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KEYNOTE ADDRESS DELIVERED AT THE 37TH ANNUAL CONFERENCE OF GENETICS SOCIETY OF NIGERIA.

POTENTIALS OF GENETICS IN STRENGTHENING AGRICULTURE AND ENHANCING THE NIGERIAN ECONOMY IN THE 21ST CENTURY

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Fellow, Agricultural Society of Nigeria;

Fellow (Hon), Entomological Society of Nigeria;

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INTRODUCTION

When I received the invitation to give a keynote address on Genetics at today's occasion, I asked myself; Shettima! What do you know about genetics anymore? I silently answered; Not much! Again I asked myself why then did you accept the invitation? Well! I told myself; if nothing else, it will give me the opportunity to open the books on genetics once more; will make me read my own postgraduate theses after so many years; I will use the opportunity to remind myself how much farther away I have been from plant breeding and genetics and more importantly I shall have the opportunity to interact with my very up-to-date colleagues from whom I shall learn more of latter day developments in that field. So I ventured into accepting the invitation.

Well! Accepting is one thing and getting down to write something and even how to start the writing became something else. Be that as it may, I reminded myself that, as a cotton breeder, there must be something in the pool of the researches my colleagues and I had left behind to pick from and kick-start this paper. I then ran to my Ph.D thesis, despite the fact that it has aged as I also have myself, but strictly speaking, knowledge never gets old. I found some relevant portions in it to use as the launching pad for this paper.

EXAMPLES OF WORK DONE PREVIOUSLY

For my Ph.D project, I studied the genetic and environmental factors affecting earliness in Cotton (*Gossypium hirsutum* L.). I used seven varieties of cotton from diverse backgrounds with wide range of characteristics.

The genetic work entailed individual crosses as well as a 7 x 7 diallel (reciprocal) hybridization between selected cotton varieties of different traits from diverse backgrounds while the agronomic studies involved different fertilizer regimes, sowing dates, insecticide sprayed versus non sprayed and other variables of interest. A wide range of characteristics were studied – earliness of maturity indices, yield, lint qualities, disease resistance, insect tolerance, plant height, flowering/fruiting habits and a few other traits. Data were collected over a three to four year period and analysed using appropriate statistical methods.

Variety 2421 was from Azerbeijan in the former USSR introduced into Nigeria in 1970, Stripper and Arkansas were from the University of Arkansas, USA; all the three varieties were early maturing but short stature, short staple with poor levels of resistance to bacterial blight (caused by the bacterium *Xanthomonas malvacearum* L.). Their yield levels were not impressive compared to some of our Samaru varieties. Two of the varieties, Samaru 71 and Samaru 72, were bred in Samaru, Nigeria, for the north-west and north-east cotton growing zones, respectively. Samaru 71 was a high seedcotton yielder while Samaru 72 was a high lint quality type. Both of them were intermediate in maturity. Of the remaining two, Samaru 26J, was bred in Nigeria and released for cultivation all over the country in 1959. It is tall, short-staple with fair yield and resistance to blight but late maturing. The last of them was UK66, introduced into Nigeria from Tanzania in 1970. It is medium height, short-staple, fair resistance to blight but very late maturing.

We came across very interesting observations and concluded that those studies have shown that earlinesss as measured by the various traits studied could be bred for, at least initially by breeding methods which utilize additive or general combining ability effects. Most of the F1 hybrids involving the early parents showed considerable earliness over their late parents or over the mid-parental value. It was also possible to combine earliness with yield and related characters.

These observations encouraged us to recommend that future improvements could be obtained using some of these varieties and their derivatives. We went further to recommend that the poor levels of resistance to blight could equally be improved by incorporating into the breeding programme another line from a family developed at Samaru code-named RASA (Reba x Samaru Allen) from which the variety named SAMARU 77 was developed and released for cultivation in 1977. I do not have the details of further progress from the research but I was informed that some of the present day cotton varieties like SAMCOT 8, SAMCOT 9, SAMCOT 10, SAMCOT 11, SAMCOT 12 and SAMCOT 13 emanated from varieties including SAMARU 71, SAMARU 72 and SAMARU 77, plus the derivatives of some of the lines developed at Samaru in the 1970s which I had the privilege of being part of the team of researchers that developed and/or released them to Nigerian farmers for cultivation. I must acknowledge the contributions, leadership and guidance of the staff of the British Cotton Research Corporation (CRC) as well as my indigenous Nigerian colleagues at the Institute for Agricultural Research, ABU, Samaru, Zaria.

FUTURE OUTLOOK

In discussing the potentials of genetics in contributing to the future agricultural development of Nigeria, let us look at some practical issues that will necessitate enormous enhancement or shall I say **quantum jump** in our capacity and capability to produce crops and animals not only for food but also for industrial uses as well as for export.

SCENARIO I

Going by the 2006 census, Nigeria's population was 140,000,000 people. Nowadays one hears projected figures of 150,000,000 or even 160,000,000, occasionally you even see 167,000,000 being mentioned in the papers. Let us for the purpose of ease of calculation take 150 million for year 2013. On average, we all eat food at least once a day; nay, in reality a minimum of two times a day. Considering what goes into our average meal – some grains/carbohydrates, meat/proteins, beans/legumes, oil, spices and vegetables, etc, each one of us eats about one kilogram of these items all put together (inclusive of wastage – such as peels, barks, etc) per meal. That means two kilograms for the two meals per day per person. Add to these some assorted fruits, eggs, tea, beverages, sugar, even kolanuts and so on and so forth. For 150 million people, you are talking of 300 miilion kilograms (300,000 metric tonnes) per day. That means in one calendar year we may be eating up to 109,500,000 (109.5 x 10^6) say 110 million tonnes of assorted food items.

SCENARIO II

Now consider also the domestic animal population. You may add another 100 million made up of cattle, sheep, goats, donkeys, horses, dogs, cats, camels, chickens and the rest of them which we must feed since we are keeping them on our farms or backyards as the case may be. I do not want to speculate but for sure some of these

animals eat probably more than twice what we humans can eat at any given time. For this, you may also add nearly as much quantity (or at least 200,000 metric tonnes) of food items – that works out to about 500,000 metric tonnes per day totaling to about 180 million tonnes per year approximately.

The figures above are all for ease of argument. In actual fact an average beef/milking cow if optimal performance is expected from her, should be fed about 12kg of assorted materials per day. V/Admiral Murtala Nyako, Governor of Adamawa, published a pamphlet on his **"Vision" for the Empowerment of Farming Populace Through Agriculture …in Adamawa State** titled " MISSIVE (1) TO THE PEOPLE OF ADAMAWA STATE. In it he gave the following figures for dual purpose cow that produces both dairy and beef, the feed requirement is a feed mixture of 12kg/day made up of: **6kg of maize; 2.5kg soya beans; 1.8kg of cotton cake; 1.2kg groundnut cake and 0.5kg premix**. For 10,000 cows you require **36,600** tons and for million cows, **3,660,000** tons. This is just for one million slightly improved varieties of cows. In the same document, for 2,500,000 chicken, Nyako gave an annual feed requirement of **139,975** (**approximately 140,000**) tons of assorted feed materials. You can now imagine the quantities we require to enhance our food and agricultural production in Nigeria. Added to the above will be the quantities of water that we and our animals drink or use to prepare food with or wash with.

SCENARIO III

Let me bring in another angle. You know nowadays nobody walks naked in this country; even an infant gets wrapped up in pampers and some warm clothing. By the nature of our traditional dresses – the kaftaan, agbada complete with jumper and sokoto and matching caps, or even the foreign dresses we wear such as suits, jackets and safaris consume quantities of clothing materials. For example, a set of a gentleman's or lady's complete dress will require a minimum of five (5) or ten (10) meters of materials. Most of us here and elsewhere I know we own more than one set of kaftaan and babban riga or lady's gowns and wrappers. That means an average man or woman in Nigeria could have at least 20 meters of clothing material per year on average. If you multiply this by 150 million, you will find it to be about 3,000,000,000 ($150 \times 20 \times 10^6$) meters of cloth of assorted types. In addition, we also have a whole range of items at home (and offices) comprising mattresses, bedsheets, pillow cases, rugs, carpets, towels, dusters, settees, curtains and so on and so forth – all of which require one kind of clothing materials or the other, mostly cotton.

Consider the tonnage of cotton or even artificial fibres that are required to supply a billion meters of clothing materials; the farm sizes, the number of farmers, quantities of inputs required, farm power needed, service providers and a whole paraphernalia of items needed to produce, process, market and handle all these quantities. Then think of all the tailors, the spinners, weavers – in short textile mills of all descriptions, crude, native or modern, the colouring materials for the prints and designers, transporters, advertisers, hawkers, sellers, buyers, etc, ad infinitum, that could benefit from such an effort. Can you now imagine the volume of business transactions that these chains of activities could generate? Who will provide all these materials for us? Or, with due apologies, are we waiting for the Chinese, the Indians, Brazilians or other "lovers" of Nigeria in foreign lands to come and feed us, clothe us and run all this business for us? Are we then going to go on an importation spree of items that we can produce comfortably and economically in Nigeria. I think as a nation we should endeavour to produce our needs by ourselves and resort to importation only as filling the obvious gap. It is a challenge for us and not for the nationals of other countries. In any case what does Nigeria, as a nation,want?"

WAY FORWARD

Going by the present day best yield performances of our commodities (both crops and animals) of 2.5 tonnes per hectare of rice produced more or less once in a year, may be 3 or 4 tonnes of maize per hectare again produced more or less once in a year, hardly one tonne of seedcotton per hectare, 250 to 350 kilogrammes live weight of cows, may be 300 to 400 litres of milk per lactation from the local cow, etc. How about the way we go about throwing up children every year, that way, we may, if care is not taken, hit the 250 million mark population by 2040 or 2050. When this is juxtaposed against our nonchalant attitude towards the development of top scientists in the various fields of agriculture, more especially breeders, I wonder how long will it take us to meet the stage of self sufficiency in food and other agricultural commodity needs of the

nation? That is where a **quantum jump** phenomenon comes into the picture and in all seriousness quantum jumps do not simply happen without the proper planning and application of genetics and biotechnology to improve the performance of Nigeria's agriculture. This can then guarantee the attainment of our future goal.

Under a conventional breeding regime, starting from the crosses (hybridization) through selecting progenies, strains, lines, and testing them first under research fields then out in the different environments likely to use these lines ultimately and then producing breeders seed, foundation seed and finally certified seeds takes a long time. These steps are far more than simply designing experiments to examine straight forward inheritance of simple characters or experiments to show the adaptation of a variety to a given environment. For instance, the SAMARU 77 Variety I referred to earlier was code-named AASA(71)114 in our research record – this meant that after all the crossing works and initial screenings, it was first selected as a **progeny** in 1971. It went through various tests as a **strain**, a **line**, a **breeders seed**, and a **foundation seed** before being released for cultivation by farmers in the Gombe area in 1977 – minimum of **seven (7) years** or so.

Let us now bring in the advanced biotechnology into our breeding programme, as in the case of **bt cotton**, or any other transgenic exercise. It will be recalled that following the realization of the problems posed to cotton by the bollworm (*Helicoverpa armigera* – American bollworm; *Pectinophora gossipiella* – pink bollworm; and *Earias vitella* –spotted bollworm) complex, scientists discovered from a bacterium *Bacillus thuringiensis* a chemical that could kill the larvae of these insects. So, they set forth to transfer the gene to a variety of cotton – which eventually became bt cotton having good measure of resistance to pests. Details of the methods adopted will not be discussed in this paper but for the sake of clarity let me briefly mention some of the steps.

You start from the identification and isolation of the required gene, go through with its transfer to your plant or tissue culture using the medium of an agrobacterium or a gene gun or whatever. Then you start developing that plant or tissue culture to the level you will incorporate it into your breeding programme. Subsequently, you go through various tests, screening, selection, etc, before you can conveniently claim that you have succeeded in the transfer of the required gene for a sustainable long term future usage. This exercise could take up to **ten (10) years**. Details can be found in an article on the Bollgard variety of cotton developed in Australia in which two genes (Cry1Ac and Cry2Ab) were transferred into this variety (anonymous writer on bt cotton in the internet). Another example can be found in an article titled "Transgenic Bt Cotton" – Technical Bulletin CGIR No. 22, Central Institute for Cotton Research, Nagpur, India, written by Indian authors – C. D. Mayee, P. Singh, A. B. Dongre and Sheo Ray.

In between, we shall not fail to mention the other variants of biotechnology from the age old budding/grafting as in fruit trees to tissue culturing and cloning in both animals and plants. These technologies, no doubt, have contributed, and are still contributing, their quota to the development of our agricultural varieties.

In all of the above, geneticists and other related scientists have a crucial role to play as they are responsible for the development of the improved varieties which if put under the right husbandry conditions they can perform maximally. Our farmers must be helped to increase the productivity of their commodities per unit of production – be it field, water, green house or whatever.

RECRUITMENT AND TRAINING OF BREEDERS AND OTHER SCIENTISTS

In order to meet this quantum jump or leap, there is need to embark on a sustained recruitment and training of agricultural scientists generally but in particular breeders. However, the present system of recruitment, training and promotion of breeders in this country, makes me feel like breeders are an endangered species. Since they are predominantly part of the university or agricultural research institutes systems, they are very much governed by the **"publish or perish"** syndrome and this is not helpful to the breeder. So if developing an improved variety takes you seven years or more, then you cannot easily meet that publish syndrome. In any case, as a breeder your pride and satisfaction is the variety you released for cultivation with positive

results. Considering the situation of developing improved varieties described above, one can appreciate the predicament of the breeder compared to some of his/her fellow scientists.

Apart from this, the study of breeding (both plant and animal) entails what is ordinarily described as the "**hard stuff**" – pure genetics, applied genetics, statistical genetics, pure statistics, a bit of mathematics and then relatively some physiology, entomology, pathology and even environmental science.

When I was at IAR, I tried recruiting some graduates to train them as cotton breeders but when each one took a good look at the involvements and the subject matter, they would simply say bye – bye. As at today, I am not sure if IAR or any of our agricultural research institutes can boast of adequate number of breeders or other required agroscientists.

A more favourable condition for recruitment, training and promotion of breeders and indeed other scientists should be developed even if that would entail some sort of prioritization of the disciplines required over a period of time. For instance, what cadre of expertise shall we require say in the next three (3) to five (5) years, or five (5) to seven (7) years, etc, and then go ahead and design a recruitment and training programme for them. You can then shift your priorities and emphasize other set/s of priorities without compromising the ones promoted earlier

CONCLUSION

In order to bridge these gaps due to low productivity, poor postharvest handling, lack of adequate encouragement of producers, processors and marketers or general handlers of farm produce and our supposed target for 2030, 2040 or 2050, the right policy instruments should be developed now for the adoption of strategies which combine improvements in agricultural production and productivity through relevant and effective research and appropriate husbandry practices. This should be coupled with effective control of wastages (in all their ramifications – rotting, pest damages, etc).

In order to achieve these aims, some mutually reinforcing approaches should be pursued. Among which are:

i. Strengthening of research and the development of appropriate technologies to fully exploit the genetic, biotechnological and agronomic potentials of agricultural commodities;

ii. Recruitment of relevant scientists and sustained training backed up with the necessary incentives so that young people can build their career;

iii. Extension be fully revived, workers recruited and adequately trained. In fact, the Local Government Councils should be made to offer extension services, while private sector supported extension should be encouraged;

iv. Effective linkages must be provided and strengthened between research – extension – input/service provider – farmer;

v. Intensive cultivation using all the modern technology backed methods supported by realistic and implementable policies and incentives (in their broad sense) to contribute a greater percentage to the envisaged demand through increased yield per unit of production;

vi. Some element of extensive cultivation or horizontal expansion should be encouraged especially since such a massive production must involve opening new land or land reclamation, and the development of new farms as well as entry of new farmers;

vii. Ensuring that our farm produce have been adequately processed and preserved and where appropriate export them; and

viii That producers, processors and all other relevant participants should be adequately trained to develop their respective skills.

Finally, let me end this address with a teaser. To a large extent the success of the work of a scientist and his satisfaction is determined or influenced by the politician who is the **boss**, the determiner of policies governing the work of the scientist and who takes the political decision for the implementation of the research result. If he/she procrastinates or takes the wrong decision or simply refuses to implement even the decision he/she has taken, then we are stuck. **THIS ISSUE IS BEYOND THE REALM OF GENETICS AND BIOTECHNOLOGY.**

ACKNOWLEDGEMENT

I wish to express my appreciation to the leadership of the Genetics Society of Nigeria and the organizers of this Conference for the opportunity given to me to address this distinguished gathering of scientists. I hope my not being too up-to-date in this field can be pardoned. Let me also thank all those who have helped in the production of this paper as well as the audience who listened to this address - I say a big THANK YOU."

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GENETICS AND THE FUTURE[1]

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ABSTRACT

Every phenomenon, including Genetics and its ambience, has a *future* that will be determined by its *present* which itself is the product of the *past*. Broadly, our subject deals with organisms and their environment and, for good or bad, in a context in which the pursuit of knowledge is not only increasingly and narrowly anthropocentric, but also distanced from collective purpose. Mendelism and the ancillary subjects had, especially since 1900 or so, contributed immensely to our understanding of the biosphere, to crop and livestock improvement, and to human health. The advent and progress in DNA science and technology has opened almost limitless possibilities for, and created new concerns about, the manipulation of life on earth, including the capacity of humans to manipulate their own genetics. First, an overview of the development of genetics shows that a critical engagement with the past of the subject had enabled, and will enable, deeper insights into the problems and the prospects of the future as the synergy of genomics with the past has shown. Secondly, as the increasing knowledge of epigenetic forces have shown, a renewed interest in general biology, natural history, ecology, behavioural science and systematic biology have become imperative and urgent in our environment where so much remains to be known about our flora and fauna. Thirdly, having regards to the products of science, their ownership and the consequences of these for the production and reproduction of knowledge and of humans themselves and their societies, geneticists and indeed all scientists need to, as a minimum, engage social and related questions such as Intellectual Property Rights.

INTRODUCTION

We need to start by clarifying what issues the theme of this conference suggest or entail and then try to harmonize the issues into some coherent perspective. In doing this, I hope to highlight the tremendous multiplication of specialized areas into which Genetics has developed, the almost complete isolation of some of these areas and the imperative for developing the *nationalist instincts and practices* of professional biologists. Well, if that is, we want to harvest the fruits of the myriads of specializations.

The theme of this conference can be contemplated, first, simply as the future of genetics as an academic discipline; the prospects and limits of what we know, what we can know and the consequences of what we know and can know generally for the biosphere—the entire gamut of organisms and their interactions with their labile biotic and abiotic environments. The second apprehension of the theme is related to the first. It is about genetics and the future of human society as they are going to the affected or shaped by genetics in terms of provisioning human needs for reproducing herself and for reproducing his societies. We must hasten to say here that this not just

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about knowledge ***per se*** but also about politics, economics and political economy. And, thirdly, the theme may lead us to apprehend the future (of man) narrowly in terms of human extant biological capabilities, limitations and disabilities as all these are prescribed by his genome and circumscribed by the plethora of epigenetic forces that man has developed almost unlimited propensity to unleash.

Obviously, the foregoing is a daunting agenda for this whole conference not to talk of a single lead paper by a single author who is in an equally obvious narrow specialty. Notwithstanding, I find it auspicious that we have this opportunity to "scan" this vast territory as it were.

PHILOSOPHERS, SPECIALISTS AND SORCERERS

From time immemorial, synthetic philosophers and specialists have always existed contemporaneously. Often times, specialists have also often been synthetic philosophers. In more recent times the sheer expansion of human knowledge and our accumulation of knowledge as collective human intellectual heritage have fractured intellectual into varying degrees of isolated specialties such that while we have gained from depth, we have lost, or we are losing, the advantage of synthesis and breadth. Ensuring some balance in the foregoing regards seems desirable.

Within the foregoing paradigms, specialists in the frontiers of science and technology tend to be especially vulnerable. While this vulnerability is, strictly, not their fault, it is desirable that they ameliorate this vulnerability by paying attention to history and to ancillary disciplines and specialties ***vis a vis*** their specialist concerns. Lack of this attention, in these regards, has considerably slowed the advancement of knowledge.

One of the consequences of the isolation and the allure of frontiers of science and technology, especially as they now tend to confer ***power*** and ***profit*** (biological weapons industry, genetic engineering and gene patenting etc.) is that they begin to appear like cults and their business acquires the image of some "sorcery" (Nicholls, 1994). In this regards, the inability or unwillingness by many of us to be "synthetic" in our approach to knowledge and pedagogy entrenches the "difficult-area-of-study" image of genetics generally!

FROM MENDELISM TO DNA DOUBLE HELIX HYPOTHESIS

As we all know, Gregor Mendel, the "father of genetics" established the mechanisms of the transmission of hereditary (genetic) factors in 1865 although the appertaining basic principles were not re-discovered to become generally publicized until 1900. Many geneticists today consider Mendelism a "revolution", if not "the revolution" in genetics (Snustad and Simmons, 2003). But if we reflect on the works of overlapping generations of geneticists and workers in ancillary areas (cytogenetics, biochemistry, immunology, agriculture, physiology, mutation sciences, medicine, systematic biology, ecology, etc. etc.), we will agree that the progress of genetics arose from "revolutions inside revolutions".

Arising from this "Pandora box" paradigm we may mention the various categories of scientists (Strickberger, 1976; Snustad and Simmons, 2003; Ryan, 2009). These include the contributions of the biometricians (Sutton, Galton, Fisher, etc.) the cytologists and cytogeneticists regarding the chromosome theory (Sutton and Boveri), the cytogeneticists of linkage and recombination (Morgan, Sturtevant, Bridges), workers in a population genetics and (Wright, Fisher, Haldane, Hardy and Weinberg), workers in medicine, biochemistry and hereditary diseases (Garrod, Herric, Lyons, Landsteiner, Beadle and Tatum), researchers on the nature of the genetic material (Avery, MacCleod and McCarthy), research on control of gene action (McClintock), workers in evolution of genomes (Stebbins, Blakeslee, Ohno, Jackson etc.) and those in genetics and sexuality and bacteria (Lederberg and others). The foregoing constitutes a sample of findings, in more or less chronological order, each of which constituted a revolution ***per se*** **(**Peters, 1959). These land-mark

advances in the study of genetics, needless to say are, of course, the results of synergies, synthesis, extrapolations and explications of the sequential leaps in genetics and other areas of biology; of chemistry, physics, mathematics (statistics); of travels and explorations around the world; of demography and epidemics, and even of wars and peace!

Without doubt, the Watson-Crick double-helix model of DNA of 1953 was also a major breakthrough especially as a foundation for molecular genetics (Watson, 1976; Weaver, 2005). The model satisfied the two dialectical elements of the genetic material: on one hand, the autocatalysis/heterocatalysis opposites, and on the other hand, the stability/mutability opposites. Three years before, in 1950, Erwin Chargaff already observed certain constancies in the 1:1 ratio of pyrimidines and purines and constancy of G + C/A + T ratios in each species.

It is left to be said that as foundational and pivotal as Darwin's ***Origin of Species*** (Darwin, 1859) was to the work of geneticists, it had been the subsequent evidence of the mechanisms of heredity (including the sources of variation and encompassing mutation and mutagenesis) that rescued Darwinism from much of the controversy, not to talk of the hostilities that greeted its enunciation.

RECOMBINANT DNA, DNA TECHNOLOGY AND GENETIC ENGINEERING

From the early 1970s i.e. in the last forty years or so, advances in recombinant DNA science and technology have opened hitherto unimaginable vistas in genetic studies. This is true especially in regard to molecular characterization of genomes and genes, the location and processes of gene action. Consequently, even though traditional Mendelian principles and related and ancillary knowledge (as we apprehended earlier) continue to make valuable contributions to plant and animal breeding, medicine, plant and animal protection, biodiversity conservation etc. (GSN, 1999; 2009); especially pure and, applied, genetics have virtually become exclusively construed as, and coterminous with molecular genetics and DNA technology (Taylor, Green and Stout, 1997).

Most biologists and, especially, geneticists are familiar and must be familiar, with the progress of molecular genetics and its various applications of genetic engineering and what is now generally circumscribed as genomes sequencing, gene cloning and production of transgenic organisms, amelioration of debilitating human conditions, the nature and initiation of epidemics, degrees of genomic identities among different evolutionary groups and life forms, identities of molecular/maps and traditional physical gene maps, control and mechanics of control of gene actions by the so-called bureaucratic genes, the role of telomeres and telomerases (Figure 1) in aging and oncogenesis, molecular characterization of plant and animal accessions, legal and forensic medicine etc., and evolution of elements of genomes such as the evolution of, and divergence between X and Y chromosomes, (Figure 2; The Arabidopsis Genome Initiative, 2000; Snustad and Simmons, 2003; Ryan, 2009). A rather elegant circumscription of the term "genomics" was given in Snustad and Simmons (Ibid) as follows:

> ……the genomics sub-discipline was divided into *structural genomics*—the study of genome structure—and *functional genomics*—the study of genome function, which, includes analyses of the *transcriptome*, the complete set of RNAs transcribed from a genome, and the *proteome*, the complete set of proteins encoded by a genome. Indeed, functional genomics has spawned an entirely new subdiscipline, proteonomics, which has as its goal the determination of the structures and functions of all proteins in living organisms.

Having apprehended the "practical" implications of what we know in genetics and, what these portend for how we are likely to approach the frontiers of genetics and biology, how do those things we know limit what we can know and what forces limit what we can know? Even if we cannot answer these questions now, we need at least to keep them in view.

One hundred years or so (1868-1965) after Miescher discovered nucleic acids, and about twenty years after Avery's team showed that DNA is the genetic material, Holley sequenced the RNA of yeast and the revolution of sequencing whole genomes of organism took off. Since then the techniques and efficiency of sequencing the genomes of organism developed by leaps and bounds. The publication of the draft of human genome on February 15, 2000 and February 16, 2000 by the ***public*** International Human Genome Sequencing Consortium and a ***private*** Celera Genomics in *Nature* and *Science* respectively constituted a watershed in a way.

MATTERS ARISING FROM THE SIZES, IDENTITIES AND DIFFERENCES IN THE GENOMES OF ORGANISMS.

Two major surprises that arose from a scrutiny of human genome are the relatively, small number of genes of humans compared with lower levels of organismal forms (bacteria, insects, worms, etc.), and the large numbers of genes shared with these lower organismal forms. Ryan (2009 pp.2-3) summarized these surprises as follows:

> The first surprise was the modest size of human genome at about 20,000 genes … we have only ten times as many genes as a bacterium, a third more than a fruit fly and not many more than a nematode worm…..Most revealing of all was the confirmation of our common inheritance with other forms of life on Earth. For example we share 2,758 of our genes with the fruitfly, 2,031 with the nematode worm—Indeed all three of us, human, fly and worm, have 1, 523 genes in common.

Perhaps a third surprise which is related to the question of shard genes is that a large proportion of the human genome (about 9%) is shared with retroviruses—the endogenous human retroviruses (EHRVs) with their long terminal repeats (LTRs) which are known to perform bureaucratic control of gene action while another 3% are DNA transposons. A related matter here is the comparatively smaller amount of the human genome shared with other vertebrates (about 1.5%) while about 52.5% of the DNA are unknown 13% and 21% of human genome are long, and short, interspersed repeat nuclear elements (LINEs and SINEs) respectively (Figure 3; 3i).

From various reflections and actual experimental work of various biologists, it had always been known or conjectured that, life is a web and that the evolution of life at different levels of complexity are vertical, horizontal or reticulate. We see many of these in the homology of organelles (chromosomes, mitochondria, ribosomes, chloroplasts etc.) organs, organisms and life forms; many of these homologies are ***conserved*** so to speak. With this intellectual heritage behind us and the new insights from genomics, a number of important facts have emerged. These include insights into the dynamic of the web of evolution as it relates in particular to control of gene action, syntheny, the evolution of genomes, and the phenomenon of epigenetics.

One of the most important matters that have arisen from the revelations of genomics is the role symbiosis and co-evolution especially of viruses have played in the evolution of the genomes of higher organisms, the reinforcement of the notion of common genomic ancestry of organisms (including, preeminently viruses) and the role of retroviral genes (and other bureaucratic genes) in the activation and deactivation of genes and the processes of development in the more complex organisms. Genomics has also enabled us to more confidently see the commonality of genetic endowments especially through studies of conserved syntheny in related animals and related plants (Chowdary, Raudshipp, Fronicke, and Scherthan, 1998; Gale, 1998; Snustad and Simmons, 2003; Figures 4, 5, 6).

The implications of the evolution of symbiosis between retroviruses and eukaryotic cells and the consequent enlargement of eukaryotic genomes point to the importance of symbiosis and

hybridizations (and evolution of sexual, mechanisms and sexuality) as critical mechanisms of genomic creativity and potentials for natural selection and evolution. Ryan (2009) referred to the creative genomic mechanisms of symbiosis and hybridization as ***symbiogenesis*** and ***hybridogenensis*** as mechanisms that are different from, but complement, ***mutation*** whose occurrence and consequences are random.

EPIGENETICS AND EPIGENETIC INTERACTIONS

Epigenetics is the study of changes (internal, external, behavioural etc) in cells, tissues, organs and whole organisms independently of DNA sequences. In this regard ***contain elements of the genome*** that can receive and process signals from the internal or the external biotic and abiotic environments of the organism are themselves stretches of DNA such as the LTRs. They respond by switching on or switching off certain genes exploring varied mechanisms as DNA methylation, modification of histones etc, all of which interact in complex and coordinated ways to control gene action—hence the term bureaucratic genes (Figure 7).

The bureaucratic genes function in specific tissues, at particular points of development by responding to the internal and external environments of the gene to induce, alter, increase certain gene products that mediate morphology (development of secondary sexual. Characteristics, flowering, leaf abscission and shedding, tropic and taxis movements, transitions from juvenile to adult forms such as moulting and juvenile – adult leaf transitions) and even behaviours like migration, homing instincts, aggression and fear, hallucinations etc., etc. perhaps one of the most spectacular example of environmentally – induced epigenetic phenomena is the story of sex change in Caribbeans of fish species – the blue-headed wrasse (Ryan, 2009: pp319-321; Figure 8).

REMEMBERING THE PAST FOR UNDERSTANDING THE PRESENT AND THE FUTURE

For whatever it is worth, I think we can proceed on the assumption that scientific progress is desirable especially if we also agree that we must strive constantly to humanize knowledge generally.

As we have seen, modern genetics, with its capacity to look at whole genomes and how genes and their expressions are controlled, grow, from Darwinism Medelism, cytogenetics, and knowledge of DNA structure; it grew from the knowledge of biochemical, behavioural and morphological (endo-and-exo-) ***end products*** or ***phenotypes*** of ***genotypes***. Darwimsm and Mendelism themselves and the related foundations of genetics developed from general biology (systematics, anatomy and histology, histochemistry and biochemistry, physiology, biology of microbes, general ecology and biogeography, and animal behaviour etc., etc.). A lot of observations and studies that today direct our attention to the modes of gene action especially in the growing area of epigenetics as demonstrated by the example of sex change in wrasse, the consequence of the large retroviral dose of the DNA of Y-chromosomes in man derive from elements of the knowledge established in the foundations of genetic studies (see Figure 7 again) and of our own observations on the transition of juvenile leaf forms to adult leaf forms in angiosperms (Figure 9; Olorode, 2012). Indeed, the homeobox gene model (Snustad and Simmons, 2003) has been invoked by various workers for the differences between simple leaves and compound leaves and for the transitions from simple juvenile for compound adult leaves (Olorode, 2012).

In the foregoing regards, we are saying that we need to pay very close attention to the general biology (taxonomy, behaviour, physiology, ecology and phenology) of our floral and fauna. This is because every constellation of floral and fauna is unique in its temporal and spatial character and is thus capable of giving unique insights into the genome and genetic processes in the constellation.

What those mean is that the conservation of flora and fauna, the vessels in which genes are sequestered, must become a matter of national priority (Hawkes, 1990; Olorode, 2004).

In regard to the study, conservation and utilization of genes and genetic material, the undying concern had been festering about private and corporate profit interests on one hand and public purpose on the other in regard to access of peoples and territories to the products of improved food and health facilities. This is obviously a political/ideological matter. Sine the earlier 1910s improvements in crop and animal yield have produced the paradox of high yield and high corporate profit on one hand, and poverty and hunger or other forms of malnutrition (such as obesity) on the other. Various critical and informed views have, since, been published on the question of who owns genes (especially genes of wild and domesticated animals and plants) and whether genes can be patented (Fedder, 1976; George, 1979; Mooney, 1983; Juma, 1989; Lesser, 1994; Olorode, 2006). Partly because of the triumph of neo-liberal and "market forces" ideology (Kargalitsky, 2001; Amin, 2004) the balance of political forces have been in favour of private corporate profit of seed companies and genomics companies. Consequently private seed and genomics companies have been having a field day in spite of the strident campaigns against hunger and the so-called "food crisis" even by organizations that instigate, rationalize and valorize market and private-profit such as the World Bank and related organizations.

The phenomena of gene-hunting and gene prospecting (Mooney, 1983; Juma, 1989; Lesser, 1994) access to, and use of data from bioinformatics and the related controversies of gene patenting and intellectual property rights will continue to attract attention and generate debate. As these are matters of power and economic-interest relations inside nations, across social classes and across national and regional boundaries, we can assert that no position is, or can be, neutral. Suffice it to say that geneticists, as intellectuals, have the responsibility to lay bare all the contending positions and issues.

The controversies surrounding gene prospecting and gene patenting have been particularly strident since the completion of the sequencing of human genome in the mid-2000s raising questions and objections among citizens and meedics concerning ***informed consent*** and ***presumed consent*** of the ***owners of the human genes*** even where genomics companies (like deCODE Genetics and pharmaceutical companies (like the Swiss "giant" Hoffman-Laroche in the case of the identification of the "familiar essential tremor" gene in Iceland) agree to compensate the owners of the gene (Snustad and Simmons, 2003: pp. 514-515).

As in many of the wars among giant corporations like the "computer wars" (Ferguson and Morris, 1994), the legal theatre not to talk of heavy-purse and political-power arenas, have been active in the controversy concerning gene prospecting and gene patenting. In a recent expose in ***New York Times,*** Joseph E. Stiglitz (2013) reviewed extensively the supreme court (USA) judgement which recently decided (Stiglitz, 2013) in regard to the legal tussle between Association of Molecular Pathology and Myriad Genetics (a private company):

> …ruled unanimously, that the genes (BRCA1 and BRCA2) cannot be patented, though synthetic DNA created in the laboratory can be.

The genes BRCA1 and BRCA2 are said to predispose their carriers to breast cancer and knowledge of their existence can be useful in early diagnosis, and prevention of the cancer. In his article, ***How intellectual Property reinforces inequality***, Stiglitz (2013) was categorically (all emphases are mine) on various elements of IPR, public welfare, alleged promotion of "incentive" and competition by IPR:

> The case (Association of Molecular Pathology v. Myriad) was a battle between those who would privatize good health …. and those who see it as a right for all—and a central component of a fair society and well-functioning economy. Even more deeply, it was about the way inequality is shaping our politics, legal institutions and the health of our population.
>
> ….. Genetic researchers have argued that the patent actually prevented the development of better tests, and so interferes with the advancement of science. ***All knowledge is based on prior knowledge, and by making prior knowledge less available, innovation is impeded.*** Myriad's own discovery—like in any science—used technologies and ideas that were developed by others….Advocates of intellectual, property rights have overemphasized their role in promoting innovation. ***Most of the key innovations—from the basic ideas underlying the computer, to transistors, to lasers, to the discovery of DNA—were not motivated by pecuniary gain.***

The importance of all of these for the galloping development of underdevelopment in the peripheries of neo-liberalism like Nigeria ought to be quite obvious. Let me add that Stiglitz is, to the best of my knowledge, not a communist—he was actually an economist with the World Bank and, at different times, an advisor to one or two recent tenants of the White House in Washington DC.

CONCLUSION

I did not set out in this presentation to tell you anything you didn't know or suspected. I have tried only to share with you my reflections on general biology and the specialty of genetics and the future: the "future" in a robust sense of the world. Let us thing globally and act nationally and locally – There are so many things that remain unknown in our environment – things we must know before, they disappear, things whose knowledge will contribute immensely to global and national intellectual heritage in biology and genetics. While building capacity for engaging in the probes of the frontiers, let us understand that the ***proximate*** and the ***distal*** (the frontier) are dialectically united.

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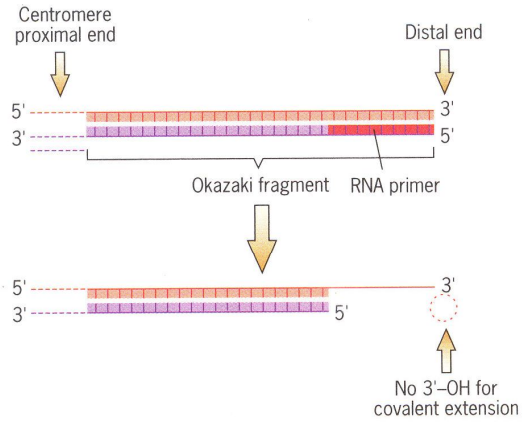
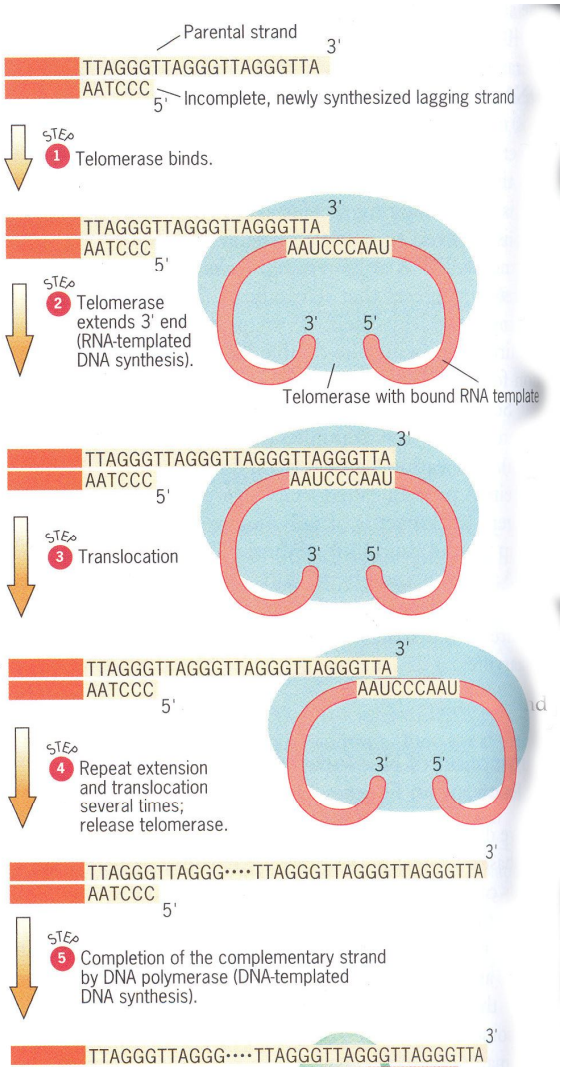


(a) The telomere lagging-strand primer problem.



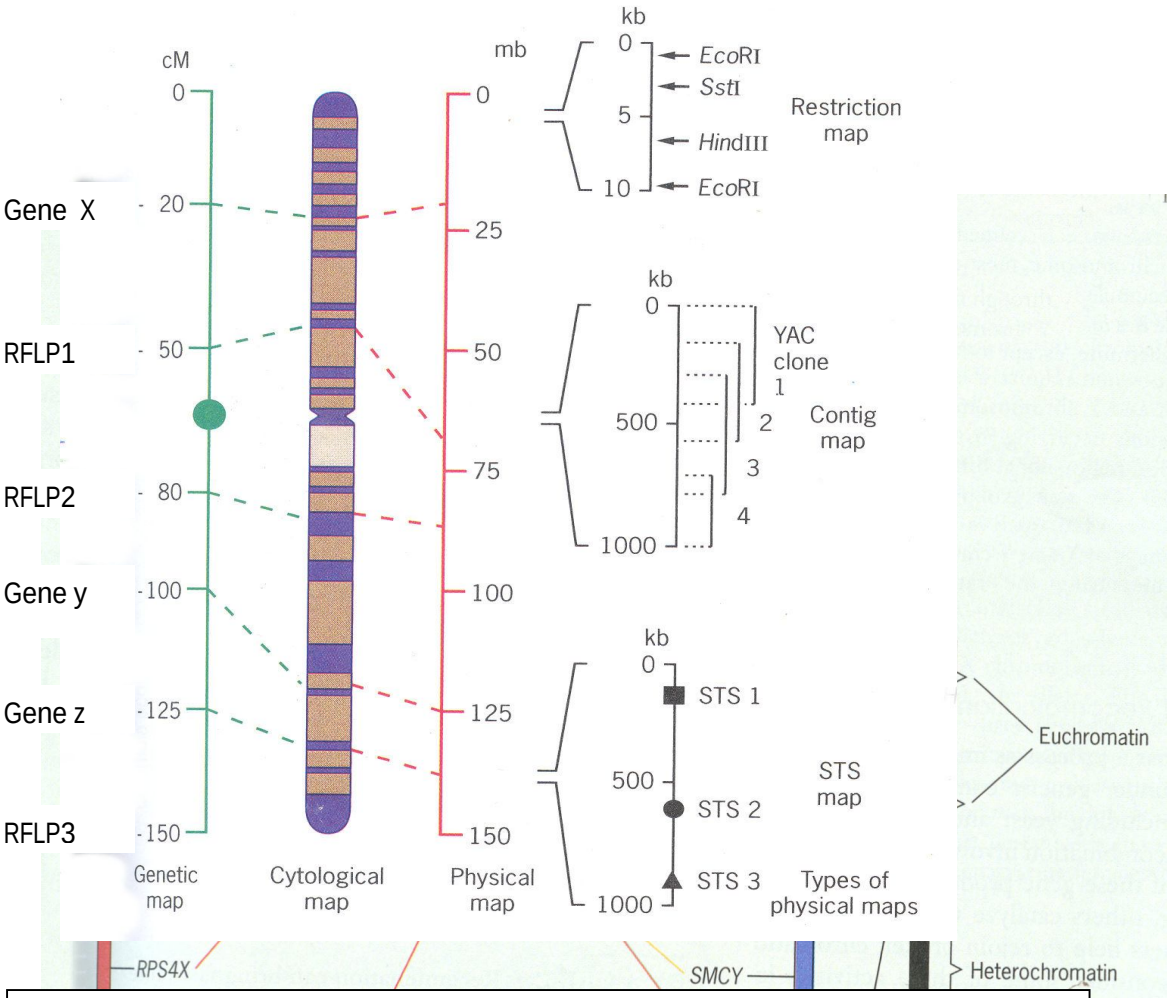
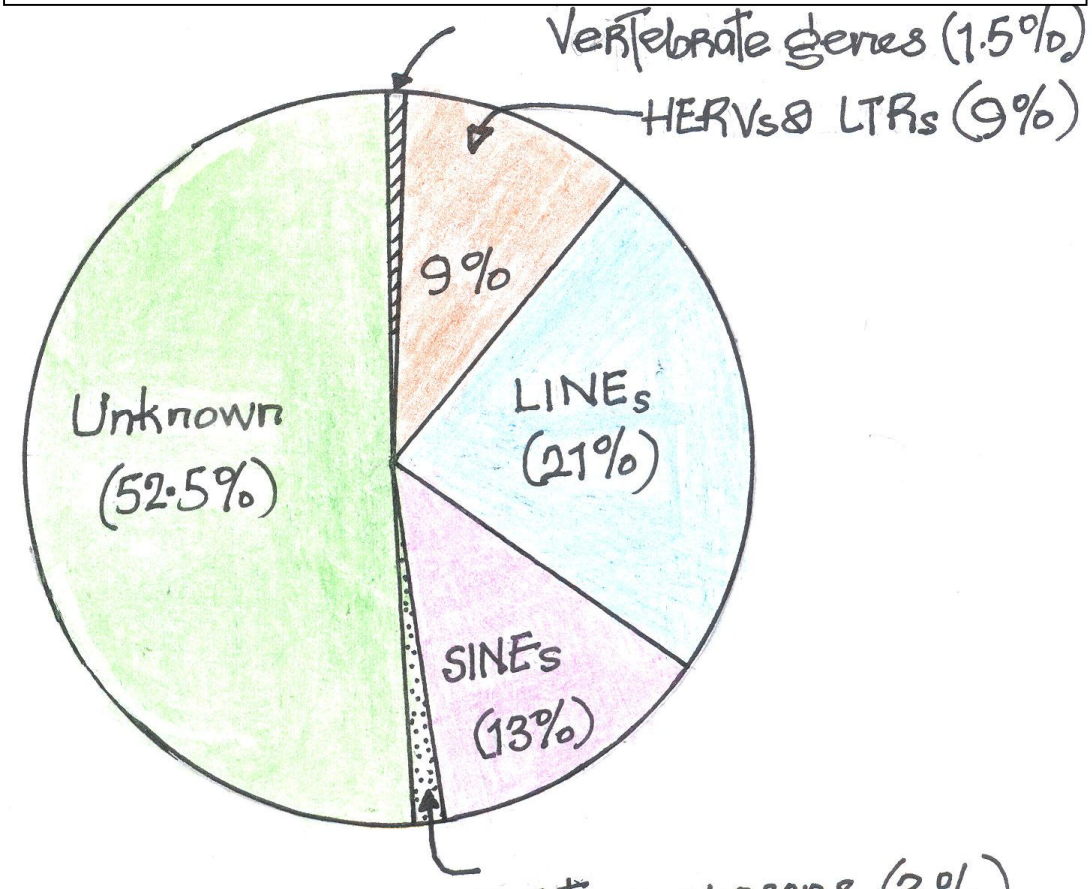


Figure 2i: Congruence of genetic, cytological and physical maps.



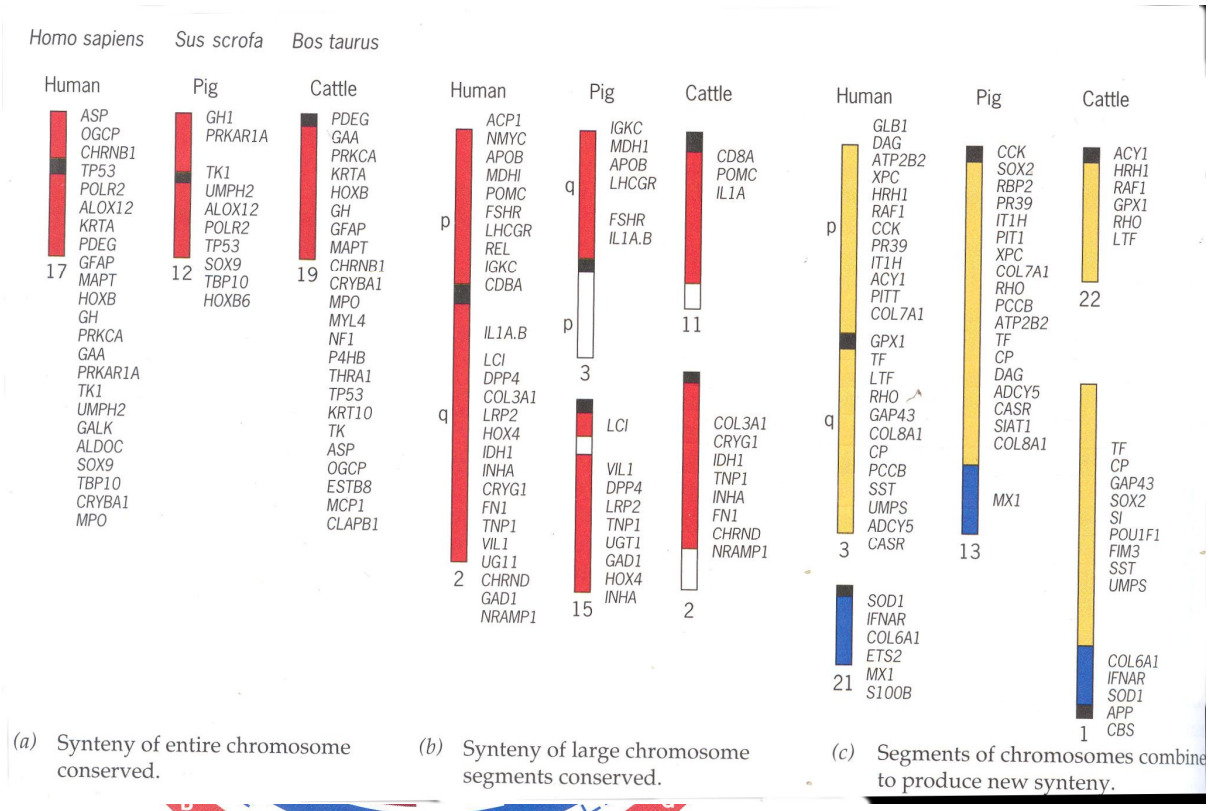


Figure 5:

Conserved syntheny in humans, pigs and cattle. (Snustad et al., op. cit., 2009).

species of cereal crops. (Modified after Snustad and Simmons, op. cit., 2009).

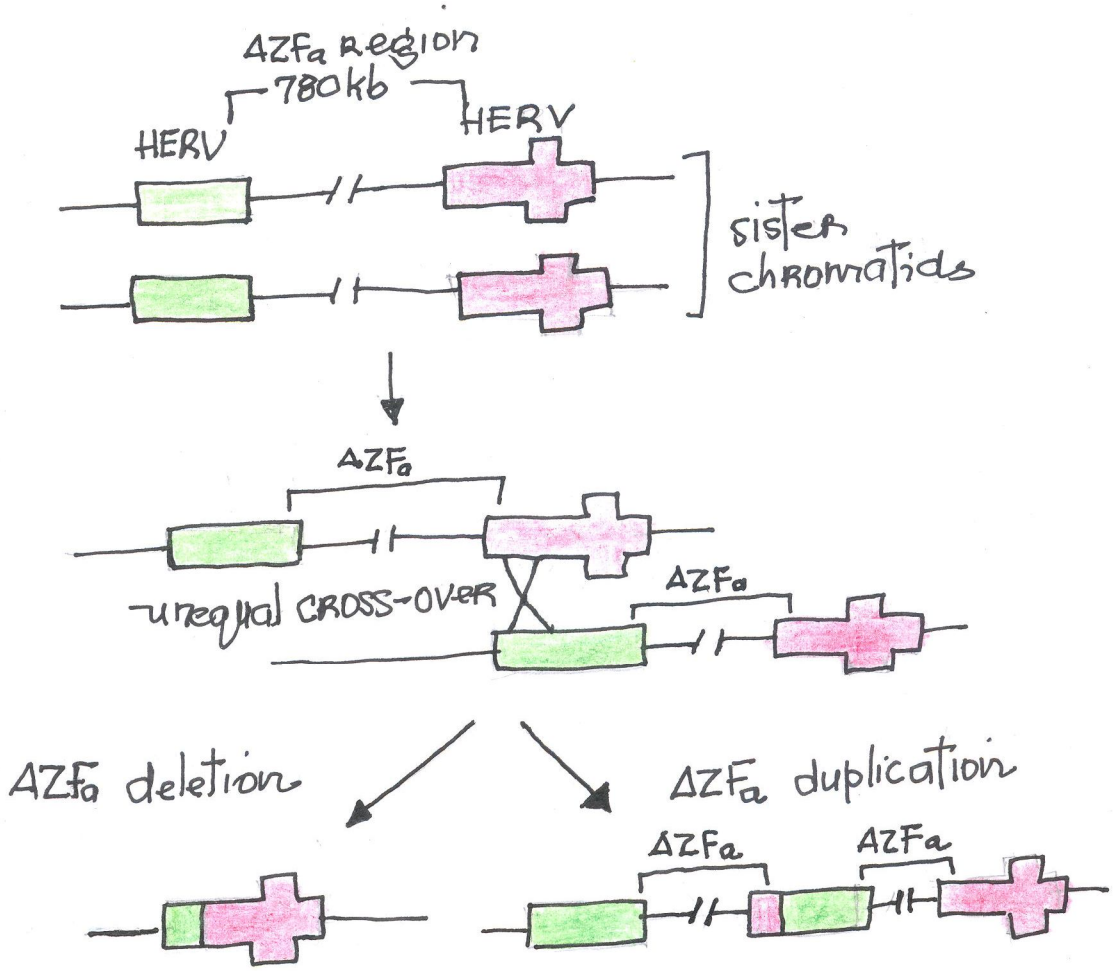


Figure 7: **AZFa region and azoospermy in Y-chromosomes**

(Modified after Ryan, 2009: p.171)

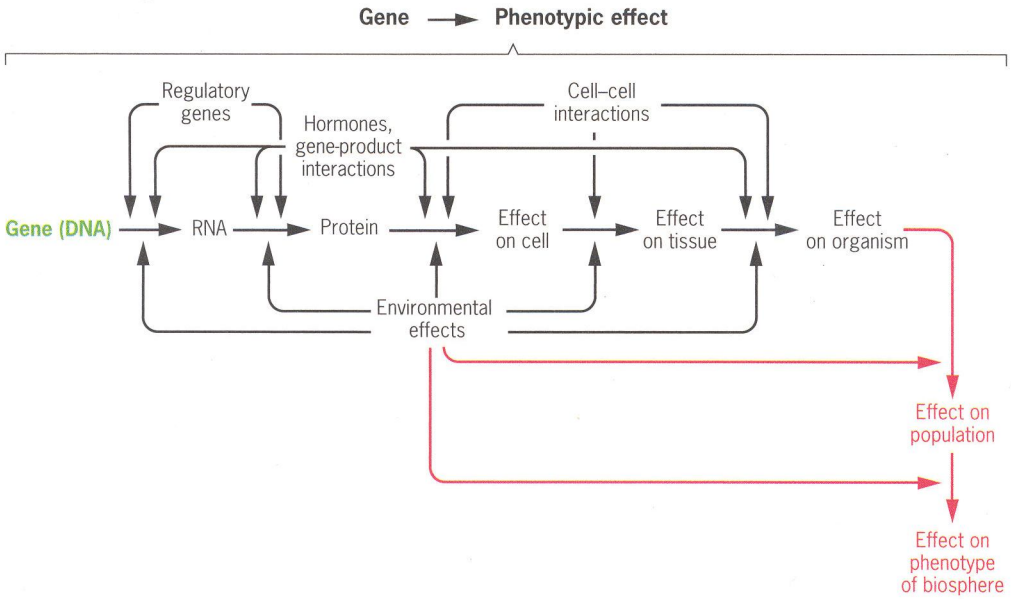


Figure 8: Gene-phenotype pathway and the influences of epigenetic factors

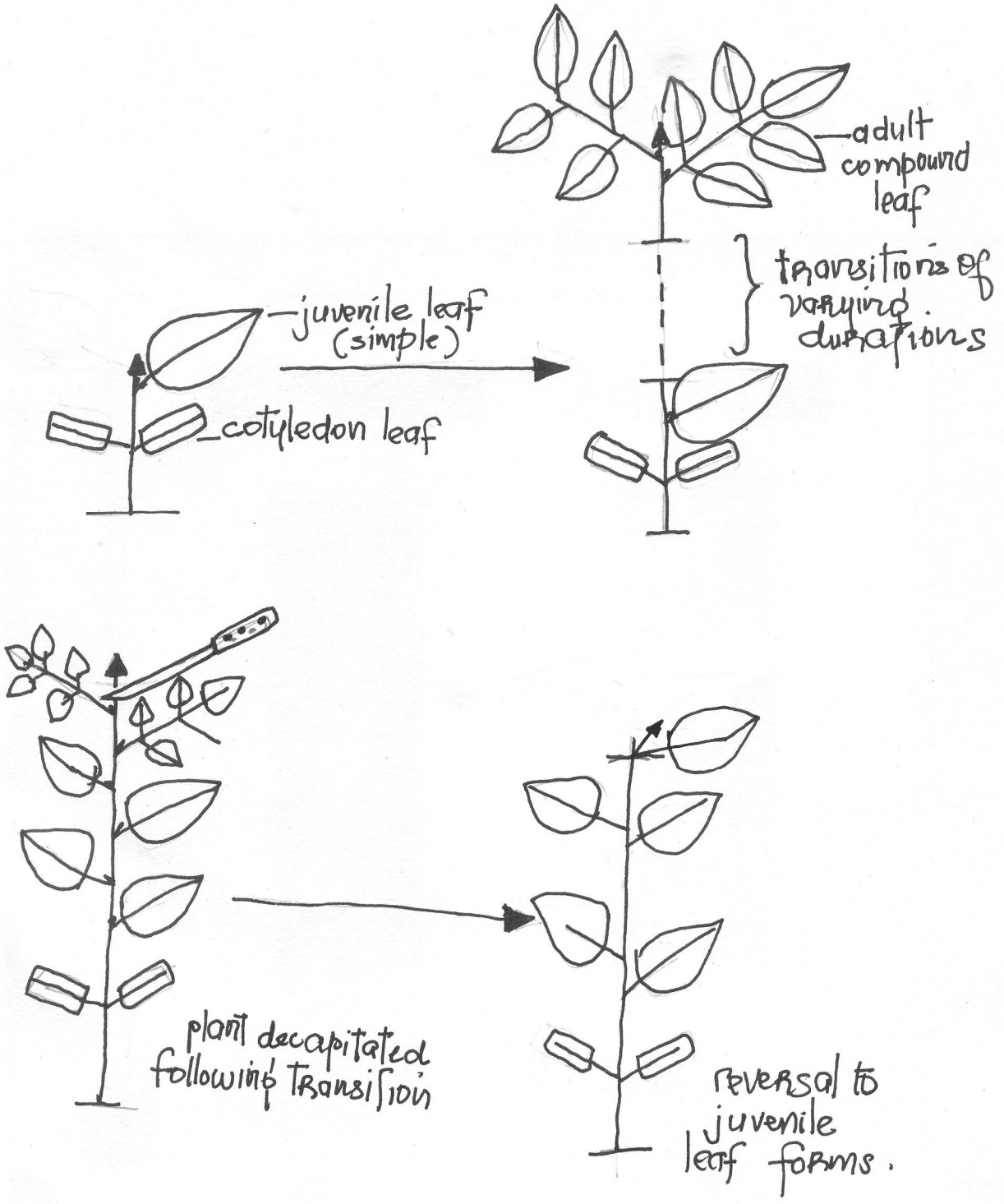


Figure 9: **Juvenile-adult leaf transition in Angiosperms: internal and external epigenetic factors**

ANIMAL BREEDING AND GENETICS IN NIGERIA AND THE FUTURE

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SUMMARY

Domestication of plants and animals using rudimentary genetics started even before written history. In Nigeria most domestic animals are kept by traditional pastoralists. These animals appear to have developed over the years into different breeds especially cattle, sheep and goats. Breed development however does not appear to have been obvious in poultry e.g. chickens. The husbandry and performance of the Nigeria livestock and poultry had not been adequate therefore they have not met sufficiently the animal protein need of the populace. Animal Breeding and Genetics utilizes the science of genetics to the improvement of animals through mainly selection and breeding especially crossbreeding. Breeding improvement utilizes statistics to estimate the genotypic values of animals using phenotypic information. The most appropriate genotypes are then selected and bred to form the next generation. Through adequate use of statistics genetic animal improvement has advanced adequately in the developed world e.g. in America. Genetic improvement however has been slower in Nigeria in comparison. To fast track genetic animal improvement in Nigeria the country must learn from the progress made in other places and apply all the appropriate genetic improvement steps that have been found useful. Of recent Molecular Genetics-Genetic Engineering in particular has been applied to animal improvement with some successes. Procedures such as marker-assisted selection and transgenesis including cloning have shown great promises and should also be applied to the Nigerian situation.

Developments of specialized breeds are usually direct products of advancement in genetic improvement. Some animals would therefore be less used or may fall out of the usual production cycle and become extinct. Efforts must be made to conserve or protect all species of farm animals including their wild ancestors and relatives because changed circumstance in the future may require their utilization.

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INTRODUCTION

Rudimentary use of genetics had allowed man to gather plant and animal food materials, discard those that do not meet his needs and domesticate some even before recorded history (Hartwell, *et al.*, 2000). In Nigeria most domestic animal especially species used for food have been in the hands of farmers/pastoralists who have little exposure to the science of modern Breeding and Genetics. They have acquired their animals mostly through ancestry but have maintained them with dignity. These livestock owners however are breeders and geneticists in their own right. For, over the years, they have developed herds/flocks of true breeding (true to type) species-cattle, sheep, goats and pigs. They have maintained their purity and distinctive characteristics especially colouration and productivity, probably through trait preference and genetic separation (natural and artificial) until recently when careless crossbreeding disturbed the status quo. Some genes, especially those for colour therefore became fixed until recently. Today multicoloured livestock are found all over Nigeria which are direct consequences of uncontrolled breeding (that the appearance of some multicolours in livestock could be due to crossbreeding can easily be demonstrated). It appears however, that distinctive breed development did not take place among most local poultry species, especially chickens as multicolouration has always been the order among them.

Natural selection has also reasonably adapted the Nigerian domestic animals to their environment. They are therefore able to withstand (survive) the vagaries-fluctuations and challenges of the environment and feed, grow, reproduce and maintain some levels of productivity. The artificial selection by traditional farmers over the years might not have been obvious. Selection is however carried out by farmers when males are castrated, bulls identified for breeding and unthrifty or sick animals culled or sold out. These processes however were not vigorously carried in systematic and sustained manner. Thus improvement progress has been slow and generally there has been low productivity. This is compounded by the overbearing effect of the relatively uncontrolled environment. Attempts have definitely been made by traditional animal owners over the years to control the environment such as little housing for smaller species e.g. sheep, goats and poultry. Deticking, a very ancient practice and, nomadism and transhumance etc are all efforts to control the environment as had been alluded to by Williamson and Payne (1978). All these have contributed to the domestic animals found around today. The authors indicated that tropical and hence Nigerian animals grow slowly, utilize food and reproduce inefficiently and therefore are unable to satisfy the animal protein demand of the society. Nigerians over the years consequently have consumed and utilized animal protein below the expected FAO (1990) recommended level of 34g per caput. Meat and eggs are a luxury in some societies and milk, of course, if available is known to be poorly utilized by 70% of adult human population due to lack of intestinal lactase to digest its high lactose content (Robinson and Mc Evoy, 1993, Montaldo, 2006). This is expected to change with future application of the science of Breeding and Genetics.

To relate Animal Breeding and Genetics to the future, it is necessary to first appreciate its position in the past and present.

THE SCIENCE OF ANIMAL BREEDING AND GENETICS AND, THE PAST AND PRESENT

Animal and Breeding and Genetics is a science of animal improvement that is researchable, taught in schools, colleges and tertiary institutions and practised on the field. Its basic scope which varies, is exposure to the science of genetics (Hartwell *et al.*, 2006) and the art of application to the improvement of animals (some people argue that the art comes before the science). Selection is its basic, albeit not the only, tool. Animals are assessed and the best selected to form future generations based on some criteria which may be objective or subjective. Thus once the criteria have been spelt out the next step is finding animals that fit them. Since genetic characteristics may but, in most cases, are not observed in animals on the outside, there must be a way of knowing the genetic make up based on the outside. Breeders therefore embark, through selection, on “blind” search for desired genetic make up-genotype using outside appearance-phenotype which may not tell much. Over the years breeders have relied on statistics to resolve the problem and the subject of statistics became so ingrained into the science of Animal Breeding and Genetics that it became difficult to appreciate the science without statistics. When mention is made of Fisher, Wright, Lush, Haldane, Dickerson, Kemp thorne, Searle, Falconer, Hill, Henderson etc with regard to work in breeding and genetics it is sometimes difficult to know whether they were breeders applying statistics as a tool to the science of Breeding and Genetics or they were Mathematicians/Statisticians using breeding and genetics in Statistics. The convergence in this respect became almost absolute.

With the aid of statistics therefore, the blind search is reduced to estimating observable values to give insight into genetic values or merits or better still breeding values of animals. This is the so called traditional (but scientific) animal breeding or improvement method using phenotype and genealogical information. Breeders therefore talk about true mean values, least squares means, best estimates and predictions etc whose elucidation may require linear modelling and matrix algebra (Searle, 1965; Henderson, 1975).

It is not uncommon therefore that Least Squares of different kinds, Maximum likelihood, Best Prediction (Estimation)(BP), Best Linear and Unbias Prediction (BLUP) procedures etc applied to mixed models (Henderson, 1975) are utilized to get the best animals for selection. The Americans at Iowa and Cornell in particular have applied these procedures and made dramatic improvement in their livestock species over the past 80 years. Procedures such as daughter dam comparisons, sire evaluation and sire studs for artificial insemination (AI), use of pedigree information, progeny testing herdmate comparison and simulation [1], nucleus breeding scheme, central breeding system and testing stations were applied to aid selection. The selection was carried out in various ways to maximize progress. Crossbreeding was also applied when quick and further improvements were desired and to benefit from the effect of heterosis. There were also various grading up policies and development of new breeds through crossbreeding. Today, animal protein in the form of meat, milk and egg is easily available in America and in many parts of the developed world and derived from different species and specialized breeds.

THE PAST AND PRESENT STATE OF ANIMAL BREEDING AND GENETICS IN NIGERIA

The Nigeria's genetic animal improvement situation is different from the Americas. The science of Animal Breeding and Genetics was slow in coming and poorly appreciated. Animal improvement was first considered in terms of nutrition and healthy. This is not completely inappropriate as genetic attributes are better appreciated only after environmental influences have been reduced.

The first crop of Nigerians to be trained in Animal Breeding and Genetics was in 1960's and early 1970's. Earlier however, the first livestock farm had been established in 1914 at Allagarno in today's Borno State to start some improvement efforts. It was closed due to lack of improved production despite improved management (Knudsen and Sohael, 1970). The Vom Livestock Investigation and Breeding Centre was established in 1920; Shika and Agege farms followed closely with others all over Nigeria, including Universities subsequently. The first few farms started with local breeds, mainly cattle.

The first recorded selection in Nigeria started at Vom in 1939 on a strain of White Fulani called Kurum Baji. It is not clear which selection procedures were followed but probably mass or individual in view of lack of adequate records and the low state of the science of breeding and genetics in the country at that time. It is on record however that the selection process was not properly executed (Knudsen and Sohael, 1970). It even became more difficult at the advent of the Second World War. The colonialists wanted plenty of butter to prosecute the war, especially during the winter. The large amount of butter required was obviously not met from home production. Colonies were looked up to. Cows were therefore retained in the Vom herd irrespective of production to boost butter quantity. Selection was again resumed in 1948 but there was poor result. It was decided at Vom and in many of the other farms that European cattle genotypes in the farms of bulls and semen should be imported to crossbreed the local herds (which have not been adequately selected) and later to form pure exotic herds. There was in addition the well known exotic cockerel exchange programme of the 1970's in most parts of Africa aimed at crossbreeding the local chickens. Sheep, goats and pigs were not spared as there have been crossbreeding on them about the same time as poultry. Therefore the Nigerian Livestock and bird population did not pass through the expected initial period of intense and sustained selection.

It has been difficult since then to convince some Nigerians to start genetic improvement through selection. To them, genetic improvement became synonymous to crossbreeding. Some of my students would want to crossbreed and quickly expose pastoralists to the crosses. My response has always been, "wait a bit". When they insist I would advise that only elite farms that can handle the

crosses should have them. This is because, if a pastoralist's herd/flock is crossbred and he is not well prepared for them, they would die and he is ruined. Even some Agricultural Development Programmes (ADP's) and elites in the society who should know better advocate immediately crossbreeding stressing that the crosses look and perform better; but on whose herd, at what cost and for how long? They also add that they have waited too long for genetic improvement, in Nigeria, through selection. My bitter experience at Butura Livestock Farm near Bokkos in Plateau State, 1977-82, might have been responsible for my present staunched perhaps stern stand. I had the unpleasant and unhappy privilege of witnessing about 80 pure Friesians and crosses with White Fulani, under my watch, perished due to dermatophilosis. The farm was not well prepared against ticks and other ectoparasites. It is only fair to mention that at the same time, the Vom herd was able to maintain similar stock with some level of productivity (Mbap and Ngere, 1989). Similarly elite poultry farms have raised exotic breeds with some levels of success, although costs of production have been quite high.

STEPS IN ANIMAL BREEDING AND GENETICS

Genetic improvement should have strong elements of selection, especially on traits of high heritabilities, such as those associated to productivity. Williamson and Payne (1978) had indicated that animal improvement in the tropics and hence Nigeria could (or in certain places had been) carried out successfully through selection, crossbreeding, grading up or rearing of pure exotic herds/flocks. However they quickly added that successes would depend on appropriateness or method, prevailing weather and management conditions. The steps may include the following:

(i) Characterization- know the phenotype, genotype and worth

(ii) Selection

(iii) Crossbreeding between local or between local and exotic breeds

(iv) Grading up, new breed development and rearing of pure exotic breeds

The last three may follow if selection results in inadequate improvement. Crossbreeding should never be the first step. Nigerian animals are poorly genetically improved today probably because of wrong concepts and steps. Part of the National Animal Production Research Institute (NAPRI) mandate is to carry out genetic animal improvement. It is gratifying that steps have been taken to include characterization, selection, crossbreeding and grading up with some successes, especially in the development of the well known NAPRI layer.

THE SCIENCE OF ANIMAL BREEDING AND GENETICS IN NIGERIA AND THE FUTURE

There have been avoidable shortcomings in genetic animal improvement in Nigeria in the past or rather the process has been relatively slow. The future state of Nigeria's livestock and poultry and contribution to living standard, health, Gross Domestic Products (GDP) and national development would depend on steps taken now and in the future. Now that the constraints of health, nutrition and other environmental conditions of animal are vigorously being tackled through research and development, sustained genetic improvement must follow. There are many attributes of the Nigerian animals that could be exploited in breeding. The fast growth and good meat conformation of the Gudali's could be utilized in beef cattle development. The breed also has good temperament for milk production. The Wadara also has some potentials for milk production. Among the sheep breeds, the Balami and Uda have high birth and mature weights and fast growth that could be utilized. The West African dwarf has the advantage of high litter production as twinning and triplets

are common features of the breeds, enabling quick herd formation and fast turnover on selection. If also selected for survivability (a very important constraint in their production) quick progress could be made in goat meat production, a product highly cherished by a large proportion of the Nigerian society. There are heavy chicken ecotypes, for example the Fulani ecotype (Atteh, 1990) that could be utilized in broiler production. The early maturity among Nigerian poultry is a trait that could also be used in both broiler and layer production. If selected against broodiness, egg production could be enhanced. These are just but few traits among many that could be utilized in future breed genetic improvement and development.

It might sound naive that we are talking about applying the basics of breeding improvement in the 21st century and post genomics. However we must get it right, carry out genetic improvement properly and be patient for results which may not come readily. Today, there is general renaissance and intensified work among breeders to properly characterize the Nigerian domestic Livestock (Moruppa and Ngere, 1986; Nwosu, 1979; Rege, 1992, Mbap and Zakar, 2000; Mancha, 2004; Egashi, 2011, Wamagi, 2012) in view of the aforementioned potentials. The other enumerated improvement steps should also follow and at national level. The Federal Livestock Department (FLD), Nigeria Institute of Animal Science (NIAS), National Agricultural Research Project (NARP) should lead and ensure rapid and sustainable genetic progress. The NAPRI should in addition to the NAPRI layer, develop more specialized breeds among other livestock species.

Procedures followed by the Americans should be reviewed, adapted and utilized. This is especially when human population is growing and available space dwindling. In 1991 the late Dr. J.N. Bincan, Director Livestock in the Federal Ministry of Agriculture (FMA) initiated a programme for improvement of all Nigerian domestic animal breeds, at a national level, through selection using the nucleus breeding scheme and other procedures. He died shortly after in 1992 and the programme also died. I call on the FMA to revisit such ingenious initiatives. The FMA should dig the archives to find out what actually happened to this particular programme and reinitiate it. As inferred earlier, traits currently considered in genetic improvement are those that emphasize increased productivity. The improvement criteria or traits to improve in the future may change. This is in view of changing environment and human population. While traits such as fast growth, early maturity, egg size and number etc may always be retained, it is possible that animal size among others may be selected against in future, in view of space constraints and other changing demands, including increase in periurban agriculture.

THE USE OF MOLECULAR GENETICS

Nigeria should not lag in the application of modern technologies in genetic animal improvement. As alluded to, the Science of Breeding and Genetics, at certain levels, was so akin to statistics that it was difficult to appreciate the difference. Increasingly the science is becoming more molecular. Any serious student or practitioner of Breeding and Genetics would not cope without proper exposure to Molecular Genetics. Thus teaching and research in Animal Breeding and Genetics and, application to the improvement of animals in Nigeria must of necessity emphasize the molecular aspect (without diminishing the conventional methods). The Animal Breeding and Genetics Laboratory of today and the future should not only be data banks and store houses for computer facilities. They should also have genetic resource banks and should contain equipment for molecular genetics and biotechnology. These facilities will expose students and researchers alike to the rudiments of the fields preparatory to stronger application in animal improvement. At Abubakar Tafawa Balewa University (ATBU) Bauchi, a course in Genetic Engineering is compulsory to all postgraduate students of Breeding and Genetics. Indeed some few universities in the country have extended it to all undergraduate Breeding and Genetics students.

The application of Molecular Genetics in Animal Breeding and Genetics is wide, varied and complex. It will only be briefly discussed to underscore its usefulness to Nigeria in the future.

When Molecular Genetics in the form of Genetic Engineering or Recombinant DNA technology is applied for the improvement of animals, it would appear that it is not blind such for the right animals any longer. Genetic Engineering allows breeders to identify, replicate, modify and transfer genetic materials (Montaldo, 2006). They range from DNA components to complete organisms. The physical map (linkage map) of special DNA's, major genes or markers, compound genes or genetic loci for production traits called quantitative trait loci (QTL) may be known through linkage disequilibrium studies in mating experiments and use of polymorphic microsatellites (Malau-Aduli, 2003) within some confidence limit. The animals that are thought to have them are then selected. However since the existence, exact location on the chromosome, function and passage of QTL to subsequent generations are still a matter of probability, phenotypic and genealogical information and hence traditional selection procedures are applied (but highly enhanced). Furthermore, as is well known, different genes may produce the same phenotype, most economic traits are due to multiple gene (or polygenic) action and attendant interactions and, complications such a linkage and plieotropy. In addition traits are also controlled by the environment. All these vitiate the initial enthusiasm that greeted the discovery of QTL. Nonetheless, even recently, it has been stated that the identification of QTL has potentials to significantly increase rate of genetic improvement through the use of Marker-Assisted Selection (MAS) (MacNeil and Gross, 2002). (The MAS being extension of traditional selection procedure using QTL). However, in view of the limitations, the use of MAS in breeding improvement is not a revolution as such but an evolution of the traditional genetic improvement (Montaldo, 2006). Although the expected gain using MAS may not be as high as initially anticipated, it is a step forward and where possible, it should be applied in future Nigerian breeding situation. The MAS is most useful for traits of low heritabilities, expressed late in life, sex limited, expensive to measure or controlled by a few genes (Davis and DeNise, 1998; Montaldo, 2006).

TRANSGENESIS AND CLONING

Transgenesis which is an introgressive procedure, in genetic engineering, makes it possible to alter an animal genetically for particular purposes e.g. disease resistance by introducing a gene or part of a DNA. Cloning of a full animal, an extreme form of transgenesis is carried out through nuclear transfer. Genetically identical individuals are produced e.g. the Dolly Sheep (Wilmut *et al*., 1997). While cloning is novel in higher animals it is the norm in some plants and lower animals. Cloning has therefore brought this type of reproduction to the remit of all living organisms. Transgenesis (cloning) if properly applied could be useful tools in the hands of breeders. With appropriate knowledge of gene combinations and functions, new and useful population could be created within a short time for the benefit of man. Again cloning is a step forward but not a panacea to all animal improvement problems. Differences still exist between clones due to the environment and the variation could be as high or even higher than 50% of total (Van Vleck, 1999). Therefore selection is still appropriate amongst them. However in selection using clonal individuals, additive and non additive genetic differences could be utilized (Visscher et al, 2000) thus increasing genetic gain. This is unlike non clonal selection where non additive variations are not utilized.

The current drawbacks to transgenesis especially cloning are low success rate, cost and some unapparent health problems amongst clones. Another dilemma is ethical and practical applicability in a country like Nigeria which has high religious culture and illiteracy rate. The negative reactions of sceptics are also not helpful. On the whole therefore, genetic engineering in animal improvement has not replaced the classical improvement procedures but aided them. However when MAS and transgenesis are applied in Nigeria in conjunction to older reproductive technologies such as

artificial insemination, semen and ova preservation, multiple ovulation and embryo transfer, semen and embryo sexing, in vitro oocyte maturation and Fertilization (Robinson and McEvoy, 1993), rapid overall progress could be made. The much needed animal protein for growth and development would be met. Furthermore, the potential of the country to export animal products in view of large number of animal species and high population would enhanced. This is particularly important as Nigeria is looked up to by many surrounding countries for support. That Nigeria sometimes imports animals for meat from other smaller neighbouring countries is not acceptable.

ANIMAL GENETIC RESOURCE AND BIODIVERSITY CONSERVATION

Genetic resource and biodiversity conservation or protection has recently become a much discussed topic. It would even be a more important concept in future breeding work. The year 2010 was declared International year of Biodiversity by the United Nations. This came at the heels of the adoption of the Global Plan of Action for Animal Genetic Resources (AnGR) three years earlier [Editorial; Animal Genetic Resources, 2010;47]. This 47th volume of the journal was published as a special edition to mark the year and all the 12 (invited) papers were on the Global Plan for Action.

Conservation of genetic resources is necessary to ensure their continuous use. For those that are not presently being used, change circumstances may require their utilization. Indeed the future food supply depends to a large extent on how the present generation handles conservation. The concept would surely gain momentum in Nigeria in view of increasing emphasis and concern about food security. Therefore, a major component of conservation is sustainable use i.e. handling genetic resources in a manner that diversity does not decline.

In general, animal genetic resources could be conserved in two ways (FAO, 1998).

(i) Maintaining the population or endangered species/breeds in the production cycle.

(ii) Cryo preservation or – conservation of gametes, embryos, somatic cells or even life animals

Initially prioritization for conservation was arrived at through phenotypic characterization. Species, breeds strains etc were evaluated for current or potential values or uses to determine those to pay more attention to. Of recent, molecular genetics -genetic engineering has been applied to enhance decision making. Genetic engineering provides in depth information on the genetic merit of animal population (Hill, 2000). There is, in addition, more accurate information retrieval. Relatedness and genetic distances are more accurately assessed, enabling better characterization. If it becomes a matter of decision on which genotype to conserve in view of storage space/facility limitations, choices could be concentrated between more, than less related individuals, thus reducing diversity erosion.

The earlier genotypic efforts/procedures utilized protein and blood type analysis using electrophoresis and immunological studies in conjunction to protein markers. Protein markers however vary with development, environment and selection (Talle *et al*., 2005). Today, gene mapping has become a particularly useful procedure in conservation. The existence of DNA sequence polymorphism enables the identification and use of different techniques/markers in conservation. Those currently in use are mitochondrial DNA markers, restriction fragment length polymorphism, amplified fragment length polymorphism, random amplified polymorphic DNA, microsatellites/micro satellites studies, DNA sequencing, single nucleotide polymorphism as individuals or in array etc (Adebambo *et al*., 2004; Talle *et al*., 2005; Agaviezor *et al.,* 2011).

It is being argued that conservation should not be limited to domestic plants and animals but also their wild ancestors and relatives. This is because there may be reasons in the future to revert to

them for some important genes or gene combinations. Since bioresource or biodiversity conservation may feature prominently in future Nigerian breeding and genetic work, the country should join and become an active participant in the global biodiversity initiative.

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ANIMAL GENETICS AND BREEDING (AGB)

AGB01

DIRECT AND PERCENTAGE HETEROSIS OF GROWTH TRAITS IN CROSSES INVOLVING INDIGENOUS AND EXOTIC BREEDS OF PIGS IN NIGERIA

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ABSTRACT
Crossbreeding in pigs in order to exploit heterosis has been the common practice in commercial pig production since better average performance of crossbred animals is achieved over their purebred counterparts. A total of 72 progenies generated from a cross involving the West African Indigenous (WAI), Landrace (LR) and Large White (LW) breeds were used to estimate the direct and percentage heterosis on bodyweight (BW) and morphometric traits such as Ear length (EL), Tail length (TL), Heart girth (HG), Height-at-withers (HW), Snout length (SL) and Body length (BL) at 56, 84, 112 and 140 days of age. Positive direct heterosis was reported on BW at 56 days for LRxLW and LRxWAI crosses only, while at 84, 112 and 140 days, negative direct heterosis were recorded for the other crosses. The morphometric traits also showed more positive direct heterosis, particularly for EL, TL, HG, HW, SL and BL at various ages and crosses than negative heterosis at other ages and crosses. The percentage heterosis ranged from 7.72% to 55.91% for BW at different ages and crosses, while for morphometric traits, it ranged from 0% to 32.00% in EL, 1.14% to 15.4% in TL, 0.77% to 21.18% in HG, 0.76% to 29.53% in HW, 0% to 13.59% in SL and 0.76% to 19.66% in BL at different ages and crosses, respectively. This implies that for those traits that exhibit positive heterosis, the exploitation of non-additive gene action such as dominance could bring about more rapid genetic improvement, while the high percentage heterosis (BW) implies that selection for such trait will lead to more rapid genetic improvement. However, low percentage heterosis recorded for some of the BW and all the morphometric traits shows that selection for these traits cannot result in rapid genetic improvements.
Keywords: Crossbreeding, growth traits, morphometric, reciprocal cross, heterosis.

INTRODUCTION
Swine breeding and genetics has advanced tremendously with rapid crossbreeding in order to exploit heterosis. Desirable characteristics of different breeds can be utilized if some breeds can be identified as good maternal breeds and others as good paternal breeds (Buchanan et al., 2005). The diallel cross is commonly used in plant and animal breeding for evaluating the genetic structure of a population of pure-bred lines. An accurate analysis of this mating design is therefore not only of theoretical but also of economic importance and has been dealt with by many authors (Virk et al.,

1985; Okoro et al., 2012a). A common assumption underlying most analyses of the diallel cross is the absence of any reciprocal differences, which are primarily caused by sex-linkage and maternal effects. Although the effects of such differences on the analysis of diallel crosses have been examined by many authors (Wearden, 1964; Durrant, 1965; Topham, 1966, and Mather and Jinks 1982); these investigators were primarily concerned with testing the significance of possible effects and with determining the probable cause of heterosis and reciprocal effects.

There is a dearth of information on systematic breeding plans in pig breeding as well as poor husbandry practices in the methods of pig production in Nigeria. Since reciprocal and heterotic effects are important in deciding on the lines of sire or dam to be used in a cross for developing commercially-superior crossbred progeny in terms of growth and reproductive characteristics; there is dearth of information on direct heterotic effects on the cross of the three major breeds commonly used for production – Large White (LW), Landrace (LR) and West African Indigenous (WAI) breeds in the tropical rainforest environment of Nigeria.

This study was therefore conducted to estimate the direct and percentage heterosis on growth traits in crosses of pigs (LW, LR and WAI breeds) in tropical rainforest zone of Nigeria.

MATERIALS AND METHODS

A modified 3x3 diallel cross comprising three breeds of pigs, namely Large White (LW), Landrace (LR) and West African Indigenous (WAI) breeds was conducted. The matings were as follows:

Main cross: LW (♂) x LR (♀); LW (♂) x WAI (♀), and LR (♂) x WAI (♀).

Reciprocal cross: LR (♂) x LW (♀); WAI (♂) x LW (♀); WAI (♂) x LR (♀).

Three boars of each breed were mated to six sows of the three breeds, randomly sampled from the population maintained in the farm. Piglets were generated from the crosses which comprised 2 parities per cross, totaling 12 litters. Data generated were replicated based on parities in order to estimate a reliable standard error of mean for crosses.

The parameters measured were growth traits which included:

1. Weaning and post weaning weight at 56 and 84 days of age (measured using 50 kg weighing scale ® Salter England)
2. Body weight towards the end of growth period at 112 and 140 days of age (measured using 200kg bridge weighing scale ® Global Universal England).
3. Morphometric traits measured at 56, 84, 112 and 140 days of age were estimated as follows:
   i. Ear length (EL) – Measured as the distance from the ear base to the tip of the ear, using a tailor's tape.
   ii. Tail length (TL) – The distance from the pin bone of the tail base to the tip of the tail, using a tailor's tape.
   iii. Heart Girth (HG) – Measured as the circumference of the animal body taken immediately posterior to the shoulder, using a tailor's tape.
   iv. Height at Withers (HW) – Measured as the distance from the highest point on the dorsum of the animal to the ground surface, at the level of the front feet, using a tailor's tape.
   v. Body length (BL) - Measured as the distance from the point of the scapular to the pin bone of the tail base, using a tailor's tape.
   vi. Snout length (SL) – The distance from the eye slit to the tip of the snout, using a tailor's tape.

Direct heterosis for each cross was estimated with the method of linear contrasts as outlined by Dickerson (1992) in expression (4) below:

Direct heterosis for each cross = Mean of the cross – Mean of parental purebreds ... (4)

In addition, percentage heterosis was obtained separately for main and reciprocal crosses as quotient between direct heterosis (expression 4) and mean purebred value multiplied by 100 as shown in expression (5) below

$$\text{Percentage heterosis} = \frac{\text{Direct heterosis}}{\text{Mean of purebreds}} \times \frac{100}{1} \quad \ldots \quad (5)$$

RESULTS AND DISCUSSION

The distribution of litters of progeny according to breed of sire (Main cross) and breed of dam (Reciprocal cross) is shown in Table 1. The resultant litter size totaled 72, comprising 27, 25 and 20 piglets from the Large White (LW), Landrace (LR) and West African Indigenous (WAI) sires respectively while the dam breed (Reciprocal cross) produced 23, 25 and 23 piglets from LW, LR and WAI, respectively. The cross between LW x LR produced the highest litter size, while NI x LW produced the least litter size.

Table 1: Distribution of litters according to Breed of Sire and Breed of Dam

	Breed of Sire[a]			
Breed of Dam	LW	LR	WAI	TOTAL
LW	*	14	9	23
LR	15	*	11	25
WAI	12	11	*	23
TOTAL	27	25	20	72

[a] LW = Large White LR= Landrace WAI= West African Indigenous.

*No purebred mating.

Bereskin and Hetzer (1986) reported an average litter distribution ranging from 6 to 10 in a diallel cross to determine the genetic and maternal effects on pig weight, growth and probe backfat in high and low fat lines of swine. Although this study was not a full diallel cross due to absence of purebred litters, it was similar to the report by Obasi and Ibe (2008) who reported a total of 72 kits in an experiment to determine the influence of additive and non-additive gene effects on body measurements in domestic rabbits. In addition, Adebambo (1986) reported a higher litter number in crosses involving LW x Hampshire (HA) breeds (8.25 to 8.75) than crosses involving LW x WAI, HA x WAI and WAI x exotic breeds, which ranged from 7.8 to 8.3.

The estimates of direct and percentage heterosis for BW are presented in Table 2. At 56 days of age, there was a positive heterosis for the reciprocal cross, LRxLW (16.21%) and main cross LRxWAI (7.92%), while for other main and reciprocal crosses, heterosis was negative with percentage heterosis ranging from 12.08% to 41.20%. At ages 84, 112 and 140days, there were negative direct heterosis for all the crosses for BW, with values ranging from -1.32 to -10.00 and percentage heterosis ranging from 3.59% to 55.91%.

Table 2: Estimates of Direct and Percentage Heterosis[a] for Body weight at 8-20 weeks

Age (Days)	Cross 1 Main LWxLR	Reciprocal LRxLW	Cross 2 Main LWxWAI	Reciprocal WAIxLW	Cross 3 Main LRxWAI	Reciprocal WAIxLR
56	-1.28	0.94	-2.06	-0.97	0.42	-0.64
	(22.07)	(16.21)	(41.20)	(19.4)	(7.92)	(12.08)
84	-3.05	-1.23	-5.20	-3.45	-1.87	-1.27
	(28.24)	(11.39)	(55.91)	(37.10)	(19.08)	(12.96)
112	-2.52	-0.46	-5.61	-3.84	-1.26	-0.29
	(19.69)	(3.59)	(50.09)	(34.29)	(10.59)	(2.44)
140	-3.55	-2.52	-10.00	-8.02	-3.29	-0.16
	(16.82)	(11.94)	(55.87)	(44.80)	(17.98)	(0.87)

[a] Percentage heterosis in parentheses.

The estimates of direct and percentage heterosis for EL and TL are presented in Tables 3 and 4. In all crosses (main and reciprocal), there was positive heterosis for EL at 56 and 84 days of age. Positive heterosis was also obtained at ages 112 and 140 days, except for LWxLR main cross in day 112, and LWxLR main and reciprocal cross and LRxWAI main and reciprocal cross in day 140. For TL, except for LWxLR main crosses at 56, 84 and 112 days, and LRxWAI main cross at 56 and 84 days, heterosis was positive in all other situations. However, the percentage heterosis ranged from 0 to 32.0% and 1.14 to 15.4% in EL and TL, respectively.

Table 3: Estimates of Direct and Percentage Heterosis[a] for Ear length between 56 -140 days.

Age (Days)	Cross 1 Main LWxLR	Reciprocal LRxLW	Cross 2 Main LWxWAI	Reciprocal WAIxLW	Cross 3 Main LRxWAI	Reciprocal WAIxLR
56	0.54	0.25	1.79	0.50	0.86	1.25
	(6.75)	(3.13)	(27.54)	(7.69)	(11.86)	(17.24)
84	0.19	0.75	2.32	0.86	0.97	1.38
	(2.24)	(8.82)	(32.00)	(11.86)	(11.76)	(16.73)
112	-0.44	0.00	1.96	1.03	0.33	0.50
	(4.51)	(0.00)	(25.29)	(13.29)	(3.67)	(5.56)
140	-1.96	-1.75	1.04	0.19	-0.69	-0.25
	(17.04)	(15.22)	(11.24)	(2.05)	(6.73)	(2.44)

[a] Percentage heterosis in parentheses.

Table 4: Estimates of Direct and Percentage Heterosis[a] for Tail length between 56 – 140 days

Age (Days)	Cross 1 Main LWxLR	Reciprocal LRxLW	Cross 2 Main LWxWAI	Reciprocal WAIxLW	Cross 3 Main LRxWAI	Reciprocal WAIxLR
56	-0.22	0.18	0.84	0.66	-0.69	0.70
	(3.41)	(2.79)	(15.41)	(12.11)	(12.55)	(12.73)
84	-0.44	0.13	0.43	0.22	-0.25	0.13
	(5.68)	(1.68)	(6.14)	(3.14)	(3.45)	(1.79)
112	-0.26	0.57	0.64	0.83	0.11	0.47
	(3.18)	(6.97)	(8.53)	(11.07)	(1.41)	(6.04)
140	0.10	0.63	0.86	1.11	0.64	1.13
	(1.14)	(7.20)	(10.76)	(13.88)	(7.76)	(13.70)

[a] Percentage heterosis in parentheses.

The estimates of direct and percentage heterosis for HG and HW are presented in Tables 5 and 6. There was positive heterosis for HG in the crosses WAIxLW, WAIxLR, LWxWAI and LRxLW in all ages studied, except at ages 112 and 140 days in LRxLW, ages 56 and 140 days in LWxWAI, and age 56 days in WAIxLR crosses. The rest of the crosses (main cross) in cross 1 and 3 had negative heterosis at all ages. For the HW, apart from the cross WAIxLR which had positive heterosis in all the ages, the rest of the crosses had negative heterosis except for crosses LRxLW, LWxWAI and WAIxLW which had positive heterosis at 56 days of age. Meanwhile, the percentage heterosis ranged from 0.77% to 21.18% and 0.76% to 29.53% in HG and HW respectively

Table 5: Estimates of Direct and Percentage Heterosis[a] for Heart Girth between 56 – 140 days.

Age (Days)	Cross 1 Main LWxLR	Reciprocal LRxLW	Cross 2 Main LWxWAI	Reciprocal WAIxLW	Cross 3 Main LRxWAI	Reciprocal WAIxLR
56	-6.45	0.58	-1.79	0.10	-8.09	-4.50
	(16.10)	(1.45)	(4.88)	(0.27)	(21.18)	(11.78)
84	-2.15	3.20	2.09	5.73	-3.81	2.75
	(5.08)	(7.57)	(5.49)	(15.73)	(9.47)	(6.83)
112	-9.50	-1.25	0.66	4.20	-6.13	6.09
	(18.81)	(2.48)	(1.50)	(9.57)	(12.79)	(12.71)
140	-9.20	-1.30	-2.79	4.83	-1.28	7.25
	(17.02)	(2.41)	(5.75)	(9.96)	(2.64)	(14.95)

[a] Percentage heterosis in parentheses.

Table 6: Estimates of Direct and Percentage Heterosis[a] for Height at Withers between 56 – 140 days

Age (Days)	Cross 1 Main LWxLR	Reciprocal LRxLW	Cross 2 Main LWxWAI	Reciprocal WAIxLW	Cross 3 Main LRxWAI	Reciprocal WAIxLR
56	-2.32	3.10	3.93	3.44	-0.22	5.70
	(7.30)	(9.75)	(14.15)	(12.38)	(0.76)	(19.66)
84	-9.66	-4.63	-0.84	-0.63	-8.08	5.95
	(21.70)	(10.40)	(2.25)	(1.68)	(19.56)	(14.41)
112	-12.61	-11.47	-3.03	-3.65	-8.44	13.88
	(24.47)	(22.26)	(6.58)	(7.93)	(17.96)	(29.53)
140	-11.06	-7.02	-2.29	-0.44	-5.64	12.38
	(20.58)	(13.06)	(4.87)	(0.94)	(11.57)	(25.39)

[a] Percentage heterosis in parentheses.

The estimates of direct and percentage heterosis for SL and BL are presented in Tables 7 and 8. SL had positive heterosis in main and reciprocal crosses of cross 3 in all ages studied, while the rest of the crosses had negative heterosis except at day 56 where no heterosis was recorded in LWxWAI. For BL, all the crosses had positive heterosis in all the ages studied, except in ages 112 and 140 days for LRxLW and LWxWAI, and day 112 of WAIxLW crosses. The rest of the crosses had negative heterosis in all the ages studied. Meanwhile, the percentage heterosis ranged from 0% to 13.59% and 0.76% to 19.66% in SL and BL respectively.

Table 7: Estimates of Direct and Percentage Heterosis[a] for Snout Length between 56 – 140 days.

Age (Days)	Cross 1 Main LWxLR	Reciprocal LRxLW	Cross 2 Main LWxWAI	Reciprocal WAIxLW	Cross 3 Main LRxWAI	Reciprocal WAIxLR
56	-0.88	-0.15	0.00	-0.11	0.29	0.05
	(13.23)	(2.26)	(0.00)	(1.83)	(4.72)	(0.81)
84	-0.49	-0.20	-0.33	-0.35	0.62	0.95
	(6.16)	(2.52)	(4.78)	(5.07)	(8.79)	13.48
112	-1.33	-1.04	-1.12	-0.88	0.22	1.08
	(13.59)	(10.62)	(13.10)	(10.29)	(2.54)	(12.46)
140	-0.90	-0.05	-0.73	-0.41	0.43	0.53
	(8.96)	(0.50)	(7.85)	(4.41)	(4.60)	(5.67)

[a] Percentage heterosis in parentheses.

Table 8: Estimates of Direct and Percentage Heterosis[a] for Body Length between 56 – 140 days.

Age (Days)	Cross 1 Main LWxLR	Reciprocal LRxLW	Cross 2 Main LWxWAI	Reciprocal WAIxLW	Cross 3 Main LRxWAI	Reciprocal WAIxLR
56	-2.32	3.10	3.93	3.44	-0.22	5.70
	(7.30)	(9.75)	(14.15)	(12.38)	(0.76)	(19.66)
84	-2.15	3.20	2.09	5.73	-3.81	2.75
	(5.08)	(7.57)	(5.49)	(15.73)	(9.47)	(6.83)
112	-1.33	-1.04	-1.12	-0.88	-0.22	1.08
	(13.59)	(10.62)	(13.10)	(10.29)	(2.54)	(12.46)
140	-9.20	-1.30	-2.79	4.83	-1.28	7.25
	(17.02)	(2.41)	(5.75)	(9.96)	(2.64)	(14.95)

[a] Percentage heterosis in parentheses.

The positive direct heterosis of BW reported for LRxLW and LRxWAI, implies that there was an increase in BW as a result of the crossbreeding in favour of the cross performance. This indicates that for the particular crosses, non-additive effects of genes could be exploited through crossbreeding to bring about genetic improvement for BW at 56 days. This finding contradicts existing knowledge that BW and conformation traits in farm animals are generally highly heritable, implying that rapid genetic improvement could be brought about by selection and exploitation of additive effects of genes, rather than crossbreeding (Ibe et al., 2005). The result obtained could be due to maternal effects of LW and WAI sows, since the main and reciprocal crosses – LWxLR and WAIxLR yielded negative heterosis for body weight at 56 days or could be due to influence of LR as sire at this age. This result is similar to those presented by Young et al. (1976), who obtained significant positive estimates of heterosis for litter weights at 42 days of 20.7% for Duroc(D) x Yorkshire (Y), 20.40% for D x Hampshire (H) and 6.00% for H x Y crosses; and by Schneider (1978) who found significant positive heterosis of 20.40% for litter weight at 56 days in Chesterwhite (CW) x D crosses and of 25.70% for D x H crosses at 56 days. For litter weight at 154 days, he found heterosis rates of 21.20, 22.00 and 27.10% for CW x H, CW x Y and CW x D crosses, respectively. According to Johnson (1981), heterosis estimates for litter weight at 21 days are highly variable but part of this variation is because similar crosses produce different estimates in independent experiments. Johnson (1980) reported a positive average heterosis of 9.4 and 2.5% for ADG (age at 56 days) and carcass average back fat thickness (CABT), respectively. McLaren et al. (1987) reported a highly significant ($P<0.01$) individual heterosis estimates for post-weaning performance traits and reasonably consistent trend between crosses of Duroc x Yorkshire, Duroc x Landrace, Duroc x Spotted breeds respectively; although the positive estimates reported in this study is obtained at pre-weaning BW stage of growth.

The negative heterosis for BW in all other crosses from ages 56 to 140 days is expected and indicates that for these crosses, additive effects of genes could best be exploited, through selective breeding, for rapid genetic improvement in BW (Ibe et al., 2005). Heterosis could subsequently be exploited by crossing different lines that had been improved by within-line selection. Medellin and Lukefar (2001) reported negative heterosis of -9.3 for market weight in rabbits. Schneider (1978) did not find a significant effect of heterosis on litter size from birth to the end of growth period, although the estimated heterosis presented by Smith and King (1964), O'Ferrall et al. (1968), Bereskin et al. (1974) and Young et al. (1976) was numerically higher than that found by Silva et al. (1996). The total heterosis according to Silva et al. (1996) was not a significant source of variation for the BW at 21, 35 and 77 days of age in crosses involving Duroc, Landrace, Yorkshire and Large White breeds of pigs.

The implication of positive heterosis on morphometric traits is that exploitation of non-additive gene action, through crossbreeding, could bring about more rapid genetic improvement for EL, TL,

HG, HW, SL and BL than selective breeding. The finding of positive heterosis in some cases contradicts existing knowledge that body weight and conformation traits in farm animals are generally highly heritable, implying that rapid genetic improvement could be brought about by selection and exploitation of additive effects of genes, rather than crossbreeding (Ibe et al., 2005). Ozimba and Lukefahr (1991) reported positive heterosis for linear body measurements in Californinan x New Zealand White crossbred than for parental purebreds. Khan and Lukefahr (1996) reported positive heterosis of 10.5% for post-weaning litter weight. Chineke et al., (2002) reported that New Zealand White x Dutch-belted crossbred recorded best performance in heart girth, height at withers and body length at pre-weaning ages of 7 and 21 days and at post-weaning age of 56 days. However, the positive heterosis obtained for EL, TL, HG, HW, SL and BL could not be explained based on maternal effects as is the case with BW, since the observed heterotic effect was shown by crosses involving different breeds of dam.

CONCLUSION

Crosses LRxLW and LRxWAI exhibited positive heterosis while others recorded negative heterosis for BW. The LBMs exhibited both positive and negative heterosis at different ages in different crosses. It is therefore recommended that in a cross-breeding programme involving these three breeds of swine – LW, LR and WAI breeds, the cross involving LR males and LW females will give the best performance in terms of growth traits measured, followed by the cross involving WAI males on LW females, and lastly using LR males on WAI females.

The WAI x LW and LR x WAI crosses had exhibited performance closest to exotic crosses which shows the high level of performance attainable when the WAI germplasm with its adaptational qualities is introduced into the exotic germplasm. The exotic breeds which are highly productive with well developed characteristics, are highly susceptible to stress and diseases in the tropical rainforest environment. Therefore, in a crossbreeding programme with the aim of improving the WAI pigs; adopting the WAI x LW and LR x WAI crosses will ensure better performance in terms of growth traits measured, thereby improving the genetic potential of the WAI pigs while conserving its valuable adaptation characteristics

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AGB02

DIFFERENTIAL DIAGNOSIS (ELISA) OF DIFFERENT BREEDS OF ASF RECOVERED PIGS AND THEIR OFFSPRING

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ABSTRACT
Data on serological test were collected from eight sows and two boars, (4 Large White sows, 2 Large Black sows, 2 Duroc sows, 1 Large White boar and 1NigerHyb boar) which are survivors of the African Swine Fever (ASF) outbreak in a farm at Abeokuta, Nigeria, in 2005). From these, fifty-two (52) pigs were generated in the F_1 and sixty (60) pigs in the F_2 generation, respectively. The pigs were used to determine the presence of ASF antibody. The serological test for determining the presence of ASF antibody showed that all the ASF recovered pigs tested positive while 18.79% of the F_1 and 6.25% of the F_2 pigs tested equally positive.

INTRODUCTION
African Swine Fever (ASF) disease can be confused with several other diseases. The differential diagnosis of ASF is implicated in the following five diseases namely: Hog cholera, haemorrhagic septicaemia encephalomycarditis of pigs, trypanosomosis and anthrax (FAO, 2000). The disease can be confirmed and differentiated from other diseases by conducting virus isolation and characterization detection of genuine DNA by PCR and serological test such as immunoblotting assay and Enzyme link immunosorbent Assay (ELISA). ELISA is a serological procedure that involves detection of antibodies in the serum of ASF infected or recovered pigs. Antibodies against ASF are detectable in serum 7 – 12 days after clinical signs appear (Blood *et al*., 1995) and persist for long periods, possibly for life in both domestic pigs and warthongs. Significant effect of breeds of pig on both productive and reproductive parameters has been reported (Adeoye and Adebambo 2010 and Adebambo, 1983).

The objective of this study was to determine the presence of ASF antibody in the serum of different breeds of pigs that recovered from the menace and in the subsequent generations produced from the recovered pigs.

MATERIALS AND METHODS
The study was carried out at the piggery Unit, Teaching and Research Farm, Federal University of Agriculture Abeokuta, Ogun State, Nigeria. A total of eight sows [4 – Large White (LW); 2 – Duroc and 2 – Large Black (LB) and 2 boars (1–Large White and 1–NigerHyb. (NH)] that recovered from ASF outbreak in 2005 were used for the study. The husbandry was intensive system whereby the animals were housed permanently in pens and daily routine management practices and mating carried out to produce F_1 and F_2 generations. Serum samples were collected from the recovered pigs, F_1 and F_2 and subjected to ELISA Test to determine the presence of ASF antibody.

1st Phase
Mating System
LW x LW – LW
NH x LB – LB NH
2nd Phase

LW x LB NH = LBNHLW
LW x DNU = DNHLW\
LW – Large White; D – Duroc, LB – Large Black
NH – Niger Hyb.

RESULTS AND DISCUSSION

The ELISA results on the recovered pigs showed that the optical density of Large White were greater than 0.50 while that for Duroc Large Black and Niger Hyb were lower than 0.50. Table 4 showed that ten animals that survived the outbreak tested positive to ASF while 18.75% of their offspring tested positive, 56.25% tested negative and 25% ambiguous. Among the F_2 individuals, 6.2% tested positive, 62.5% tested negative and 31.25% ambiguous.

Table 1: Differential diagnosis of pig sera

Animal	No tested	No Tv	No -V	No undecided	Total
Foundation stock	10	10	-	-	10
F_1	32	6(18.75%)	18(56.25%)	8(25%)	32
F_2	32	2(6.25%)	20(62.5%)	10(31.25%)	32
Total	74	18	38	18	74

No Tv= number positive; No –V= number negative

The higher optical density observed in Large White pigs compared with other breeds that survived the disease can be compared with the difference observed in productive and reproductive parameters among different breeds of pigs (Adeoye and Adebambo, 2010; Adebambo, 1983). The reduction in the percentage of pigs infected from recovered pigs to F_2 generation indicates a decrease in the shedding of the virus from the recovered pigs into the environment and subsequently a reduction in the prevailing rate of exposure of other pigs to the virus within the environment. This is to be expected because recovered pigs do continue to trap the virus within their tissues by the activities of macrophages (that eat up pathogens are infected tissues so that other parts will not be affected) and mast cells in the tissues. Together with the activities of the complement fixation antibodies (CFA), the engulfed ASF virus particles that are shared in the urine and faeces of the older pigs, originally infected by the virus drop significantly. This result agrees with the findings of Olugasa (2007) who reported that the level of infection is higher among the older stock (75.3% - 96.8%) than in younger stocks (13.8% - 39.7%). The result is also similar to findings of Fasina *et al*. (2010) who reported decrease in the percentage of infected animals from 2006 to 2007 to 2008 across Sixteen States of Nigeria through serological test.

CONCLUSION

The study revealed variation in response to ASF infection among breeds of pigs and decline in the number of pigs infected down the generation.

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AGB03

RELATIONSHIP BETWEEN BODY MEASUREMENT AND CARCASS CHARACTERISTICS OF MUSCOVY DUCKS USING CANONICAL CORRELATION ANALYSIS

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ABSTRACT

One hundred and twenty (120) seven-day old Muscovy ducklings were collected around Lafia metropolis for the experiment. The ducks were reared under semi-intensive system for 20 weeks. Body measurements (body length, breast bone, chest width, shank length, shank circumference and beak length) were taken at week 20, after which the ducks were slaughtered and carcass parameters (slaughter weight, pluck weight, eviscerated weight, breast muscle weight, leg muscle weight, heart weight, liver weight, spleen weight, gizzard weight and proventriculus) were taken. The data were generated according to sex and subjected to Canonical Correlation Analysis. The result showed significant ($P<0.01$) correlation between the two character sets having canonical correlation coefficient of 0.88 representing 77.71% of the population.

Keywords: Muscovy ducks, body measurements, carcass, canonical correlation

INTRODUCTION

Poultry in Nigeria has been growing at an average annual rate of 1.6 percent compared to the average human population growth of about 3 percent, while on the average Nigerians consume only about 10 grams of animal protein in a day as against the recommended 35 grams estimated requirement for normal healthy living (www.poultrysitenewsdesk.com, August, 2009). This implies that Nigerians need to triple their animal protein intake.

In pursuance of the above, this research seek to evaluate carcass characteristics of Muscovy ducks at 20 weeks of age and also to evaluate the canonical correlation amongst body measurement and

carcass characteristics of Muscovy ducks at 20 weeks of age. The results of this research provide information which will serve as a frame work for the development of selection criteria for improving the performance traits that will be needed in Muscovy duck production (growth and meat yield).

MATERIALS AND METHODS

The ducks were housed in open sided pens partitioned into 10 rooms to house 12 ducks per room. Each room measured 250 x 400cm. The pens also have an extended run for the ducks to bask and feed on green vegetation as prescribed by Nickolova (2004).

The ducklings were collected at a week old, irrespective of sex, randomly from different locations and villages of Lafia Local Governments of Nasarawa State. 120 ducklings were collected thereby making allowance for 5% mortality due to the shock of snatching from their mothers.

Kitchen residue, wet meal residue of beans, maize and other grains were collected while fresh and immediately given to the ducks. Properly dried forms of the residues mentioned above were also used when available.

The morphological data were generated at week 20 where linear body size measurements (body length, breast bone, chest width, shank length, shank circumference and beak length) were taken before slaughtering; while carcass data (slaughter weight, pluck weight, eviscerated weight, breast muscle weight, leg muscle weight, heart weight, liver weight, spleen weight, gizzard weight and proventriculus) were obtained when the animals were slaughtered. On the whole 19 variables were generated for the two sets.

For better understanding of sex continuum, the data for drakes and hens were analysed separately. The data were then subjected to Principle of Canonical Correlation Analysis (CCA) developed by Hotelling in 1935 (Wood and Erskine, 1976).

RESULTS

TABLE 1: CORRELATIONS BETWEEN BODY MEASUREMENTS AND CARCASS CHARACTERISTICS AT 20 WEEKS OF AGE FOR MUSCOVY HENS

	BL	BB	BWD	LL	TWD	BKL	SWT	DWT	EWT
BL	1								
BB	0.48*	1							
BWD	0.58**	0.30*	1						
LL	0.26*	0.98**	0.68*	1					
TWD	0.92**	0.95**	0.67**	0.46*	1				
BKL	0.55*	0.34*	0.38*	0.61**	0.58**	1			
SWT	0.76**	0.82**	0.44*	0.55**	0.96**	0.44*	1		
DWT	0.99**	0.92**	0.74**	0.29*	0.99**	0.57**	0.98*	1	
EWT	0.61**	0.88**	0.29*	0.43*	0.89**	0.27*	0.91*	0.89*	1
CCAS	0.39*	0.85**	0.27*	0.34*	0.88**	0.03*	0.86*	0.83*	0.92*
HRT	0.93**	0.98**	0.2*	0.36*	0.31*	0.44*	0.80*	0.78*	0.62*
SPLN	0.38*	0.46*	0.97**	0.31*	0.43*	0.64**	0.78**	0.58**	0.91**
LIVA	0.70**	0.79**	0.42*	0.29*	0.26*	0.31*	0.23*	0.37*	0.39*
LINT	0.27*	0.98**	0.23*	0.37**	0.99**	0.20**	0.26*	0.29*	0.34*
GZD	0.64**	0.49*	0.43*	0.89**	0.37*	0.24*	0.46**	0.45*	0.32*
KDNY	0.30*	0.25*	0.36*	0.31*	0.87**	0.78**	0.93**	0.92**	0.65**
AWT	0.39*	0.42*	0.22*	0.68**	0.45*	0.31*	0.42*	0.30*	0.32*
LWT	0.63**	0.75**	0.29*	0.35*	0.41*	0.02*	0.27*	0.26*	0.32*
KDNY	0.41*	0.82**	0.91**	0.56**	0.27*	0.26*	0.05*	0.41*	0.03*

	CCAS	HRT	SPLN	LIVA	LINT	GZD	AWT	LWT	KDNY
CCAS	1.00								
HRT	0.70*	1.00							
SPLN	0.37*	0.38*	1.00						
LIVA	0.93**	0.16*	0.26*	1.00					
LINT	0.68**	0.93**	0.26*	0.26*	1.00				
GZD	0.32*	0.54**	0.45*	0.27*	0.86**	1.00			
AWT	0.34*	0.98**	0.23*	0.37**	0.99**	0.20**	1.00		
LWT	0.82**	0.04*	0.45*	0.82*	0.41*	0.34*	0.28*	1.00	
KDNY	0.39*	0.42*	0.22*	0.68**	0.45*	0.31*	0.42*	0.30*	1.00

*= correlation is significance at the 0.05 level ** = correlation is significance at the 0.05 level

BL = Body length TWD = Thigh width EWT = Eviscerated weight LIVA = Liver length LWT = Leg weight BB = Body width
BKL = Beak length CCAS = Carcass weight LINT = Length of intestine KDNY = Kidney weight BWD = Body width
SWT = Slaughter weight HRT = Heart weight GZD = Gizzard weight LL = Length of leg
DWT = Dressed weight SPLN = Spleen weight AWT = Arm weight

From table 1 above, the highest correlation between body measurement and carcass characteristics for Muscovy hens was observed between thigh width and dressed weight; and between arm weight and heart weight, both having the correlation value of 0.99 at 0.01 level of significance.

Table 2: Pearson Correlation Analysis of Body Measurements and Carcass Characteristics at Week 20 for Muscovy Drakes

	BB	BWD	LL	TWD	BKL	SWT	DWT	EWT

BB	1.00							
BWD	0.62*	1.00						
LL	0.70**	0.67**	1.00					
TWD	0.59*	0.64**	0.73*	1.00				
BKL	0.66*	0.38*	0.33*	0.47*	1.00			
SWT	0.21*	0.55**	0.86**	0.59**	0.75**	1.00		
DWT	0.36*	0.53**	0.89**	0.87**	0.83**	0.89*	1.00	
EWT	0.47*	0.58**	0.82**	0.98**	0.62**	0.67*	0.93*	1.00
CCAS	0.4*	0.80**	0.64**	0.80**	0.77**	0.79*	0.95**	0.96**
HRT	0.42*	0.80**	0.50**	0.67**	0.96**	0.68**	0.89*	0.92*
SPLN	0.34*	0.77**	0.34	0.43*	0.96**	0.57**	0.35*	0.11*
LIVA	0.13*	0.11*	0.95**	0.35*	0.52**	0.40*	0.47*	0.37*
LINT	0.31*	0.32*	0.95**	0.96**	0.97**	0.66**	0.94**	0.55**
GZD	0.13*	0.12*	0.68**	0.49*	0.60**	0.45*	0.4*	0.57*
AWT	0.72**	0.52**	0.95**	0.62**	0.31*	0.56**	0.75**	0.81**
LWT	0.32*	0.57**	0.43	0.52**	0.82**	0.81*	0.85*	0.78*
KID	0.35*	0.54*	0.93**	0.60**	0.78**	0.12*	0.49*	0.42*

	CCAS	**HRT**	**SPLN**	**LIVA**	**LINT**	**GZD**	**AWT**	**LWT**	**KID**
CCAS	1.00								
HRT	0.94*	1.00							
SPLN	0.10*	0.15	1.00						
LIVA	0.30*	0.32	0.58**	1.00					
LINT	0.86**	0.74**	0.37*	0.87**	1.00				
GZD	0.46*	0.40*	0.40*	0.30*	0.2*	1.00			
AWT	0.77**	0.59**	0.34*	0.26*	0.12*	0.48*	1.00		
LWT	0.89*	0.89*	0.10*	0.29*	0.42*	0.37*	0.55**	1.00	
KID	0.42*	0.53**	0.95**	0.30*	0.26*	0.71**	0.27*	0.2*	1.00

From table 2 above, the highest correlation between body measurement and carcass characteristics in Muscovy drakes is between eviscerated weight and thigh width which is 0.97 at 0.01 level of significance.

First Set	**Second Set**	**Cancorr. Coef.**	**Prop.**	**P.V.**
Body measurement (7 characters)	Carcass characteristics (12 characters)	ʎ 1 = 0.881493	0.7771	0.0001
		ʎ 2 = 0.705716	0.0865	0.4375
		ʎ 3 = 0.632047	0.0925	0.6640
		ʎ 4 = 0.599482	0.0097	0.8362
		ʎ 5 = 0.532898	0.0098	0.9656
		ʎ 6 = 0.342313	0.0099	0.9365
		ʎ 7 = 0.233568	0.0145	0.9509

TABLE 3: The Canonical Correlation Analyses between Body Measurement and Carcass Characteristics at Week 20 for Muscovy Hens

Cancorr. Coef. = Canonical Correlation Coefficient represented by ʎ
Prop. = Proportion, it can be converted into percentage by multiplying directly with 100
P.V. = probability value

From table 3 above it can be observed that the highest canonical correlation coefficient between body measurement and carcass characteristics is 0.881493 representing 77.71% of the total population.

TABLE 4: Canonical Variants for Significant Correlation between Body Measurement and Carcass Characteristics for Muscovy Hens

Character	Formation of Canonical Variant
Body measurement and carcass characteristics	$\mathbf{V_1} = 0.0043X_1 + 0.20X_2 + 0.18X_3 - 0.0068X_4 + 0.19X_5 + 0.047X_6 + 0.50X_7$ $\mathbf{W_1} = 0.013X_8 - 0.024X_9 + 0.0084X_{10} + 0.0052X_{11} - 0.56X_{12} + 0.025X_{13} - 0.0043X_{14} + 0.0034X_{15} + 0.037X_{16} - 0.021X_{17} - 0.011X_{18} + 0.0044X_{19}$

In table 4 above, the highest contributor to the canonical significance in the body measurement set of variable was beak length while the least was thigh width. In the carcass character set, it

was observed that gizzard weight had the highest contribution while heart weight had the least contribution.

TABLE 5: The Canonical Correlation Analysis between Body Measurement and Carcass

Characteristics for Muscovy Drakes

From table 5 above, it can be seen that the highest canonical coefficient between body measurement and carcass characteristics for Muscovy drakes was 0.851171 representing 56% of the total population while the least was 0.683582 representing 0.13% of the population.

TABLE 6: Canonical Variants for Significant Correlation between Body Measurement and Carcass Characteristics for the Drakes

Character	**Formation of Canonical Variant**
Body measurement and carcass characteristics	$V_1 = -1.04X_1 + 298.18X_2 + 243.75X_3 - 1365.78X_4 + 13.61X_5 - 93.86X_6 - 3039.10X_7$ $W_1 = 1.90X_8 - 13.76X_9 + 29.92X_{10} - 9.60X_{11} + 174.35X_{12} - 0.0022X_{13} + 0.011X_{14} - 0.081X_{15} - 0.13X_{16} + 0.07X_{17} + 0.95X_{18} + 0.85X_{19}$

From table 6 above, the highest contributor to the function as observed in the body measurement data set was body length and the least was beak length, and for the carcass characteristics set, heart weight had the highest contribution while heart weight had the least.

DISCUSSION

In drakes the canonical correlation coefficients for body measurements and carcass characteristics had significance of 0.851171 and total correlation proportion of 56.00% of the character set at 0.01 level of significance. This is lesser to that obtained in the hens where body measurement and carcass characteristics had higher significance, 0.881493 representing 77.71% of the total population.

First Set	**Second Set**	**Cancorr. Coef.**	**Prop**	**P.V.**
Body measurement (7 characters)	Carcass characteristics (12 characters)	ʎ 1 = 0.851171	0.5600	0.0001
		ʎ 2 = 0.706813	0.1728	0.9821
		ʎ 3 = 0.668522	0.0367	0.9995
		ʎ 4 = 0.382935	0.0146	0.9954
		ʎ 5 = 0.253045	0.2135	0.9541
		ʎ 6 = 0.961266	0.0011	0.0013
		ʎ 7 = 0.683582	0.0013	0.1103

Canonical variants corresponding to canonical correlation coefficient between characters in Muscovy hens was shown in Table 2. For the first pair (V_1 W_1) of canonical variants. In V_1, beak length had the highest contribution followed by body length while within W_1 gizzard weight and spleen weight had the highest and the next highest contribution respectively.

The canonical variants corresponding to the canonical correlation coefficients between characters in Muscovy drakes were presented in Table 4. Significant correlation between body measurement and carcass characteristics V_1 and W_1, the highest canonical correlation coefficient for V_1 in the analysis of characters was for body length followed by breast bone, and for the corresponding W_1 heart weight and eviscerated weight had the highest and the next highest contributor to the correlation between the characters set respectively.

Significance of the Results

In the hens it was observed from the result that beak length and body length were the most important predictors of the carcass characteristics. This differs from that obtained for the drakes where body length and breast bones were the most important predictors. This may be as a result of the usage and roles they play in each sex at this age. It also indicated that more attention should be paid to sex when it comes to the Muscovy ducks.

The results obtained by canonical correlation analysis demonstrated the main contradiction among the multitudinous correlation variables and has reflected the correlative essence of two character sets that could not be settled by the simple correlation. This is because often times, other factors can influence simple correlation such that it only reflects the exterior, non-essential correlation.

CONCLUSION

The following conclusions can be drawn from the results obtained;

- From the results of canonical correlation and coefficients of canonical variant, it is clear that there is significant morphological dimorphism in Muscovy ducks.
- In body measurement, for drakes, it was body length and breast bone that were the highest contributors while it was beak length and body length that were the highest contributors for hens.
- Within the carcass characteristics, heart weight was the highest contributor in drakes while it was gizzard weight in hens.

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AGB04

BREED AND PARITY EFFECTS ON REPRODUCTIVE PERFORMANCE OF RABBITS IN ZARIA, NIGERIA

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ABSTRACT
This research work was conducted to investigate the effect of breed and parity on the reproductive performance of rabbits. A total of 48 adults (12 bucks and 36 does) were used and the parameters considered included litter size at birth (LSB) and weaning (LSW), litter weight at birth (LWB) and weaning (LWW), individual kit weight at birth (IKWB) and weaning (IKWW) and gestation length (GL). Three breeds were used namely Chinchilla (CHC), New Zealand White (NZW) and California White (CAW) and only three parities (first, second and third) were considered. Weaning was done at 35 days of age. The results obtained revealed that breed significantly ($P<0.05$) affected all the parameters studied except GL and WM. Among the three breeds used, CAW produced the largest LSB (7.33±0.19) while CHC had the smallest LSB (6.05±0.29). The CHC breed had the highest LWB (163.68±5.76g) while NZW had the lowest LWB (149.25±3.92g). IKWB was higher (27.05±2.14g) in CHC breed than in the other two breeds. Gestation length and weaning mortality were unaffected by breed. Parity significantly ($P<0.05$) affected all the tested reproductive parameters except GL and WM. The results revealed significantly ($P<0.05$) higher values in the third parity than in the first and second parities. It was concluded that CHC breed produced kits that were heavier at birth (IKWB) and at weaning (IKWW) while CAW and NZW breeds produced more number of kits per litter (LSB) than the CHC breed. Furthermore, third parity is recommended for rabbit farmers in Zaria, Nigeria due to its benefits in terms of improved LSB, LSW, LWB and lowered mortality as observed in the present study.
Key words: Breed, Parity, Rabbit, Zaria.

INTRODUCTION
Rabbit farming is becoming more and more attractive due to high reproductive potentials (Kabir *et al*., 2012b), high mothering ability (Lukefahr and Cheeke, 1990; Kabir *et al*., 2012a), adaptability in wide range of climatic conditions, high genetic variability (Kabir *et al*., 2011c), high roughage utilization potentials (Iyeghe-Erakpotobor *et al*., 2009) and low cost of production (Aduku and Olukosi, 1990). Moreover, detailed information about the effect of breed, effect of parity and effect of mating frequency on the reproductive performance of rabbit in the Northern Guinea Savannah zone of Nigeria is not available for commercial rabbit farming. Hence, the need for this study.

MATERIALS AND METHODS

The study was conducted at the Rabbitry Unit of the Teaching and Research Farm of the Department of Animal Science, Ahmadu Bello University, Zaria. Zaria is located between latitude 11^{o} 30'N and longitude 12^{o} 33'E and on altitude of 686 meters above sea level. Detailed description of Zaria had been given by Kabir *et al*., 2011a).

Three breeds of rabbit were used namely Chinchilla (CHC), New Zealand White (NZW) and California White (CAW), each having 12 adult females (does) and 4 adult males (bucks). The 36 does were in the age group of 7–8 months and weighed 2.25 to 2.45kg, while the 12 bucks belong to the age category of 8–9 months and weighed 2.3 to 2.6kg. The mating plan adopted was as described by Kabir *et al.* (2011b). There were three parities. Mashed concentrate diet was given at 100g in the morning and green roughage was supplied *ad libitum* in the afternoon. Composition of feed was similar for all experimental rabbits and in accordance with specifications of Aduku and Olukosi (1990): maize - 40%, maize offal - 22%, groundnut cake - 12%, soya bean meal – 18%, trace ingredients - 5%, vitamin and mineral mixture - 2.5%, common salt - 0.5%. The proximate composition of the diet was DM - 93.04, CP - 14.08, Ash - 7.12, EE - 10.33, CF - 10.64, NFE - 57.83 and OM - 92.88%, respectively. Other routine management was the same. Feed was analyzed regularly once a month as per standard method described in A.O.A.C. (1980).

Total of 185 data on different reproductive parameters recorded over 18 months (June 2007–December 2008) on 48 rabbits were considered. The parameters included litter size at birth (LSB), litter size at weaning (LSW), litter weight at birth (LWB), litter weight at weaning (LWW), individual kit weight at birth (IKWB), individual kit weight at weaning (IKWW), gestation length (GL) and weaning mortality (WM). The weight measurements were obtained using a digital scale calibrated in grams (g).

The experiment followed a completely randomized design (CRD). The general linear model of SAS (SAS, 2002) computer programme was used for computing ANOVA. Means were compared for significant difference using the Duncan's Multiple Range Test (DMRT) (Duncan, 1955).

RESULTS AND DISCUSSION

Breed significantly ($P<0.05$) affected the reproductive performance of the rabbits (Table 1). The CAW produced the largest LSB (7.33±0.19) with a corresponding LWB of 155.94±4.34g. This agrees with the earlier submissions of Kabir *et al.* (2012b). The NZW rabbits gave a LSB of 6.89±0.25 weighing 149.25±3.92g, while CHC rabbits gave a LSB of 6.05±0.29 which had the heaviest LWB of 163.68±5.76g. CAW had significantly ($P<0.05$) higher LSB than the CHC and NZW rabbits, respectively. This result agrees with the reports of Irekhore (2007), who stated that California breed produced higher litter size at birth than New Zealand White, New Zealand Black and Flemish Giant breeds. Liang (1996) reported much higher LSB (7.50) and LWW (3.32 kg) in NZW rabbits in China than the value obtained in this study. However, Rastogi (1996) reported lower LSB (5.20) and LSW (4.30) in NZW rabbits in Trinidad.

Similar to the present findings Das *et al*. (2006) reported significantly ($P<0.05$) higher LSW and LWW in the NZW rabbit than the Soviet Chinchilla; while Das and Bujarbarua (2005) found no effect of breed on LWB. Iraqi *et al*. (2006) corroborated with this finding in respect of LSB (6.60) and LSW (4.80) but contradicted with this finding in respect of LWB (429 g) and LWW (2.97 kg) in the New Zealand White in Egypt. Though the LSB obtained in this study compares with the report of Patial *et al*. (1991), it was higher than the report of Odubote and Akinokun (1991). The range of 6.05-7.33 for LSB obtained herein is higher than the LSB values of 4.4 (Iyeghe *et al*., 1996), 4.77 (Fayeye and Ayorinde, 2003), 5.8-6.61 (Irekhore, 2007), 4.27-5.33 (Zalla *et al*., 2007) and 5.69 (Akpa and Alphonsus, 2008). It is also higher than other reported values in literature (Ayorinde, 1997; Oseni *et al*., 1999; Akanno *et al*., 2004). The differences in literature values with those obtained from this study could be attributed to the combined effects of breed and environment; study location, nutrition, management and diseases (Kabir *et al*., 2011a). The CAW rabbits recorded the least WM (20%) while CHC rabbits had the highest WM (24%).

Parity had significant (P<0.05) effect on all the reproductive parameters measured except GL. Litter size at birth (LSB), LSW, LWB, LWW, IKWB and IKWW were significantly (P<0.05) higher in the third parity than in the first and second parities (Table 2). This observation agrees with the earlier reports in literature (Kabir *et al.,* 2012b; Das and Yadav, 2007). Reporting further, Das and Yadav (2007) argued that in the third parity due to maturity of doe more ova were released from the ovary, hence more chance of increasing litter size at birth in third parity than first and second. The present findings however, contradict earlier submissions of Das and Bujarbarua (2005), who reported significant (P<0.05) effect of parity on LWB. Variation in milk production has also been implicated (Paufler, 1985) whereby the NZW females produce less milk in their first lactation than subsequent lactations. This has been advanced as another reason for the low weaning weights observed in the litter of first parity does (Lukefahr *et al*., 1981). Average milk yield of a medium heavy doe on *ad lib* concentrate feed was 250g over a four week period of lactation (Paufler, 1985). Maximum daily milk yield is attained between the 18^{th} and 23^{rd} day after kindling and by the 42^{nd} day it amounts to only 30–40% of maximum yield (Paufler, 1985). All kits in this study were weaned at 35 days postpartum, which was regarded early as compared to the weaning practices in other conventional and commercial setups. Fortun-Lamothe *et al*. (2001) observed that early weaning provides higher viability and faster growth in the weaned rabbits. The peak of milk production in the rabbits is considered to be at the third week of lactation following the reports that lactation increases until the end of the third week of lactation (Kustos *et al*., 1996; McNitt and Lukefahr 1996). Generally, differences in the results obtained from this study with other literature reports could be attributed to differences in breed, management and method of data analysis used.

CONCLUSION

The CAW and NZW rabbits produced higher LSB with a corresponding higher LWB than the CHC rabbits. The CHC rabbits on the other hand, produced the heaviest kits in terms of IKWB and IKWW. Therefore, if the interest of the rabbit farmer is higher LSB and LSW, then CAW and/or NZW should be exploited. Otherwise, CHC is the best breed for individual kit weight at birth and weaning. Rabbit farmers in the Northern Guinea Savannah zone of Nigeria could take advantage of maturity in the third parity does in terms of improved LSB, LSW, LWB and lowered mortality as revealed by the present study.

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Table 1: Effect of breed on reproductive performance of rabbits

	Breed performance		
Parameter	CHC	NZW	CAW
Litter size at birth (LSB)	6.05±0.29^{c}	6.89±0.25^{b}	7.33±0.19^{a}
Litter size at weaning (LSW)	4.58±0.24^{c}	5.39±0.23^{b}	5.86±0.22^{a}
Litter birth weight (LWB) (g)	163.68±5.76^{a}	149.25±3.92^{b}	155.94±4.34^{b}
Litter weaning weight (LWW) (g)	1596.93±66.31^{C}	1764.05±64.36^{b}	1838.40±66.22^{a}
Individual Kit birth weight (IKWB) (g)	27.05±2.14^{a}	21.66±1.61^{b}	21.27±1.39^{b}
Individual Kit weaning weight	348.67±2.77^{a}	327.28±2.14^{b}	313.72±2.55^{c}

(IKWW) (g)			
Gestation length (GL) (days)	30.00±0.04[b]	29.02±0.02[a]	30.00±0.04[b]
Weaning mortality (WM) (%)	24.30±0.11[c]	21.80±0.06[b]	20.00±0.05[a]

SEM = Standard Error of Means; Figures having different superscripts in a row differ significantly (P<0.05)

Table 2: Parity effect on reproductive performance of rabbit

Parameter	Parity		
	First	Second	Third
Litter size at birth (LSB)	5.82±0.13[c]	6.59±0.08[b]	7.42±0.16[a]
Litter size at weaning (LSW)	4.69±0.03[c]	5.12±0.17[b]	6.44±0.14[a]
Litter birth weight (LWB) (g)	154.26±1.36[c]	183.41±2.11[b]	242.96±2.38[a]
Litter weaning weight (LWW) (g)	1460.56±52.52[c]	1577.89±61.58[b]	2065.53±74.82[a]
Individual Kit birth weight (IKWB) (g)	26.50±0.09[c]	27.83±0.07[b]	32.74±0.08[a]
Individual Kit weaning weight (IKWW) (g)	311.42±2.57[b]	308.18±2.10[b]	320.73±2.05[a]
Gestation length (GL) (days)	29.02±0.03	29.05±0.14	29.05±0.06
Weaning mortality (WM) (%)	19.41[b]	22.30[c]	13.20[a]

SEM = Standard Error of Means; Figures having different superscripts in a row differ significantly (P<0.05)

AGB05

GENETIC PARAMETERS OF HYLA F_1 NEW ZEALAND PUREBRED RABBITS USING ANIMAL MODELS

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ABSTRACT
Data on kit weight at different ages of 74 F_1 progeny Hyla purebred New Zealand White rabbits were analyzed to provide estimates of genetic parameters such as heritability, repeatability, genetic and phenotypic correlations. Genetic analysis was estimated using the least square mixed model likelihood and mean weight procedure of Harvey algorithm programme. Heritability estimates of 0.53±0.32, 0.39±0.29, 0.64±0.35, 0.99±0.41, 1.30±0.44 and 0.89±0.39 were obtained for individual kit weight at preweaning ages (birth, 7, 14, 21, 28 and 35 days, respectively). Repeatability

estimates were found to be generally moderate to high. Genetic and phenotypic correlations were positive and moderate to high. The genetic trends for kit weights suggested that mass selection of litters at preweaning ages will be more effective in the improvement of growth traits.

Keywords: Rabbit, kit, heritability, repeatability, correlations,

INTRODUCTION

Hyla rabbits are pedigree breed used to produce grandparent male and female lines for multiplication farms or grand-parent pool in production farms. Estimation of genetic parameters are primordial to the establishment of strategies to be used in Hyla rabbit breeding programmes and the evaluation of response to selection for traits and genetic associations among traits. The understanding of genetic architecture of traits such as growth and body composition has become a primary focus for agricultural and biomedical research (Terčič and Holcman, 2008). The two main tools for genetic improvement are selection and mating system. In order to employ these tools, however, baseline information on genetic parameters -heritability, repeatability, genetic and phenotypic correlations must be determined. The baseline information of the genetic parameters will serve as a guide that enables breeders to decide on the best method of selection to achieve rapid genetic progress. Khalil *et al*. (1988) reported that estimates of heritability for bodyweight were highest at younger ages, declining to the lowest values after weaning and increasing again at older ages in rabbits. Estimates of repeatability for growth traits were reported to be moderate at preweaning ages (Ndjon and Nwakalor, 1998). However, without the knowledge of genetics of imported exotic rabbits population such as Hyla New Zealand purebreds, planned improvement of meat rabbits in Nigeria would be limited. Therefore, this study was undertaken to estimate the heritability, repeatability, genetic and phenotypic correlations of Hyla New Zealand White purebred rabbits under the tropical conditions of Zaria, Nigeria.

MATERIALS AND METHODS

The study was conducted in the Rabbitry of the National Animal Production Research Institute (NAPRI), Shika, Zaria. Shika is located in the Northern Guinea Savannah zone of Nigeria, on latitude 11^0 12' of the equator and longitude 7^0 33' with altitude of about 610mm.
All the rabbits were housed in metallic cages and fed *ad libitum* with pelletized ration containing 20 % crude protein and 2800 kcal ME/Kg. *Tridax procumbens* was also fed as supplementary ration. Vitamin C was added to the drinking water during the hot period. Matings were carried out early in the morning. Inbreeding was avoided in the herd using pedigree information as a guide.

Data on F_1 kit weight were collected at birth, 7, 14, 21, 28 and 35 days respectively using a sensitive metallic scale. The data was analyzed using the least square mixed model likelihood and mean weight procedure of Harvey (Harvey, 1990).
$Y_{ijkl} = \mu + B_1 + S_j + e_{ijk}$
Y_{ijkl} = Observation on K_{th} litter from j_{th} sire in i_{th} breed
μ = Overall population mean
B_1 = effect of i_{th} breed (i= New Zealand white purebred rabbits)
$B{:}S_j$ = effect of j_{th} sire of the i_{th} breed
e_{ijk} = random error

Genetic analysis was computed using the sire variance:
Heritability model

$$h^2 = \frac{4\sigma_s^2}{\sigma_T^2}$$

h^2 = heritability estimate

σ^2_S = variance due to sire

σ^2_T = total variance

Repeatability was estimated as the ratio of variances by summing genetic and permanent environmental variances to phenotypic variance:

$$t = \frac{\sigma^2_s + \sigma^2_{pe}}{\sigma^2_s + \sigma^2_{pe} + \sigma^2_e}$$

σ^2_s = variance due to additive effect

σ^2_{pe} = variance due to permanent environmental effect

σ^2_e = error variance

The repeatability model employed was as follows:

$Y_{ijkl} = u + B_i + P_l + D_{ij} + e_{ijk}$

Y_{ijkl} = animal record

μ = the population mean

B_i = random effect of i^{th} sire

P_l = fixed effect of I^{th} parity (I = 3)

D_{ij} = random effect of j^{th} doe nested within i^{th} sire

e_{ijk} = random deviation of k^{th} litter of j^{th} doe and i^{th} sire, assumed to be independently and randomly distributed (0, 1).

RESULTS AND DISCUSSION

The least squares analysis for the bodyweight are shown in Table 1. The average bodyweight at birth to weaning ranged from 57.97 ± 1.41 - 744.94± 16.66g. The heritability estimates were moderate to high which ranged from 0.39 ± 0.29 - 1.30 ± 0.44. The repeatability estimates were also moderate to high for all the traits (Table 2). Genetic and phenotypic correlation among the traits were found to be generally positive and significant ($P<0.01$) (Table 3). Values of 57.97g reported in this study was higher than the reported value of 55.6 g in France and 54.4g in Republic of Benin by Chrystosome *et al*. (2001) in Hyla pure New Zealand rabbits. Yamani *et al*. (1994) reported kit weight at birth of 46g in Sam Elgar project in Egypt for Hyla rabbits. Weaning weight of 744.94g obtained in this study was heavier than the average weaning weight of 671.11g versus 646.58g of California and New Zealand rabbits obtained by Ferraz and Eler (1994). Values obtained at different ages were slightly lower than the values reported by Nizza and Moniello (2000) for Hyla rabbits and also values reported by Italian hybrids. Moderate to high heritability estimates obtained at different ages indicated high genetic influence. Thus selection for any of these traits should result in genetic improvement of the traits. Heritability value of 1.30 which was above unity might be due to smaller sample size (n = 74) used for this study. This also agrees with the report of Orunmuyi *et al*. (1996) who obtained heritability estimates above 1. Khalil *et al*. (1986) reported that maternal effects resulted in the high heritability estimates obtained for preweaning traits. The moderate to high repeatability estimates showed that great reliability can be put on selection or culling of does and sires based on 2 or 3 records, thus leading to improvement in the productivity of the herd. The moderate to high genetic and phenotypic correlations obtained are consistent with the reports of Garcia *et al*. (1982). In conclusion, genetic improvement of bodyweight could be achieved at rapid rate by selection and culling strategies at early ages in Hyla New Zealand White purebred rabbits under the Nigerian conditions.

Table 1: Least squares means and standard errors of preweaning bodyweight of Hyla purebred rabbits

Period	N	Bodyweight
Birth	205	57.97±1.41
7	195	138.14±2.12
14	172	269.25±5.26
21	160	420.43±8.17
28	147	585.50±11.54
35	142	744.94±16.64

Table 2: Heritability and Repeatability estimates of preweaning bodyweight

Traits (Bodyweight)	h^2	R
Birth	0.77±0.002	0.53±0.32
7	0.21±0.002	0.39±0.29
14	0.25±0.003	0.64±0.35
21	0.43±0.003	0.99±0.41
28	0.36±0.002	1.30±0.44
35	0.33±0.003	0.89±0.39

h^2 = heritability, R = repeatability

Table 3: Genetic (below diagonal) and Phenotypic correlation (above the diagonal) of Hyla purebred rabbits

TRAITS	BW	IK7	IK14	IK21	IK28	IK35
BW		0.61	0.60	0.28	0.40	0.71
IK7	0.79		0.30	0.36	0.54	0.71
IK14	0.63	0.67		0.67	0.63	0.75

IK21	0.39	0.42	0.69		1.00	0.96
IK28	0.20	0.25	0.51	0.85		0.91
IK35	0.09	0.15	0.37	0.68	0.87	

R- Repeatability, H - Heritability, BW- Birth weight, IK- Individual kit weight

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AGB06

EVALUATION OF THE DAIRY POTENTIAL OF FRIESIAN, WADARA AND THEIR CROSSBREDS IN BAUCHI STATE

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ABSTRACT
A total of 244 lactation records of cows that calved from 1976 to 1989 were analysed to evaluate the dairy potential of Friesian, Wadara and their crossbreds. The lactation records consisted of 120, 36 and 88 records of Friesian, Wadara and their crossbreds, respectively. The records were subjected to least square means to determine the mean performance across the breeds. The estimated 305-day milk yield for Friesian, Wadara and their crossbreds were 2,359kg, 879kg and1,643.5kg, respectively. The lactation length for the crossbreds was longest (338 days) compared to 324 days and 186 days obtained for Friesian and Wadara, respectively. 453, 436 and 374 days were obtained as average calving interval for the crossbreds, Friesian and Wadara, respectively. However, the differences in the calving interval were not significant**.**

Keywords: Cow, breed, crossbreds, lactation, calving interval,

INTRODUCTION

In the tropics, dairying involves the use of indigenous breeds of cattle which are characterized by low genetic potential for milk production. Thus, the production of milk and milk products in the tropics are grossly inadequate and this has resulted in importation from temperate countries to sustain the demand for these products, which entails a huge financial investment. Other constraints to remarkable increase in milk production in the topics have been attributed to inadequate nutrition, prevailing diseases and hot climate. However, improvement in the productivity of the animal dairy inducing is needed to meet present and future demands for livestock production. This improvement can be achieved through breeding programmes, nutrition, disease control and provision of conducive environment.

The role of European breeds of dairy cattle in improving the dairy cattle potential of indigenous breeds in the tropics is well known because of their high milk production potential adaptability to modern milking practice and early maturity ability. Therefore, they have been introduced for pure breeding and for crossing with the indigenous breed, in order to blend their high performance with adapt ability in the indigenous tropical breeds (Buvandran *et al*., 1950). The progeny from such cross breeding perform better than pure breed indigenous breeds in dairy production traits.

Attention is focused on increasing the milk yield of indigenous cattle (especially white Fulani) by crossing them with exotic breed (Friesian). However, the number of these reports with respect to other indigenous cattle in Nigeria is few. Thus, the present study involves the evaluation of the dairy potentials of pure bred Friesian, Wadara and their crossbreds in Bauchi State, Nigeria.

MATERIALS AND METHODS

The data used for this study were obtained from records of milking cows kept at the Gubi Dairy Farm of the Bauchi State Integrated Development Authority (BASIDA) Bauchi, Nigeria. The data for the study consisted of a total of 244 lactation records. Out of these. 120 records of 53 cows were from Friesian cross; 36 records of 21 cows from Wadara breed and 88 records of 26 cows were from the crossbreds (Friesian x Wadara).

The Friesian cattle were maintained intensively while Wadara and crossbreds were managed semi intensively. The animals were vaccinated yearly against prevalent diseases and exo-parasites were also controlled by spraying the animals. The cows were hand milked twice daily (morning and evening), with Wadara calves standing closely to their dams to induce milk let-down. Cows were dried off 60 days prior to parturition.

Milk records were compiled weekly on the basis of daily milk weight (morning and evening). From these record books, production records of each cow and for the different lactation numbers were compiled. The total lactation yield and lactation length were calculated for each lactation, while the 305 day yield was estimated for each lactation. The calving intervals were computed from the recorded dates of calving. The days dry were also computed. All these records were used to evaluate the performance of the breed groups.

The records were subjected to least squares means to determine the mean performance across the breeds.

RESULTS AND DISCUSSION

The least square mean (Table 1) revealed that Friesian breed had the highest values of 2359kg for estimated 305-day milk yield. The crossbred had 1643.5kg for estimated 305-day milk yield. The lowest value was obtained for Wadara breed 879kg, for estimated 305-day yield. The crossbred had the longest lactation length (338 day) compared to 324days and 186days obtained for Friesian and Wadara, respectively, although, the differences were not significant. The calving interval averaged 453, 436 and 374 days for crossbred, Friesian and Wadara cattle, respectively. However, the differences in their calving interval were not significant.

Table 1. Least Square Mean (LSM) ± SE of dairy traits across breeds of cattle

	Lactation Length (Days)		**Estimated 305-Day milk yield (kg)**		**Days Dry (Days)**		**Calving interval (Day)**	
	No	**LSM**	**No**	**LSM**	**No**	**LSM**	**No**	**LSM**
Overall Mean	244	318	244	1904.8	146	117	156	421
Breed	120	324.4a ± 24.0	120	2359.3a ± 229.4	66	60 ± 33.4	66	436 ± 39
Friesian								
Wadara	36	186.4b ± 27.3	36	879.9c ± 261.4	15	117.7 ± 39.5	17	374 ± 46.5

Friesian x Wadara	88	338.1a 27.2	±	88	1643.5b ± 250.0	65	98 ± 31.5	70	453 ± 34.6

The results of this study revealed that Friesian breed is better than the crossbreds and Wadara in estimated 305-day yield, which was highly significantly (P< 0.01) different. This is an indication that dairy performance is a function of both the genetic composition of the animal and the environment since Friesian breed is known for their high milk potential under good feeding and management. The crossbred performed better in milk production than the indigenous Wadara cattle which had the lowest lactation yield. This observation agrees with the findings of earlier researchers (Kiwuwa *et al*., 1983 and Letenneur, 1983).

The average 305-day yield estimated for Friesian in this study is higher than that reported by Ibeawuchi (1987), but lower than that reported by Maroof and Tahir (1990). The estimated 305-day yield for Wadara was similar to that obtained for Bunaji (Knudsen and Sohael, 1990). The estimated 305-day yield for the crossbreds is higher than the indigenous Wadara but lower than that reported by Ibeawuchi (1987). The lactation length obtained for Friesian is similar to that reported in Kenya (Meyn and Wikin, 1974) and Nigeria (Sohael, 1984), respectively.

The lactation length obtained for Wadara (186days) falls within 150-200 days reported by Mahadevan (1958). The lactation length obtained for crossbreds is in agreement with that reported by Wijeratue (1970), but higher than the value reported by Sohael (1984). The non-significant difference between the lactation length of Friesian and crossbreds observed in this study is in agreement with the findings of Alba and Kennedy (1985). The increased length of crossbreds over the local breed Wadara in this study is in line with the findings of Sohael (1984).

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AGB07

DETERMINATION OF THE BEST NON-LINEAR GROWTH MODEL FOR INDIGENOUS SHEEP IN NIGERIA.

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ABSTRACT
This study, aimed at determining the best non-linear model for indigenous sheep, was conducted at the University of Maiduguri Livestock Teaching and Research Farm, Maiduguri. Weekly body weights (1-20 weeks) obtained from 51 Yankasa crossbred lambs were fitted to three non-linear models; Gompertz, Logistic and Monomolecular. The goodness of fit statistics; Coefficient of determination (R^2), Mean Square Error (MSE), Standard Deviation (SD) and Akaike Information Criteria (AIC), in addition to model parameters were used for model comparison. The age at Point of Inflection for the Gompertz and Logistic were 5.33 and 7.97 weeks, respectively with corresponding weights of 8.53 and 9.87kg. The asymptote weights of the Gompertz, Logistic and Monomolecular models were 23.191, 19.749 and 39.876kg, respectively with corresponding R^2 values of 0.9907, 0.9909 and 0.9913. The Monomolecular had the least values (3.6596, 1.9130 and 238.73) of MSE, SD and AIC while the Logistic had the highest (3.6861, 1.9199 and 240.03). Based on these statistics, the monomolecular fitted the data better than the other models. Generally, residual variations were higher at early than later ages, though the Gompertz and Logistic models overestimated the early weights more than the Monomolecular and predictions may be more accurate at later than early ages. Monomolecular is thus the best model for describing growth of indigenous sheep in Nigeria.
Key words: Growth, non-linear, models, crossbred Yankasa lambs

INTRODUCTION

The world population of sheep and goats increased from 1.35 billion in 1961 to 1.94 in 2006 (FAOSTAT, 2008). Africa has a population of over 205 million sheep representing more than 17% of the world's total (FAO, 1990). According to the Federal Department of Livestock, sheep population estimate in Nigeria as at 2009 was 34.69 million (FDL, 2010). Sheep with their small body size, high productive capacity and rapid growth rates are ideally suited to production by resource-poor smallholders. It is thus a very important animal genetic resource in Nigeria.

Growth is one of the most important characteristics of farm animals and has been investigated for many years (Topal *et al.*, 2004; Lambe *et al.*, 2006; Keskin and Daskiran, 2007; Kum *et al.*, 2010). It is an increase in body size of animals per unit time and influenced by genetic and environmental effects (Kucuk, 2004). The scientific analysis of growth requires mathematical models running with

data obtained over periods (Ozdemir and Dellal, 2009). Growth has been measured at various intervals; such as weekly (Kocabas *et al*., 1997), bi weekly (Kor *et al*., 2006), monthly (Akbas *et al.,* 1999; Tekel *et al.,* 2005; Keskin and Daskiran, 2007) and once in three months (Bilgin *et al*., 2004). A typical growth curve can be divided into two phases, an early phase where the weight gain rate increases and a later phase where the weight gain rate decreases (Trangerud *et al*., 2007).
Growth curves have been used to estimate mature body weight and increase in live weight in goats and sheep by many researchers (Topal *et al*., 2004; Kor *et al*., 2006; Lambe *et al*., 2006; Keskin and Daskiran, 2007; Kum *et al*., 2010). They can also be used for early selection of animals as they provide prediction of future growth at any age (Tekel *et al*., 2005). Linear and non-linear models have been used to describe growth in animals. Non-linear models have commonly been preferred, since animals reach asymptotic body weight at a certain age (Akbas *et al*., 1999; Topal *et al.,* 2004; Tekel *et al.,* 2005; Kor *et al*., 2006; Keskin and Daskiran, 2007). Tekel *et al.* (2005) reported that some non-linear models used in explaining lifetime weight and age relationship of animals are Logistic and Gompertz, Richards, Weibull and Monomolecular. These authors observed that the best growth models in predicting change of body weight of Awassi male lambs were Gompertz and Logistic models with equal determination coefficients of 98%. Akbas *et al.* (1999) stated that Gompertz growth model with coefficients of determination of 99.28 and 99.63% in Kıvırcık and Daglic breeds was the best growth model. In contrast, Kucuk and Eyduran (2010) reported the best model for determination of growth in the Akkaraman and its crossbred lambs to be Monomolecular. Since sheep are among the most reared and consumed animals in Nigeria, it is important to determine the best growth model, which can explain weight and age relationships. Growth models have been use extensively in many regions and in different species to describe growth, but few are in Nigeria. The aim of this study therefore was to determine the best growth model for crossbred Yankasa lambs in Nigeria.

MATERIALS AND METHODS

The study was conducted at the University of Maiduguri Livestock Teaching and Research Farm, Maiduguri, Borno State. Maiduguri is located within the Sahelian region of West Africa on Longitude 11.38° North and Latitude 32.77° East and 354 m above sea level (Alade *et al.,* 2008).

Maiduguri experiences a short rainy season (2-4months) usually between June and September. There is extreme dryness during the rest of the year. Average annual rainfall is estimated at 645mm with monthly (July, August and September) estimates of 138.12mm, 198.6mm and 157.4mm, respectively. Based on the temperature of this area, the months are grouped into three distinct seasons; hot dry (February- May), wet (June-September) and dry cold (October-January). The state has a relative humidity of 5-45%, which increases from dry to wet season. The hot dry season has a temperature range of 39.8-40.7^{o}C; during the wet season it can fall to 31.0^{o}C.
The management of the experimental animals was generally semi-intensive. The animals were allowed to graze twice daily (morning and evening) in a range of up to 86 ha though, local farmers carried out seasonal cultivation of annual crops in some portions. Species of plants found in the area included *Acacia obtusifolia, Strigal asiatical, Ziziphus macronatal* etc. Few days to lambing pregnant ewes were isolated and housed in a well-littered lambing pen. After parturition, all necessary cleaning and identification processes were observed. Newly born animals were housed together with their ewes under close observation for 24 h to ensure colostrum feeding. Ewes were allowed to graze leaving behind their lambs after two weeks

The data collected were for 51 Yankasa crossbred lambs. Body weight was recorded weekly for each animal from 1 – 20 weeks of age. The data collected were analysed using non-linear regression procedure of Statistix 9.0. The goodness of fit statistics, coefficient of determination (R^2), Mean Square Error (MSE), Standard Deviation (SD) and Akaike Information Criteria (AIC), in addition to model parameters were used for model comparison. Growth curve functions were fitted

individually to the observed data by using Levenberg-Marquardt nonlinear least-squares algorithm in Statistix 9.0. During the iteration procedure, when any parameter value at a current iteration did not change in the successive iteration, the procedure stopped and it was assumed that the convergence criterion of 1.0E-05 was attained.
The models fitted were as follows:
Gompertz :

$$W(t) = A*\exp(-B*\exp(-k*t))$$

Logistic:

$$W(t) = A*(1 + B*\exp(-k*t))^{-1}$$

Monomolecular :

$$W(t) = A*(1 - B*\exp(-k*t))^{1}$$

For each model, W_t is the body weight (kg) of sheep at t week(s) of age (t = 1, 2,…, 20); A, B and k are model parameters: A is asymptotic weight when time goes to infinity; B is a scaling parameter (constant of integration), which is related with initial values of W, and k is maturing rate.
Weight and age at the Point of Inflection (POI) were calculated as **W = A/e** and **t = ln(B)/k**, respectively for Gompertz and **W = A/2** and **t = ln(B)/k** for Logistic. e is base of natural logarithm or Eulerian number (2.71828). The monomolecular model has no inflection point.

RESULTS AND DISCUSSION

Growth parameters, derivatives and goodness of fit criteria for different models fitted to live weight data of crossbred Yankasa lambs are presented in Table 1. The asymptote weights of the Gompertz, Logistic and Monomolecular models were 23.191, 19.749 and 39.876 kg, respectively. Based on asymptotic weight, the Monomolecular ranked first, followed by the Gompertz and then the Logistic. The asymptote weights obtained from the models are attainable by crossbred Yankasa lambs but lower than those reported by Lambe *et al.* (2006) and Kum *et al.* (2010) for Texel and Scottish black face and, Norduz lambs. The difference could be because the mature weights of the breeds may be higher than that of the Yankasa cross breeds. In addition, differences could be due to genotype and environmental variations. The trend in terms of ranking of models based on asymptote weights was however similar to that of Kucuk and Eyduran (2009) in Akkaraman crossbreds.
Coefficients of determination have been used to evaluate the goodness of fit of models in some studies (Lewis *et al*., 2002; Topal *et al*., 2004). Models with the highest R^2 and lowest MSE values have been accepted as best fitting (Tedeschi, 2006). The coefficients of determination (R^2) for the different growth models (Gompertz, Logistic and Monomolecular) were 0.9907, 0.9909 and 0.9913, respectively. Kucuk and Eyduran (2009) and Kum *et al*. (2010) also reported high R^2 values in lambs using the same models. High R^2 for all the models implied, they all fitted the data adequately. This is buttressed by Figure 1, where the points on the curves for all models were very close at most ages. All the growth models presented similar prediction patterns at the same stages of growth. They under- or overestimated the body weight to a greater or lesser extent. However, they all provided less accurate predictions at the beginning of the growth curve and predictions were more accurate after 6 weeks of age. Forni *et al.* (2009) made similar observations.
When Mean Square Error (MSE), Standard Deviation (SD) and AIC were used for comparison, the Monomolecular had the least values (3.6596, 1.9130 and 238.73) while the Logistic had the highest (3.6861, 1.9199 and 240.03). Based on these statistics, the monomolecular fitted the data better than the other models. Bilgin *et al*. (2004), Kor *et al*. (2005) and Kucuk and Eyduran (2009) also made similar observation based on MSE for Morkaraman lambs, Akkeci kids and Akkaraman lambs,

respectively. The age and weight at POI for the Gompertz were 5.33 weeks and 8.53 kg respectively, while the corresponding values for the Logistic were 7.97 weeks and 9.87 kg. These values indicate the ages and weights where the estimated growth rate changed from an increasing to a decreasing function.

The observed, predicted and residual weights for the different growth models of indigenous sheep are presented in Table 2. The range of residuals for the Gompertz, Logistics and Monomolecular from 2 - 20 weeks were 0.03 - 0.61, 0.02 - 0.66 and 0.00 - 0.56, respectively. The corresponding values for percentage deviations were 0.21 – 6.59, 0.21 – 7.08 and 0.02 – 5.99%. Residuals and percentage deviations were generally low except in the first week; an indication that the models fitted the weight data adequately. Among the models, the monomolecular had a narrower range of residual and percentage deviation, indicating that it might have a better fit than the other models. It was also observed that no model described early periods of growth as adequately as the later ones. However, the Gompertz and Logistic models overestimated the early weights more than the Monomolecular. Generally, residual variations were higher at early than later ages. Brown *et al*. (1976) made similar observations and concluded that predictions may be more accurate at later than early ages.

CONCLUSION

It could be concluded from this study that the Gompertz, Logistic and Monomolecular models all fitted the live weight data of the crossbred Yankasa lambs . However, the best model was the Monomolecular based on higher coefficient of determination and lower MSE. This is followed by the Gompertz.

Table 1. Growth parameters, derivatives and goodness of fit criteria for different models fitted to live weight data of crossbred Yankasa lambs

Model parameters	Gompertz	Logistic	Monomolecular
A	23.191	19.749	39.876
B	0.3731	0.9347	0.0179
C	0.070	0.1173	-7.7822
POI (age in weeks)	5.33	7.97	-
POI (weight in Kg)	8.53	9.87	-
R^2	0.999	0.999	0.999
MSE	3.6734	3.6861	3.6596
SD	1.9166	1.9199	1.913
AIC	239.4	240.03	238.73

A = Asymptotic weight, B = Integration constant, C = Maturing rate, R^2 = Coefficient of Determination, MSE= Mean Square Error, SD= Standard Deviation, AIC= Akaike Information Criteria, POI = Point of inflection

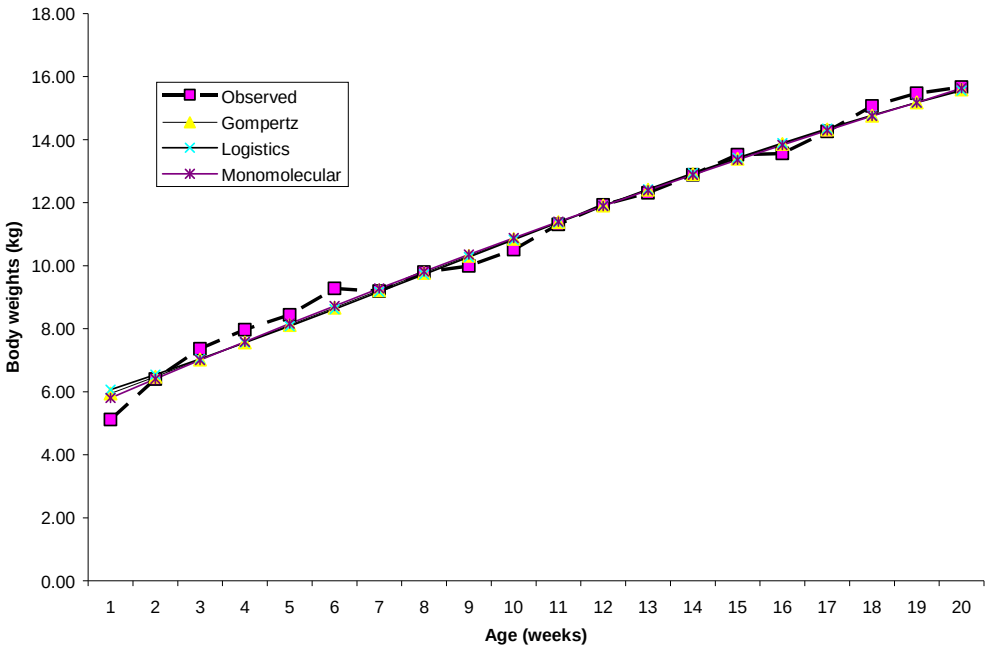

Figure 1. Growth curves for indigenous sheep from the different models

Table 2. The observed, predicted and residual weights for the different growth models of crossbred Yankasa lambs

Age	observed	Gompertz			Logistics			Monomolecular		
(week)	Weights	P	R	D	P	R	D	P	R	D
1	5.12	5.95	0.83	16.14	6.06	0.94	18.40	5.80	0.68	13.28
2	6.40	6.48	0.08	1.19	6.54	0.14	2.25	6.41	0.01	0.15
3	7.36	7.02	-0.34	-4.66	7.04	-0.32	-4.34	7.00	-0.36	-4.84
4	7.97	7.56	-0.41	-5.09	7.56	-0.41	-5.20	7.59	-0.38	-4.80
5	8.44	8.12	-0.32	-3.85	8.08	-0.36	-4.22	8.16	-0.28	-3.31
6	9.28	8.67	-0.61	-6.59	8.62	-0.66	-7.08	8.72	-0.56	-5.99
7	9.19	9.22	0.03	0.33	9.17	-0.02	-0.21	9.28	0.09	0.94
8	9.80	9.77	-0.03	-0.31	9.72	-0.08	-0.80	9.82	0.02	0.20
9	9.99	10.32	0.33	3.26	10.27	0.28	2.84	10.35	0.36	3.64
10	10.51	10.85	0.34	3.27	10.82	0.31	2.99	10.88	0.37	3.50
11	11.31	11.39	0.07	0.66	11.37	0.06	0.51	11.40	0.08	0.75
12	11.93	11.91	-0.03	-0.21	11.90	-0.03	-0.23	11.90	-0.03	-0.27
13	12.31	12.41	0.10	0.84	12.43	0.12	0.94	12.40	0.08	0.69
14	12.88	12.91	0.03	0.24	12.93	0.05	0.42	12.88	0.00	0.02
15	13.52	13.40	-0.13	-0.92	13.42	-0.10	-0.71	13.36	-0.16	-1.16
16	13.56	13.86	0.30	2.24	13.90	0.33	2.47	13.83	0.27	2.01
17	14.26	14.32	0.06	0.42	14.35	0.09	0.60	14.30	0.04	0.25
18	15.07	14.76	-0.31	-2.06	14.77	-0.30	-1.96	14.75	-0.32	-2.13
19	15.47	15.19	-0.29	-1.84	15.18	-0.29	-1.89	15.18	-0.30	-1.91
20	15.67	15.59	-0.08	-0.49	15.56	-0.11	-0.70	15.63	-0.04	-0.23

P= Predicted weight, R= Residual weight, D = percentage deviation from observed weight

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AGB08

HERITABILITY ESTIMATES OF LITTER BODY WEIGHT IN A POPULATION OF NON-DESCRIPT BREEDS OF DOMESTIC RABBITS RAISED IN A HUMID TROPICAL ENVIRONMENT OF SOUTHERN NIGERIA

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ABSTRACT
Heritability of litter body weight traits at various ages were estimated in a population of domestic rabbits raised in Asaba, Southern Nigeria using the paternal and maternal half-sib method. Litter traits studied were litter bodyweight at birth (LBW), litter weight at 7days (7BW), litter weight at 14days (14BW), litter weight at 21days (21BW) and litter weight at weaning (42BW). The variance components and heritability were obtained using standard expressions in a hierarchal design. The data consisted of 224kits obtained from a mating involving fifteen dams and five sires in three parities each from sires and dams. Variance components were higher from dam components than sire components except for litter birth weight (LBW) and litter weaning weight (LWW). Heritability of LBW, 7BW, 14BW, 21BW and LWW from sire (dam) components were 0.84(0.34), 0.28 (0.92), 0.90(0.96), 0.33(0.63) and 0.79(0.74), respectively. The moderate to high heritability estimates of litter body weight suggest improvement of these traits by simple selection method such as one based on individual performance or pedigree records.

Keywords: Heritability, hierarchal, litter, bodyweight, half-sibs

INTRODUCTION
Rabbits have a number of characteristics that would make them particularly suitable as meat-producing animals, especially when compared with other herbivores. Rabbits could contribute significantly in solving the problem of meat shortage (Lebas, 1983). One of the pre-requisites for genetic improvement is knowledge of genetic parameters for important economic traits (Akanno and Ibe, 2005). As rabbits can be fed with forages and do not compete directly with humans for grains, they can be a very important source of high quality animal protein in developing countries (1raqi, 2003). Heritability is the proportion of the total phenotypic variance (VP) attributable to effect of genes (Falconer, 1989). Heritability of litter traits for domestic rabbits in the humid tropics have been reported to range from low, moderate to high when estimates are obtained using paternal and maternal half-sib methods (Sorhue *et al*., 2013; Ibrahim *et al*., 2007; Akanno and Ibe, 2005). Nofal *et al*. (2008) reported that estimate of variance is highest for litter weight at weaning (6 weeks) of age which may be due to mothering ability, which is continued to the end of suckling period. There is need for more research in this area of animal breeding in other to predict selection response. This study was therefore designed to estimate the variance components and heritability of litter body weight traits in this rabbit population from birth to weaning.

MATERIALS AND METHODS

The study was conducted at the rabbitry unit of the Department of Animal Science, Delta State University, Asaba Campus, Asaba, Nigeria. Asaba Campus is located at latitude 06^0 14'N and longitude 06^0 49'E. It lies in the tropical rainforest zone, characterized by seven months of rainy season between April and October punctuated by a short break in August with annual rainfall of 1500mm-1849mm (NIMET, 2005).

Kits obtained from a mating involving fifteen dams and five sires. The experimental stocks were Non-descript breeds of domestic rabbits (commercial rabbit).The parental stock produced 224 kits which were weaned at 42days of age.

There were five (5) pens of 90x60x65(cm) for the five (5) sires, five (5) pens of 90x80x65 for the fifteen (15) dams with 3 dams per pen and three (3) pens of 100x60x65 for dams and litters after kindling. The design was a balanced design with equal numbers of sub-class. It was a two way nested classification, dams were nested between sires and litters were weaned at 6weeks (42days).

Feed and water were provided *ad libitum* throughout the period of the experiment. The rabbits were raised in wooden cages with wire mesh. The feed used was commercial pellets with forages and grasses supplied to meet the nutrient required by the experimental animals. Prior to the experiment, the feed's proximate composition was determined to ensure conformation with the NRC standard at the Nutrition and Biochemistry Laboratory of the Department of Animal Science, Delta State University, Asaba Campus.

Litter body weight traits were collected from progeny of a particular dam, mated to a particular sire separately. The kits of a certain litter from a certain Dam mated to a certain sire were marked. The litter traits were measured from birth to weaning at 42days of age. There were three parities per dam with the same sire.

The following parameters were measured and data collected included:

1. Litter birth weight (LBW)
2. Litter weight at 7days (7BW)
3 Litter weight at 14days (14BW)
4 Litter weight at 21days (21BW)
5. Litter weight at weaning (LWW).

Litter weight was collected with the aid of a weighing scale.

All data collected were subjected to analysis of variance using SAS (2001). Variance components and Heritability were estimated using standard expressions given by Becker (1984).

The statistical model used for the analysis of variance was

$Y_{ijk} = \mu + Si + Dij + e_{ijk}$

where:

Y_{ijk} = record of the k-th progeny of the Jth dam mated to the I-th Sire.
μ = the overall population mean
Si = the random effect of the i-th sire
Dij = the random effect of the jth dam mated to the i-th sire.
Eijk = the error term.

Heritability was estimated from sire and dam components as follows:

$h^2s=4\sigma^2s/ (\sigma^2s + \sigma^2d +\sigma^2w)$

$h^2d= 4\sigma^2d / (\sigma^2s + \sigma^2d + \sigma^2w)$

where:

h^2s = Heritability from sire
h^2d = Heritability from dam
σ^2s = Sire variance component

$\sigma^2 d$ = Dam variance component
$\sigma^2 w$ = Within progeny variance component

RESULTS AND DISCUSSION

Table 2. Proximate composition of experimental diets

	Pelletized commercial growers mash	Guinea grass	*Tridax procubens* stem	*Tridax procubens* leaf
Moisture	-	66.20	84.30	87.55
Crude protein	15.4	12.30	36.04	35.16
Ash	9.4	14.50	5.17	2.49
Ether extract	4.5	3.15	1.05	5.02
CHO	62.0	52.20	42.40	52.12
crude fiber	8.7	18.04	16.91	5.88

Table 3. Means and standard errors for litter size and body weight traits of domestic rabbits

Traits	No of observation	Mean		S.E
LBW	195	0.05	±	0.04
7BW	187	0.10	±	0.07
14BW	181	0.19	±	0.12
21BW	179	0.28	±	0.13
42BW	174	0.59	±	0.02

LBW- litter-birth-weight, 7BW-7day bodyweight, 14BW - 14day body weight, 21BW -21day body weight, LWW - 42 day body weight.

Table 4.Variance components for litter body weights traits of sire (σ_s^2), dam (σ_d^2), progeny (σ_e^2) and total phenotypic variance (σ_p^2)

Traits	σ_s^2	σ_d^2	σ_e^2	σ_p^2
LBW	0.0020	0.0008	0.0068	0.0096
7BW	0.0027	0.0089	0.0271	0.0387
14BW	0.0040	0.0042	0.0094	0.0176
21BW	0.0003	0.0007	0.0032	0.0042
LWW	0.0022	0.0020	0.0067	0.0109

σ_s^2- sire component of variance σ_d^2 –Dam component of variance σ_e^2-progeny component of variance σ_p^2- Total phenotypic variance.

Table 5. Heritability and standard errors of heritability for litter body weight traits

Traits	$h^2\sigma s$ + se	$h^2\sigma d$+ se
LBW	0.84 ± 0.24	0.34 ± 0.64
7BW	0.28 ± 0.65	0.92 ± 0.13
14BW	0.90 ± 0.15	0.96 ± 0.07
21BW	0.33 ± 0.64	0.63 ± 0.48
LWW	0.79 ± 0.31	0.74 ± 0.19

$h^2\sigma s$ – paternal half-sib heritability $h^2\sigma d$-Maternal half-sib heritability se-standard error of heritability.

The proximate composition of the experimental diet is presented in Table 2. The crude protein level ranged from 12.30% for guinea grass to 36.04% for the *tridax procubens* stem while the ash content ranged from 2.49 for *tridax procubens* leaf to 14.50% for guinea grass. Crude fiber content varied from 5.88 for *tridax procubens* leaf to 18.04 for guinea grass.

Means and standard errors for litter body weight traits are presented in Table 3. The mean values ranged from 0.05±0.04 for litter birth weight (LBW) to 0.59±0.02 for litter weaning weight (LWW). The variance components for litter body weight traits in this study ranged from 0.0003 to 0.004 (sire), 0.0007 to 0.009 (dam) and 0.003 to 0.027 (progeny) as shown in Table 4. Heritability estimates for dam component were higher than the corresponding heritability from sire components for the traits studied except for LBW and 42 BW, respectively. This may be due to the fact that Sire components of variance were lower than the corresponding dam component of variance for those traits except for LBW and LWW. Heritability estimates for dam component ranged from 0.34 for LBW to 0.96 for 14BW. Heritability of LBW, 7BW, 14BW, 21BW and LWW from sire (dam) components were 0.84(0.34), 0.28 (0.92), 0.90(0.96), 0.33(0.63) and 0.79(0.74), respectively. The high standard errors obtained in the estimate of heritability could be due to the low accuracy of sire and dam component of variance in the traits studied as well as the sample size.

The variance components obtained in this studied is comparable to earlier reports by Sorhue *et al*. (2013) for litter size traits at birth and weaning. Litter Body weight traits using sire components and dam component were moderate to high. Moderate heritability values of 0.37 and 0.34 were also reported by Lukefahr *et al*. (1983) and Okoro *et al*. (2011) using paternal half sib method for litter body weight (LBW) at birth. The values of 0.84, (0.34), 0.28 (0.92), 0.90 (0.96), 0.33 (0.63) and 0.79 (0.74) reported for LBW, 7BW, 14BW, 21BW and LWW for both sire and dam component are higher than 0.01 reported by Youssef *et al*. (2008) using animal model.

The estimate of 0.34 for LBW obtained in the present study is the same with that reported by Okoro *et al*. (2011) using the paternal half sib method. The moderate heritability of 0.28 for 7BW is lower than 0.49 estimated by Ibrahim *et al*. (2007) using paternal half-sib method while the high heritability estimate from maternal half-sib of 0.92 for 7day bodyweight was far higher than the value of 0.17 reported by Ibrahim *et al*. (2007) using maternal half sib method.

Literature on 14BW heritability was scarce but high heritability values of 0.90 and 0.96 from sire and dam components were recorded and are comparable to estimates of 0.94 (paternal half-sib heritability) and 0.96 (maternal half-sib heritability) reported by Sorhue *et al*. (2013) for litter size at weaning. The moderate to high values for 21BW heritability of 0.33 for sire and 0.63 for dam component of variance is in line with values reported by Ibrahim *et al*. (2007) using paternal half-sib and maternal half-sib methods, respectively. However, these values are higher than estimates for 21BW reported by Rastogi *et al*. (2000), Iraqi (2008) and Youssef *et al*. (2008) with values of 0.08, 0.05 and 0.21 respectively using different animal models. The high values of heritability for LWW of 0.79 and 0.74 for sire and dam component are similar to 0.66 obtained by Castellini and Panella (1988) but far higher than reports from Youssef *et al*. (2008) and Niranja *et al*. (2010) with values of 0.23 and 0.25 using single trait and multi-trait animal models, respectively. Values out of heritability range of 2.10 using paternal half-sib method was recorded by Ibrahim *et al*. (2007)\ and Okoro *et al*. (2011). Ibrahim *et al*. (2007) also reported very high value of 1.26 for LWW heritability using maternal half-sib method which is higher than estimates in the present study. Discrepancies between the estimates in this study and those reported in literature are expected since heritability values depend on the genetic make up of the stocks, management and climatic conditions and period of study as well as differences in data size and method of analysis (Khalil *et al*., 1986) as well as the variance that exist in the population. Moderate to high heritability values indicate strong contribution of additive genes in the expression of these traits and suggest possible improvement of litter body weights in rabbits in the experimental population by use of either pedigree or individual selection method.

CONCLUSION

The heritability estimates of litter body weight were moderate to high and were consistent. Moderate and high genetic improvement is possible through selection on the basis of individual or pedigree testing methods. Moderate to high heritability values imply that selection would be efficient to improve these traits and the characters are susceptible to genetic influence.

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AGB09

HERITABILITY AND REPEATABILITY ESTIMATES FOR GROWTH AND BODY LINEAR MEASUREMENTS IN MALE AND FEMALE BROILER LINES

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ABSTRACT
A total of 350 broiler chickens, which consisted of 100 each for sire and dam line and 75 each for sire control and dam control, , kept at the National Animal Production Research Institute (NAPRI) Shika, Zaria were used. The parameters considered were body weight (BW), body length (BL), Body girth (BG), Thigh length (TL), keel length (KL) and Shank length (SL) which were measured fortnightly. The results of heritability (h^2) estimates obtained for BW and body linear measurements from 2 to 8 weeks ranged from low (0.05±1.63) to high (0.58±0.73) values. The estimate obtained for TL at 8 weeks was high (0.81±1.27) in sire line while a range from low (0.04±1.50) to high (0.90±0.11) values was obtained in dam line. The h^2 estimates for sire control and dam control also ranged from low to high values. The repeatability (R) estimates for BW were generally low for both the selected lines and the control, ranging from 0.001 to 0.193 across all ages. The R for body linear measurements were also low though moderate to high values for BG at 2 weeks (0.35) and BG at 4 weeks (0.25) for dam line, keel length at 6 week (0.27) for sire line and keel length at 6 weeks (0.29) for dam line were obtained. The results obtained from this study were in line with literature reported values for broiler chickens. Any observed variation in estimates of h^2 and R could be attributed to line effects, method of estimation and sampling error due to small data size. The results finally indicated that the population of collapsed Anak and Hubbard broilers into sire and dam line as well as sire and dam control, kept at NAPRI were stable. Furthermore, variations abound for exploitation in the measured traits as interbreeding within and without lines continue.
Keywords: Broiler chickens, growth, genetic parameters, sire, dam, control line

INTRODUCTION
The performance of broiler birds is determined by its genotype and environmental factors (Boukwamp *et al.,* 1973; Edward and Denman, 1975). In animal breeding, it is imperative to determine breeding value with the objective of classifying the best individuals that will be the parents of the next generation, and quantifying its contribution to the genetic gain (Grosso *et al.,* 2010). Selection of better breeds or strains has gone a long way in producing quick and rapid transformation in animal proteins supply (Nawathe and Lamorde, 1987). Some of the genetic parameters used for selection by breeders are repeatability, heritability and genetic and phenotypic correlations.

According to Falconer (1989), fewer records are required to realize a high expected response from selection in traits with high repeatability estimates while those with low repeatability estimates will require larger number of records. Gaya *et al.* (2006) had shown genetic correlation between body weight at different ages and carcass traits and suggested that direct selection for body weight at 38 and 42 days of age could produce indirect genetic gain for breast muscle, leg and eviscerated body weight. The authors further indicated that heritability estimate for body weight at different ages for evaluation of genetic variability and considerable direct additive genetic effects seemed to exist in the expression of body composition traits. Kabir *et al.* (2006*)* reported that mean values of body weight at various ages showed good performance. They also noted that heritability estimates observed for body weight and shank length decreases with increasing age of birds. The National Animal Production Research Institute (NAPRI) Shika Zaria, recently collapsed the population of

Anak and Hubbard broilers, leading to the formation of two lines of sire and dam as well as two control of sire and dam, respectively. This was due to exhaustion of the additive genetic variation. Periodic evaluation of such population is pertinent and hence this study, which was designed to estimate the genetic parameters (h^2, R) for growth and body linear measurements in sire and dam broiler lines.

MATERIALS AND METHODS

The research was conducted at the Poultry Research Unit of National Animal Production Research Institute (NAPRI) Shika, Zaria, Kaduna State. Shika lies between latitude 11^0 12`N, longitude $7^0$ 33`E and at altitude of 640m above sea level. The area falls within the Northern Guinea Savannah having an average annual rainfall of 1100mm. Detailed description of the experimental site was given by Kabir *et al.* (2010).

Total number of 350 broiler birds was used for this study, which comprised of 100 each of sire line and dam line, 75 each of sire control and dam control, obtained from a collapsed population of Hubbard and Anak broiler birds at the National Animal production Research Institute (NAPRI). They were kept in deep litter system for a period of eight weeks. Feed and clean drinking water were provided *ad-libitum.* Broiler starter mash containing crude protein of 24.96% and ME of 2767.62Kcal/kg was fed to the chicks for the first four weeks while broiler finisher mash with crude protein of 23.23 and ME of 2839.64 Kcal/kg was fed for the last four weeks. All rations were formulated and mixed at the feed mill of the Institute (NAPRI), the composition is as shown in Table 1.

Table 1. Composition of the experimental diets

	PERCENTAGE	
Ingredients	Broiler Starter	Broiler Finisher
Maize	45.00	52.00
Groundnut cake	30.00	30.00
Soyabean meal	15.00	10.00
Maize offal	4.60	2.50
Lime stone	3.00	1.50
Bone meal	1.50	3.00
Salt	0.30	0.30
Lysine	0.15	0.20
Methionine	0.15	0.20
Premix*	0.25	0.30
Total	100	100
Calculated analysis		
ME Kcal/kg	2767.62	2839.64
Crude Protein	24.96	23.23
Crude Fibre	3.82	3.45
Ether Extract	5.16	5.22
Methionine	0.47	0.50
Methionine + Cysteine	0.85	0.86
Lysine	1.20	1.13
Calcium	1.75	1.74
Available Phosphorous	0.90	0.89

*The premix used in this study supplied the following nutrients (Kg/diet): Vit A: 20,000,00, IU Vitamin E. 500 I, thiamin (B) 2,000mg, Riboflavin (B2) 3500mg, Vit (B3) 20000mg, Panthothenic acid (B5) 6,600ml, Pyridoxine (B6) 3600mg, Vitamin (B12) 20mg, folic acid 400mg, Vitamin 20000mg, Methionine 10,000mg, antioxidant 12.5g, Ca 18%, P.Mn 8.0g, Zn ug Iodine 0.12g.

The weight of individual birds and other body linear measurements were taken every two weeks for a period of eight weeks using a measuring scale in grams (g) and measuring tape in centimeter (cm). The body linear measurements considered were body length (BL), body girth (BG), thigh length (TL), keel length (KL) and shank length (SL). Data collected were subjected to variance components of SAS (2002) and their heritability (h^2) and repeatability (R) were estimated using the expression described by Falconer (1989). The formulae used for h^2 and R estimation are given below:

Heritability: $$h^2 = \frac{4\delta^2 s}{\delta^2 T}$$

Where; h^2 = heritability estimates, $\delta^2 s$ = Variance due to sire, δ^2_T = Total variance

Repeatability: $$Rs = \frac{\delta^2 ts}{(\delta^2 t + \delta^2 te)s}$$

Where; $\delta^2 ts$ = individuals variance component; $\delta^2 e$ = variance due to error;
$(\delta^2 t + \delta^2 e)s$ = total phenotypic variance

RESULTS AND DISCUSSION

Estimates of h^2 and R for body weight and body linear measurements are presented in Tables 2 and 3. The h^2 estimates ranged from low to moderate for body weight in sire line at 2 (0.07±1.67), 4 (0.18±0.41), 6 (0.19±0.36) and 8 (0.27±1.31) weeks of age, respectively. These estimates agreed with the reports of Siripholvat *et al.* (1995) who reported low h^2 estimates. Adeyinka *et al.* (2004) however obtained moderate to high h^2 estimates for body weight at different ages in naked neck broilers. There was an increasing trend in the estimates of h^2 for body weight with age in sire line, which agreed with the reports of Chambers (1990). The h^2 estimates for body weight in dam line decreases with increasing age of birds (Table 2 and 3). This observation is in line with the report of Kabir *et al.* (2006) who reported similar results in male and female lines of Rhode Island chickens. Differences in h^2 obtained could be attributed to method of estimation, strain or small sample size.

The h^2 estimates for body linear measurements ranged from low to high for dam line, sire control and dam control. This concur with the reports of Singh and Julvan (2007) who reported low to moderate h^2 for body linear measurements in van-cob broiler chickens. The low h^2 estimates obtained in this study for some of the body linear measurements from 2 to 8 weeks of age is in line with the reports of Adeyinka *et al.* (2004) who reported similar results for naked neck broiler chicken.

Low to moderate R estimates for the two lines and two control groups for body weight and body linear measurements across all ages were obtained (Tables 2 and 3). The low to moderate estimates of R obtained in this study disagreed with the earlier result of Kabir *et al.* (2010), who reported higher R of 0.921 to 0.985 for body weight at 2 to 4 weeks of age in broiler chickens. The values for body linear measurements are within the range for body linear measurements (0.170 to 0.962) reported by Kabir *et al.* (2010). The values observed in this study also disagreed with reports of Sola-Ojo *et al.* (2011), who reported high R for body weight (0.99) and body parts measured (0.61 to 0.99) at week 2, 4 and 6 for Arbor Acre broiler strain. The differences in the observed estimates with literature values could be as a result of breed/or line difference and environmental effect. Generally, low R estimates implies that larger numbers of records are required to retain or cull parent chickens as opposed to fewer records required if the R estimates were high.

CONCLUSION

Variations observed in the estimate of h^2 with respect to all the lines are indication of genetic influence on these parameters. Low h^2 obtained for body weight and body linear measurements imply that high environmental effects could be responsible and it means that selection based on individual performance alone may not be desirable. On the other hand, low R estimates implies that lines used in this study have lower ability to repeat their present performance in the future and also high numbers of records are required to realize expected response for selection.

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Table 2: Estimates of h^2 (±SE) and R for BW and body linear measurements at starter phase in broiler chickens

Ages		BW		BL		BG		TL		KL	
(weeks)	Line	R	h^2s	R	h^2s	R	h^2s	R	h^2s	R	h^2s
2	Sire	0.018	0.07±1.67	0.119	0.48±0.94	0.129	0.52±0.87	0.102	0.41±1.06	0.112	0.32±1.
	Dam	0.069	1.27±0.42	0.190	0.76±0.37	0.350	1.40±0.44	0.194	0.78±0.33	0.079	0.31±1.
	S/C	0.084	0.34±1.25	0.021	0.08±1.75	0.045	018±1.56	0.005	0.02±1.86	0.063	0.25±1.
	D/C	0.100	0.4±1.14	0.108	0.43±1.08	0.165	0.66±0.91	0.098	0.27±1.39	0.029	0.12±1.
4	Sire	0.050	0.18±0.41	0.145	0.58±0.73	0.013	0.05±1.63	0.083	0.31±1.19	0.107	0.43±0.
	Dam	0.193	0.77±0.36	0.188	0.75±0.39	0.251	1.00±1.12	0.227	0.91±0.14	0.039	0.16±1.
	S/C	0.030	0.12±1.90	0.021	0.09±1.96	0.006	0.02±2.11	0.032	0.13±1.88	0.015	0.06±2.
	D/C	0.001	0.01±1.89	0.040	0.16±1.59	0.065	0.26±1.84	0.064	0.26±1.84	0.089	0.36±1.

BW=Body weight, BL= body length, BG=Body girth, TL= Thigh length, KL=keel length, SL=Shank length, R=repeatability, h^2=heritability, SE=standard error, S/C=sire control, D/C=dam control.

Table 3: Estimates of h^2 (±SE) and R for BW and body linear measurements at finisher phase in broiler chickens

Ages		BW		BL		BG		TL		KL	
(weeks)	Line	R	h^2s	R	h^2s	R	h^2s	R	h^2s	R	h^2s
6	Sire	0.049	0.19±0.36	-	-	0.032	0.13±1.50	0.058	0.2±1.37	0.271	1.09±0.76
	Dam	0.097	0.32±1.12	0.020	0.08±1.16	0.010	0.04±1.58	0.021	0.08±1.57	0.291	0.90±0.11
	S/C	0.043	0.17±1.68	0.086	0.34±1.40	0.115	0.46±1.09	0.065	0.26±1.50	0.090	0.36±1.30
	D/C	0.037	0.15±1.72	0.047	0.19±1.16	0.069	0.28±1.45	0.041	0.17±1.86	0.111	0.44±1.13
8	Sire	0.069	0.27±1.31	0.161	0.06±1.69	0.101	0.4±1.26	0.202	0.81±1.27	0.077	0.31±1.25
	Dam	0.045	0.18±1.41	0.161	0.64±0.62	0.037	1.49±0.85	0.048	0.19±0.55	0.071	0.28±1.24
	S/C	0.044	0.18±1.66	0.080	0.32±1.37	0.035	0.14±1.74	0.014	0.05±1.92	0.082	0.33±1.36
	D/C	0.013	0.05±1.98	0.048	0.19±1.54	0.040	0.16±1.6	0.048	0.19±1.54	0.007	0.03±1.85

BW=Body weight, BL= body length, BG=Body girth, TL= Thigh length, KL=keel length, SL=Shank length, R=repeatability, h^2=heritability, SE=standard error, S/C=sire control, D/C=dam control.

AGB10

SELECTION RESPONSE OF REPRODUCTIVE TRAITS AT DIFFERENT GENERATION INTERVAL IN QUAIL UNDER THE TROPICAL CONDITIONS OF NIGERIA

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ABSTRACT

A study was conducted to estimate genetic parameters of egg production and reproductive traits in Japanese quail. A total of five hundred and twenty six Japanese quails, made up of three hundred and ninety seven females and one hundred and twenty seven males were used to conduct the study. The response to selection for egg production after two generations of selection was estimated. Egg number (EGN), Egg weight at 12 weeks of age (EWT12), Age at sexual maturity (ASM) and Body weight at 6 weeks of age (BWT6) averaged 46.04, 8.73gm, 39.73days and 163.28gm in generation 1 and the corresponding values for generation 2 are 45.36, 9.06gm, 39.86days and 163.70gm. Percent fertility (Fert %) and percent hatchability (Hatch%) were recorded as, 80.43% and 77.99% for the first generation and the corresponding values for the second generation were 82.05% and 67.14%. Heritability estimates of production traits ranged from low to high (0.05 - 0.96). Egg number (EGN) had a negative correlation with Age at sexual maturity (ASM) (-1.21) but positively correlated with Body weight (BWT) (0.14). Response to selection for egg number was 3.91. There was a highly significantly ($P<0.01$) increase in egg number, from 36.55 at generation zero to 45.36 at the second generation of selection. In conclusion, selection in generation 0 based on egg number to 12 weeks of age improved the egg number and BWT6 in generation 2.

Keywords: Egg number, Heritability, Age at sexual maturity, selection

INTRODUCTION

Poultry production is a fast means of meeting the ever-increasing demand for protein supply, especially in Africa, where intake of protein is relatively low. This is because poultry production has a rapid turnover rate. In other words, several tons of meat and eggs can be produced in a relatively short interval of time. This prompted breeders to put more interest in the breeding of quail, the laying performance of which is relatively high. Over six months laying period, the total egg production in quails was ten times higher than female's body weight, whereas in chicken such a relation is reached only by the production gathered from 12 months (Richtrova, 1999).

The production of Japanese Quails has gained tremendous interest among Nigerian populace especially because of the medicinal value of the egg. Japanese quails are also known for their low caloric values in addition to having quality protein of high biological value (Haruna *et al.,* 1997). Studies using Japanese Quails in breeding experiments have demonstrated that this species offers scientist several advantages in exploring breeding systems and certain applied problems of poultry breeding. Improvement through selection requires estimates of genetic parameters. This study was therefore designed to estimate the genetic parameters of egg production and reproductive traits in Japanese quail.

MATERIALS AND METHODS

The research was conducted at the Poultry Unit of the Animal Science Department, Ahmadu Bello University, Samaru – Zaria. Zaria is geographically located between latitude $11^0$12'N and longitude $7^0$33'E, at an altitude of 610m above sea level. (Google Earth, 2011).

250 birds were bought from National Veterinary Research Institute Jos at two weeks of age. The birds were raised together until four weeks of age before they were sexed. They were made up of 130 males and 120 females. The females were then put in individual cages and tagged according to cage number. 40 sires were randomly selected to meet the mating ratio of 1:3. These formed the base population. The dams were placed in individual cages with one sire mated to three dams by introducing the sire into the cages, with the sire spending one night in each cage. The sires were placed such that half-sib or full sib mating was completely avoided. The birds were fed with starter diets of 2741 Kcal/Kg ME and 26% CP, for the first five weeks of age and then breeder diets of 2990Kcal/Kg ME and 23% CP (Dafwang, 2006). Water and feed were given *ad libitum*.

Fertile eggs were marked according to sire number over a seven-day period. The eggs were incubated for a period of 16 days, 14 days in the setter and 2 days in the hatcher. The setter and hatcher were equipped with separate boxes which were marked according to sire number in order to pedigree hatch the chicks for the first generation. The hatched chicks were brooded in separate boxes marked according to sire number, and then wing banded after 21 days.

Selection of females was based on each hen's production plus the average of its full and half sibs, while males were selected based on the performance of their female sibs. The selection procedure was repeated to produce the second generation. Selection index constructed was based on the type developed by Henderson (1963).

In notational form, the indexes can be written thus:-

$I♀ = (P - \bar{x}) + b_1 (D - \bar{x}) + b_2 (S - \bar{x})$

$I♂ = b_3 (D_1 - \bar{x}) + b_4 (S_1 - \bar{x})$

Where $\bar{x}$ = population mean for the trait

P = a female breeding candidate's own performance

D and D_1 = average phenotypic values for the trait of full sisters of a female and male breeding candidate, respectively.

S and S_1 = average phenotypic values for the traits of half sisters of a female and male breeding candidate, respectively.

b_1, b_2= regression coefficients of the trait on the index for females.

b_3 and b_4 = regression coefficients of the trait on the index for males.

$$b_1 = \frac{2n(1-h^2)}{4+(n-2)h^2} \qquad b_2 = \frac{4nd\,(1-h^2)(2h^2)}{[4+(n-2)h^2][4+n(d+1)-2h^2]}$$

$$b_3 = \frac{(nh^2)}{4+(n-2)h^2} \text{ and} \qquad b_4 = \frac{2nd\,(1-h^2)(2h^2)}{[4+(n-2)h^2][4+n(d+1)-2h^2]}$$

Where

d = the number of dams; n = the number of offspring per dam

h^2 = the heritability estimate

Body weight:

Individual body weights were recorded biweekly from hatch until 6 weeks of age to the nearest 0.1 gm. Body weights at two, four and six weeks of age were recorded (BW2, BW4 and BW6).

Growth rate:

Individual absolute body weight gain during the different studied growth periods from two to four and from four to six weeks of age were obtained according to (Brody, 1945) as follows:

$$G.R = \frac{W_2 - W_1}{\frac{1}{2}(W_2 + W_1)} \times 100$$

Where,

G.R = Growth Rate

W_1 = the weight at the beginning of the period.

W_2 = the weight at the end of the period

Age at sexual maturity for females was individually recorded in days (ASM), total egg production (numbers and weights) were recorded from the onset of lay till 12 weeks of production. However daily egg mass was estimated as the average egg number multiplied by the average egg weight per week (DEM).

Individual fertility and hatchability of each female were recorded accordingly. The hatched eggs were recorded and the residual eggs in the hatcher were broken to determine the fertile eggs. Percent fertility and percent hatchability were calculated as follows.

$$\text{Percent Fertility} = \frac{\text{Total number of fertile eggs}}{\text{Total number of egg set}} \times 100$$

$$\text{Percent Hatchability} = \frac{\text{Total number of chicks hatched}}{\text{Total number of fertile eggs}} \times 100$$

Genetic parameter estimates

Genetic parameters were estimated using the sire model. The variance component was partitioned into those due to sire or environment. The statistical model used was:

$$y_{ij} = \mu + a_i + e_{ij}$$

Where y_{ij} = the record of the j^{th} progeny of i^{th} sire.

μ = the common mean

a_i = the effect of the i^{th} sire

e_{ij} = the uncontrolled environmental and genetic deviations attributable to the individuals. All error terms were random, normal and independent with expectation equal to zero.

Heritability

Heritabilities of egg production, serum alkaline phosphatase activity and economic traits were estimated using the formula

$$h^2 = \frac{4\sigma_s^2}{\sigma_T^2}$$

h^2 = heritability estimate

σ_S^2 = Variance due to sire

σ_T^2 = Total variance

Estimation of correlations

The coefficients of genetic correlation between different traits studied were computed from the sire component of variance as follows:

$$r_g = \frac{4\,\text{cov}_{s(xy)}}{\sqrt{4\sigma^2_{s(x)}.4\sigma^2_{s(y)}}}$$

$$\text{S.E of } r_g = \frac{1-\sigma^2_g}{\sqrt{2}} \sqrt{\frac{SEh^2_{(x)} xS.Eh^2_{(y)}}{h^2_{(x)} h^2_{(y)}}}$$

Estimating phenotypic correlation from sire component of variance

$$r_p = \frac{\text{cov}_{w(xy)} + \text{cov}_{s(xy)}}{\sqrt{\sigma^2_{w(x)} + \sigma^2_{s(x)}.\sigma^2_{w(y)} + \sigma^2_{s(y)}}}$$

RESULTS AND DISCUSSION

Table 1 shows the least squares means (±standard error) and coefficient of variation for growth traits for generation 1 and 2. Body weight at 2, 4 and 6 weeks was averaged 39 gm, 96.66 gm and 163.29 gm respectively after two generation of selection. This is similar to what was reported by Aboul-Hassan (2000) who observed estimates of body weight at 2 weeks as 35.2 gm. Higher estimates were reported by Aboul-Hassan (2001) as 46.4 gm for the Brown strain of Japanese quail and 40.2 gm for the White strain for body weight at two weeks of both sexes. For 4 weeks body weight, Sharaf (1992) reported estimates ranging between 94.46gm and 100.45gm. For 6 weeks body weight, El–Fiky (1991) reported an estimate of 128.1gm and 140.8 gm for males and females, respectively. Body weight at 2, 4, and 6 weeks of age generally increased at the end of the first and second generation after selection, when compared to the base generation. However body weight for generation 1 was slightly higher than that of generation 2. Table 2 shows the least square means of egg quality parameters of Japanese quails for generation 0, 1 and 2. The average EWT6, EWT8, EWT12, EGN, and DEM were found to be 8.72gm, 9.04gm, 8.95gm, 46.04, and 8.61gm/day respectively. These values are similar to what is found in literature. Abdul-Hasan (2004) reported EWT and DEM as 10.56gm and 9.18gm/day respectively. Table 3 shows the heritability estimates with standard error of heritability for generation 1 and 2. Heritability estimate obtained for EGN (1.21), and ASM (1.63) were outside the parameter estimate. This could be due to low population size. This is similar to what was reported by Wilhelmson (1979) and El-Fiky *et al.* (1994) who both reported heritability estimates of 1.35 and 1.42 for ASM in Japanese quail. The heritability estimate for EWT12 (0.56) differs from the findings of Abdel-Mounsef (2005), Saatci *et al* (2006) and Abou Hassan (2001) who reported heritability of 0.12, 0.25, and 0.10 respectively. Estimates for other egg production traits were low. Table 5 shows selection response for egg number and correlated response for some economic traits**.** Egg number highly significantly ($P<0.01$) increased from 36.55 in generation zero to 45.36 at the second generation of selection. There was a slight decrease though in the EGN recorded, from 46.04 in generation 1, to 45.36 in generation 2. The same trend was reported by Aboul-Hassan (1997) and Aboul-Hassan (2001) when he selected Japanese quail for increased BWT6 and EGN produced for the first ten weeks of laying. Other correlated responses were observed as a result of selection for egg number. Negative response (-1.84) was observed in ASM. This is so because the ASM reduced across the generation as EGN increased. Generally,

positive response of varying magnitude was observed for EWT12 (0.05), BWT6 (0.72) and DEM (0.92).

CONCLUSION

From the results obtained in this study, selection in generation 0 based on egg number to 12 weeks of age improved the egg number by 3.91, ASM by -1.84 days, EWT by 0.05gm, BWT6 by 0.72gm and DEM by 0.92gm after two generations of selection.

Table 1. Least squares means (±standard error) and coefficient of variation for growth traits of Japanese Quails (Generation 1 and 2)

	Gen 1		Gen 2	
Traits*	LSM ± SE	C.V (%)	LSM ± SE	C.V (%)
BWT2	40.39 ± 0.20	6.27	40.06 ± 0.17	6.19
BWT4	97.17 ± 0.22	2.86	96.88 ± 0.19	2.93
BWT6	163.79± 0.44	3.43	163.00 ± 0.41	3.67
GR 4	80.96 ± 0.77	11.98	83.02± 0.41	7.15
GR 6	53.89 ± 0.82	19.22	50.83± 0.29	8.56

BWT2 =Body Weight at 2 weeks; BWT4= Body Weight at 4; BWT6= Body Weight at 6; GR4 = Growth rate at 4 weeks; GR6= Growth rate at 6 weeks.

Table 2. Least Square Means (±standard error) of Egg Quality parameters of Japanese quail for generation 0, 1 and 2

	Gen 0		Gen 1		Gen 2	
Traits	LSM±SE	CV%	LSM±SE	CV%	LSM±SEM	CV%
EGN	36.55±0.92^{b}	24.72	46.04±0.29^{a}	7.27	45.36±0.21^{a}	6.29
EGW6	8.41±0.09^{b}	10.80	9.16±0.07^{a}	9.54	8.56±0.06^{b}	10.07
EGW8	8.89±0.06^{b}	6.37	9.15±0.04^{a}	5.32	9.04±0.04^{a}	5.97
EGW12	9.02±0.09	10.09	8.73±0.18	23.59	9.06±0.06	9.86
AGW	8.77±0.06^{b}	6.68	9.02±0.07^{a}	8.77	8.87±0.04^{a}	6.22
EGH6	2.19±0.01	5.79	2.14±0.05	27.07	2.14±0.03	23.00
EGD6	1.89±0.05^{b}	24.66	2.11±0.06^{a}	35.70	2.04±0.05^{a}	34.13
ALH6	0.11±0.00^{b}	26.53	0.14±0.01^{a}	93.50	0.13±0.01^{a}	86.41
ALW6	4.04±0.06	15.14	4.02±0.05	14.47	3.98±0.04	16.49
YLH6	0.58±0.00^{b}	10.37	2.16±0.51^{a}	68.03	1.72±0.37^{a}	89.06
YLW6	3.13±0.08	28.01	3.08±0.06	23.35	3.20±0.05	21.53
SHT6	22.22±0.51^{a}	22.67	19.87±0.70^{b}	39.67	20.59±0.53^{a}	34.36
EGH12	2.69±0.01^{a}	4.71	2.52±0.06^{b}	28.60	2.57±0.04^{a}	24.11
EGD12	2.037±0.05^{b}	24.18	2.27±0.07^{a}	37.44	2.20±0.05^{a}	35.45
ALH12	0.11±0.00^{b}	30.54	0.15±0.01^{a}	99.36	0.14±0.01^{a}	92.30
ALW12	4.55±0.06	14.24	4.50±0.05	14.77	4.47±0.05^{a}	16.28
YLH12	0.63±0.00^{b}	9.49	2.29±0.54^{a}	64.79	1.82±0.39	84.69
YLW12	3.22±0.09	29.19	3.01±0.08	33.39	3.18±0.06	28.25

SHT12	23.25±0.52	22.09	23.88±0.15	7.48	23.78±0.19	10.64
DEM	6.43±0.17^{c}	26.99	10.07±0.47^{a}	52.89	8.75±0.06^{b}	9.26
HGU6	57.58±1.84^{a}	2.68	58.99±1.24^{b}	1.98	59.95±1.03^{b}	1.92
HGU12	58.98±1.75^{a}	6.55	59.88±2.05^{b}	5.37	59.11±1.45^{b}	2.02
YIN6	1.53±0.00^{a}	5.49	1.61±0.01^{a}	6.86	0.61±0.01^{b}	1.85
YIN12	0.12±0.01^{a}	0.62	0.18±0.01^{a}	0.15	0.20±0.01^{b}	2.53

Means with different superscripts across the row are significantly different ($P < 0.05$)
EGW= Egg Weight; EGN= Egg Number; DEM= Daily egg mass. EGN=Egg number; EGW=Egg weight, SHT= Shell thickness; ALP20= Plasma alkaline phosphatase activity at 20 weeks; HGU= Haugh Unit; YIN= Yolk Index; ALH=Albumen height; ALD= Albumen width; EGD= Egg width; YLW=yolk weight

Table 3. Heritability Estimates (±standard error) of Growth, Production and Egg Quality Traits for Generations 1 and 2

	Gen 1	Gen 2
Traits	Heritability±SE	Heritability±SE
EGN	1.20±0.42	0.05±0.15
ASM	0.29±0.28	1.63±0.44
EGW12	1.25±0.42	0.56±0.29
HGU6	0.64±0.35	0.22±0.20
YIN6	0.90±0.39	0.42±0.26
SHT6	1.55±0.44	0.33±0.23
HGU12	1.14±0.41	0.42±0.27
YIN12	0.96±0.39	0.16±0.18
SHT12	0.58±0.34	0.20±0.19
BWT6	0.39±0.25	0.20±0.20

+SEE TABLE 2 FOR MEANING

Table 4. Selection response of reproductive traits at different generation intervals

Traits				Response		Cumulative Response±SE
	G0	G1	G2	G1	G2	
EGN	36.55	46.04	45.36	9.49	-0.68	3.91±0.35
ASM	43.97	39.73	39.86	-4.24	0.13	-1.84±0.17
EGW12	9.02	8.73	9.06	-0.29	0.33	0.05±0.08
SHT12	23.25	23.88	23.78	0.63	-0.1	-0.15±0.11
BWT6	162.09	163.30	163.02	1.21	-0.28	0.72±0.36
DEM	6.43	10.07	8.75	3.64	-1.34	0.92±0.21

EGN=Egg number, EGW= Egg weight, SHT= Shell thickness, ASM=Age at sexual maturity, DEM= Daily egg mass

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AGB11

REPEATABILITY OF CLUTCH SIZE AND HATCHLING SIZE IN TRADITIONALLY-MANAGED YORUBA AND FULANI ECOTYPE CHICKENS

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ABSTRACT

Progeny history of 408 and 350 traditionally-managed dam families of Yoruba and Fulani ecotype chickens were used to estimate the repeatability of clutch size and hatchling size. Mean clutch size and hatchling size for Yoruba ecotype chicken were 5.68 ± 5.37 eggs and 5.02 ± 4.86 chicks, respectively. Corresponding mean values for the two traits in Fulani ecotype chicken were 4.13± 5.84 eggs and 2.94± 4.44 chicks, respectively. Clutch size and hatchling size were higher in Yoruba ecotype than Fulani ecotype chicken. Generally, both clutch size and hatchling size declined in the two ecotypes as the hatch number increased. Repeatability of clutch size and hatchling size in Yoruba ecotype chicken were -0.41± 0.17 and -0.43± 0.01, respectively. Corresponding values for the two traits in Fulani ecotype chicken were lower (-0.28±0.16 and -0.23±0.14, respectively). The negative repeatability estimates obtained in the two flocks suggest that both clutch size and hatchling size would likely decline with increasing hatch number per hen. The low mean repeatability estimates obtained for hatchling size suggest that collection of additional records and improvement of non-genetic factors are needed to improve the accuracy of characterizing bird's inherent transmitting ability for this trait.

Keywords: Clutch size, Hatchling size, Repeatability, Yoruba ecotype, Fulani ecotype

INTRODUCTION

Repeatability is the proportion total variation attributable to differences among individuals (Wolak *et al.*, 2012). It tells how an animal will repeat its performance in a given trait during its lifetime. Statistically, it is the correlation between records from the same animal (Dalton, 1982). Repeatability estimate of reproductive traits indicates the extent at which selection will influence future animal reproductive performance (Ibe, 1995). Indigenous poultry population in Nigeria include the Yoruba and Fulani ecotype chickens. Fulani ecotype chicken is one of the best-preserved local chickens in Nigeria because of the cultural lifestyle of the Fulani keepers (Fayeye and Oketoyin, 2006). These birds are important genetic resources because of their adaptability to the stressful tropical environment. NRC (1993) recommended a study of the level of genetic diversity in different populations as the first step to bring about improvement in the performance of chicken in developing countries. Most of the works done on local chicken by animal breeders in Nigeria have been limited to morphometric characterization (Olori, 1992, Fayeye *et al.*, 2006,

Olawunmi *et al.,* 2008) and their crossbreeding potential. For instance, Olori (1992) reported that Fulani ecotype chicken has superior bodyweight and fleshing than the Yoruba ecotype chicken. Clutch size and hatchling size are important reproductive parameters that influence sustainability of flock size of smallholder poultry producers. Knowledge of these two basic reproductive parameters is invaluable for adequate characterization and genetic improvement of both Yoruba and Fulani ecotype chickens. No previous work is known on the repeatability of clutch size and hatchling size in traditionally managed Yoruba and Fulani ecotype chickens. The present work is therefore aimed at determining the repeatability of clutch size and hatchling size in traditionally managed Yoruba and Fulani ecotype chickens.

MATERIALS AND METHODS

Origin of flock: The Yoruba ecotype chickens were obtained from four Yoruba communities (Ogbomoso, Igbon, Gambari and Gbede) in Oyo state. The last three communities have close proximity with Ogbomoso (Longitude, 08:15^0 N; Latitude, 04: 15^0 E, Altitude 300-600 mm above sea level, Temperature, 27^{0}C, Rainfall, 1247mm). The Fulani ecotype chickens were obtained from eighteen (18) Fulani kraals (Table 1). All the kraals have close proximity with Ilorin (Longitude, 08: 29^0 N; Latitude, 04: 350 E, Altitude 305m, 1001', Temperature, 33-37^{0}C, Rainfall, 600-1200 mm). The two coordinates are 51.36km apart.

Animal genotypes and data collection: Progeny History Technique of the Participatory Rural Appraisal (Kassaye et al., 1992; Iles 1994) was used to collect clutch size records and hatchling size of 408 and 350 traditionally-managed dam families of Yoruba and Fulani ecotype chickens. The animals were identified as Yoruba or Fulani ecotype chickens based on their phenotypic characteristics and the information given by flock owners.

Statistics: Data on clutch size and hatchling size obtained from the two ecotype chickens were subjected to Analysis of Variance (ANOVA) of the SPSS (SPSS, 1996) to obtain the required mean square between and within class of the hens' records. The clutch size and hatchling size per hen (i.e. k_1) were estimated as the harmonic mean of the records obtained from the dam families of Yoruba and Fulani ecotype chickens. Mean squares obtained from ANOVA were equated to their expected values and the resulting equation solved for the required variance components. Repeatability of clutch size and hatchling size were obtained from between and within class variance components using the formula below (Becker, 1992).

$$\text{Repeatability (R)} = \frac{\boldsymbol{\sigma^2_I}}{\boldsymbol{\sigma^2_I + \sigma^2 e}}$$

Where σ^2_I =variance due to the effect of individual hen of either Yoruba or Fulani-ecotypes and $\sigma^2 e$ = variance due to within individual hen's records or random error

The Standard Error of Repeatability or S.E (R) was obtained from the equation given by Swiger et. al. (1964) as follows:

$$\text{S.E (R)} = \frac{\sqrt{2\,(M-1)\,(1-R)\,2\,[1 + (K1 - 1)\,R]^2}}{K12\,(M-N)\,(N-1)}$$

When M = total member of record for hen belonging to Yoruba or Fulani ecotype chickens

N = Numbers of hens

K1 = harmonic mean of the records obtained from the 408 and 350 traditionally-managed

Dam families of Yoruba and Fulani ecotype chickens, respectively

K1 was estimated as follows:

$$\frac{1}{N-I} \quad X \quad \frac{(M - \sum mk2)}{Mk}$$

Where Mk = numbers of records per ith hen

The statistical model for obtaining the variance components used in calculating repeatability was as follows:

$Yij = \mu + \alpha i + eij$ where

Yij = record from the jth clutch or hatch by the ith hen

μ = population mean

αi = effect of the ith hen

eij = random error.

All the effects were assumed to be random, normal and independent with their expectation equals to zero.

RESULTS AND DISCUSSION

The mean clutch size and hatchling size for Yoruba ecotype chicken were 5.68 ± 5.37 eggs and 5.02 ± 4.86 chicks, respectively. Corresponding mean values for the two traits in Fulani ecotype chicken were 4.13± 5.84 eggs and 2.94± 4.44 chicks, respectively (Table 2). Clutch size and hatchling size in the two ecotype chickens were influenced by hatch number. Generally, the clutch size and hatchling size declined in the two ecotypes as the hatch number increased (Table 2). Repeatability of clutch size and hatchling size in Yoruba ecotype chicken were -0.41± 0.17 and -0.43± 0.01, respectively (Table 3). Corresponding values for the two traits in Fulani ecotype chicken were lower (-0.28±0.16 and -0.23±0.14, respectively). Mean clutch size for Yoruba and Fulani ecotype chickens were lower than 10.7 eggs reported by Gondwe (2005) for local Malawian chicken. Such variation is common in laying performance of African village chickens (Gueye, 1998), perhaps due to genetic and vagaries of environmental effects. The mean hatchling size observed in this study for both Yoruba and Fulani-ecotypes were within the preponderance range (Adebayo *et al*., 2013) for local chicken obtained from rural communities in Kwara state. Repeatability estimates obtained in the present study for both Yoruba and Fulani-ecotypes fell within 0.05-0.85 reported for two commercial layer strains by Udeh (2010). Negative repeatability estimates obtained in the two flocks suggests that both clutch size and hatchling size will likely decline with increasing brooding records. The low mean repeatability estimates obtained for the hatchling size suggest that collection of additional records and improvement of non-genetic factors are needed to improve the accuracy of characterizing the inherent transmitting ability of both Yoruba and Fulani ecotype chickens for this trait.

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Table 1: Communal distribution of sampled Fulani ecotype chicken

Location	*settlement*	*No. of hens*	*No. Of chicks*
ILORIN SOUTH	*Bolunduro*	*24*	*310*
	Gaa Seriki Sambata	*11*	*193*
	Gaa Mogaji	*3*	*65*
	Gaa Mumiri	*6*	*117*
ILORIN EAST	*Aleniboro*	*6*	*98*
	Gaa Alhaji Baare	*28*	*347*
	Gaa Atende	*24*	*247*
	Gaa Atirun	*39*	*364*
	Gaa Adire Hara	*13*	*219*
	Gaa Gahara	*14*	*179*
	Gida Idi	*15*	*130*
	Gida Mogaji	*6*	*48*
	Gida Idi Ose	*40*	*424*
IFELODUN	*Gaa Mubari*	*39*	*385*
	Gaa Oseri	*42*	*464*

	Gaa Ibata	*16*	*244*
	Gaa Mogaji	*12*	*104*
	Gaa Aljaji Osere	*12*	*154*
3	*18*	*350*	*4,092*

Table 2: *Mean (± SD) Clutch size and hatchling size in Yoruba and Fulani ecotype chickens.*

	No of eggs laid± SD		*No of egg hatched± SD*	
Hatch Number	*Yoruba ecotype*	*Fulani ecotype*	*Yoruba ecotype*	*Fulani ecotype*
1	*10.05±2.02*	11.12±2.69	*8.93±2.32*	7.86±3.00
2	*7.10±5.12*	4.86±6.57	*6.33±4.64*	3.54±5.11
3	*4.10±5.37*	0.50±2.54	*3.59±4.84*	0.36± 1.95
4	*1.46 ±3.86*	*	*1.24±3.23*	*
Overall	*5.6789±5.37*	4.13±5.84	*5.02 ±4.86*	2.94±4.44

*Records not used because of small sample size

Table 3: *Variance components and repeatability estimates of Clutch size and hatchling size in Yoruba*
and Fulani ecotype chickens

Characteristics	Egg laid		Egg hatched	
	Yoruba-ecotype	*Fulani-ecotype*	*Yoruba-ecotype*	*Fulani-ecotype*
Variance between	-7.54	-8.9	-6.31	-4.17
Variance within	25.75	40.41	21.07	22.64
Repeatability ± S.E	-0.41± 0.17	-0.28±0.16	-0.43± 0.010	-0.23±0.14

AGB12

HETEROSIS, GENERAL AND SPECIFIC COMBINING ABILITY OF TWO BREEDS OF RABBIT AND THEIR CROSSES UNDER PREVAILING SOUTHERN GUINEA SAVANNA ENVIRONMENTAL CONDITIONS OF NIGERIA

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ABSTRACT
An experiment was conducted to estimate heterosis, general combining ability (GCA) and specific combining ability (SCA) of two breeds of rabbit. The rabbit breeds used for the experiment were the New Zealand White (NZW) and Chinchilla (CH). Six breeding bucks (three/breed) and eighteen breeding does (nine/breed) served as the foundation animals. Data were collected on litter size at birth (LSB), litter body weight (LBW), gestation length (GL), kindling loss (KL), coefficient of milking capacity (CMC), litter size at weaning (LSW), litter weight at weaning (LWW), litter weight gain (LWG) and survival rate to weaning (SRW). Data were also collected on body weight (BW), nose to shoulder length (NTS), shoulder to tail length (STL), heart girth (HG), trunk length (TL) and length of ear (LE). Results revealed that, positive heterosis was estimated for LSB (11.89 %), LBW (13.51 %), GL (7.23 %), KL (22.22 %), CMC (5.13 %) and LSW (1.25 %) while negative heterosis was observed for LWW (-3.69 %), LWG (-8.02 %) and SRW (-2.45 %). Superiority percentage was positive only for LSB (2.60 %), LBW (5.00 %) and GL (5.88 %) while the other parameters showed negative values. Significant GCA was observed only for IBW and NTS in the CH breed while significant SCA was observed in the NZW x CH cross for STL, HG and TL, and for HG, TL and LE in the CH x NZW cross, respectively. It was concluded that crossing the two breeds of rabbit, led to hybrid vigour for LSB, LBW, GL, KL, CMC and LSW, respectively. IBW and NTS could also be improved upon in the CH at the genetic level while STL, HG and TL (NZW x CH), and HG, TL and LE (CH x NZW) could be improved upon by improving the environment of the rabbits.

Key words: Heterosis, general combining ability, specific combining ability, breed, and rabbit.

Introduction

Breeding is an option towards increasing dietary protein supply through the production of animals of high genetic merit. This is because genetic differences exist in animals even of the same breed. These differences are important potential raw materials necessary for genetic improvement of animals. Crossbreeding as a breeding system, exploits heterosis in animal breeding and it could be fruitfully employed in rabbit breeding for increasing productivity (Reddy *et al.,* 2003). Positive effects of crossbreeding have been reported on growth traits in rabbits (Orengo *et al.,* 2004; Abou Khadiga *et al.,* 2008). General combining ability (GCA) is a measure of the influence of additive genes effects, while Specific combining ability (SCA) measures the effect of non-additive genes. The performance of all crosses that derive from one breed is designated the general combining ability of the breed while, specific combining ability, a joint attribute of two breeds signifies the deviation of crosses from the sum of the general combining abilities of the crosses parents (Rubio-Rubio *et al.,* 2004). Analysis of diallel crosses enables the breeder to partition total genetic variation into additive (GCA) and non-additive (SCA) genetic variance (Nagpure *et al.,* 1991). Both additive and non-additive genes have an impact on traits evaluated in rabbits (Obasi and Ibe, 2008). Knowledge of the type of gene action operating in animals therefore will enable breeders to formulate suitable breeding plans for the genetic improvement of characters of economic importance in such animals. The objectives of this study therefore, are to estimate heterosis, general and specific combining ability of two breeds of rabbit in a southern guinea savannah area of Nigeria.

MATERIALS AND METHODS

The experiment was carried out at the Rabbitry section of the Teaching and Research Farm of the Department of Animal Production, Federal University of Technology, Minna, Niger State, Nigeria. Rabbits used for this study were NZW and CH breeds. The rabbits were housed in groups (i.e according to breed) in well ventilated and shaded hutches. Feed (16 % CP; 2776 Kcal/Kg formulated concentrate, *Tridax procumbens* as well as legume hay supplement) and water were given *ad libitum.* Does were randomly assigned to one of the three bucks within their breed. Thereafter, does from the second breed were mated to bucks from the first breed and vice versa to obtain the crossbred. Mating began when the rabbits were between 4-5 months of age (i.e 120-150 days). Does were monitored for pregnancy through palpation of the abdominal region. Five days to kindling, nesting boxes were placed in the doe's hutch. The litter and weaning traits measured were:

LSB, LBW, GL, KL, CMC, LSW, LWW, LWG, and SRW. The body dimensions measured using flexible tape rule were: NTS, STL, HG, TL and LE. Data obtained from the purebred and crossbred matings were used to estimate heterosis and superiority percentages. Heterosis and superiority percentages of crossbreds were calculated according to Abdel-Azeem (2007). The formulae are:

Heterosis % = $[(MF_1 - MP) / MP] X 100$

Where MF_1 = Mean of crossbred generation and MP = Mid-parent value. Mid-parent value is = 1/2 (MP_1+MP_2) where P_1 and P_2 are parents 1 and 2 respectively.

Superiority % = $[(MF_1 - BP)/BP] X 100$

Where MF_1 = Mean of crossbred generation and BP = Better-parent value.

General and specific combining abilities were estimated using the statistical model below.

$$Y_{ijkl} = \mu + g_i + g_j + s_{ij} + r_{ij} + 1/bc\sum e_{ijkl}$$

Where Y_{ijkl} = the mean of the i^{th} x j^{th} genotype over $_k$ and $_l$, μ = overall mean, g_i = general combining ability (GCA) effect of the i^{th} parent, g_j = general combining ability (GCA) effect of the j^{th} parent, $_{sij}$ = interaction i.e specific combining ability (SCA) effect, r_{ij} = reciprocal effect and $1/bc\sum e_{ijkl}$ = random error effect. General combining ability (GCA) was estimated using the expression

$$GCA = 1/2n (Y_{i.} + Y_{.i}) - 1/n^2Y$$

Specific combining ability (SCA) was estimated using the expression

$$SCA = ½ (Y_{ij} + Y_{ji}) - 1/2n (Y_{i.} + Y_{.i} + Y_{j.} + Y_{.j}) + 1/n^2Y$$

Where n = number of records considered or number of breeds involved in the cross; Y= the sum of the observations $Y_1 + Y_2 + Y_3 + \ldots + Y_n$ for the respective breeds (i or j) of rabbit. The expressions were fitted to a Microsoft Excel generated programme.

RESULTS AND DISCUSSION

Estimate of heterosis and superiority of the crossbred in litter and weaning traits are presented in Table 1. The positive heterosis observed for LSB, LBW, GL, KL, CMC and LSW as well as,

positive superiority of the crossbred over their parents in LSB, LBW and GL means that the magnitude of non-additive gene effect (mainly dominance) for these traits is comparatively substantial. This could be because the base population differ in the frequency of genes affecting the traits. This means that the less the degree of genetic resemblance, the greater the magnitude of the heterosis. Some of the traits however showed negative heterosis. This means that crossbreeding is associated with negative effect or has little significance on these traits (although this is not applicable to all the traits). Keambou *et al.* (2010) attributed strong negative heterosis to greater genetic distance between tested breeds. The negative sign in no way invalidate the definition of heterosis however as the nature of heterosis really is dependent on the nature of the measurement. The negative heterosis and superiority effect observed for SRW is actually advantageous as it indicates the positive effect of crossbreeding in diminishing the negative effect of the trait. This is because a larger proportion of the crossbred litter will survive. This is of great economic importance to rabbit farmers.

Estimates of GCA and SCA for body weight and linear body measurements are presented in Table 2. The significant GCA effect observed for IBW and NTS is indicative of the importance of additive genes for the expression of these traits. The superior performance of the CH breed suggests that it has the upmost preponderance of genes which impact additive gene effect on the growth traits. This demonstrates that CH rabbits could possibly increase in growth performance because of their higher GCA values. Reports by Rubio-Rubio *et al.* (2004) indicate that breed differences exist for GCA in rabbits for litter and weaning traits. Maximum utilization of additive genetic variance could be made therefore using CH rabbits for better body weight and nose to shoulder length. Kabir *et al.* (2009) opined that this is because heritability values for these traits are expected to be moderate to high.

The combination CH x NZW was superior for all the traits studied but there was no advantage pertaining to the use of male or female lines for any of the breeds to exploit non-additive genetic variance in IBW, NTS (both crosses), STL (CH x NZW cross) and LE (NZW x CH cross) since no significant effect was observed for these traits. Significant SCA observed for some of the traits however, is indicative of non-additive gene action. Such traits could therefore be improved upon genetically through the utilization of non-additive gene effects such as dominance and epistasis, and also by improved management of the environment. Kabir *et al.* (2009) also reported on the superior performance of CH x NZW cross over those involving NZW x CH and California white x chinchilla cross when they evaluated litter traits in three breeds of rabbit. The negative non-significant

($p>0.05$) SCA observed for the NZW x CH cross is according to Nagpure *et al.* (1991), indicative of such crossing resulting in the depression of such traits.

In conclusion, results from the study showed that crossing the two breeds of rabbit, led to hybrid vigour for some litter and weaning traits (LSB, LBW, GL, KL, CMC and LSW respectively). Individual body weight and NTS could be improved upon in the CH at the genetic level due to significant and positive GCA attributable to additive genetic variance, while STL, HG and TL (NZW x CH), and HG, TL and LE (CH x NZW) could be improved upon by improving the environment of the rabbits.

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Table 1: Estimates of heterosis and superiority of two breeds of rabbits and their crosses

Traits	Pure breed average	Crossbred average	Heterosis (%)	Superiority %
Litter				
LSB	4.585	5.13	11.89	2.60
LBW (g)	185	210	13.51	5.00
GL	32.585	34.94	7.23	5.88
KL (g)	135	165	22.22	-2.94
CMC	0.195	0.205	5.13	-2.38
Weaning				
LSW	3.60	3.645	1.25	-4.08
LWW (g)	1355	1305	-3.69	-8.74
LWG (g)	1185	1090	-8.02	-13.49
SRW (%)	83.145	81.11	-2.45	-11.84

LSB= litter size at birth; LBW= litter body weight; GL= gestation length; KL= kindling loss; CMC= coefficient of milking capacity; LSW= litter size at weaning; LWW= litter weaning weight; LWG= litter weight gain; SRW= survival rate to weaning.

Table 2: Estimates of General (GCA) and Specific (SCA) combining ability for body Weight and body linear measurements

Combining ability	IBW	NTS	STL	HG	TL	LE
GCA						
NZW	-3.790	5.921	1.184	-1.776	-2.369	-5.921
CH	1.895*	1.184*	-1.184	2.961	5.921	-2.961
SCA						
NZW x CH	-10.492	-0.035	-0.258*	-0.161*	-0.144*	-0.028
CH x NZW	18.321	0.093	0.090	0.128*	0.181*	0.106*

**Significant (p<0.05); IBW= Individual body weight; NTS=Nose to shoulder length; STL= Shoulder to tail length; HG=Heart girth; TL= Trunk length; LE=Length of ear; NZW= New Zealand White; CH= Chinchilla; GCA=general combining ability; SCA=specific combining ability.*

AGB13

GENETIC RELATIONSHIP BETWEEN *CLARIAS ANGUILLARIS* AND *HETEROBRANCHUS BIDORSALIS* FROM THREE ECOLOGICAL ZONES IN NIGERIA

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ABSTRACT
The phylogenetic relationship among Clariidae species (Teleostei Siluriformes) from different ecological zones in Nigeria were assessed using Histone 3 gene promoter. Two different species form two different genera were examined namely, *Clarias anguillaris* and *Heterobranchus bidorsalis.* The result showed that the species have a common ancestor though the distance in relationship revealed variations among them. There were also variations in the sites of the nucleotides in the different strains. Estimated genetic distances between populations were directly correlated with geographical distances. The unweighted pair group method with averages (UPGMA) dendrogram showed three clusters, the Maiduguri, Onitsha, Kainji, Yola *C. anguillaris* and India *C. gariepinus* population forming one cluster. Kainji *H. bidorsalis* was alone on the second cluster and Maiduguri *H. bidorsalis* and the Genbank AF416497.1 on the third cluster. Genetic variation of *C. anguillaris* is a useful trait for developing a good management strategy for maintaining genetic quality of the species.
Keywords: DNA Sequence, Phylogenetic relationship, *Clarias, Heterobranchus*, Nigeria.

INTRODUCTION
The Clariid catfishes, order Siluriformes, are distributed in Africa, Asia Minor and South-east Asia and the Indian subcontinent (Teugels and Adriaens, 2003). Two genera of these, *Clarias* and *Heterobranchus*, with the Cichlids are the most used in African aquaculture production (Agnese *et al*., 1995). The *Clarias* (Teugels, 1982, 1986) made up of two valid species, *Clarias gariepinus* and *C. anguillaris* that cannot be differentiated morphologically except by counting the number of gill rakers on the dead fish dominate the Nigeria aquaculture production. *C. gariepinus* occurs thoughout Africa, while *C. anguillaris* is geographically restricted to West Africa where they occur sympatrically.

C. anguillaris (Linnaeus, 1758) like *C. gariepinus* is also of interest to aquaculture (Volckaer *et al.*, 1994). This species is used in aquaculture production systems in Africa (Sylla, 1994). It is often used in place of *C. gariepinus* because of the close resemblance. Earlier researches have been carried out on the growth performance of two strains of *C. anguillaris* from Niger and Bouake (Da Costa, 1997), morphometric and meristic characters (Onyia and Iliya, 2008) and generic characterization of sympatric populations of *Clarias gariepinus* and *Clarias anguillaris* from Senegal (Agnese *et al.*, 1997).

According to Olken (2002), phylogenetic trees are computed to understand evolutionary history, map pathogen strains diversity for vaccines, assist in epidemiology of infectious diseases and genetic defects, aid in the prediction of function of novel genes, biodiversity studies and understanding microbial ecologies. *C. anguillaris* and *H. bidorsalis* are widely distributed in Nigerian water bodies. It is therefore necessary to study the phylogenetic relationship of the strains from different ecological zones in Nigeria having different hydrological characteristics. The objective of the study described in the present paper was to assess the genetic variation and relatedness in four strains of *C. anguillaris* and two strains of *H. bidorsalis* populations from different ecological zones.

MATERIALS AND METHODS

Clarias anguillaris strains were collected form Jos (Montane Vegetation). Kainji (Guinea savanna), Onitsha (Rainforest zone) and Maiduguri (Sahel savanna). *Heterobranchus bidorsalis* strains were also collected form Kainji and Maiduguri, while *Clarias gariepinus* from India was also used. Genomic DNA was extracted using phenol method from the blood of *Clarias gariepinus* and was confirmed on 0.8% agarose TBE gel electrophoresis. The amount of DNA was determined using Nano spectrophotometer.

The histone gene promoter was amplified using polymerase chain reaction approach; this was achieved by using Histone 3 Forward and Histone 3 Reverse primers. The reaction volume was 25ul containing 2.5ul dNTPs, 16.5ul ddH20, 2.5 ul 10X PCR buffer, 5 pmol H3 Forward primer, 5 PMOl H3 Reverse primer, 1 ul of template (genomic DNA) and 0.5 ul Tag polymerase were used. The reaction condition which was done using MJ Research Thermo Cycler 200 involved hot start 95oC for 5 mins, and 35 cycles of denaturaion at 94oC for 30 secs, annealing at 60oC for 30 seconds and extension at 68oC for 1 minute. A final extension at 68oC for 10 minutes was included. (H3 forward primer: GAGAAAGGCCGTCAAAGCCAAGT and H3 reverse primer: AAGAAGGAAGCTAGCTAGCGCC). PCR product was confirmed on 0.8% agarose gel using 100bp marker.

The PCR product was sequenced along with the sequence of other Histone 3 gene promoter sequences derived from fish samples from Nigeria. A phylogenetic analysis was carried out. PCR product was given chloroform treatment followed by pK treatment before lighting into pMOS Blue vector for 20 hrs at 37oc. Clones were transformed in bacterial competent cells and the colonies were culture overnight from where plasmid DNA were isolated and checked on 0.8% gel electrophoresis to confirmed mobility ship due to presence of foreign DNA. The PCR product was sequenced using dideoxy chain termination method with fluorescently labeled ddNTP in automate DNA sequencer.

RESULTS AND DISCUSSION

From Table 1, the different nucleotide sites are shown. A close relationship among *C. anguillaris* strains from Maiduguri, Onitsha and Yola was found at close observation on the sites of the nucleotides. *C. anguillaris* from Kainji and *C. gariepinus* from India, differ from them in the genus *Clarias* based on the sites of the nucleotides. *C. anguillaris* had consistently different sites of the nucleotides in the analysis. *H. bidorsalis* from Maiduguri and Kainji also had variations in the sites of the nucleotides.

A total of 500 sites were analysed to give eight sequences of the different strains of the species. The total number of sites (including sites with gaps or missing data) was 485. The number of variable sites was 17 while the total number of mutation was 18. From the phylogenetic tree, the pattern among the lineages has the same homogenous pattern. There were uniform rates among the sites (Table 1).

The values on the phylogenetic tree (Figure 1), revealed 71% for *Clarias anguillaris* strains form Maiduguri, Onitsha, Kainji and Yola; 35% for *C. anguillaris* from Maiduguri and *Clarias gariepinus f*orm India. All the different strains of *C. anguillaris* and *H. bidorsalis* from Kainji were 99%. The pairwise genetic distance (Table 2), showed that the different samples are similar and very close.

Table 1. Histone 3 gene Promoter variable sites and nucleotide changes in *C. anguillaris* and *H. bidorsalis* form different ecological zones in Nigeria.

Strains of Clariids	Histone 3 variable sites and nucleotides changes in Clariid strains									
	1	2	3	4	5	6	7	8	9	10
Mai. C.a	A (49)	C(97)	G(147)	T(197)	T(247)	G(297)	C(345)	A(395)	A(445)	C9496)

Ind. C.g A(50) C(98) G(148) T(198) T(248) G(298) C(346) A(396) A(446) C(496)
Onit. C.a. A(49) C(97) G(147) T(197) T(247) G(297) C(345) A(395) A(445) C(494)
Kainji C.a. A(47) C(95) G(145) T(195) T(245) G(295) C(343) A(393) A(443) C(496)
YolaC.a. A(49) C(97) G(147) T(197) T(247) G(297 C(345) A(395) A(445) C(495)
Kainji H. b. A(46) C(96) G(146) T(196) T(246) G(296) C(344) A(394) A(444) C)495)
Mai. H.b. A(49) C(94) G(143) T(193) T(243) G(293) C(340) A(389) A(438) C(489)
GenBank A(49) C(94) G(143 T(193) T(243) G(293) C(343) A(392) A(441) C(492)
416497.1
Keys:
Mai. C.a. = Maiduguri *Clarias anguillaris* Ind. C.g. = Indian *Clarias gariepinus*
Onit. C. a. = Onitsha *Clarias anguillaris* Kainji C.a. = *C. anguillaris*
Yola C.a. = *C. anguillaris* Kainji H. b. = *Heterobranchus bidorsalis*
Mai. H. b. = Maiduguri *H. bidorsalis*

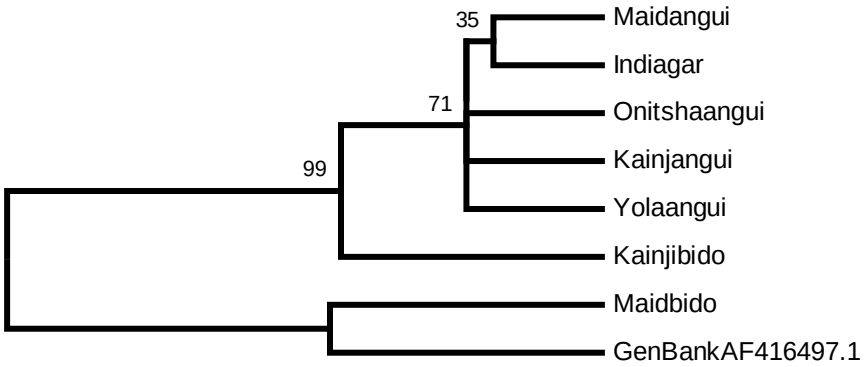

Figure 1: Phylogenetic tree of *Clarias anguillaris* and *Heterobranchus bidorsalis* from four ecological zones in Nigeria.

Table2: Correlation of *C. anguillaris* and *H. bidorsalis* from different ecological zones of Nigeria

[1 2 3 4 5 6 7 8]
[1]
[2] 0.004

[3] 0.004 0.006
[4] 0.008 0.008 0.006
[5] 0.004 0.006 0.004 0.006
[6] 0.012 0.010 0.008 0.010 0.008
[7] 0.019 0.017 0.019 0.021 0.015 0.015
[8] 0.029 0.027 0.029 0.032 0.025 0.025 0.010

Key:
[1] Maidangui [2] Indiagar [3] Onitshaangui [4] #Kainjangui
[5] Yolaangui [6] Kainjibido [7] Maidbido [8] GenBankAF416497.1

A representative Unpaired Group method of Analysis (UPGMA) based on Nei's genetic distance (Nei, 1972) is shown in Figure 1. The dendrogram segregated three distinct clusters of Clarias anguillaris and *H. bidorsalis* populations form three ecological zones in Nigeria. *C. anguillaris* populations form Maiduguri, Onitsha, Kainji, Yola and *C. gariepinus* from India being the first cluster while *H. bidorsalis* population form Maiduguri also alone on the third cluster.

The first cluster was further separated into two subgroups, Maiduguri *C. anguillaris* population and *C. gariepinus* from India in one subgroup and *C. anguillaris* populations form Onitsha, Kanji and Yola in the second subgroup. The estimation of genetic distance produced UPGMA dendrograms with similar clustering patterns. It also detected correlations between genetic and geographical distances for some population pairs, with large genetic distance being found between distantly located populations. The three populations have a common ancestor from the phylogenetic tree (Figure 1) but with genetic variations which led to their separation into different clusters and subgroups.

Distinguishing valid species from geographic population of same species usually begins by studying variability of good character among samples. Buth and Mayden (1981) stated that characters variability often describe clines, which are directed changes in sample mean of character over without abrupt discontinuity between ranges of gradual change. Genetically based cline in character means reflect an evolutionary response by means of natural selection, to geographically varying environmental factor such as temperature. This is shown by frequency correlation between clines in morphological characters.

Alhstrom (1957) and Ajado *et. al.* (2004) reported that partial or complete isolation of groups of fish result in slight differences in body proportion. The differences might be due to environmental or hereditary factors. It could be inferred that differences observed in the three strains of *C. anguillaris* from different ecological ones may be due to environmental factors in the different locations. Yola is located within the Sudan savannah and lies between latitude 7^0 and 11^0 N of the equator and between longitudes 11^0 and 14^0 E of Greenwich meridian. The mean annual rainfall is about 1000mm and an average maximum temperature of 40^{0c} (Adebayo, 1999). Kainji is located in derived guinea savannah and lies between the latitudes10^0 11' and 13^0 53' N and longitudes 10^0 14' and $14^0$30' E., the maximum temperature is above 41^0C in the hottest months. The estimation of genetic distances produced UPGMA dendrograms with similar clustering patterns. It also detected correlations between genetic and geographical distances for some population pairs, with large genetics distance being found between distantly located populations. Geographical isolation of their water bodies and may result from restricted intermingle and subsequent morphological differentiation. This result is in line with the work of swaine *et al.* (1991), that environmental changes and modification of morphology mitigate the effects of environmental variation. The difference in the environmental conditions between the locations could be responsible for the variations in the amino acid constitution.

Maiduguri samples were collected from Lake alau isolated in the Northeast of Nigeria, which is far from the other three *C. anguillaris* populations from Onitsha, Kainji and Yola. Contrastingly, the close relationship between Onitsha, Kainji and Yola *C. anguillaris* population could be due to the connecting River Benue and Niger. Since River Benue is a major tributary of River Niger, there is

the possibility of intermixing of fish from the two rivers, likely leading to high levels of gene flow and inter-population similarities between these riverine populations. These result agreed with the study on catla catla from different rivers and geographical locations in Bangladesh (Islam and Alam, 2004, Islam *et al*., 2005, Islam *et al*., 2007; Rahman *et al.*,2009 Volckaer *et al.*,1994).

The phylogenetic tree showed that the samples were divided into three distinct clusters. This result agreed with Rahman *et al.*, 2009 that worked on different populations of Indian major carp from different rivers in Bangladesh. The result of this study could be attributed to their different ecological locations and hydrological zones. The close genetic variation between Kainji, Onitsha and Yola populations of *C. anguillaris* could be due to genetic mix between them, since there could be interbreeding in the wild. The upper Benue River is a tributary of River Niger; there is the likelihood that the *C. anguillaris* from the two river can interbreed. Maiduguri C. *anguillaris* population was separated alone and this could be because of the ecological zone and non-connectivity to any of the rivers the other populations were found. This also could be applicable to *H. bidorsalis* population from kainji and Maiduguri in this study. The study also showed that wild stocks of *C. anguillaris* and *H. bidorsalis* represented a diversified genetic resource which indicated that in situ management practices, such as preventing the wanton capture of fish and creating sanctuaries for protecting small stocks such as those from Maiduguri (Lake Alau), can help to maintain and conserve the present diverse gene pool.

In conclusion, the phylogenetic tree of the samples in this study revealed three distinct evolutionary linkages. The four strains of *C. anguillaris* belonged to the same ancestors through separated due to ecological differences and rivers of collection. Crossbreeding of these different strains of *C. anguillaris* will lead to the development of strain with better growth parameters for hatchery managers. Furthermore, breeding between two genetically distinct and distance populations may have a positive impact on aquaculture production.

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AGB14

MULTIFACTORIAL ANALYSES OF MORPHOLOGICAL TRAITS OF HELMETED GUINEA FOWLS *NUMIDIA MELEAGRIS*

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ABSTRACT
A cross-sectional design was used to study possible variations in a population of helmeted guinea fowl (HGF). Data was collected on some qualitative and quantitative traits of morphologically distinct HGF and were analysed using Principal Component Analysis (PCA) procedure and cluster analysis. The study showed that the first two components accounted for 53.3% of the total variations obtained in the entire study zones. Variations among the entire population was due to quantitative traits such as body weight (BWT), body length (BOL), shank length (SKL), shank circumference (SKC) and wing span (WGS). Qualitative traits such as neck colour (NKC), wattle colour (WTC), eye colour (EYC), breast colour (BRC), beak colour (BKC) and shank colour (SHC) that were positively and significantly related to body weight varied between the entire populations of HGF. The study also indicated that there are five distinct varieties of HGF in the study zone. Variations observed in some qualitative and quantitative traits would be useful in selection and in breeding commercially improved strains of HGF for meat purposes at genomic level.

Key words: breeding, helmeted guinea fowl, markers, selection

INTRODUCTION
Multifactorial analyses of morphological traits have proven to be suitable in assessing the variation within a population and can discriminate different population types when morphological variables are considered simultaneously (Yakubu and Ibrahim, 2011). Various multivariate techniques such as PCA, cluster analysis, multivariate regression analysis, canonical correlation analysis and others have been applied for multivariate variable data analysis in the field of animal science and other related fields. PCA is designed to transform original variables into new, uncorrelated variables (axes) called principal components (PCs) which are linear combinations of the original variables (Shrestha *et al.*, 2008). PCA has capacity to reduce the original variables measured into few components/factors to provide information on the most meaningful parameters which will describe a whole set affording data reduction with minimum loss of original information (Helena *et al.*, 2000). Independent factor scores derived from this multivariate technique can be used to estimate body weight (Yakubu and Ayoade, 2009),

AGB15

THE EFFECTS OF GENOTYPE, PROXIMATE COMPOSITION AND CHARACTERISTICS OF THREE STRAINS OF LAYER TURKEYS ON EGG QUALITY TRAITS

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ABSTRACT

This study was conducted to determine the influence of egg genotype on internal, external and some proximate composition on egg traits. Ninety (90) fresh eggs of the three genotypes (exotic, crossbred and local strains) of layer turkeys were used. Genotype had significant effect ($p < 0.05$) on egg proximate composition and other egg traits. Egg quality trait in terms of crude protein highly favoured exotic compared to others. The analysis of variance showed significant genotype effect on egg weight and egg production traits. The mean weights of exotic turkey eggs (76.10g) were much heavier than the crossbred and local turkey eggs (65.85g), respectively. The egg length and egg width followed the same pattern. The proportion of shell weight to the egg weight was higher in exotic turkey (7.40g) than the local turkey (6.15g). Similarly, the exotic turkey eggs showed highest value in internal and external egg traits. The present study therefore indicates that genotype significantly affect egg weight and egg quality traits. The implication is that the egg quality traits are influenced by both genetic and non genetic factors.

Keywords: Local, crossbred, exotic, genotype, egg quality.

INTRODUCTION

In Nigeria, there are many varieties of poultry including Turkey. Turkeys are emerging as an important source of animal protein and provide essential substances as other meat but has comparatively low percentages of fat and high percentages of proteins (Nixey and Grey, 1985). The productivity and quality of the breeding egg has an overall effect for poultry flock and for economic breeding (Isidahomen *et al.*, 2011).Moreover, the external and internal quality traits are important in poultry breeding because of their influence on the yield on the progeny generation. The egg production of local turkeys can rose up to 99 eggs per hen per year with improved feeding, housing and health care (Tadelle *et al.*, 2000). The relationship between weight, length and width of eggs has been reported by Danilov (2000) who also noted the proportion of yolk, albumin and shell that contribute to the egg weight increase with hen's age. Thus egg weight is one of the important phenotypic traits which influences egg quality and reproductive fitness of the chicken parents (Islam *et al.*, 2001; Farooq *et al.*, 2001). Egg quality is composed of those characteristics of an egg that affects its acceptability to consumers such as cleanliness, freshness, egg weight, shell quality, yolk index etc (Song *et al.*, 2000). The assessment of proximate composition of different strains of turkey has been given less attention. Hence, this study examines the quality characteristic of egg of three strains. This study, therefore, was conducted to evaluate the proximate composition, egg quality of different strains of local, crossbred and exotic turkey eggs.

MATERIALS AND METHODS

This study was conducted at the Poultry Unit of the Teaching and Research Farm, Ambrose Alli University, Ekpoma, Edo State, Nigeria. Ninety fresh eggs each from three strains namely: local, crossbred and exotic turkeys were used to obtain the eggs quality traits of these turkeys. These comprised 30 eggs from each genotype. The eggs collected were sorted and pedigreed along each sire line. All hens were wing tagged for proper identification and subjected to the same management practices throughout the experimental period. The birds were fed *ad libitum* with layer mash containing 16% Crude Protein and 2800kcal/kg Metabolisable Energy.

Data were collected on:

Body Weight: This was taken on individual bird from each female turkey with the aid of a scale balance in kg.

Egg Weight: This was taken on individual eggs from each layer with the aid of an electronic balance having sensitivity of 0.01g.

Egg Length: A Venier caliper with an accuracy of 0.1mm was used to determine the egg length. It was taken as the longitudinal distance between the narrow and the broad ends.

Egg Width: It was measured to the nearest 0.1mm with venier caliper. The egg width was taken as the diameter of the widest cross-sectioned region.

Egg shell weight: This was taken on individual eggs from each layer with the aid of an electronic balance having sensitivity of 0.01g.

Egg shell Thickness: It was measured to the nearest 0.1mm with micrometer screw gauge

Yolk weight: This was taken on individual eggs from each layer with the aid of an electronic balance having sensitivity of 0.01g.

Yolk length: A Venier caliper with an accuracy of 0.1mm was used to determine the egg yolk length. It was taken as the longitudinal distance between ends.

Yolk height: It was measured to the nearest 0.1mm with venier caliper. The egg height was taken as the distance between the base and the height.

Proximate composition: The Proximate composition of eggs was determined according to the method of AOAC (1980).

All data collected were subjected to Analysis of Variance using generalized linear model (GLM) of SAS (1999). Significant differences were computed using New Duncan multiple range test (Gomez and Gomez, 1984) to determine the significance of specific classes.

The data were analyzed using the model specified below:

The model is stated thus:

$Y_{ijk} = \mu + G_i + \Sigma_{ij}$

Where,

Y_{ijk} = dependent Variable

μ = overall mean

G_i = effect of the i^{th} genotype on egg traits

Σ_{ij} = random residual error

RESULTS AND DISCUSSION

Least square means and standard error of proximate composition as affected by genotype are presented in Table 1. Genotype significantly affected ($P< 0.05$) proximate composition. The crude protein value was highest in Exotic egg strain (22.03) while the least value was recorded in Local egg strain (19.45), the ash content was highest in the Local egg strain (9.52%) and lowest in the Exotic (3.79%). The Moisture content was highest in the Local egg strain (30. 68%) and lowest in the Exotic egg strain (27.14%).

Least square means and standard error of egg weight as affected by genotype are presented in Table 2. Egg weight were found to have significant ($P<0.05$) effect in this study. Exotic egg strain had the

highest mean value (76.10) while the Local egg strain had the least (65.85). Egg length followed the same trend with egg weight (6.27), while Local egg strain had the least mean value of egg width (5.85). For albumin weight, yolk weight and yolk length and other parameters measured favoured the exotic chicken when compared with their local and crossbreds.

Table 1: Least-squares means and standard error of means on turkey eggs proximate composition as affected by genotype

Parameters	**Local**	**Exotic**	**Crossbred**
Either Extract (%)	33.77 ± 0.09^{b}	36.79 ± 0.82^{a}	34.54 ± 0.01^{b}
Crude Protein (%)	19.45 ± 0.00^{c}	22.03 ± 0.00^{a}	20.70 ± 0.01^{b}
Ash (%)	9.52 ± 0.88^{a}	3.79 ± 0.40^{c}	6.66 ± 0.13^{b}
Nitrogen Free Extract (%)	6.98 ± 0.19^{c}	12.06 ± 0.09^{a}	9.11 ± 0.01^{b}
Moisture (%)	30.68 ± 0.09^{a}	27.14 ± 0.00^{c}	28.99 ± 0.01^{b}

a,b,c means in the same row with different superscripts are significantly different ($P < 0.05$)

Table 2.Least square means and standard error of means of weight, external and internal egg quality of turkey as affected by genotype

Parameters	Local	Exotic	Crossbred
Egg weight(g)	$65.85\pm0,87^{c}$	76.10 ± 1.71^{a}	70.98 ± 0.92^{b}
Egg length(cm)	5.85 ± 0.09^{b}	6.27 ± 0.16^{a}	6.09 ± 0.09^{ab}
Egg length (cm)	4.04 ± 0.05^{b}	4.32 ± 0.07^{a}	4.14 ± 0.06^{b}
Shell weight(g)	6.20 ± 0.09^{c}	7.35 ± 0.10^{a}	6.55 ± 0.15^{b}
Shell thickness (%)	0.34 ± 0.00^{b}	0.36 ± 0.00^{a}	0.36 ± 0.00^{a}
Albumin weight (g)	43.70 ± 0.47^{c}	54.00 ± 0.32^{a}	47.45 ± 0.39^{b}
Yolk weight (g)	25.10 ± 0.16^{a}	24.45 ± 0.34^{a}	23.15 ± 1.13^{a}
Yolk length (cm)	3.90 ± 0.02^{c}	4.32 ± 0.06^{a}	4.13 ± 0.04^{b}
Yolk Height(MM)	0.82 ± 0.02^{b}	1.03 ± 0.02^{a}	1.01 ± 0.01^{a}

Means and in the same row with different superscript are significantly different ($P<0.05$)

Crude protein in this study were found to have significant ($P<0.05$) effect in this study. Exotic genotype had the highest value while the local had the least value. This is in agreement with findings of (Faga *et al.*, 1989; Isidahomen *et al.,* 2009) who observed that genotype significantly affected crude protein irrespective of the size. Also the values fall within the range reported by Babangida *et al.,* (2006). Moisture content favoured the local turkey eggs showing the highest mean value and the least value was observed among the exotic. The reason could be due to their genetic make-up. However, the values recorded were lower compared to the report of Olomu (2003). Also the values fall within the range according to Babangida *et al.*, (2006) and Olomu (2003). The values for ether extract was also highest in exotic genotype and the lowest was observed in local which may also be due to their genetic make-up, which is in agreement with the report of Isidahomen *et al*. (2013). Exotic birds also recorded the lowest ash value while the highest value was recorded in local egg genotype. However, the value did not agree with the work of Babangida *el al*., (2006), but in consonance with the report of Isidahomen *et al*. (2013) who reported that the exotic chicken eggs had the highest value and the least value was recorded in the Normal local chicken. This could be attributed to environment and the analytical procedure involved. Exotic birds also recorded the lowest moisture value while the local had the highest value. However, the value did not agree with the work of Babangida *el al*. (2006).

The exotic turkey weight was much higher than the crossbred and local. This is basically due to the vast difference in size of this genotype (Isidahomen *et al*., 2011). The absolute weight of external and internal egg characteristics were significantly ($P<0.05$) higher in exotic and crossbreds compared to local turkeys. The differences were obviously due to much higher egg weight in the

turkeys. The effect of genetic group on egg weight were significantly (P<0.05) different. Exotic turkey had higher egg weight than local turkey. The difference between the three might be expected. In general, the egg weight of local turkey is low compared to exotic turkey. The reason for the higher weight might be due to the fact that it is an improved genotype. (Sharma *et al.,* 2006). Egg weight variations in different genetic groups have been reported by many authors (Washburnn, 1990; Padhi *et al.,* 1998; Chatterjee *et al.,* 2007a). The effects of genetic group on egg length and egg width were also significantly (P<0.05) different from each other. The exotic turkey showed higher values in egg length and egg width than the local turkey. Shell weight was significantly (P<0.05) affected by genetic group. The egg shell weights were significantly higher in exotic turkeys than those of local turkeys (Padhi *et al.,* 1998). Shell thickness varied significantly (P<0.05) between genetic groups. The shells of exotic turkey eggs were thicker than their local counterparts. The mean shell thickness was better for their suitability (Parmer *et al.,* 2006; Padhi *et al.,* 1998; Wani *et al.,* 2007; Chatterjee *et al.,* 2007b). The albumin weight differed significantly (P<0.05) between the genetic groups. Exotic turkey eggs had better albumin weight than the local and this is in agreement with the report of Parmer *et al.* (2006) and Chatterjee *et al.* (2007b). The reason for the higher weight might be due to the fact that it is an improved genotype. Yolk weight value were significantly (P<0.05) influenced by genotype. The yolk weights were significantly higher in local than exotic birds (Isidahomen *et al.,* 2011). Parmer *et al.* (2006) also observed lower yolk weight index for kadknult birds. However, higher yolk length and yolk height and were also observed in this experiment. The values support the reports by Singh *et al.,* 1993 and Sachdera *et al.,* 2006).

CONCLUSION

The present study therefore indicates that genotype, significantly affect egg weight and egg quality traits. The implication is that the egg quality traits are influenced by both genetic and non genetic factors. The crossbred eggs were very close to the exotic, suggesting that eggs quality traits of turkey could be improved by crossbreeding.

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AGB16

RELATIONS BETWEEN AGE AND WEIGHT AT FIRST EGG AND EGG PRODUCTION TRAITS OF JAPANESE QUAILS.

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ABSTRACT
The relationship between age and weight at frst egg and egg production traits of the Japanese quail were investigated. The study, carried out at the Poultry unit of the University of Maiduguri Livestock Teaching and Research farm, involved 180 female Japanese quails housed individually in cages. The age and weight at first eggs were 65.15 days and 148.44g, respectively. The total egg number (52 weeks) was 275.69 with egg mass and hen day egg production of 2539.6g and 78.84%, respectively, while the weight of first egg was 8.75g. Age at first egg significantly ($P<0.05$) affected all the egg production traits while weight at first egg did not. Birds that matured earlier (8 weeks) had significantly ($P<0.05$) higher total egg number, mass and hen day egg production. However, they had lower first egg weight. Age and weight at first egg had low but positive correlation (0.11). The correlation between age at first egg and egg production traits were high and negative (-0.4687

to -0.5167) indicating that early maturity results in higher egg production. Thus, selection for early maturity in Japanese quail may result in higher egg production.
Keywords: Age, weight, first egg, egg production, Japanese quails

INTRODUCTION

The Japanese quail is gradually becoming a popular poultry species among Nigerians. It is the smallest avian species farmed for egg and meat production in the world. Some of its distinct characteristics include small body size, early sexual maturity, high rate of production (290 - 300 eggs/year), short generation interval, low maintenance cost and high resistance to common poultry diseases (Hassan *et al.,* 2003). Age and weight at sexual maturity and egg production are important economic traits in the Japanese quail. Jadhav and Siddiqui (2007) observed that quails start to lay at 6 - 7 weeks of age and reach peak production at 13 – 14 weeks with a decline from 25 weeks. Ages at sexual maturity of 65.6 (Sachdev and Ahuja, 1986), 48.9 - 49.6 (Thomas and Ahuja, 1988), 58 (Kocak *et al.,* 1995), 39.8-51.1 (Inal *et al.,* 1996), 45.9 (Gunes and Cerit, 2001) and 44.9 days (Camci *et al.,* 2002) have been reported. Similarly, weights at sexual maturity reported by some authors were 181 – 200 g (Sachdev and Ahuja, 1986), 122.9 -128.2 g (Sreenivasaiah and Joshi, 1988), 145.2 g (El-Ibiary *et al.*, 1966) and 202.2 g (Kocak *et al.,* 1995). A number of authors posited that age at sexual maturity was fairly related to body weight and that quails with higher body weights at sexual maturity had higher egg production rate (Gunes and Cerit, 2001; Camci *et al.,* 2002). The report of Camci *et al.* (2002) indicated that birds that matured late (50-56 days) had higher body weight and lower hen-day egg production than those that matured early (36-42 days). Gebherdt-hendrich and Marks (1995) reported a correlation of 0.25 between age at sexual maturity and body weight. While Kocak *et al.* (1995) reported a value of 0.29. Correlation values of 0.33 and 0.18 were reported by Camci *et al.* (2002) and Gunes and Cerit (2001), respectively. Eitan and Soller (2001) observed that several factors contribute to variability in onset of egg production in chickens, turkeys and quails. Oruwari and Brody (1988) observed that chronological age alone is not a primary effector of sexual maturity rather there is a complex relationship between age, body weight, body composition and sexual maturity. This is supported by Soller *et al.* (1984) and Zelenka *et al.* (1984) who postulated that there are minimum ages, body weight and body composition values for attainment of sexual maturity in female birds. Thus, to select for good egg producers, it is important to establish the relationship between age and weight at first egg and egg production traits. The aim of this study is to determine the relationship between age and weight at first egg and, egg production traits of the Japanese quail.

MATERIALS AND METHODS

The study was carried out at the Poultry Unit of the University of Maiduguri Livestock Teaching and Research Farm, Maiduguri, Borno State, Nigeria. Maiduguri, the Borno State capital is situated on latitude $11^0 5^{'}$ N, longitude $13^0 09^{'}$ E (Encarta, 2007) and at an altitude of 354 m above sea level. The area falls within the Sahelian region of West Africa, which is noted for great climatic and seasonal variations. It has very short period (3 – 4 months) of rainfall of 645.9 mm/annum with a long dry season of about 8 – 9 months. The ambient temperature could be as low as 20^0C during the dry cold season and as high as 44^0C during the dry hot season. Relative humidity is 45% in August which usually lowers to about 5% in December and January. Day length varies from 11 to 12 hours. One hundred and eighty (180) four-week old female Japanese quails housed in individual cages (30x30x45 cm) fitted with improvised feeders and drinkers, were used for the study which lasted 60 weeks. They were fed commercial broiler starter ration containing 23% Crude Protein and 3000 kcal/kg of Metabolizable Energy (ME) to 6 weeks of age and breeder diet containing 18% Crude Protein and 2800 kcal/kg of ME subsequently (NRC, 1994). They had access to the feed and water *ad libitum*. Age at sexual maturity was taken as the age (days) when the bird laid its first egg. The weight was also recorded as the weight at first egg and egg production then recoded for each hen till the end of the experiment. For statistical analysis, hens were grouped according to their age at first

egg into 8 (56 – 62 days) and 9 (63 -70 days) weeks. They were also grouped according to body weights into 120 – 140, 141 – 160 and 161 – 180 g with 20 g between groups. Data collected were subjected to Analysis of Variance using Statistix 8.0 Software and significant means separated by Least Significant Difference (LSD). The model used for the analysis was as follows:

$Y_{ij} = \mu + S_i + W_j + e_{ij}$

where

Y_{ij} = observation on individual measurement based on the i,j classification

μ = overall mean

S_i = fixed effect of age at first egg

W_j = fixed effect of weight at first egg

e_{ij} = random error

Phenotypic correlation between variables was also calculated using the same software.

RESULTS AND DISCUSSION

Descriptive statistics of egg production traits are presented on Table 1. Age at first egg was 65.15 days with a body and egg weight of 148.44 and 8.75 g. The total egg number was 275.69 with an egg mass and hen day egg production of 2539.6 g and 78.8%. The age at first egg for birds in this study was similar to 65.6 days reported by Sachdev and Ahuja (1986) but higher than 58, 45.9 and 44.9 days obtained by Kocak *et al.* (1995), Gunes and Cerit (2001) and Camci *et al.* (2002), respectively. Similarly, weight at first egg was similar to 145.2 g reported by El-Ibiary *et al*. (1966), higher than 122.9 -128.2g obtained by Sreenivasaiah and Joshi (1988) but lower than 202.2g reported by Kocak *et al.* (1995). The total egg production obtained was close to 282 reported by Cerit (1997) but lower than 287 and 290 obtained by Gunes and Cerit (2001) and Sundaram (1989). It was however higher than 205.7 reported by Sachdev and Ahuja (1986). The variations in egg production traits may have been due to differences in environment, nutrition and management.

The means of egg production traits as affected by age and weight at first egg are presented on Table 2. The effect of age at first egg was significant ($P<0.05$) on egg production traits while weight at first egg did not affect them significantly. Birds that matured earlier (8 weeks), had higher total egg number and mass and, hen day egg production. However, they had lower first egg weight. This may be due to the fact that egg weight is more a function of body weight than age, and early maturing birds had lower body weights than late maturing ones. Consequently, they laid smaller eggs. However, egg mass was higher because they laid more eggs than late maturing quails. The non significant effect of weight at first egg on egg production was also reported by Gunes and Cerit (2001).

The phenotypic correlations between egg production traits are presented on Table 3. The correlation between age and weight at first egg was positive and significant ($P<0.05$) but low. Positive correlation indicates that early maturity results in lower body which was implicated in the significantly ($P<0.05$) lower weight of first egg. Similar result was reported by Gunes and Cerit (2001) though the magnitude of the relationship was higher (0.29 and 0.33) in the reports of Kocak *et al.* (1995) and Camci *et al.* (2002), respectively. The correlation between age at first egg and total egg number and mass, and hen day egg production was high, negative and significant ($P<0.01$). This implies that early maturing quails had higher values for the egg production traits except weight of first egg with which it had a positive relationship. Similar findings were reported by Kocak *et al.* (1995) and Camci *et al.* (2002).

CONCLUSION

In this study, Japanese quails that matured early had higher egg production indicating that selection for early age at first egg will lead to higher egg production.

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Table 1. Descriptive statistics of egg production traits

Variables	Mean	SD	SE	CV
Age at first egg (days)	65.15	4.12	0.72	6.3233
Weight at first egg (g)	148.44	14.39	2.54	9.6978
Total Egg number	275.69	19.32	3.41	7.0109
Total Egg mass (g)	2539.60	185.05	32.71	7.2867
Egg weight (g)	8.75	0.49	0.088	5.6854
Hen day egg production (%)	78.84	3.94	0.697	5.0004

Table 2. Means and SE of egg production traits as affected by age and weight at first egg in the Japanese quail

	Total egg number	Egg weight (g)	Total egg mass (g)	Hen day egg production (%)
Age at first egg (weeks)				
8	288.78 ± 5.26[a]	8.49 ± 0.12[b]	2680.0 ± 47.34[a]	81.19 ± 1.11[a]
9	269.63 ± 4.28[b]	8.98 ± 0.10[a]	2481.6 ± 38.61[b]	77.79 ± 0.90[b]
Weight at first egg (g)				
120 -140	275.14 ± 5.29	8.54 ± 0.12	2505.7 ± 47.67	78.78 ± 1.12
141- 160	278.15 ± 4.54	8.71 ± 0.11	2573.9 ± 40.94	79.23 ± 0.96
161-180	284.31 ± 7.87	8.95 ± 0.19	2662.8 ± 70.83	80.46 ± 1.66

Means within columns with different superscripts are significantly (P<0.05) different

Table 3. Correlation coefficients between egg production traits of the Japanese quail

	Age at first egg	Weight at first egg	Total Egg number	Egg weight	Total Egg mass
Weight at first egg	0.1147*				
Total egg number	-0.5167**	0.0490			
Egg weight	0.4790**	0.3652*	-0.2218*		
Total egg mass	-0.5056**	0.1842*	0.9382**	-0.1936*	
Hen day egg prod.	-0.4687**	0.0416	0.9539**	-0.2210**	0.8957**

* P<0.05 ** P<0.01

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TILAPIA GENETIC RESOURCE CONSERVATION IN NIGERIA

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ABSTRACT

Tilapia aquaculture has experienced rapid development globally in recent years, which has made China the largest tilapia producing country in the world. The paper reviews the major species of tilapia in Nigerian water which include *Oreochromis niloticus, Tilapia guineensis, T.zilli, Sarotherodon galileaus* and *S. melanotheron*. However, there are a number of unidentified cichlid which could contribute significantly to national fish production among which is the ecotype cichlid commonly called 'wesafu', with eco-fidelity to Epe lagoon, Lagos where it grows to 1,500g and 414mm in the wild. Previous studies have revealed that Nigeria has a pool of tilapia genetic resources of great growth potentials yet to be exploited. The study of growth performance index of natural populations of tilapia revealed that *Oreochromis niloticus* caught from Kainji Lake in Nigeria had the highest growth performance index (3.11) when compared with other strains across the globe. The high growth performance index may be an indication of better growth when brought into captivity for domestication. Such information is important to the development of tilapia culture in Nigeria. Genetic breeding and biotechnology have not been explored in Nigeria due to a number of challenges which include poor funding of genetic research, poor manpower development, inadequate research facilities as well as poor documentation of the genetic resources. For Nigeria to benefit from the revolution in the tilapia industry globally, efforts should be made to assemble and characterize our tilapia genetic resources and explore the knowledge of biotechnology and genetic breeding to improve the stocks.

Keywords: Tilapia, genetic resource, conservation, Nigeria

INTRODUCTION

Throughout the world, aquaculture is being looked upon as a panacea for meeting the increasing demand for fish, as catches from open waters are declining due to over exploitation and degradation of fish habitats. Fish production from inland open waters declined due to over exploitation, intensive agriculture, industrial development, erosion and siltation, reclamation of land for human

settlement, pollution, destruction of mangrove forests, e.t.c. Fish farming therefore appears to hold the key for enhanced global fish production.

Among the numerous species of fish for culture, tilapia is widely recognized as one of the most popular species for a wide range of aquaculture systems worldwide. It is an ideal candidate for warmwater aquaculture (Tahoun *et al*., 2008). Tilapia generally differs greatly in size and taxonomic group (Olojo, 2003). Essentially, there are three genera of Ttlapia based on reproductive behaviour. They are; *Oreochromis, Sarotherodon and Tilapia. Oreochromis species* are maternal mouthbrooders, *Sarotherondon species* are bi-parental mouthbrooders while *Tilapia* are substrate spawner (Popma and Lovshin, 1996). In the early 1970s, all commercially important tilapias were grouped under the genus tilapia. But by mid-1970, the mouth brooding species were separated from the species that incubated their eggs externally and were placed in the genus *Sarotherodon.* About 1983, the maternal mouth brooders species of *Sarotherodon* were separated again, this time to the genus *Oreochromis.* Consequently, an important aquacultural species such as Nile tilapia now reported as *Oreochromis niloticus* was called *Sarotherodon niloticus* in 1980, and prior to that time, was identified as *Tilapia nilotica*, the author reported.

Worldwide, Nile tilapia (*Oreochromis niloticus*) is the leading species accounting for over 80% of tilapia production globally, with China as the leading producer. Production of this species increased during the year, 2001-2006 from 1,113,737MT to 1,988,726MT representing a growth of 79% (FAO, 2008), thus making it one of the fastest growing freshwater aquaculture production. Globally tilapia production is growing at a very high rate, with a 12.2% average annual increase in production during the past decade (El-Sayed, 2006).

TILAPIA PRODUCTION AND GENETIC RESOURCES IN NIGERIA

Nigeria was the largest producer of farm-raised tilapias in Africa, after Egypt a few decades ago (El-Sayed, 2006). In 1950, there were only two countries in Africa that had record of tilapia production, namely, Egypt with production figure of 700 Metric tons and Nigeria with production figure of 208 Metric tons the author reported. It is sad however, to note that, while Egypt's production of tilapia is in excess of 500, 000 Metric tons, Nigeria produces less than 50,000 Metric tons. In West Africa, Nigeria is one of the largest producer of tilapia (Table 1)

Table 1: A table of West African countries and tilapia production

Country	**Inland fisheries Production(MT)**	**Tilapia Production(MT)**
1.Benin	35,000.0	7,000.0
2.Burkina Faso	7,500.0	1,500.0
3.Cote d'Ivoire	11,650.0	2330.0
4.Gambia	2,500.0	500.0
5.Ghana	75,580.0	14,716.0
6.Guinea	4,000.0	800.0
7.G. Bissau	250.0	50.0
8.Liberia	4,000.0	800.0
9.Mali	111,910.	22,382.0
10.Niger	4135.0	827.0
11.**Nigeria**	**67**,**794**.**0**	**13**,**558.0**
12. Senegal	47**,**500.0	9**,**500.0
13.Sierra Leone	14,500.0	2,900.0
14 Togo	5,000.0	1,000.0
Total	**389 319.0**	**60 578.0**

Source: Abban and Agyakwa (2004).

The bulk of tilapia production in Nigeria is from natural population in rivers, lake and lagoons. In Nigeria tilapias are cultivated in ponds, reservoirs and cages in Nigeria (Fagbenro *et al*., 2004) and are suitable in low-tech farming systems. This is because of their relatively fast growth rate, ability to convert low protein feed to flesh, resistance to environmental variables, ease of reproduction in captivity and tolerance to wide ranges of disease conditions (Fagbenro, 1987). Tilapia farming in Nigeria remained largely a subsistence level activity until 2000, when it began to expand rapidly following the successful commercial farming of catfishes (Fagbenro, 2006; Afolabi *et al.,* 2007). There is a wide range of tilapia genetic resources in Nigeria. They include, *Tilapia zillii*, *T. guineensis* (substrate spawners, macro-phytophagous (generally herbivorous), *Sarotherodon galilaeus*, *S. melanotheron* (bi-parental mouth-brooders, micro-phytophagous (planktophagous), *Oreochromis niloticus* and *O. aureus* (maternal mouth-brooders, omnivorous).

There are however a number of unidentified tilapia in our waters. Among this is the ecotype cichlid commonly called 'wesafu' having eco-fidelity to Epe lagoon. This fish grows to 1,500g and 414mm in the wild (Fashina-Bombata *et al*., 2006, 2007; Megbowon and Fashina- Bombatta, 2010). It has a deep body that makes a candidate for filleting. Recent studies on 'wesafu' indicated that it is maternal mouth brooder (Oreochromis) (Fashina-Bombata and Megbowon, 2012). The fish had improved crude protein over other cichlid fishes of Epe lagoon where it is abundantly caught (Bombata *et al*., 2013). DNA analysis using RAPD further showed 'wesafu' is unique in its band when compared with known species. However, molecular studies on the fish using mtDNA, using cytochrome oxidate sub unit 1 revealed that 'wesafu' could be one of the three known species namely, *Sarotherodon boulengeri* (99.45% confidence), *Oreochromis niloticus* (99.36%) and *Oreochromis aureus* (99.33% confidence) (Jayasaker *et al*., 2012). Considering the morphological features of these species which is at variance with 'wesafu', it may be right to say that 'wesafu' is the product of hybridization of any of these known species.

It is heartwarming to note that Nigerian waters have tilapia genetic resources of outstanding status. The report of Moreau *et al.* (1986) who reported that *O. niloticus* obtained from Kainji, Nigeria had the highest growth performance index of 3.11 when compared with other natural populations from different continents of the world is remarkable. Today fishermen still catch tilapia weighing over 1.5kg from our waters. It is therefore necessary to first assemble information on the genetic status of these fish for possible genetic improvement programme. The high growth performance index of this strain of *O. niloticus* may be an indication of better growth when brought into captivity for domestication. Such information is important to the development of tilapia culture in Nigeria.

PROBLEMS AND PROSPECTS OF TILAPIA IN NIGERIA

Although the potential for tilapia culture is high, the production in Africa and more importantly, Nigeria is very low; the draw-back being the precocious maturity, uncontrolled reproduction in ponds leading to increased competition for food, reduction in growth rate which results in a phenomenon referred to as stunting (Bombatta *et al.,* 2005; Baroiller and Toguyemi, 1996). This early maturation and frequent spawning are management challenges when working with tilapia. However, the culture of monosex produces a better result. Male tilapia is preferred for culture because of their faster growth. It is however usually difficult to differentiate male and female tilapia when they are young (less than 3-4"). When the fish are larger, they can be separated by inspecting the genital papilla on the ventral or underside of the fish. The papilla of the male tends to be elongated with one opening. The papilla of the female tends to be wider, and has two openings, one of which is a transverse slit.

Furthermore, we need to properly identify the genetic status of our tilapia and genetically improve them. However, genetic improvement of tilapia in Nigeria is likely to face a major setback due to lack of fish genetic research facilities, poor funding of genetic research, poor manpower

development, inadequate research facilities as well as poor documentation of the genetic resources. Genetic resources are global assets (Megbowon, 2011). Information on tilapia genetic resources in Nigeria is lacking. Many of tilapia species have high growth potential. The report of Moreau *et al.* (1986) who reported that *O. niloticus* obtained from Kainji, Nigeria had the highest growth performance index of 3.11 when compared with other natural populations from different continents of the world is remarkable. Today fishermen still catch tilapia weighing over 1.5kg from our waters (Megbowon *et al.*, 2009). It is therefore necessary to first assemble information on the genetic status of these fish for possible genetic improvement programme.

STRATEGIES FOR IMPROVED TILAPIA AQUCULTURE IN NIGERIA

Agricultural production is presently enhanced through genetic improvement of germplasm leading to improved varieties (Megbowon *et al.*, 2009). For improved tilapia production in Nigeria, there must of necessity, be a program on the characterization of our tilapia genetic resources. The resources should be assemble and characterize using modern tools such as molecular assays (DNA analysis), considering the fact that many cichlid fishes are genetically similar. This should then be followed with genetic improvement. Our genetic improvement program might begin with several generations of selective breeding, as it is done in GIFT (Genetic Improvement of Farmed Tilapia).

Tilapia has great potential in Nigeria as an alternative and/or additional species of farmed fish. The mud catfish (*Clarias gariepinus*) is presently experiencing glut in Nigeria market with attendant poor market price, it become necessary to have an alternative species that command high market acceptance. Tilapia is the first candidate for consideration as a scaly fish having no religious or cultural resistance to consumption. Considering tilapia as one of the important and potential fish species, the following developmental areas and strategies are identified for necessary consideration:

•There abounds hundreds and thousands of seasonal water bodies (>0.1 ha) in the form of ditches, shallow ponds, road side canals and barrow pit that retains water for 4-6 months. These bodies of water have great potential for the culture of fish species having short generation period and characterized by faster growth rate requiring low input support (Hussain *et al.*, 2000). In such cases, tilapia can be a promising candidate for aquaculture in the suitable seasonal water bodies.

• Tilapia occupies an important position in rural aquaculture (Megbowon, 2010). Across the country, there abound countless number of dams, rivers, lagoon and lakes where cages can be installed. The installation of cages will fast track the production process as the cost of water procurement/ pumping is eliminated. Furthermore, aeration is important to the culture and profitability of tilapia farming. In such bodies of water, particularly flowing water (rivers and lagoons) the cost of aeration will be reduced. In cage culture, tilapia prolific spawning is eliminated as the egg released pass through the mesh of the cage and get lost thus preventing reproduction which will in effect eliminate the phenomenon of stunting, a disincentive to tilapia farming.

• Furthermore, Nigeria must explore the knowledge of biotechnology and genetic breeding to improve her stocks. Such biotechnology tools such as chromosomal manipulation through polyploidy, transgenic and production of YY super male technology could be the future focus of our tilapia genetic resources development.

CONCLUSION

Tilapia holds the key to rural aquaculture in Nigeria. However, its potentials will only be optimized if adequate attention is given to its genetic resources and its development. This development will boost food security, poverty eradication and sustainable livelihood of the rural dwellers.

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AGB18

POLYMERASE CHAIN REACTION DETECTION OF ASFV GENOME IN NIGERIAN INDIGENOUS PIGS

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ABSTRACT
This study was carried out at the Piggery unit of the Institute of Agricultural Research and Training (I.A.R&T.) Ibadan, Nigeria. Blood of pure Nigerian indigenous pigs (NIP) was collected from the jugular vein and the DNA extraction was done by using DNA kit (Zymobeads). Diagnostic Polymerase Chain Reaction for African Swine Fever Virus (ASFV) was performed according to the Manual of Diagnostic Tests and Vaccines. The ASF primers [PAS 1 (Forward) and PAS 2 (Reverse)] were utilized. A single discrete and specific band was observed in NIP and the infected samples collected from the University of Ibadan, Nigeria as positive control of the expected size

[278 base pairs (bp)]. The result showed that pure NIP was also infected with ASFV without it showing any clinical symptoms.

Keywords: Nigerian Indigenous pigs, polymerase chain reaction, African Swine Fever, tolerance

INTRODUCTION

The population of pig in Nigeria increases from 2 million in 1984 to 7 million in 1997 before the widespread of African Swine Fever (ASF) epizootic (Dafwang, 2010). The Nigerian Indigenous Pig (NIP) is becoming extinct as livestock genetic resource due to the high rate of genetic erosion that is caused by extensive indiscriminate and unplanned mating with exotic pig breeds. It has been acknowledged that the NIP is resistant to ASF but it has not been scientifically investigated and documented.

Disease is one of the factors that affect the livestock production in Nigeria (Abubakar, 2003). Jovanoic *et al.* (2009) stated that diseases can have a significant impact on animal productivity and production, human health and, consequently, on the overall process of economic development. Pigs harbour a range of parasites and diseases some of which are zoonotic. One of these is the ASF that is caused by a virus.

ASF is a highly contagious viral disease of pigs and of such concern that it is included among the List A diseases by the United Nations Office International des Epizooties (OIE) (Owolodun *et al.*, 2010; Sánchez-Vizcaíno *et al.*, 2009, 2010; OIE, 2008; Penrith, *et al*., 2004; FAO, 2010). It causes a devastating haemorrhagic fever of pigs with mortality rates approaching 100 per cent with the acute and peracute forms. It causes major economic losses, threatens food security and limits pig production in affected countries. The disease causes significant economic losses in affected countries due to the high mortality rates associated. The transmission of the disease, as it now occurs in sub-Saharan Africa, is through the African soft tick (*Ornithodoros moubata porcinus*) and Warthogs or domestic pigs. The transmission through the warthog and soft ticks does not occur in West Africa, although ASF virus has been detected from Warthog in Nigeria (Luther, 2008), and the presence of soft ticks has also been confirmed (Penrith *et al*., 2004). This study aimed at screening pure NIPs in the piggery unit of Institute of Agricultural Research and Training (I.A.R.T) in Ibadan to verify disease resistance of NIPs to ASF.

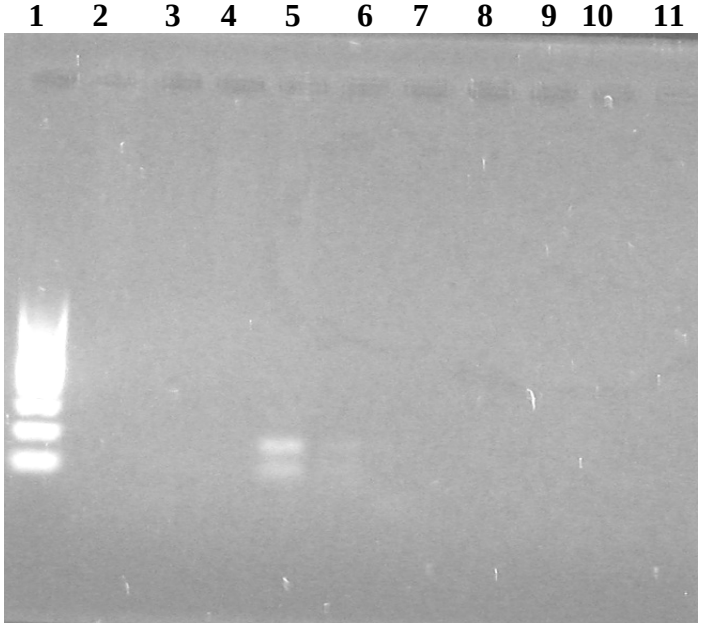
MATERIALS AND METHODS

Blood sample (5ml) of the pure NIPs was collected from the jugular vein into anticoagulant container. The DNA extraction was done by using DNA kit (Zymobeads). Diagnostic Polymerase Chain Reaction (PCR) was performed according to the Manual of Diagnostic Tests and Vaccines (OIE, 2008). ASF-specific primers (oligonucleotide primers) targeting the major capsid protein (VP72 gene) amplifying a 278-bp fragment within the conserved region was employed: PAS_1F: 5'-ATG GAT ACC GAG GGA ATA GC-3' and PAS_2R: 5'-CTT ACC GAT GAA AAT GAT AC-3' (Luther *et al*., 2007; OIE, 2008). The final reaction volume of 25 µl PCR master mix comprised 1·0 µl extracted DNA template, 10µl Nuclease Free Water, 1·0 µl oligonucleotide primers (for both Forward and Reverse) and 12 µl of already prepared Master Mix. Each tube was placed in an automated PCR thermal cycler (MG48+; Mygene^{TM} Series) for amplification for 35 cycles as follows: initial denaturation at 94°C for 3minutes for 35 cycles, with 3 steps of denaturation at 94°C for 30 seconds, annealing at 57°C for 45 seconds and extension at 72°C for 30 seconds and final extension at 72°C for 5 minutes. Amplification products were analyzed by electrophoresis on a 1% agarose gel containing 0.5 µg of ethidium bromide per ml. The gel was visualized under Ultra violet light and photographed.

RESULTS AND DISCUSSION

From the PCR for molecular investigation, a single discrete and specific band of the expected size (278 base pairs (bp) was observed for NIP in lane 6 while discrete band was observed for infected

animals collected from university of Ibadan used as positive control in lane 5 and no band was observed in lane 7 as negative control. The result showed that pure NIP was also infected with ASFV without showing any clinical symptoms.



Amplification at 278bp of NIP in lane 5, infected sample from University of Ibadan as a positive control in lane 6 and lane 7 showing the negative control without the DNA and molecular marker (100bp) in Lane1.

The 278bp of ASFV observed in NIP was corroborated by the findings of Luther, *et al*. (2007), where the same virus band was observed in Bush pigs and Warthogs tested at National Veterinary Research Institute (NVRI), Jos. The resistance of NIP to ASFV for long period without any clinical symptom or death was explained by Adeoye and Adebambo (2010) as the ability of host to trap ASFV within their tissues by the activities of macrophages that eat up the pathogens and infected tissues so that other parts and their mast cells in the tissues are not affected.

This observation was also explained by the work of Adeoye and Adebambo (2010) where serological tests were carried out on ASF outbreak survivors, their offspring and F_2 showed a decline in antibody levels against ASF from 100% to 18.79%. This phenomenon was explained as the ability of engulfed ASFV to be broken down easily and effectively by macrophages leading to decreasing circulation of ASFV in the blood and other tissue. Thus, the amount of shed ASFV particles observed in urine and faeces was seen to drop significantly in their offspring (Adeoye and Adebambo, 2010). This observation was also corroborated by Olugasa (2007) who also reported that level of infection in the serum dropped from 96.8% in the stock to 13.8% in young stock. The ability of the virus to persist in one host while killing another genetically related host has been established by Palgrave *et al.* (2011) where a particular sequence found in warthog and bush pigs was absent in domestic pigs.

There is the question of defining NIP so called ‘resistance’ to ASFV as whether it is ‘resistant’ or ‘tolerant’? An animal as a host can only evolve two types of defense mechanism to increase its fitness when challenged with pathogen which are resistance and tolerance (Doeschl-Wilson, 2012). It is important to distinguish between these two defense mechanisms in NIP because they have different pathological and epidemiological effects. An increased understanding of tolerance to pathogen infection could lead to more efficient treatments for infectious diseases and a better description of host–pathogen interactions. Jovanovic (2009) defines resistance as ability of an animal to resist infection (which means that the virus will not be seen in the animal), while tolerance signifies a condition in which the host is infected by the pathogen but displays very limited adverse effects. By this definition, we can classify NIP as being tolerant.

Both host resistance and tolerance enhance host fitness but major difference between the two is important in genetic improvement programme. The effects of resistance and tolerance can lead to striking difference in epidemiological and evolutionary outcomes in affected animals.

Disease control strategy using genetic improvement to obtain host resistance is better than disease control strategy using breeding to obtain host tolerance. This is because of their different epidemiological and evolutionary consequences, meaning that the ASF eradication in a population can only be achieved through increasing resistance while the tolerance will not constraint ASF replication. It has been argued that selective breeding may be more evolution-proof than manipulations in resistance because tolerance does not impose selection for pathogen counter-measures. FAO (2012) also stated that the breeding for increased resistance to ASFV may be possible, but there are several factors to be considered before embarking on such a program. One consideration is that resistant pigs that are unable to be infected by ASFV will be difficult to achieve. It is more likely that pigs will express a phenotype that will not succumb to the clinical effects of ASFV. While these type pigs may not express clinical disease, they may become infected and could shed ASFV into the environment. As such, these pigs could pose a risk to susceptible pigs in the area or undermine control strategies. Instead transcriptome analysis of ASFV-infected macrophages using microarrays can be used which will provide new candidate genes that are differentially regulated during infection. Such candidate genes could be used for development of DNA marker tests for selection of animals with reduced susceptibility to disease. Therefore conservation of resistant breeds is critical for progress in genetic resistance to ASFV.

CONCLUSION

From this study, it can be concluded that NIP has ASFV but do not exhibit any clinical sign.

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AGB19

PHYSIOLOGICAL EVALUATION OF PRE-WEANING GROWTH TRAITS IN NIP CROSSBREDS

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ABSTRACT

The study was carried out at the Piggery unit of the Institute of Agricultural Research and Training (I.A.R&T.) Ibadan, Nigeria. Forty-seven hybrid progenies from crossbreeding between the Nigerian Indigenous Pig (NIP) and Large White pigs were used. Body measurements and live weight were recorded weekly from first week of birth to their weaning date. Body measurements taken were Body Weight (BW), Body Length (BL), Snout Length (SL), Ear Length (EL), Body Height (BH), Heart girth (HG) and Rump circumference (RC) of crossbred progenies. The correlation between the reproductive parameters and growth performance of hybrid pigs were established with good management practice. The mean for weaning weight was 6.72±0.96, birth weight 0.91±0.15, litter size at birth 5.36 ±1.87, litter size at weaning 5.29 ±1.97, litter weight at birth 4.56 ±1.57, total litter weight at weaning 33.91±11.6, average daily weaning weight 0.73±0.12, average litter size at birth 0.93±0.11 and sex ratio 97.78±8.61%**.** The male and female mean values for weight of animals were 6.96±1.0 and 6.52± 0.9 with males heavier in weight and higher in morphometric traits such as BL, HG and RC, while the females exhibited higher SL, EL and BH. The correlation matrix for BW against linear body measurements in pre-weaned NIP crossbreds indicates that all the parameters could be used to select for BW. The linear equation generated by regressing BW on SL, BH, RC, HG and BL could be used by resource poor pig farmers in the estimation of BW of pre weaned crossbreds pigs if they cannot afford weighing scales.

Keywords: Morphometric measurement, pig, hybrid, correlation, regression

INTRODUCTION

Crossbreeding is a successful management practice for improving litter productivity in swine (Oseni, 2005). It is also an effective means of improving reproductive performance i.e. heterosis or hybrid vigour that comes from an increase in heterozygosity, which leads to better average genotypic values at dominant loci. Genetic improvement for reproductive and growth traits of Nigerian Indigenous Pig can be brought about by crossbreeding and long term selection within the existing population, provided additive genetic variance exists. This offers the opportunity to increase genetic variation from which leaner and more efficient animals can be selected (Wheeler and Campion, 1993). Evaluation of the performance of animals constitutes an essential part of successful breeding plans for sustainable genetics improvement. In order to develop a very good model for the genetic improvement of crossed pigs, it is important to measure the traits of interest. Pigs are mostly kept for their meat and the most important trait of interest for their genetic improvement is the body weight. According to Cam *et al.* (2010), body weight is a very important characteristic in animal husbandry due to its effect on economical profit. Live weight might be affected by different management, environment and enterprise feeding conditions. Proper measurement of this trait on-farm is sometimes difficult because of unavailability of weighing scale in the rural areas. Therefore use of simple linear body measurement parameters to predict live weight will be appreciated by the farmers. Some traits are usually regulated by the same pair of genes. Hence information on associations between traits is highly valuable in genetic improvements. In pig production, growth and reproductive traits are important (Mungate *et al.*, 1999; Hermesch *et al*., 2000a; Zhang *et al*., 2000). According to Adeola (2005) and Oke *et al*. (2006), age had been shown to have influence on morphological measurement of crossbred pigs. According to Adebambo (1983), productivity of breeding stock depends majorly on the reproductive efficiency, growth performance and feed efficiency. Many works have been carried out on Nigerian indigenous crossbreds (LW 50% X NIP 50%) by Adebambo and Detmers (1979), Adebambo (1981, 1983). They have reported superior values for exotic and crossbreds over the NIP in body weight, weaning weight at 52 days of age, average daily gain and milk yield.

This study focused on age, reproductive parameters and the relationship between live weight and morphological parameters such as snout length (SL), body length (BL), heart girth (HG), body height (BH) and rump circumference (RC). It is also to determine the strength of relationship and prediction of bodyweight from linear body measurements.

MATERIALS AND METHODS

The study was carried out at the Southern Farm, Piggery Unit of the Institute of Agricultural Research and Training (I.A.R&T.). Forty-seven hybrid progenies from crossbreeding between the NIP and Large white pigs were used. Body measurements were recorded weekly from first week of birth to their weaning date. Body measurements taken were Body Weight (BW), Body Length (BL), Snout Length (SL), Ear Length (EL), Body Height (BH), Heart girth (HG) and Rump (RC) of the progeny of crossed breed. Body Weight (BW), was measured with weighing scale, (BL), the length of the animal from the last cervical to the lumbar vertebra (base of the tail), Heart Girth (HG), the circumference of the chest region and rump circumference (RC) the circumference of the loin region; were measured with a measuring tape in centimeter. The following parameters were taken Litter size at birth (total number of piglets farrowed), Litter birth weight (Weight of all the piglets farrowed), Average birth weight (total weight of the number born alive divided by the total weight of the live litter size at birth), Litter size at weaning (number of piglets at weaning), Litter weaning weight (total weight of the piglets in each litter) Average daily gain pre – weaning (ADGPW) (a weakly difference of piglet weight). The data were analyzed using the general linear model (GLM) procedures where the differences between the characteristics of the growth Data weren summarized by using obtain variances for the estimation of morphometric traits and phenotypic correlations among pre-weaning traits such as BW, WW, LSB, LSW, ADWG,, TBW, TWW, SR%.

RESULTS AND DISCUSSION

There was no significant effect of sex on the birth weight as shown below. This result was corroborated with findings of Adeoye *et al*. (2012) where the pre-weaning weight of piglets from ASF survivors parents were not affected by sex. The heavier weight of male than females with 6.94kg was in corroboration with Adeoye *et al.* (2012), where the male was heavier than female with 7.13kg

Tables 1, 2 and 3 show the mean for reproductive traits, the morphometric traits .of hybrid pigs from age 1 to 7 weeks and the morphometric traits of male and female. The mean for weaning weight was 6.72±0.96, birth weight 0.91±0.15, litter size at birth 5.36 ±1.87, litter size at weaning 5.29 ±1.97, litter weight at birth 4.56 ±1.57, total litter weight at weaning 33.91±11.6, average daily weaning weight 0.73±0.12, average litter size at birth 0.93±0.11 and survival rate 97.78±8.61%**.** The values obtained are similar to those reported by Adeoye *et al.* (2012) in birth weight (1.05), weaning weight (7.08), litter size at weaning (5.72), but lower in litter weaning weight (38.85); while it was higher than that of Orheruata (2000) in weaning weight (4.87) and lower than is 14.50 reported by Ngere (1975). The litter size at birth is lower than that of Adebambo (1981) and Nwakpu and Ugwu (2009).

Table 1. Mean for reproductive traits

Traits	Mean (kg)
WW	6.72±0.96
BW	0.91±0.15
LSB	5.36 ±1.87
LSW	5.29 ±1.97
TLWB	4.56 ±1.57
TLWW	33.91±11.6
ADWG	0.73±0.12
ALSB	0.93±0.11
S.R%	97.78±8.61

BW-Body weight, BW- Birth weight, WW-Weaning weight, LSB-Average Litter size at birth, LSW- Litter size at weaning, ALSB-Average S.R-survival rate,

Table2: Mean for morphometric traits from week 1-7 weeks

	Traits					
WK	BW	SL	BL	BH	RC	HG
1	1.44	3.69±0.3	23.03±4.7	20.33±0.9	22.90±5.8	25.28±3.0
2	2.79	3.98±0.3	27.08±1.2	24.17±0.8	28.00±2.7	30.33±2.13
3	3.28	4.50±1.4	30.64±4.3	26.09±1.8	32.91±2.6	34.27±2.6
4	4.41	5.27±0.5	34.00±1.2	29.00±1.8	34.54±2.7	36.96±2.6
5	5.18	4.77±0.0	36.37±4.8	29.05±1.8	39.18±2.6	39.05±2.6
6	6.09	5.82±0.0	40.55±4.8	32.09±1.8	44.27±1.9	41.73±2.4
7	6.71	5.77±0.5	42.73±4.5	34.09±2.4	46.46±2.6	43.36±2.6

BW-Body weight, BL- Body Length, HG- Heart girth, NC- Neck circumference, SL- Snout Length, SC, TL – Tail length, RC- Rump circumference, BL- Body length, BH-Body height (Height at wither)

Male and female mean values for weight of animals were 6.96±1.0 and 6.52± 0.9 with male heavier in weight and higher in morphometric traits such as BL, HG and RC, while the female were high in morphometric traits such as SL, EL and BH.

Table 3: Mean (kg) for the morphometric traits of males and females

Traits	Male	Female
WT	6.96±1.0	6.52± 0.9
SL	6.86 ±0.8	6.88± 0.6
EL	9.21±1.2	9.39±1.2
BL	44.33±5.7	44.18± 4.3
HG	41.10±3.7	40.84±0.7
BH	34.19±3.1	34.95 ±3.3
RC	39.95±6.2	37.89±4.6

All the body parameters measured were positively and highly significantly (P< 0.001) correlated with BW (Table 4). The correlation coefficient ranged between 0.74 and 0.85. RC and BH had the highest correlation coefficient of 0.85 followed by HG and BH with values of 0.81, respectively.

Table 4. Pearson correlation Matrix of body weight and linear body measurements in preweaned NIP crossbreds.

Variables	WT	SL	BL	BH	RC	HG
WT		0.81	0.74	0.85	0.85	0.81
SL			0.68	0.71	0.73	0.76
BL				0.76	0.84	0.79
BH					0.78	0.68
RC						0.86
HG						

WT= weight, BL=Body length, SL=Snout length, RC=Rump circumference, BH= Body height, HG=Heart girth.

The best prediction equation for BW from body measurement variables is shown in Table 5. For a unit increase in SL, BH, RC and HG, the BW of pre weaned hybrid pigs will increase by 0.66, 0.20, 0.01 and 0.11Kg, respectively.

Table 5. Linear regressions relating body weight to various body linear measurements in preweaning NIP crossbreds.

Prediction Equations	Coefficient of determination (R^2)
BW=-7.80-0.01BL+0.66SL+0.20BH+0.01RC+0.113HG	0.86

M=Body linear measurement, BW=Body weight, BL=Body length, SL=Snout Circumference, RC=Rump circumference, HG=Heart girth.

There was low correlation between the weaning weight and other reproductive traits with the exception of average daily weight gain ADWG as shown in table below.

Table 6 . Pearson correlation matrix for reproductive traits

Traits	WWT	BW	ADWG	ALSB	TLWTB	TLWW	S.R %
WWT	1.00						
BW	0.23	1.00					
ADWG	0.99	0.08	1.00				
ALSB	0.21	0.99	0.06	1.00			
TLWTB	-0.32	0.06	-0.33	-0.00	1.00		
TLWW	-0.01	-0.26	0.03	-0.34	0.87	1.00	
S.R%	0.37	0.48	0.41	-0.08	0.41	-0.08	1.00

The high correlation observed between litter size at birth and at weaning (Table 6) is expected because an increase in the number of piglet in a litter will cause an increment in the total litter weight. The correlation between the litter size and weaning weight is corroborated with the findings of Nwakwu *et al.* (2007) and Nwagu et al. (2000), that there is positive and significant correlation between the liter size, weaning weight and survival rate of piglets. The negative correlation observed between litter size and average litter weight suggested that the factors that work for the increment of the litte**r** size also cause reduction of average weight of the piglets. A highly negative and significant correlation between litter size and mean kit weight at birth of rabbit was reported by Nwagu *et. al.* (2010). The relationship between average piglet weight and liter size is however not invariable. Litter size has low heritability (Rico *et al.*, 2000) and crossbreeding has been found to improve it (Adebambo, 1986)

The superior weaning weights of the crossbred pigs in this study also mean that the total litter weight at weaning was higher for the crossbred pigs. Such findings could support the argument that crossbred pigs can be utilized under smallholder farming systems. Whittemore (1993) suggested that the high weaning weights of crossbred pigs could also have been a reflection of their higher birth weights. Ncube *et. al*. (2003) reported that the heavier piglets of the crossbred were better able to compete for milk

because they were thriftier and hence had higher chances of surviving up to weaning.

One of the most common and most useful statistics that describes the degree of relationship between two variables is the correlation (Cam *et al.,* 2009). The estimation of accurate BW from animal's simple body measurements will make it easier for farmers in the rural areas, who has little or no access to weighing scale. Due to affordability of measuring tapes a producer can measure all the body measurements easily from a live animal and can determine body weight approximately. Teghe and Olorunda (1998) and Adeola (2009) reported similar results between BW and body measurements in pigs while Afolayan *et al*. (2006), Salako (2006) and Cankaya *et al*. (2009) reported same for sheep

According to the correlation modules, BW was found to be very highly correlated with all body dimensional traits measured (0.74-0.85). Of the body dimensional characters, Rump circumference and body height were the most related trait to weight and the correlation between these two traits was 0.85. Variables such as heart girth, body height, body length, which are directly related to the size and weight of animal, showed moderate to very high positive correlations with each other (0.68-0.86). However, the measure of snout length was lowly correlated with body length (0.68).The high correlation coefficient observed between body weight and the linear body measurement parameters shows that selection for these traits will result in correlated responses in these traits.

In most studies HG was found to be highly correlated with BW in pigs (Teghe and Olorunda, 1998), in sheep (Topal and Macit, 2004; Atta and khidir, 2004; Afolayan *et al*., 2006), in cattle (Koenen and Groen. 1997; Goe *et al.,* 2001; Heinrichs *et al.,* 2007) and in goats (Khan *et al.,* 2006; Nsoso *et al.,* 2003). The difference between this result and the mentioned literature can be attributed to the differences in age, nutrition and rearing conditions. Fattening status should be taken into consideration in order to predict an animal's BW from its body measurements. In this study, results suggest that variables with high correlation coefficients might be used to predict BW of preweaned NIP crossbreds. Khan *et al*. (2006) suggested that the highest relationship amongst body measurements may be used as selection criterion in traditional production systems in rural areas.

CONCLUSION

The correlation between the reproductive parameters and growth performance of hybrid pigs were established with good management practice. The correlation matrix for BW and linear body measurements in pre-weaned NIP crossbreds indicates that all the parameters could be used to select for BW. The linear equation generated by regressing BW on SL, BH, RC, HG and BL could be used by resource poor pig farmers in the estimation of BW of pre weaned crossbreds pigs if they cannot afford weighing scales

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AGB20

GROWTH PERFORMANCE OF MONOSEX AND MIXED POPULATION OF *OREOCHROMIS NILOTICUS*

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ABSTRACT

Growth performance of hand-sexed: male mono-sex, female mono-sex and mixed-sex population of tilapia *(Oreochromis niloticus)* was conducted in six aquaria tanks (60cm×30cm×30cm). The experimental tanks were stocked with 12 fingerlings per tank. Fish were cultured for 49days and fed at a daily rate of 5% of their body weight, the results of the experiment showed that male mono-sex tilapia showed significantly ($P<0.05$) higher growth rate (weight, length, DWG, SGR) than female and mixed sex group. Generally, male mono-sex fishes reached a larger final individual sizes (24.33±0.2g) , and female mono-sex (18.66±0.6g) while (17.89±1.2g) for mixed population group. The daily growth rate showed 0.23±0.2g for males, 0.1±0.01g for females and 0.09±0.02g for mixed population tilapia, respectively. Based on this result, male mono-sex *Oreochromis niloticus* grows faster than female mono-sex and mixed population.

Keywords: Monosex, *Oreochromis niloticus*, growth

INTRODUCTION

Tilapia have been successfully farmed under a wide range of environmental conditions and are important group of cultured fish species in many parts of the world, particularly in developing countries (El-sayad, 2006). Among the tilapia, *Oreochromis niloticus* was found to be suitable for semi-intensive culture system because of its ability to utilize a wide range of feed stuff originating from plants and animals (Liti *et al.*, 2005). *Oreochromis niloticus* is an important tropical freshwater fish because of its relative abundance due to their high fecundity, *Oreochromis niloticus* can be recognized by the characteristic pattern of dark and light bands crossing the caudal fin. The body is elongated and usually shows a number narrow bands on the back, it is one of the largest tilapia; reaching the considerable length of 50cm. However, their breeding habit has undesirable consequences. Some of the problems associated with the reproductive efficiency of *Oreochromis niloticus* are prolific reproduction and stunted growth in pond culture system (Phelps and Popma, 2000). Within a few months of culture period, the ponds get packed with various sizes of fishes and later, due to overpopulation the growth of the fish gets slower and the fish farmer virtually gets no revenue.

There exist a number of methods to control reproduction in a mixed-sex population of *Oreochromis niloticus;* one of these methods is the rearing of male mono-sex tilapia (Phelps and Popma, 2000). There is significant sex specific difference in the growth of fish where males usually grow faster and more uniform in size than females (Bwanika *et al.*, 2007). This is mainly attributed to reproduction which drains energy primarily for the production of eggs and offsprings (Eyualem and Getachew, 1998; Tadesse, 1998). Notwithstanding, in a mouth brooder fish species like *Oreochromis niloticus*, females fast during the early stages and probably throughout the brooding period which causes inconsistent feeding and subsequently affects the body condition (Tadesse, 1988; Demeke, 1994). Meanwhile, the culture of all male tilapia is well established for increased production potential and low management requirements in semi-intensive culture system. Moreover

monosex culture of this species has been carried out by several authors to ascertain its advantage over the usual practice of mixed sex culture of tilapia, which necessitates this study.

MATERIALS AND METHODS

The experiment was carried out at the Fish Biotechnology Research Laboratory of the National Institute for Freshwater Fisheries Research (NIFFR), New-Bussa, Niger State, Nigeria.

Growth performance and survival rate of monosex (males, females and mixed populations) of *Oreochromis niloticus* were conducted for 49 days in aquaria tanks of 60cm×30cm×30cm. Seventy two (72) *Oreochromis niloticus* fingerlings having average weight of (13.09±0.4) g were obtained. Sexing was done manually by visual inspection of the external urogenital pores with the aid of magnifying hand lens, after which twelve (12) fingerlings were randomly weighed using electronic sensitive weighing balance OHAUS-LS-200g model, and was assigned to each of the experimental tanks that was made of three treatments which were replicated using a Complete Randomized Design (CRD).

The fish were fed twice daily with commercial feed (Coppens) 0.8mm-1.2mm at 5% body weight from 6am-7am, and 7pm-8pm, in the morning and evening respectively for seven weeks. Each tank was supplied with compressed air via rubber hose and air stones from air pump, siphoning of debris from each aquaria was done daily, after which an equal volume of freshwater was added as replacement. Sampling was carried out weekly to determine their growth rate. Dead fish were removed and recorded as soon as observed indoor to evaluate the survival rate of the stocks.

Food conversion ratio was computed as follows:

$$FCR = \frac{\text{Total feed given}}{\text{Total weight gained}}$$

*Specific Growth Rate (SGR) as:

$$SGR = \frac{(\text{Inwf} - \text{Inwi})}{\text{Time (days)}}$$

where: Wf = final weight (g), Wi = initial weight (g), In= natural logarithms, Time (days) = duration of trial.

RESULTS AND DISCUSSION

Data on the growth performance, feed conversion ratio, specific growth rate, daily growth rate and survival rate of monosex (all males, all females) and mixed populations (male and female) of *Oreochromis niloticus* are presented in Fig. 1 and 2. Significant variations were observed in growth performance among male, female and mixed populations of *Oreochromis niloticus* reared under the same conditions after 49 days (7weeks). The fish attained an average weight of 24.33±0.2g, 18.66±0.7g and 17.89±1.2g for male, female and mixed populations, respectively. The net weight and daily weight growth per fish were 11.16 g and 0.23g/d for male, 5.12 g and 0.1g/d for female and 4.58g and 0.09g/d for mixed population, respectively. The specific growth rate (SGR) per fish for the male (0.6g) , 0.3g for the female and 0.3g for the mixed populations were recorded. The survival rates for the fish were 83.33%, 83.33% and 79.17% for male, female and mixed populations, respectively.

The mean value of water quality parameters of the experiment for dissolved oxygen 6.05mg/l, ph. 6.8, air temperature 26°c and water temperature 26.5°c, respectively. Based on the data obtained, the water quality parameters; temperature, dissolved oxygen and p^H. measured during the study period were all within the optimum range for rearing tilapia (Boyd and Tucker, 1992; Xu *et al.*, 2005; Azaza *et al.,* 2008).

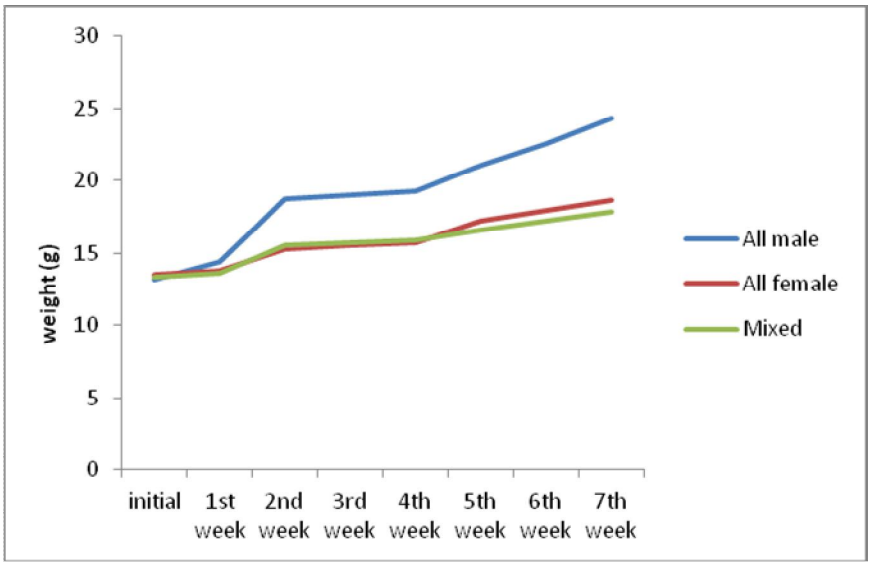

Figure 1: Growth curve of live body weight for monosex, and mixed population of *Oreochromis niloticus* during the study period

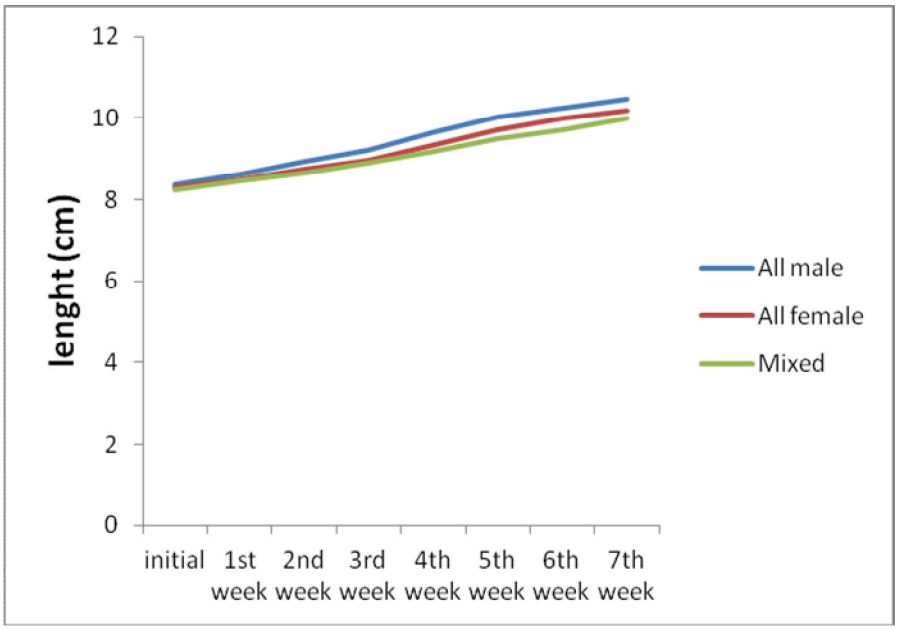

Figure 2: Growth curve of live body length for monosex, and mixed population of *Oreochromis niloticus* during the study period.

Although the growth performance of *Oreochromis niloticus* is highly influenced by genetics, quality and quantity of food, stock management and environmental factors (El-sayad, 2006), sex-specific differences in the growth of *Oreochromis niloticus* is apparent (Green *et al.*, 2007).

The results of the present study revealed that the growth performance between all male, all female and mixed populations *Oreochromis niloticus* reared for 49days under the same conditions was significantly difference ($P<0.05$), where the male monosex attained a larger final individual size. Several investigators have studied the sex-specific growth difference of *Oreochromis niloticus* under semi-intensive culture system, for example, Chakraborty *et al.* (2011) documented the faster growth of all male tilapia than females and mixed-sex, this might be attributed to sex-specific growth ability, female mouth brooding behavior or the efficient feeding habits of males. In a mouth brooding fish like *Oreochromis niloticus* females fast during the early stages and probably throughout the brooding period which causes inconsistent feeding and subsequently affects the body condition (Tadesse, 1988; Demeke, 1994). Pandian and Sheela (1999) and Green *et al.* (1997) further reported similar result, where all male tilapia showed superior growth rate over the females and mixed populations which are in agreement with the results of the present study.

They attributed this to the fact that energy is not utilized for reproduction and there exist no competition with younger fish in all male tilapia culture.

CONCLUSION

The result of the present study revealed that the growth performance between male, female and mixed population of *Oreochromis niloticus* reared under the same condition was significantly different, where the male monosex fish grow faster and attained a larger size than the female monosex and mixed populations. Therefore culturing of male monosex *Oreochromis niloticus* is recommended to fish farmers for increased income.

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AGB21

RELATIONSHIP BETWEEN BODY WEIGHT AND LINEAR BODY MEASUREMENTS IN JAPANESE QUAIL (COTURNIX COTURNIX JAPONICA)

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ABSTRACT

A total of 108 Japanese quail chicks (55 males and 53 females) were used to study the relationship between body weight and linear measurements at 2, 4, 6, and 8 weeks of age and to predict body weight (BW) from early linear measurements of body length (BL), body girth (BG), wing length (WL), shank length (SL), shank diameter (SD) and drum stick (DS). Mean chicks' body weight at 2^{nd}, 4^{th}, 6^{th} and 8^{th} week of age were 35.23g, 93.67g, 138.95g and 143.78g, respectively. Weekly body weight gain was rapid between 2 and 6 weeks of age and thereafter decreased with age. Female chicks were significantly ($P< 0.05$) heavier than their male counterparts at 6^{th} and 8^{th} weeks of age. Correlations between BW and body measurements was significantly positive ($P<0.01$) at 2^{nd}, 4^{th} and 8^{th} week of age. The best correlation was obtained between BW and BG at the 2^{nd} week of age (0.70). Estimates of Coefficient of Determination (R^2) showed that the best two single predictors of body weight of birds at 2 weeks of age were BG and BL. A combination of all body measurements however enhanced the efficiency of prediction of BW at 2^{nd} and 4^{th} week of age. The predictive equation showed that BW in Japanese quail is linearly related to body measurements especially with BG and BL. Prediction of BW from these measurements is therefore possible as early as 2 weeks of rearing. It is also possible for the breeder to use these easily measured parts as criteria for assessment and early selection for BW.

Key words: Body weight, linear measurements, correlation and Japanese quail.

INTRODUCTION

Japanese quail is the smallest farmed avian specie for egg and meat (Minvielle, 1998) and it is becoming increasingly important in the Nigerian poultry industry (Musa *et al*., 2008). Apart from its conventional use as a laboratory animal (Odunsi *et al.* 2007 and Minviellie, 2010), Japanese quail has the potential to serve as an excellent and cheap source of protein (Raji *et al.*, 2008). The high prolificacy and hardy nature of the bird (Robins, 1981; Annon, 1991) as well as the recent discovery of the health benefits of its egg, have made rearing of Japanese quail suitable for the resource poor tropical countries.

Body weight, body conformation and yield have been reported as important traits to poultry breeders and processors (Adeniji and Ayorinde, 1990). Body weight plays an important role in determining several other economic characteristics of the farm animals (Pesmen and Yardimci, 2008). It is an important attribute of farm animals as it forms the basis for assessing growth, feed efficiency and also in making economic decisions (Momoh and Kershima, 2008). It is also important in determining the market prices of animals especially in an organized market (Momoh and Kershima, 2008). Maciejowski and Zeiba (1982) reported positive correlation between body weight and a number of linear body measurements. These include shank length and diameter which are regarded as indicators of leg development, body girth and length which are indicators of breast development. Indirect method of estimating body weight using body measurements has been reported to be practical, faster, easier, and cheaper approach, especially in the rural areas where the resources are insufficient and the acquisition of expensive sensitive weighing scale is unaffordable (Semakula *et al*., 2011). Estimates of the relationship between body weight and linear measurements is not only important in developing predictive equations, it could also be employed in genetic improvement strategies to achieve an optimum combination of body weight and good conformation (Chineke *et al.* 2002).

This study therefore examined the relationship between body weight and linear body measurements in the Japanese quail and also developed regression equations for predicting body weight from linear measurements at different ages.

MATERIALS AND METHODS

The experiment was conducted at the Poultry Unit of the Department of Animal Production, Faculty of Agriculture, University of Ilorin, Nigeria. All experiments were implemented in accordance with Institutional guidelines on the care and use of animals for scientific studies, and in compliance with generally accepted rules of best practice worldwide.

A total of one hundred and eight (108) day old Japanese quail of mixed sex (55 males and 53 females) were obtained from a random-bred population that has been maintained in the department for three generations (Ojo *et al*. 2011). These birds were initially developed at the National Veterinary Research Institute (NVRI) station, Vom (Jos, Nigeria) from fertile eggs obtained from the Republic of Benin in 1992. Day-old birds were tagged on their wings and kept in brooding pen. Feed and water were supplied *ad- libitum* throughout the eight (8) weeks period of the experiment. Standard prophylactic procedures were also followed.

Body Weight (**BW**): Body Weight in gram (g) was recorded to two decimal places using a sensitive weighing scale (Scout II brand).
Body Length (**BL**): Body Length was taken in centimetre (cm) with a measuring tape stretched from bird's nasal opening, along its gently stretched neck and back, to the tip of its pygostyle.
Body Girth (**BG**): Body Girth was taken in centimetre (cm) when a measuring tape was looped round the region of the breast under the Wing.
Wing Length (**WL**): Wing Length was measured in centimetre (cm) as the distance from the humerus-coracoid junction to the distal tip of the phalange digits, using a measuring tape.
Shank Length (**SL**): The Shank Length was taken as the distance in centimetres (cm) between the foot pad and the hock joint, measured by a set of Venier calipers.
Shank Diameter (**SD**): Shank Diameter was taken as the width of the shank in centimetres (cm), measured by the use of a Venier calipers.
Drum Stick (**DS**): Drum stick was taken as the distance from the tip of hock to the ball joint of femur, measured in centimetres (cm) by the use of a measuring tape.

Data were subjected to analysis of variance (ANOVA) for a Completely Randomized Design (Steel and Torrie, 1980) using SPSS (version 13). Significantly different means ($P<0.05$) were further separated by the use of Duncan's Multiple Range procedure option in SPSS 13 (SPSS IBM). Correlation, linear and multiple regression analysis between BW and the various body size parameters were also determined. The coefficient of determination (R^2) for each parameter in the regression equations was determined to show the relative contribution of each body measurement to the BW of Japanese quail at different ages. The following linear regression equation was used to predict BW from linear measurements.

$Y = a + bx$

Where Y = body weight or dependent variable, a = constant in the regression equation, b = regression coefficient and, x = various body measurements

RESULTS AND DISCUSSION

Table 1 shows the means (±SEM) and the coefficients of variation of BW and linear measurements taken on the Japanese quails at different ages. The data indicated a progressive increase in BW and linear measurements over the eight weeks period. Mean BW increased from 35.23g at 2 weeks of age to 143.78g at 8 weeks of age. The highest increase in BW occurred between two and four weeks of age (58.44g). BL increased from 11.84cm at week two to 19.45cm at week eight. BG increased

from 8.02cm at week 2 to 13.67cm at week 8. SL, SD and DS increased from 2.31cm to 2.96cm, 0.32 to 0.44cm, and 3.04 to 5.16cm between weeks two and eight, respectively. This result agrees with the reports of Sonaiya *et al.* (1986) and Ojedapo *et al.* (2012) who reported that age is a major determinant of growth and physiological development. The estimates of coefficient of variation in this study suggest that there was an increased uniformity in body size measurements as the birds advanced in age.

There was no significant effect ($P>0.05$) of sex on most body measurements except for SD and BG (Table 2). Female chicks had significantly higher ($P<0.05$) SD at the 2^{nd} (0.33cm) and 4^{th} (0.41cm) weeks of age and a higher BG at the 6^{th} week. Sex effect on BW was not significant ($P>0.05$) at the 2^{nd} and 4^{th} weeks of age, although female quails were nominally better in mean BW at these ages. However, Females were significantly higher ($P<0.05$) than the males in BW at 6^{th} (150.71g vs 127.62g) and 8^{th} (157.98g vs 130.10g) weeks of age. The BW and linear measurements obtained in this study are lower than values reported by other authors (Almeida *et al.*, 2002; Reddish *et al.* 2003; Sezer *et al.*, 2006 and Tulobaev *et al.* 2011). Ojo *et al.* (2012) had suggested that differences in genetic sublineage and rearing environmental conditions may account for such differences. Coefficient of variation for body measurements was higher in males than in females but decreased with successive rearing age. This pattern suggests that there was an increasing uniformity in BW and linear measurements of both sexes with age. Sexual dimorphism has previously been reported in favour of the male in duck (Raji *et al.*, 2009), pigeon (Hassan and Adamu, 1997), chicken (Momoh and Kershima, 2008), guinea fowl (Ogah, 2006) and pheasants (Kuzniacka and Adamski, 2010). The growth pattern of male and female Japanese quails have been well documented (Balcioglu *et al.*, 2005; Sezer and Tarhan, 2005). The result of the present study agrees with the pattern reported by Hort *et al.* (1999) and Sezer *et al.* (2006). Sezer *et al.* (2006) reported that there were no sex differences in hatchling weight and that the degree of sexual dimorphism was low until after 4 weeks of age.

Table 3 shows the correlation between BW and body measurements in Japanese quail. BW was positive and significantly ($P<0.01$) correlated with all body measurements at 2^{nd} and 4^{th} weeks of age except for WL (0.35) at week four. BG had the highest correlated value with BW at 2^{nd} (0.70) and 4^{th} (0.68) weeks. At weeks six and eight, correlation coefficient had reduced for all body measurement except for BG. Estimates obtained for WL, SL and diameter and DS at weeks six and eight were between -0.01and 0.27.

These results are in agreement with earlier reports on correlation between BW and linear measurements in poultry species. For instance, Ibe and Nwakalor (1987) reported high and positive correlation between linear measurements and BW in the Nigerian local chicken. Adeniji and Ayorinde (1990) also reported a linear relationship between BW and body measurements in broiler chicken while Hassan and Adamu (1997) obtained a similar result in pigeon. Raji *et al.* (2009) reported a positive and highly significant correlation between BW and zoometric body measurements in local Muscovy ducks. These authors noted that chest girth had the strongest correlation with BW followed by BL. Raji *et al.* (2009) opined that the higher association between BW and CG was due to relatively large contribution to BW by chest girth which consists of bones, muscles and viscera. The present study indicates that DS and WL are less strong compared with SL and BG as indicators of BW in the Japanese quail. Maciejowski and Zeiba (1982) observed that SL and SD were good indicators of leg development. The present result on correlation between BW and WL contradicts the earlier report of Teguia *et al.* (2008) who reported highest correlation between BW and WL in Muscovy duck.

Tables 4 and 5 show the linear and multiple regression equations and coefficient of determination (R^2) for predicting BW at different ages in the Japanese quail. Live BW had a significant ($P<0.05$) simple linear relationship with all body measurement at all ages except with WL and the SD at sixth week of age. R^2 was highest for BG at 2^{nd} (0.49) and 4^{th} (0.46) weeks and lowest for DS (0.08) at the 2^{nd} and WL (0.12) at the 4^{th} weeks. R^2 values reduced as the birds advanced in age. The R^2 values suggest that BG contributed 49 and 46%, BL contributed 44 and 20% to BW at 2^{nd} and 4^{th}

weeks, respectively. Conversely, WL contributed as little as 0.13 and 0.12% to BW at 2nd and 4th week. This result supports the findings of Raji *et al.* (2009) in Muscovy duck where highest R^2value (0.728) was obtained when chest girth was used singly, followed by BL (0.704) and WL (0.704), respectively. These authors explained that the high association of BW and chest girth was due to the relatively large contribution of chest girth (which consists of bones, muscles and viscera) to BW. R^2 value increased when all body measurements were combined in a multiple regression with the BW. R^2 value was 0.677, 0.572, 0.376 and 0.414 at 2nd, 4th, 6th and 8th week, respectively. This supports the result of Momoh and Kershima (2008) who also reported an increase in coefficient of determination when body measurements were combined in a multiple regression in the local chicken. Raji *et al*. (2009) also reported similar findings in the Muscovy duck especially when chest girth, body length and chest width were combined in a multiple regression equation.

CONCLUSION

This study shows that BW in Japanese quail is linearly related to body measurements, especially with BG and BL. Prediction of BW from these measurements is therefore possible as early as 2 weeks of rearing. It is also possible for the breeder to use these easily measured parts as criteria for assessment and selection for BW at this early age. Thus a breeding programme to achieve an optimum combination of BW and good conformation for maximum economic returns in the Japanese quail can be easily organized.

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Table 1. Means of Body Weight and Linear Measurements at Different Ages in the Japanese quail (sexes combined)

	2nd week		4th week		6th week		8th week	
Traits	Means±S.E	C.O.V	Means±S.E	C.O.V	Means±S.E	C.O.V	Means±S.E	C.O.V
BW(g)	35.23±0.61	17.85	93.67±1.18	13.09	138.95±1.81	13.54	143.78±1.82	13.14
BL (cm)	11.84±0.08	7.26	17.40±0.07	4.43	19.24±0.13	6.86	19.45±0.07	3.95
BG (cm)	8.20±0.07	9.27	11.92±0.08	6.96	13.70±0.06	4.82	13.67±0.06	4.75
WLcm)	5.95±0.08	13.45	8.79±0.05	6.26	8.70±0.05	6.44	8.90±0.46	5.43
SL(cm)	2.31±0.03	12.55	2.95±0.02	7.46	2.99±0.01	5.02	2.96±0.01	5.07
SD (cm)	0.32±0.004	12.50	0.41±0.002	4.88	0.43±0.003	6.98	0.44±0.003	6.82
DS (cm)	3.04±0.03	10.20	4.78±0.05	9.83	5.15±0.02	4.47	5.16±0.02	4.65

BW- body weight; BL- body length; BG-body girth; WL-wing length; SL-shank length; SD- shank diameter; DS-drum stick. S.E- Standard error of mean; C.O.V- Coefficient of variation.

Table 2. Effect of Sex on Body Weight and some linear measurements in the Japanese quail

	2 weeks				4 weeks				6 weeks				8 weeks			
	Male		Female		Male		Female		Male		Female		Male		Female	
Traits	Mean	COV	Mean	C.OV	Mean	COV	Mean	COV	Mean	COV	Mean	COV	Mean	COV	Mean	COV
BW(g)	34.51	19.12	35.98	16.48	92.22	13.27	95.17	12.84	127.62[b]	11.64	150.71[a]	9.92	130.10[b]	9.21	157.98[a]	8.54
BL(cm)	11.78	7.22	11.90	7.39	17.32	4.79	17.51	3.93	19.20	4.06	19.27	8.87	19.35	4.03	19.55	3.84
BG(cm)	8.09	8.66	8.31	9.03	11.80	6.95	12.04	6.89	13.42[b]	4.40	13.99[a]	4.36	13.45	4.91	13.90	3.81
WL(cm)	5.83	16.98	6.08	8.55	8.73	6.41	8.86	6.09	8.66	6.24	8.74	6.75	8.86	6.21	8.94	4.59
SL(cm)	2.31	10.39	2.32	15.52	2.95	7.46	2.96	7.09	3.00	5.33	3.00	5.33	2.95	5.76	2.96	4.73
SD(cm)	0.31[b]	11.29	0.33[a]	12.12	0.40[b]	5.0	0.41[a]	4.88	0.43	6.98	0.44	6.82	0.43	6.98	0.44	6.82
DS(cm)	3.02	10.23	3.06	10.13	4.67	10.06	4.78	9.62	5.15	3.88	5.16	4.84	5.13	4.48	5.20	4.62

[a,b]Means in the same column having different superscript within the same week differs significantly (P<0.05).COV-coefficient of variation. BW- body weight; BL- body length; BG-body girth; WL-wing length; SL-shank length; SD- shank diameter; DS-drum stick

Table 3. Correlations between Body Weight and Body Measurements in the Japanese quail at Different ages.

	Body weight / Age			
Traits	2 weeks	4 weeks	6 weeks	8 weeks
Body length	0.66**	0.45**	0.26**	0.39**
Body girth	0.70**	0.68**	0.57**	0.61**
Wing length	0.38**	0.35	0.12	0.25**

Shank length	0.45**	0.47**	0.25*	0.27**
Shank diameter	0.48**	0.36**	-0.01	0.19**
Drum stick	0.28**	0.42**	0.20*	0.25**

**, **significant at P<0.05 and P<0.01, respectively*

Table 4. Linear Regression Equation for predicting Body Weight at Different Ages in the Japanese quail

	Age	Intercept (a)	Regression Coefficient (b)	Coefficient of Determination (R^2)	Significance
Body Length	2	-21.73	4.81	0.44	S
	4	-31.44	7.18	0.20	S
	6	68.42	3.67	0.07	S
	8	-44.14	9.68	0.15	S
Body Girth	2	-11.84	5.73	0.49	S
	4	-26.07	10.05	0.46	S
	6	-81.96	16.12	0.32	S
	8	-97.50	17.67	0.37	S
WingLength	2	18.10	2.88	0.13	S
	4	24.96	7.82	0.12	S
	6	103.88	4.03	0.01	NS
	8	52.64	10.30	0.06	S
Shank Length	2	13.37	9.46	0.20	S
	4	14.74	26.74	0.22	S
	6	49.76	29.67	0.06	S
	8	50.40	31.71	0.07	S
Shank Diam.	2	11.47	75.0	0.23	S
	4	18.45	185.01	0.13	S
	6	142.22	-7.53	0.00	NS
	8	88.72	127.03	0.04	S
Drum Stick	2	17.76	5.74	0.08	S
	4	41.62	11.02	0.18	S
	6	54.53	16.38	0.04	S
	8	42.21	19.75	0.06	S

S- significant, NS-Not significant.

Table 5. Multiple Regression Equations for estimating bodyweight at Different ages in the Japanese quail.

Age (weeks)	Predicting Equations	R^2	Significance	SE of Estimate
2	Y= -38.02+2.31(BL)+3.51(BG)+0.85(WL)+5.15(SL) +11.54(SD)+(-1.12)DS	0.677	**	3.68
4	Y= -106.20+2.49(BL)+7.35(BG)+1.81(WL)+9.49(SL) +39.83(SD)+1.88(DS)	0.572	**	8.25
6	Y= -179.78+0.98(BL)+15.08(BG)+1.65(WL)+25.08(SL) +1.04(SD)+0.63(DS)	0.376	**	15.30
8	Y= -171.18+1.89(BL)+16.78(BG)+6.45(WL)+14.68(SL) +(-80.63)(SD)+(-3.14)(DS)	0.414	**	14.89

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GENETIC PARAMETERS OF WEEKLY BODYWEIGHT IN JAPANESE QUAIL

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ABSTRACT
The Harvey Mixed Model Least-squares and Maximum Likelihood Computer Programme was used to estimate the heritability, genetic and phenotypic correlations of live body weight of 684 Japanese quails. The results revealed that Japanese quails are sexually dimorphic for live body weight at all ages. Heritability of live body weight ranged from 0.12±0.02 to 0.91±0.11. All genetic correlations between live body weights were positive. Phenotypic correlations between live body weights at all ages were positive and very high (P<0.001). It was concluded that selection for live body weight within the first two weeks of age may lead to improvement of body weight at later stages of life.
Keywords: Body weight, heritability, genetic correlation, Japanese quail.

INTRODUCTION

Quail breeding offers excellent opportunity for diversification and early marketing age, hence increasing activity in the production of Japanese quail in developing countries. Despite the small body size of Japanese quail, its meat and eggs are widely consumed and therefore ameliorates the problem of animal protein shortage.

The Japanese quail is a sexually dimorphic bird with females having a larger body size than males, unlike other poultry species. Sexual dimorphism is believed to evolve under the pressure of natural and sexual selection, which implies that genes controlling sexually dimorphic characteristics differ between males and females (Mignon-Grasteau *et al*., 2004). Growth is the most important trait for evaluating different livestock species, especially in meat producing animals and birds. Growth traits such as bodyweight and bodyweight gain are affected by genetic and non-genetic factors and the phenomenon of growth is usually measured by observing differences in bodyweight recorded at different ages and/or bodyweight gain obtained during different growth periods (Chambers, 1993). Growth traits in the Japanese quail have been estimated by several researchers (Marks, 1993, EL-Full *et al.,* 2001, Almeida *et al*., 2002, Abdel-Fattah, 2006). The genetic parameter estimates cited in literatures for growth traits would be expected to differ in diverse genotypes and under different environments.

Therefore the objective of this study was to estimate the genetic parameters of body weight in Japanese quail in a tropical environment like Nigerian as a step towards genetic improvement.

MATERIALS AND METHODS

The study was conducted at the Poultry Unit of the Teaching and Research Farm of the Faculty of Agriculture, Kogi State University, Anyigba Nigeria. Anyigba lies between longitudes 5^0 15^1 and 7^0 45^1 North and latitude 5^0 45^1 and 8^0 45^1 East with mean annual rainfall of 1,808mm. The Natural day length of Anyigba is 12-13hrs with average monthly temperature that varies from 17^0c – 36.2^0c. The relative humidity varies from an average of 65-85% throughout the year (Amhakian, 2009).

The foundation stock from which the birds used for the study were hatched consisted of 90 females and 30 males maintained in the farm as separate non-pedigreed, unselected and unimproved population. A mating ratio of 1(male) : 3 (females) generated 684 day old chicks in three hatches. At hatching, the chicks were leg banded with small plastic bands to indicate individual and sire identities. The chicks were brooded on a floor pen with wood shavings as litter materials. Brooding temperature started with 37.5^0C for the first week after which the temperature was reduced by $2\text{-}3^0$C weekly until the end of 3 weeks of age when the birds were transferred to the rearing pens. In the rearing pens, birds were managed on deep litter from the 4^{th} week to 8 weeks of ages using standard management procedures. Chicks were fed diet containing 24% crude protein and 2741/kcal/kg of feed from hatch to 5 weeks of age, thereafter the birds were fed diet containing 18% crude protein and 2707 kcal/kg of feed as recommended by Dafwang (2006). Both feed and water were provided *ad libitum.*

Live bodyweight at hatch (0 week), 1-week, 2-weeks, 3-weeks, 4-weeks, 5-weeks, 6-weeks, and 7-weeks of age were individually recorded to the nearest gram for all the quails using a sensitive digital electronic weighing scale. Degree of sexual dimorphism in live weight was calculated using the formula as applied by Sezer *et al.* (2006).

$$\text{Degree of sexual dimorphism (DSD)} = Fw_t - \frac{Mw_t}{F_{Wt}} \times \frac{100}{1}$$

where, F_{Wt} = the mean female live weight at time t

M_{Wt} = the mean male live weight at time t

Data obtained on bodyweight were analysed using the Generalized Linear Model (GLM) procedure of SPSS 14.0 (2004). The model employed was:

$Y_{ijk} = \mu + S_{¿} + B_j + (SB)_{ij} + e_{¿jk}$

where,
Y_{ijk} = Individual quail's bodyweight,
μ = the population mean, $S_{¿}$ = effect of sex (i = 1, 2), B_j = effect of the j^{th} hatch (j = 1,..3), $(SB)_{ij}$ = interaction effects of sex and hatch, e_{ijk} = residual random error.
The data were further subjected to genetic analysis using the mixed model least – squares and maximum likelihood computer programme of Harvey (1990). The reduced sire model (Becker, 1992) was used to fit the data.
$Y_{ij} = \mu + a_{¿} + e_{ij}$

where,
Y_{ij} = Observation on the j^{th} progeny of the $¿^{th}$ sire
μ = Population mean, $a_{¿}$ = Random effect of the $¿^{th}$ sire ($_{¿ = 1,....30}$)
e_{ij} = Residual random error.

The Harvey programme computes estimates of genetic and phenotypic correlation as well as heritability estimates of traits from sire variance components.

RESULTS AND DISCUSSION
Table 1 presents the least-square means of weekly body weight and degree or sexual dimorphism in Japanese quail. Regardless of sex, the mean bodyweights remarkably increased as the quails progressed in age. The female chicks were significantly ($P<0.05$) heavier in body weight than the males. The degree of sexual dimorphism estimates were 3.23, 3.73, 5.26, 3.58, 3.93, 5.54, 10.78 and 11.48% at 0, 1, 2, 3, 4, 5, 6 and 7 weeks of age. Degree of sexual dimorphism tend to increase with increase in age.
The bodyweight at hatch obtained in this study is in agreement with Abdel-Fattah (2006) and Abdel-Tawab (2006) who reported values that ranged between 6.0 and 9.3g. Bodyweight at 1, 2, 3, 4, 5, 6 and 7 weeks of age were lower than those reported by El-Full *et al.* (2001), Abdel-Fattah (2006) and Abdel-Tawab (2006). The observed differences between the various estimates reported at particular ages could be due to the differences in climate and managerial conditions under which different flocks were reared and to the possible differences in genetic make-up of the different flocks or to the differences in the statistical manipulation of the data obtained used to obtain the estimates. Female quails were significantly ($P<0.05$) heavier than the males from 0 (hatch) week of age up to 7 weeks of age. This observation is similar to those of Soltan *et al*. (1987), Oguz *et al.* (1996) and Abdel-Fattah (2006). The degree of sexual dimorphism (DSD) reported in this study follow the same trend with results presented by Hort *et al.* (1999) and Sezer *et al*. (2006). The occurrence of sexual dimorphism in the Japanese quail indicates potentials for their possible development as sire and dam lines in breed development.
Heritability from sire variance component, genetic correlation and phenotypic correlation among bodyweights at different ages in Japanese quail are presented in Table 2. Heritability estimates ranged from 0.12±0.02 at 6 weeks of age to 0.91±0.11 at 0 week (hatch) of age. All genetic correlation estimates between bodyweights at different ages were positive. The genetic correlation estimates of body weight ranged from 0.18 to 1.17. These were cases when genetic correlation estimates were outside parametric range (1.01, 1.05 and 1.17, respectively). Generally, phenotypic correlation between bodyweights at all ages were positive and very highly significant ($P<0.001$).
The heritability of body weight at hatch is in close agreement with the value reported by El-Fiky (1991). The heritability estimate of 4-week body weight in this study generally fall within the range of 0.17-0.60 reported by Bahie El-Deen (1994) for Japanese quail. Heritability tends to reduce with age. This similar observation was earlier reported by Saatei *et al*. (2002) for Japanese quail. The moderate to high heritabilities reported indicate that response to selection at 7, 4, 3, 2, 1 and 0

weeks of age could be rapid while the low heritabilities implies that response to selection at the 5th and 6th week of age could be slow.

The genetic and phenotypic correlation estimates between body weights at different ages were similar in magnitude and direction. Similar trends were reported by Sharaf (1992), Farahat (1998) and Shalan (1998). Genetic correlations greater than 1 obtained between bodyweights at some ages in this study were outside parametric range. El-Full *et al*. (2001) who used 3, 150 birds also estimated genetic correlations among some growth traits with values greater than 1, in Japanese quail in Egypt. Problems associated with small group data size, sampling errors and data imbalance (unequal group sizes) could indicate very high genetic correlations between traits involved, which sometimes can be outside the parametric range. The strong and positive genetic relationships between bodyweights at different ages could be attributed to pleitropic and linkage effect of genes. This means that the same genes were controlling the bodyweight traits at different ages with increasing expressivity.

CONCLUSION

On the basis of heritability estimates obtained for bodyweights at various ages, selection for body weight can start within the first two weeks of age due to high body weight heritability at this age. The low to moderate heritability of body weight at older ages may indicate that environmental deviations were more important in influencing body weight at these ages than additive genetic variances. Greater attention should therefore be paid to optimal conditions of feeding and management at these stages. The high and positive genetic correlation observed between bodyweights at different ages revealed the same quantitative traits loci (QTL) acting to express body weight at different ages. Selection for bodyweight at early stages of life would lead to improvement of body weight at later stages of life in the Japanese quail.

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Table 1. Least-squares Means ± SEM for weekly body weight and degree of sexual dimorphism (DSD, %) in Japanese quail**.**

Age (weeks)	Sex	Bodyweight (g)	DSD (%)
O (Hatch)	Male	6.60±0.07[b]	
	Female	6.82±0.08[a]	3.23
1	Male	13.42±0.19[b]	
	Female	13.94±0.20[a]	3.73
2	Male	27.74±0.44[b]	
	Female	29.28±0.46[a]	5.26
3	Male	50.93±0.76[b]	
	Female	52.82±0.80[a]	3.58

4	Male	72.11±0.92[b]	
	Female	75±06.097[a]	3.93
5	Male	95.95±1.05[b]	
	Female	101.58±1.10[a]	5.45
6	Male	117.39±1.13[b]	
	Female	131.58±1.19[a]	10.78
7	Male	124.49±1.11[b]	
	Female	140.64±1.16[a]	11.48

a, b = Means within sex-subgroup with different superscripts are significantly different ($P<0.05$)
DSD = Degree of sexual dimorphism

Table 2. Heritability from sire variance component (on Diagonal), Genetic correlation (above diagonal) and phenotypic correlation (below diagonal) among bodyweights at different Ages in Japanese quail.

	O week	1 week	2 week	3 week	4 week	5 week	6 week	7 week
O week	**0.91±0.11**	0.74	0.59	0.90	0.81	0.80	0.38	0.40
1 week	0.66***	**0.88±0.27**	0.93	0.82	0.75	0.89	0.72	0.23
2 Week	0.61***	0.82***	**0.50±0.02**	0.85	0.97	1.17	0.92	0.61
3 week	0.47***	0.47***	0.69***	**0.32±0.19**	0.94	0.98	0.67	0.37
4 week	0.46***	0.52***	0.72***	0.92***	**0.27±0.18**	1.05	1.01	0.66
5 week	0.46***	0.47***	0.65***	0.79***	0.87***	**0.18±0.06**	0.95	0.34
6 week	0.30***	0.35***	0.51***	0.60***	0.68***	0.79***	**0.12±0.02**	0.18
7 week	0.19***	0.13***	0.28***	0.43***	0.49***	0.59***	0.83***	**0.21±0.06**

*** = **(**P<0.001)

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GENETIC DISTANCE BETWEEN POPULATIONS OF THE TIV LOCAL CHICKEN IN THE DERIVED GUINEA SAVANNAH ZONE OF NIGERIA

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ABSTRACT
A total of 1378 body linear measurement and body weight were obtained at four locations of about 30 kilometers minimum apart, from kastina-Ala local government area of Benue State. The data were subjected to the general linear model procedure and a discriminant analysis to estimate the effect of location and mahalanobis square (D^2) distance between locations. There was significant variation in body length, shank length, tail length, tail width and comb length due to location. There were also large and significant genetic distances between the locations except between location 4 and 2. There is a wide genetic diversity in body dimensions between isolated populations of the local chicken ecotypes. Superior birds could be identified, selected and bred for genetic improvementKEY WORDS: Genetic distance, local chicken's ecotypes and population.

INTRODUCTION
Local chicken ecotypes are more adapted to local environmental conditions and diseases (AL-Aliyat, 2009). The local chickens contribute greatly to human supply of eggs and meat in tropical and subtropical areas. They are the only livestock, which could be kept by the poorest rural families (AL Aliyat, 2009). Horst (1989) considered the local chicken ecotypes as genes reservoir, especially, there genes that have adaptive values in the tropical conditions.
Nigeria local chicken had been grouped on ecological zones on the bases of body size and body weight as light and heavy ecotypes (Momoh *et al*., 2007). Olori (1992) noted two ecotypes characterized as forest and savannah ecotypes. Nwosu (1979) reported three main strains among the forest ecotype. Oluyemi *et al*. (1982) also reported variation in many traits of the local chicken from southern region of Nigeria. Adebambo *et al*. (2009) however found no significance differences in the genetic distance of local chickens from South west, North West and, Northeast ecological zones of Nigeria. The cited literature indicated that there appeared to be no consistency in literature about genetic diversity in the Nigeria local chicken ecotypes. However, most literature accepts the existence of diversity in the Nigerian local chicken ecotypes. Classification of genetic resources based on geographical location appeared to provide based estimates of genetic diversity (Pimm and Lawton, 1988) of the local chicken genetic resources of Nigeria. The genetic distinctiveness of an animal forms the base for distinguishing it among different animal genetic resources and for assessing the available diversity (FAO, 1984). The present and future improvement and sustainability of the local chicken's production systems are dependent upon availability of this genetic variation (Benitez, 2002). Therefore, the evaluation of the local chicken population genetic resources includes the determination of genetic distance between the available populations (Hammond, 1994).
The objective of this study was to assess the genetic distance between populations of the Tiv local chicken ecotypes based on body linear measurements with the view of highlighting genetic diversity within isolated populations of the ecotypes that can be selected and breed for genetic improvement.

MATERIALS AND METHODS

The study was conducted at Kastina-Ala Local Government Area of Benue State at four locations Weghgyina village, Kenvanger village, Kpuntgo village and Udende village that were more than 30 Kilometers apart. These were rural farming communities that practiced crop/livestock integration. Local chickens were the predominant poultry species owned. Kastina-Ala local government area is located between Latitude 7° 11^{11} 3411 N and Longitude 9° 20^{11} 21^{11} E. The mean annual rainfall was 11.75mm. There is two seasons (dry and wet seasons). Temperature during the rainy season ranges from 21.7^{o}C. The relative humadity is about 68%.

The local chickens were reared under the free range population system. The birds seek for their own feed by scavenging kitchen waste, farm by-products and foraging for insects and worms. Cereal grains were offered occasionally as feed supplement. Water was provided through not ad-labium. Medication was never provided. Inhabitation, hatching and blooding were all by natural processes.

Measurements were taken on 1,378 birds consisting of 360 at Kpuntgo, 400 at Kenvanger, 320 at Weghyuia and 298 at Udende villages, respectively. Traits measured were body length, body height, shank length, thigh length, tail length, tail width, comb length, comb height, wattle length, wattle height and body weight.

The data generated were subjected to general linear procedure of SPSS, (2004) to estimate the effect of location, sex and their interaction on body dimensions of the birds. The following model was used.

$Y_{ijk} = \mu + Li + Sj + (LS)\ ij + e_{ijk}$

where,

Y_{ijk} = single observation

μ = population mean

Li = effect of the ith location (i = 1, 2, 3, 4)

Sj = effect of sex (j = 1, 2).

$(LS)_{ij}$ = effect of location by sex interaction

e_{ijk} = error variance component

The data were also subjected to a discriminant analysis to estimate the Mahalanobis distance between the locations using the CANDISC procedure. The Mahalanobis squared distance (D^2) between locations was estimated by:

$D^2\ (i/j) = (xi - \bar{x}j)\ cov^{-1}\ (xi - xj)$ (SAS, 1990).

Where D^2 = genetic distance between populations in a m-Dimensional space.

Ij = the element of the i^{th} row and j^{th} column of the inverse matrix.

$\bar{x}i - xj^{-}$ = mean set of original variables

Cov = covariance of the original data set.

RESULTS AND DISCUSSION

The analysis of variance indicated significant ($p>0.05$) effect of location on body length, shark length highly significant ($p>0.001$), thigh length ($p>0.05$), tail length ($p>0.01$), law width highly significant ($P>0.001$), comb length ($P>0.05$), comb height ($P<0.05$) and wattle length ($P<0.05$). Body weight and body height did not vary significantly ($P>0.05$) across the locations (Table 1). Sex effect on body measurement was highly significant ($P<0.001$) for all the traits measured. The effect of sex by location interaction significantly ($P<0.05$) affected only body height. The other interactions were not significant ($P>0.05$). The significant ($p<0.05$) effect of body length, thigh length, wattle length, comb length and comb height due to location indicated that these parameters varied between the isolated populations to the Tiv chicken ecotypes. The univariate test also indicated that shark length, tail length and width were most varied between the isolated population's Gwaza et al. (2012) also reported variation in there traits. These parameters determine adaptation and fitness of the birds to their environment. The variation in there parameters between the population would mean variation in the genetic resources of the local chicken between the population (Yakubu, 2011).

Mahalanobis squared distance (D^2) from location 1 to 2, 1to 3 and 4 were o.64854, 0.92750 and 0.54760 respectively. Location 2 to 3 and 4 were 1.20128 and 0.15311 and distance from location 4 to 1, 2 and 3 were 0.54760, 0.15311, and 0.99809 respectively (Table 2). The highest F statistic value were recorded for Mahalanobis squared distance between locations 1 and 2(7.10656) followed by that between location 1 and 4 (4.56086). This was followed by the distance between location 2 and 3 (2.91620), location 1 and 3 (2.46385), location 3 and 4 (2.26458). The least F statistics was obtained for the squared distance between location 2 and 4 (0.98429) (Table 3). There were significant ($p>0.0$) differences in F statistics between location 1 and 2 ($p<0.05$), location 1 and 3 ($p<0.02$) and between location 1 and 4. Location 2 to 3 and between location 4 to 3 different significantly ($p>0.05$) difference in the squared distance between location 2 and 4 (Table 3). Although the univariate analysis revealed difference in body dimensions between the isolated populations of the Tiv chicken ecotypes multivariate analysis indicated that there was significant genetic distance between the isolated populations of the Tiv local chicken ecotypes. This may be due to cultural practices, movement and settlement patterns of the Tiv rural farming communities. As then rural farmer's family size increases, some members of the farming communities relocate to new settlements taking along with them a small group of the local chicken from the original population to form a new population. The random sample of alleles in the just formed new populations is expected to grossly misrepresent the original population (Neil, 1996). When a new formed population is small, its founders can strongly affect the populations genetic make-up far into the future (http://www.pbs.org/wgbh/evolution /library/06/3/1-063-03.html) .
The difference in the gene frequencies between the original and the new populations may also trigger the groups to diverge significant over the course of many generations (small et al., 2007). As the difference increases, the separated populations may become distinct, both genetically and phenotypic ally with wide genetic distance as observed in this study. Natural and artificial selection gene flow and mutation may have certainly contributed to this divergence.

TABLE 1:Analysis of variance result on effect of location, sex and their interactions on body linear measurement.

Sources of Variation	degrees of freedom	sum of squaressquares	means	F value
Loc				
bol	3	42.090	14.030	1.456*
boh	3	16.089	5.363	0.766^{ns}
shl	3	36.555	12.185	12.355***
thl	3	7.588	2.529	1.670*
tal	3	48.522	16.174	5.333**
taw	3	60.186	20.062	6.570*
Comh	3	21.674	7.225	4.068*
Comh	3	2.222	0.741	1.242*
Wal	3	3.415	1.138	1.123^{ns}
Wal	3	4.285	1.1428	3.027*
Bow	3	0.055	0.018	0.421^{ns}
Sex				
bol	1	1386.483	1386.483	143.918***
Bol	1	1597.375	157.375	228.133***
Shl	1	242.961	242.961	246.347***
Thl	1	273.679	273.679	180.696***
Tal	1	518.721	518.721	171.049***
Taw	1	41.409	41.409	13.562***
Coml	1	978.114	978.114	550.768***
Coml	1	346.610	346.610	581.304***
Wal	1	153.011	153.011	150.939***
Wal	1	276.316	276.316	585.657***
Bow	1	8.518	8.518	195.747***
Bol	3	30.847	10.282	1.468*
Error				
bol	721	6947.788	9.636	
Boh	721	5048.414	7.002	
Shl	721	711.092	0.986	
Tal	721	1092.013	1.515	
Tail	721	2186.497	3.033	
Toilw	721	2201.489	3.053	
Coml.	721	1280.431	3.053	
Wal	721	429.905	0.596	
Wal	721	730.897	1.014	
Wah	721	340.172	0.472	
Bow	721	31.373	0.044	

* Significant at 5 percent

*** Significant at 10 percent.

Table 2: Mahalanobin squared distance (D^2) to location.

From location	1	2	3	4
1	0	0.649	0.928	0.548
2		0	1.201	0.153
3			0	0.998

Table 3: F statistic for squared Mahalanobin distance (D^2) to Location.

From location	1	2	3	4
1	0	7.107**	2.464*	4.561**
2		0	2.916*	0.984^{ns}
3			0	2.265*

* Significant at 5 percent, ** significant at 10 percent.

CONCLUSION

There existed significant genetic diversity between isolated population of the Tiv local chicken ecotypes. This diversity may have been induced by cultural practices, isolated settlement patterns in addition to natural and artificial selection, gene flow and mutation. Superior birds could be identified, selected and bred for genetic improvement of the Tiv local chicken performance. There is need to conduct molecular characterization, that will provide, molecular data for unbiased estimates of genetic diversity within this ecotype.

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AGB24

IMPROVING EGG PRODUCTION IN THE NORMAL FEATHERED NATIVE CHICKENS OF NIGERIA USING THE NAKED NECK GENE

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ABSTRACT
Part period egg production was monitored in straight bred F_1 progeny of two genetic groups of Nigerian local chicken (normal feathered and naked neck) and their crossbred (using the naked neck as the sire) to 280 days of age. Eggs traits considered during the part period were total egg number, egg mass and average egg weight. The age at first egg (AFE) and the weight of first egg (WFE) were also monitored in the genetic groups. The heritability and genetic correlations between these traits were also evaluated. Part period egg number, egg mass and average egg weight varied significantly ($P<0.05$) between the genetic groups. Similarly, AFE and WFE varied significantly between the genetic groups. Though part period egg number was significantly higher in the normal feathered (NF) genetic group, it did not translate to higher egg mass due smaller egg size. The introgression of the naked neck gene (Na) into the normal feathered significantly ($P<0.05$) improved egg mass in the crossbred over the straight bred normal feathered birds. The study therefore recommends the exploitation of the Na gene in improving egg production in the normal feathered native chicken of Nigeria.

INTRODUCTION
Native chickens are important in breaking the vicious cycle of poverty, malnutrition and disease especially among the rural poor. These birds have been reported to have adapted well to the local scavenging production system under which they are managed. Phenotypically, four genetic groups of the Nigerian local chicken have been identified. These are the normal feathered, frizzle feathered, naked neck and the dwarf chickens. The egg production characteristic of these genetic groups is common expression in contemporary literature. In general, several workers (Hanzi and Somes, 1993; Cahaner *et al.*, 1994; Eberhart and Washburn, 1993) have demonstrated the advantage of the naked neck (Na) birds over their normally feathered counterparts when reared at constant high ambient temperatures (AT). Consequently, the Na birds have been variously reported (Horst, 1988; Ibe, 1993) to have better productivity in terms of body weight gain, egg number and egg size over the normal feathered and frizzled feathered birds under same stressing conditions usually imposed by high AT in the tropics. However, there is a dearth in literature on the production characteristics of the Na gene acting in concert with other genes of the native

chickens in Nigeria. The current study was therefore undertaken to evaluate the egg production characteristics of the cross between the naked neck and the normal feathered birds.

MATERIALS AND METHODS

Thirty parent stock dams of normal feathered (NF) and naked neck (Na) genotypes housed on deep litter with a mating ratio of 1:10 sire to dam, respectively were used to generate the F_1 pedigreed chicks used in the experiment. Similarly, a mating ratio of 1:10 naked neck sire to normal feathered dams replicated three times was used to generate the crossbred genetic group. The resulting chicks were brooded on deep litter under standard conditions. Twenty pullets from each genetic group were randomly selected and reared to 280 days of age during which part period egg production was measured. Parameters evaluated include part period egg number (PPEN), part period egg mass (PPEM) and average part period egg weight (PPEW). The age at first egg (AFE) and the weight of first egg (WFE) were also evaluated.

Data collected were analysed using the general linear model multivariate analysis as outlined in SPSS (2004) statistical package. The model fitted was:

$$Y_{ij} = \mu + a_1 + e_{ij}$$

Where

Y_{ij} = single observation (egg number, egg weight)

μ = overall mean

a_i = effect of i^{th} genetic group

e_{ij} = residual error.

RESULTS AND DISCUSSION

Table 1 presents the summary of the part period egg production characteristics in the genetic groups studied. The total part period egg number ranged from 88.8±1.98 in the Na straight bred to 105.25±2.57 in the NF straight bred genotype. It varied significantly ($P<0.05$) between the genetic groups with the NF genotype exhibiting a significantly ($P<0.05$) higher egg number among the straight bred genotypes.

Mean part period egg weight ranged from 33.45±1.04 in the NF straight bred genotype to 38.86±0.95 in the Na straight bred genotype. There was significant variation between the straight bred the cross bred genotypes for egg mean weight.

Part period egg mass was significantly higher ($P<0.05$) in the cross bred genotype than in the respective straight bred genetic groups. The part period egg number for the genetic group of the Nigerian local chicken in the current study is higher than those reported by Momoh (2005) for the heavy and light ecotype chickens. The observed differences in the current genotypes of the Nigerian local chicken may be a reflection of the true genetic diversity of these birds or environmental differences. However, the observed significant ($P<0.05$) differences between the genetic groups for egg number is at variance with the report of Adedokun and Sonaiya (2001) who noted that the Nigerian indigenous chicken from three agro-ecological zones did not differ significantly in egg production characteristics. The range obtained in the current study for egg number during the part period are within the range reported by Udeh and Omeje (2005) and Asuquo *et al.* (1992) for the Nigerian local chicken.

The heritability estimates for part period egg characteristics are presented in Table 2. In general, heritability estimate observed in the current study ranged from low to high. The heritability estimates for short term egg number obtained in the current study are in agreement with the values reported previously by Oni *et al.* (1991) for Nigerian local chicken and Kiaani-Manesh *et al.* (2003) for Iranian native chickens. The low to moderate heritability estimate for egg number observed in the current study is indicative that improvement for egg number in the genetic groups may not be rapid through mass selection. Thus, crossbreeding and other selection procedures (individual selection) may be profitable in improving egg number in the genetic groups. The mean short term heritability estimate for egg number, egg weight and egg mass in the crossbred genotype are marginally higher than those of the respective straight bred genotypes. This is suggestive that genetic improvement for these traits could be achieved through crossbreeding.

Tables 3 present the genetic correlation between the traits of interest. The range of values obtained for genetic correlation in the current study is within the range reported by Momoh (2005) for the light and heavy ecotypes of chicken of Nigeria.

CONCLUSION

In summary, based on the values for the genetic correlations obtained between the various parameters, it may be concluded that any improvement in part period egg number would lead to a concurrent improvement in egg mass and age at first egg in the genetic groups because of the positive genetic correlation. Furthermore, selection for part period egg number will lead to improvement in annual egg number. This is true since there is high genetic correlation between part period egg number and annual egg number reported by several authors.

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Table 1. Summary of part period egg production characteristics in the genetic groups

Parameter	NF/NF	Na/Na	Na/NF
PPEN	105.25 ±2.57[a]	88.8 ±1.98[c]	100.5 ±2.04[b]
APPEW	33.45 ±1.04 [c]	38.86 ±0.95[a]	35.99 ±1.35[b]
PPEM (g)	3520.61 ±79.25[b]	3450.76 ±78.51[c]	3616.99 ±85.47[a]
AFE (days)	161.05±0.72[a]	180.05 ±1.36[c]	163.90 ±0.83[b]
WFE (g)	28.21 ±0.37[b]	30.40 ±0.27[a]	30.42 ±0.35[a]

a,b,c… means within the same row having different superscripts are significantly different (P<0.05)

NF-Normal feathered genotype. Na- Naked neck genotype

PPEN = Part period egg number **A**PPEW = average part period egg weight PPEM = Part period egg mass

AFE = Age at first egg WFE=Weight of first egg

Table 2. Heritability estimates for short-term egg production from sire variance components in the genetic groups

Parameter	NF/NF	Na/Na	Na/NF
Egg number	0.31±0.26	0.27±0.21	0.32±0.23
Egg weight	0.45±0.14	0.44±0.21	0.51±0.21
Egg mass	0.17±0.12	0.31±0.22	0.35±0.15
AFE	0.42±0.11	0.28±0.18	0.26±0.17

NF-Normal feathered genotype.

FF- Frizzle feathered genotype.

Na- Naked neck genotype

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DIMORPHISM OF BODY WEIGHT IN TWO TYPES OF NIGERIAN INDIGENOUS CHICKEN IN DERIVED SAVANNAH ZONE

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ABSTRACT
The study sought to evaluate sources of variation of bodyweight in Yoruba and Fulani Ecotype chickens on free range system. A total of 2,041 chickens from five different flocks were weighed individually with the aid of weighing scale with sensitivity of 0.01 kg. Data generated were subjected to T-Test statistics. It was revealed that within each ecotype sex significantly ($P<0.05$) influenced bodyweight in favour of male chicken while ecotype significantly ($P<0.05$) influenced bodyweight in favour of Fulani ecotype. Flock had no significant ($P>0.05$) effect on bodyweight in both ecotypes. It can therefore be concluded that during selection to improve body weight of indigenous chickens, male chicken should be given more preference than female and that Fulani ecotype may respond positively to selection than Yoruba ecotype.

INTRODUCTION
Dimorphism is a natural phenomenon in all growing animals characterised by the manifestation of visible differences between the male and female species. Various investigations in sexual dimorphism in relation to body weight, feed and water intake of chicken have been made. In domestic chicken, this was observed from the body weight gains, size, shape and behaviour of the birds. It was reviewed by Laseinde and Oluyemi (1992) that male broilers were heavier than females at hatching. The average body weight at day old for male was 40.31g and 36.6g for the female. At the growing and finishing stages, also the males were heavier than the females. Musa *et al.* (2006) reported that males had a significantly higher body weight and carcass weight, a better feed conversion and less carcass fat than females. Garcia *et al.* (1993) found that the body weight at slaughter and carcass yield were higher in male than in female. Kirchgessner *et al.* (1993) also reported that females had a lower feed consumption and growth rate than the males and also had a poorer feed efficiency by 3.4%
In the experiment conducted by Soarce *et al.* (1992) males had significantly higher body weight, better feed conversion efficiency and less carcass fat than females. High significant differences were evident between sexes of the commercial broiler stocks in an experiment conducted by Hamcock *et al.* (1995), with respect to the mature weights. It was reviewed by Burke (1994) that male chick was significantly heavier than females. Burke (1994) also noted significant sex differences in body weight of turkey poults of one strain on the day of hatch, but in another strain, the difference was not significant until 6 weeks of age. Akinokun (1990) reported that higher body weight values for male in indigenous chicken than females in a non descript population.
This study was therefore designed to document sources of variation of bodyweight in Fulani and Yoruba ecotype chickens in derived savannah zone of Nigeria.

MATERIALS AND METHODS
Data used for this study were generated from 2,041 Indigenous chicken comprising of 767 Fulani Ecotype and 1,274 Yoruba ecotype chickens under free range system in the derived savannah zone of Nigeria. These chickens were individually weighed with the aid of weighing scale with sensitivity of 0.01kg. The study was carried out at Ogbomoso, it was located in the derived savannah zone of Nigeria. The climate is characterized by fairly high uniform temperature (36.2^0C) and Moderate to

high relative humidity (60% - 70%) (Oladuntan Oladimeji, 1999). The Nigeria indigenous chickens in this study are Yoruba and Fulani ecotype, reared under traditional Animal Husbandry where they scavenge for most feed resources that are no longer directly useful to man, such as crop residues and kitchen waste with little or no grain supplement

Least square mean (x), standard deviation (S.D), standard error (S.E) and coefficient of variation (C.V) associated with body weight were estimated using GLM procedure of Statistical Analysis System (SAS, 1990) package. T – Statistics procedure was used to test the significance of the mean differences between values of sexes and ecotype using the same statistical package.

RESULTS AND DISCUSSION

Table 1 shows the descriptive statistics of body weight of Yoruba and Fulani ecotype flocks. In Yoruba Ecotype, the result showed that mean live weight across location ranged from 0.98 ± 0.22kg to 1.21±0.1kg with 1.06 ± 0.02 kg to 1.36 ± 0.02kg for males and 0.88 ± 0.02kg to 1.06 ± 0.02kg for females. Coefficient of variation ranged from 12.86% – 22.14% for males and 10.50% – 18.88% for females. Males were significantly heavier than females (Table 2). In Fulani Ecotype, the result showed that mean live weight across location ranged from 1.32 ± 0.03kg to 1.77 ± 0.04kg with 1.87 ± 0.06kg to 1.75 + 0.05kg for males and 1.65 ± 0.06kg to 1.27 ± 0.03kg for females. Fulani Ecotype had higher coefficients of variation (28.27% - 35.68%). Males were significantly heavier than females. Generally, Fulani ecotype were heavier (1.77 ± 0.04kg) than their Yoruba ecotype counterpart (1.21 ± 0.01kg). Highest value was recorded for male. Coefficient of variation and standard deviation did not follow any definite pattern, thus live weight were variable in the populations studied.

Table 1. Least Square Means(X*)*, Standard deviation (S. D.), Standard Error (S. E.) and Coefficient of Variation (C. V.) of Body Weight of Yoruba and Fulani ecotype Chicken.

		Yoruba Ecotype			Fulani Ecotype		
Population		Male	Female	Total	Male	Female	Total
Ikoyi	N	131	122	253	78	80	158
	$\bar{X}$ (kg)	1.06	0.88	0.98	1.75	1.27	1.32
	S. D.	0.24	0.17	0.22	0.43	0.24	0.43
	S. E.	0.02	0.02	0.01	0.05	0.03	0.03
	C. V.	22.14	18.88	22.79	24.76	19.08	28.27

Iluju	N	130	123	253	80	75	155
	$\bar{X}$ (kg)	1.26	0.97	1.11	1.87	1.60	1.72
	S. D.	0.17	0.10	0.20	0.52	0.43	0.50
	S. E.	0.02	0.01	0.01	0.06	0.05	0.04
	C. V.	13.70	10.50	18.40	27.99	27.09	29.82
Iresaadu	N	127	123	250	75	71	146
	$\bar{X}$ (kg)	1.36	1.06	1.21	1.86	1.60	1.74
	S. D.	0.17	0.18	0.23	0.50	0.50	0.52
	S. E.	0.02	0.02	0.01	0.06	0.06	0.04
	C. V.	12.86	17.10	19.12	26.84	30.93	29.71
Onipaanu	N	126	123	249	76	73	149
	$\bar{X}$ (kg)	1.18	1.06	1.09	1.84	1.65	1.77
	S. D.	0.19	0.18	0.18	0.51	0.53	0.52
	S. E.	0.02	0.02	0.01	0.06	0.06	0.04
	C. V.	15.70	11.53	16.39	27.91	32.08	29.52
Ibaiyaoje	N	144	125	269	80	79	159
	$\bar{X}$ (kg)	1.07	0.95	1.01	1.83	1.55	1.66
	S. D.	0.21	0.15	0.19	0.56	0.42	0.51
	S. E.	0.02	0.01	0.01	0.06	0.05	0.04
	C. V.	19.36	15.43	19.08	30.76	26.89	30.68

Table 2. Summary of T – Test of Mean Difference of Body weight between Sexes and Ecotype

	YORUBA		FULANI		POOLED	
FLOCK	MALE	FEMALE	MALE	FEMALE	YORUBA	FULANI

Ikoyi	1.06[a]	0.88[b]	1.75[a]	1.27[b]	0.98[a]	1.52[b]
Iluju	1.26[a]	0.97[b]	1.87[a]	1.60[b]	1.11[a]	1.72[b]
Iresaadu	1.36[a]	1.06[b]	1.86[a]	1.60[b]	1.21[a]	1.74[b]
Onipaanu`	1.18[a]	0.99[b]	1.84[a]	1.65[b]	1.09[a]	1.77[b]
Ibaiyaoje	1.07[a]	0.95[b]	1.83[a]	1.55[b]	1.07[a]	1.66[b]

Means with the same superscript along the same row within ecotype and body parameters are not significantly different (p>0.05)

Body weight has been widely reported as the most common measure of size in domestic animal populations. Akinokun (1990), Nwosu *et al.* (1985), Hossain and Ahmed (1993) and Gueye *et al.* (1998) all reported the significance of body weight in local chickens. Gueye *et al.* (1998) reported values of 1.367 ± 0.3kg and 1.120 ± 0.23kg for male and female indigenous chicken of Senegal which were higher than value reported for Yoruba ecotype and lower than value reported for Fulani ecotype chickens in this study. Within each ecotype, males were generally heavier than females which may be due to sexual dimorphisms that exist in indigenous chicken populations. This agrees with reports of Ngou Ngoupayou (1990) and Missohou *et al.* (1997) in indigenous chickens and Hassan and Adamu (1997) in indigenous pigeons. The authors further explained that males were generally more aggressive than females which consequently aid their ability in search of feeds during scavenging as well as during feeding. Fayeye *et al.* (2006) reported values of 1.49 ±0.43kg and 1.13±0.29kg for male and female, respectively which agree with the values reported in this study and Gonzalez *et al.* (2003) also reported that males were generally heavier than females in native chicken of South Eastern Mexico. The present results also agree with the earlier submission of Adedokun and Sonaiya (2001) in the study conducted on the effect of sex on body weight of indigenous chicken population of Nigeria. The result of this study is also in line with the work of Morathop *et al.* (2007) who reported values of 1.1kg and 0.85kg for males and female, respectively in decoy chickens in upper North of Thailand. Islam and Nishebiri (2009) shared the same view of sex effect on native chickens of Bangladesh. Oluyemi and Ogunmodede (1979) reported on the physical characteristics of the indigenous fowl with matured body weight of 1.18 – 1.25kg for male and 0.9 – 1.02kg for female.

Although, information on the age of the birds in this study could not be obtained because indigenous chicken keepers were ignorant of it, even most indigenous chicken keepers did not know the exact age of their bird so as to relate it to bodyweight. Sonaiya (1997) reported similar constraints in his study. However, Olori (1992) observed sexual dimorphism in indigenous chickens under intensive system at adult age of fifteen week and the differentiation became apparent with male being significantly heavier.

Between ecotypes, Fulani ecotype were significantly heavier than Yoruba ecotype in this study and this may be due to strain effect which plays a significant role in relation to genetic effect on variation in body weight of chickens. Giordani *et al.* (1992) and Garcia *et al.* (1993) also reported significant differences in the growth performance of different strains of birds in their studies. Edriss *et al.* (1995) earlier reported that strain groups had significant effect on body weight in indigenous chickens of Iran. Fulani Ecotypes chickens tend to have more access to crop residues and farm wastes than Yoruba Ecotype chickens. Atteh (1990) and Olori (1992) observed that Fulani Ecotype were heavier than other ecotypes in their various studies. Olori (1992) further concluded that Fulani Ecotype Chicken grew faster than Yoruba ecotype chicken.

The values reported for Body Weight in this study was lower than literature values of exotic chicken which thus indicates that indigenous chickens are small in body size. Nwosu and Asuquo, (1985), Nwosu and Omeje (1985) all reported that indigenous chickens are characterised with small body size and small egg size. Nwosu *et al.* (1985) opined that indigenous chickens belong to light breed group. Conclusively, this study revealed that sex is a source of variation in indigenous chicken population.

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Table 3. Genetic correlations between egg production characteristics in the straight and crossbred genetic groups

	Parameter	NF					Na		
		PPEN	PPEM	AVPPEW	AFE	WFE	PPEN	PPEM	APPEW
NF	PPEN		0.98***	-0.78***	0.17	0.14			
	PPEM			0.82***	0.14	0.18			
	APPEW				-0.15	0.11			
	AFE					0.95***			
Na	PPEN		0.87***	-0.77***	0.17	0.13		0.97***	-1.13***
	PPEM			0.86***	0.08	0.23			0.85***
	PPEW					-0.22			
	AFE					0.87***			

*P<0.05 ** P<0.01 ***P<0.001 PPEN-part period egg number PPEM-part period egg mass

APPEW-part period egg weight. AFE- age at first egg. WFE-weight of first egg

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ECOTYPES OF INDIGENOUS CHICKENS IN SOKOTO SOUTH LOCAL GOVERNMENT AREA: VARIATION IN WEIGHTS OF BIRDS AND EGGS

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ABSTRACT

Fifteen (15) flocks of domestic fowls comprising 83 birds (42 hens, 9 cocks and 32 chicks) and 60 eggs were monitored in Gagi village between August and November 2001. The aim of the study was to characterize the traditionally-managed native domestic fowl diversity in terms of variation in live weight of adult birds and weight of eggs. Monitoring visits were paid to the flocks weekly during which live weights of birds and egg weights were taken. Results of the study revealed that the mean live weight of hens was 1.10±0.25kg. Hens that belong to the Red (*Ja*) strain were-significantly heavier (P<0.05} than those of White (*Fari*) of Black/white (*Wake-wake*) strain. Live weight of a

hen was significantly influenced by its current reproductive phase ($P<0.05$). As such, live weight of hens that were laying, incubating, and brooding averaged 1.15±0.30kg, 1.16±0.29kg, and 1.19±0.26kg, respectively. The mean live weight of cocks was 1.07±0.13kg. This value varied significantly due to strain ($P<0.05$). Cocks of the Black/white plumage (*Wake-wake*) were significantly heavier than those with Black (*Baki*), White (*Fari*) or Red (*Ja*) plumage. The mean live weight of chicks at about 34 days of age was 59.3±26.8g. This value also varied significantly between flocks ($P<0.05$). Mean weight of egg of the native chickens was 41.6±4.5g. No significant differences in the weights of eggs as a result of strain and flock effects were recorded. The observed significant effects of strain and flock on the live weights of hens and cocks, haphazard though, point to some level of variation in the performance potential of the various strains and husbandry of local chickens in the area.

INTRODUCTION

The main types of domestic poultry in Nigeria are chickens, pigeons, ducks, guinea fowls and turkeys. Chickens are by the far the most important poultry species numerically (FDLPCS, 1992). In this country, there has been a substantial development of commercial enterprises complementing village poultry production. Nevertheless, poultry production is still dominated by peasants, who own the birds in small numbers and raise them under what was variously described as extensive, low or zero husbandry system (Matthewman, 1977). Earlier studies on traditional poultry production in Sokoto State reported some baseline information on husbandry practices and flock composition (Eshiett *et al*., 1988; Hassan *et al*., 1989; Otchere *et al*., 1993) and species combination (Okoro *et al*., 1990) and reproductive performance (Hassan and Aliyu, 1996). The present study set out to characterize the domestic fowls kept under the traditional system of management. Specifically, the study aimed at assessing the birds under their natural rearing conditions using live weight and egg weight as criteria.

MATERIALS AND METHODS

The present study was carried out in a random sample of households in Gagi in Sokoto South Local Government of Sokoto State, Nigeria. Geographically, Gagi is located about three kilometres East of Sokoto, the state capital. Sokoto lies in the Sudan savannah (Goh *et al*., 1975). It is characterized by alternate rainy and dry seasons. The average annual rainfall is about 800 mm. The monthly temperature is between 21°C and 40°C. Hamattan season stretches from November to March, when there is dry and ladden wind accompanied with dust (Udo, 1970). The people of Gagi are Sulubawa (Fulani) from Rikina in the present-day Dange Shuni Local Government.

After securing the permission of the District Head of Gagi, weekly visits were paid to the study households for about three months. Before the monitoring visits, questionnaires were administered to know the actual number of birds owned by each selected household and gain the consent of the household head for flock performance monitoring. With the aid of the pre-prepared format, random samples of domestic fowls in each household were monitored. The format covered items like bird identification number, flock number, source of bird, sex of bird, date of hatching, strain (ecotype), colour of feathers of wings and tail, comb type, shank colour and reproductive phase. One to five birds were monitored per household. Birds were marked on the legs for identification. Weighing of the birds was done using a 5-kg scale. Eggs of the monitored hens were weighed using a 1-kg weighing scale. Information was also collected on the husbandry (housing feeding, and health care) of the birds. Photographs were taken to illustrate the various strains of domestic fowls found in the monitored flocks.

The data collected were collated for statistical analysis. Frequency, mean, standard deviation, minimum and maximum values were calculated. Data on live weight and egg weight were subjected to analysis of variance on a PC version of the Statistical Package for Social Sciences (SPSS, 1997). The fixed effects included in the final model were strain, flock, and reproductive phase. Statistically significant subclass means were separated using the Duncan's Multiple Range Test of the same data analytical package..

RESULTS AND DISCUSSION

The overall mean live weight of hens was 1.10±0.20kg (Table 1). This value is almost similar to the 1.04kg reported for mature local domestic hens under three rearing systems in Central Mali (Wilson *et al.*, 1987), but higher than 0.89 kg reported for mature Desi hens in Bangladesh (Sazzad *et al.*, 1986). In agreement with Wilson *et al*. (1987), there were significant differences between the weights of the hens in different phases of reproductive process. Thus, the resting hens (1.06±0.23kg) were lighter than those that were laying (1.15±0.30kg), incubating (1.16±0.29kg) or brooding (1.19±0.26kg). Wilson *et al.* (1987) got a comparable weight (1.17kg) for laying hens as obtained from the present study. However, they reported smaller weights for incubating hens (0.85kg) and brooding hens (0.94kg).

Among the strains of native chickens encountered in this study, the White (*Fari*) and Red (*Ja*). hens (Plates I and II, respectively) were significantly heavier ($P<0.05$) than the remaining ones (Table 1). The flock effect on body weight of hens was also found to be significant ($P<0.05$). As such, the hens in flock No. 2 recorded the highest value (1.54±0.25kg) while those in flock No. 10 recorded the lowest value (0.90±0.10kg) (Table 2). This is an indication of the variation in the level of husbandry practices adopted by the keepers of the birds.

Table 3 shows the overall mean live weight of cock as 1.07±0.13kg. This value was higher than 0.80kg reported for mature local cocks in the tropics (Anthony *et al*., 1986), but lower than 1.60kg reported for local cocks in Central Mali (Wilson *et.al*., 1987). Cocks of the *Wake-wake* (Plate III) recorded the highest value for live weight (1.24±0.08 kg). This value was significantly higher than those values recorded for the other strains ($P<0.001$). Generally, the live weights of hens and cocks obtained from the present work fall within 0.9±1.8kg reported for mature indigenous) domestics fowls in the tropics (Payne, 1990).

Table 1: Means, standard deviations, minimum and maximum values for live weight of hens (kg) according to strain and reproductive phase

Characteristic	No. of values	Mean	S.D.	Min	Max
Overall	368	1.100	0.254	0.600	1.900
Strain of hen)					
Black (*Baki*)	93	1.063[*]	0.196	0.800	1.650
White (*Fari*)	39	1.204[c]	0.328	0.800	1.800
Silver (*Kankara*)	20	1.039[a]	0.185	0.800	1.400

Black/White (*Wake-wake*)	69	0.979[a]	0.175	0.600	1.400
Red (*Ja*)	147	1.161[bc]	0.276	0.800	1.900
Reproductive phase of hen					
Incubating	34	1.155[b]	0.293	0.800	1.800
Brooding	74	1.189+c	0.258	0.800	1.860
Laying	23	1.151[b]	0.304	0.800	1.800
Resting	237	1.059[a]	0.232	0.600	1.900

*Means in the same column with same letters are not significantly different (P<0.05)

Table 2: Means, standard deviation, minimum and maximum values for live weight of hens (kg) according to flock number

Characteristic	No. of values	Mean	S.D.	Min.	Max
Overall	364	1.102	0.254	0.600	1.900
Flock No.					
1	30	1.107*	0.209	0.800	1.500
2	18	1.543[g]	0.247	1.000	1.860
3	20	1.498[g]	0.246	1.075	1.800
4	16	0.919[b]	0.259	0.600	1.200
5	50	0.988[b]	0.102	0.800	1.200
6	30	1.037[c]	0.117	0.800	1.270
7	50	1.058[c]	0.101	0.900	1.300
8	50	0.991[b]	0.146	0.800	1.400
9	18	1.144[d]	0.271	0.800	1.650
10	10	0.895[a]	0.101	0.800	1.100
11	20	0.920[b]	0.108	0.800	1.175
12	36	1.311[f]	0.298	1.100	1.900
13	10	1.182[e]	0.128	1.000	1.400
14	6	0.967[b]	0.137	0.800	1.100

*Means in the same column with same letters are not significantly different (P<0.05)

Plate I: **The White (Fari) incubating hen in Gagi**

Plate II: **The Red (Ja) hen in Gagi**

Table 3: Means and standard deviation for live weight of cocks (kg) according to strain

and flock number

Characteristic	No.	Mean	S.D	Min.	Max.
Overall	64	1.069	0.128	0.800	1.400
Strain of cock					
Black (*Baki*)	32	1.073[a]	0.132	0.800	1.300
White (*Fari*)	10	0.980[a]	0.092	0.900	1.100
Black/White (*Wake-wake*)	6	1.241[b]	0.080	1.200	1.400
Red (*Ja*)	16	1.050[a]	0.089	0.800	1.100
Flock number of cock					
4	10	1.030	0.108	0.800	1.100
5	10	1.120	0.079	1.000	1.200
6	20	1.020	0.110	0.900	1.200
11	16	1.112	0.185	0.800	1.400
12	8	1.075	0.046	1.000	1.100

*Means in the same column with same letters are not significantly different (P<0.05)

Plate III: The Black/White (*Wake-wake*) hen in Gagi

The live weight of chicks averaged 59.3±26.8g at about 34 days of age (Table 4). It was impossible to obtain the age of the chicks at day old due largely to variation in the ages of the chicks at the start of monitoring. Nevertheless, the 28.6g obtained for chicks that were younger than one week was

lower than 35g reported for day old chicks in the humid zone of Nigeria (Oluyemi and Roberts, 1979), but higher than 21.7g reported for day old chicks of local domestic fowls in Central Mali (Wilson *et al.*, 1987). The observed increase in the live weight of chicks with age is normally physiological. The observed significant differences in live weights of chicks caused by strain and flock effects (Table 4) need to be interpreted with care, because the chicks in the various classes and sub-classes were of varying ages. This caution applies to the chicks', growth pattern as depicted in Figure 1, though the continuous increase in gain up to the last week agrees with the trend reported for local chicks at Nsukka (Nwosu and Asuquo, 1985). On-station performance evaluation of the chicks will help to ascertain the true trend of these environmental and physiological events.

The overall mean weight of eggs of local domestic hens was 41.6±4.5g (Table 5). Previous studies gave average egg weight of local domestic fowls as 43.9g (Hill and Modebe, 1961), 42.8g (Trail, 1962), 33.4g (Hertrampf, 1979), 34.4g (Wilson *et al*., 1987), 40.6g (Wilson, 1979) and 32.7g (Akinokun, 1990). The value got from the present study fell on the upper limit of the range of the earlier reported values. It is noteworthy however that no significant differences were recorded in the weights of the eggs as a result of differences in strain and flock ($P>0.05$).

Table 4: Means and standard deviations for weight of chicks (g) according to strain of hen, flock number and age group of chick

Characteristic	No. of values	Mean	S.D.	Min.	Max
Overall	210	59.3	26.8	25	100
Strain of hen					
Black (*Baki*)	21	64.0[b]	9.8	50	80
Black/White (*Wake-wake*)	41	49.9[a]	19.4	25	75
Red (*Ja*)	148	61.2[ab]	29.6	25	100
Flock No.					
1	22	32.7[ab]	5.5	25	42
2	36	36.9[b]	10.3	25	62
4	13	29.2[a]	4.9	25	40
5	44	72.8[c]	12.9	50	100
6	24	29.2[a]	4.0	25	35
7	19	69.7[c]	5.1	60	75
9	7	73.6[c]	3.8	70	80
10	45	95.1[d]	5.6	80	100
Age of chick (week)					

Less than 1	14	28.6[a]	13.4	25	75
1-4	85	47.9[b]	18.5	25	80
4-8	82	64.8[c]	27.3	25	100
Above 8	29	91.9[d]	7.8	70	100

*Means in the same column with same letters are not significantly different (P<0.05)

CONCLUSION

The values obtained for live weights of the various categories of domestic fowls and weight of eggs from the present study have added to the baseline information on the performance of the Nigerian native chickens under the traditional rearing conditions in the semi-arid zone of Nigeria. The observed significant effects of strain and flock on the live weights of hens and cocks, haphazard though, point to some level of variation in the performance potential of the various strains and husbandry of local chickens in the area. These findings can be exploited for stock genetic improvement. Investigation of the feeding regimes and health care practices adopted under the traditional production system will be helpful in this direction.

Table 5: Means, standard deviations, minimum and maximum values for weight of eggs (g) according to strain and flock number of hen

Characteristic	No. of values	Mean	S.D.	Min.	Max
Overall	60	41.6	4.5	30.0	47.2
Strain of hen					
Black (*Baki*)	11	42.5	4.8	30.2	47.0
White (*Fari*)	4	42.2	2.2	40.2	45.2
Black/White (*Wake-wake*)	35	40.8	4.5	30.0	46.2
Red (*Ja*)	10	42.9	4.8	30.2	47.2
Flock No. of hen					
1	9	42.4	2.2	40.2	46.2
3	11	40.0	5.2	30.0	45.5
5	5	40.0	6.0	30.2	45.0
6	4	40.1	7.0	30.2	45.4
7	5	43.1	2.4	40.5	45.5
9	12	40.0	4.9	30.3	45.5

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ENVIRONMENTAL GENETICS (EG)

EG01
BEHAVIOURAL RESPONSE OF INTENSIVELY MANAGED WEST AFRICAN DWARF GOATS TO VARIATIONS IN DIURNAL TEMPERATURE

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ABSTRACT
Response of intensively managed West African dwarf goats at different daily ambient temperature was evaluated. 12 goats were used for the study. Temperature and relative humidity in the goat pen were monitored across seasons (rain and dry) and across day periods (minimum temperature in the morning and maximum temperature in the afternoon) using thermo-hygrometer to compare parameters in normal and heat stress conditions. Activities of the animals were observed and classified as eating, ruminating, standing and lying. Data collected were analysed using inferential statistics of Chi-square test. Summary statistics for climatic variations were also calculated within each season. The animals were found lying more than standing during the cool hours of the day

while they were seen standing more during the hot hours of the day; the animals ate more during the cool hours of the day and ruminated less during this period but during hot hours of the day, they ate less and ruminated more The result obtained in this experiment support the hypothesis that goats behavioural responses are useful indicators of heat stress in terms of changes in diurnal ambient temperature.
Keywords: Behavioural response, climatic variation, diurnal temperature, seasons

INTRODUCTION

West African Dwarf (WAD) goats are found in large number in the Southern part of Nigeria, they possess the widest margin of adaptation amongst the ruminants (Oni, 2003). They are small, hardy, early maturing, prolific, non-seasonal breeders (Osuagwuh and Akpodje, 1982) and are trypanosome-tolerant (Ozoje, 2002). However, WAD goats are exposed to stressful climatic conditions in tropical regions, which influence their productivity and welfare. In such regions, high temperature and relative humidity are major environmental factors that result in heat stress which in turn influence the productivity and physiological development of animals (McNitt *et al*., 2000; Marai *et al*., 2002a). This effect is aggravated when heat stress is accompanied by high ambient humidity (Marai *et al*., 2000a; Abdel-Hafez, 2002). Climatic conditions in these regions are such that the warm hot season is relatively long with intense radiant energy for an extended period of time accompanied with high relative humidity. The environment surrounding an animal at any particular instant influences the amount of heat exchange between it and the environment. It has been reported that acclimation of domesticated ruminants to heat stress imposes behavioural, physiological and metabolic adjustments to reduce the strain and enhances the likelihood of surviving the stress; it also frequently reduces their performance and compromises their health (Bernabucci *et al*., 2010). Although many animals have special heat loss mechanisms that enable them control their body temperature, such as sweating or panting, these activities involve the use of stored energy and water. Modifications of behaviour patterns or behavioral thermoregulation, however, may be adequate to enable an animal to maintain acceptable comfort levels without involving these mechanisms (Bradley, 2008). Animals respond to thermal stress in different ways, between species, breeds and between individual within a breed. Therefore, there is a need to develop a simple, most practical, easy and relatively trust worthy non- invasive means of assessing the potential of an animal that is able to maintain expression of its inherited functional trait during when raised under hot conditions, either when introduced to a new locality or for selection for heat tolerance. Thus, this study sought to evaluate interaction of change in diurnal ambient temperature and behaviour of WAD goats under hot humid conditions.

MATERIALS AND METHODS

The study was conducted at the Teaching and Research Farm of the Federal College of Animal Health and Production Technology, Ibadan Nigeria, between December, 2012 and May, 2013. Temperature and relative humidity in the goat unit were monitored across seasons (rain and dry) and across day periods (minimum temperature in the morning and maximum temperature in the afternoon) two to three days using a DeltaTrak thermo-hygrometer. As far as possible, this instrument was hung on the wall inside the pen to provide a record of the temperature and relative humidity experienced by the goats.

Based on the recordings of farm ambient temperature and relative humidity, the study was conducted during rainy and dry seasons to compare parameters in normal and heat stress conditions. Months of December, 2012 to February, 2013 were considered as the dry season, while the months of March, 2013 to May, 2013 were considered as the rainy season periods. Activities of the animals were observed and classified on the basis of visual observation of animal behaviour as follows: eating, ruminating, standing and lying. Behavioural observations were recorded for 3 hours during the cool period of the day as well as during the hot periods of the day; this was done twice a week. The cool part of the day for this study was considered to be 6:30 am, whilst the hot part of the day was

determined by taking ambient temperature readings at an hour intervals from 6:30am to 5:30pm daily over three continuous days and the hot part of the day was found to be 1:00pm.

Data collected were analysed by the Statistical Analytical Software (SAS, 2004) using inferential statistics test Chi-square test to test the hypotheses stated for the study (the association between behaviour of WAD goats and variation in diurnal ambient temperature). The summary statistics for climatic variations were also calculated within each season.

RESULTS AND DISCUSSION

The average temperature and relative humidity in the pen during cool and hot hours of the day across the two seasons of the study are presented in Table 1. The climatic data obtained in wet season differed from the data obtained in the dry season. Values obtained for ambient temperature during the cool period (AM) and hot period (PM) of the day in the rainy season were less than that obtained during these periods in the dry season. However, relative humidity during cool and hot periods in the rainy season was higher than that of dry season.

Table 1. Mean temperature and relative humidity in the pen during cool (AM) and hot hours (PM) of the day across seasons

	Farm ambient temperature (^{o}C)		Farm ambient relative humidity (%)	
Seasons	AM	PM	AM	PM
Rain	23.62 ± 0.56	28.88± 1.23	84.50 ± 0.95	55.80 ±1.12
Dry	25.63±0.97	31.70 ± 1.35	63.70 ±1.03	49.30± 0.56

Table 2 shows the results of the degree of relationship between the goats' posture and rising diurnal temperature. There was significant difference (P< 0.001) between the animals' posture and change in diurnal ambient temperature. The animals were found lying more than standing during the cool hours of the day while they were seen standing more during the hot hours of the day. This result agreed with report of (Nazan *et al*., 2009) in a comparative study between heat stress ability of pigmented and unpigmented goats that unpigmented goats stood (0.8 vs. 1.2 h) less, but lay down (2.2 vs. 1.8 h) more than pigmented goats.

Table 2. Degree of association between behavioral response (standing and lying) of WAD goats and rising diurnal temperature

Behavioral responses					
Diurnal periods	Standing N (%)	Lying N (%)	Overall N (%)	Test	
				P-value	χ^2
AM	201 (34.9)	375 (65.1)	576 (100)	0.001	42.75
PM	222 (38.5)	354 (61.5)	576 (100)		

N=Number of observation, χ^2=Chi-square, AM = cool hours, PM = hot hours

There was significant difference (P<0.001) between the goats eating pattern and change in ambient diurnal temperature .The animals ate more during the cool hours of the day and ruminated less during this period but during hot hours of the day, they ate less and ruminated more (Table 3). Similar results were reported in earlier studies; that as temperature increased; less time was spent consuming food, probably to minimize or curtail body heat production and to keep the body cool (Ogebe *et al*., 1996) WAD goats have reduced rumination rates during rainy season when compared to that of dry season due to smaller amount of forage ingested, inducing a smaller absorption of nutrients. Hirayama, (2004) also reported that, time spent by goats eating in the heat treatment was

highest, while ruminating time was the lowest, indicating that stressed goats ate more but ruminated less than non-stressed goats.

Table 3. Degree of association between behavioral response (eating and ruminating) of WAD goats and rising diurnal temperature

Diurnal periods	Behavioral responses			Test	
	Eating N (%)	Ruminating N (%)	Overall N (%)	P-value	χ^2
AM	357 (62.0)	219 (38.0)	576 (100)	0.001	54.05
PM	250(43.4)	326 (56.6)	576 (100)		

N=Number of observation, χ^2=Chi-square, AM = cool hours, PM = hot hours

CONCLUSION

Exposure of goats to change in daily ambient temperature resulted in significant change in behaviuoral responses in terms of their activities - standing, lying, change in feeding pattern (eating and ruminating). Hence, these are useful indicators of heat stress as reflected in the animal behaviour in response to changes in diurnal ambient temperature.

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EG02

TOLERANCE MECHANISMS IN PTERIDOPHYTES (FERNS) AND THEIR USE AS REMEDIATORS OF HEAVY METAL CONTAMINATED SITES

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ABSTRACT

Pteridophytes (ferns) are lower plants with no well developed vascular bundle, yet they have shown high potentials in remediating heavy metals contaminated soils due to their inherent biological characteristics. They have ability to hyperaccumulate heavy metals such as Arsenic, Lead, Nickel, Chromium and Mercury in the soil and at the same beautify the contaminated site. Understanding the tolerance mechanisms of ferns would be helpful for using them to remediate heavy metal polluted sites (pterido-remediation). It is cost effective, environmental friendly and aesthetically pleasing approach which makes it suitable for developing countries. Therefore, Pterido-remediation is an effective tool or technology for cleaning up soil contaminated with heavy metals. Despite this, it is yet to become a commercially available technology in Nigeria. This paper provides a review of some ferns reported as excellent in removal of heavy metals from the soil and the molecular and physiological mechanisms that enable them tolerate these heavy metals. Benefits, limitations and factors influencing phytoremediation were also reviewed.
Key words: fern, heavy metals, hyperaccumulation, pterido-remediation, soil

INTRODUCTION

Ferns are non-flowering vascular plants which appeared in the fossil record around 400 million years ago (Kenrick and Crane, 1997). They are a group of about 9000 – 12000 species of plants classified in the Division Pteridophyta (Kartesz, 1994). Ferns are quite successful plants which grow as perennial or annual herbs, trees, epiphytes, aquatic or terrestrial plants. They differ from primitive thallophytes by having true leaves called megaphylls. Ferns also differ from gymnosperms and angiosperms by being seedless. Like all other vascular plants, ferns exhibit alternation of generation characterized by a diploid sporophytic and haploid gametophytic phases (Bierhorst, 1971). The distribution of ferns is similar to that of the mosses. They occur almost in all habitats but are most abundant in moist, montane forests, along streams and rivers most especially in the tropics (Agnew, 1974). Many ferns also grow within specific PH ranges; for instance the climbing fern *Lygodium* will only grow in moist, intensely acid soils, while the bulblet bladder fern, *Cystopteris bulbifera* is only found on limestone (Bierhorst, 1971). In Nigeria, ferns occur abundantly in rainfall belt of the south (Odu and Opapeju, 1986).

Bioindicators are plant species, substances or chemicals used to monitor pollutants of an environment or ecosystem. They are any biological species or group of substances whose functions, population or status could be used to determine ecosystem or environmental integrity (Rasheed,

2010). The principle behind the bioindicator approach is the analysis of an organism heavy metals contents and compared the metal concentration with the soil metal levels. However, phytoremediation is the process of decontaminating or cleaning of soil and water by using plants to absorb heavy metals or other pollutants. It is an emerging plant- based technology and has been receiving increased attention. The pre-requisite for successful phytoremediation is the existence of hyperaccumulator in some plants which are able to accumulate large amount of the metal contaminants in their above ground tissues with a high biomass (Mrittunjai *et al.,* 2005). Salt *et al.* (1998) referred to the method of using green plants to detoxify or remediate heavy metals contaminated soil sites as phytoextraction. The term 'hyperaccumulator' was first used to describe a plant species that hyperaccumulate nickel (Jaffre *et al.,* 1976). The term was later broadened to characterize plants achieving metal concentration greater than 1000 mg/kg (Reeves and Baker, 2000).

In general, Mosses, liverworts and ferns are also capable of growing on metal-enriched substrates. These plants possess anatomical and physiological characteristics enabling them to occupy unique ecological niches in natural metalliferous and manmade environments. For example, groups of specialized bryophytes called 'copper mosses' are found on Cu enriched substrates and come from widely separated taxonomic groups. Other bryophytes are associated with lead and zinc enriched substrates. Pteridophytes (ferns) are associated with serpentine substrates in various parts of the world. Brake fern, *Pteris vittata*, a fast growing plant is reported to tolerate soils contaminated with arsenic as much as 1500 ppm and its fronds concentrate the toxic metal to 22,630 ppm in 6 weeks (Ma *et al.,* 2001).

The objective of this paper is to provide a review of some pteridophytes that are found to be efficient in remediating heavy metal contaminated sites, the molecular and physiological mechanisms of their tolerance to heavy metals uptake, the benefits, limitations and factors influencing phytoremediation.

HYPERACCUMULATION AND PTERIDOREMEDIATION

Hyperaccumulation can be defined as uptake and sequestration of exceptional concentration of an element in aboveground parts of a plant under field conditions (Pollard, 2000). Hence, the threshold metal content used to define a hyperaccumulator depends upon the particular metal accumulated. For instance, proposed thresholds on a dry weight basis are 100 µg/g for cadmium, 1000 µg/g for cobalt, copper, nickel and lead while 10,000 µg/g is for manganese and zinc (Baker and Brooks, 1989). Once the metals are taken up, they are concentrated in less sensitive locations such as vacuoles, cell walls, epidermal cells and trichomes (Boyd *et al.,* 2000). The key process of pteridoremediation is the rate of metal removal that depends upon the biomass harvested and metal concentration in harvested biomass. A large number of hyperaccumulators are known mostly for nickel, zinc and selenium whereas most widespread and hazardous soil pollutants are arsenic, lead, cadmium often occurring in combination with other metals (Kraner, 2000). The process of hyperaccumulation of heavy metals by ferns is a complex phenomenon. It involves several steps, such as (a) transport of metals across the plasma membrane of root cells; (b) xylem loading and translocation; and (c) detoxification and sequestration of metals at the whole plant and cellular levels (Lombi *et al.,* 2002).

Unlike angiosperms, fern hyperaccumulators are equipped with inherent biological characteristics that could be exploited in the phytoremediation strategies aimed at decontaminating polluted sites. For instance, *Asplenium adylterium* is an indicator and hyperaccumulator of nickel (Vogt, 1942) while *Asplenium septentrionale* is an hyperaccumulator of lead and copper (Page, 1988). Sela *et al.* (1989) reported some aquatic ferns such as *Azolla filliculoides* which were able to hyperaccumulate heavy metals in their shoots. Other ferns with metal accumulating capabilities include *Salvinia*

natans, for copper and *S. minima* for chromium (Sen and Mondal, 1990). Other than heavy metals, ferns have also been known to concentrate large quantities of trace elements in their tissues (Woolson *et al.*, 1971). Hyperaccumulation of arsenic was discovered only recently, and the majority of plants that hyperaccumulate arsenic are fern species. First was *Pteris vittata* L. (Ma et al., 2001); followed *Pityrogramma calomelanos* L. (Francesconi *et al.*, 2002) and many other species of the *Pteris* genus such as *P. cretica* L., *P. longifolia* L., *P. umbrosa* L., *P. argyraea* L. (Zhao *et al.*, 2002), *P. quadriaurita* L., *P. ryiunkensis* L. and, *P. biaurita* (Srivastava *et al.*, 2005).

The phylogenetic relationship of ferns has been established based on the ability to hyperaccumulate arsenic. Plants that can hyperaccumulate arsenic were said to have arrived relatively late in fern evolution and might have evolved in arsenic-rich environment (Meharg, 2002). Many plants have been reported to accumulate more than 1000 mg/kg arsenic in their tissues (Porter and Peterson, 1975). However, they cannot be classified as hyperaccumulators since arsenic accumulation in these plants occur very slowly over an extended period of time. In addition, a large portion of the arsenic is sequestered in the roots. Most importantly, a lack of rapid growth, large biomass production and high uptake capacity render these plants unsuitable for phytoremediation (Meharg, 2002). A plant that accumulates a minimum arsenic concentration of 1000 mg/kg in the aboveground biomass and has a higher concentration in the aboveground than in both roots and the soil is said to be arsenic hyperaccumulator (Bombada and Ma, 2003).

Komar *et al.* (1998) reported the first known arsenic hyperaccumulating plant, *Pteris vitata* L. also known as Chinese brake fern from a site that was contaminated from pressure – treating lumber using chromated – copper- arsenate (CCA). *P. vittata* was also found to hyperaccumulate up to 60,000 mg/kg of arsenic in Nigeria which is more than the ones ever reported in literatures (Oloyede *et al.*, 2013). Ma *et al*. (2001) also reported three cultivars of *Pteris cretica* i.e *albolineata, mayii* and *parkerii* as arsenic hyperaccumulators with concentrations ranging from 1114 to 2046 mg/kg. Mrittunjai *et al*. (2005) identified additional new arsenic hyperaccumulating ferns (*Pteris biaurita, P. quadriaurita* and *P. ryukyuensis*) and reconfirmed *P. vitata* as an hyperaccumulator. *P. longifolia*, and *P. umbrosa* were also identified as hyperaccumulators by Ma *et al.* (2001).

SOURCES OF HEAVY METAL POLLUTION

Geological and anthropogenic activities are sources of heavy metal contamination (Dembitsky, 2003). Sources of anthropogenic metal contamination include industrial effluents, fuel production, mining, smelting processes, military operations, utilization of agricultural chemicals, small-scale industries (including battery production, metal products, metal smelting and cable coating industries), brick kilns and coal combustion (Zhen-Guo *et al.*, 2002). Arsenic is a major contaminant of soil and water around the world. It is a by-product of many mining processes and has been used extensively in pesticide industry and until recently, was widely used as a wood preservative (Azcue *et al.*, 1994). Man made sources of the world environmental arsenic production has been estimated as follows: about 70% in the preservation of timber, 22% in agricultural chemicals / pesticides and the remainder in pharmaceutical products, glass and non-ferrous alloys. Of these, mining, smelting of non-ferrous metals and burning of fossil fuels are the major industrial processes that contribute to anthropogenic arsenic contamination of air, water and soil (Jalal, 2008).

There are a variety of industrial processes that involve the use of lead such as mining, smelting, manufacture of pesticides and fertilizers, dumping of municipal sewage and the burning of fossil fuels that contain a lead additive. Many commercial products and materials also contain lead including paints, ceramic glazes, television glass, ammunition, batteries, medical equipment (i.e., x-ray shields, fetal monitors), and electrical equipment. Lead battery recycling sites, of which 29 have been labeled Superfund sites, and manufacturers use more than 80% of the lead produced in the

United States. On average, recycled lead products only satisfy half of the nation's lead requirements (Meagher, 1998).

Table 1: Summary of some ferns used as hyperaccumulators of heavy metals

S/N	SPECIES	SOURCE
1	*Adiantum caudatum* L.	Supaporn *et al.,* 2008
2	*A. philippense*	Supaporn *et al.,* 2008
3	*Angiopteris erecta*	Supaporn *et al.,* 2008
4	*Asplenium adylterium*	Vogt 1942
5	*A. septentrionale*	Page 1998
6	*Azolla filiculoides*	Sela 1989
7	*Colysis pothifolia*	Supaporn *et al.,* 2008
8	*Lindsea ensifolia*	Supaporn *et al.,* 2008
9	*Pteridium aquilium*	Supaporn *et al.,* 2008
10	*Pteris biaurita*	Supaporn *et al.,* 2008
11	*P. venusta*	Supaporn *et al.,* 2008
12	*P. vittata*	Ma *et al.,* 2001; Komar *et al.,* 1998
13	*P. cretica*	Zhao *et al.,* 2002
14	*P. longifolia*	Zhao *et al.,* 2002
15	*P. umbrosa*	Zhao *et al.,* 2002
16	*P. argyraea*	Zhao *et al.,* 2002
17	*P. quadriaurita*	Srivastava *et al.,* 2005
18	*P. ryukyuensis*	Srivastava *et al.,* 2005
19	*P. biaurita*	Srivastava *et al.,* 2005
20	*P. mayii*	Ma *et al.,* 2001
21	*P. parkerii*	Ma *et al.,* 2001
22	*P. albolineata*	Ma *et al.,* 2001
23	*Pityrogramma calomelanos*	Francesconi *et al.,* 2002
24	*Lygodium spp*	Supaporn *et al.,* 2008
25	*Tectaria impressa*	Supaporn *et al.,* 2008
26	*T. herpetocaulos*	Supaporn *et al.,* 2008

MECHANISMS OF TOLERANCE OF HEAVY METALS BY FERNS

Understanding the effects of heavy metals on ferns and the tolerance mechanisms would be helpful for using them to remediate heavy metal polluted sites. Plants growing on metal-contaminated sites need to develop some degree of tolerance to metal toxicity in order to survive. Since all plants contain at least some metal in their tissues, they clearly are incapable of completely excluding potentially toxic elements, but simply of restricting their uptake and/or translocation. Ferns growing on metal-contaminated sites need to develop some degree of tolerance to metal toxicity in order to survive. Tolerance to metals can either be achieved by avoiding the metal stress, by tolerating it or both (Levitt, 1980). Avoidance by exclusion is the most common mechanism of plant adaptation to metal toxicity. It depends on various kinds of reduced metal uptake: (i) by deposition in cell wall components; and (ii) by chelate secretion (Meharg, 2002). Tolerance to metal stress relies on plant capacity to detoxify metals having entered cells. The mechanisms for metal tolerance proposed are: (a) metal sequestration by specially produced organic compounds; (b) compartmentalization in certain cell compartments; (c) metal ion efflux; (d) organic ligand exudation. Plant protection against metal toxicity involves, with others, the control of root metal uptake and of long distance metal

transport. Inside cells, proteins such as ferritins, metallothioneins and phytochelatins and related peptides, participate in excess metal storage and detoxification, together with low molecular weight organic molecules, mainly organic acids and amino acids and their derivatives. When these systems are overloaded, oxidative stress defense mechanisms are activated. The naturally tolerant ferns which hyperaccumulate metals form the basis for investigations on the improvement of metal resistance (Briat and Lebrun, 1999). The largest group of metal resistance systems function by energy-dependent efflux of toxic ions (Silver and Phung, 1996).

Metallothioneins are small proteins that sequester excess amounts of certain metal ions. Their synthesis is transcriptionally activated by metal ions. Plant metallothioneins have received little attention until it was reported that plants indeed contain functional metallothionein homologs. Two *Arabidopsis thaliana* cDNAs, named MT1 and MT2, share all the structural characteristics of yeast metallothioneins (Zhou and Goldsbrough, 1994). Since then, three protein bands, corresponding to six MT genes, have been isolated from *Arabidopsis*, and the amino acids sequenced for nine fragments (Rauser, 1999). The term phytochelatin (PC) have been given to a unique family of thiol containing metal-binding polypeptides derived from glutathione (GSH) (Rauser, 1990). Maitani *et al.* (1996) used root cultures of *Rubia tinctorum* and confirmed that arsenic, lead and mercury induced PCs. The analysis of a PC-deficient mutant of *Arabidopsis* showed a detoxifying role for PCs against mercury (Howden and Cobbett, 1992). Exposure to excess of arsenate and arsenite induced the biosynthesis of phytochelatins in vivo and in vitro in ferns.

The rapid induction of the metal-binding PCs has been reported in cell suspension cultures of *Rauvolfia serpentina*, in seedlings of *Arabidopsis*, and in enzyme preparations of *Silene vulgaris*. Gel filtration studies and inhibition studies have demonstrated the complexation and detoxification of arsenic by the induced PCs (Schmöger *et al.*, 2000). Furthermore, activities of PC-deficient mutants of *Arabidopsis* and *Schizosaccharomyces pombe* showed an increased sensitivity towards arsenate (Ha *et al*., 1999). Conversely, the over expression of a plant PC synthase in *S. pombe* resulted in increased resistance to arsenite and arsenate (Vatamaniuk *et al.*, 1999). Mercury-stressed (1–10 mg/l) plant cells showed increased activities of antioxidants like superoxide dismutase and catalase in varying degrees and presented a positive endogenous protection effect. However, the protection effect disappeared at higher levels (50 mg/l).

Ferns exhibit considerable constitutional tolerance to heavy metals and, in some cases, it reaches levels of inducible tolerance (Wierzbicka, 1999). Constitutional tolerance to heavy metals shows that after an initial phase in which lead is toxic to cells, defense processes appear. Lead in the root symplast is detoxified in vacuoles, cell walls and dictyosomal vesicles. Initial cells of the meristem (quiescent centre) which plays a basic role in root regeneration processes are protected against lead penetration. This is in agreement with the absence of any symptoms of lead poisoning in ferns growing in natural conditions, and suggests that there is a defense mechanism specific only to plant cells (Wierzbicka, 1995). The mechanism of tolerance of ferns to heavy metals may involve one or more of the several methods suggested for metal tolerance like binding of metal to cell wall material (Cumming and Taylor, 1990); complex-formation with organic acids and then removal to the vacuole (Godbold *et al.*, 1984); and binding to specific thiol-rich proteins or phytochelatins (Lolkema *et al.*, 1984; Rauser, 1984).

INFLUENCE OF ENVIRONMENTAL FACTORS ON PTERIDO-REMEDIATION

A variety of environmental factors affects or alters the mechanisms of pterido-remediation. Soil type and organic matter content can limit the bioavailability of petroleum contaminants. Water content in soil and wetlands affects plant/microbial growth and the availability of oxygen required for aerobic respiration. Temperature affects the rates at which various processes take place. Nutrient availability can influence the rate and extent of degradation in oil-contaminated soil. Finally, sunlight can transform parent compounds into other compounds, which may have different toxicities

and bioavailability than the original compounds (Frick *et al.,* 1999). Some of the environmental factors are discussed briefly below.

Soil Structure, Texture, and Organic Matter Content

Soil type is defined according to various characteristics including structure, texture, and organic matter content. In terms of the influence of soil structure, Alexander *et al.* (1997) identified that phenanthrene may be trapped within and sorbed to the surfaces of nanopores (Soil pores with diameters < 100 nm) that are inaccessible to organisms (i.e., not bioavailable). Soil texture can also affect pterido-remediation efforts by influencing the bioavailability of the contaminant. For example, clay is capable of binding molecules more readily than silt or sand (Brady and Weil, 1996). As a result, the bioavailability of contaminants may be lower in soils with high clay contents. Soil organic matter binds lipophilic compounds, thereby reducing their bioavailability (Cunningham *et al.,* 1996). A high organic carbon content (>5%) in soil usually leads to strong adsorption and, therefore, low availability, while a moderate organic carbon content (1 to 5%) may lead to limited availability (Otten *et al.,* 1997).

Water and Oxygen Availability

Water and oxygen are important to the general health of plants and microbes (Eweis *et al.,* 1998). Water is not only a major component of living organisms, it also serves as a transport medium to carry nutrients to biota and carry wastes away. If the moisture content of the soil is low, there will be a loss of microbial activity and dehydration of ferns. Too much moisture results in limited gas exchange and the creation of anoxic zones where degradation is dominated by anaerobic microorganisms. Interestingly, oxygen may be provided to the rhizosphere as a plant exudate. The extent of oxygen-transfer from the root depends on the type of plant (Vance 1996).

Temperature

Temperature affects the rates at which the various mechanisms of pterido-remediation take place. In general, the rate of microbial degradation or transformation doubles for every 10 °C increase in temperature (Eweis *et al.,* 1998). In an experiment involving oil bioremediation in salt marsh mesocosms, degradation of applied hydrocarbons averaged 72% during summer compared to 56% during winter, even though the winter exposure was day's longer (Wright *et al.,* 1997). The seasonal difference was thought to be the result of a difference in temperature between the warm summer and cool winter periods.

Nutrients

Adequate soil nutrients are required to support the growth of ferns and their associated microorganisms. This may be especially true during pterido-remediation efforts, when the plant/microbe community is already under stress from the contaminant. Xu and Johnson (1997) have shown that soil contaminants can significantly reduce the availability of plant nutrients in soil. Low nutrient availability results from the fact that petroleum hydrocarbons have high carbon contents, but are poor suppliers of nitrogen and phosphorus. As soil microorganisms degrade the soil organic carbon, they use up or immobilize available nutrients (i.e. nitrogen and phosphorus) creating nutrient deficiencies in contaminated soil. Biederbeck *et al.* (1993) found that, following initial applications of an oily waste sludge to sandy soil, the soil had very low nitrate levels due to immobilization of nitrogen by rapidly growing populations of bacteria as well as suppression of nitrogen-fixing bacteria.

Weathering

Weathering processes include volatilization, evapotranspiration, photomodification, hydrolysis, leaching and biotransformation of the contaminant. These processes selectively reduce the concentration of contaminants, with the more recalcitrant compounds remaining in the soil. The contaminants left behind are typically non-volatile or semi-volatile compounds that preferentially partition to soil organic matter or clay particles, which limits their bioavailability and the degree to which they can be, degraded (Cunningham *et al.,* 1996). Carmichael and Pfaender (1997) noted that contaminant bioavailability was a major factor limiting the degradation of contaminants.

BENEFITS AND LIMITATIONS OF PHYTOREMEDIATION

Direct Benefits of Phytoremediation

Phytoremediation is an in situ, solar driven technique, which limits environmental disturbance and reduces costs (Shimp *et al.*, 1993). Moreover, it is particularly well-suited to the treatment of large areas of surface contamination, when other methods may not be cost effective (Schnoor, 1999). In general, both the public and government regulators look favourably upon phytoremediation because it involves exploiting the natural ability of the environment to restore itself (Cunningham *et al.*, 1996). Indeed, there was a high level of public support for the use of ferns in phytoremediation at a series of public focus group meetings to gauge public perceptions and awareness of environmental applications of biotechnology in Canada (McIntyre and Lewis, 1997). Pterido-remediation also is considered to be more aesthetically pleasing than other remediation techniques (Shimp *et al.*, 1993; Cunningham *et al.*, 1996).

Plant samples can be harvested and used as indicators of the extent of remediation or, conversely, contamination (Shimp *et al.*, 1993). Similarly, a field of plants may serve as a direct, visual bioassay (Cunningham *et al.*, 1996). There is also the potential to grow various fern species together on the same site in an attempt to simultaneously remediate various contaminants, including salts, metals, pesticides, and petroleum hydrocarbons. Plants help contain the region of contamination by removing water from soil, thereby keeping the contaminants from spreading or confining them within or near the root-system (Shimp *et al.*,1993). Finally, phytoremediation may be applied with relative ease using existing agricultural practices at contaminated sites (McIntyre and Lewis, 1997).

Indirect Benefits of Phytoremediation

An indirect benefit of phytoremediation is improvement of soil quality by improving soil structure (aggregates and peds), increasing porosity/aggregation and, therefore, water infiltration, providing nutrients (nitrogen-fixing legumes), accelerating nutrient cycling, and increasing soil organic carbon (Schnoor *et al.*, 1995; Cunningham *et al.*, 1996). The use of plants in a remediation effort stabilizes the soil, thus preventing erosion and direct human exposure (i.e., by preventing the consumption of contaminated soil by children and the inhalation of soil particles carried in the wind) (Schnoor *et al.*, 1995; McIntyre and Lewis, 1997). Likewise, phytoremediation has the potential to help reduce greenhouse gas emissions.

CONCLUSION AND RECOMMENDATION

Conclusively, with all these tolerance mechanisms, a lot of fern species have been found to be very effective in the hyperaccumulation and remediation of heavy metal contaminated sites as they can also be easily propagated with other beneficial roles to the environment. However, more attention should be paid to their use in Nigeria and further study be carried out on their phytovolatilization ability i.e. the movement of a contaminant out of the soil, into, through and out of a plant, and then into the atmosphere instead of bioaccumulation in the plant body. Phytovolatilization is a mechanism to remove contaminants out of plant body by transforming toxic metal to volatile forms that can easily transpire out of the plant body. This method will not only reclaim contaminant soil but also clean up plant body.

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HUMAN GENETICS (HG)

HG01

SICKLE CELL ALLELLIC FREQUENCIES IN THE NORTHERN GUINEA- SAVANNAH OF NIGERIA

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ABSTRACT

A study, aimed at estimating the frequencies of sickle cell trait in 3 populations of Northern Guinea-Savannah Nigeria was conducted. The population studied were ABUTH (Kaduna State), AKTHK (Kano State) and IBBSH (Niger State). 675 homozygote dominants (wild types), 263 heterozygote and 25 homozygote recessives (mutant types) genotypes were recorded in the ABUTH populations. The allelic frequencies in this population were 0.84(84%) wild type and 0.16 (about 16%) mutant. However in AKTHK population, the genotypes recorded were 837 homozygote dominant, 341 heterozygote and 31 homozygote recessives. The estimated allelic frequencies in these populations were 0.83(83%) wild types and 0.17(about 17%) were mutants. While in the IBBSH population the genotypes recorded were 350 homozygote dominant, 247 heterozygote and 23 homozygote recessive. Allelic frequencies estimated in this populations were 0.76(76%) wild types and 0.24 (24%) mutant. To investigate whether the three populations conformed to Hardy-Weinberg principle, the observed genotypes in the three populations were compared with expected genotypes under Hardy-Weinberg principle. The calculated chi square values for the deviations between the population and the idealised Hardy-Weinberg population at $\chi^2_{0.05}$ level of significance was not significant, (0.01) for ABUTH, (0.302) for AKTHK and for IBBSH 0.005 suggesting that none of the Hardy-Weinberg assumptions (random mating, migration, mutation and selection) were violated in the populations.

Keywords: Alleles, Sickle Cell, Genotype, ABUTH, AKTHK, IBBSH

INTRODUCTION

Sickle cell is a hereditary blood anomaly, depicted by erythrocytes that have rigid sickle shape. Sickling decreases the cell flexibility and result in various serious complications. Under low oxygen tension, the sickle cell haemoglobin polymerised (Betty Pace, 2007). The deoxy form of the haemoglobin exposes a hydrophobic patch on the protein, which associates with the hydrophobic residue of valine at position six of the beta chain, causing haemoglobin S molecule to aggregate and polymerised. This polymerization , in the homozygote recessive individual distort the shape of red blood cell from smooth and doughnut-like in normal individuals (homozygous dominant) , producing blood cells that are sickle shaped, ragged and full of spikes, making it fragile and susceptible to breaking within capillaries (Mary Louise, 2005). Heterozygote individuals, show symptoms only

under low oxygen tension. The trait is as a result of autosomal recessive inheritance resulting from point mutation at position number six in the haemoglobin protein chain (146 amino acid long), where valine, the mutant replaces glutamic acid , the wild type (Freeman and Herron, 2007). Individuals heterozygotes for the trait have both normal and abnormal haemoglobin, a condition known as co-dominance. The first description of the haemoglobinopathy now known as sickle cell was reported by Herrick in 1910, when he reported his observation of sickle-shaped erythrocytes in the peripheral blood of a severely anaemic patient (Taiwo *et al., 2011*). Sickle cell disease occurs more commonly among people who live in tropical and sub-Saharan regions as well as those whose ancestors originated from these regions, where malaria is common(Austin, *et al.*, 2007). According to secretariat report (WHO, 2006) 200,000 infants are born with sickle cell disorder in Africa each year. The prevalence of the trait (healthy carriers or heterozygous) ranges between 10% and 40% across equatorial Africa.

Due to the morbidity and mortality that always ensue, as a result of sickling, it has become an area of challenge to the health industries. Despite all these, there are no comprehensive literatures regarding the distribution of the trait in the areas of the study. The interaction between the alleles at the population level has not been elucidated. Such an undertaking would sound novel in an area that hitherto remain untouched as far as population studies are concern.

The objectives of the present studies are to measure the diversity of sickle cell alleles in the Northern Guinea-Savannah of this country, as well as to confirm if the population conformed with Hardy-Weinberg principles.

MATERIALS AND METHODS

This study was conducted in three states within the Northern Guinea- Savannah (Kaduna, Kano and Niger). The subjects that participated in these study comprises 965 individuals from Ahmadu Bello University Teaching Hospital Zaria (ABUTH), 1229 from Aminu Kano Teaching Hospital Kano (AKTHK) and 620 from Ibrahim Badamasi Babangida Specialist Hospital Minna (IBBSH). The data were of two types. Already genotyped record was obtained from the haematological units of the various hospitals, the second data originated from information acquired in questionnaire completed by voluntary participants. All the aforementioned hospitals are the largest and most densely populated in terms of patients within the states that form the study areas. In the haematological laboratories of the various hospitals where the data were collected, the genotyping was done as follows;

A 2.5ml, blood sample was collected from antecubital vain of each subject that participated in the study and stored in Ethylinediaminetetraacetic acid (EDTA) coated bottles prior to electrophoresis. Blood sample was then haemolysed using saline solution. Little quantity of haemolysed blood from each individual was placed on cellulose acetate membrane and then introduced into electrophoretic container, containing Tris-EDTA borate buffer, P^H 8.9. The electrophoresis was run for 20 min. at a voltage of 160v. The resulting genotypes were compared with standard ladder for their identification. In each of the three populations studied, genotypes were grouped into three columns; homozygote dominant (AA), heterozygote (AS), and homozygote recessive (SS).

The allelic frequencies were calculated by multiplying the number of individuals tested in each population by two, to get the total number of alleles (remember that allelic frequency is twice the number of genotype).The total number of alleles were then used to divide the number of copies of the sickle cell alleles (one from the heterozygote plus two from the homozygote) as shown below.
AA=2 alleles
AS=1 allele

SS=2alleles

The genotypic frequencies (observed genotypic frequencies) are simply the number of individuals tested that fall under each genotypic group divided by the total number of individuals in the population;
AA/n, AS/n, SS/n

The expected genotypic frequencies under Hardy-Weinberg principle, given the allele frequencies were estimated as follows; according to the Hardy-Weinberg equilibrium principle, if the frequencies of two alleles are p and q, then the frequencies of genotypes would be : $p^2 + 2pq + q^2$, represented as;

(AA)	(AS)	(SS)
P^2	2pq	q^2

The expected number of individual genotypes in each population under Hardy- Weinberg equilibrium is simply the expected frequency of each genotype, multiply by the number of individuals in the population.

$n(p^2)$	n(2pq)	$n(q^2)$

The number of individuals observed (the number of genotypes in each population) were then compared with the number of individuals expected to confirm if the population conformed to the assumption of Hardy-Weinberg principle. The presence of discrepancy between the expected and the observed number of individuals entails that the population is not in conformity with the principle; one or some of the conditions in the principle are violated. A chi square test (Pearson, 1914) was then used to test the significant level of the difference.

$$\chi^2 = \sum \frac{(observed - expected)^2}{expected}$$

RESULTS AND DISCUSSION

Table1 provides information on allelic and genotypic frequencies of sickle cell traits in the tested populations. The allelic frequencies for sickle cell in the studied populations were less than 20% for ABUTH and AKTHK, while for IBBSH it was 24%. The homozygote frequencies for sickle cell in the studied populations were low with SS ranging from 0.03 (ABUTH) to 0.04 (AKTHK and IBBSH). The heterozygote condition was intermediate with AS ranging from 0.27 (ABUTH and AKTHK) to 0.04 (IBBSH). Overall, in the northern guinea-savannah zone of Nigeria the allelic frequency of sickle cell was 0.19, while the normal allele was 0.81. The genotypic frequencies in the zone were 0.65(AA), 0.31 (AS) and 0.04 (SS).

Table 1. Allelic and Genotypic Frequencies of Sickle Cell Trait In The Tested Populations.

POPULATION	NO. Tested	Genotypic Frequencies			Allelic Frequencies	
		AA	AS	SS	A	S
ABUTH	963	0.70	0.27	0.03	0.84	0.16
AKTHK	1209	0.69	0.27	0.04	0.83	0.17
IBBSH	620	0.56	0.40	0.04	0.76	0.24

Table 2 depicts the variations between the observed and expected genotypes in the studied populations. There was no significant (P> 0.05) difference in the observed and expected genotypic distributions in the 3 studied populations in the northern guinea-savannah zone of Nigeria.

Table2: Variation Between Observed and Expected Number of Individuals Across Genotypic Groups In The Three Populations.

POPULATION		GENOTYPES				
		AA	AS	SS	χ^2 values	LOS
ABUTH	observed	675	263	25		
	expected	675.4	262.1	25.42	0.01	ns
AKTHK	observed	837	341	31		
	expected	839.5	335.7	33.5	0.302	ns
IBBSH	observed	350	247	23		
	expected	349.9	246.8	22.9	0.005	ns

Both the estimated genotypic and allelic frequencies in this study are in conformity with an estimate made earlier by World Health Organisation (WHO, 2006) for the sub-region. It is also within the range estimated by Taiwo *et al.* (2011), for the Yoruba community in Lagos.
The low frequency of sickle trait in the population does not come as a surprise, studies on autosomal recessive alleles example cystic fibrosis (Lyczak *et al.*, 2003) , spinal muscular atrophy (Wirth *et al*., 1997), Gaucher disease (Beutler, 1993) had revealed low frequencies in such alleles. Most recessive mutant alleles are deleterious and therefore natural selection acts to eliminate such mutants from the population. The effect of migration in changing allelic or genotypic frequencies in these populations is negligible when one compares the rate of gene flow and the sizes of the populations. Mutation is inconsequential in changing allelic frequencies in the populations due to their vastness, and the time it takes for a mutant allele to be fixed by genetic drift. Selection (an important force in changing allelic frequency) has limitation here in eliminating the mutant allele completely from the populations, as the recessive mutant allele confer some degree of fitness, when it is in the heterozygote form. The heterozygote is selected for, because of the resistance it bestows against malarial infection.

The deviation of the observed number of individuals from the expected in the three populations is not significant at $\chi^2_{0.05}$ level. This is suggesting that none of the assumptions of Hardy-Weinberg principle is violated in the three populations. This finding supports the fact that marriages among the population is panmictic (non assortative). The vastness of the area covered by this study (Northern Guinea-Savannah) and the heterogeneity of the population made it outstanding among similar studies done previously (Taiwo *et al.*, 2011) only for the Yoruba community in Lagos and (Bakare *et al.*, 2006) conducted in Ogbomosho only.

CONCLUSION

This work provides an opportunity for population genetic studies. The frequencies of alleles and genotypes estimated may be valuable information to the health sector, for the purpose of budget forecasting and planning, when the need to control the trait in these areas arises.

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VARIETAL RESPONSE OF POTATO *(SOLANUM TUBEROSUM L.)* TO IRRIGATION REGIMES IN JOS PLATEAU, NIGERIA.

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ABSTRACT

A field experiment was carried out in Kuru ($09^0$44N, $08^0$47E) and 1239 meters above mean sea level in Jos, Plateau State of Nigeria during the dry season of 2012 /2013. The treatment consisted of four irrigation regimes (once in fourteen days, once in ten days, once in seven days and once in three days) and six potato varieties (Diamant, RC 7716-2, BR63-18, Nicola, Agria and Bertita) laid out in a split-plot design with three replications. The study aimed to assess the varietal responses of the different potato varieties to the variable irrigation regimes so as to get recommendations for low water input for dry season potato production on the Jos Plateau. The varieties exhibited highly significant variability ($P<0.01$) for most traits assessed. Significant differences ($P<0.05$) were recorded in plant emergence, plant height, plant vigour, Stem girth, number of stems, number of tubers, average tuber weight and tuber yield. The irrigation regimes affected the varieties significantly ($P<0.05$) with plants that were irrigated once in three days producing the highest yields in all varieties. The plants that were irrigated least produced the lowest yields. Agria and Diamant performed better on receiving the least irrigation regimes compared to others. The interaction between varieties and irrigation regimes were significant ($P<0.05$) for most traits assessed. Days to

maturity, number of tuber and average tuber weight had a positive significance ($P<0.05$) correlation with tuber yield per plant. The inter-relationship between growth and yield components in this study suggested that adequate shoot development (number of stem, plant height, number of leaves), number of tubers/plant, average tuber weight/plant are the yield indicators for potato varieties which suggest that both attributes are important criteria for selection for improved yield and drought tolerance of potato.Diamant and Nicola Produced the highest tuber yield while irrigation regimes once in three days produced the highest yield. The suggestions of these outcomes are further discussed in line with the water use requirements for this crop on the Plateau.

INTRODUCTION

Yield response to irrigation of different crops is of major importance in production planning where water resources are limited. The cultivated potato *(Solanum tuberosun L.)* varieties grown outside its South American centre of origin evolved from only a few Andean potato genotypes (Hawkes, 1978, Birhman and Kang, 1993). Potato rate fourth among the world's various agriculture production volume after wheat, rice and corn (Faberio, *et al.,* 2001). It is a temperate crop that grows and yields well in cool and humid climates. Production of potato takes a very important place in world agriculture, with a production potential of about 327 million tons harvested and 18.6 million hectares planted area (FAO, 2004).

Studies have shown that water is the most important limiting factor for potato production and it is possible to increase production levels by well-scheduled irrigation program throughout the growing season (Boujelben*et al.,* 2000; Deblonde and Ledent, 2001; Faberio*et al.,* 2001; Chowdhung*et al.,* 2001; Panigrahi*et al.,* 2001; Ferreira and Carr, 2002, Kashyap and Panda, 2003; Shocks *et al*., Yuan *et al.,* 2003 Onder*et al.,* 2005). Because average rainfall and water resources are limited, research on the relationship among yield, irrigation regimes and potato varieties is of great importance for the selection of high yielding varieties that can tolerate water stress. This study aims to determine the effect of different irrigations regimes on the growth and tuber yield of six potato cultivars, study the inter- relationship between tuber yield and other yield related components and to suggest varieties that show superiority in tuber yield and other agronomic attributes under different irrigations regimes and could be utilized in a drought improvement programme.

MATERIALS AND METHODS

Six potato varieties were evaluated under four different irrigation regimes in the research substation of the National Root Crops Research Institute in Kuru (Lat. 09^{o} 44N, Long. 08^{o}47E and 1239 masl) on the Jos Plateau State of Nigeria between November 2012 to February 2013. The experiment was laid out in a split plot design using three treatments. Gross plot size was 27m x 20m while the net plot size was $6m^2$. Seed tubers were planted one per stand at a population density of 33,333 plants per hectare. Galex® was applied as a pre-emergence herbicide at the rate of 5 liters product per hectare to control weeds. Further weeding was done manually at six weeks after planting (WAP). Fertilizer was applied at the rate of 100kg Nitrogen, 100kg Phosphorus as P_2O_5 and 40kg potassium as K_2O at 3 WAP. Data was collected on the following plant attributes at different periods of development of the crop ranging from 2 weeks after planting (2 WAP) to 12 WAP:Plant emergence, Plant height (cm), Number of leaves per plant, plant vigour, number of stems per plant, stem girth (cm), number of days to maturity, dry matter content (%), number of tubers per plant (kg), average tuber weight (kg) and tuber yield per plant (kg). The data obtained were subjected to analysis of variance (ANOVA) using SPSS computer software at $P<0.05$ and means compared with Duncan's new multiple range test (DNMRT). Pearson's correlation analysis was also used to compare the inter- relationships of yield with some growth related traits.

RESULTS

Plant emergence varied significantly between potato varieties ($P<0.01$, Table 1). The variation ranged from 10 stands per plot in Agria, 13 stands per plot in RC 7716-2, 14 stands per plot in Diamant, 15 stands per plot in Bertita, 16 stands per plot in BR68-18 and 17 stands per plot in Nicola

(Table 1). There were also significant differences (P<0.05). In the irrigation regimes means. Plants that were irrigated once in 3 days produced significantly higher number of plant that emerged. Irrigation regimes once in 14 days produced the least number of plant emergence. The irrigation regimes once in 7 days and 10 days produced plant emergence that were not significantly different.
The interaction between irrigation regimes and varieties were not significant while the coefficient of variation was 23%.

Variability in the height of the varieties was significant (P<0.05, Table. 1). In all the growth stages Diamant had the tallest plants, while Bertita produced the shortest plant. Irrigation regimes were also significant (P<0.05). The interactions between varieties and irrigation regimes were not significant. The coefficient of variation (%) was 49.96.

Table 1 shows the effect of variety and irrigation regimes on number of leaves per plant. The means number of leaves ranged from 661 in Nicola and 512 in Agria. The differences in this attribute between the varieties were significant (P<0.05). There was also a significant difference (P<0.05) in the treatments. Plants irrigated once in 3 days produced the highest number of leaves per plant (669) while irrigation regimes once in 14 days produced the least number of leaves (460).
The interaction between varieties and irrigation regimes were not significant while the coefficient of variation was 80.21%.

The means plant vigour is shown in Table 1. It ranged from 5.78 in Diamant to 2.89 in Agria. The difference in this attribute between the varieties was highly significant (P<0.01). The means irrigation regimes was also significant (P<0.05, Table 1). Irrigation once in 3 days produced the most vigorous plant while irrigation regimes once in 14 days produced the least vigorous plants.
The interaction between irrigation regimes and varieties were also significant while the coefficient of variation was 41.13%.

The mean number of stem per plant varied significant (P<0.05, Table 1) between the potato varieties. Bertita produced the highest number of stem (3). This however did not differ significantly from the stem number of 2 others varieties. RC7716-2, Diamant and Agria Produced the least number of stem (2). The mean irrigation regimes also varied significantly (P<0.05, Table 1).
The interaction between varieties and irrigation regimes were also significant and the coefficient of variation was 46.62%.

Variation between the varieties in the stem girth was significant (P<0.05, table 2). Stem girth was highest in Diamant (4.75) while the least was BR68-18 (2.93) RC7716-2, BR68-18, Nicola and Bertita produced stem girth that were not significantly different. The interaction between the varieties and irrigation regimes were significant while the coefficient of variation was 29.36%.

The mean number of days from planting to maturity varied significantly amongst potato varieties (P<0.01) ranging from 70 days in Bertita to 93 days in Diamant (Table 2). There was also a highly significant difference (P<0.01) in the irrigation regimes means. The interaction was also significant between the potato varieties and the irrigation regimes. The coefficient of variation was 11.49%.

Table 2 shows the mean dry matter content for the potato varieties. There were no significant differences in the dry matter content in regard to the varietal means. The irrigation regime was not also significant. However, the interaction between the varieties and irrigation regimes were significant while the coefficient of variation was 12.77% (Table. 2).

There was a highly significant variability in the number of tubers produced by the varieties (P<0.01). Nicola Produced highest tubers followed by Bertita (4). Diamant produced the least tubers but did

not differ in this regard from 2 other varieties. The mean irrigation regimes also differ significantly with irrigation regime once in 3 days producing the highest tubers while once in 10 days produced the least (Table 2). Interaction between variety and irrigation regimes was significant while the coefficient of variation was 60.28%

The mean average tuber weight was not significantly different in terms of the varieties and also the irrigation regimes. However, the interaction between variety and irrigation regime was significant and the coefficient of variation was 65.52% (Table 2).

There was a significant variation between the varieties in their tuber yield ($P<0.05$). Diamant had the highest tuber yield while RC7716-2 gave the lowest yield. Nicola and Bertita gave yields that were not significantly different from each other. There was also a significantly different ($P<0.05$) in terms of the irrigation regimes with irrigation regimes once in 3days producing the highest yields.
The interaction between varieties and irrigation regimes were significant while the coefficient of variation was 47.87% (Table 2).

Table 3 shows the simple coefficient of correlation matrix between the traits studied. Tuber yield correlated positively and significantly ($P<0.05$) with dry matter content. Tuber yield also correlated positively and highly significantly ($P<0.01$) with average tuber weight ($r=0.437$), number of tubers/plant ($r=0.843$), days to maturity ($r=0.341$), number of leaves/plant (0.391), stem girth ($r=0.191$) and plant height ($r=0.421$). Plant emergence had a negative correlation with dry matter content. Plant height had a positive and significant correlation with most traits assessed except average tuber weight ($r= -0.061$) and dry matter content ($r= -0.176$) that were negatively correlated. The attribute also showed significant association with one another. Stem girth had a highly significant correlation with number of leaves ($r=1.00$), number of stems ($r=1.00$) Plant vigour ($r=1.00$) while days to maturity had a significant but negative correlation ($r= -0.102$). Number of tubers had a positive and significant correlation with average tuber weight ($r=0.239$).

Table 1 Effect of Varieties and Irrigation Regimes on Some Growth Parameters of Potato.

Treatments	Plant emergence	Plant heights (cm)	Number of leaves	Plant vigour	No. of stem per plant
Irrigation regimes(I)					
Once in three days	15.89a	53.11a	440. 88a	4.79a	2.54a
Once in seven days	14. 83ab	49.28ab	424.40a	3. 81b	2.1ab
Once in ten days	14.28ab	44.61b	403.67ab	4.00b	2.65a
Once in fourteen days	13.28b	47.37a	316.97b	3.74b	1. 83c
Significance	*	*	*	*	*
SE ±	0.55	5.70	74.94	0.28	0.20
Varieties (V)					
Diamant	14. 83bc	52.51a	369.17a	5.78a	1.97b
RC7716-2	13.08c	48.21a	392.42a	3.61c	1.75b
BR68-18	16.00ab	48.34a	397.27a	4.28b	2.64a
Nicola	17. 08a	52.43a	448.12a	4.72b	2.64a
Agria	10.08ab	44. 88a	341.22a	2. 89d	1.97b
Bertita	15.58b	37.70b	430.68a	3.22cd	2. 81a
Significance	**	*	*	**	*
S.E ±	0.67	6.98	91.79	0.35	0.25
Interaction					
I×V l	Ns	Ns	Ns	**	*
Coefficient of variation (CV)%	23.00	49.96	80.21	41.13	46.62

Means followed by the same letter(s) within the same column and treatment are not significantly different at 5% level of probability.
*=significant at 0.05 level of probability
**= significant at 0.01 level of probability.
NS= not significant
SE= standard Error
C.V= Coefficient of variation (%)

Table 2 Effect of varieties and Irrigation Regimes on Some Potato Attributes

Treatment	Stem girth (cm)	Days to Maturity	Number of tubers/plant	Average Tuber weight(kg)	Tuber yield/plant(kg)	Dry Matter content (%)
Irrigation (I)						
Once in three days	3.59a	91.72a	4.22a	0.23a	0.39a	21.94a
Once in seven days	3.63a	83. 89b	3.12ab	0.11a	0.23b	22.30a
Once in ten days	3.34a	80.61c	2.74b	0.15a	0.27b	22.00a
Once in fourteen days	3.35a	75.50d	3.32ab	0.12a	0.25b	21.78a
Significance	Ns	**	*	Ns	*	Ns
SE ±	0.20	0.36	0.39	0.06	0.03	0.66
Varieties (V)						
Diamant	4.75a	92.92a	1. 87d	0.28a	0. 83a	22.39a
RC7716-2	3.19c	83.03d	2.74d	0.27a	0.26d	20.59a
BR68-18	2.93c	80.67d	3.73bc	0.10a	0.69ab	22.11a
Nicola	2.94c	83.33c	5.28a	0.09a	0.28d	22.36a
Agria	3.96b	89.00b	2.13d	0.13a	0.56c	22.70a
Bertita	3.93c	70.83e	4.35ab	o.10a	0.29d	22.70a
Significance	*	**	**	Ns	*	Ns
S.E ±	0.17	0.44	0.48	0.07	0.04	0. 81
Interaction						
I×V	*	**	*	*	**	*
C.V (%)	29.36	11.49	60.28	65.51	47. 87	12.77

Means followed by the same letter(s) within the same column and treatment are not significantly different at 5% level of probability.
*=significant at 0.05 level of probability
**= significant at 0.01 level of probability.
NS= not significant
SE= standard Error
C.V= Coefficient of variation (%)

Table 3: Matrix for correlation coefficient of some growth and yield parameters of potato in Jos, Plateau State, Nigeria.

Traits	Plant height	Stem girth/pt	Number of leaves/pt.	Plant vigour	Number of stem/pt	Days to Maturity	Number of tubers/pt	Average tuber
Plant Emergence	**	**	**	**	**	-0.17	**	.
	.331	0.942	.942	.942	.942		.261	
Plant Height		*	*	*	*	*		
		.297	.297	.297	.297	.280	.104	-.
Stem Girth/pt.			**	**	**	**	*	
			1.000	1.000	1.000	-.102	.261	.
Number of leaves/pt				**	**		*	
				l.0S00	1.000	-.102	.261	.
Plant Vigour					**		*	
					1.000	-.102	.261	.
Number of Stems/pt							*	
						-.102	.261	.
Days of Maturity								
							-.155	.
Number of Tubers/Pt								
								.
Average tuber weight								
Tuber yield/pt								

* = Significant at 0.05 level of probability
** = Significant at 0.01 level of probability

DISCUSSION

The Varieties exhibited significant variability ($P<0.05$) for most traits assessed. Variation amongst potato genotypes for different attributes has been reported by various others (Birhman and Kang, 1993; Jefferies, *et al.*,1993; Paterson *et al.*, 1996; and Shock, *et al.*, 1998). Highly significant variability in plant attributes within a population suggests the existence of sufficient variability upon which selection for improvement in these characters can be based.

Nicola and Diamant were observed to have recorded the highest number of plant emergence, tallest plants and most vigorous plants. These growth parameters showed significant ($P<0.05$) difference in their means. This could be attributed to the environmental influences.
Analysis of the association between days to maturity, number of tubers per plant and average tuber weight with tuber yield in this study revealed a significant positive correlation. Amadi (2005) showed Via a path analysis that the functional relationship between number of stem/plant and yield is mainly indirect since it operated largely through the number of tuber/plant hence the positive correlation between the number of stem/plant and number of tubers/plant (Table 3).
Correlation between tuber yield, number of tubers/plant and average tuber weight/plant were positive and significant ($P<0.05$). potato tuber yield is a function of the number of tuber and average tuber weight Birhman and Kang, 1993; Amadi*et al.*, (2005). Amadi *et al.*, (2005) reported that compared with other attributes, tuber number and average weight were by far the most important determinants of tuber yield as shown by their relatively high correlation

In this study, result revealed a significant ($P<0.05$) effects of irrigation regimes on most of the growth and tuber yield parameters assessed. The irrigation regimes once in 3 days recorded the highest means in all the traits assessed except; stem number per plant and days to maturity. This could be attributed to the fact that water stress increases early maturity of crops. The differences observed in the performance of the potato varieties with respect to the different irrigation regimes were in agreement with the findings of (Shock, *et al.*, 1994; Shae *et al.*, 1999) who reported that the capacity of water utilization varied with plant varieties.
The Yield parameters were observed to be highly significant in terms of the irrigation regimes with plants that were water once in three days producing the most yields followed by once in seven days, once in ten days and once in fourteen days producing the least yield. This showed that the assimilation from the leave and nutrients in the soil were better utilized in the presence of much moisture, thus increasing the sinking ability. Clarke, *et al.*, (1992) and Hall, *et al.*, (1997) reported that relative yield performance of genotypes in moisture stressed and non-stressed environment could be the starting point in identifying traits related to drought tolerance and selection of desired genotypes. Comparison of the performance of the genotypes in well – watered and moisture stressed conditions showed that some varieties performed well in both environment. Diamant and Agria, performed better compared to others under irrigation regime once in fourteen days. However Nicola required much water for optimal tuber yield. Yield both increased with increases in irrigation regimes in all the varieties. Low yield recorded in irrigation regime once in fourteen days suggest that potato needs relatively much moisture for optimal yield as reported by Eldredge, *et al.*, (1992).
Highly significant interactions were observed between variety and irrigation regimes for plant height, days to maturity, stem girth, plant vigour, number of stems per plant, number of tuber per plant, average tuber weight and tuber yield. Other authors have found strong potato-genotypes x water stress interaction (Jeffreries and Mackerron, 1993b). Interactions between Diamant, Nicola

and irrigation regimes once in three days produced the highest yield. The interaction between varieties and irrigation regimes shows that yield responded linearly to applied water. In arid regions studies has shown that potato yield responded linearly to water supply (Hane and Pumphrey , 1984; Martin, *et al.,* (1992).

The insignificant interaction of variety and irrigation regime on plant emergence could be attributed the fact that the initial moisture in the soil was better utilized by the plants.
The observed highly significant ($P<0.01$) correlation between tuber yield and three attributes namely; days to maturity ($r=0.341$), number of tuber ($r=0.843$) and average tuber weight ($r=0.437$) is similar to the result obtained by Lopez, *et al*., (1987). This result showed that any positive increases in such traits with suffice the boost in tuber yield as reported by Galarreta, *et al*., (2005).

CONCLUSION

Significant variability was observed for most attributes of the varieties evaluated suggesting the existence of satisfactory variability upon which selection for improvement in these attributes can be based. The irrigation regimes also differ significant with the potato varieties. Plant emergence, number of stem per plant, average tuber weight, number of tubers and tubers yield were mostly attributed to environmental influence while plant vigour and other traits were mostly genotypic. The inter-relationship between growth and yield components suggested that adequate shoot development (number of stem, plant height and number of leaves), number of tuber/plant and average tuber weight per plant) were the yield indicators. All the varieties studied required relative irrigation regimes once in three days for optimal yield. Maximum yields from potato production on the Jos Plateau during the dry season therefore require relative irrigation regimes of once in three days.

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PGB02

EVALUATION OF CYTOGENOTOXIC AND ANTIMUTAGENIC POTENCY OF WATER EXTRACT OF *CENTELLA ASIATICA* LINN. USING THE *ALLIUM CEPA* ASSAY

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ABSTRACT

In this study, the toxicological safety and therapeutic assessments of water extract of *Centella asiatica* Linn. were carried out in the *Allium cepa* (onion) cells for the evaluation of mutagenic and antimutagenic activities, respectively. The mitotic index (MI) at 6.25% concentration of the extract alone decreased significantly from 3.13 to 2.05 after 24 and 48 hours, respectively, however, it was significantly increased by 60% and 400% at 12.5% and 50.0%, respectively. There was total arrest of cell division at 100% after 24 and 48 hours. The percentage chromosomal aberrations (CA) induced by the water extract alone decreased significantly throughout the tested concentrations except at 50.0%. The mutagenic activity of cyclophosphamide was significantly suppressed above 50% at the tested concentrations except 100% where there was no dividing cell. These results suggest the application of antimutagenic potency of water extract of *C. asiatica* in anticancer chemotherapeutics.

INTRODUCTION

Herbs are usually consumed by humans because of their nutritive and medicinal values which are functions of phytochemicals in them. Recent scientific reports have shown that some plant extracts contained toxic phytochemicals which can interract with biomolecules in the cells to cause mutagenic, cytotoxic and genotoxic effects in *in vitro* and *in vivo* assays (Schimmers, 1994; Akinboro and Bakare 2007 ; Akinboro *et al*., 2012). *Centella asiatica* is an important medicinal herb recognized for its various healing activities such as the treatment of leprosy, ulcer, asthma, eczemza, anxiety and elephantiasis (Siddique *et al*., 2008; Seema and Meena, 2012), because it contained various biochemical compounds such as alkaloids, flavonoids, glycosides, triterpenoids and Saponins (Babu *et al*., 1995; Siddiques *et al*., 2007; Siddique *et al*., 2009; Seema and Meena *et al*., 2012). So far, the available results of scientific experiments on

the genotoxic and antigenotoxic evaluations of the extract of *C. asiatica* were carried out using *in vitro* assays, suggesting the validation of the reported results in *in vivo* experiments which better mimic the normal human system. Thus far, the present study aimed at evaluating water extract of *C. assiatica* for mutagenic and antimutagenic effects on cell division and chromosomes using the *in vivo Allium cepa* assay.

MATERIALS AND METHOD

Centella asiatica plant was identified and given voucher specimen number 11268 at the herbarium unit of the School of Biological Sciences, USM, Penang, Malaysia. Leaves were dried at the room temperature and ground using an electric blender. The powdered plant material (50 g) was added with 1000 ml distilled water and placed in a water bath at 40 $^{\circ}$C for 10 h. The aqueous extract was seived with a filter paper and kept at 4 °C for cytological studies. The stock aqueous extract of *C. asiatica* at 100% was diluted to 6.25% , 12.5 % , 25 % and 50 % for the mutagenic evaluation after 24 and 48 hrs (Akinboro *et al*., 2011a & b).

The antimutagenic test was similar to the mutagenic evaluation except that 0.1 % cyclophosphamide (CP) was added to the water extract. Distilled water and cyclophophamide served as the negative and postive controls, respectively. Root tips were processed for the slide preparation and scoring as previously described (Akinboro *et al*., 2011a & b; Akinboro *et al*., 2012). Mitotic index (MI), CA percentage and reduction percentage of CP-induced CA were calculated as follows:

$$MI = \quad \times 100$$

Where A = Number of dividing cells, B = Total number of counted cells.

$$CA = \quad \times 100$$

Where A = Number of aberrant cells , B = Total number of counted cells.

$$\text{Reduction of CP-induced CA (\%)} =$$

Where A = Proportion of CA in the MI induced by the positive control (CP) , B = Proportion of CA in the MI induced by the mixture of CP and aqueous extract of *C. asiatica*, C = Proportion of CA in the MI induced by the negative control (distilled water).

Data were analyzed for the level of significance set at $P \leq 0.05$ using Duncan's multiple range comparison in One-way ANOVA using SPSS version 18.0.

RESULTS

The effects of water extract of C*entella asiatica* on cell division in the root tips of the exposed onions for 24 and 48 hrs are shown in Figure 1. There was a significant reduction ($p \leq 0.05$) in the mitotic index (MI) at the tested concentrations when compared to the negative control. After 48 hrs., the water extract at 12.5 % produced highest MI of 3.69%, where as, there was a complete arrest (0%) of cell division at 100% concentration. The MI values at 6.25% and 25% concentrations after 24 hrs. were 3.13%, 2.52%, respectively which were more than those obtained after 48 hrs. However, 1.62% MI obtained at 50.0% concentration after 48 hours was

lower than 0.35% MI recorded after 24 hrs. The positive control produced 2.30% and 1.93% MI values after 24 and 48 hrs., respectively.

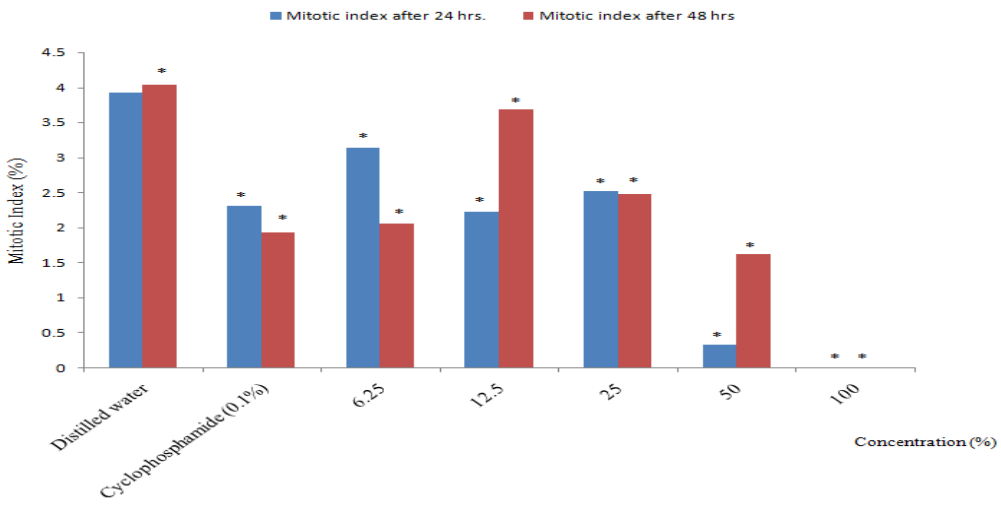

Figure 1. Mitotic indices induced by water extract of *Centella asiatica* in *Allium cepa* cells after 24 and 48 hours of planting. Asterisked MI values are significantly different from the negative control (24 hrs. planting time) at $p \leq 0.05$.

The water extract of *Centella asiatica* induced different types of chromosomal aberrations (CA) such as disturbed spindles, laggard chromosome, anaphase bridge, sticky bridge polyploid and fragmentations as presented in Figure 2. Highest CA percentage was 1.40% induced by 0.1% cylophosphamide after 48 hrs. No CA was observed at 100% concentration. After 24 and 48 hrs. of planting at 50.0% concentration, and after 48 hrs. of planting at 6.25% and 25.0% concentrations, there was induction of significantly lower percentages of CA compared to the negative control. However, the percentage CA at 12.5% concentration was not sigficantly different from the negative control ($p \geq 0.05$).

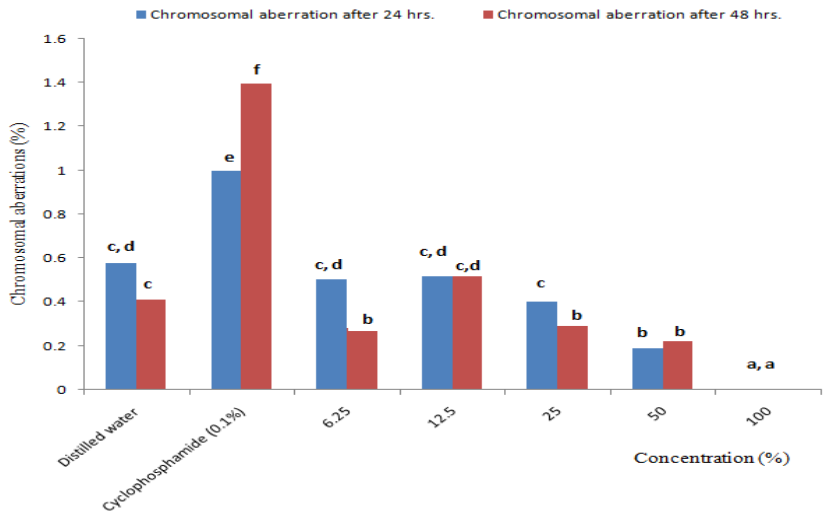

Figure 2: Chromosomal aberrations induced by water extract of *Centella asiatica* in *Allium cepa* after 24 and 48 hours of planting. CA percentages with different alphabelt are significantly different at $p \leq 0.05$.

Table 1 has the reduction percentage of CP-induced chromosomal aberrations (CA). The highest reduction percentage of 92.86% was recorded at 6.25% concentration, while the least percentage reduction of CA was 53.57% recorded at 50.0% concentration. The percentage reduction of CA at 100.0% could not be calculated because there was no dividing cells at this concentration. The manner of reduction of CP-induced CA by the water extract of *C. asiatica* was inversely proportional to the concentrations except at 25.0% concetration which caused 89.29% reduction.

Table 1: Antimutagenic activity of water extract of *Centella asiatica* against CP-induced chromosomal aberrations in *A. cepa* cells.

Concentration (%)	Mitotic index (%)	% Chromosomal aberrations	CA/ MI	% reduction of CP-induced CA
Distilled water	3.93	0.58	0.15	-
Cyclophosphamide	2.31	1.00	0.43	-
6.25 + CP	3.13	0.52	0.17	92.86
12.5 + CP	2.22	0.52	0.23	71.43
25.0 + CP	2.52	0.46	0.18	89.29
50.0 + CP	0.33	0.19	0.58	53.57
100.0 + CP	0.0	0.0	0.0	TA

TA: Total arrest of cell division; CA: Chromosomal aberration; MI: Mitotic index; CP: Cyclophosphamide.

DISCUSSION

The water extract of *C. asiatica* at the tested concentrations signficantly reduced the number of dividing cells in the root tips of *A. cepa* compared to the MI values of distilled water group after 24 and 48 hrs of the treatment. This effect was mitostatic in *A. cepa* cells, and its total arrest of

cell division at 100% could mean cytotoxic through the induction of cell death. The results of similar investigation (Seema and Meena, 2012) using the cultured human peripheral blood lymphocytes *in vitro* assay was in contrary to our results of this *in vivo Allium cepa* assay. This disperity could be due to the series of metabolic enzymatic reactions on the aqueous extract of *C. asiatica* to produce cytotoxic metabolites that were capable of causing non continous interferrence with the progression of cell cycle in the root tip of *A. cepa*. However, this inconsistent increase and decrease in the MI values after 24 and 48 hrs of root growth at the tested concentrations except at 100% was an indication of mitostatic effect, possibly to be observed with the non continuous use of aqueous extract of *C. asiatica* as a food or medicinal herb.

Aside the evaluation of the aqueous extract on the cell division in *A. cepa* cells, induction of chromosomal aberrations was also used in this study to determine its mutagenic effect. The frequency of aberrant cells observed in non-concentration dependent manner, and which were not significantly different from the negative control except at 50% suggests lack of mutagenic activities in the *in vivo A. cepa* assay. This was in accordance with the previous results of *in vitro* genotoxic investigations of the extract of *C. asiatica* on; cultured human lymphocytes (Siddique, 2008; Siddique *et al*., 2009) and human peripheral blood lymphocytes (Seema and Meena, 2012). The antimutagenic activity of the aqueous extract against cyclophosphamide-induced mutagenicity was similar to the earlier reports. The suppression of mutagenicity of cyclophosphamide above 50% at the tested concentrations, except 100%, (where to total arrest of cell dividion was observed) could be considered a strong antimutagenic effect. It is possible that metabolic activation of cyclophosphamide to free radicals (that are mutagenic metabolites) was perfectly inhibited by the aqueous extract of *C. asiatica* through its free-radcals scanvenging phenolic compounds with antioxidant properties (Siddique *et al*., 2008; Siddique 2009).

CONCLUSION

This study revealed that the effect of water extract of *C. asiatica* on cell division in *A. cepa* was mitostatic and not cytotoxic except at 100% concentration. Its activity on the chromosomes of the treated cells was not mutagenic. However, it showed strong antimutagenic effectivness against cyclophosphamide-induced chromosomal aberrations in the *A. cepa* cells, suggesting its possible use as a promising anticancer chemotherapy.

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PGB03

INDUCED GENETIC VARIABILITY IN SESAME (*SESAMUM INDICUM*(L) USING FAST NEUTRON IRRADIATION AND SODIUM AZIDE.

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ABSTRACT

Induced Genetic variability's in sesame was studied. Variety kenena-4 was exposed to fast neutron irradiation (FNI) from an Am-Be source with a flux of $1.5\times10^{4}ncm^{-2}s^{-1}$, using doses of 0,4,8,12 and 16μsv and also treated with sodium azide using doses of 0.0%,0.2%,0.4%,0.6%,0.8%. Plant height, survival percentage, length of petiole, number of leaves per plant and leave surface area were observed for quantitative character .There were significant differences (at $p<0.05$) in kenana-4 at different doses of fast neutron irradiation and sodium azide with most of the parameters used. Both radiation and chemical showed negative correlation with most of the parameters used.

Key words: Mutagenesis, FNI, sodium azide, sesame.

INTRODUCTION

Sesame is considered to be the oldest oilseed crop known to man. The crop has been domesticated well over 5000 years (Bisht *et al.*,1998). It belongs to the family Pedaliaceae and genus *Sesamum*. The genus consist of about 36 species out of which the commonly recognized is *Sesamum indicum* L. (Falusi, 2006). *Sesamum indicum* is very drought tolerant. It has been called a survivor crop because of its ability to grow where most plants fail. The crop is believed to have originated from Africa where the greatest diversity of the genus sesame and its family Pedaliaceae is present (Falusi and Salako, 2003). Some of the local names of the crop in Nigeria are ("Ridi" Hausa) ("Ishwa" Tiv), ("Gorigo" Igbira), ("Eeku" Yoruba) and ("Doo"Jukun) (Falusi *et al*, 2001)

Currently it is cultivated in the tropical and sub tropical region of Africa, South America, North America and Asia principally for its seeds which contains about 50-52 % oil, 17-19 % Protein and 16-18 % carbon hydrate (Falusi and Salako, 2003).It is an annual plant growing to 50 - 100cm (1.6 to 3.3 ft)tall, with opposite leaves 4 -14cm (1.6 - 55in) long with an entire margin :they are broad lanceolate, to 5cm(2in) broad at the base of the plant, narrowing to just 1 cm (0.4in) broad on the flowering stem . The flowers are yellow, tabular, 3 to 5cm (1.2 to 2.0m) long, with four lobed mouths. The flower may vary in colour with some being white, blue or purple. Sesame fruit is a capsule, normally pubescent, rectangular in section and typically grooved with a short triangular beak. The length of the fruit capsule varies from 2 to 8 cm. Its width varies between 0.5 to 2cm, and the number loculi from 4 to 12. The fruit naturally splits opens (dehisces) to release the seed by splitting along the septa from top to bottom or by means of two apical pores, depending on the varietal cultivar. Sesame seeds are small, about 3to4millimeter long by 2millimeter wide and 1millimeter thick. The seeds are ovate, slightly flattened and somewhat thinner at the eye of the seed(helium)than the opposite end with the weight of the seed between 20to 40 milligrams. Sesame is grown primarily for it's oil-rich seeds. The oil is used locally for cooking as well as for medicinal purposes such as the treatment of ulcers and burns. The stem and the oil extracts are equally used in making local soup.The products are locally processed and utilized in various forms. Principally among the products are "KATUN RIDI" and "KANUN RIDI". After oil has been extracted from the seeds, the cake is made into "Kuli Kuli" which together with the leaves are used to prepare local soup known as "MIYAR TAUSHE". Artificial induction of mutation is of scientific and commercial interest as it is one of the methods used in improving the growth and yield of economic plants. It provides raw materials for the genetic improvement of economic crops (Adamu et al., 2004). Although various mutagens were known to induce mutation in plants, this work has made use of fast neutron and sodium azide in inducing genetic variability through mutagenesis to improve both

the quality and quantity of sesame. The aim of the present study is to induce mutation through the use of various concentrations of sodium azide and fast neutron in sesame (S. indicum L. Var. Kenana-4) to improve the quality and quantity of the plants.

MATERIALS AND METHODS

The study was carried out at the experimental garden; Centre for Preliminary and Extra-mural Studies, Federal University of Technology, Minna, Niger State, Nigeria.

The seeds were obtained at National Cereal Research Institute (NCRI) Baddegi, Niger State.

The seeds were irradiated with fast neutron at the Centre for Energy and Research training (CERT), Ahmadu Bello University Zaria, Kaduna state, Nigeria. Kenana 4 was subjected to different doses of fast neutron. The variety was divided into five equal parts and exposed to 0, 4,8,12 and16µsv.

Sodium azide was used to treat the seeds, there were five different concentrations, 0%,0.2%,0.4%,0.6%,0.8%. Sodium azide was diluted to the required concentration by using distilled H2O.Seeds were soaked in the H2O for six hours to initiate Biochemical reaction. The chemical reaction is found to be affected by the frequency and spectrum of mutagens depending on the type of cell division during the process of germination. If the chemical treatment is synchronized with DNA synthesis stage (G1, s and G2) then we get better results.

The presoaked seeds were put in flask and Sodium azide was added and left for eight hours. Usually the quantity of Sodium azide 10 times the volume of the seeds. Intermittent shaken was given to ensure uniform exposure of the chemicals. The chemical was drained after the treatment time is over. The seeds were washed immediately not less than 30mins.

Two factors were involved; the variety and irradiation for physical, variety and sodium azide for the chemical. Factorial design was adopted with two (2) plants per pot with a total of 15 combinations per plot. The arrangement used was randomized block design with thirty (30) pots per block (figure 1).The experiment was replicated in three making a total of 90 pots for physical and 90 pots for chemical. Ten seeds were planted per pot (i.e. five per hole in a pot).Three weeks after planting; each pot was thinned to two plants per pot. A total of eight (8) pots for each treatment combination were used.

The following data were taken during the period of study;

Plant height at 2, and 4weeks after planting and at maturity: The distance from ground level up to the terminal bud on main axis of a plant in cm using metre rule, length of petiole(cm) using metre rule, leaf surface area in cm^2.Survival rate 21 days after planting: this was taken in percentage. The result of this research was subjected to analysis of variance (ANOVA) to show whether there were significant differences among the morphological parameters and yield parameters. Duncan multiple range was used to separate the means. The survival rate, flowering percentage and the spearman rank correlation was used to show the relationship between the treatments and parameters.

RESULTS

For the effect of fast neutron irradiation kenana 4 variety at 2 weeks, 0usv assumed the highest with a mean of 6.87a, Followed by 8usv, 12usv, 16usv and the least was recorded in 4usv with the mean of 5.67a and there were no significant difference observed in the various doses at $p<0.05$, but there was a negatively very weak correlation(-0.148). At 4 week 12usv showed the highest plant height with the mean of 25.73a, then 0usv, 4usv, 8usv, and the least was recorded in 16usv with a mean of 20.93b. There were significant difference observed between 12usv and all other doses at $p<0.05$. There was a negatively weak (-0.287) not significant correlation between the doses and the plant height However, at 6 week 12usv assumed the highest height (70.25a) than other doses, while the least was recorded in 16usv. With the mean of (53.60b). There were significant difference observed between 12usv and the other doses (0usv, 4usv, 8usv, 16usv) at $p<0.05$. But there was a positively weak correlation (0.100) and not significant. For the effect of sodium Azide on plant height at 2 weeks variety kenana 4 treated with 0.2% and 0.8% were significantly different from 0.4%, 0.6% and 0.0% (controls) with the means of (6.45a and 6.20a) respectively while the lowest was 0.6% with the mean of (3.80b).The correlation was a weak positive correlation (0.238) and not significant.At 4^{th} week 0.6% recorded the least plant height with the mean of 12.64c, while 0.0% (control) has the highest mean (23.78a) followed by 0.2%, 0.4% and 0.8%. 0.0% and 0.2% were statistically different with the other doses at $p<0.05$. The correlation was a strong negative correlation (-0.757) and was not significant.At 6^{th} week, 0.2% had the highest mean of (58.29a) followed by 0.0%, 0.8%, 0.6% and 0.4% recorded the lowest mean of (45.36b). A modest negative correlation (-0.629) not significant was recorded. 0.2% and 0.0% were statistically different from the other doses at $p<0.05$.

For the effect of fast neutron irradiation (FNI) on the number of leaves per plant kenana 4, 16usv assumed the highest (11.10a) and the least recorded 4usv(9.80a). But there were no statistical difference in all the doses at $p<0.05$. There was a strong positive correlation and not significant (0.827).

For the effect of sodium Azide on the number of leaves per plant in kenana 4, 0.2% has the highest number of leaves (27.30a) and the least was recorded in 0.0% (control) with the mean of (10.20c) 0.2% and 0.4% were statistically different from the other doses 0.8%, 0.6% and 0.0% at $p\leq0.05$. The correlation was a weak positive correlation (0.278).

Kenana 4, radiated at 12usv had the longest petiole (5.10a) followed by 4usv, 8usv, 0usv and the least was 16usv with the mean of (2.18c). There were statistical difference between 12usv and the other doses at $p<0.05$. The correlation was a negative weak correlation and not significant. For the effect of sodium Azide, kenana 4 treated with 0.0% had longest petiole (2.90a) the least was recorded in 0.6% with the mean of (1.11b). There were statistical difference between 0.0% and the other doses at $p\leq0.05$. The correlation was a negative modest correlation and not significant.

For the effect of fast neutron irradiation (FNI) kenana 4, 0usv had the highest leave surface area(42.18a) and the least was 16usv(25.61c). There were statistical difference in all the doses at $p<0.05$. There was a weak negative correlation (-0.417) and not significant

For the effect of sodium Azide in kenana 4, 0.0% had the highest leave surface area (42.18a) and the least was recorded in 0.6% with the mean of (27.11b) there were statistically different

between 0.0% and all the other doses at $p \leq 0.05$. The correlation was a weak negative correlation (-0.315) and not significant.

For the effect of fast neutron irradiation on survival percentage, 16usv and 8usv in kenana 4 performed better (53% and 50%) than the control 0usv (45%). For the effect of sodium azide on survival percentage in kenena 4 0.8%,0.2% and 0.6% (93%,73%and 50%)performed better than the control(45%).

Table 1: Some morphological parameters of the Kenana-4 variety at different doses

TREATMENT	PLANT HEIGHT 2 WEEKS	4 WEEKS	6 WEEKS	NO. OF LEAVES PER PLANT	LENGTH OF PETIOLE	LEAVE SURFACE AREA
FAST NEUTRON						
Ke0	6.87±1.76a	23.78±1.74ab	57.30±14.99ab	10.20±1.22a	2.90±0.96bc	42.18±12.63a
Ke4	5.67±1.42a	23.71±3.80ab	58.89±17.7ab	9.80±1.54a	3.84±1.32b	38.18±4.79ab
Ke8	6.70±1.68a	21.22±2.83b	61.50±17.10ab	10.90±1.59a	3.45±0.84b	37.43±23.57ab
Ke12	6.63±1.35a	25.73±3.45a	70.25±20.93a	10.90±1.72a	5.10±1.55a	30.95±2.50ab
Ke16	6.16±1.89a	20.93±2.57b	53.60±13.83b	11.10±1.37a	2.18±0.50c	25.61±9.84c
SODIUM AZIDE						
Ke0	3.90±0.68b	23.78±5.32a	57.30±14.99a	10.20±1.22c	2.90±0.96a	42.18±12.63a
Ke2	6.45±1.37a	22.60±5.39a	58.29±15.47a	27.30±7.74a	2.23±0.92ab	38.70±4.85ab
Ke4	4.29±1.18b	21.97±5.73ab	45.36±10.80b	25.00±7.87a	1.09±0.16b	39.93±22.63a
Ke6	3.80±1.15b	12.64±5.06c	48.60±7.67ab	16.60±10.37bc	1.11±0.32b	27.11±2.93b
Ke8	6.20±1.12a	17.80±3.88b	51.05±13.07ab	21.60±11.22ab	2.39±3.37ab	32.05±8.56ab

*Values are mean±SD. Values followed by the same letter(s) within the same row do not statistically differ at the 5% level according to DMRT

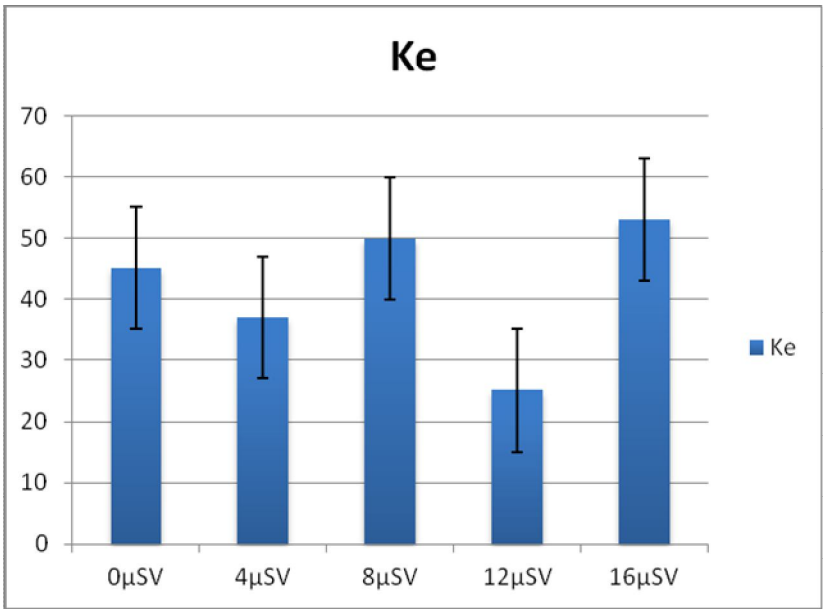

Figure 4.1: Survival Percentages of Kenana-4 at different doses of FNI

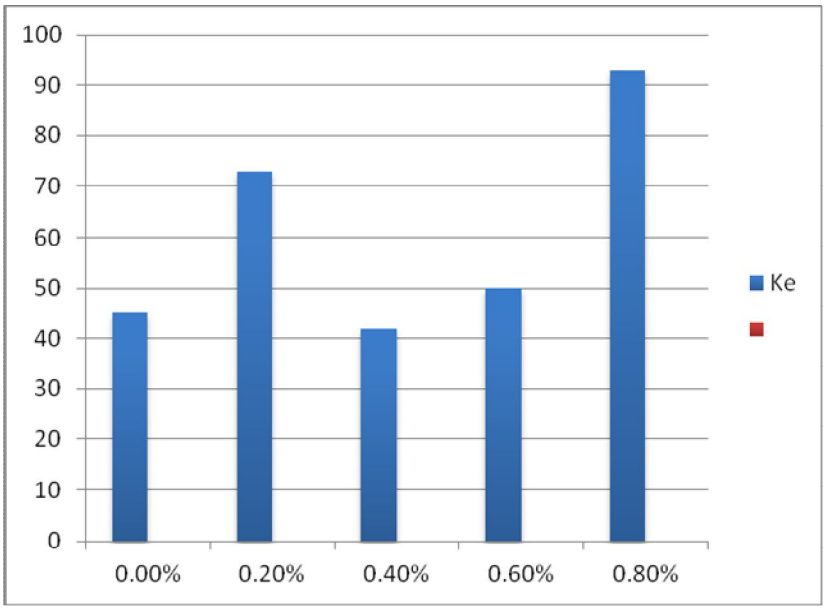

Figure 2: Survival Percentages of kenana-4 at different concentration of sodium azide

DISCUSSION

Mutation induction through the use of different concentrations of sodium azide and fast neutron irradiation has proved vital in inducing variability that could be exploited in the improvements of sesame growth and yields. It is therefore the origin of genetic variability as suggested by Tamarin (1999). The mean increase in plants heights at maturity of the sesame variety induced

by sodium was due to the alteration of their genome integrated by environmental signals as reported by Uno et al. (2001); probably by increasing the rates of cellular division and expansion at their meristematic regions. This is also in agreement with the findings of Hoballah (1999) who reported increased in plant heights of sesame due to radiation mutagenesis; but is in contrast to the findings of Anandakumar and Sree- Rangasamy (1995) and Maluszynski et al. (2001) who independently reported decrease in plant height due to induced mutation in rice and other cereals. The increase in leaf number and internodes length with decrease in the concentrations of colchicines was in agreement with the findings of Hoballah (1999) who reported increased in leaf number and internodes length among sesame mutants due to gamma irradiation. The increase in the leaf area of sesame due to colchicines means an increase in the surface area for gaseous ex-change which consequently affects the photosynthetic process. This agrees with the work of Maluszynski et al. (2001) who reported increase in the leaf area among Zea mays mutants due to irradiation. Artificial induction of mutation through the use of sodium azide proves vital in the improvement of genetic variability in sesame. Certain concentrations of sodium azide (0.2 through 2.0mM colchicines concentration) have the potentiality of inducing variability that could be used in the improvement of the yield of sesame.

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PGB04

GROWTH AND REPRODUCTIVE CHARACTERISTICS OF INBRED FLUTED PUMPKIN

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ABSTRACT

Landraces from five states of Anambra (AN), Imo (IM), Abia (AB), Enugu (EN) and Rivers (RV) in South Eastern Agro-ecology of Nigeria were collected and established ex-situ at the Teaching and Research Farm in Federal University of Technology, Owerri between 2003 and 2004 cropping seasons. Selected plants of each parent landraces were selfed and the growth and reproductive characteristics of individual inbreds assessed. The Abia inbred (AB/AB) performed better than all other inbreds. They produced the longest vine length plant^{-1}, highest number of branches and nodes plant -^{1}, internode length and leaf number plant $^{-1}$ at 6 weeks after planting (6WAP). The male (AB) inbred also flowered earlier (10WAP) than other inbreds while those of (AN) flowered later (13 WAP) than the rest. The female Anambra inbreds flowered earlier (12WAP) than other female inbreds while those of Rivers flowered last (16WAP). The highest number of female flowers plant^{-1} (150) was obtained from Anambra inbreds and their fruits also matured (13WAP) earlier than others while the female Abia inbreds had the least number of flowers and fruits which also matured last (18WAP). Our findings showed potential for genetic enhancement of fluted pumpkin of different landraces from this ecological zone.

INTRODUCTION

Telfairia occidentalis belongs to the genus *Telfaira* Hooker, Tribe *Joliffeae*, sub-family *Cucurbitoideae* and family *Cucurbitaceae* (Jeffrey, 1980).

It is an important crop in Tropical West Africa, especially in Nigeria, Sierra Leone, Ghana and Benin Republic where it is used as food and as commercial garden vegetable (Purseglove, 1968; Irvine, 1969; Eziaba, 1982). In Nigeria, according to Akoroda, (1990) the largest diversity in plant population of this crop can be found in the South-Eastern Agroecology encompassing Imo, Anambra, Enugu, Ebonyi, Cross-River, Akwa-Ibom and Abia states of Nigeria. The edible parts include the young vines or shoots, leaves, seeds and petiole and are important sources of carbohydrate, protein vitamins and minerals (Achinewhu, 1993; Asiegbu, 1987). In a survey on the pattern of consumption of leafy vegetables in Nigeria, Hart *et al.* (2005) gave the per capita consumption as 91-130kg. This range was reported to be among the highest in Africa and fluted pumpkin was also listed among the Regionally Consumed Indigenous and Traditional Leafy Vegetables for West Africa, (Smith and Pablo 2007). The oily seeds apart from nutritional

properties also have lactating properties while the root extracts are used to kill rats, mice and fish (Schipper, 2000). Now, the economic and nutritional benefits of blending fluted pumpkin seed into wheat flour for bread because of its nutritional value has been revealed in Nigerian economy (Giami *et al.*,2003).

The plant is dioecious having only staminate (male) flower or the pistilate (female) flower on individual plants. This makes *T. occidentalis* 100% cross-pollinated and thus characterized by high genetic variability. The land races of cross-pollinators are heterogeneous genetically and form a relative continuum of agronomic types in the field (Heiser, 1981) According to Thompson (1976) and Izumolu (1987), the agronomic problem encountered when growing *T. occidentalis* is that the plants exhibit variations in many quantitative and qualitative characters. These variations, they reported, are expressed in their differences in stem length, number of leaves, length and size of pods, time of pod maturity and effective duration of vegetative growth.

The main benefit of hybridization is to eliminate variability and to produce seeds that produce fairly uniform plants with high yields. (Kuckuch *et al.*,1991). In *Cucurbita*, demand for uniformity and selection had resulted in high homozygosity and true breeding cultivars. Inbred lines have been used to develop hybrids which were more uniform and homogenous, than open-pollinated cultivars (Paris, 1989). *Cucurbita* like *Telfairia* belongs to the same family of *Cucurbitaceae.* Very limited research has been targeted on the genetic enhancement of *T. occidentalis*. This work reports on the growth and reproductive characteristics of inbred landraces targeted for use in hybridization of. *T. occidentalis.*

MATERIALS AND METHODS

Two field experiments were conducted in 2003 and 2004 at the Teaching and Research Farm of the Federal University of Technology Owerri, located at latitude 5.29^0 N and longitude 7. 02^0 E and 17 meters above sea level. The rainfall pattern is bimodal with peaks in June and October while the dry season falls within November and February. The mean annual rainfall varies and ranges between 2000 and 2400mm while the annual mean temperature ranges between 25 and 28 ^{0}C. Sunshine averages 4.2 hours per day, ranging from 2 hours in September to 6.1 hours in February (FAO 1984).

The soils are generally classified as sandy ultisols (Vine, 1970 Hulugalle et al, 1990; Eshett and Anyahucha, 1992.)

The treatment for the experiment consists of twenty fruits of traditional landrace morphotypes of *T.occidentalis* obtained locally from selected home gardens within five states in South-Eastern agro-ecological zones of Nigeria. Four fruits were obtained from each of the states which are centers of genetic variability, which include Imo (IM), Abia (AB), Anambra (AN) Enugu (EN) and Rivers (RV) and were characterized for length, width and circumference. These were split open and the seeds scooped, processed, counted and bulked. The seeds were then weighed and fairly uniform seeds of same weights (12 + 0.5g) were selected and used. These treatment lots were randomized in plots and replicated four times in a Randomized Complete Block Design (RCBD) according to the methods described by Wahua (1999) and SPSS (2006) for Randomized Complete Block experiments. The seeds were planted on ridges at a rate of one seed per hole at a depth of 5cm and with a spacing of 2 x 2m between and within rows. Selfing among selected male and female plants from each treatment population was carried out in the field. In the

process, immature buds of the female parents were protected from foreign pollen with pollination bags till they were matured and receptive. Pollen from the selected male parents were then collected and shed on the receptive stigma. Parents were selected on the basis of superior growth rate, early flowering and increase in leaf size. In addition the male parents were selected for fewer number of tendrils and flowers.

The selfed plants were labeled accordingly and their fruits harvested at maturity as S1 (selfed) progenies. The seeds of S1 progenies produced were planted out the following year (2004) and evaluated to identify promising S1 families based on vegetative and reproductive yield. characteristics. Data collated from the field were subjected to Statistical Analysis (descriptive and bivariate statistics), using the SPSS 15.0., (2006) Evaluation version for windows.

RESULTS AND DISCUSSION

It is desirous that vegetable production be profitable during the early stages of growth therefore growth characteristics and leaf yield within 6 weeks after planting T. occidentalis is important. The result of the vegetative characteristics and leaf yield of inbred *T. occidentalis* at 6 WAP is as shown in Table 1.

The AN/AN inbred had the longest vine length of 120cm which was not different from those of AB/AB and IM/IM but differed significantly from those of EN/EN and RV/RV inbreds which had the shortest vine length of 87.8 and 87.8cm at 6 weeks after planting (6WAP). The internode was also significantly the longest (15.8cm) from AB/AB inbreds. Similarly, the number of branches (6.3) which was produced by the AB/AB inbreds was significantly different from other inbreds except EN/EN that had 4.2 branches at 6WAP. The lowest number of branches 2.3 was produced by RV/RV which however, did not differ from IM/IM and AN/AN that had 3.0 and 3.3, respectively.

The number of nodes and leaves plant $-^{1}$ at 6WAP also followed the same trend with AB/AB being consistently the highest and RV/RV the lowest.

The leaf area per plant did not differ amongst the inbreds which is an indication that the gene controlling leaf area is fairly constant in all the landraces. The highest leaf yield of 109.5 kg ha^{-1} was however obtained from AB/AB inbred which was significantly different from the yield of all other inbreds. This can simply be adduced to the significantly higher number of leaves per plant (50) produced by the AB/AB inbreds.

S1 Inbred	Vine length (cm)	Internode length (cm)	No.of Branches $Plant^{-1}$	No. of Nodes $Plant^{-1}$	No. of leaves $Plant^{-1}$	Leaf area $Plant^{-1}$ (cm^2)	Leaf yield (kg) ha^{-1}
EN/EN	87.8	7.3	4.3	32.0	38.3	79.0	68.0
AN/AN	120.0	7.5	3.3	31.3	36.0	94.8	45.5
AB/AB	115.0	15.8	6.3	42.3	50.0	82.0	109.5
IM/IM	113.3	9.3	3.0	32.3	38.0	99.7	55.3

RV/RV	87.0	11.0	2.3	26.0	31.3	92.9	4.0
LSD *0.05*	40.3	5.41	2.51	6.47	9.22	29.66	7.01

Table1: Growth and leaf yield characteristics of *T. occidentalis* inbreds at 6WAP

Growth characteristics and leaf yield at 6 WAP were consistently the highest with AB/AB inbreds while the RV/RV had the lowest. The vigor in growth characteristics recorded for the AB selfed plants may be due to the fact that only physiologically good plants were selfed, this according to (Assman,1970) can result in favorable gene combination that hastened the physiological process that enhanced faster and better growth as manifested in the AB/AB plants at the early growth stage. These growth characteristics of the inbred lines grown under the same condition which revealed that the AB/AB plants had the most desired growth characteristics and leaf yield than the other inbreds therefore lends itself for use as the best material for any improvement program for increased vegetable production of *T. occidentalis* in Southern Nigeria. The result of flowering and fruit yield characteristics of inbred lines of *T. occidentalis* as presented in. Table 2 shows that the number of days to 50% flowering differed amongst the male and female plants. Between the male plants AB/AB flowered earlier (69DAP) than other inbreds but did not differ from that of EN/EN (70DAP). It is generally known that, male plants flower earlier than their female counterparts in *T. occidentalis.* The inbred AN/AN female plant flowered earliest (82.3DAP) to 50% flowering but was not significantly different from EN/EN, IM/IM and AB/AB inbreds. The highest was with RV/RV which attained 50% flowering at 109DAP and differed significantly from the rest inbreds. Percent male and female plants also differed significantly amongst the inbreds (Table2) AB/AB and RV/RV had more males than females,whereas IM/IM and AN/AN had more females than males. The highest percent of female plants 55% was obtained with EN/EN and the lowest (36%) was with RV/RV while it was observed that equal proportions of male and female plants (48%) were obtained with AN/AN. Plants with more females are preferred because of expected high yields of both leaf and seeds. The number of matured fruit harvested from the inbreds also differed significantly, IM/IM inbreds had the highest number of fruits (84) per treatment and the lowest number (44) was with RV/ inbred.

The low number of matured fruits obtained by RV/RV can be attributed to the delayed fertilization of the female flowers of RV/RV inbreds as a result longer days to the attainment of 50% female flower, moreover the short anthesis period of the male and female flower coupled with the low number of female plants will definitely cause decrease in number of matured fruits. The result on Fruit weight indicated that IM/IM inbred had the highest fruit weight of 7.3kg fruit^{-1} followed by AB/AB and RV/RV which had 6.8 kg fruit^{-1} both and did not differ significantly from EN/EN inbred.

Table 2: Flowering and fruit yield characteristics of *T. occidentalis* Inbreds

S1 Inbred	Number of DAP to 50% flowering	No. of Days to end of flowering Male	Percent (%) of Treatment Male	Female	No. of Matured fruits treatment^{-}	Fruit weight kg fruit^{-1}	No. of seeds No. Fruit^{-1}

	Male Female	Female		[1]		
EN/EN	70.0	107.3	36.0	60	4.6	42
	92.0	141.7	55.0			
AN/AN	93.7	120.0	48.0	58	4.1	47
	82.3	114.3	48.0			
AB/AB	69.0	95.3	60.0	48	6.8	58
	85.7	145.3	40.0			
IM/IM	91.0	111.3	47.0	84	7.3	69
	94.0	146.7	53.0			
RV/RV	89.7	114.7	61..0	44	6.8	75
	109.0	156.0	36.0			
LSD	13.13	40.0	1.49	2.92	2.23	14.67
0.05	16.5	24.78	1.60			

CONCLUSION

It is important to make recommendation based upon the result of this experiment when the target of any hybridization program is for the enhancement of vegetable and or fruit production of *T. occidentalis* that the AB/AB followed by IM/IM inbred families will be better materials because of the desirable performance across various growth and reproductive characteristics assessed. These families can form the basic unit for selection and recombination with any other landrace. Our findings showed potential for genetic enhancement of fluted pumpkin from different landraces of this ecological zone, having identified desirable traits in the inbreds.

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PGB05

GENOTYPIC POTENTIAL FOR GERMINATION CAPACITY, GROWTH AND YIELD IN SUGARCANE *(SACCHARUM OFFICINARUM* L.) GERMPLASM ACCESSIONS IN A SAVANNA ECOLOGY OF NIGERIA

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ABSTRACT

Assessment of germplasm materials is a prerequisite for their utilization either as cultivars *per se* or as parents in hybridization programme aimed at the development of future varieties. This

study was therefore conducted to evaluate germination capacity, growth and yield potentials in thirty exotic sugarcane germplasm accessions and six check varieties in a Savanna ecology of Nigeria, with the aim to identify superior clones that will be suitable for cultivation on the estates or in a hybridization programme aimed at development of high yielding sugarcane varieties for cultivation on the estates. The study was conducted at the Research Farm of the Unilorin, Sugar Research Institute, Ilorin, Kwara State for two cropping seasons using a Randomized Complete Block Design (RCBD) with three replications. Data were collected on germination count, tiller count, number of stalks/stool, stalk length, stalk girth, number of internodes/stalk, internode length, number of millable canes, single stalk weight and cane yield. Results showed that the genotypes differed significantly ($P<0.01$) for the characters studied, with many of the introductions showing superiority for cane yield (t/ha^{-1}) over the existing cultivars. Notable among the accessions were DB 851062, KNB 9252, B93638 DB 7867 B 78697 and B 881607 with cane yield between 75 and 81t/ha^{-1}, indicating that they could be utilize in hybridization schemes to evolve superior progenies which can eventually replace the current low yielding varieties on sugar estates in Nigeria.

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INTRODUCTION

The primary goal in germplasm evaluation is to assess them for their yield potentials and general adaptation to the ecosystems where they are likely to be utilized either as variety *per se* or as parents in hybridization programme. However, a major factor militating against the attainment of a faster goal in sugarcane (*Saccharum officinarum* L.) breeding and varietal development in Nigeria is due in part to lack of access to germplasm with high yield potential. For example, majority of the parental clones which are currently used in hybridization in the two institutes involved in sugarcane varietal development in Nigeria {National Cereals Research Institute (NCRI) Badeggi and Unilorin Sugar Research Institute (USRI), Ilorin}, are old. Recently, the National Sugar Development Council (NSDC), Abuja, imported over 100 exotic sugarcane varieties intended for evaluation and selection of high yielding (cane yield and sucrose content) genotypes for industrial cultivation on the estates. Therefore, selection of superior genotypes from among the new exotic germplasm accessions either directly as industrial sugarcane varieties or as parents in the development of adapted sugarcane varieties for Nigeria's sugarcane

plantations, will increase the productivity of the existing varieties (50 -75 t/ha^{-1}) to as high as $\geq$100 t/ha^{-1} obtainable in other sugarcane producing countries in Africa.

From the breeding perspective, germplasm materials are also assessed for their breeding behaviour with the objective of utilizing them as parents in hybridization for evolving new and superior progenies intended to replace the existing cultivars. For example, previous evaluation of germplasm accessions (Olaoye and Agbana, 1987; Olaoye and Fatunla, 1991; Olaoye, 1995; 2006) has succeeded in identifying superior genotypes that have been used as parents in hybridization programme. The study reported here was therefore carried out to assess yield potential and breeding values of thirty (30) exotic sugarcane germplasm accessions representing batch one (1) of the accessions imported from Barbados (West indies).

MATERIALS AND METHODS

Thirty (30) exotic sugarcane germplasm accessions representing the first batch of genetic resources from Barbados (West Indies) and six (6) check standard varieties (as checks) were evaluated at the Research Farm of the Unilorin Sugar Research Institute (USRI), Ilorin, Kwara State in a typical Southern Guinea Savanna agro-ecological zone of Nigeria (latitude 8^0 29N and longitude 4^0 35E). Three (3) of the check varieties Co957, Co62175 and B47419 are commercial varieties, while the remaining three (3) (ILS-001, ILS-002 and USRI/85/31) were developed at USRI, two (ILS-001 and ILS-002) of which have already been released.

The rainfall pattern of the ecology is bimodal with the highest peak in July and September with a break usually from mid-July and late August every year. The average annual precipitation of the area is 1250-1500mm with temperature ranging from 19-33^{0}C. The accessions were obtained from Josepdam Sugar Company Estate Bacita, Kwara State. The experimental design used was a Randomized Complete Block Design (RCBD) with three (3) replicates. The genetic materials were planted in single row plots measuring (5m x 1.6m) that is 5m long and 1.6m wide, with inter and intra-row spacing of 0.5m and inter plot spacing of 1m during 2010/2011 growing seasons. Three (3) budded sugarcane sets were cut and laid in furrows at a depth of 15cm and covered with soil. Pre-emergence herbicide was applied immediately after planting to control weeds. Supplementary weeding was thereafter carried out as necessary throughout the period of the experiment.

Fertilizer application was carried out as split-dosage at the recommended rate of 150kgN/ha. The first dose was applied immediately after planting while the second dose was applied six (6)

months after the initial application. The fields were irrigated from November, 2010 through April, 2011 to ensure adequate moisture supply throughout the period of the dry season and also after harvest in December, 2011 to May, 2012 to sustain the ratoon crop until rains became steady. Data were collected on germination percentage, tiller counts, number of stalks/stool, stalk length (cm), stalk girth (cm) number of internodes/stalk, stalk length (m), number of millable canes/plots, single stalk weight (kg) cane yield at harvest (t/ha^{-1}) and cane yield in tones/hectare. Germination and tiller counts as well as the number of stalks/stool were done by physical examination and counting the buds that sprouted and shoots that developed. Stalk length (m) internode length (cm) and stalk girth (cm) were carried out by measurement, using meter tape. These were carried out at specific growth and developmental stages beginning from fourteen days after planting (14DAP) at two-weekly intervals up to 42 DAP (germination) and three months after planting (3MAP) to 12 MAP (tiller count and brix content). Millable cane population was based on counting the number of matured stalks in a plot while the weight was determined by weighing them on weighing scale and recorded in kilograms. The single stalk weight was also recorded in kilograms while cane weights were converted into tones/hectare (t/ha^{-1}). The estimate of sugar contents was obtained by extracting the sucrose in the juice of the matured and ripened stalks using hand punch and values read as degree brix (^{o}Brix) with the aid of a hand refractometer. The data collected were subjected to the analysis of variance (ANOVA). Pertinent means were thereafter separated with least significant difference (LSD) according to Steel and Torrie (1980).

RESULTS

Means, ranges in the means and coefficient of variation (%CV) for germination count, growth characteristics as well as cane yield and related traits are presented in Table 1. Germination count increased with increasing days from planting with the largest variation among the genotypes recorded at 42DAP. Tiller count also showed similar trend, increasing with maturity in all the genotypes. Brix reading increased with maturity period until 12 MAP but decreased at harvest. The highest variability among the genotypes was recorded for cane yield followed by millable cane population while the least variation was recorded for stalk length and stalk girth respectively.

Mean germination and tiller counts in the thirty (30) exotic sugarcane germplasm accessions and six (6) check varieties are presented in Table 2. The results showed that there were significant differences among the genetic materials ($P \leq 0.05$) at all the periods of observation. Accession B 85106 consistently had the highest number of germinated buds followed by varieties ILS-001 and USRI/85/31. Some of the accessions (KNB9211, BT74209, B76251, KNB92101, B881607, B62163, B93638 and varieties ILS-002, Co-62175, and B 47419) had low germination count, while accessions B 79474 and B76621 failed to germinate even14 DAP. Many of the genotypes with high germination count also had high tiller counts. Consequently, three genotypes - KNB 9252, USRI 85/31 and DB 85106 in that order had high tiller counts which were superior to those of other genotypes. Differences in tiller counts in respect of these genotypes and accession B 82233 with the lowest tiller count at harvest were 99, 96 and 79 respectively.

The genotypes also differed significantly ($\leq P$ 0.05) for stalk characteristics (Table 3). Var. USRI/85/31 had the highest number of stalks/stool, followed by accessions DB85106, B93638, B63118, B76621, B88107 in that order. Accession DB7867 had the longest stalk length followed by accession DB8113 while accession KWB9252 had shortest stalk length. Accession DB7867 also had the thickest stalk-girth while accession BT871646 and var. Co957 which had 3.1cm each had the thinnest girth. Accession B78697 had the highest number of internodes/stalk, followed by accession B63118, while variety B47419 had the least number of internodes/stalk. Accession B881607 had the longest internode while accessions D8687 and KNB 9252 had the shortest internodes respectively.

Means for cane yield and related traits (Table 4), revealed significant differences ($P \leq 0.05$) among the genotypes for number of millable canes/plot, cane yield and brix reading while differences among them was not significant for single stalk weight. Accession BT74209 had the heaviest single stalk weight followed by accession B82238.Accessions BR 8230 and B80689 had the highest sucrose content followed by accession BT74209 while accession B62163 had the least sucrose content. Fifteen (15) genotypes which included eleven (11) accessions, yielded between 90.3 (var. Co 957) and 99.8t/ha^{-1} (i.e. Accession D 8415). The differences between the highest yielding and the five (5) poorest yielding genotypes (BR 8230, B 76621, B 85266, B 93638 and Co 62175) which recorded yields that were below 50t/ha^{-1}, were 72.7, 70.6, 61.8, 60.5

and 58.6t/ha^{-1} respectively. Var. USRI/85/31 with the highest number of millable canes was the third highest yielding genotypes. All the high yielding genotypes except D8687 also had high brix content.

DISCUSSION

The results from this study revealed that the genotypes differed from one another for almost all the characters except stalk length and single stalk weight (kg). This is in consonant with earlier report of Nair *et al*., (1998) who reported that stalk length, and stalk weight have no contribution to genetic variation because the genes controlling height and weight may be identical at the loci. Similarly Olaoye and Fatunla (1991) hypothesized that the observed negative genetic variance estimates recorded for stalk length and leaf length in sugarcane in their own study may probably be due to absence of genetic variability for the two traits among the genotypes tested.

The significant difference observed for number of stalks/stool, stalk girth, number of internodes/stalk and stalk length is also in conformity with the reports of James (1971), Singh *et al*., (1981) and Kang *et al*., (1983). Furthermore, the variation observed in the number of millable canes/plot and cane yield could be as a result of inherent genetic variability among the genotypes which also agreed with reports of Lawrence and Sunnel (1997) as well as Bakshi and Hemaprabha (1998) who reported in their independent studies on estimate of genetic variance in sugarcane populations, confirmed that additive genetic variance estimates were responsible for cane yield and sucrose contents.

CONCLUSION

The results obtained from this study revealed that most of the accessions were found superior and acceptable to the existing varieties for germination, growth and yield characteristics. This suggests that there is possibility of finding replacement to existing varieties which are low in yielding ability. However, the identified genotypes still need to undergo further testing in the ratoon crops in order to make a definite pronouncement of their potential either as cultivar *per se* or as parents in breeding programme.

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Table 1: Means (SE±) ranges and coefficient of variation (%CV) for germination, growth parameters, cane yield and related traits in 30 exotic sugarcane germplasm accessions and six check varieties (Ilorin, 2011).

Trait	Mean (±SE)	Range	%CV
Germination count (no) 14DAP	2.40±1.07	6	78.0
Germination count (no) 28DAP	8.81±2.30	16	45.0
Germination count (no) 42DAP	20.06±4.08	31	35.0
Tiller count (no) 3MAP	36.56±5.15	64	24.0
Tiller count (no) 6MAP	45.82±6.44	79	24.0
Tiller count (no) 9MAP	52.39±7.07	84	23.0
Tiller count (no) 12MAP	61.94±7.90	99	22.0
^{o}Brix reading 8MAP	17.38±0.81	4	8.0
^{o}Brix reading 9MAP	17.85±0.77	5	8.0
^{o}Brix reading 10MAP	18.56±0.84	4	8.0
^{o}Brix reading 11MAP	18.67±1.05	4	10.0
^{o}11rix reading 12MAP	20.00±1.28	4	16.0
^{o}Brix reading at harvest	21.48±1.57	7	10.0
Stalks/stool (no)	9.39±0.65	13	29.0
Stalk length (m)	2.90±0.16	4	39.0
Stalk girth (cm)	2.77±2.26	1	9.0
Internodes/stalk (no)	27.7±1.14	16	14.0
Internode length (cm)	12.48±7.27	9	16.0
Millable canes (no)	48.44±1.11	86	26.0
Single stalk weight (kg)	2.18±15.57	7	88.0
Cane yield (t/ha^{-1})	65.14±15.57	124	40.0

DAP =Days after planting; MAP= Months after planting.

Table 2: Mean Germination and tiller counts in thirty exotic sugarcane germplasm accessions and six check varieties (Ilorin, 2011)

	Germination			Tiller Count			
Genotype	14 DAP	28 DAP	48 DAP	3 MAP	6 MAP	9 MAP	12 MAP
B77602	3	9	19	44	65	68	74
KNB9211	1	7	25	33	39	43	57
B82233	2	3	7	14	18	19	21
BT74209	1	6	22	38	45	50	56
B76251	1	6	20	46	52	62	67
B80689	2	8	17	37	40	45	54
BR8230	2	7	18	34	39	50	55
B991037	2	9	23	48	52	58	61
B85877	5	16	27	55	61	72	79
B74541	2	6	11	19	29	35	38
B93310	3	7	16	46	63	66	76
D8415	5	14	28	35	41	46	60
KNB9252	3	17	25	36	77	96	120
B85266	3	5	15	22	25	33	38
DB8113	4	11	26	31	43	51	62
DB85106	6	18	34	61	67	77	100
KNB92101	1	10	22	27	35	39	48
B881607	1	9	25	38	44	51	58
D8687	2	13	26	36	41	48	51
B78697	4	9	22	39	48	54	72
B62163	1	2	3	9	13	18	22
B93638	1	4	9	15	17	19	30
B79474	0	5	15	36	46	50	58
DB7867	2	9	26	42	51	61	70
BJ82112	2	9	25	33	38	46	53
B98653	3	16	28	50	57	65	72
B63118	2	11	26	44	56	62	65
B76621	0	2	6	13	16	21	24
B82238	3	8	23	29	45	50	60
BT871646	2	11	21	26	36	39	48
Co957	3	8	11	48	67	71	76
ILS-001	6	12	19	55	65	76	90
ILS-002	1	9	24	41	50	56	75
Co62175	1	2	8	16	21	25	39
B47419	1	7	21	37	56	63	82
USRI/85/31	4	14	30	73	92	102	117
Mean	2.4	8.8	21.1	36.6	45.8	52.3	61.9
LSD	3.006	6.497	11.497	14.582	18.16	19.94	22.84
%CV	78.49	45.26	30.20	24.39	24.34	23.38	22.1

DAP = Days after planting, MAP = Months after planting

Table 3: Stalk characteristics in thirty exotic sugarcane germplasm accessions and six check varieties (Ilorin, 2011)

Genotype	Stalk/Stool (no)	Stalk length (cm) ns	Stalk girth (cm)	Internodes/Stalk (no)	Internode length (cm)
B77602	8	2.8	2.6	28	11.7
KNB9211	7	2.8	2.9	29	11.4
B82233	11	2.4	2.9	22	11.4
BT74209	9	2.6	3.0	28	10.8
B76251	10	2.3	2.9	27	13.4
B80689	7	2.8	2.9	31	10.2
BR8230	8	2.3	2.5	29	12.3
B991037	9	3.0	2.7	29	13.1
B85877	4	2.8	2.9	28	12.0
B74541	7	2.7	2.6	22	11.9
B93310	9	2.8	2.9	26	12.8
D8415	6	3.1	2.9	31	13.8
KNB9252	9	2.1	2.1	28	9.2
B85266	7	4.1	2.9	30	11.5
DB8113	7	3.3	3.0	30	13.9
DB85106	14	2.5	2.6	27	11.0
KNB92101	6	2.9	2.8	31	13.5
B881607	12	2.9	2.9	28	16.8
D8687	6	2.5	2.9	32	8.2
B78697	12	3.3	2.8	35	15.2
B62163	12	3.1	2.7	28	13.3
B93638	13	3.0	2.7	28	12.2
B79474	8	2.3	2.5	24	12.2
DB7867	11	6.0	3.3	26	13.6
BJ82112	8	2.9	2.6	28	11.3
B98653	7	3.2	2.7	26	12.8
B63118	13	2.8	2.7	33	13.1
B76621	13	2.5	2.7	27	12.6
B82238	12	3.1	2.7	31	15.5
BT871646	6	2.8	3.1	28	13.4
Co957	10	2.7	3.1	29	12.6
ILS-001	10	3.0	2.7	26	12.1
ILS-002	9	2.9	2.7	26	12.8
Co62175	11	2.9	2.8	26	11.0
B47419	8	2.5	2.5	19	13.8
USRI/85/31	18	2.4	2.2	24	12.9
Mean	9.4	2.9	2.8	27.7	12.5
LSD	4.434	1.815	0.4393	9.542	3.221
%CV	29.00	38.62	9.99	14.15	15.84

Table 4: Cane yield and related traits in thirty exotic sugarcane germplasm accessions and six check varieties (Ilorin, 2011)

Genotype	Millable canes (no)	Brix at harvest	Single stalk weight (kg)	Cane yield (t/ha^{-1})
B77602	44	22.3	1.6	69.38
KNB9211	40	25.5	1.9	77.79
B82233	20	23.0	2.1	49.88
BT74209	48	23.8	8.5	68.42
B76251	47	23.2	2.0	91.71
B80689	43	25.0	2.0	91.71
BR8230	39	23.7	1.3	27.08
B991037	40	22.2	2.4	81.33
B85877	60	21.3	2.3	94.29
B74541	33	21.2	1.4	56.96
B93310	60	21.8	1.9	91.46
D8415	49	22.8	2.3	99.79
KNB9252	96	18.5	2.2	90.13
B85266	29	21.5	2.6	38.08
DB8113	53	20.8	1.5	99.75
DB85106	85	22.7	1.3	97.00
KNB92101	37	20.2	1.7	58.75
B881607	50	21.8	2.0	85.29
D8687	44	19.3	1.6	93.00
B78697	60	21.7	2.0	98.00
B62163	18	17.8	2.1	59.79
B93638	25	19.7	2.0	39.29
B79474	45	21.7	1.5	64.17
DB7867	62	21.5	2.8	96.38
BJ82112	42	22.8	1.6	50.58
B98653	56	19.8	1.8	89.25
B63118	52	19.7	2.3	72.25
B76621	19	21.8	1.6	29.17
B82238	41	20.2	4.6	91.92
BT871646	35	20.2	2.8	63.08
Co957	60	23.2	1.8	90.29
ILS-001	64	23.5	1.6	92.50
ILS-002	54	18.7	1.8	54.67
Co62175	33	20.7	1.9	41.25
B47419	65	22.5	1.6	53.33
USRI/85/31	104	20.5	1.7	96.75
Mean	48.4	21.5	2.2	81.44
LSD	20.51	3.614	3.128	0.04391
%CV	26.00	10.30	88.65	0.04137

PGB06

RICE BLAST PATHOGENICITY AND ITS EFFECT ON SOME RICE CULTIVARS IN NIGERIA.

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ABSTRACT

Screen house experiment to compare the virulence of blast inoculum collected at various locations in Nigeria and its effects on some rice cultivars were determined at a screen house studies conducted at Badeggi Central Nigeria. The blast inoculum was collected from some locations in North West, North East. North Central, South East and South West of Nigeria. The experiment was laid out in a factorial design fitted into a split plot. There were 60 treatment combinations. The rice cultivars serve as the main plot while the inoculum serves as the subplot. The experiment was replicated three times. Inoculation was done at two weeks after sowing with a control plot that was not inoculated. Leaf, neck and panicle blast were scored on all the buckets. Also grain weight at harvest was scored. Result indicated that blast pathogen from South west was most virulent. Blast pathogen from South East was the second most virulent on all the varieties of rice tested. Blast pathogens from North East and North Central were almost the same in terms of pathogenicity on all the varieties of rice tested. Blast pathogen from North West was the least virulent on all the varieties of rice tested. There was a progressive increase in pathogenicity from the day of inoculation to 4 weeks after inoculation across all the treatments. The result showed that the local varieties used in the trial holds promise for blast control and for breeding for blast resistant varieties.

Key words: Blast Pathogen, inoculum, Rice, Variety.

INTRODUCTION

Rice is a grass plant which belongs to the genus *Oryza* of the family *poaceae* (Vaughan, 1994). Two species *(Oryza sativa* and *Oryza glaberrima)* are cultivated (Crawford and Lee, 2003). Rice is the world's most important food crop based on the cultivated area and serves as a major source of calories for 40% of the world population (Heinrichs, 1992a). Most of the world rice production occurs in tropical Asia in irrigated and rainfed lowland fields (Heinrichs, 1992a). In Nigeria rice is produced in all agro-ecological zones from Sahel to coastal swamps of the country (Singh *et al.*, 1997). Nigeria produces about three million metric tons of rice annually, with harvested area of about 1.7 million hectares. Rice per capital consumption is put at 21.2kg annually (WARDA, 1996).

Rice blast caused by *Pyricularia oryzae* is now the most destructive fungal disease of rice in the West African Subregion (Fomba and Taylor, 1994). The fungus produces spot or lesions on

leaves, nodes and different parts of the panicles and the grains (Ou, 1985). The leaf spots are typically elliptical with more or less pointed ends. The centre of the spots is usually gray or whitish and the margin is usually brown or reddish brown. Fully developed lesions reach 1-1.5cm long, 0.3-0.5cm broad and usually develop a brown margin. On resistant cultivars only minute brown specks of pinhead size may be observed. Numerous spots may occur on the leaf, which may soon be killed. This is followed by the drying up of the leaf sheath. Seedling or plant at the tillering stage is often completely killed in the field.

MATERIALS AND METHOD

The experiment was conducted in the screen house of National Cereals Research Institute (NCRI) Badeggi in 2011. Badegi is located in North Central Nigeria. The blast innoculum were sourced from five locations across the agro ecology of Nigeria. North West (Wurno), North East (Damarmari), North Central (National Cereals Research Institute Badeggi) South East (Abakaliki,) and South West (Ogbomoso,). The local varieties of rice used were collected from various locations in Niger state. Also five rice blast differentials were collected form African Rice Center. The Experiment was laid out in factorial arrangement fitted into a split plot design. The experiment consists of 60 treatment combinations and replicated three times. Each of the fungus (*Magnaporthe grisea*) collected from five different rice growing regions in Nigeria, was Isolated from lesions on leaves of infected rice by conidial isolation technique (Shanta, 2000 and Awoderu, 1990). Conidial suspensions (25×10^3 spores/ml) of monoconidial culture of blast fungus, were used to inoculate the seedlings of 10 varieties of rice. Inoculation was done 2 weeks after planting (by spraying the conidial suspensions (25×10^3 spores/ml) on rice seedling). Blast scoring was done at 2, 3 and 4 weeks after inoculation for leaf blast, and at 3 weeks after heading for neck and panicle blast. Degree of infection was measured using a visual scale of 0-9 (0 = no infection, 1 = mild infection, 3 = moderate infection, 5 = high infection, 7 = severe infection and 9 = very severe infection) IRRI disease evaluation scale (1996). Disease progression was measured using the differences between the intervals of record taken (i.e, 2WKS – 4WKS). To determine the stage (s) of rice growth in which the pathogens are more virulent. Scoring was based on the number of plants and leaves infected, lesions and sizes of lesion on the leaves, necks and panicles infested (WARDA, 1999). Also data on plant height at maturity, grain weight at harvest were also taken

RESULT

Result from Table 1 shows the mean score for blast at 2, 3 and 4 weeks after inoculation. The location result showed that South West had the highest value and was significantly different from other locations at 2 WAI. The same trend was expressed at 3 and 4 WAI. Result at 3 WAI showed the highest value of 6.0. Blast collected from North East and North Central were significantly similar. They were higher that than the collection from North west and the control. At 4 WAI significant differences were observed among the treatments. The control had the lowest value of 1.60. The highest value was from the South west, followed closely by value obtained from the South east. All the locations showed significant difference from each other. Reaction of the varieties at 2 WAI showed that RAM 28 had the highest value but was not significantly different from RAM 114 and OS6, it was however different from others. At 3 WAI, RAM 28 had the highest value but it was not significantly different from TOG 80711, OS 6 and Jina. Result at 4 WAI also showed that RAM 28 had the highest value and was

significantly different from others. The interaction between location and variety were not significantly different.

Table 1: Blast mean score at 2, 3, 4 weeks after inoculation (WAI) for both location and variety

Treatment	2WAI	3WAI	4WAI
Blast Isolate From			
North West	1.17b	2.40d	3.33e
North East	1.10b	3.07c	3.80d
North Central	1.27b	3.47c	4.33c
South East	1.77b	4.67b	5.07b
South West	2.67a	6.00a	6.13a
Control	0.13c	0.93e	1.60f
S E±	**0.23**	**0.20**	**0.16**
Variety			
RAM 114	2.22ab	3.72cb	4.22bc
RAM 28	2.72a	4.67a	5.44a
TOG6711	0.61d	3.06cd	3.06e
TOG 80711	1.06cd	3.89ab	3.89dc
OS 6	2.11ab	4.33ab	5.22bc
Maitudunkurshi	0.56d	3.00cd	3.67edc
Jina	1.72cb	4.67a	4.78b
Yarkuma	0.44d	2.72d	3.78dc
Majalisa	1.06cd	2.44d	3.44ed
Zokwandami	1.00cd	1.72e	3.28f
S E ±	**0.30**	**0.26**	**0.21**
Interaction			
Blast Isolates x Varieties	**NS**	**NS**	**NS**

NS=Not significant at 5%.

Means with the same letter (s) in a column are not significantly different by Duncan Multiple range test

The result from table 2 indicates the mean values for neck and panicle blasts and the grain yield. Neck blast result showed that South east had the highest value and was significantly different from other locations. The control had the lowest value. The same trend showed also for the panicle blast. The varieties showed a susceptible value for South west but resistant reaction for the control. North West, North East and North central showed moderately resistant to moderately susceptible reaction. The grain yield result showed that the control had the highest value and was significantly different from others. Varietal reaction showed that RAM 28 had the highest value for neck blast and was significantly different from others. The same variety had the highest value for panicle blast also. The yield result were generally the same. However there were interaction between blast isolates and the varieties for neck blast. The interaction result is as shown in table 3. Result from North west showed that RAM 28 had the highest value and was significantly different from others. This trend was repeated in all the locations. However RAM 114 was significantly the same with RAM 28 the North east and North central. Control result showed lowest values in all the locations and the varieties.

Table 2: Mean Score of Neck and Panicle Blast 3 Weeks after Heading (WAH) and Grain Weight (Kg/Ha)

Treatment	Neck Blast 3 WAH	Panicle Blast 3WAH	Grains Weight at Harvest (Kg/Ha)
Blast Isolate From			
North West	2.47d	3.67d	266.69b
North East	3.53c	4.67c	210.54c
North Central	4.03c	5.33c	183.63cd
South East	5.07b	6.20b	153.75d
South West	5.87a	7.45a	100.18e
Control	1.10e	1.43e	539.31a
S E±	**0.20**	**0.27**	**16.23**
Varity			
RAM 114	5.56b	4.89bc	235.21ab
RAM 28	6.56a	6.89a	130.70d
TOG6711	2.61d	4.22dc	296.59a
TOG 80711	4.22c	4.78bc	267.36ab
OS 6	2.72d	4.39c	279.84ab
Maitudunkurshi	4.11c	5.67b	165.41cd
Jina	5.00b	5.56b	215.02cb
Yarkuma	1.78e	4.44c	281.48a

Majalisa	2.56d	3.22d	285.93a
Zokwandami	1.67e	3.89d	265.96ab
S E ±	**0.26**	**0.34**	**20.93**
Interaction			
Blast Isolates x Varieties	*****	**NS**	**NS**

* = Significant at 5%.

Means with the same letter (s) in a column are not significantly different by Duncan Multiple range test

The result of the interaction between variety and sources of innoculum is presented in table 3. Across the variety RAM 28 had the highest value and was significantly different from others in the North West. The same variety gave similar result across the locations but was significantly similar to RAM 114 with innoculum collected at North East and North Central. Result of the individual varieties across the innoculum sources showed that North West had the highest value across the varieties and was significantly different from others except for Zokwandami at South East. The overall highest value was obtained with RAM 28 (8.33), this gave a highly susceptible value. This was significantly different from all the other values in the interaction. The control had the lowest value across the varieties. Majilisa and Zokwandami (control treatment) had the lowest value of 0.33 for all the treatment combinations. However it was significantly not different from Yarkuma under the North West innoculum.

Table 3: Interaction of Blast Isolates and Variety of Rice on the Neck of Rice 3WAH

	Variety									
TREATMENT	RAM 114	RAM 28	TOG 6711	TOG 80711	OS 6	*Maitudunkurshi*	*Jina*	*Yarkuma*	*Majalisa*	*Zokwandami*
Blast Isolate										
North West	3.00ij	6.33d	1.67mn	3.00ij	1.33no	2.67jk	3.67h	0.67pq	1.00op	1.33no
North East	7.00c	7.00c	1.00op	3.00ij	2.00 lm	3.67h	4.33g	2.33kl	3.67h	1.33no
North Central.	7.00c	7.00c	3.67h	3.76h	3.33no	5.00f	5.67e	1.00op	3.00ij	1.00p
South East	7.00c	7.67b	3.67h	7.00c	4.33g	5.67e	7.00c	2.33kl	3.00ij	3.00ij
South West	7.67b	8.33a	5.00f	7.67b	5.00f	6.33d	7.67b	3.67h	4.33g	3.00ij
Control	1.67mn	3.00ij	0.67pq	1.00p	0.33q	1.33no	1.67mn	0.67 pq	0.33q	0.33q
S E±	**0.64**									

Means followed by the same letter (s) within treatment columns and between rows are not significantly different at 5% level of probability using DMRT

DISCUSSION

The effect of blast pathogens on the ten varieties of rice confirmed the detrimental effect of this disease to the rice production in Nigeria (Maji, 2000). The disease cycle is short and most damage is caused by secondary infections (Jahn *et al*., 2007). The mark difference between the control revealed the inability of these varieties to confer resistance to blast races across the locations in the country

Several blasts resistant cultivars have been developed and traditional landraces including ROK 16, 63-83, Moroberakan, Lac 23 and OS6 which possess high level of stable resistance to blast (Alluri *et al.,* 1987). These traditional varieties are often cross with Asian semi dwarf to improve yields. In a study on upland rice cultivars in Senegal, Mbodj *et al.,* (1989b) observed high level of quantitative resistance to blast in IRAT 10, IRAT 112 and IRAT 133 while Dj 8-14 and Dill-509 were moderately resistant. Among the lowland rice cultivars studied TOX 103, ITA 123, BKN 6986-38-1 and BR 51-46-5 showed high degree of partial or incomplete resistance, which was stable in time and with rice cultivars (Mbodj *et al.,* 1989b). In this study blast innoculum collected from South west was more virulent. The control had better resistant reaction to blast. The varieties showed a susceptible value for South west but resistant reaction for the control. North West, North East and North central showed moderately resistant to moderately susceptible reactions. The grain yield result showed that the control had the highest value and was significantly different from others. Varietal reaction showed that RAM 28 had the highest value for neck blast and was significantly different from others. The same variety had the highest value for panicle blast also.

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AGB07

GENOTYPE ASSESSMENT AND GROUPING OF MAIZE ON YIELD AND STABILITY OF PERFORMANCE IN A SOUTHERN GUINEA SAVANNA AGROECOLOGY OF NIGERIA

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ABSTRACT

Selection for high yield and consistency of crop performance in a particular environment are major concerns to plant breeders. Five inbred lines and two local cultivars of maize were evaluated on an experimental field across two (wet and dry) growing seasons in a Randomized Complete Block Design with three replicates. Data were collected on average kernel yield and analysed using Analysis of Variance and means were separated by Least Significant Difference at p=0.05. Genotype yields in each season showed significant differences. The genotypes were grouped on average yield performance and stability according to Francis and Kannerberg (1978) using average mean yield and coefficient of variation. Genotype MG4 in group I gave best performance with highest mean yield (3.48 t/ha) and low variability (8.08%) across growing seasons. Genotypes MG5 and MG7 had poorest performance with respective mean yields (3.06 t/ha; 3.20 t/ha) and high variability (23.95%; 29.34%) showing low stability across seasons. Genotypes gave higher yield average (3.92 t/ha) in dry season than wet season (2.73 t/ha). Genotypes variability was higher in wet season (22.41%) than dry season (17.36%). Planting of maize in late season from May to September is recommended in Ogbomoso due to better performance of genotypes.

Key words: maize, genotype, variability, growing season, mean yield, agroecology.

INTRODUCTION

Maize is regarded as that which feed the nation in India, the golden crop in Mexico and a major staple food for man and important source of animal feeds and industrial raw materials, including power and energy (Borlaug, 1988; Kim, 1993). Environment constitutes complex structures and

functions of interactions involving biotic and abiotic factors resultantly affecting maize production despite its tolerance to stress (Kim, 1993). Hence, there is need for genotype screening for better performance in a particular location for ease of cultivation and enhancing productivity. Climate as an important abiotic structure combining rainfall, temperature, humidity, photoperiod, wind and sunshine, together in their distribution characterize a geographical location differently from others. Ogbomoso in the southern guinea savanna agroecology of Nigeria has 10 hours daylight, over nine months 1,000mm bimodal annual mean rainfall, 74% humidity, 33^0C maximum and 28^0C minimum temperature, 9km/hr south-western wind trade and 101.3 kPa pressure (Idinoba, 2004). This climate favours maize cultivation in wet and dry growing seasons. Objectives of this research study were aimed at: (i) studying selected maize genotypes for yield performance across wet and dry growing seasons in Ogbomoso; (ii) grouping the genotypes based on their average yield and stability of performance across the seasons.

MATERIALS AND METHODS

The experiment was carried out at Teaching and Research Farm of Ladoke Akintola University of Technology, Ogbomoso, Oyo state (Lat. 8^0 10''N, Long. 4^0 10'' E) during the 2007 cropping season. Research materials (Table 1) used included five maize inbred lines sourced from International Institute of Tropical Agriculture, IITA, Ibadan and two local cultivars sourced from agro-marketers in Ogbomoso. All seeds were sown in three replicate of Randomized Complete Block Design in wet (April-July) and dry (May-September) seasons. Proper agronomic operations were duly observed on the field and controlled pollination was done manually. Data were collected on average kernel weight for each genotype and average yield per hectare were calculated. Yields data were analyzed using Analysis of Variance (ANOVA) and means were separated where significant by Least Significance Difference (LSD) at p=0.05. Genotypes were grouped into four classes according to Francis and Kernneberg technique, using average mean yields and coefficient of variation, viz:

Group I genotypes with above average mean yield and below average coefficient of variation.

Group II genotypes with above average mean yield and above average coefficient of variation.

Group III genotypes with below average mean yield and below average coefficient of variation.

Group IV genotypes with below average mean yield and above average coefficient of variation.

RESULTS AND DISCUSSION

Maize mean yields (Table 2) observed across wet and dry seasons for genotypes had respective ranges 1.25t/ha to 3.55 t/ha and 2.85 t/ha to 5.99 t/ha with total mean yields 2.73 t/ha and 3.94 t/ha. Coefficient of variation (CV) expressed genotypes stability of performance, CV recorded across wet and dry seasons had mean values range of 8.08% to 29.34% with average 19.89%; and respective values of 22.41% and 17.36%. Effect of seasonal factors of the environment on genotypes total average yields across the two seasons (Fig. 1) showed better performance and good stability in dry season over wet season in the agroecology. Genotype grouping technique (Table 3) had MG4 in group I with better average yield, low variability and high stability; MG2 and MG3 in group II expressed better yield, high variability and low stability; and MG5 and MG7 in group IV expressed poor yield, low variability and high stability. These observations established variation in performance of maize genotypes across seasons, due to wide genetic divergence characteristics and influence of seasonal differential factors.

CONCLUSION

Breeding methods make better tools for screening high yielding and better stable genotypes for particular environment. This study recommended planting of maize in dry season from May to September in Ogbomoso agroecology due to better performance of genotypes. Maize growers are advised to plant MG4 genotype across wet and dry seasons for better yield and stability of performance, while other genotypes should be given further research attention to improve their yield and stability to perform better in the agroecology.

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Table 1:Maize genotypes description and sources

Genotype	Name	Source	Type	Maturity
MG1	TZUTSR-Y/W	IITA	Yellow	Intermediate
MG2	OBA./TZL	IITA	White	Late
MG3	POPSR/TUUTSR	IITA	Yellow	Intermediate
MG4	DMR-ESR	IITA	White	Early

MG5	ACR-SWAN	IITA	Yellow	Late
MG6	LOCAL VAR.	OPEN MARK.	Yellow	Late
MG7	LOCAL VAR.	OPEN MARK.	Yellow	Late

Table 2: Maize genotype yields and coefficient of variation (CV) recorded across wet and dry seasons

Genotype	Wet Grain Yield (t/ha)	Dry Grain Yield (t/ha)
MG1	2.33	3.13
MG2	3.31	5.99
MG3	3.41	3.94
MG4	2.72	4.24
MG5	2.55	3.57
MG6	1.25	3.86
MG7	3.55	2.85
Total	**19.12**	**27.58**
Mean	**2.73**	**3.94**
CV (%)	**22.41**	**17.36**
LSD (P=0.05)	**0.53**	**0.52**

Table 3:Maize genotypes grouping based on average yields and stability of performance across wet and dry seasons in Ogbomoso agroecology.

Genotype	Average mean yield (t/ha)		Average coefficient of variation (%)		Group
	Above	Below	Above	Below	
MG1	-	+	-	+	III
MG2	+	-	+	-	II
MG3	+	-	+	-	II
MG4	+	-	-	+	I
MG5	-	+	+	-	IV
MG6	-	+	-	+	III
MG7	-	+	+	-	IV

Mean	3.34	19.89

+ represents value recorded

- represents nil

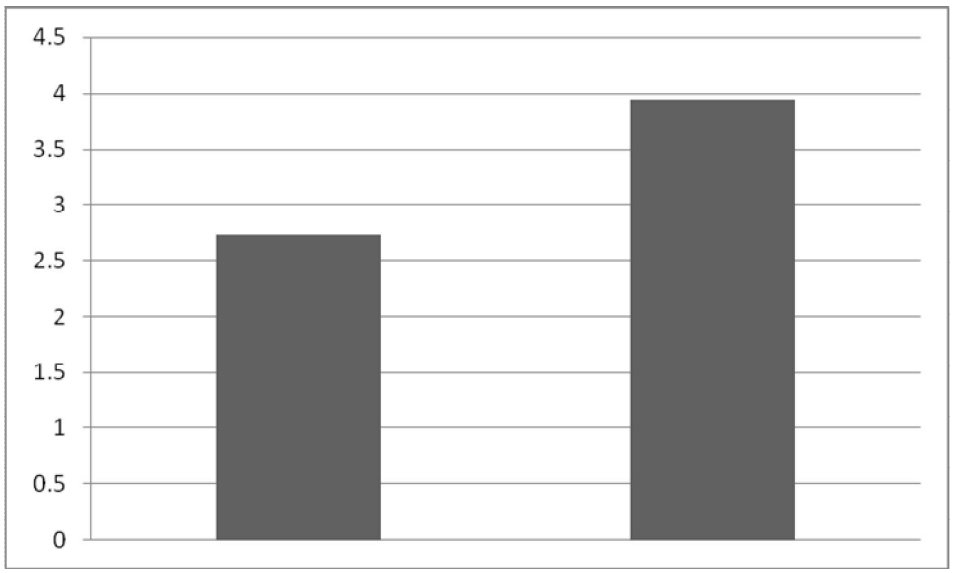

Fig. 1: Maize genotypes total average yields performance in each wet and dry season in Ogbomoso agroecology.

PGB08

CYTOTOXIC AND GENOTOXIC EVALUATION OF AQUEOUS LEAF, ROOT AND SEED EXTRACTS OF *CARICA PAPAYA* L. USING *ALLIUM* TEST.

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ABSTRACT

Cytotoxicity and genotoxicity of aqueous leaf, root and seed extracts of *Carica papaya* were assayed using *Allium cepa* root tip meristems. The onion bulbs were sprouted over water before transferring to the water extracts. The duration of treatment in diverse water extracts were 1 h, 6 h, 12 h and 24 h. The layout of the experiment was a 4 x 4 factorial in completely randomized design (CRD). The results obtained showed that the extracts significantly reduced cell reproduction. Cells entering into mitosis in all the treatments were significantly ($P \leq 0.01$) lower than the control. The abnormalities observed included: clumped prophase, sticky and star metaphase cells, anaphase with single and multiple bridges, precocious, lagging and sticky chromosomes at anaphase and sticky telophase. Others include micronuclei and cytokinetic failure leading to multiple nuclei. Treatment durations equally had adverse effects on the dividing cells. All these abnormalities are pointers to the potential toxicity of these plant extracts which has great benefits in ethno medicine. The implications of the results were discussed with a concluding statement on the need to standardize the dosages of herbal medicine to maximum benefit without adverse health effects.

Key words: *Allium* test, aqueous extracts, *Carica papaya*, cytotoxic, multiple nuclei

INTRODUCTION

Carica papaya L. belongs to the family Caricaceae. The common names are pawpaw, papaya, papaw and others. Pawpaw is a herbaceous succulent plant with self supporting stems. It has a weak soft wooden stem which is straight, cylindrical with prominent leaf scars (Purseglove, 1968). The pale green leaves are clustered near the apex of the trunk with large spiral petiole. Pawpaw has a high level of natural self-defense compounds that makes it highly resistant to insects and disease infestation. Pawpaw has been shown to be a source of vitamins like thiamine, riboflavin, ascorbic acid and important minerals like calcium, magnesium, potassium, manganese by various researchers (Ayoola and Adeyeye, 2010; Aravind *et al.*, 2013). Aravind *et al.* (2013) reported that pawpaw is a powerhouse of nutrients and is available throughout the year, being the rich source of three powerful antioxidants, Vitamins A, C and E.

Pawpaw plant parts are used in many countries in herbal medicine to treat malaria, diabetes, cardiovascular diseases, arthritis, wounds like sores and ulsers and as worm expeller (Ayoola and Adeyeye, 2010). It has been reported that whole plant parts: leaves, fruits, roots, bark, peel, seeds and pulp are all known to have medicinal properties (Aravind *et al*., 2013). The authors went further to report that all the ingredients in papaya has been said to improve cardiovascular system, protect against heart disease, heart attacks, strokes and prevent colon cancer. Pawpaw contains many biological active compounds including chymopapain and papain which is the ingredient that aids digestive system and help in the treatment of arthritis. The juice from pawpaw roots is used in some countries like Asia to ease urinary troubles while the seeds have

anti-bacterial properties and are effective against *E.coli*, *Salmonella* and *Staphylococcus* infections. The seeds also protect the kidney from toxin induced kidney failure, detoxify the liver, cure piles and typhoid, has anti-helminthic and anti-amoebic properties (Aravind *et al*., 2013).

The contraindication of this valued fruit and herbal medicine has also been reported, continued consumption of the plant especially in pregnancy could have teratogenic (abnormalities of physiological development) and abortifacient (can induce an abortion) effects. Papain could also act as prostaglandin and oxytocin. Latex can cause marked oedema and hemorrhagic placentas which leads to severe complications in pregnancy and could induce early delivery (Aravind *et al*., 2013). Seed extracts have contraceptive effects. It has been reported that women in India, Bangladesh, Pakistan, Sri Lanka and other countries have long used green papaya as an herbal medicine for contraception and abortion.

Herbal medicine has several advantages to humanity, however, extracts of herbal plants have no actual dosage in herbal medicine, and only a rough volume dosage is given by herbal practitioners. Therefore the actual concentration is difficult to ascertain. In line with the above, Amadi *et al*. (2011) reported that in Nigeria and many other developing countries, herbal preparations are sold over the counter in general stores and not in pharmaceutical stores. The indiscriminate use of such preparations might adversely affect fertility/reproductive health when used over a long period of time or when used in high doses for the treatment of other human diseases (Srivastava *et al*., 2005). Birdi *et al*. (2010) reported that toxicological evaluation of medicinal plants has often been neglected since prolonged and apparently uneventful use is usually considered as a testimony of its safety. People generally consider herbal medicines to be safe because they are 'natural' inspite of the fact that there is dearth of information on the precise nature of the constituents and on the likely effects. (Tyler, 1999; Srivastava *et al*., 2005; Amadi *et al*., 2011).

Toxicity assessments are usually done using *Allium* test. *Allium* test has been accepted as standard in monitoring and toxicity assessment of complex molecules. Medicinal plant parts have been assessed by various authors using *Allium* test and other test systems, some of which include; Water extracts of *Pulicaria crispa* (Shehab, 1979), *Teucrium pilosum* (Shehab, 1980), *Vernonia amygdalina* and *Boerhaeria diffusa* (Ene-Obong and Amadi, 1987a), *Vinca rosea* and *Borrera filiformis* (Ene-Obong and Osuala, 1990), *Azadirachta indica* (Akaneme and Amaefule, 2012) and a host of others. The aim of the present work is to assess the cytotoxicity and genotoxicity of aqueous leaf, seed and root extracts of *Carica papaya* on *Allium cepa* root tip chromosomes.

MATERIALS AND METHODS

Collection and preparation of the samples: Fresh leaves, roots and seeds of *Carica papaya* (Pawpaw) were collected from Pawpaw trees within the University of Nigeria, Nsukka staff quarters. The ripe pawpaw fruits were cut open and the seeds were collected. All the samples were dried in the oven at 40^0C and the dried plant parts were ground into powdered form using an electric grinder. The powdered samples were stored in polythene bags until use. Two hundred grams of each of the powdered samples was weighed out for extraction into 1.5 litres of water. The extraction process was by maceration and the set up was left for 24 hours before filtration, with the aid of Whatman filter paper, peforation funnel and suction pump the filterate was evaporated to dryness under reduced pressure. One gram of the aqueous extract of each of plant

parts (leaf, root and seed) was added to 100ml of distilled water. This stock was used in this study.

Fresh and healthy onion (*Allium cepa*) bulbs of the purple variety were purchased from Nsukka main market. The bulbs were sprouted over tap water in transparent plastic cups for about 6 days to ensure adequate rooting. The well rooted bulbs were transferred from the transparent plastic cups containing tap water to beakers containing the extract solutions of *C. papaya* leaves, roots and seeds. The bulbs with poor rooting were discarded and a set of three well rooted bulbs were left in the tap water to serve as control. The bulbs in the different extracts were treated for different durations. The durations of treatment ranged from 9am – 10am (1 h), 9am – 3pm (6 h), 9am – 9pm (12 h) and 9am – 9am (24 h). At the end of each treatment duration 6 – 10 roots were chopped off from each bulb. They were washed 3 times in tap water and fixed in Carnoy solution (1:3 acetic acid to absolute alcohol). All the fixed root tips were stored in refrigerator for at least 24 h before use. The fixed roots of the different treatments were collected one after the other from the refrigerator for hydrolysis and further studies. They were hydrolysed in 0.1 N hydrochloric acid for 6 – 8 minutes at 60^{o}C in a water bath. The hydrolsed root tips were washed 3 times with tap water and the milky portion was cut on a glass slide for squashing and preparation.The stain used was acetic orcein. The slides were examined under the microscope and good ones were sealed with nail varnish and photomicrographs were taken at oil immersion (X100).

The experimental design was a 4 x 4 factorial in CRD with 3 replications (Table 1). Factor A were extracts of *C. papaya* while factor B were the durations of treatment. Analysis of variance (ANOVA) using GenStat discovery edition was used to analyse the data obtained on the number of dividing cells at different mitotic phases and the number of cells with diverse abnormalities. Mean separation was done using least significant difference (LSD) where the variance ratio is significant.

RESULTS

The analysis of variance of the number of dividing cells at various mitotic phases showed significant effects of the extracts, durations of treatment and the interaction on various mitotic stages (Table 2). At prophase and metaphase, the extracts induced significant effects at 0.1% probability level while at anaphase their effects were significant at 1% probability level. It could be observed that the treatment duration affected all the mitotic stages significantly ranging from $P \leq 0.01$ to $P \leq 0.05$. The interaction between the extracts and duration of treatment also affected dividing cells at all the mitotic stages significantly at $P \leq 0.01$. In the actual number of cells at different mitotic stages, it could be observed that there is significant reduction in the number of cells that enter prophase (M phase of cell cycle) across the treatment extracts (Figure 1). As mitotic division progressed from prophase to other stages, some of the extracts had higher number of dividing cells than the control. For instance, at telophase stage the number of cells in the control treatment was 2.3, while those induced by leaf, root and seed extracts were 11.3, 9.5 and 7.8 respectively. The seed extract had significantly the least number of cells at all stages except at telophase. Treatment duration equally affected the mitotic stages significantly (Figure 1). Twenty four hours treatment duration had the least number of dividing cells in all the stages except at prophase, however, the values did not differ significantly with that at 6 h in metaphase stage.

The analysis of variance of abnormal nuclei and cytokinetic failure involved cells with micronuclei, multiple nuclei and nuclear disintegration (Table 3). The analysis showed that the extracts of *C. papaya* and durations of treatment had significant effects in the induction of abnormal and multiple nuclei in *A. cepa* cells. In cells with micronuclei both the extract and durations of treatment together with their interaction were significant at $P \leq 0.001$. In addition to inducing micronuclei; cytokinesis failure signified by binucleate, trinucleate and tetranucleate cells were also induced by the extracts at significant levels. The treatment duration and the extract x treatment duration equally induced multiple nuclei in *A. cepa* cells at varying levels of probability except at tetranucleate cells where the duration and the interaction was not significant. Only the effects of the extracts were significant ($P \leq 0.05$) in causing nuclear disintegration, the treatment durations and the interaction were not significant (Table 3).

It was equally observed that most of the dividing *A. cepa* cells treated with the extracts at different durations were abnormal (Table 4 and Plates 1 - 3). Abnormalities were rated according to their different forms as follows:

i). Prophase: clumped prophase – root extracts induced the highest value in this abnormality, disturbed prophase – the leaf extract induced the highest abnormality.

ii). Metaphase: sticky metaphase – leaf extract followed by root extract induced the highest abnormality, star metaphase was also observed (Plate 1).

iii). Anaphase: anaphase with single and multiple bridges and other forms of abnormalities – anaphase with precocious chromosomes, lagging chromosomes, sticky late anaphase and clumping chromosomes.

iv). Telophase: sticky telophase were also observed and the extracts and treatment duration had significant effects.

v). Abnormal nuclei: micronuclei – seed extract and 24 h treatment duration had the highest significant effect in inducing micronuclei (Table 4), the effect of 24 h was however, not different from that of 12 h. Some nuclei were also observed appearing like the normal ones but on a closer observation they are slightly smaller than the other normal ones (Plate 3).

vi). Cytokinetic failure: binucleate, trinucleate and tetranucleate cells were the observed effects of cytokinesis failure. The seed extracts did not induce any multiple nuclei while leaf extract induced the highest bi- and tri- nucleate cells. The effects of leaf and root extracts were not significantly different in inducing tetranucleate cells. Twelve hour treatment significantly induced the highest binucleate cells, however, the effects of treatment time was not significant as regards tetranucleate cells. One hour treatment had the highest values in inducing the following abnormalities – clumped prophase, disturbed prophase, sticky metaphase, abnormal anaphase and anaphase bridge. However, these effects were not significantly different from 12 h treatment in disturbed prophase, sticky metaphase and abnormal anaphase (Table 4 and Figure 4).

DISCUSSION

There are rising concerns over the safety of herbal medicines in many countries. The aqueous extracts of *C. Papaya* and treatment duration affected the mitotic process at different stages. The significant reduction of phase cells in all the extracts and durations of treatment as compared to control seems to suggest the adverse effects of the extracts on the interphase cells, or probably an

arrest of the cells at the interphase nucleus. It seems that the extracts had inhibitory effects on cells entering into M phase of the cell cycle leading to reduction in cell reproduction. Ene-Obong, (1991) reported that the inhibitory effects of medicinal plants extracts at interphase stage lowers cell reproduction. On the other hand, it could be possible that the extracts had effects on the cell respiration and the cells could not generate enough ATP to enter into mitosis. Similar reports include Epel, (1963) and Jain and Sarbhoy, (1987), who reported that the rate of mitosis and chromosome movement are influenced by the resultant level of ATP in a cell. The length of usage of these extracts could equally affect cell reproduction as 24 h treatment duration affected mitotic stages of *A. cepa* more than the other durations, especially at metaphase to telophase stages. The significance of treatment duration on phase index depicts the adverse effects of the extracts at long term intake, especially as it has been reported that toxicological evaluation of medicinal plants has often been neglected since prolonged and apparently uneventful use is usually considered as a testimony of its safety (Birdi *et al.*, 2010).

Most of the observed dividing cells in the extracts are abnormal. This is a pointer to cytotoxicity and genotoxicty of these extracts. Abnormal dividing cells-clumped prophase, disturbed prophase, sticky prophase, anaphase bridges and other observed anaphase abnormalities were higher in 1hr duration of treatment. It could be that there is a cell recovery mechanism as the duration of treatment increased. The first reaction of the cells in coming into contact with the extract was to divide abnormally and gradually there seems to be a switch reducing or blocking cells entering into mitosis or progressing to other stages and equally a recovery of the initial shock. Rayburn *et al*. (2002) reported that tolerance as measured by reduced chromosome stickiness did not occur until the plants were grown in very high soil aluminum saturation. This implies that cells could develop tolerance as concentration increased and probably with continued use.

Chromosome instability as triggered off by the *C. Papaya* extract lead to diverse abnormalities observed in this work. Ayoola and Adeyeye (2010) reported the presence of saponins in *C. Papaya* leaves while Okwu and Okwu (2004) in an earlier report stated that saponins are cytotoxic causing permealization of the intestine. Rayburn *et al.* (2002) reported that chromosome stickiness is defined as a chromosomal agglutination of unknown nature which results in a pycnotic or sticky appearance of chromosomes. There are several reports on the cause of chromosome stickness - chromosome stickiness could be caused by depolymerization of DNA (Abraham and Kashy, 1979); DNA condensation (Osterberg *et al.*, 1984); physical adhesion of chromosomal proteins (Patil and Bhat, 1992). There is a general consensus that stickiness reflects highly toxic and usually irreversible effect that probably leads to cell death (Liu *et al*., 1992; El-Ghamery *et al*., 2000; Tipirdamaz *et al*., 2003; Akaneme and Amaefule, 2012). Liu *et al*. (1995) in Rayburn *et al.* (2002) while testing aluminum toxicity reported severe cytological abnormalities (such as anaphase bridges) in dividing cells of onion roots resulting from chromosomal stickiness. Chromosome bridges and fragments are signs of clastogenic effects resulting in chromosome and chromatid breaks (Evandri *et al*., 2000). Hall and Giaccia (2006) equally reported that anaphase bridge is one of the 3 types of aberrations that are lethal to the cell, the other two being dicentric and ring chromosomes. Bridges have been reported to cause structural chromosome mutation (duplications and deletions in DNA double-strand) (Evandri *et al.*, 2000; El-Ghamery *et al.*, 2000).

Star metaphase and associated anaphase abnormalities classified as disturbed anaphase-multipolar anaphase, precocious chromosomes at anaphase, chromosome clumping at anaphase have been reported by other researchers on diverse medicinal plants and other complex molecules (Amer, 1965; Mercy Kulthy and Stephen, 1980; Abu and Mba, 2011; Akaneme and Amaefule, 2012). The precocious chromosomes have been attributed to unequal spindle movement where some chromosome arms are pulled towards the extremity of the pole (Stakykova *et al*., 2005; Bhatta and Sakya, 2008).

Cytokinesis is the final step in cell division. Cytokinetic failure leading to multinucleate cells have been reported as a severe deleterious effect that can lead to cancerous cells in tissues and play a major role in development of tumor cells (Normand and King, 2010). Cytokinesis is a highly ordered process requiring an intricate interplay between cytoskelectal, chromosomal and cell cycle regulatory pathways (Normand and King, 2010). The authors went further to report that cytokinesis being a highly regulated complex process, it is surprising that cytokinesis sometimes fail. The process of cytokinesis can be divided into 4 stages and each stage of cytokinesis is dependent on the proper execution of the prior stage and thus interference with any stage may result to cytokinesis failure. This explains the high level of cytokinesis failure in this work; the extracts might have interfered with the cytokinetic process at one or more stages. The interference of the extracts on the formation of cell plate (cytokinesis) could also explain the significantly higher number of cells at mitotic telophase in all the extracts than the control.

Multinuclei could result in cells with different ploidy level or number of nuclei especially in a previously uninucleate cells. Moreover, micronuclei in cells leads to aneuploidy conditions and seed extracts induced the highest number of micronuclei. Leaf and root extracts induced both micronuclei and multinucleate cells via cytokinetic failure. The inductions are higher at longer durations of treatment. This calls for caution in the consumption of this extract especially as it has been reported that *Allium* test has high correlation with other test system (Fiskesjo and Levan, 1993). Moreover, Fiskesjo (1995) reported that a positive result in *Allium* test system should be taken to indicate a potential biological hazard and that false negatives have been shown to rarely occur in either the *Allium* test or other similar plant test. The potentially high mutagenic effects of *C. Papaya* plant extracts are evidenced by the abnormalities observed in this work. Several researchers working with similar and other test systems have reported the adverse effects of Papaya plant extracts. Aravind *et al*. (2013) reported the use of green Papaya as contraception and abortion drugs among women in India, Bangladesh, Pakistan, Sri Lanka and other countries. Seed extracts have been reported to cause contraceptive effects on rats and monkeys, and equally causes toxicity-induced kidney failure (Aravind *et al*., 2013).

The acute toxicity of the leaf extracts on rat's hemoglobin (HGB), hemotocrit (HCT), red blood cells and total protein was reported by Halin *et al*. (2011) while Tarkang *et al*. (2012) reported liver and Kidney toxicity of leaf extracts on rats. All these evidences are pointers to the potential toxicity of these plant extracts which also have great benefits in ethno medicine. The results of this research, together with other similar results in plants and animal systems call for urgent need to standardize the dosages of medicinal plants extracts for the treatment of different ailments. This would go a long way in helping the maximization of their benefits with minimal side effects.

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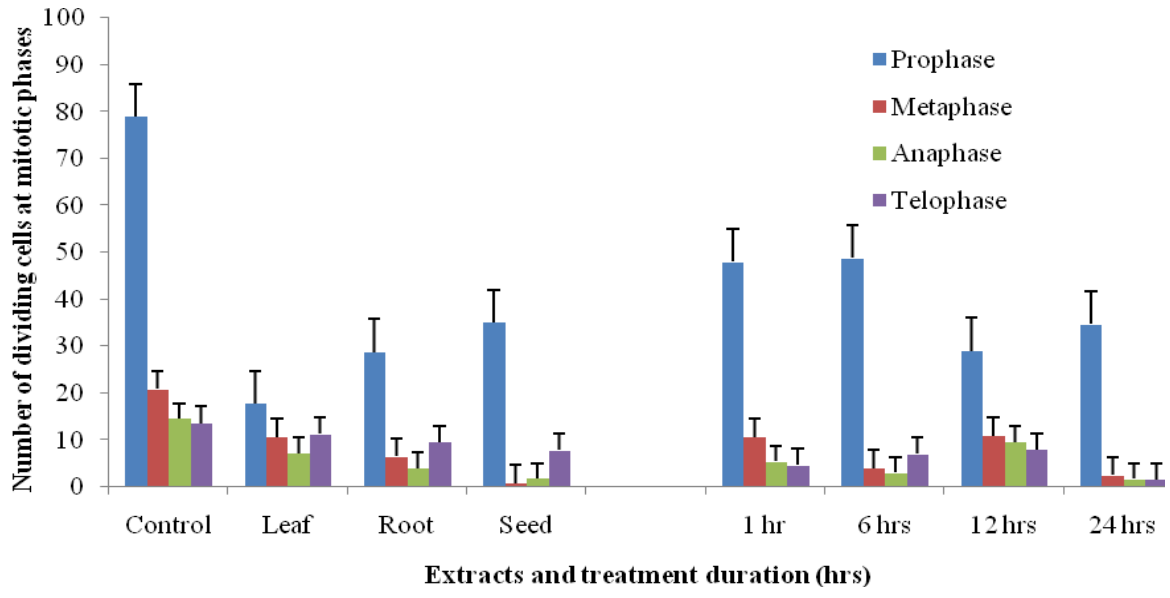

Figure1. The main effects of extracts and treatment time on mitotic phase indices.

Table 2. The analysis of variance of the number of dividing cells at various mitotic stages

Sources of variation	DF	Prophase			Metaphase			Anaphase			Telophase		
		SS	MS	VR	SS	MS	VR	SS	MS	VR	SS	MS	VR
Extracts	3	25931.1	8643.7	29.37***	721.64	240.55	10.63***	224.54	74.85	4.74**	542.2	180.73	2.13^{ns}
Durations	3	3469.9	1156.6	3.9**	684.11	228.04	10.07***	432.88	144.29	9.15***	1049.91	349.97	4.13*
Extracts x durations	9	8299.5	922.2	3.13**	619.85	68.87	3.04**	522.09	58.01	3.68**	3399.39	377.71	4.46**
Residual	32	9416.9	294.3	-	724.3	22.63	-	504.8	15.78	-	2708.89	84.65	-
Total	47	47117.5	-	-	2749.91	-	-	1684.31	-	-	7700.38	-	-

DF: Degrees of freedom; SS: Sum of squares; MS: Mean square; VR: Variance ratio; *** Significant at 0.1% probability level; ** Significant at 1% probability level; * Significant at 5% probability level, ns: Not significant

Table 3. The analysis of variance of abnormal nuclei of *A. cepa* treated with *C. papaya* leaf, root and seed aqueous extracts at four treatment durations

Sources of variation	DF	Micronuclei			Binucleate cells			Trinucleate cells			Tetranucleate cells			Nuclear disintegration		
		SS	MS	VR	SS	MS	VR	SS	MS	VR	SS	MS	VR	SS	MS	VR
Extracts	3	14992.92	4997.64	91.73***	387.0	129.0	18.16***	138.08	46.03	12.92***	58.56	19.52	5.04*	12,25	4.08	4.26*
Durations	3	4462.92	1487.64	27.31***	221.17	73.72	10.38***	65.75	21.92	6.15**	6.4	2.13	0.55 ns	4.75	1.58	1.65ns
Extracts x duration	9	27762.08	3084.68	56.62***	249.5	27.72	3.9***	224.08	24.90	6.99***	33.52	3.73	0.96 ns	14.25	1.58	1.65ns
Residual	32	1743.33	54.48		227.33	7.1		114.0	3.56		124	3.88		30.67	0.96	
Total	47	48961.25			1085.0			541.92			222.48			61.92		

DF: Degrees of freedom; SS: Sum of squares; MS: Mean square; VR: Variance ratio; *** Significant at 0.1% probability level; ** Significant at 1% probability level; * Significant at 5% probability level, ns: Not significant

Table 4. Main effects of *C. papaya* extracts and treatment duration in the induction of diverse abnormalities in *A. cepa* mitotic cells.

Extracts and Treatment Time	Clumped prophase	Disturbed prophase	Sticky metaphase	Abnormal anaphase	Anaphase bridge	Sticky telophase	Micro-nuclei	Binucleate cells	Trinucleate cells	Tetranucleate cells
Control	0	0	0	0	0	0	0	0	0	0
Leaf	1.17±0.56	7.08±2.6	8.58±2.19	6.08±2.79	0.17±0.1	2.83±0.31	24.5±4.0	6.5±1.8	4.08±1.6	2.25±0.88
Root	11.58±2.84	3.75±1.48	4.5±1.19	1.67±0.8	0.08±0.04	0.5±0.2	29.3±3.08	4.5±1.41	2.08±0.68	2.17±0.68
Seed	0	3.08±1.64	3.5±2.0	0.58±0.3	0.5±0.2	0.33±0.23	49.7±14.98	0.0	0.0	0.0
LSD =	2.15*** (P = 0.001)	3.3** (P = 0.01)	4.2* (P = 0.01)	3.7* (P = 0.05)	0.3* (P = 0.05)	1.9* (P = 0.05)	6.14*** (P = 0.001)	2.21*** (P = 0.001)	1.57*** (P = 0.001)	1.6* (P = 0.05)
1 hour	6.25±3.36	6.92±2.57	6.33±2.23	4.42±2.7	0.5±0.29	0.58±0.36	13.0±5.24	1.0±0.41	0.25±0.18	0.58±0.42
6 hours	2.58±1.22	1.0±0.7	2.42±1.6	0.17±0.09	0.3±0.01	1.5±1.0	20.2±6.55	1.58±0.66	1.5±0.85	1.25±0.83
12 hours	3.0±1.6	5.33±1.98	4.5±1.89	1.17±0.75	0.0	0.17±0.11	34.5±11.5	6.4±2.19	1.0±0.77	1.58±0.73
24 hours	0.92±0.52	0.67±0.45	2.03±1.25	1.58±1.22	0	1.42±0.83	35.8±11.56	2.0±1.07	3.42±1.5	1.0±0.49
LSD =	2.15*** P = 0.001	3.3*** (P = 0.001)	4.2 ^{NS}	3.79 ^{NS}	0.3** (P=0.01)	1.9^{NS}	6.14** (P = 0.01)	2.2** (P = 0.01)	1.57** (P = 0.01)	0.6^{NS}

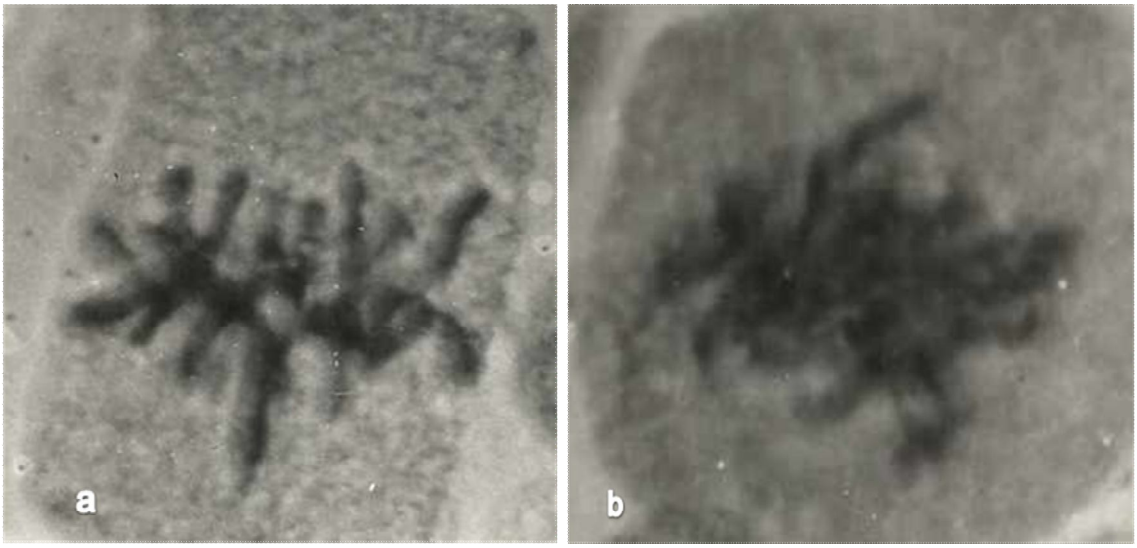

Plate 1. Abnormal metaphase cells showing: a, star metaphase; b, sticky metaphase.

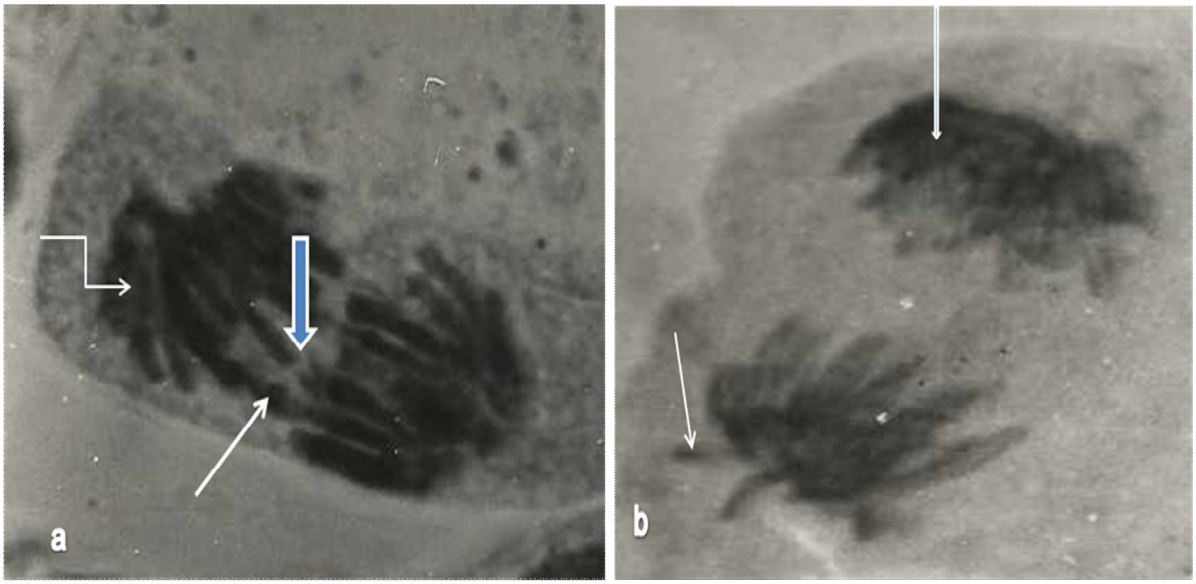

Plate 2. Abnormal anaphase cells showing: a, anaphase bridge – straight arrow, lagging chromosome/chromatid – bold arrow, sticky chromosomes at late anaphase – bent arrow; b, precocious chromosome – straight arrow, clumping chromosomes – bold arrow.

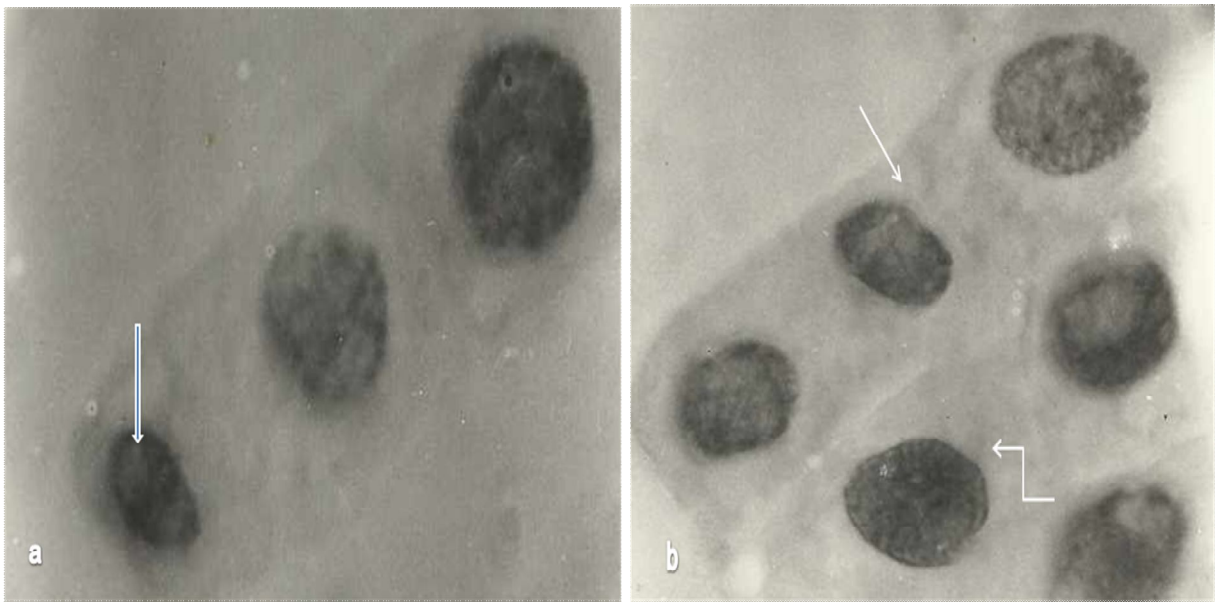

Plate 3. Cytokinetic failure showing: a, trinuclaete cell, note unequal size of the nuclei – arrowed, b, binucleate cell – bent arrow and trinuclate cell – straight arrow, also note the smallness of the centre nucleus in trinucleate cell.

PGB09

GENETIC STUDIES OF DURATION TO ANTHESIS IN SOME NIGERIA KENAF *(HIBISCUS CANNABINUS L.)* COLLECTIONS.

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ABSTRACT

Photoperiod sensitivity has been one of major constraint to kenaf production in Nigeria and countries in the tropics, because it reduces vegetative growth and therefore leads to poor yield. To understand the genetic architecture of days to flowering for kenaf, two early to mature Nigeria kenaf accessions (NHC (12)1, NHC (3)2 and two late to mature (NHC (9)2, (NHC) were crossed and F1 hybrid were planted out at a spacing of 20cm x50cm in Randomized Complete Block Design with three replicates and 16 treatments (parents, F1 and Reciprocals). Data taken on days to anthesis (DTA), height (HAH), girth (GAH), base diameter (BDAH) and fresh weight at harvest (FWAH) were analyzed. The mean square of GCA and SCA are both significant for days

to anthesis, height and girth at harvest; these indicate that the gene actions for the characters are controlled by both additive and non additive gene actions. However, fresh weight at harvest was controlled mainly by non additive gene action. GCA/SCA ratio observed in HAH and GAH are greater than 1 while it is less than 1 in DTA, BDAH and FWAH indicating that non additive is most important for the DTA, BDAH, FWAH and additive gene action is most important for HAH and GAH traits . Parent NHC (12)1, NHC (9)2 are the best general combiners (-7.47 and -6.25 respectfully) for earliness to maturity. Hybrid NHC (3)2 x NHC (9)2 are the best in combination for early to maturity with positive fibre yield component. It should therefore be used for further yield improvement in breeding programme.

Keywords: Photoperiod sensitivity, *Hibiscus cannabinus* anthesis, GCA/SCA ratio, kenaf breeding.

INTRODUCTION

Kenaf (*Hibiscus cannabinus* L.) is a member of the Malvaceae family cultivated for the soft core fiber in its stem. Kenaf originates from Africa (Chen *et al.*, 2004). Kenaf is recently used for energy and paper pulp production. Kenaf production is faced with constraints like lack of disease resistant hybrid and poor yield compared to other developed countries, Africa produces about 2.91% of the global production (FAO, 2003). Xu (1994) found predominantly additive effects determining the number of days from seedling emergence to first flowering. Liliana (2006) revealed that some dominance effects also occurred in the form of a partial dominance for early flowering. The onset of anthesis usually marks a reduction in vegetative growth which is the economically important part of kenaf (Webber *et al.*, 2002). Therefore, understanding the genetic component of days to anthesis trait is important to develop cultivars that would produce maximum fibre yield within a growing season. The objectives of these studies are; to estimate the combining ability, additive and non-additive gene effects of days to anthesis and fibre yield in selected accessions of kenaf from Nigeria.

MATERIALS AND METHODS

Matured F1 (hybrids) seed obtained from four parents (two early to mature and 2 late to mature) crossed in all possible ways in the preliminary experiment were planted in the Crop Garden of Crop Protection and Experimental biology, university of Ibadan located on latitude 7°34' and

longitude 3°54', altitude 220m, in a Randomized Complete Block Design with three replicates and 16 treatments at a spacing of 20cm x50cm. Necessary agricultural management practices were carried out when due. Data were taken on day to flowering and height, basal girth, diameter and fresh weight at harvest at about 160 days after planting. Analyses of variance were done and means were separated by least significant difference (Lsd < 0.05). Analysis of the combining ability for the experiment was done following Griffing's Method 1, where parents, F1's and reciprocals are included

RESULTS AND DISCUSSION

Mean squares for parents and their F1s (Table 1) revealed highly significant variations for all

Source	Df	DTA	HAH	BDAH	GAH	FWAH

characters. That may indicate a wide genetic variability for studied characters, which may facilitate genetic improvement using such genetic pools of kenaf.

The means squares of GCA and SCA are both significant (Table 1), for days to anthesis, height and girth at harvest. This indicates that the gene action in kenaf for these characters is controlled by both additive gene and non- additive which was similar to what Su, (2004) reported. The variance due to GCA, hence additive gene action, was more pronounced for height and girth at harvesting. Meanwhile, variance due to SCA, as an indicator of non-additive gene action, was greater for days to anthesis, basal diameter and fresh weight at harvesting.

Table 1: Mean squares from analysis of variance, general combining ability (GCA), specific combining ability (SCA) for five characters in some selected Nigeria kenaf.

Treatment	15.00	1466.82*	3142.11*	0.46*	3.47*	38059.082*
REP	2.00	6.57	1006.24	0.10	1.95	6128.34
GCA	2.00	777.90*	1712.68*	0.14	2*	6604.09
SCA	6.00	1689.51*	1218.10*	0.24	1.5*	23184.54*
GCA/SCA		0.46	1.41	0.61	1.33	0.28
Reciprocal	6.00	118.30*	829.43**	0.10	0.73	6330.00
ERROR	30.00	18.64	317.89	0.07	0.56	3819.69

*- significant at 0.05, **- significant at 0.01.

REP = Replicate, GCA = General combining ability, SCA = Specific combining ability, DTA= Days to anthesis, HAH=Height at harvest, GAH= Girth at harvest, FWAH= fresh weight at harvest and BDAH= Base diameter at harvest

Table 2: Estimates of GCA on five characters in some selected Nigeria kenaf

Parents	DTA	HAH	BDAH	GAH	DWAH
NHC(12)1	-7.47*	4.41	0.10	0.41*	27.58*
NHC(3)2	5.16*	-3.15	-0.01	-0.03	7.53
NHC(9)2	-6.25*	13.48*	0.06	0.17	-7.14
NHC 15	8.55*	-14.74*	-0.15*	-0.55*	-27.97*
SE	1.32	5.46	0.08	0.23	18.92

*- significant at 0.05

Table 3: Estimates of SCA effect and reciprocal effect on five characters in selected Nigeria kenaf genotypes.

Specific combining effects	DTA	HAH	BDAH	GAH	WAH
NHC(12)1xNHC(3)2	-8.88*	10.74	0.07	0.13	52.02
NHC(12)1xNHC(9)2	18.01*	16.17	0.18	0.32	83.49*
NHC(12)1 x NHC 15	-11.80*	16.30	0.13	0.41	21.55
NHC(3)2x NHC(9)2	-5.75*	12.58	0.33*	0.85*	91.46*
NHC(3)2x NHC 15	-18.07*	5.09	0.16	0.26	59.24
NHC(9)2x NHC 15	-13.09*	11.59	0.11	0.49	-17.76
Standard error	2.41	9.97	0.14	0.42	34.55
Reciprocal Effects					
NHC(12)1xNHC(3)2	-0.40	7.89	-0.11	-0.32	17.22
NHC(12)1xNHC(9)2	-18.02*	-20.10*	-0.23	-0.61	-99.58*
NHC(12)1 x NHC15	0.44	21.09*	0.26	0.71	39.31
NHC(3)2x NHC(9)2	-4.71	14.19	-0.01	-0.28	-2.50
NHC(3)2x NHC 15	-2.03	-19.71	0.01	0.01	-65.28
NHC(9)2x NHC 15	-1.90	31.43*	0.41*	1.07*	54.44
Standard error	3.05	12.61	0.18	0.53	43.70

*- significant at 0.05

Comparison between GCA effects associated with each parent (Table 2) revealed that NHC(3)2 and NHC 15 showed positive and highly significant, effects for days to anthesis, while it showed significant negative effect for height, base diameter and girth at harvest. NHC (12)1 has positive significant GCA in girth and weight at harvesting and NHC (9)2 has positive significant on height at harvest, Thus the negative estimates in days to anthesis and positive estimates in girth and fresh weight at harvest for NHC (12)1, and the negative estimates in days to anthesis and positive estimates in height at harvest for NHC (9)2 accessions can be used for development of hybrids with early days to maturity with high yield.

Six crosses (NHC(12)1xNHC(3)2, NHC(12)1 x NHC 15, NHC(3)2x NHC(9)2, NHC(3)2x NHC 15, NHC(9)2x NHC 15 and NHC(12)1xNHC(9)2) had negative significant SCA effects for days to anthesis (Table 3). However among all the crosses only NHC (3)2x NHC (9)2 has a significant SCA effects in base diameter, girth and fresh weight at harvest with significant negative SCA estimates for days to anthesis. In the reciprocal effect, only NHC (9)2xNHC 15 gave negative significant SCA effects in days to anthesis and positive significant values in height, girth, base diameter at harvest. Hybrids having significant positive SCA are due to favourable combinations of dominance effects when those parents are crossed

CONCLUSION

These crosses could further be explored to breed for kenaf hybrid that produce high fibre yield despite the earliness to physiological maturity in country located in the low altitude. Hybrid NHC (3)2x NHC (9)2 and NHC (12)1x NHC (9)2 was the best crosses combiners for early to maturity and high fibre yield component. It is recommended that based on the combining ability of the accessions for various traits studied, the selected accessions can be used for further heterotic breeding research

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PGB10

DEVELOPMENT OF NEW SWEETPOTATO VARIETIES: EVALUATION OF ADVANCE SWEETPOTATO BREEDING LINES AT THE UNIFORM YIELD TRIAL STAGE IN CONTRASTING AGRO-ECOLOGIES IN NIGERIA.

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ABSTRACT
In our quest to develop new sweetpotato varieties, fifteen selected promising sweetpotato lines were evaluated in three contrasting locations for their yield and yield components. The trials were established using randomized complete block design with three replications in $9m^2$ plots. Analysis of variance for genotype, location and genotype-by-location interaction

showed significant (<0.01 P<0.001) differences for number of marketable roots, marketable roots weight (kg/plot), and total roots weight (kg/plot). Genotypes NRSP/E2 and NRSP/B3 had higher mean number of marketable roots of 40.00 and 35.67 respectively compared tothe controls (TIS 87/0087 and Ex-Igbariam) with mean number of marketable roots of 32.11 and 30.33 respectively (P>0.05). Mean number of marketable roots were significantly higher at Abuja than the other two locations, while genotypes NRSP/E2 and Ex-Igbariam had the highest values for the trait at Abuja. , Line NRSP/C6 had the highest values of 12.12 and 12.40 kg/plot respectively for weight of marketable and total roots across locations. Also, the highest weight of total roots of 20.53 kg was recorded by genotype NRSP/C6 at Otobi, followed by TIS 87/0087 with 18.50 kg at the same location. The least total roots weight of 0.93 kg was recorded by NRSP/B2 at Umudike. Abuja had the highest mean total root weight across the genotypes (12.46kg/plot) while Umudike had the least total root weight (3.35kg/plot). Otobi also supported the growth of sweetpotato with a total root weight across genotypes of 11.44 kg. However, Otobi appears to correctly classified the genotypes as the good lines gave high yields while the poor lines gave poor yields. The significant (P<0.0001) correlation of mean number and weight of marketable roots with weight of total roots support the fact that the two traits are important sweetpotato yield components.

INTRODUCTION

Sweetpotato (*Ipomoea batatas* L.[Lam.]) is a dicotyledonous root crop and a member of the family *Convulvulaceæ* (Woolfe, 1992). It is the only member of *Ipomoea* of major economic importance (Woolfe, 1992). Globally, it is the 7th most important crop in terms of annual production and the third most important root and tuber crop after cassava and yam in Nigeria. China, with production figure of 75.6 million tonnes in 2011, is the largest producer of sweetpotato in the world, while Tanzania and Nigeria with annual production figures of 3.57 and 2.73 million tonnes respectively (FAOSTAT, 2013) are the second and third largest producers in the world.

Today in Nigeria, sweetpotato has become a more important root crop than it was in 1970s and 1980s. A recent (July, 2013) sweetpotato-based agro-enterprise survey (data unpublished) conducted in selected towns in Abia, Kwara, Lagos, Oyo and Plateau states indicated emerging small-scale commercial utilization of sweetpotato in the fries, crisp, chips, flour, fermented non-alcoholic beverage (Kunnu) and bread (in Ilorin alone) enterprises. These are in addition to the popular boil and eat as well as portage forms of consumption. However, cultivation of the crop in the country is still largely dominated by landraces and unproductive cultivars. To enhance the growth of these emerging enterprises, new sweetpotato varieties must dominate the production system. The development of new varieties is in cycle and the uniform yield trial (UYT) is at the tail end of the selection cycle. Yield has been identified as one of the most important farmer-preferred traits (Rees *et al.*, 2003). Any variety that will be acceptable to farmers must first be high yielding. This work was carried out in order to identify high-yielding genotypes across locations at the uniform yield trial stage.

MATERIALS AND METHODS

Fifteen sweetpotato breeding lines in advanced yield selection stage were evaluated in three locations (Umudike, Abuja and Otobi). The locations are situated within two distinct agro-

ecologies. The agro-meteorological characteristics of the three locations are presented in Table 1.

Table 1: Agro-meteorological characteristics of the three locations involved in the evaluation of the 15 sweetpotato genotypes at the uniform yield trial phase.

		Agro-meteorological characteristics						
Location	State	Longitude	Latitude	Altitude	Soil type	Total annual rainfall (mm)	Average monthly temp (^{0}C)	Agro-ecology
Umudike	Abia	$07^0$0331E	$05^0$0291'N	122 m	Ultisol	2064.10	30.2	Rain forest belt
Otobi	Benue	$08^0$0632E	$07^0$696'N	141 m	Alfisol	914.30	31.8	Guinea savannah
Nyanya	Abuja	$07^0$37'E	$09^0$04'N	426 m	Alfisol	952.52	32.5	Southern guinea savannah

Sources: *Agro-meteorological Unit, National Root Crops Research Institute, Umudike, Abia State.

The fifteen genotypes were laid out in a randomized complete block design with three replications. The plot size was $9m^2$ containing 30 plants per plot with plant spacing of 1m x 0.3m, giving plant density of 33,333 stands per hectare. NPK 15:15:15 fertilizer was applied at the rate of 400kg/hectare immediately after first weeding at four weeks after planting. Data were collected, on plot basis, on number of large (roots > 150g) roots, weight (kg/plot) of large roots, and total root yield (kg/plot). Combined analysis of variance was performed on the data using the SAS GLM procedure (SAS, 1992). Means were separated by Fisher's LSD ($_{0.05)}$. The genotypes were compared against the checks (TIS 87/0087 and Ex-Igbariam). Principal component biplot was also used to show genotype – location relationship.

RESULTS AND DISCUSSION:

New sweetpotato varieties are often bred for varied attributes. Fresh sweetpotato root yield is one of the most important traits for developing new sweetpotato varieties. The number of roots (Gasura *et al.,* 2008; Afuape *et al.,* 2011) and weight of marketable roots (i.e. large root size) (Afuape *et al.,* 2011) are some of the most important root yield components. However, the cultivation environment often influences the expression of most traits of the crop. Table 2 shows that significant ($P<0.01$ to $P<0.0001$) genotypic and location variation still existed among the fifteen genotypes for number and weight (kg/plot) for large roots, as well as the total root yield (made up of weights of large and small roots). Genotypic and location effects had been reported severally for root yield and number and weight of roots among elite genotypes of sweetpotato (Islam *et al.,* 2002; Afuape *et al.,* 2011).

Crop performance is a function of the genotype of the crop and the nature of the environment in which it is produced (Cooper and Byth, 1996). Table 3 shows that mean

number of large (>150g) roots of the advanced lines differed across and within locations. Genotype NRSP/E2 had the highest mean number of large roots of 40.44, followed by NRSP/B3 with 35.67 (P>0.05), and both were more than most of other lines. The Abuja location supported the development of more large roots than the other two locations (Otobi and Umudike). However, NRSP/E2 at Abuja had the highest mean number of large roots of 67.67 per plot.

High number of large roots seemed not to literally translate to high mean weight of the roots, and this can be so only when mean weight of roots of each genotype differ. Genotype NRSP/C6 had the highest combined mean weight of large roots of 12.12kg/plot, followed by TIS 87/0087 with mean weight of 11.25 (P>0.05) (Table 4). Comparing the locations, the Abuja location recorded the highest mean large root weight of 11.54 kg compared to 10.80 kg of Otobi (P>0.05) and 2.94 kg of Umudike (P<0.05). However, genotypes NRSP/C6 at Otobi had the highest mean large root weight of 20.33 kg/plot.

Mean total root yield is made up of mean weight of both large (>150g) and small roots (<150g). For total root yield (Table 5) across locations, genotype NRSP/C6 with yield level of 12.40 kg had the highest root mean total root yield, followed by the check TIS 87/0087 with yield level of 12.03 kg (P>0.05). Overall, NRSP/C6 had the highest yield performance of 20.53kg/plot at Otobi, followed by TIS 87/0087 with yield level of 18.50 kg. This suggests that the Otobi production environment may be better suited for commercial production of sweetpotato using specific genotypes. Both Abuja and Otobi locations were not different in their overall mean yield level across the genotypes, but both recorded higher yield than Umudike (P<0.05).

Figure 1 presents the biplot of the principal component analysis (PCA). The tool was used to show which genotype(s) were more adapted to which location(s). This tool has been used by Afuape *et al.* (2011) to show the relationship between genotypes and traits. Genotypes NRSP/F8, Ex-Igbariam NRSP/E2 and NRSP/B2 were more adapted to Abuja in root yielding ability. Genotypes NRSP/C6, TIS 87/008 and NRSP/A5 seem to be more adapted to the Otobi location, while the yield of NRSP/B3 and NRSP/OP were better supported by the Umudike location. Genotype NRSP/E3 seems to be the most stable genotype across the three locations in term of yield, while NRSP/D10 and NRSP/C7 also showed relative stability in the three locations.

CONCLUSION

The presence of genotype-by-environment interaction in the evaluation of the advanced sweetpotato breeding lines in the three locations for important traits has shown the necessity for multi-locations evaluation of breeding lines. It has afforded the opportunity for the selection of location-specific and generally adapted breeding lines for further field evaluations.

Table 2: Mean squares of the analysis of variance of yield and yield components of advanced fifteen genotypes of sweetpotato.

		Mean squares		
Sources of	Degrees of	Number of large	Weight (kg/plot)	Total root yield

variation	freedom	(>150g) roots	of large roots	(weight/plot)
Genotype	14	406.8963**	40.3294**	41.2319**
Location	2	6658.0519***	1021.5407***	1121.8531***
Replication	2	42.8741ns	11.4029ns	16.4389ns
Genotype * Location	28	320.3158**	45.0908***	48.7743***
Error	88	153.1923	11.2172	11.8417
Total	134			

Table 3: Genotype-by-location interaction means for number large roots of fifteen advanced genotypes of sweetpotato evaluated in three locations.

Genotypes	**Locations**			
	Abuja	**Otobi**	**Umudike**	**Mean Genotype)**
TIS 87/0087	46.67	36.00	1.67	32.11
NRSP/A5	32.00	29.33	13.67	25.00
NRSP/B1	41.67	13.00	20.33	25.00
NRSP/B2	37.33	21.67	5.00	21.33
NRSP/B3	48.00	32.33	26.67	35.67
NRSP/C6	29.33	36.67	12.33	26.11
NRSP/C7	26.67	23.67	10.67	20.33
NRSP/D10	30.67	26.00	15.67	24.11
NRSP/D7	18.00	8.33	17.00	14.44
NRSP/E2	67.67	44.00	9.67	40.44
NRSP/E3	36.00	20.33	19.00	25.11
Ex-Igbariam	61.67	19.67	9.67	30.33
NRSP/F8	56.67	17.33	7.67	27.22
NRSP/OP	19.33	21.67	17.67	19.80
NRSP/OP5	24.33	21.67	13.33	19.78
Mean (Location)	38.40	24.78	14.12	

$FLSD_{0.05}$ for comparing the means of genotypes across locations = 11.60

$FLSD_{0.05}$ for comparing the means of locations across genotypes = 5.19

$FLSD_{0.05}$ for comparing genotype * location means = 20.08

Table 4: Genotype-by-location interaction means for weight (kg/plot) of large roots of fifteen advanced genotypes of sweetpotato evaluated in three locations.

Genotypes	**Locations**			
	Abuja	**Otobi**	**Umudike**	**Mean Genotype)**
TIS 87/0087	13.53	17.70	2.53	11.26
NRSP/A5	11.73	15.40	2.67	9.93
NRSP/B1	11.80	3.85	4.60	6.75
NRSP/B2	13.50	10.97	0.67	8.38
NRSP/B3	13.00	12.20	5.83	10.34
NRSP/C6	11.93	20.33	4.10	12.12
NRSP/C7	9.93	13.47	2.07	8.49
NRSP/D10	9.73	11.00	3.44	8.06
NRSP/D7	3.60	2.40	4.30	3.43
NRSP/E2	15.00	10.93	1.13	9.02
NRSP/E3	14.33	9.00	4.90	9.41
Ex-Igbariam	14.47	4.37	1.53	6.79
NRSP/F8	16.00	3.60	1.13	6.91
NRSP/OP	5.2	14.87	3.33	7.80
NRSP/OP5	9.27	11.93	1.87	7.69
Mean (Location)	11.54	10.80	2.94	

$FLSD_{0.05}$ for comparing the means of genotypes across locations = 3.14

$FLSD_{0.05}$ for comparing the means of locations across genotypes = 1.40

$FLSD_{0.05}$ for comparing genotype * location means = 5.43

Table 5: Genotype-by-location interaction means for total root yield (kg/plot) of fifteen advanced genotypes of sweetpotato evaluated in three locations.

Genotypes	**Locations**			
	Abuja	**Otobi**	**Umudike**	**Mean Genotype)**
TIS 87/0087	14.37	18.50	3.23	12.03

NRSP/A5	13.13	15.82	3.37	10.77
NRSP/B1	12.50	3.97	5.08	7.18
NRSP/B2	14.47	11.40	.93	8.93
NRSP/B3	13.87	13.00	6.33	11.07
NRSP/C6	12.37	20.53	4.30	12.40
NRSP/C7	10.13	14.20	2.25	8.86
NRSP/D10	10.60	12.27	3.67	8.85
NRSP/D7	4.40	2.80	4.63	3.98
NRSP/E2	17.07	12.97	1.40	10.48
NRSP/E3	14.80	9.32	5.20	9.77
Ex-Igbariam	16.57	4.93	1.97	7.82
NRSP/F8	17.20	4.36	1.34	7.64
NRSP/OP	5.53	15.22	4.00	8.25
NRSP/OP5	9.90	12.33	2.50	8.24
Mean (Location)	12.48	11.44	3.35	

$FLSD_{0.05}$ for comparing the means of genotypes across locations = 3.22

$FLSD_{0.05}$ for comparing the means of locations across genotypes = 1.44

$FLSD_{0.05}$ for comparing genotype * location means = 5.58

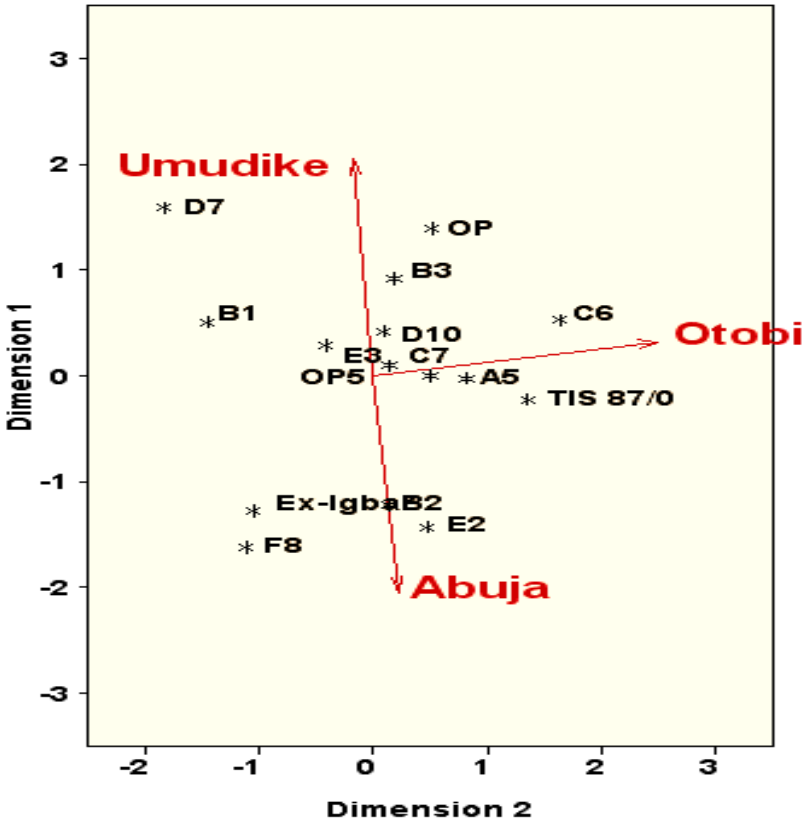

Figure 1: Principal component biplot of genotypes and locations showing genotypes that perform best in each location.

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PGB11

COMBINING ABILITY FOR MAIZE GRAIN YIELD, AGRONOMIC TRAITS AND *STRIGA HERMONTHICA* RESISTANCE UNDER ARTIFICIAL *STRIGA* INFESTATION

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ABSTRACT
A study was conducted at Institute for Agricultural Research, Samaru Teaching and Research Farm during 2011 rainy season to determine general and specific combining abilities for grain yield, agronomic traits and *Striga hermonthica* resistance in maize. Nine *Striga* resistant maize inbred lines were mated in design II fashion to produce F_1 hybrids. The results revealed that general and specific combining ability effects were low for grain yield and other morphological traits. However, parent TZEEI 19 is a good general combiner for grain yield while hybrids TZEEI 1 x TZEEI 34 and TZEEI 78 x TZEEI 19 are good specific combiners for grain yield. Also, parents TZEEI 6, TZEEI 28, TZEEI 19 and TZEEI 78 are good general combiners for earliness while hybrids TZEEI 1 x TZEE 34, TZEEI 78 x TZEEI 19 and TZEEI 78 x TZEEI 28 are good specific combiners for earliness. Simlarly, general and specific combining ability effects were low for *Striga* related traits with some parents (TZEEI 6, TZEEI 19 and TZEEI 78) and F_1 hybrids (TZEEI 1 x TZEEI 34 and TZEEI 78 x TZEEI 28) recording negative estimates, thus showing resistance to *S. hermonthica*. Therefore, these hybrids that showed good performance for grain yield, agronomic traits and *Striga hermonthica* resistance may be further tested for commercial maize production for *S. hermonthica* endemic areas of Northern Guinea Savanna.

Keywords: Combining ability, grain yield, agronomic traits, *Striga hermonthica.*

INTRODUCTION

Maize is the third most important principal cereal food crop of the world after wheat and rice (Rafique *et al*., 2004). It provides the bulk of raw materials for livestock and agro-based industries in the production of starch, corn chips, corn bread, glucose and oil (Nuhu *et al*., 2008). It is cultivated both as rainfed and under irrigation across the six agro-ecological zones of Nigeria, with Northern Nigeria accounting for more than half of the total production (NAERLS, 1987). Despite great potential of maize, *Striga*

hermonthica (Del.) Benth. is one of the most serious production constraints to maize production by small holder farmers in Sub-saharan Africa. Infestation results in substantial yield losses ranging from 10 to 100% depending on the variety and environmental conditions (Kroschel, 1999). The estimated economic loss attributable to this parasitic weed has not been quantified in recent years (Badu-Apraku *et al*., 2009), however, M'Boob (1986) reported an estimate of US $7 billion per annum. Previous research effort identified control measures such as hand pulling, crop rotation, trap and catch cropping, higher rate of fertilizer application, fallow, seed treatment, chemical control and breeding (Eplee, 1992; Shaxson and Riches, 1998; Odhiambo and Ramson, 2000). However, for most African small holder farmers, the most appropriate strategy would be one that requires limited financial outlay and could be adapted to their farming systems. One such simple, control method, is the use of resistant/tolerant variety (Badu-Apraku *et al*., 2004 and Badu-Apraku *et al*., 2005). The use of resistant variety is not only compatible with low cost input requirement of small scale farmers but also environmental friendly as it reduces the detrimental consequences of chemical sprays on non-target organisms and environment. Many researchers have used combining ability to solve maize agronomic problems. Olaoye and Bello (2009) using partial diallel to study the combining ability for grain yield among 45 maize hybrids in *Striga* endemic and non-endemic environments, revealed that SCA effects for *Striga* related characters such as *Striga* shoot count and flowering *Striga* shoot were generally low. In another study, Olakojo and Olaoye (2005) using combining ability technique reported that GCA effects of the parent inbreds for *Striga* shoot count and *Striga* syndrome rating were generally low with some parents recording negative values. The objectives of this study were (1) to determine the general and specific combining abilities of the parent inbreds for agronomic traits and resistance to *S. hermonthica* and (2) to identify maize hybrid which combine *Striga* resistance with grain yield for possible use in commercial hybrid maize production.

MATERIALS AND METHODS

The experiment was conducted at Institute for Agricultural Research Teaching and Research Farm *Striga* sick plot, Samaru during 2011 rainy season (Lat. 11^0 11', Long. 7^0 38' and 686m above sea level). A design II mating scheme was used to intermate nine *Striga* resistant maize inbred lines to produce 20 F_1 hybrids. However, because of poor performance of the parents which resulted to seed shortage only six parents and six hybrids were evaluated. The land was prepared by mechanical ploughing, harrowing and ridging at onset of the rainy season before commencement of the research. Entries which included six parents and six hybrids were made in a row plot of 3.0 x 0.75m each. The trial was laid out in 4 x 4 partially balanced lattice design replicated thrice. Two maize seeds were sown per hill. Spacing of 75 x 50cm was used to obtain plant population of about 55,333 plants per hectare. *Striga* seeds were sourced from Institute for Agricultural Research, Samaru. *Striga* inoculum was prepared by thoroughly mixing *Striga* seeds with sand at a ratio of 1:39 by weight to obtain approximately 3000 germinable seeds per gram of sand to seed mixture (Berner *et al*., 1997). One gram of sand to seed (1:1) mixture was placed in each sowing hole before maize seeds were sown on a hill. Low fertilizer was applied at the rate of 50kg N ha^{-1}, 30kg P_2O_5 ha^{-1} and 30kg K_2O ha^{-1} (NPK 20:10:10) in split doses, half of N and all of P_2O_5 and K_2O were applied at two weeks after sowing (WAS) and the remaining N was applied at 6 WAS to minimize the likelihood of N suppressing *Striga* emergence as described by Olakojo and Olaoye (2005). Weeds other than *Striga* were removed by hand pulling at 4, 8 and 10 WAS to ensure survival of emerged *Striga*. Data were collected on *Striga* related traits such as *Striga* count 1 (8WAS), *Striga* count 2 (10WAS) and number of flowering *Striga* plants. Other maize agronomic traits included plant height, days to 50% anthesis, days to 50% silking, cob weight, 100-grain weight and grain yield were measured. Data collected were subjected to design II analysis as described by Hallauer *et al*. (2010). General and specific combining abilities (GCA and SCA) were computed

using Singh and Chaudhary (1985) for six parents and six hybrids with respect to *Striga* related and maize agronomic traits.

RESULTS

General combining ability effects is presented in Table 1. Among the parents, TZEEI 78 recorded desirable GCA effects for *Striga* count 1 and *Striga* count 2 and low GCA effects for number of flowering *Striga* plants. TZEEI 1 revealed significant ($P \leq 0.05$) positive GCA effects for *Striga* count 1 and *Striga* count 2 and low GCA effects for number of flowering *Striga* plants. On the other hand, TZEEI 6 exhibited significant ($P \leq 0.05$) negative GCA for *Striga* count 1 and *Striga* count 2 and insignificant negative GCA effects for number of flowering *Striga* plants. TZEEI 19 revealed significant ($P \leq 0.05$) negative GCA effects for *Striga* count 1 and insignificant GCA effects for *Striga* count 2. It also recorded low GCA effects for number of flowering *Striga* plants. Parent TZEEI 34 exhibited low positive GCA effects for *Striga* count 1 and *Striga* count 2 and negative GCA effects for number of flowering *Striga* plants. Specific combining ability effects for *Striga* related traits are presented in Table 2. The hybrid TZEEI 78 x TZEEI 19 recorded positive SCA effect for *Striga* count 1, *Striga* count 2 and number of flowering *Striga* plants. Hybrid TZEEI 1 x TZEEI 34 revealed significant ($P \leq 0.05$) negative SCA effects for *Striga* count 1 and insignificant negative SCA effects for *Striga* count 2. It showed low positive SCA effects for number of flowering *Striga* plants. TZEEI 78 x TZEEI 34 showed low positive SCA effects for *Striga* count 1 and *Striga* count 2 and low negative SCA effects for number of flowering *Striga* plants. The hybrid TZEEI 1 x TZEEI 28 recorded low negative SCA effects for *Striga* count 2 and positive SCA effects for *Striga* count 1 and number of flowering *Striga* plants. The hybrid TZEEI 78 x TZEEI 28 revealed negative SCA effects for *Striga* count 1, *Striga* count 2 and number of flowering *Striga* plants. TZEEI 6 x TZEEI 19 exhibited positive SCA effects for *Striga* count 1 and *Striga* count 2 and low negative SCA effects for number of flowering *Striga* plants.

General combining ability effects for grain yield and maize agronomic traits are presented in Table 3. Parent TZEEI 78 recorded significant positive GCA effects for grain yield and desirable GCA effects for the other traits. TZEEI 1 revealed significant ($P \leq 0.05$) negative GCA effects for cob weight and grain yield. The same parent recorded desirable GCA effects for number of leaves per plant, days to 50% anthesis and days to 50% silking. TZEEI 6 exhibited negative GCA effects for plant height, days to 50% anthesis, cob weight and grain yield. It also revealed desirable GCA effects for days to 50% silking and 100-grain weight. Parent TZEEI 19 exhibited highly significant ($P \leq 0.01$) positive GCA effects for cob weight and grain yield. It also recorded negative GCA effects for days to 50% anthesis and days to 50% silking. TZEEI 34 depicted significant ($P \leq 0.05$) negative GCA effects for days to 50% anthesis and days to 50% silking. It recorded low positive GCA effects for plant height, cob weight, 100-grain weight and grain yield. TZEEI 28 revealed highly significant ($P \leq 0.01$) negative GCA effects for grain yield and cob weight. It exhibited significant ($P \leq 0.05$) negative GCA effects for days to 50% silking. It also revealed desirable GCA effects for plant height, number of leaves per plant, days to 50% anthesis and 100-grain weight. Specific combining ability effects are presented in Table 4. The hybrid TZEEI 78 x TZEEI 19 recorded significant ($P \leq 0.05$) positive SCA effects for cob weight and grain yield. It also showed desirable SCA effects for the other traits. Another hybrid TZEEI 1 x TZEEI 34 revealed significant positive ($P \leq 0.05$) SCA effects for grain yield and significant ($P \leq 0.05$) negative SCA for days to 50% anthesis. It exhibited desirable performance for the rest of the traits. TZEEI 1 x TZEEI 28 exhibited desirable SCA effect for grain yield, 100-grain weight and cob weight. The hybrid TZEEI 78 x TZEEI 34 recorded positive SCA effects for days to 50% anthesis and days to 50% silking. It also exhibited negative SCA effects for the other traits. The hybrid TZEEI 78 x TZEEI 28 recorded desirable SCA effects for all the characters except grain yield and cob weight. TZEEI 6 x TZEEI 19 exhibited

significant ($P \leq 0.05$) negative SCA effects for grain yield with desirable SCA effect for the rest of the traits except cob weight and 100-grain weight.

DISCUSSION

In breeding for *Striga* resistance, the lower the value obtained for *Striga* related traits the better the genotypes. The significant GCA effects recorded for *Striga* count 1 and *Striga* count 2 among the parents suggest differential reaction of the parents to *S. hermonthica* infestation. These results show that additive gene effects played a major role in the inheritance of resistance to the parasite in the parental lines. Low GCA effects exhibited for number of flowering *Striga* plants in some parents is \indicative of high resistance to *S. hermonthica* emergence and survival, consequently, a reduction in the rate of *Striga* seed multiplication in the soil. Parents TZEEI 1 with high positive GCA effects for *Striga* count 1 and *Striga* count 2 could be regarded as *S. hermonthica* susceptible, while TZEEI 6 and TZEEI 19 recorded high negative GCA effects, thus, indicating their resistance to *S. hermonthica*. The low negative GCA effects recorded in parent TZEEI 78 for *Striga* count 1 and *Striga* count 2 and low GCA effects for number of flowering *Striga* plants suggest its resistance to *S. hermonthica* infestation. In a similar study, Kim (1994) reported low GCA effect for *S. hermonthica* emergence and host-plant response for most tolerant maize inbreds and high GCA effects for the susceptible. The low negative and positive SCA effects recorded for *Striga* related traits indicated differential response of the crosses to the *Striga* related parameters. In other words, non-additive gene effects played a vital role in the inheritance of *Striga* resistance in the crosses. The highly resistant crosses are TZEEI 78 x TZEEI 19 and TZEEI 1 x TZEEI 34 which were both derived from different *Striga* resistant parents. Kim (1991) reported that the highest level of tolerance to *S. hermonthica* was obtained from crosses involving two resistant parents while most of the susceptible hybrids were from crosses involving susceptible x susceptible parents.

There were differential responses among the parent inbred lines for maize agronomic characters under *S. hermonthica* infestation. The Low GCA effects recorded for maize grain yield in some of the parents indicate poor combining ability in terms of grain yield under *Striga* infestation. However, parent TZEEI 19 exhibited highly significant positive GCA effects for grain yield and cob weight, while TZEEI 78 recorded significant GCA effects for grain yield. The results obtained indicate that these parents will be suitable for yield improvement under *Striga* infestation. Badu-Apraku and Lum (2007) reported that varieties differed significantly in grain yield under both *Striga* endemic and *Striga* free environments. Similarly, Badu-Apraku *et al.* (2008) reported low grain yield for most of the parents used in their studies under *Striga* infestation. The significant negative GCA effects for grain yield and cob weight recorded by TZEEI 1 and TZEEI 28 under *Striga* infestation indicate susceptibility to *Striga*. This further reveals poor combining ability of these parents with respect to these traits. Plant height is an important trait to be considered in maize breeding especially since very tall maize plants could lodge easily. An optimum plant height is required to prevent the crop from lodging and protect the cob from rodent damage. Thus, TZEEI 1, TZEEI 6, TZEEI 28 and TZEEI 34 are potential parents which recorded negative GCA effects for plant height. These findings corroborate Das and Islam (1994) and Hussain *et al*. (2003) who adjudged that inbred lines are good general combiners for short plant height in their studies. The significant positive GCA effects recorded for flowering traits (days to 50% anthesis and days to 50% silking) in the parent TZEEI 34 indicates probable lateness to maturity. However, TZEEI 28 showed significant negative GCA effects for days to 50% silking reveals probable earliness to maturity. Also, the negative GCA effects for flowering traits in the parents TZEEI 19, TZEEI 6 and TZEEI 78 indicate possible earliness to maturity. This further reveals the potential importance of these inbred lines in the improvement of these traits. Legesse *et al.* (2009) reported several parental inbred lines with desirable GCA effects for days to 50% silking.

Specific combining ability effect is an index to determine the importance of a particular cross combination in the exploitation of heterosis. Three hybrids (TZEEI 78 x TZEEI 34, TZEEI 78 x TZEEI 28 and TZEEI 6 x TZEEI 19) expressed negative SCA effects for grain yield which were considered undesirable. However, out of the three hybrids that revealed negative SCA effects for grain yield, TZEEI 6 x TZEEI 19 recorded significant negative SCA effect which was considered as a poor specific cross combination. The hybrid TZEEI 78 x TZEEI 19 was the best specific cross combination because it showed significant SCA effects for cob weight and grain yield. Similarly, TZEEI 1 x TZEEI 34 recorded significant positive SCA effects for grain yield. These hybrids appeared to be ideal specific combiners for grain yield under *Striga* infestation. This further suggests that non-additive gene effects played a major role in the expression of grain yield among crosses under *S. hermonthica* infestation. Olaoye and Bello (2009) reported the importance of non-additive gene effects for grain yield among crosses under *Striga* infestation in the Southern Guinea Savanna of Nigeria. Similarly, in a related study conducted in the South-western ecological zone of Nigeria, Olakojo and Olaoye (2005) revealed that non-additive gene effects played a significant role for grain yield among crosses under *S. lutea* infestation. Positive SCA effects among the following hybrids: TZEEI 1 x TZEEI 28, TZEEI 78 x TZEEI 34 and TZEEI 6 x TZEEI 19 for flowering traits indicated probable lateness to maturity of the hybrids, while those with negative effects revealed probable earliness to maturity. These results show differential response of the crosses with respect to these traits. The hybrids TZEEI 1 x TZEEI 34, TZEEI 78 x TZEEI 19 and TZEEI 78 x TZEEI 28 which showed negative SCA effects for flowering traits could be crossed with other promising germplasm to generate populations with early maturity and high yield under *Striga* infestation. Similar result was reported by Olaoye and Bello (2009). Three hybrids (TZEEI 1 x TZEEI 34, TZEEI 78 x TZEEI 19 and TZEEI 78 x TZEEI 28) showed positive SCA effects for plant height reflecting an increasing trend in plant stature. The other hybrids (TZEEI 1 x TZEEI 28, TZEEI 78 x TZEEI 34 and TZEEI 6 x TZEEI 19) revealed negative SCA effects which is considered important for lodging resistance. This result was similar to that of Sharma (2006). TZEEI 1 x TZEEI 34 and TZEEI 1 x TZEEI 28 recorded desirable SCA effects for cob weight and 100-grain weight. The hybrid TZEEI 78 x TZEEI 19 also revealed desirable SCA effects for cob weight. This indicates the importance of non-additive gene effects for yield related traits under *S. hermonthica* infestation. Dhaliwal and Sharma (1990) reported similar findings.

CONCLUSION

The results obtained from this study indicated that the general and specific combining ability effects were low for grain yield and most agronomic traits. Similarly, general and specific combining ability effects were low for *Striga* related traits with some parents (TZEEI 6, TZEEI 19 and TZEEI 78) and F_1 hybrids (TZEEI 1 x TZEEI 34 and TZEEI 78 x TZEEI 28) and recording negative estimates, thus indicating resistance to *S. hermonthica*. Also, the hybrids TZEEI 1 x TZEEI 34 and TZEEI 78 x TZEEI 19 are good specific combiners for grain yield and could be adopted for improvement of grain yield and *Striga* resistance for *S. hermonthica* endemic areas of Northern Guinea Savanna of Nigeria.

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Table 1: General combining ability effects for *Striga* related traits evaluated at Samaru during 2011 rainy season under artificial *S. hermonthica* infestation.

Parents	*Striga* count 1 (8WAS)	*Striga* count 2 (10WAS)	Number of flowering *Striga* plants
TZEEI 1	6.389*	9.389*	0.222
TZEEI 6	-6.944*	-9.111*	-1.111
TZEEI 19	-5.278*	-6.944	1.222
TZEEI 28	4.222	6.556	-0.944
TZEEI 34	1.056	0.389	-0.278
TZEEI 78	-1.944	-3.222	0.222
SE (gca effects)	2.132	3.827	1.514

* refers to significant at 0.05 probability level

Table 2: Specific combining ability effects for *Striga* related traits evaluated at Samaru during 2011 rainy season under artificial *S. hermonthica* infestation.

Hybrids	*Striga* count 1 (8WAS)	*Striga* count 2 (10WAS)	Number of flowering *Striga* Plants
TZEEI 1 x TZEEI 28	2.444	-0.389	-0.944
TZEEI 1 x TZEEI 34	-7.722*	-6.556	-0.278
TZEEI 6 x TZEEI 19	5.278	6.944	-1.222
TZEEI 78 x TZEEI 19	3.611	5.389	2.111
TZEEI 78 x TZEEI 28	-6.889	-5.778	-1.389
TZEEI 78 x TZEEI 34	3.278	0.389	-0.722
SE (sca effects)	3.692	6.629	2.621

* refers to significant at 0.05 probability level

Table 3: General combining ability effects for maize agronomic traits evaluated at Samaru during 2011 rainy season under artificial *S. hermonthica* infestation.

Parents	Plant height	Number of leaves per plant	Days to 50% anthesis	Days to 50% silking	Cob weight	100-grain weight	Grain yield
TZEEI 1	-3.127	0.111	0.667	0.333	-0.094*	-1.444	-0.397*
TZEEI 6	-3.276	-0.389	-0.167	0.833	-0.037	0.889	-0.157
TZEEI 19	4.876	-0.056	-0.667	-0.333	0.173**	1.556	0.744**
TZEEI 28	-4.686	-0.222	-0.667	-1.167*	-0.164**	-0.444	-0.704**
TZEEI 34	-0.191	0.278	1.333*	1.500*	-0.009	-1.111	-0.041
TZEEI 78	3.177	0.056	-0.389	-0.500	0.075	0.667	0.317*
SE (gca effects)	3.839	0.199	0.514	0.568	0.039	1.697	0.154

*, ** refer to significant at 0.05 and 0.01 probability levels, respectively.

Table 4: Specific combining ability effects for maize agronomic traits evaluated at Samaru during 2011 rainy season under artificial *S. hermonthica* infestation.

Hybrids	Plant height	Number of leaves per plant	Days to 50% anthesis	Days to 50% silking	Cob weight	100-grain weight	Grain yield
TZEEI 1 x TZEEI 28	-6.293	-0.278	1.167	1.000	0.044	0.111	0.184
TZEEI 1 x TZEEI 34	11.169	0.222	1.833*	-1.333	0.129	1.444	0.561*
TZEEI 6 x TZEEI 19	-4.876	0.056	0.667	0.333	-0.173	-1.556	-0.744*
TZEEI 78 x TZEEI 19	4.975	0.278	-0.111	-0.667	0.135*	0.000	0.584*
TZEEI 78 x TZEEI 28	6.243	0.111	-1.444	-0.833	-0.025	0.667	-0.104
TZEEI 78 x TZEEI 34	-11.218	-0.389	1.556	1.500	-0.110	-0.667	-0.481
SE (sca effects)	6.649	0.344	0.890	0.984	0.068	2.940	0.266

* refers to significant at 0.05 probability level.

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COMPARATIVE EFFECTS OF HORMONE-INDUCED SEEDS ON GERMINATION AND SEXUAL EXPRESSION OF FLUTED PUMPKIN (*TELFAIRIA OCCIDENTALIS* HOOK) IN THE HUMID TROPICS OF SOUTHERN NIGERIA.

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ABSTRACT
A green house and field experiments were carried out to study the comparative effects of seeds induced with different growth hormones on germination and sex expression of Fluted Pumpkin (*Telfairia occidentalis* Hook) at the Teaching and Research Farm of the Rivers State University of Science and Technology, Port Harcourt in 2010. Induction of seeds with growth hormones was done by soaking in aqueous solutions of 0, 100, 200 and 300 parts per million(ppm) each of Gibberellic acid (GA3), Indole-3- acetic acid (IAA) , Naphthalene acetic acids (NAA) and Ethrel (ET) before planting and exogenous foliar application on young leaves during vegetative growth of fluted pumpkin. The treatments significantly affected the number of days to 50% seed germination. Seeds induced with (GA_3) germinated earlier while those with NAA were the least. With 300ppm NAA significantly delayed germination by the increase in the number of days to 50% seed germination. The effects of IAA, NAA and GA_3 were similar on sex expression of the plant, while that of ET differed significantly from the rest. Induction with $GA_3$300ppm significantly reduced number of days before first male flower initiation (94days) after planting but increased the number of days before first female flower initiation. Generally, the numbers of female and male flowers vine^{-1} were significantly reduced by the hormones but GA_3 200ppm gave the highest number of 57 male flowers vine^{-1} .The highest number of 20.92 female flowers vine-$^{-1}$ obtained was with NAA300ppm which was significantly less than that of the control (23) female flowers vine^{-1}. The lowest sex ratio (M/F) of 0.30:1 was obtained with IAA300ppm**.** This reduction in sex ratio indicates favourable increase in the femaleness of induced fluted pumpkin with the benefit of increase in yield.

INTRODUCTION
In Southern Nigeria, the production and utilization of fluted pumpkin as leafy vegetable is on the increase more than ever before because of increased awareness of its nutritional and economic values, In a survey on the pattern of consumption of leafy vegetables in Nigeria, Hart *et al.* (2005) gave the per capita consumption as 91-130kg. This range was reported to be among the highest in Africa and Fluted pumpkin was also listed among the Regionally Consumed Indigenous and Traditional Leafy Vegetables for West Africa, (Smith and Pablo 2007). The seeds of fluted pumpkin are also nutritious and rich in fat (50%) making it a potential raw material for the pharmaceuticals and soap-making industry (Okoli and Mgbeogu, 1983). Furthermore, the economic and nutritional benefits of blending fluted pumpkin seed into wheat flour for bread because of its nutritional value in a Nigeria economy has been revealed (Giami *et al.*,2003).

Presently, the seeds which are the only means of propagation present some problems, which include high cost and its scarcity at the time of planting, and poor storability (Akoroda, 1990). It is a common knowledge that female plants have more luxuriant leaves and is more productive than the male plants; they also produce pods which bear seeds. The high productivity of the female plant makes it more preferred to the male by farmers particularly for seed production. It is however not yet possible to identify the sex of a seed before planting in order to ensure increased leaf, fruit and seed production.

The difficulty to differentiate between male and female plants before flower initiation in the crop also adds to the problem and limitation of fluted pumpkin production by local farmers

(Opukiri and Nwonuala, 2011). Various attempts have been made to find an alternative method of propagation and preservation such as the use of vine cuttings and the in-vitro culture of embryos of fluted pumpkin (Nwonuala, *et al.*2007). Recently, Ogbonna (2009) studied portion and type effects on sex, growth and yield of fluted pumpkin and indicated no significant differences in sex ratio. In all these cases, the desired result of identifying the sexes in order to increase the production of fluted pumpkin per unit land area has not been attained. Experimental modification of sex expression of flowering plants has been earlier reported by Heslop-Harrison, (1957). The work of Rudich *et al*., (1972) suggest that ethylene participate in the endogenous regulation of sex expression by promoting femaleness in cucumber plant

Later, Michaele *et al.* (1977) indicated that exogenous Ethephon treatment on cucumber increased the female tendency in monoecious plants, and decreased it in gynoecious ones. According to the work of Kshirsagar *et al*. (1995), plant growth regulators were confirmed to increase female flowers and yields in cucurbits. It is now well established that ethylene is the main hormonal regulator of sexual expression in the *Cucurbitaceae* family, controlling not only the sexual fate of individual floral buds, but also the female flower transition, that is, the time at which the first female flower appears and therefore the number of female flowers per plant (Susan *et al*., 2013).

The role of growth hormones on the growth and sex expression of Fluted pumpkin has not been studied in details. This research will therefore, provide useful scientific information on the effects of different plant hormones on Seed Germination and Sexual expression of fluted pumpkin thus paving the way towards the increase in productivity of the female plant.

MATERIALS AND METHODS

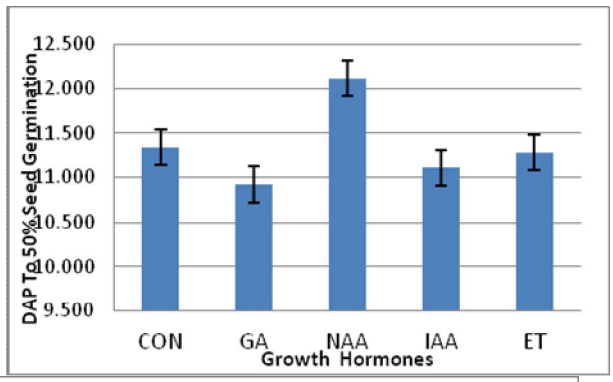
In 2009 and 2010, a Green House and field experiments were conducted at the Research and Teaching farm of the Rivers State University of Science and Technology, Port Harcourt located at latitude 4.51^0 N and longitude 7.01^0 E and 18 meters above sea level, the rain fall pattern is bimodal with peaks in June and September and ranges between 2000mm to 2484mm per annum with an annual mean temperature of 25^0 C. Experimental materials are four plant growth hormones and the seeds of fluted pumpkin obtained within four major clusters of production in Rivers State of Southern Nigeria during the farming seasons.

The experimental design was a Randomised Complete Block (RCB) with 3 replicates. The treatments consist of seeds from matured pods induced by soaking them in prepared aqueous solution of the growth hormones: - Indole-3-acetic acid (IAA), Naphthalene acetic acid (NAA), Gibberellic acid (GA_3) and 2-Chloroethyl phosphonic acid (CEPA used in the commercial form as Ethrel) each at 0, 100, 200, and 300 parts per million (ppm) for 60 minutes, drained and sundried for another 60 minutes before planting. Seeds induced with hormones were planted at a rate of one seed per hole on the ridge and with a spacing of 1 x 1m (10,000 plant ha^{-1}). Compound Fertilizer (N:P:K 15:15:20) was applied at the rate of 150g $vine^{-1}$ (750kg ha^{-1}) by ring application on the ridge, four weeks after planting. Data collated from the Greenhouse and field were subjected to statistical analysis (descriptive and bivariate statistics), using the SPSS 15.0., (2006) Evaluation version for windows.

RESULTS AND DISCUSSION

The results of effects of induction with different hormones and levels on germination in the Green house and sexual expression of Fluted pumpkin in the field are presented in Figures 1-6. The effect of hormones on number of days after planting to 50% seed germination as shown in Figure1 indicate that seeds from the control plots attained 50% germination 11days

after planting (DAP). The number of days to 50% seed germination was earlier and less than 11 DAP with GA_3 treatment, while NAA had the highest and significantly above 12 DAP.



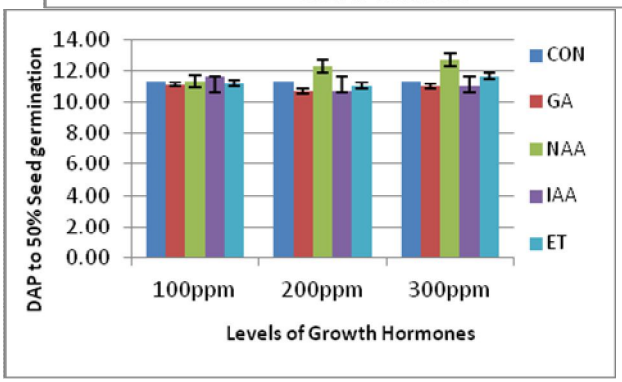


Fig1: Effect of Growth Hormones on seed germination. Fig.2: Effect of Levels of Hormone on germination.

The effect of ET and IAA were similar and differed from that of control. This result indicates that the growth hormones can delay or promote seed germination as shown by the effects of NAA and GA_3 respectively. In this experiment all the growth hormones except NAA enhanced early seed germination by reducing the number of days to 50 % seed germination below 11DAP.

The result of the effect of different levels of hormones presented in Table 2, shows that there was no significant difference at a low level of 100ppm which did not differ with that of the control. With increase in levels of hormones, however, the number of days to 50% seed germination was significantly increased above 12 DAP with NAA at 200 and 300ppm. The effects of GA_3, and IAA were similar at 200ppm which enhanced seed germination by reducing the numbers of days to 50% seed germination to less than 11DAP. At 300ppm NAA significantly increased the number of days to 50% seed germination above 12 and half DAP while GA_3 and IAA attained 50% germination in less than 11 DAP.

On sex of plant, it is basically the expression of male or female flower buds that reveals the sex of the Fluted pumpkin plant. The effect of the growth hormones and their levels as presented on Figure 3 show that the expression of male flowers occurred before the females in all the hormone treated and control plots of the field experiment. The induction of Hormones significantly increased the number of days before first the female flower expression. The mean time for the initiation of first male and female flowers according to the results of this experiment occurred 116 and 124 DAP respectively in the control plots (Fig 3). The effect of GA_3 significantly reduced the number of DAP to 106 before male flower

expression, but all the hormones significantly increased the number of DAP before the Female flower (139-146 DAP).

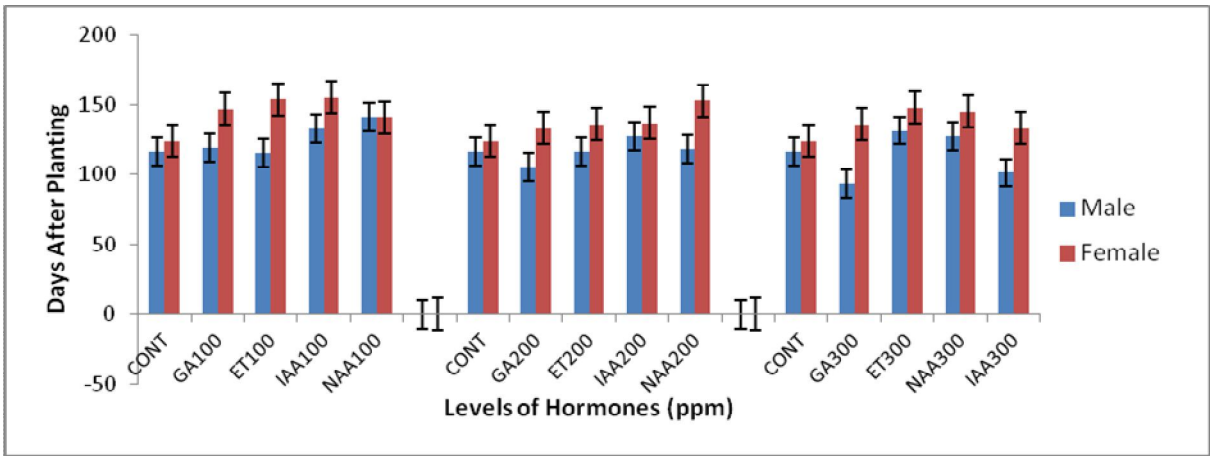


Fig 3: Effects of Hormones and their levels on Days after Planting to the Expression of Male and Female Flowers.* Ethrel is abbreviated as ET, a trade name for 2 chloroethyl phosphonic acid (CEPA)

The results indicate that increase in the level of all the hormones caused a decline in the number of DAP for both the male and female flowers, but were significantly higher than that of the control at all levels. Hormone treatment significantly reduced the number of days before first male flower initiation (94 DAP) with $GA_3$300ppm. Conversely, the same treatment significantly delayed the time before first female flower expression by increasing the number to 139 DAP (Fig 3). The longest delay in the number of days to first female flower initiation (155 DAP) was obtained with IAA300ppm.
The response by the reduction in the number of days before the first male flower initiation is observed to be in agreement with the findings of Atsmon and Tabbak (1979) that GA_3 induces staminate flower formation in cucumber plant. The response however, is of reverse effect on the expression of female flower by the extension up to 7 days beyond that of the control when compared with $GA_3$200 and IAA 300ppm, female flowers were expressed 133 DAP. This result is in contrast to the response of cucumber when treated with similar concentrations of Ethrel and NAA which resulted in delay in appearance of first male flower and enhanced that of female flower (Kshiragar et al. 1995).

The effect of the hormones and their levels on Number of flowers per vine is shown in Fig.4. Generally, the number of male flowers was more than that of female flowers at all levels of treatment and the control . Hormone induction also significantly affected number of female and male flowers vine^{-1}. Induction with $GA_3$200ppm produced 57 male flowers vine^{-1} which was the highest followed by the control. Except for $GA_3$200ppm, the number of male flowers vine^{-1} obtained with other treatments was less than that of the control. The least number of 16 male flowers was obtained with Ethrel 200ppm while the control had 39 male flowers vine^{-1}. It is observed therefore, that the number of male flowers generally decreased as the days before male flower initiation was reduced by the hormone treatments. There was also significant reduction in the number of female flowers vine^{-1} as the control plot had 23 female flowers as the highest number of flowers vine^{-1}. The least number of female flowers vine^{-1} (12.71) was obtained with GA_3 100ppm.The number of female flowers, decreased with increase in the level of the hormones to 200ppm, but NAA300ppm produced the highest number of female flowers for all the hormone treatment

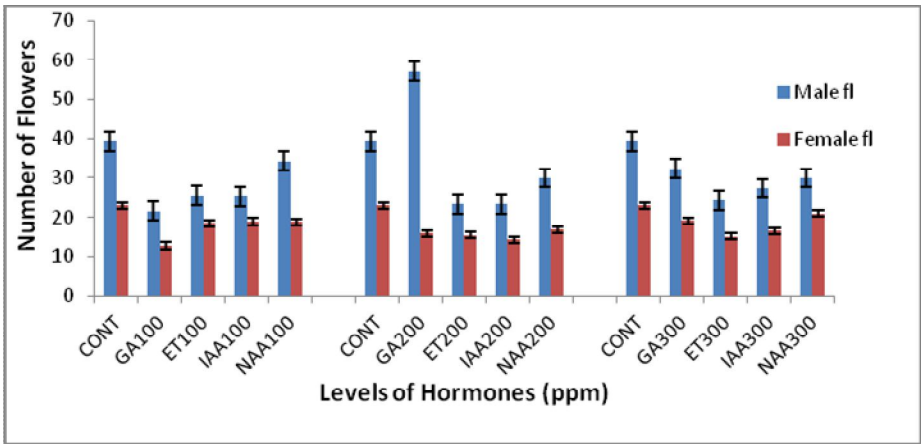


Fig 4: The Effect of Hormones and their Levels on Number of Male and Female Flower Expression

The effect of induced hormones also significantly influenced the sex ratio (M/F) of Fluted pumpkin. The graphical representation of the comparative expression of male and female plants observed in Figure 5 from the field experiment is as a result of treatment effect. The control plot had a ratio of 1 female plant to 1.28 male plants (1.28:1). It was observed that with seed induction and leaf treatment, all the hormones differ in their effect on sex ratio. The highest ratio of 1.85:1 was obtained with $GA_3$100ppm. Sex ratio however decreased with increased levels of GA_3, NAA, and IAA while the effect of Ethrel was contrary, ET300ppm (1.83:1) i.e. increase in level of ET resulted in increase in sex ratio. The lowest but the best sex ratio of 0.3:1 was obtained with IAA 300ppm which was not significantly different from those of NAA and GA_3 at 300ppm. The reduction in sex ratio indicates favourable increase in the femaleness of fluted pumpkin as a result of induced hormones.

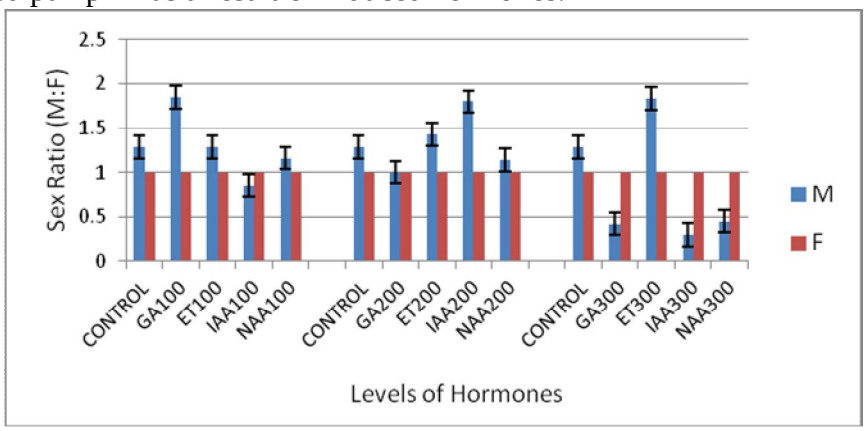


Figure 5: The effect of levels of Hormones on Sex ratio (M/F)

The ratio of male plants to female for a dioecious Fluted pumpkin plant is an indication of its productive capacity since the female plants are responsible for seed and better vegetable yields.
of Fluted Pumpkin.

CONCLUSION

The effects of GA, IAA and ET on seed germination are observed to be significant in promoting seed germination although Fluted pumpkin does not have dormancy problem but enhancement of germination has agronomic benefits. The similarity in the response to the

different hormones vary slightly, the trend however indicate similarity in the effects of GA_3, NAA, and IAA on sex expression as observed in the number of male and female flowers vine $^{-1}$; and sex ratio. With increase in levels of treatment, the reduction in sex ratio indicates favourable increase in the femaleness of Fluted pumpkin. The lowest and the best sex ratio of 0.3:1 obtained with IAA300ppm which was not significantly different from those of NAA and GA_3 at 300ppm.The response to Ethrel is contrary but is in conformity with the findings Michaele *et al.* (1977) who indicated that exogenous Ethephon treatment on cucumber increased the female tendency in monoecious plants, and decreased it in gynoecious ones.

The exogenous induction of plant hormones on the seeds and leaves of fluted pumpkin can be regarded with all certainty to influence seed germination and sexual expression towards femaleness. The implication is that the benefits of female Fluted pumpkin can be maximised through the exogenous induction of Hormones which is in no doubt directly related to increase in vegetable and pod yield.

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PGB13

STUDIES ON EXPLANTS OF PEPPER (*CAPSICUM* SP) TREATED WITH DESIGNATED HORMONES.

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ABSTRACT

A study was conducted in the Biotechnology Advanced Laboratory (BAL) of Sheda Science and Technology Complex (SHESTCO) Abuja on the growth and yield of 4 pepper varieties (*Capsicum annum* L.) cultured on Murashige and Skog (MS) basal medium supplemented with different plant growth regulators (PGRs) at various concentrations. Regenerated plant were obtained from cotyledon explants of pepper varieties by a culture procedure including rate of germination, shoot elongation, rooting capacity and fruit yield.$AgNo_3$ significantly increased the frequency of germination rate in different pepper varieties.Gibberellic acid (GA_3) was the key factor in shoot elongation.MS basal medium with indole-3-butyric acid (IBA) were easier to root for the highest numbers of root were obtained in MS with Nicotinic acid and fruit yield. An efficient protocol for regeneration of pepper through economically viable explants of indigenous pepper varieties was established.

INTRODUCTION

Pepper (*Capsicum specie* L.) an economically important vegetable and spice crop worldwide, is the fruit of plants from the genus, Capsicum, member of the nightshade family, Solanaceae. The genus Capsicum consists of approximately 22 wild species and 5 domesticated species (Bosland, 1994), domesticated for vegetable and industrial (Oleoresin and Capsaicin) purposes. Pepper is widely cultivated throughout the world, mainly in Asia, South and North America and part of Africa According to Contreras Padilla(Yahia, 1998; Kumar *et al.*,2006).

The propagation of pepper through seeds is further restricted by short span of viability and low germination rate. Since the plants also lack natural vegetative propagation, tissue culture methods provide a novel way for the asexual multiplication of pepper plant (Morrison *et al.*,

2004). Tissue culture technique in pepper, one of the most important vegetable crops in the world, lag behind most other vegetable crops, mainly due to its recalcitrance to regeneration (Diaz *et al.*, 2000). Low differentiation frequency, difficulty in shoot elongation, and low response (Dabauza *et al.*, 2001), are main barriers to the development of pepper gene engineering. This study project describes the development of a simple and efficient procedure for plant regeneration, in a PGRs medium, applicable to different cultivars of pepper. In addition he study aimed to study the efficiency of selected hormones and create variability in local varieties of pepper in Keffi through *in vitro* culture.

MATERIALS AND METHODS

The study was conducted in the Biotechnology Advanced Laboratory (BAL) of Sheda Science and Technology Complex (SHESTCO), Abuja.

Local seeds of pepper varieties: Atarugu, Shumbo, Borkonu Kanana and Tatasai were commercially, obtained from Keffi Market at Keffi Local Government Area of Nasarawa State.

Plate 1: Local seed of pepper from Keffi market

1mg/ml of $AgNO_3$ and 0.1mg/ml each of IBA, GA_3 and Nicotinic acid were prepared for the study. Murashige and Skoog (MS) basal media were prepared in four places using 1L (1000ml) beaker each, about 500ml of distilled water was poured into each of the beaker and placed on a magnetic stirrer with the magnetic bar inside the water. Four different media were prepared for this study. 1L each of Murashigea and Skoog basal medium were prepared into four places, 50ml/L of Macro salt + 5ml/L of micro salt + 30g/L of sucrose and 2.8g/L of Agar (geltrite) were dissolved into each of the beaker one after the other. pH of 5.8 were taken, using 1M hydrochloric acid (HCL) or 1M sodium hydroxide (NaOH). The media was made up to 1L (1000ml) in a graduated measuring cylinder using distilled water, each of 1L media prepared were divided into 4 (250ms each), different concentrations of the plant growth hormones were added into each of the 250mls media as follows: 0.3ml, 1.3ml, 2.5ml and 3.8ml of IBA were added into each of 250ml of the MS medium.

1.5ml, 2ml, 2.5ml and 3ml of Nicotinic acid were added into each of the 250ml of 1L MS medium. 0.5ml, 1ml, 1.2ml and 2ml of $AgNO_3$ were added into each of 250ml of the 1L MS medium and 2.5ml, 3.8ml, 5ml and 6.3ml of GA_3 were added into each of 250ml of the 1L MS medium. Each 250mls medium were poured into culture bottles, the media were

sterilized by autoclaving for 15 minutes at 121^{o}C and a pressure of 1.05kg/cm^{2} (Merck, 2005), and transferred into biosafety cabinate to cool for culturing.

Plate 2: Prepared media for study

Local seeds of pepper varieties were washed under running tap to remove dirts, using morning fresh, seeds were soaked in worm water for 10 minutes due to its recalcitrance, under the laminar flow hood, seeds were transferred into a sterile flask and soaked in 70% ethanol for 10 seconds, the ethanol were decanted and the seeds were rinsed thoroughly, and were immersed in 20% sodium hypochloride (NaOCl) for 10 minutes, 2 drops of tween 20 were added and rinsed three (3) times with sterile distilled water, the seeds were picked wit autoclaved flamed forceps (sterile) and placed on the cutting board to dry.

Under the biosafety cabinate, my hands were sterilized with absolute ethanol and the whole hood was swamped with absolute ethanol. The equipments used: blade holder, scalpel and forceps all were in a dip containing 70% ethanol and kept always in the laminar flow hood. The spirit lamp was lighted which further sterilized the laminar flow hood. Sterilized seeds were cultured into the prepared medium (Murashige *et al.,* 1962). Cultures were kept for 3 days under continuous dark, then transferred to 16 hours photoperiod per day at light intensity of 17.7μ mol/m^{2}/s were provided by cool white fluorescent tubes and temperature were set at 25^{o}C.

Cotyledons of seedlings after germination without petiole and apical parts were cut into small parts say 0.25cm^{2}. Explants were cultured into ordinary MS media (control) and MS supplemented with each of the growth hormones (treatment) that is; IBA, GA_3, $AgNO_3$ and Nicotinic acid at a specific concentration. Explants were subcultured at two weeks intervals into the same medium (Dabauza and Pena, 2001). Explants with roots were acclimatized for 48 hours after washing off the Agar (gelrite) with deionized water to pots with a mixture of substrate and perlite (5:1) in a screen house and transferred into green house, were they developed into normal plants and bearing normal fruits.

Plate 3: Cultures kept in the dark

Plate 4: Geminated seeds after 2 weeks of culture

Data was collected for g, after two weeks after planting in pots, Shoot elongation after six weeks after planting in pots, Rooting capacity (number of roots) after four week after planting in pots and fruit yield after eight weeks after planting in pots. Mean and mean effect of the result were calculated and subjected to analysis of variance using (ANOVA), treatment means were separated using the least significant difference (LSD) at p=0.05.

RESULTS

Table 1: Efficacy of PGRs (mg/ml) on germination of different pepper varieties (%).

Trt	MS	MS+IBA				MS+GA_3				MS+$AgNo_3$				MS+Nicotinic acid			
	0.0	0.3	1.3	2.5	3.8	2.5	3.8	5.0	6.3	0.5	1.0	1.2	2.0	1.5	2.0	2.5	3.0
Ata	4.7	8.7	8.3	14.0	9.7	7.0	12.7	13.3	9.3	8.7	16.7	12.0	10.0	15.3	8.7	9.0	9.0
Bor	6.0	8.3	8.3	13.7	8.0	8.7	10.7	10.7	8.3	10.3	16.0	11.7	10.3	13.3	9.3	10.0	9.7
Sh	5.3	6.7	7.0	11.0	9.3	7.7	9.7	10.7	10.7	9.7	15.3	11.3	9.7	12.7	8.3	9.7	9.3
Ta	4.3	6.0	5.3	10.3	8.7	8.7	9.3	9.3	8.3	9.0	14.7	12.3	10.0	11.7	8.7	8.7	8.0

$LSD_{0.05}$ =1.50

Trt= Treatment, Ata = Atarugu, Bor = Borkonu, Sh = Shombo, Ta = Tatashe

Any difference between a pair of treatment mean, that is higher than 1.50 is considered to be significant at 5% level.

The result showed that there is significant different among treatment among treatment means

Table 2: Efficacy of PGRs (mg/ml) on rooting capacity (number) of different pepper varieties (%)

Trt	MS	MS+IBA				MS+GA_3				MS+$AgNo_3$				MS+Nicotinic acid			
	0.0	0.3	1.3	2.5	3.8	2.5	3.8	5.0	6.3	0.5	1.0	1.2	2.0	1.5	2.0	2.5	3.0
Ata	3.0	6.3	6.0	7.3	5.7	6.0	6.7	7.0	9.7	5.0	6.3	7.3	7.7	5.3	6.7	7.7	6.0
Bor	3.0	5.7	5.7	6.7	5.0	5.0	5.0	9.0	9.3	4.0	4.7	4.3	5.3	4.7	5.0	6.0	6.0
Sh	3.0	4.0	4.7	5.0	4.7	4.7	6.3	8.0	8.7	4.7	5.0	5.3	6.0	4.3	5.7	7.3	6.7
Ta	4.0	4.3	5.3	6.3	4.3	7.0	8.0	8.0	6.3	4.0	6.0	5.3	7.0	3.7	5.7	7.0	7.3

$LSD_{0.05}$ = 0.46

Trt= Treatment, Ata = Atarugu, Bor = Borkonu, Sh = Shombo, Ta = Tatashe

Any difference between a pair of treatment mean, that is higher than 0.46 is considered to be significant at 5% level.

The result showed that there is significant different among treatment among treatment means.

Table 3: Efficacy of PGRs (mg/ml) on shoot elongation of different pepper varieties (cm)

Trt	MS	MS+IBA				MS+GA_3				MS+$AgNo_3$				MS+Nicotinic ac		
	0.0	0.3	1.3	2.5	3.8	2.5	3.8	5.0	6.3	0.5	1.0	1.2	2.0	1.5	2.0	2.5

Ata	17.7	26.6	27.9	28.3	24.5	32.0	32.8	57.7	39.7	42.9	54.0	39.3	31.9	25.4	27.2	28.9
Bor	17.7	25.4	26.3	29.5	26.5	35.8	46.7	62.6	52.6	42.0	56.0	39.7	33.5	34.2	30.5	30.5
Sh	17.7	26.7	21.8	31.8	29.1	46.4	49.5	57.3	50.3	36.3	52.7	39.7	33.5	32.6	24.7	25.9
Ta	17.7	20.7	23.3	20.0	30.7	32.7	39.8	32.9	39.2	51.7	41.3	26.9	24.2	20.1	22.3	22.3

$LSD_{0.05} = 0.46$

Trt= Treatment, Ata = Atarugu, Bor = Borkonu, Sh = Shombo, Ta = Tatashe

Any difference between a pair of treatment mean, that is higher than 0.46 is considered to be significant at 5% level.

The result showed that there is significant different among treatment among treatment means.

Table 4: Efficacy of PGRs (mg/ml) on number of fruit yield per pepper variety (%)

Trt	MS	MS + IBA				MS + GA_3				MS + $AgNo_3$				MS+Nicotinic acid			
	0.0	0.3	1.3	2.5	3.8	2.5	3.8	5.0	6.3	0.5	1.0	1.2	2.0	1.5	2.0	2.5	3.0
Ata	2.7	4.3	9.3	11.3	7.7	5.0	6.7	8.7	4.0	11.0	9.0	6.7	5.0	6.0	8.0	15.7	11.3
Bor	2.7	5.3	13.0	15.7	15.7	10.0	11.0	16.0	8.7	18.7	5.0	5.0	6.0	8.0	9.7	22.0	14.7
Sh	2.7	6.0	8.3	11.3	9.7	7.0	7.7	9.3	6.3	9.3	7.0	6.0	7.0	5.3	5.7	9.3	7.0
Ta	2.7	5.0	6.1	7.7	7.0	4.0	4.7	8.0	5.3	4.0	4.0	6.3	8.0	5.0	6.7	8.3	8.0

$LSD_{0.05}$ =0.61

Trt= Treatment, Ata = Atarugu, Bor = Borkonu, Sh = Shombo, Ta = Tatashe

Any difference between a pair of treatment mean that is higher than 0.61is considered to be highly significant at 5% level.

The result showed that there is significant different among treatment among treatment means.

DISCUSSION

The results of the study revealed that treatments significantly affected germination of pepper varieties ($p<0.05$). IBA showed the highest number of germination at concentration of 2.5ml in all pepper varieties, GA_3 showed highest number of germination in concentration of 5ml in Atarugu, 3.8ml concentration in Tatashi, Borkonu and Shumbo probably because of the variation in pepper type. In Nicotinic acid, germination rate was highest in concentration of 1.5ml on Borkonu, Shumbo and Tatashi but showed highest yield of germination on Atarugu at 2.5ml concentration and in $AgNO_3$, the highest yield of germination rate of the four pepper varieties was obtained in 1ml concentration of $AgNO_3$.

The shoot elongation of pepper varieties was obtained in Basal medium supplemented with different concentration of IBA but the highest yield of elongated shoots in IBA was obtained in 2.5ml concentration in the four pepper varieties which is in accordance with those reported in some studies (Dabauze and Pena, 2001; Peddaboina *et al.,* 2006; Guadalupe *et al.,* 2009).

GA_3 also induced shoot elongation in all pepper varieties and the best result was obtained with the medium supplemented with 5ml GA_3 in all pepper varieties.

$AgNO_3$ also promoted shoot elongation of the four pepper varieties at different concentrations but the highest elongated shoot were obtained at concentration of 1ml $AgNO_3$ in all the pepper types which is in agreement with (Chen Qin *et al.,* 2005; Mezghani *et al.,* 2007; Ashrafuzzaman *et al.,* 2009) that found Ms with GA_3 or $AgNO_3$ to be the best elongation medium. Nicotinic and also showed significant variation in the promotion of shoot elongation of the pepper varieties at different concentration, that is in Atarugu, the highest yield of elongated shoot was obtained from concentration 3ml Nicotonic acidic, while inn Borkonu, Shumbo and Tatashi, the highest shoot elongation was obtained from concentration of 1.5ml Nicotinic acid (Chen Qin *et al.,* 2005).

On the basis of rooting capacity, the four treatments significantly ($p<0.05$) promoted the roots of the pepper varieties at different concentration though some concentrations showed highest yield than others. The highest yield of roots were obtain in concentration 2.5ml IBA, 6.3ml GA_3 on Atarugu, Borkonu, Shumbo and 5ml GA_3 on Tatashi, 2.5ml Nitotinic acid on Atarugu and Shumbo, 3ml Nitotinic acid on Tatashi and Borkonu.

Plate 5: Roots of explants

Plate 6: Roots of explants

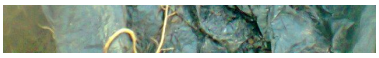

Plate 7: Elongated shoot of explants in screen house

Plate 8: Some explants with fruits

$AgNO_3$ on the other hand significantly promoted rooting ($p<0.05$) capacity in all pepper types but the highest root was obtained on 2ml $AgNO_3$ concentration.

On the basis of fruit yield, the four treatments significantly promoted ($p<0.05$) the yield of pepper fruits in the pepper types though at some concentration, the yield was higher than others. IBA gave the highest yield at concentration 2.5ml in all pepper types, in treatment with GA_3, the highest number of fruit was observed at 5ml GA_3 concentration, in treatment with Nicotinic acid, the highest number of fruit was observed at concentration 2.5ml in Atarugu, Shumbo and Tatashi, and at 3ml concentration on Brokonu. $AgNO_3$ also had the highest number of fruit observed at concentration 0.5ml on Atarugu, Brokonu and Shumbo and showed a difference at higher yield in Tatashi at 8ml $AgNO_3$ concentration which could be due to pepper type.

Overall findings of the present study are significant in obtaining the maximum regeneration or yield with proper concentration of growth regulator.

CONCLUSION

In conclusion, four the local pepper varieties were found to regenerate on proper medium, but they have difference in differentiation rates and yields resulting from gene type, explants type, seedling stage and ingredients in the media (Dong Zhaolong, 2003). The best formula

for all the medium used for germination test in this study is MS + 1ml $AgNO_3$ which made explants germinate and differentiate at high rates with good development.

Hyde *et al.,* (1996) observed that $AgNO_3$ influenced shoot induction of two cultivars. Explants were not able to elongate at high rate in the medium containing only MS without plant regulators, $AgNO_3$ was optimum in all pepper varieties, in order to confirm whether the action of $AgNO_3$ is affected by gene type or not, $AgNO_3$ was regarded as an induction promotion factor added to the medium. According to (Van *et al.*, 1989), $AgNO_3$ was an ethylene inhibitor. Ethylene suppresses callus to differentiate and $AgNO_3$ climates the ethylene action, which in return favours explants differentiation.

In the present study, GA_3 promoted shoot elongation that is to say GA_3 is an elongation – promotion factor. Though work has been carried out on pepper treated with different growth hormone, no work has been done on local peppers in Keffi, I therefore recommend that more work should be carried out to improve on the invitro yield and propagation of local pepper varieties in Keffi.

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PGB14

SCREENING OF COWPEA LINES FOR DROUGHT TOLERANCE

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ABSTRACT

Thirty nine cowpea lines were screened for drought tolerance to provide information on cowpea lines that can be used for genetic improvement of the acceptable varieties. The experiment was carried out using wooden boxes filled with top soil. Cowpea lines were

planted in three replications and the seedlings were watered daily using a small watering can of four litres for two weeks until partial emergence of the first trifoliate leaves of all the varieties was observed. Thereafter, watering was stopped for thirty five days and wilted plants in each variety were counted daily. Watering was resumed for fourteen days to ascertain regeneration potentials of each variety. Significant differences were observed among the cowpea lines for drought tolerance Stress effect was first noticed on the unifoliate leaves twelve days after watering was stopped, followed by the emerging trifoliates and finally the growing tip dried. Wilting percentage at different days after termination of watering indicated TVx 3236, NG/SA/07/132 and IT95K-193-12 to be the most susceptible to drought. The recovery percentage after watering ranged from 0% for NG/SA/01/09/004 to 100 % for IT81D-994 and Oloyin. All the cowpea lines were grouped into three. Group 1 comprises three lines (TVx 3236, NG/SA/07/130 and NG/SA/01/09/004) which are highly drought susceptible while Group 2 and 3 comprise of 14 and 22 lines respectively that were tolerant at varying degrees. The screening has provided information on cowpea lines that can be used in breeding for drought tolerant cowpea varieties.

Keywords: Cowpea, drought tolerance, screen house.

INTRODUCTION

Cowpea (*Vigna unguiculata (L.) Walp*) belongs to the family *Fabaceae* and sub family papilionoideae. It is indigenous to West Africa where its cultivation was taken to other part of the world such as Latin America, Europe and Asia. It is popularly known as beans and grows best in dry area of the Northern part of West Africa (Thomas, 2005). It is one of the most important food legumes in the tropic and sub-tropic regions of Africa because it is a major source of protein, minerals and vitamins in daily human diets and are equally important as nutritious fodder for livestock (Singh *et al.*, 1997).

In spite of several research work conducted on cowpea improvement, cowpea production is still low when compared to production potentials of the crop in Nigeria. Field research has indicated that the potential yield of cowpea can go up to 3,000kg/ha if most of the production constraints are addressed. Among the factors militating against cowpea production is low yield caused by insect pests; diseases; parasitic flowering weeds and drought. Cowpea is relatively sensitive to soil water deficit. Cowpea responds differently to water stress through leaf area reduction, delay in reproductive cycle or by developing a deep root system depending on timing and the magnitude of the water deficit (Gwathmey and Hall, 1992). Recent global warming and climate change has been reported to cause reduction in the potential yield of so many crops including cowpea. Drought tolerance is defined as the ability of plants to live, grow and yield satisfactorily with limited soil water supply or under periodic water deficiencies (Ashley, 1993). The development of cowpea cultivars with enhanced levels of drought tolerance is necessary in Nigeria but only a few studies have been reported in the selection of cowpea varieties regarding genetic variability for drought tolerance among cowpea lines and cultivated varieties grown in Nigeria. It is based on this fact that this study was set to screen some cowpea lines for drought tolerance using simple screening method for shoot drought tolerance to identify cowpea lines that are drought tolerant and can be used for genetic improvement of the acceptable varieties.

MATERIALS AND METHODS

Thirty nine cowpea lines were collected from three Institutions namely: International Institute of Tropical Agriculture (IITA), Institute of Agricultural Research and Training, Ibadan (I.A.R. &T.) and National Centre of Genetic Resources and Biotechnology, Ibadan (NACGRAB). The cowpea lines, according to the Institutions were collected from different

parts of the country. List of the cowpea lines, seed coat colour and their sources are presented in Table 1.

Table 1: List of cowpea lines used for the experiment, their seed coat colour and sources

No	**Cowpea Lines**	**Seed coat colour**	**Source**
1	1T93K-452-1	White	IITA
2	NG/SA/07/167	White	NACGRAB
3	IT90K-277-2	White	IITA
4	IT86D-719	White	IITA
5	IT98K-205-8	White	IITA
6	IT97K-499-35	White	IITA
7	NG/SA/07/159	White	NACGRAB
8	NG/SA/01/09/008	White	NACGRAB
9	NG/SA/07/089	White	NACGRAB
10	Cowpea-2	White	NACGRAB
11	NG/SA/07/155	White	NACGRAB
12	O311109	White	NACGRAB
13	NG/SA/01/09/009	White	NACGRAB
14	NG/SA/07/083	White	NACGRAB
15	NG/AO/11/08/084	White	NACGRAB
16	NG/AO/11/08/089	White	NACGRAB
17	NG/SA/07/141	White	NACGRAB
18	NG/SA/JAN/09/003	Brown	NACGRAB
19	TVx 3236	White and brown	IITA
20	IT8ID-994	Brown	IITA
21	IT89KD-288	Brown	IITA
22	NG/SA/07/135	Brown	NACGRAB
23	O304107	Brown	NACGRAB
24	NG/SA/JAN/09/004	Brown	NACGRAB
25	NG/SA/07/132	Brown	NACGRAB
26	NG/SA/07/130	Brown	NACGRAB
27	NGB/06/043	Brown	NACGRAB
28	NGB/06/110	Brown	NACGRAB
29	NA/SA/JAN/09/015	White	NACGRAB
30	IT84S-2246-4	Brown	IITA
31	NG/SA/01/09/011	White	NACGRAB
32	IFE BROWN	Brown	IAR&T
33	IFE BPC	Brown	IAR&T
34	IT82E-18	Brown	IITA
35	ERUSU	White	IAR&T
36	MODUPE	Brown	IAR&T
37	IFE 98-14	Brown	IAR&T
38	IT 95K-193-12	White	IITA
39	OLOYIN	Brown	Private Agro dealer

The screening was carried out in the screen house of I.A.R. &T, Moore plantation, Ibadan, Oyo State, Nigeria between March and July, 2013 using a modified protocol of Singh *et al.* (1999). Three wooden boxes of 240cm length, 116cm width, and 20cm depth each were made from plank of 2.5cm thickness. Each box represents each replicate. The bottom and sides of the boxes were lined with polyethylene to ensure even distribution of water. Top soil collected from southern farm of I.A.R. &T, Ibadan was used to fill the boxes to 16cm depth,

leaving about 4cm space on the top for watering. Thereafter, the boxes were arranged on concrete platform inside the rain-protected screen-house. The top soil was air-dried and sieved. Equidistant holes were made in straight rows 10cm apart with a hill-hill distance of 5cm within the rows.

Two handpicked healthy seeds of the cowpea lines were sown in hole of 2cm deep and thinned to one plant per stand after germination. Each box contained one row of each of 39 cowpea varieties with 6 plants and constituted one replication. The boxes were watered daily using a small watering can of four litres for two weeks when partial emergence of the first trifoliate leaf of all the varieties was observed. Thereafter, watering was stopped for thirty five days (7 weeks). Wilted plants in each variety for each replicate were counted daily. Atmospheric temperature and relative humidity of the environment (screen house) was also taken daily throughout the period of the experiment. Watering was then resumed for fourteen days (2 weeks) to ascertain regeneration percentage for each variety.

The percentage of wilted plants /day (*% wp*) was calculated using the formula: $\frac{Npw}{Nps} X100$

Where *Npw* is number of plants wilted and *Nps* is numbers of plants standing.

1. Percentage recovery was estimated after watering has resumed for fourteen days (two week) as: : $\frac{Npr}{Npw} X100$

   Where *Npr* is the number of plant that recovered after water stress and *Npw* is the total number of plants that wilted.

Data obtained were subjected to statistical analysis using SAS ™ and based on the days taken to wilt, the percentage recovery was used to construct dendogram, using PAST software.

RESULTS AND DISCUSSION

The average temperature and relative humidity of the screen house in the morning and afternoon during the experiment are presented in Table 2. The temperature in the morning ranges between 26.5^{o}C and 28.1^{o}C while afternoon temperature was between 27.7^{o}C and 33.5^{o}C.

The relative humidity in the morning ranges between 73.1% and 87.2% while that of the afternoon was 64.5% and 75.6%. The result indicates that the weather condition was optimum during the experiment. However, the environment was generally cooler and has high moisture in the morning than in the afternoon throughout the period of the experiment.

Table 2. Average temperature and relative humidity of the screen house on weekly basis during the experiment.

Weeks	Morning		Afternoon	
	Temperature (^{o}C)	Humidity (%)	Temperature (^{o}C)	Humidity (%)
Week 1	27.3	87.2	34.2	64.5
Week 2	27.4	83.4	27.7	69.4
Week 3	27.3	84.3	32.7	70.6
Week 4	28.1	86.1	33.5	69.4

Week 5	26.7	73.1	32.6	73.0
Week 6	27.5	80.1	30.9	75.6
Week 7	26.5	81.4	32.3	72.3

The result from the analysis of variance for percentage wilting during water stress and percentage recovery after water stress of the cowpea lines shows that there was significant difference among the cowpea lines at 5% probability level. (Table 3) This result indicated variation in drought tolerance among the cowpea germplasm lines Watanabe *et al.* (1997) has also identified some cowpea lines with better drought tolerance than many improved breeding lines. This result suggests that progress could still be made in the development of cowpea varieties with enhanced levels of drought tolerance.

Table 3: Mean Square of percentage wilting at 35 days of water stress and percentage recovery of cowpea lines.

Source of variation	Degree of freedom	% wilting at 35 days of water stress	% recovery after water stress
Cowpea lines	38	1041.76*	1501.96*
Error	78	40.99	16.32

*Significant at P<0.05 probability level

Drought tolerance ability of the cowpea lines are presented in Table 4. Seed germination and initial growth of plants of all the thirty nine lines were normal. Stress effects started appearing on susceptible varieties at twelve (12) days after the termination of watering while differences among varieties became visible and progressively more pronounced with advancing days of moisture stress (Figure 1). The stress effects were first noticed on the unifoliate leaves which became wilted, followed by the emerging trifoliates, and finally the growing tip dried (Figure 2) The data on wilting percentage at different days after termination of watering showed that TVx 3236, NG/SA/07/132 and IT95K-193-12 were the most susceptible to drought. The recovery percentage after watering ranged from 0% for NG/SA/01/09/004 to 100 % for IT81D-994 and Oloyin.

Table 4: Relative drought tolerance of the cowpea lines.

S/N	Cowpea lines	Percentage wilting after termination of watering (No of days)												% recovery after water stress
		12	14	16	18	20	22	24	26	28	30	32	35	
1	IT93K-452-1	0	0	0	0	0	0	0	17	42	58	58	58	79
2	NG/SA/07/167 (NAGRAB)	0	0	9	9	9	9	9	9	18	41	68	68	71
3	IT90K-277-2	0	0	0	0	0	0	0	0	17	67	67	67	84
4	IT86D-719	0	0	12.5	12.5	12.5	12.5	25	25	50	50	62.5	75	78
5	IT98K-205-8	0	0	0	0	0	0	0	33	33	67	67	67	84
6	IT97K-499-35	0	0	13	13	13	13	13	13	13	67	67	67	74
7	NG/SA/07/159	0	8	37.5	37.5	37.5	37.5	37.5	62.5	62.5	62.5	62.5	71	75

	(NAGRAB)													
8	NG/SA/01/09/008 (NAGRAB)	0	0	0	10	10	10	10	24	38	48	62	71	45
9	NG/SA/07/089 (NAGRAB)	0	0	28	28	28	28	39	50	50	61	61	61	65
10	Cowpea - 2 (NAGRAB)	0	0	44	44	44	44	70	70	70	70	70	88	57
11	NG/SA/07/155 (NAGRAB)	0	0	0	0	25	25	37.5	37.5	75	75	75	75	25
12	0311109	0	0	12.5	12.5	12.5	12.5	25	37.5	37.5	62.5	62.5	75	50
13	NG/SA/01/09/009 (NAGRAB)	0	0	14	14	14	14	14	69	78	78	78	78	54
14	NG/SA/07/083 (NAGRAB)	0	0	15	15	15	15	15	25	25	60	70	90	91
15	NG/AO/11/08/084 (NAGRAB)	0	0	0	0	0	0	0	25	33	42	50	50	63
16	NG/AO/11/08/089 (NAGRAB)	0	30	30	30	30	30	30	62	88	88	88	100	29
17	NG/SA/07/141 (NAGRAB)	0	0	0	0	0	14	14	38	52	62	62	76	57
18	NG/SA/01/09/003 (NAGRAB)	0	0	0	10	10	40	40	50	50	50	60	60	40
19	TVx 3236	8	8	8	20	20	20	20	33	67	67	67	92	2
20	IT81D-994	0	0	0	0	0	0	0	0	0	0	67	67	100
21	IT89KD-288	0	0	0	11	11	11	11	11	56	56	56	72	80
22	NG/SA/07/135 (NAGRAB)	0	0	22	39	39	50	50	50	61	78	78	78	27
23	0304107	0	0	12.5	12.5	12.5	44	57	57	57	89	89	89	30
24	NG/SA/01/09/004 (NAGRAB)	0	0	50	50	50	50	100	100	100	100	100	100	0
25	NG/SA/07/132 (NAGRAB)	17	33	33	33	50	83	83	83	100	100	100	100	67
26	NG/SA/07/130 (NAGRAB)	0	0	25	25	33	42	42	75	75	83	83	92	2
27	NGB/06/043 (NAGRAB)	0	17	17	33	44	61	61	61	72	89	89	89	61
28	NGB/06/110 (NAGRAB)	0	12.5	31	31	31	44	62.5	62.5	75	87.5	87.5	87.5	57
29	NG/SA/01/09/015 (NAGRAB)	0	0	21	21	31	45	67	67	67	76	76	76	47
30	IT84S-2246-4	0	0	24	38	50	50	50	50	64	76	76	88	89
31	NG/SA/01/09/011 (NAGRAB)	0	0	18	18	18	50	50	50	62	74	88	88	57
32	IFE BROWN	0	0	20	33	33	53	53	53	67	67	77	100	40
33	IFE BPC	0	11	11	44	44	44	44	61	72	72	89	89	61

34	IT82E-18	0	17	17	17	17	33	33	50	61	78	89	89	60
35	ERUSU	0	0	0	15	15	15	15	44	59	59	72	72	52
36	MODUPE	0	17	17	17	33	50	50	50	67	67	83	83	57
37	IFE-98-14	0	0	0	10	10	43	43	43	43	57	57	57	43
38	IT95K-193-12	17	17	17	17	17	50	50	67	67	67	83	83	58
39	OLOYIN	0	0	0	0	0	0	0	0	0	0	100	100	100

Figure 1: Cowpea varieties twelve days after water stress.

Figure 2: Cowpea varieties thirty-five days after water stress

The dendogram constructed based on percentage wilting at 35 days of water stress and percentage recovery of the cowpea lines is presented in Figure 3. The dendogram revealed that the 39 cowpea lines were majorly grouped into three. Group 1 comprises of three lines (TVx 3236, NG/SA/07/130 and NG/SA/01/09/004) which are drought susceptible while Groups 2 and 3 comprises of 14 and 22 lines respectively that were tolerant at varying degrees.

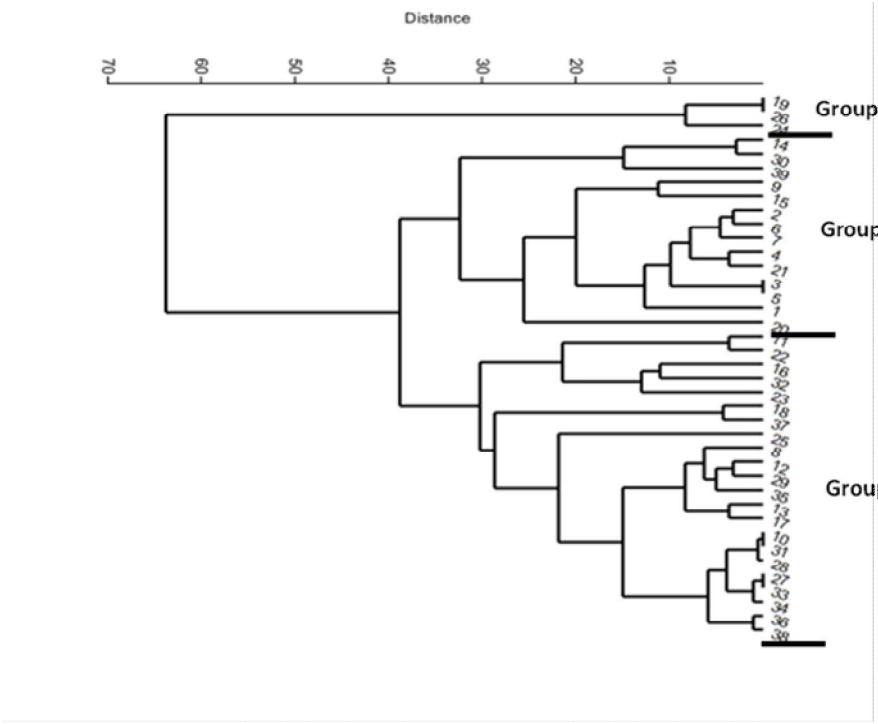

Figure 3: Dendogram from Euclidan paired group based on % wilting on 35 days after water stress and % recovery after water stress.

CONCLUSION

Traditional approach of studying drought tolerance on a whole plant basis makes the trait very complex and therefore difficult to manipulate by plant breeders. The wooden box screening for shoot drought tolerance as made it very simple to understand the mechanism behind the trait thereby removing the influence of roots and vice versa. This screening method have provided information on the cowpea lines that can be used in developing drought resistant and tolerant cowpea lines which may lead to faster progress in breeding for drought tolerance in cowpea.

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PGB15

EVALUATION OF TURMERIC (*CURCUMA LONGA* L) ACCESSIONS IN NIGERIA

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ABSTRACT

Fifteen promising accessions of turmeric selected from the germplasm held at National Root Crops Research Institute Umudike, Nigeria were evaluated during the rainy season of 2012 at 4 locations - Kuru (8.3833° N, 7.1833° E, 1200m asl), Otobi (7.11667° N and 8.08333° E), Umudike (5.4758° N, 7.5489° E), and Igbariam (6.4° N and 6.93333° E). The objective of the trial was to select turmeric accessions with high yield across locations for release in Nigeria. At each location, the experiment was laid out in RCBD in 3 replications. Plot Size was $9m^2$. Data was collected on the following growth and harvest parameters: sprout count, plant height, number of tillers, number of leaves, main stem girth, rhizome number and weight. Analysis of variance was carried out on the combined data using genstat discovery edition software. Results based on the combined data from 4 locations indicate that turmeric accessions did not vary in percentage emergence and number of leaves. They however varied significantly $P<0.05$ in height, main stem girth, tillering, number and yield of fresh rhizomes. The effect of location on all attributes was significant ($P<0.05$) with Jos location giving consistently the least values for all attributes thus suggesting that this location may not be suitable for the commercial production of turmeric. Genotype environment interaction for most attributes was not significant indicating that the accessions behaved in the same way across the locations. Ten accessions viz UT39 (28.37 t/ha), UT44 (27.15 t/ha), UT46 (25.39 t/ha), UT58 (24.73 t/ha), UT50 (24.10 t/ha), UT14 (23.81 t/ha), UT41 (21.53 t/ha), UT6 (20.62 t/ha), UT38 (19.43 t/ha), and UT35 (18.64 t/ha) were identified as promising and merits further evaluation preparatory for nomination as candidates for official release.

Keywords: Turmeric, Accessions, Variation, Rhizomes, Yield

INTRODUCTION

Turmeric (*Curcuma longa* Linn) is a monocot belonging to the family *Zingiberaceae* (Jilani *et al*., 2012). It is an important spice used for centuries in food preparation and in medicines to treat numerous diseases and conditions. (Ishimine, *et al*., 2003; Pari, *et al*., 2008; Maheshwari, *et al*., 2006). Turmeric is valued for its underground rhizome which contain a yellow coloured phenolic pigment called curcumin (Karim *et al*., 2010, Keith Singletary, 2010) which is used as natural colouring agent for food, cosmetics and dye (Olojede *et al*., 2009). Curcumin the main active ingredient of turmeric functions as a medicine with anti-inflammatory, anti-mutagenic anti-carcinogenic, anti-tumor, anti-bacterial, anti-oxidant, anti-fungal, anti-parasitic and detoxifying properties (Akanime *et al*., 2007). In addition to the rhizome's richness in curcuminoid pigments (6%) and essential oils (5%), it also contains 69.43% carbohydrate, 6.30% protein, 3.50% mineral and other important nutrients on dry weight basis (Olojede, *et al*., 2005).

India is considered as the largest producer, consumer and exporter of turmeric in the world and contributes about 50% of the world trade (Chaudhary, *et al*., 2006)). Other major producers are China, Myanmar, Nigeria, Bangladesh, Pakistan, Sri-lanka, Taiwan, Burma and

Indonesia, etc., The increasing demand for natural products as food additives makes turmeric an ideal produce for a food colorant. Additionally, anti-cancer and anti-viral properties of turmeric may also increase its demand from the pharmaceutical industry.

Its production in Nigeria is mainly in small plots around homes (Olojede *et al*., 2005). Turmeric can be found growing from low altitude (5m a.s.l.) in the Southern coastal plains of the rainforest to the mid-altitude (823m a.s.l.) in the derived Savanna within Longitude 3'02'E - 09'30'E and latitude 4'37'N - 10'04'N (Olojede and Nwokocha, 2011). No variety of turmeric has been officially released in Nigeria. Official release of improved varieties of this crop is likely to stimulate production thereby helping to unlock its potentials. The objective of the trial is to select high yielding turmeric accessions for release in Nigeria.

MATERIALS AND METHODS

The experiment was carried out during the rainy season of 2012 in 4 locations - Kuru (8.3833° N, 7.1833° E), Otobi (7.11667° N and 8.08333° E), Umudike (5.4758° N, 7.5489° E), and Igbariam (6.4° N and 6.93333° E). Fifteen accessions were laid out in RCBD containing 3 treatment replications. Plot size was $9m^2$. Method of cultivation was by means of raised beds. Seed rate was 1 rhizome/stand. The plants were spaced 50cm x 30cm apart between and within rows respectively. The beds were mulched soon after planting. Fertilizer was applied at the rate of 400kg/ha NPK 15:15:15 at 8WAP. The experiment were kept weed free by the application of pre-emergence herbicide followed by manual weeding. The plants were harvested when leaves have dried.

Data was collected on the following growth and harvest parameters: sprout count (4 & 8WAP), plant height (8, 12, 16 and 20 WAP), number of tillers (8, 12, 16 and 20 WAP), number of leaves (8, 12, 16 and 20 WAP), leaf area (8, 12, 16 and 20 WAP), main stem girth (8, 12, 16 and 20 WAP), rhizome number and weight. Analysis of variance was carried out on the combined data using genstat discovery edition. Means were separated using Standard Error of the Difference of means (SED)

RESULTS AND DISCUSSION

Turmeric accessions did not vary in plant emergence. Percentage emergence was higher at Umudike and Igbariam compared to Otobi and Jos (Table 1).

Plant height varied significantly with turmeric accession from 75 cm in UT39 to 54 cm in UT16 (Table 2). In an experiment conducted in 2008 & 2009 cropping seasons at Umudike, Nigeria, Njoku, *et al.*, (2012) recorded maximum and minimum turmeric heights of 70.6 and 43.9cm respectively. Jilani *et al.*, (2012) reported significant differences in plant height of turmeric cultivars. Plant height was highest at Igbariam and lowest at Jos. The lowest heights were recorded consistently in Jos location for all the genotypes (Table 2). The cold temperatures of Jos plateau may have had an adverse effect on plant growth leading to reduced height.

Most turmeric accessions did not differ in number of leaves per plant (Table 3). However, significant variations in number of leaves in different turmeric cultivars have been reported (Detpiratmongkol, *et al.*, 2009; Jilani, *et al.*, 2012). Effect of location on the leafiness of turmeric was significant with the highest number of leaves for most accessions recorded at Umudike (Table 3).

Main stem girth of UT58 (9.99 cm) and UT38 (9.91 cm) were significantly wider than most other accessions while UT35 with a mean girth of 6.26 cm was lower than most accessions (Table 4). Main stem girth varied significantly with location. Turmeric grown at Umudike

had the widest main stem girth (10.94 cm) while plant at Jos location had the least (4.23 cm) (Table 4).

The effect of accession and location on tillering in turmeric is presented in Table 5. Mean number of tillers per plant ranged from 4.62 in UT14 to 2.92 in UT39. UT14 with the highest number of tillers did not differ significantly with eight other accessions in this attribute. Tillering was highest at Igbariam compared to other locations. It was least in Jos. Hrideek *et al*. (2006) did not find significant differences between turmeric accessions in number of tillers per plant.

Turmeric accessions differed significantly in number of rhizomes (Tables 6). UT46 produced a mean of 30 rhizomes per plant which was significantly lower than the number produced by eight other accessions. Olojede, *et al*. (2009) also reported significant differences between 2 cultivars of turmeric in their rhizome number. The effect of location on rhizome number was also significant ($P<0.05$). Rhizome number was highest at Umudike and lowest at Jos location (Table 6).

Rhizome yield (t/ha) varied significantly with both accession and location (Table 7). Accessions UT50 and UT46 gave the highest yield at Jos and Otobi respectively while UT39 gave the highest yield at both Umudike and Igbariam. UT39 also gave the highest yield and UT16 the lowest yield across locations. Sisikumar *et al*., (1996) reported significant variation in fresh rhizome yield of entries in a turmeric multilocation trial in India. Other authors (Nayak *et al.*, 2006; Rao, *et al.* 2004) have also reported significant variation in rhizome yield among turmeric cultivars. Effect of location on rhizome yield was significant ($P<0.05$). Yield was highest at Igbariam and least at Jos. The yield in Jos for most of the varieties was very poor (Table 7). Chaudhary *et al*., (2006), suggested that the variation in rhizome characters, fresh yield and recovery percentage among various turmeric varieties could be due to genetic factors rather than the environmental conditions as reported by Subharayadu *et al.* (1976).

Genotype (Accession) x location interaction was not significant for most attributes including rhizome yield of turmeric. This is because the accessions responded in the same manner across the locations with Jos consistently giving the least values for all the attributes while Umudike and Igbariam gave the highest values for most attributes.

CONCLUSION

Most of the turmeric accessions performed relatively well at Igbariam, Umudike and Otobi but performed poorly in most attributes at kuru thus suggesting that this location may not be suitable for the commercial production of turmeric. Ten accessions viz UT39 (28.37 t/ha), UT44 (27.15 t/ha), UT46 (25.39 t/ha), UT58 (24.73 t/ha), UT50 (24.10 t/ha), UT14 (23.81 t/ha), UT41 (21.53 t/ha), UT6 (20.62 t/ha), UT38 (19.43 t/ha), and UT35 (18.64 t/ha) are promising and merits further evaluation preparatory for nomination as candidates for official release.

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Table 1: Percentage Emergence of Turmeric Accessions across 4 location

	Location				
Accession	**Jos**	**Otobi**	**Umudike**	**Igbariam**	**Mean**
UT6	88.89	93.33	100.00	86.67	92.22
UT14	88.89	100.00	96.67	100.00	96.39
UT16	91.11	73.33	100.00	96.67	90.28
UT25	95.56	93.33	100.00	100.00	97.22
UT30	85.56	73.33	100.00	100.00	89.72
UT35	84.44	86.67	96.67	96.67	91.11
UT37	92.22	93.33	100.00	100.00	96.39
UT38	90.00	83.33	100.00	100.00	93.33
UT39	91.11	93.33	96.67	100.00	95.28
UT41	88.89	100.00	100.00	100.00	97.22
UT44	75.56	93.33	100.00	96.67	91.39
UT46	74.44	100.00	96.67	100.00	92.78
UT50	91.11	80.00	100.00	100.00	92.78
UT58	78.89	100.00	100.00	100.00	94.72
UT60	90.00	93.33	100.00	96.67	95.00
Mean	87.11	90.44	99.11	98.22	

SED Accession - 3.58, SED Location - 1.85, SED Acn x Loc. - 7.16, CV% - 9.4

Table 2: Height (cm) of Turmeric Accessions across 4 Locations

	Location				
Accession	**Jos**	**Otobi**	**Umudike**	**Igbariam**	**Mean**
UT6	34.06	64.67	57.06	75.50	**57.82**
UT14	34.06	75.00	64.44	82.92	**64.10**
UT16	34.94	47.00	61.33	74.08	**54.34**
UT25	36.72	70.00	73.17	85.67	**66.39**
UT30	32.06	59.33	66.17	78.92	**59.12**
UT35	31.86	56.67	55.22	82.00	**56.44**
UT37	34.81	69.33	102.50	74.83	**70.37**
UT38	33.75	70.33	55.44	74.83	**58.59**
UT39	35.36	89.00	88.17	87.33	**74.97**
UT41	35.22	87.33	62.44	110.58	**73.90**
UT44	29.22	74.67	75.67	88.25	**66.95**
UT46	29.03	95.33	90.28	76.03	**72.67**
UT50	36.03	79.00	65.61	84.50	**66.28**
UT58	30.06	83.00	83.61	99.50	**74.04**
UT60	34.25	79.67	72.50	75.33	**65.44**
Mean	**33.43**	**73.36**	**71.57**	**83.35**	

SED Accession - 5.08, SED Location - 2.63, SED Acn x Loc - 10.17, CV% - 19.0

Table 3: Leafiness of Turmeric Accessions across 4 Locations

	Location				
Accession	**Jos**	**Otobi**	**Umudike**	**Igbariam**	**Mean**
UT6	7.38	11.67	20.94	9.25	**12.31**
UT14	9.77	12.00	25.33	9.67	**14.19**
UT16	9.03	9.33	18.89	9.25	**11.63**
UT25	8.88	10.00	20.22	9.92	**12.26**
UT30	8.64	15.00	20.61	8.83	**13.27**
UT35	10.87	9.00	22.17	9.42	**12.86**
UT37	8.28	11.00	13.56	9.50	**10.58**
UT38	7.86	8.67	20.39	9.25	**11.54**
UT39	11.45	16.00	21.00	8.92	**14.34**
UT41	9.08	11.33	20.67	9.25	**12.58**
UT44	9.32	12.67	23.89	9.17	**13.76**
UT46	6.33	10.67	20.22	9.67	**11.72**
UT50	9.43	9.00	21.67	9.67	**12.44**
UT58	6.45	11.33	21.78	9.33	**12.22**
UT60	8.03	11.33	20.17	9.33	**12.22**
Mean	**8.72**	**11.27**	**20.77**	**9.36**	

SED Accession - 1.46, SED Location - 0.75, SED Acn x Loc - 2.91, CV% - 28.5

Table 4: Main stem girth (cm) of Turmeric Accessions across 4 locations

	Location				
Accession	**Jos**	**Otobi**	**Umudike**	**Igbariam**	**Mean**
UT6	3.56	7.53	9.39	7.80	**7.07**
UT14	4.71	7.60	9.94	8.43	**7.67**
UT16	3.83	4.87	9.50	7.84	**6.51**
UT25	5.03	8.33	9.28	9.21	**7.96**
UT30	5.16	6.60	10.78	8.17	**7.68**
UT35	3.99	5.33	8.33	7.39	**6.26**
UT37	3.98	7.17	14.06	7.62	**8.20**
UT38	3.77	6.43	9.11	8.30	**6.90**
UT39	5.25	9.33	13.67	11.38	**9.91**
UT41	4.73	9.10	9.89	11.86	**8.90**
UT44	3.70	8.67	13.56	10.99	**9.23**
UT46	3.56	8.40	13.50	9.21	**8.67**
UT50	5.17	7.43	9.06	9.23	**7.72**
UT58	3.28	9.10	14.28	13.31	**9.99**
UT60	3.78	6.40	9.78	7.55	**6.88**
Mean	**4.23**	**7.48**	**10.94**	**9.22**	

SED Accessions - 0.53, SED Location - 0.27, SED Acn x Loc - 1.05, CV% 16.2

Table 5: Tillering ability of Turmeric Accessions across 4 locations

	Location				
Accession	**Jos**	**Otobi**	**Umudike**	**Igbariam**	**Mean**

UT6	1.47	3.67	5.83	6.50	**4.37**
UT14	1.46	3.67	6.28	7.08	**4.62**
UT16	1.94	2.67	5.28	6.33	**4.06**
UT25	2.03	3.00	4.94	6.08	**4.01**
UT30	1.82	2.33	5.89	6.75	**4.20**
UT35	1.79	2.67	5.22	6.75	**4.11**
UT37	1.56	3.00	2.22	5.00	**2.95**
UT38	1.92	3.33	5.50	7.17	**4.48**
UT39	2.30	3.00	2.56	3.83	**2.92**
UT41	1.37	3.00	4.83	3.83	**3.26**
UT44	1.96	3.00	2.67	4.75	**3.09**
UT46	1.65	3.00	2.72	5.67	**3.26**
UT50	1.87	3.33	4.94	5.58	**3.93**
UT58	1.43	3.00	2.39	5.17	**3.00**
UT60	1.84	3.00	5.22	5.58	**3.91**
Mean	**1.76**	**3.04**	**4.43**	**5.74**	

SED Accession - 0.38, SED Location - 0.20, SED Acn x Loc - 0.76, CV% - 24.8

Table 6: Rhizome Number of Turmeric Accessions across 4 locations

	Location				
Accession	**Jos**	**Otobi**	**Umudike**	**Igbariam**	**Mean**
UT6	8.55	46.62	89.13	64.54	52.2
UT14	11.34	70.12	54.30	65.17	50.2
UT16	11.11	25.04	88.70	58.80	45.9
UT25	14.47	45.19	69.93	82.70	53.1
UT30	12.85	51.25	69.97	51.13	46.3
UT35	14.12	27.82	81.51	74.42	49.5
UT37	9.34	47.88	88.80	53.53	49.9
UT38	9.27	43.94	68.60	54.80	44.2
UT39	12.57	49.91	84.01	47.83	48.6
UT41	9.39	46.22	71.03	32.63	39.8
UT44	8.81	61.00	79.50	62.90	53.1
UT46	10.68	14.33	36.03	58.30	29.8
UT50	19.34	33.57	67.07	65.97	46.5
UT58	7.90	53.68	70.57	50.90	45.8
UT60	10.16	51.56	52.93	50.04	41.2
Mean	11.3	44.5	71.5	58.2	

SED Accession - 8.04, SED Location - 4.15, SED Acn x Loc - 16.08, CV% - 42.5

Table 7: Rhizome Yield (t/ha) of Turmeric Accessions across 4 Locations

	Location				
Accession	**Jos**	**Otobi**	**Umudike**	**Igbariam**	**Mean**
UT6	1.99	16.08	36.00	28.41	20.62
UT14	2.61	30.22	30.42	32.00	23.81
UT16	2.77	14.07	20.00	24.72	15.39

UT25	4.14	17.67	15.56	34.44	17.95
UT30	3.57	18.15	20.89	24.22	16.71
UT35	3.48	9.81	24.79	36.47	18.64
UT37	5.37	18.07	21.78	25.78	17.75
UT38	2.88	21.27	19.11	34.44	19.43
UT39	5.98	28.94	39.90	38.67	28.37
UT41	3.08	33.93	20.89	28.22	21.53
UT44	2.21	36.79	34.22	35.38	27.15
UT46	2.95	40.37	26.81	36.22	26.59
UT50	16.19	14.67	37.33	28.22	24.10
UT58	2.86	36.07	29.33	30.67	24.73
UT60	2.13	24.44	18.22	26.62	17.85
Mean loc	4.15	24.04	26.35	30.97	

SED Accession - 4.21, SED Location - 2.18, SED Acn x Loc - 8.42, CV% - 48.3

PGB16

GENOTYPE × ENVIRONMENT INTERACTION OF DISEASE AND AGRONOMIC TRAITS ON SIX CASSAVA GENOTYPES (*MANIHOT ESCULENTA* CRANTZ) IN NIGERIA

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ABSTRACT

The study was carried out to quantify the genotype × environment interaction (GEI) on cassava mosaic disease (CMD), harvest index (HI), fresh root yield (FRY), dry matter content (DMC) and carotene content (CC) of six cassava genotypes in humid rainforest (Umudike) and guinea savanna (Otobi) agroecologies in Nigeria. The study was laid out in a randomized complete block design (RCBD) with three replications. Genotype main effect was significant ($P < 0.001$) for harvest index, fresh root yield, dry matter content and carotene concentration. Environment main effect was significant ($P < 0.01$) for cassava mosaic disease, harvest index and fresh root yield, and G × E interaction effect was significant ($P < 0.001$) for dry matter content and carotene content respectively. The high genotype and low environment effects, and the relatively low interaction on dry matter content imply that evaluation and selection can be effectively done in fewer environments to select genotypes with high performance for the trait whiles fresh root yield requires multiple environments to identify clones with broad and specific adaptation. Genotype x environment interactions (GEI) played a significant role in this study and should be given considerable attention in cassava breeding program for development of genetic materials adapted to a wide range of environments.
***Keywords*:** Genotype, Environment, GEI, Cassava, Biofortification, carotenoids

INTRODUCTION

Cassava is an important energy staple in Nigeria. It provides over 70% of the energy requirement for over 70% of Nigerian Population (Njoku *et al.,* 2011). Cassava is the most important of the root crops in the tropics and ranks fourth after rice, sugarcane and maize as a source of calorie for human needs (FAO, 2010). The spread of cassava from its native land of

origin in Amazon in Brazil has been mainly due to its adaptability and predominant use as a food crop for human nutrition, source of calorie for livestock feed, and lately as an industrial crop. Cassava as a crop is widely adapted but an individual cultivar has very limited adaptation because cassava cultivars are very sensitive to G x E interaction (Ssemakula and Dixon, 2007). An improved genotype will have its maximum value in a particular environment but may also represent an improvement for neighbouring environments (spill-over effect). Also, the response of individual genotype to different environments follows a diverse pattern due to the influence of the climate and soil variations. It is on this pattern that selection for high root yield, pest and disease resistance, and stable root yield are based.

Quantitative traits such as those associated with root qualities for example carotene content, dry matter content, starch and HCN content may show considerable interaction with the environment. Therefore, the testing of new lines requires evaluation in different locations (environment) to establish their genetic potential. When G x E interactions is present, the breeder faces major problems in comparing the performance of cultivars across environments between genotype, resulting in weak inferences from field data relevant to crop improvement (Ngeve, 1993). Other factors such as uneven germination of seeds may also complicate the work of a plant breeder (Collard *et al.,* 2005). In addition to high mean yields, stability of a genotype's performance in different environments is necessary to assist breeders in selecting superior cultivars to meet varying growing conditions. One approach is to reduce the number of replications used in a single field trial, assuming that performance can still be evaluated accurately.

Yellow-fleshed cassava genotypes have featured prominently in biofortification because they have higher levels of micronutrient, such as carotenoids (Chavez *et al.,* 2005) than the white-fleshed genotypes. Adoption of micronutrient biofortified genotypes will largely depend on their agronomic, including fresh and dry root yield, resistance to major pests and diseases, and the stability of these traits over time and space. Though cassava is widely adapted to a variety of environmental conditions, usually the adaptability of most white fleshed varieties is narrow and shows large GEI effects.

There were conflicting reports on G x E interaction on carotenoid concentration in cassava. Ssemakula *et al.* (2007) in a trail with 26 yellow flesh cassava in 10 environments in Nigeria had significant G x E interaction on total carotene content, dry matter content and cassava mosaic disease. There is need to conduct extensive trails to confirm these reports. The objective of the study was to study the G x E and to assess the CMD, HI, FRY and DMC of six cassava clones at different carotenoid levels.

MATERIALS AND METHODS

Six cassava genotypes (Table 1) at clonal yield stages were used for the study. The environments were Umudike and Otobi which represent humid forest and guinea savanna transition zones respectively. The soils for the trial sites were Umudike (Dystric Luvisol with sandy loam top soil over sandy clay) and Otobi (Ferric Luvisol with sandy loam top soil). Annual rainfall for the environments during the trial period was Umudike (2289 mm) and Otobi (1500 mm). Plantings were done at different dates for the two environments. The materials were grown under rainfed conditions in a randomized complete block design with three replications.

Table 1: Description and sources of cassava genotypes used for the evaluation studies

Clone	Clone type	Origin	Root fresh colour

TMS 01-1368	Released (2011)	IITA	yellow
TMS 05-1636	Non-release	IITA	yellow
TMS 05-0473	Non-release	IITA	yellow
TMS 97-2205	Released (2005)	IITA	white
TMS 98-0505	Released (2005)	IITA	white
TMS 98-0002	Released (2005)	IITA	white

Planting was done using disease-free stakes planted on 4 row plots of 5 plants / row with a plot size of $20m^2$. Weeding was done with both herbicides and manual methods when necessary. Data were collected from the 10 inner plants within a plot. Severity ratings of cassava mosaic disease were taken at 1, 2, 3, 4, 4 and 6 months after planting (MAP) using a scale of 1 to 5 (1 = no symptoms; 5 = severe symptoms). At harvest (12 MAP), data were collected from the 10 inner plants within a plot for harvest index, storage fresh root yield, dry matter percentage and carotene concentration. Dry matter percentages of storage roots were determined from a random bulk sample of four plants selected from the inner rows. The roots were peeled and shredded after washing. Hundred grammes (100 g) of fresh root was taken in the form of chips and dried at 65°C for 72 h in a forced air oven. The dried samples were then reweighed to obtain the dry weighs, and the dry matter percentage was calculated as the ratio of the dry weight over the fresh weight and multiplied by 100. Data collected were first analyzed separately, then combined over environments using GenStat 14 edition.

RESULTS AND DISCUSSION

Some notable significant interaction existed in this study. Umudike recorded the highest grandmean for harvest index (HI) (0.6). Also, Umudike recorded the lowest score for cassava mosaic disease severity (CMD) (1.6). However, Otobi recorded the highest grandmean for storage fresh root yield (SFRY) and dry matter content (DMC) of 33.5 t/ha and 34.5 % respectively. Both locations recorded the same grandmean values for carotene concentration (CC) of 4.0 (Table 2). In the combined analysis (Table 3), storage fresh root yield ranged from 13.7 t/ha to 37.8 t/ha with a mean of 25.7 t/ha. TMS 98-0002 had the highest root yield of 37.8 t/ha, while the lowest value of 13 t/ha was recorded for TMS 05-0473. Dry matter content ranged from 28.3% to 36.5% with a mean of 33.3%. Harvest index ranged from 0.4 to 0.6 with a mean of 0.5, and carotene concentration ranged from 1.3µg/g to 8.2µg/g with a mean of 4.0µg/g (Table 3). However, the reaction of the clones to cassava mosaic disease (CMD) across the two environments did not vary significantly.

Analysis of variance (ANOVA) showed that storage fresh root yield, harvest index, dry matter content and carotene concentration varied significantly ($P < 0.001$) among the genotypes (Table 4). G x E accounted for 9.7% of the total sum of squares for storage root yield, while environment accounted for 17.7% and genotype 32.0%. Similarly, genotype, environment and G x E sources of variation also accounted for 20.5%, 0.2% and 66.7% of the total sum of squares respectively, on dry matter content. Also, G, E and G x E accounted for 95.9 %, 1.1% and 1.9% on carotene concentration (Table 5).

The high genotype and low environment effects and relatively low G x E interaction for storage fresh root yield, dry matter content and carotene concentration suggest that these traits are not drastically influenced by environment and, therefore, that fewer environments may be needed to distinguish clones with high and stable performance. This also suggests good prospects for the improvement of the clones for these traits since simple phenotypic

recurrent selection will be needed. Ssemakula and Dixon (2007), and Benesi *et al.* (2004) also reported higher genotype than environment effects on dry matter content in cassava. The high genotype effects on mosaic disease has also been reported by Maroya *et al.* (2012) when working on G x E interaction on cassava mosaic disease, storage fresh root yield and carotene concentration of yellow-fleshed cassava in Nigeria. Also, this work is in agreement with the work of Peprah *et al.* (2013) who reported greater genotype effect on fresh root yield than environment effect.

Table 2: Performance of six cassava clones planted across two environments in Nigeria

Clone	**Umudike 2012**					**Otobi 2012**				
	CMDs	HI	SFRY	DMC	CC	CMDs	HI	SFRY	DMC	CC
TMS 98-0002	2.0	0.6	27.2	39.8	2.0	1.7	0.6	48.3	35.7	1.1
TMS 05-0473	1.7	0.5	9.6	26.6	4.0	2.6	0.3	17.9	35.8	5.1
TMS 98-0505	1.0	0.6	35.1	39.9	1.2	1.7	0.4	37.7	38.8	1.4
TMS 01-1368	1.7	0.6	14.9	29.7	8.5	3.0	0.4	23.3	26.9	7.9
TMS 05-1636	1.3	0.5	6.2	30.0	6.2	2.3	0.3	21.2	30.6	7.0
TMS 97-2205	2.0	0.6	14.8	32.6	2.3	2.0	0.5	52.4	33.4	1.8
Grandmean	1.6	0.6	18.0	33.1	4.0	2.2	0.4	33.5	34.5	4.0
SED	0.51	0.07	10.6	1.18	0.17	0.55	0.05	10.20	1.78	0.50
CV (%)	26.0	2.0	36.9	1.4	2.1	18.9	14.2	29.6	2.5	7.6
LSD (0.05)	0.39	0.15	0.14	<.001	<.001	0.17	0.006	0.026	<.001	<.001

Table 3: Mean performance of six cassava clones evaluated across two environments (combined data)

Clone	CMDs	HI	SFRY (t/ha)	DMC (%)	Carotene Conc
TMS 98-0002	1.8	0.6	37.8	36.5	1.5
TMS 05-0473	2.2	0.4	13.7	31.2	4.5
TMS 98-0505	1.3	0.5	36.4	39.3	1.3
TMS 01-1368	2.3	0.5	19.1	28.3	8.2
TMS 05-1636	1.8	0.4	13.7	30.3	6.6
TMS 97-2205	2.0	0.5	33.6	33.0	2.1
Grandmean	1.9	0.5	25.7	33.3	4.0
SED	0.2	0.1	12.0	1.5	0.4
CV (%)	19.0	5.5	57.3	5.5	11.8

Table 4: Mean squares of fresh root yield, dry matter content, harvest index, cassava mosaic disease and carotene concentration

Source	Df	CMDs	HI	SFRY	DMC	CC
Genotype	5	0.72^{ns}	0.04***	783.7**	114.19***	49.7***
Environment	1	3.36*	0.24***	2167.4**	1.80^{ns}	0.1^{ns}
Gen X Env	5	0.63^{ns}	0.01^{ns}	237.5^{ns}	33.52***	0.9**

Table 5: Combined ANOVA of the 5 traits of six cassava clones in two environments

		CMDs		HI		FRY (t/ha)		DMC (%)		CC (ug/g)	
Source	Df	SS	Variation (%)	SS	Variation (%)	SS	Variation (%)	SS	Variation (%)	SS	Variation (%)
Gen	5	3.58	15.7	0.18	30.5	3918.3	32.0	570.9	66.7	248.3	95.9
Env	1	3.36	14.8	0.24	40.7	2167.4	17.7	1.8	0.2	0.01	0.0
G x E	5	3.14	13.8	0.02	3.4	1187.7	9.7	167.6	20.5	4.9	1.9

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PGB17

HORMONAL INDUCTION OF SEEDLINGS FROM LEAF SUBCULTURE IN SESAME SESAMUM INDICUM L. GENOTYPES

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ABSTRACT

Three Sesame genotypes, Alaede (N3), E8 (N5) and Ex Sudan (N9) obtained from NCRI, Badeggi, Nigeria, were studied using tissue culture techniques to examine their responses in vitro. Growth media with different concentrations and combinations of hormones were used for shoot formation from callus subculture and seedling development from leaf subculture. Ex Sudan recorded the highest shoot formation frequency on full strength MS media only and produced the highest mean in seedling development from sub cultured leaves at $0.1mg*L^{-1}$ Kinetin + $0.2mg*L^{-1}$ NAA and $0.3mg*L^{-1}$ Kinetin + $0.1mg*L^{-1}$ 2,4 D. The latter concentration showed significant difference among the three genotypes. From the experiments, Ex Sudan responded better than the other varieties therefore stands as a candidate for improvement of the other varieties.

Keywords: callus subculture, growth hormones, in vitro, leaf subculture, seedlings development, sesame, shoot formation

INTRODUCTION

Sesame belongs to the family Pedaliaceae and genus *Sesamum* (Hutchinson and Dalziel 1963; Purseglove 1974). The genus consists of about 36 species of which 19 species are indigenous to Africa (Weiss 1983; Uzo 1998). In Nigeria, three species, which include *S. alatum* (Thonn), *S. indicum* L. and *S. radiatum* Schum & Thonn, are widely cultivated for different purposes (Dabir 2000). The most popular species is *S. indicum*, which has hundreds of varieties and strains with considerable variation in size, form, growth pattern, colour of flowers, seed size, seed colour and composition.

Since antiquity, sesame has been used as a valued oil crop. Today it is grown mainly in the tropics, although its cultivation reaches from 40^oN to 40^oS latitude. It is typically grown by small holders with nearly all of its production in developing countries. China (825,531 MT) and India (620,000 MT) are the world's principal producers (FAO 2004). Myanmar (390,000 MT), Sudan (122,000 MT), Uganda (110,000 MT), Nigeria (75,000 MT), Pakistan (61,600 MT), Bangladesh (49,000 MT) and Thailand (40,000 MT) are other major sesame growing countries. (IPGRI and NBPGR , 2004)

Sesame is grown for its seeds, prized oil, and oil paste. The oil paste, tahini, is obtained by grinding the seeds. The seed is also used on breads and cakes. Sesame is useful as an extra

rich source of protein in many developing countries (Uzun, et al. 2002). Sesame seeds contain 50-60% oil. Sesame is known as the queen of oil seeds because its oil not only has nutritive value but also is of high quality and quantity (Bedigian 2000). According to research, sesame has many beneficial effects for human health. For instance, scientists showed that sesame leads to reduction of total serum cholesterol and low density lipoprotein (LDL) cholesterol and improvement of antioxidant capacity in hypercholestrolemic patients (Chen, et al. 2005). Sesame also increases vitamin E concentrations in plasma (Frank 2005)In addition to its effects on animals, sesame has significant effects on microorganisms.

Nigeria has a great potential for sesame production for the domestic and export markets but the yield of this valuable crop is relatively low and varies from one area to another, due to a lack of improved varieties. Based on this, the National Cereals Research Institute (NCRI), Badeggi, has been given the national mandate for the genetic improvement of sesame. A number of studies have been carried out on various aspects of sesame development. Taskin, *et. al*. (1997) studied the *in vitro* regeneration of sesame while George, *et al*. (1989) worked on *in vitro* propagation and shoot tip culture of different cultivars. Sesame breeding work in Nigeria is progressing. The need to evaluate materials for selection and subsequent use in breeding programmes with the purpose of developing improved sesame varieties suited to Nigerian conditions has been highlighted(Akpan-Iwo et al, 2006)

The aim of this study therefore is to determine the responses of these three varieties of sesame to different types of growth hormones combinations and concentrations with a view to developing seedlings from in vitro culture for the improvement of the crop.

MATERIALS AND METHODS

Three genotypes of sesame seeds used for this study were obtained from the National Cereals Research Institute, (NCRI), Badeggi, Niger State, Nigeria. The genotypes were designated based on the genotype and NCRI name (the latter in parenthesis). These are N3(Alaede); N5(E8) and N9(Ex- Sudan). The explants used for the study were calluses earlier obtained from embryo culture of the three varieties. (Jayeoba, 2010)

The basal media used for the experiment was Murashige and Skoog (1962) modified with 3% Sucrose, 0.1g*L^{-1} Inocitol and growth hormones concentrations. The growth hormones used for the study were obtained from the National Center for Genetic Resources and Biotechnology (NACGRAB) Ibadan, Nigeria. They are abbreviated as follows : 2,4 (2,4 dichlorophenoxyacetic acid);CM(Coconut Milk);K(Kinetin);BAP(6,benzylaminepurine) and NAA(Napthalene-1-acetic acid). The forceps used was sterilized in glowing splint after rinsing in ethanol and allowed to cool. The mouth of the medium test – tube was flamed in the glowing splint and a piece of the callus was carefully placed on the medium. The media bottle was closed with paraffin to prevent contamination, and the test tubes labeled and dated. The culture was transferred to the growth room for incubation at 28^0 C ± 2^0 C with a 16/18 hour photoperiod from cool-light fluorescent lights with an intensity of 2000 lux. For each treatment, three replications with 10 tubes per replicate were maintained. The cultured calluses were scored for the appearance of shoot formation. The leaves from the shoots were also sub cultured to produce more seedlings.

The data obtained was analyzed using ANOVA according to Steel and Torre (1980). Significant means were separated using Duncan's Multiple Range Test (Duncan, 1955).

RESULTS AND DISCUSSION

Table 1: Mean of shoot formation from callus subculture in Sesame genotypes.

Treatment	Genotypes		
	N3	N5	N9
100ml*L^{-1} CM	0.3 ± 0.14	0.4 ± 0.15	0.4 ± 0.15
0.05mg*L^{-1} BAP +0.01mg*L^{-1} IAA	0.1 ± 0.09	0.3 ± 0.14	0.5 ± 0.16
MS Only			
Full strength	0.3 ± 0.14	0.5 ± 0.16	0.7 ± 0.14
Half strength	0.5 ± 0.16	0.5 ± 0.16	0.6 ± 0.16

Table 2: Mean of seedling development from leaf subculture in Sesame genotypes.

Treatment	Genotypes		
	N3	N5	N9
K(mg*L^{-1}) + NAA(mg*L^{-1})			
0.1 + 0.01	0.4 ± 0.15	0.4 ± 0.15	0.7 ± 0.14
0.1 + 0.02	0.4 ± 0.15	0.7 ± 0.14	0.8 ± 0.13
K(mg*L^{-1})+2,4 D(mg*L^{-1})			
0.1+ 0.3	0.2± 0.13	0.1 ± 0.14	0.2± 0.15
0.3+0.1	0.3 ± 0.14[b]	0.6 ± 0.16[ab]	0.8 ± 0.13[a]
MS Only			
Full strength	0.2 ± 0.13	0.20 ± 0.13	0.3 ± 0.14
Half strength	0.1 ± 0.9	0.2 ± 0.13	0.2 ± 0.13

[ab]Means with different superscripts in the same row are significantly different.

There was significant difference in the responses of the three genotypes with N9 producing the highest mean of 0.8 at the concentration of 0.3mg*L^{-1} 2, 4D and 0.1mg*L^{-1} kinetin (Table 1, Fig I). The highest callus production was recorded at the combination of 0.08mg*L^{-1} kinetin and 0.25mg*L^{-1} 2, 4D with N9 producing a mean of 0.9 and N5 and N3, 0.7 and 0.5 respectively. Full strength MS produced a significant difference (when subjected to statistical analysis in callus production in the three genotypes). N9 produced the highest mean of 0.9 and N3 the lowest of 0.5.

The culture on MS only produced higher means in the three genotypes with N9 having the highest mean of 0.7 and N3 the lowest mean of 0.3, the result was reduced with half strength MS. Addition of 100ml*L^{-1} CM reduced the shoot production of N9 from 0.7 in MS to 0.4, while N3 was not affected. Modifying the MS with 0.005mg*L^{-1} BAP plus 0.01 mg*L^{-1}NAA however reduced the rate of shoot production from 0.7 in N9, MS, to 0.5; and 0.3 in N3, MS to 0.1.

The responses of the genotypes to MS only (full strength and half strength) for the production of seedlings from leaves subculture was low compared to the modified Ms. N9 produced the highest mean of 0.3 with full strength MS, while the least mean in the MS treatment was 0.1 produced by N3 at half strength MS treatment. N9 and N5 showed increase in mean of seedling production as the concentration of NAA was increased from 0.1 to 0.2mg*L^{-1} but N3 remained unaffected (Table 2, Fig II). Replacing NAA with 0.3mg*L^{-1} 2, 4D reduced shoot production drastically in the three genotypes. Increasing kinetin concentration to 0.3mg*$L^{-1}$and reducing that of 2, 4 D to 0.1mg*L^{-1} produced a significantly different increase in seedling production in the three genotypes with N9 producing the highest number of seedlings.

As the calluses were sub cultured to produce leaves, even though N9 produced a higher mean on MS in comparison with the others, the means were not significantly different when subjected to ststistical analysis. The same applied to half strength MS. Reduction in the means of the three genotypes when compared to full strength MS is as a result of the reason given in callus production. MS modified with 0.05mg*L^{-1} BAP and 0.01mg*L^{-1}IAA produced higher mean in N9 and less in N3 and N5. Since the increment is not significantly different, it can be deduced that BAP and Coconut Milk had the same effect on shoot production in the three genotypes. The ratio of BAP: IAA (Cytokinin to Auxin) in this work was 5:1; this is close to 5.5:1 obtained by Saravanan and Nadarajan (2005) in their shoot multiplication experiment in in-vitro sesame culture.

In leaf subculture to produce seedlings, N9 responded best of all the three genotypes to all the treatments they were subjected to. The responses were generally low with MS only; this means that modifying the media was important for shoot production from leaves in these genotypes. Increasing the ratio of cytokinin (K) to auxin (NAA) to 1:20 from 1:10 (i.e. from 0.1mg*L^{-1}K + 0.01mg*L^{-1} NAA to 0.1mg*L^{-1} K + 0.02mg*L^{-1} NAA) increased the responses of N9 and N5 without any effect on N3 (Table 2). It can be deduced from here that the three genotypes would produce seedlings from leaves at K:NAA ratio of 1:20, and that the response of N3 is as a result of its genotype. The reduction in seedling production in the

three genotypes when NAA was replaced with 2, 4 D (Table 2) implies that hormones belonging to the same class may not necessarily produce the same effect on the same plant species. The significant difference observed in the means when K was increased to 0.3 and 2, 4 D reduced to 0.1 shows that seedlings could be regenerated faster from leaves at that concentration and combination. It also showed that the three genotypes responded differently to that treatment.

CONCLUSION

The response of N9 is higher in almost all the studies carried out when compared with other two genotypes. This could be traced to its performance in the viability test in which it gave the highest germination rate. The reason for this performance may have arisen from its genetic constitution which confers an advantage on it. The seeds of N9 and N5 were also relatively bigger than that of N3 (N9 was 2mm while N5 was 1.5mm in length). This could have also contributed to the performances as N3 responded least in all the treatments. It has been observed in this study that Kinetin is a better cytokinin for callus development in the three genotypes under study than coconut milk. Also, BAP and coconut milk have been found to produce similar effects on shoot production in the three genotypes. Seedling development from leaf subculture was found to improve significantly when MS was modified with hormones. Individual hormone rather than class produced different effects on the three genotypes.

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PGB18

ASSESSMENT OF POLLEN FERTILITY, CANE YIELD AND ETHANOL CONTENT IN SUGARCANE PROGENIES DEVELOPED BY THE MODIFIED POLYCROSS METHOD

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ABSTRACT

Performance of breeding lines in advanced yield trials is prerequisite to identification of superior genotypes intended as replacement to the existing cultivars. However, apart from yield potential, sugarcane breeders also determine the sexuality of flowering genotypes that are highly productive so that they can be used either as male or female in crosses aimed at the development of future varieties. To this end, 10 advanced sugarcane lines from the Unilorin Sugar Research Institute (USRI) breeding programme were assessed for their flowering behaviour, sugar (cane yield and sucrose content) and ethanol yields, using a randomized complete block design with four-replications during the 2011/2012 cropping season at the institute's research farm. Our results showed that all the progenies were highly fertile and so could be utilized as males in crosses. On the basis of pollen morphology, the genotypes were classified as either Sulcate or Colpate. Many of the progenies yielded significantly higher ($P<0.001$) than some of the check varieties with Progeny USRI/08/63 recording the highest cane yield but which was comparable to the yield of the best standard variety (var. Co6806). Among the progenies, the highest ethanol yield was obtained from progeny USRI/08/03 with 15% ethanol followed by four other progenies (USRI/08/16, USRI/08/63, USRI/08/68 and USRI/08/85) with 10% ethanol respectively. Since different genotypes were identified in respect of cane yield and ethanol, a separate breeding programme can therefore be designed for the development of high ethanol content sugarcane varieties.

Key words: Saccharum officinarum, pollen morphology, sugar yields, ethanol content, polycross,

INTRODUCTION

Sugarcane (*Saccharum officinarum* L.) breeders routinely carry out hybridization procedures which normally involve the use of highly fertile sugarcane genotypes as source of pollen (males) in crosses with male sterile types (as females), followed by raising of the fuzz (true sugarcane seeds). Although the degree of anther dehiscent when viewed with the hand lens gives an indication of sexuality of a flowering variety, classification based on microscopic examination of the pollen grains is a more realistic procedure for correctly classifying flowering sugarcane varieties either as male or female. This is because the use of hand lens in classifying flowering sugarcane varieties on the basis of degree of pollen shed has to be carried out regularly during the breeding season in order to ensure success in pollination.

The occurrence of flowering under field conditions is variable and is also influenced by variety as well as prevailing environmental conditions in a locality. Previous studies have shown that flowering is a complex process consisting of multiple stages of development with each stage having specific environmental and physiological requirements. The environmental conditions may include a combination of factors such as diurnal temperatures, specific day length, elevation, temperature and moisture requirements (Van-Breeman *et al*., 1962;Clements and Awada 1967; Coleman, 1969; Gosnell, 1973; Moore, 1987; Moore and Nuss, 1987; Araldi *et al*., 2010), rainfall amount and distribution (Olaoye, 1996), sub-optimal photoperiod (Nayamuth *et al*., 2003; Berding, 2005), rising atmospheric concentrations of CO_2 (Rosenzweig *et al*., 1995) and pollution levels.

Furthermore, as the world demand for alternative source of fuel increases, attention has been focused on non-fossil source of fuels which include crops such as sugarcane, cassava (*Manihot utilissima*), jatropha (*Jatropha cacus*) among others. According to Deepland (2005), sugarcane is one of the plants having the highest bioconversion efficiency of captured sunlight through photosynthesis to fix around 55 tonnes of dry matter/ha of land on an annually renewable basis. For example, the crop has been used in Mauritius as energy conservation and efficiency measures to minimize cogenerated energy (steam and electricity) utilized in cane processing and also export excess electricity to the grid. Similarly, Brazil has diversified sugarcane breeding efforts to include development of varieties for ethanol (biofuel) generation from the crop, as source of fuel for their automobile by transforming sugarcane into about 12 x 109 litres, 1/5 of which is in anhydrous form (Gonzalez and Galvez, 1998). A corollary is that sugarcane breeding efforts in other sugar producing countries have been diversified into development of varieties for specific end uses such as high sugar, high fibre, and ethanol content sugarcane varieties.

Secure, reliable and affordable energy supplies are fundamentals to global economic stability and growth. The challenges of sustainable development are great and the importance of energy in achieving sustainable development predicated upon search for sustainable programme for generation of energy from biomass. Access to affordable energy services is fundamental to human activities, development, and economic growth. Biomass is considered to be one of the key renewable resources of the future at both small and large scale levels. The development of biomass as a source of clean and renewable energy has been encouraged because of its benefits especially environmental sustainability (Keeney and DeLuca, 1992).

Olaoye (2011) reported that production of biofuels has the beneficial effect in increasing a sustainable fuel supply for the future. The activities through the production chains of biofuels provide jobs and socio-economic developments in rural areas. The use of ethanol as fuel is capable of reducing the adverse foreign trade balance. COLMAC (2009) and Van Gerpen *et al*., (2007) in Olaoye (2011), noted that the cost benefit ratio of production of biofuels may be higher compare to fossil fuel but biofuel does not contribute to greenhouse effect problem which is a major problem with other known energy source.

Since the inception of sugarcane varietal development activities in Nigeria, breeding efforts have concentrated on the development of high yielding (cane yield and sucrose content) varieties without diversifying breeding efforts to the development of varieties for specific end-uses such as high fibre (for coenergy generation) or high ethanol (biofuel) content sugarcane varieties. Although previous studies (Oworu, 1987; Fadayomi *et. al*., 1995), have shown that flowering is not a desirable trait in sugarcane because of the diversion of photo assimilates into flowering and seed production to the detriment of sucrose accumulation, it is required in sugarcane breeding for varietal development. Consequent upon our interest to diversify breeding efforts into the development of improved sugarcane varieties for other specific end uses other than manufacturing of refined sugar, 10 of the 97 progenies from our 2007 modified polycross scheme which combined high cane yield with high sucrose in the juice at the preliminary yield testing stage (which are also the flowering type), were selected for further yield evaluation in the savanna ecologies. In this part of the study, the performances of the progenies for cane yield and related traits under large plot size as well as their ethanol contents were investigated. The fertility status of the flowering types was also determined with the view to correctly classify them either as male or female for effective hybridization purposes.

MATERIALS AND METHODS

The genetic materials used comprised 10 flowering sugarcane progenies which were selected from among 97 progenies evaluated for their yield potential and other attributes at the research farm of the Unilorin Sugar Research Institute (USRI), Ilorin in 2009 (Olaoye *et al.*, 2010). The progenies came out of the 2007 modified polycross breeding scheme which was developed in the institute to generate planned crosses in recognition of lack of specialized glasshouse and stock solution for effective hybridization under a controlled condition to prevent contamination from unwanted pollen source. The details of the scheme have been described in an earlier paper (Olaoye, 2001).

The study was conducted during 2012/2013 growing season at the USRI, farm, Ilorin in the Southern Guinea Savanna (SGS) agro-ecological zone of Nigeria (Lat 8^0 29 and Long 4^0 35E). The rainfall pattern is usually bimodal with its highest peak in July and September and a break between Mid-July and Late August. The average annual precipitation of the area is 1250 – 1500mm with temperature ranging between 19^0C and 33^0C. The 10 sugarcane progenies were evaluated along with five commercial varieties as checks. The experimental design was a randomized complete Block (RCBD) with three (3) replicates. The trials were laid out in four row plots, 5 meters long with 1.5m between the plots and an alley of 1m between plots. Three-budded sugarcane sets which were, used as planting materials were laid in horizontally in the furrows and eight (8) sets were planted per row. All agronomic

practices including weed control and fertilizer application were carried out according to the standard practices.

Data were collected from five (5) random stools selected from the two middle rows on yield parameters of tiller count, stalks/stool, stalk length, stalk diameter, millable cane population, internodes/stalk and length of internode. Data were also collected at harvest on cane yield, single stalk weight and sucrose accumulation in the juice. For cane yield, all millable cane stalks from the two middle rows were harvested and weighed on scale and recorded in kilograms (kg). The weights were later converted into cane yield in tonnes per hectare. Single stalk weight was measured as the weight of three (3) randomly selected single cane stalks per plot and recorded in kg. ^{o}Brix which is the percentage by weight of the soluble solids in the juice when squeezed from a matured or crushed sugarcane stalk with an extractor and measured and read on a refractometer, were collected from three (3) randomly selected millable stalks in a plot.

Arrows (sugarcane flowers) were collected from three stalks/plot and taken to the laboratory of the Department of Plant Biology for microscopic examination of the pollen grains. Matured anthers on the spikelets at shedding period were collected in sample bags and examined for pollen morphology and viability tests using the light microscope. The anthers were squashed on the microscope slide using a broad base material to remove the pollen grain from the anthers. Few drops of stain Lacto-phenol (cotton blue) were added and covered with cover slip to prevent the pollen grains from displacement. The prepared slides were then examined under the light microscope. Viable (fertile) pollen grains appeared large, fully round and dark in colour while inviable and (infertile) pollen grains appeared clear, empty and colourless. The pollen grains were then counted and sorted into fertile and infertile pollen grains and then expressed into percentage as

$$\frac{No\ of\ fertile\ pollens}{Total\ no\ of\ pollens} \times 100 = \text{percentage of fertile pollen}$$

Based on the percentages of fertile and infertile pollen grains, the genotypes were classified into males and females. Genotypes with high percentages (50 – 100%) were rated as males and genotypes with lower percentages (0-49) were rated as females.

The structure and characteristic of the pollen grains were determined using the photomicrographic scanning machine in the Department of Plant Biology, University of Ilorin. On the basis of structure and characteristics, the pollen grains were characterized either as inviable or viable while the viable pollen grains were further grouped as either colpate (elongated aperture or furrow) or sulcate (many pores).

The biofuel component comprising of sugarcane juice extractor, fermenter and distillation unit were designed and constructed in the Department of Agricultural and Biosystems Engineering of the University of Ilorin. (Plate 1). Three (3) litres of sugarcane juice was extracted from each of the progenies with the aid of the juice extractor. This was followed by the addition of 1.2g of commercial Baker's yeast, dry *Saccaromyces cerevisiae* to each of the three (3) litres of sugarcane juice/progeny. The concentrate was fermented for a period of 48 hours in the fermenter with stirring under anaerobic conditions. The juice was later distilled and bioethanol yield determined for each genotype using the hydrometer values. Brix was determined with the hand refractometer while a viscometer was used to determine the Kinematic Viscosity of the slurry after distillation at 27^{o}C. The procedure was repeated

three times for each genotype. Other data collected included time of grating, weights of grated canes, volume of juice, brix value and machine loss. Amount of juice yield was later calculated using the formula:

Juice yield (%) = [Je/Je+ Wr] 100

Where Je = weight of extracted juice, Wr = weight of residue.

RESULTS AND DISCUSSION

Means with standard errors attached (SE±) ranges in the means and coefficient of variation (%CV) for pollen characteristics in (10) USRI progenies and four (4) check varieties are presented in Table 1. The results showed that number of viable pollen grains were quite high than the inviable pollen grains with a difference of greater than 95 percent (%). The range in the means for the viable pollen grains among the genotypes which is an indication of differences among them for this trait, as well as coefficient of variation (%CV) was also large compared to the values obtained in respect of inviable pollen grains.

Plate 2 shows the different pollen characteristics encountered among the flowering genotypes. The inviable pollen grains (top) had clear, collapsible, and colourless morphology which failed to absorb the stain. This feature was observed in USRI/08/58 which had the highest number of inviable pollen grains relative to total pollen count. Viable pollen grains appeared round and took the blue colour of the stain (lactophenol or cotton blue) and majority of the USRI progenies are in this category as they exhibit high percentage of pollen grains which stained the cotton blue and therefore were characterized as viable. The viable pollen grains were further classified as either *Sulcate* (middle) or *Colpate* (bottom). The sulcate type were characterised by possession of numerous spores in ring when viewed under light microscope while the colpate type is characterised by presence of two apertures in their pollen after viability test is carried out. Three of the progenies (USRI/08/03, USRI/08/43 and USRI/08/85) as well as the three standard varieties (ILS-001, ILS-002 and Co 6806) were classified as colpate because they have aperture in their viable pollen grain while the others could be classified as sulcate because they posses many spore in their viable pollen grain.

The mean values for pollen characteristics among the USRI progenies and check varieties are presented in Table 2. Many of the progenies have higher percentage of viable pollen than the check varieties with USRI08/85 having the highest pollen viability and USRI/08/58 having the lowest percentage viable pollen. Sexuality based on pollen viability is usually used to classify flowering sugarcane genotypes as either female (0-49%) or male (≥50%). Since all the test genotypes had high pollen fertility, they can be correctly classified as male fertile and source of pollen in our hybridization programme. However, many of the genotypes with high pollen count also had high % pollen fertility which is contrary to earlier reports (Olaoye, 1996) indicating inverse relationship between pollen production and fertility. Some of the progenies used in this study as well var. ILS-002 were actually the non-flowering types, either at the time of selection (progenies) or release (ILS-002). However, results from this study showed that they now flower (and some of them profusely). This may not be unconnected with the effects of climate change which tend to support recent observation from our yield testing programme (Olaoye *et al*., 2010) and consistent with earlier reports that flowering behaviour (flowering or non-flowering), its extent (profuse or shy) as well as sexuality (male or female) in sugarcane do change relative to changes in climatic factors, (Badalou, Personal communication).

Cane yield and associated traits in the progenies and check varieties are presented in Table 3. There were significant differences among the genotypes for almost all the traits except stalk length and stalk diameter. Single stalk weight and millable cane population jointly contributed to overall cane tonnage as the high yielding genotypes (for example USRI/08/63, Co 6806, USRI/08/08 and USRI/08/46) showed superiority for these two traits. Low yielding genotypes on the other hand (Co 957, Local check and USRI/08/43) had high brix content which also supports earlier findings (Smith and James, 1969; Miller and James, 1971) of an inverse relationship between cane yield and sucrose in the juice and that different genes probably code for each trait. All the progenies yielded significantly higher than the check variety. Progeny USRI/08/63 had the highest cane tonnage which was comparable to the yield of the best standard variety (var. Co6806). Two other progenies (USRI/08/03 and USRI/08/46) also combined high cane yield with acceptable brix content. The difference in cane yield between the two highest yielding genotypes (USRI/08/63 and progeny and the check variety was 23t/ha-1 representing a yield advantage of 32.77%.

The ethanol yields in the progenies and those of three standard varieties are presented in Table 4. Among the progenies, the highest ethanol yield was obtained from progeny USRI/08/03 with 15% ethanol followed by progenies USRI/08/16, USRI/08/63, USRI/08/68 and USRI/08/85 with 10% ethanol respectively while the lowest value of 5% was recorded in progenies USRI/08/46, USRI/08/58 and USRI/08/80 had 5% ethanol all after 48 hours of fermentation. The slurry from progeny USRI/08/68 had the highest kinematic viscosity of 8.5 cm^3/s while USRI/08/63 had the least of 1.0 cm^3/s. The ethanol yield obtained in respect of the progenies was low when compared to values obtained in the standard varieties. This may be due to the fact that the determinations in 2011 was were carried out as soon as flowering commenced while the activity in 2012 was carried out long after flowering process was completed.

CONCLUSION

The results from the present study revealed that different genotypes exhibited superiority of performance especially with respect to sugar and ethanol yields. This implies that development of high ethanol content sugarcane varieties is also feasible using the current genetic resources at our disposal. Furthermore, since these progenies are highly fertile, they can serve as sources of genes for the development of high sugar and ethanol content sugarcane varieties.

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Table 1: Means with standard errors (SE±) for pollen fertility in ten sugarcane progenies and four check varieties (Ilorin, 2012).

Trait	Mean±SE	Min	Max	Range	%CV
Total Pollen count	582±174	88	1104	1016	53.0
No. of viable pollen grains	523±173	65	1026	961	63.4
No. of inviable pollen grains	26.6±8.52	8.7	44.0	35.3	12.9
% Viability	96.72±3.48	88.07	96.06	7.99	5.4

Table 2: Pollen characteristics and sexuality of 10 sugarcane progenies and two check varieties (Ilorin, 2012).

			Number of			
S/N	Genotype	Total pollen count	Viable pollen	Inviable pollen	% Viability	Sexuality
1.	USRI/08/03	727	692	34.7	95.18	Male
2.	USRI/08/16	392	374	17.3	95.41	Male
3.	USRI/08/43	1104	609	35.0	55.16	Male
4.	USRI/08/46	826	788	37.7	73.86	Male
5.	USRI/08/58	88	65	23.3	98.65	Male
6.	USRI/08/63	592	584	8.7	92.84	Male
7.	USRI/08/68	489	454	35.7	93.10	Male
8.	USRI/08/80	449	418	31.7	98.84	Male
9.	USRI/08/85	1038	1026	16.0	95.45	Male
10.	USRI/08/87	462	441	21.0	98.04	Male
11.	CO6806	614	602	12.3	95.70	Male
12.	ILS-002	396	379	16.7	94.55	Male
13.	ILS-001	808	764	44.0	74.10	Male
14.	Local Check	162	123	39.0	75.92	Male
	SED	246.5	245.4	12.14	4.93	
	LSD(0.05)	506.6	504.4	ns	10.14	
	F-Test	**	**	ns	**	
	%CV	51.9	57.5	55.8	6.7	

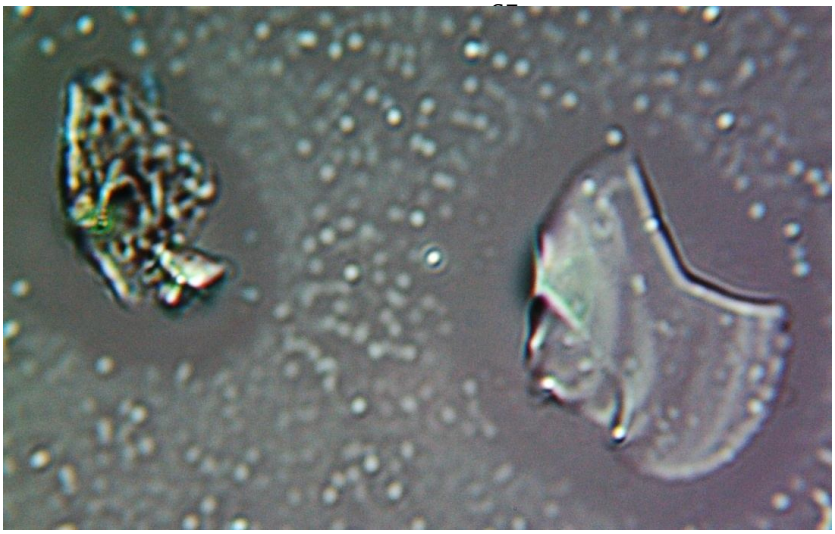
Table 3: Cane yield and associated traits in10 sugarcane progenies and five check varieties (Ilorin, 2012)

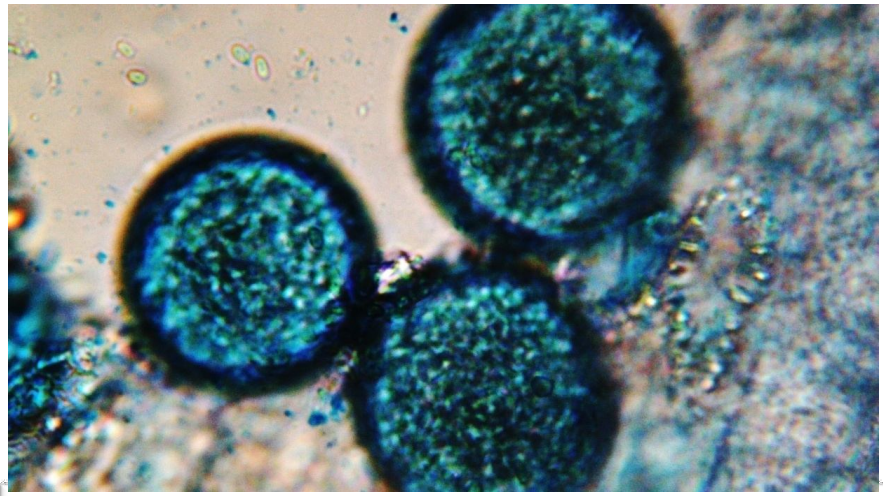
Genotype	Stalks /stool (no)	Tiller count (no)	Stalk length (m)	Stalk diameter (cm)	Internode length (cm)	Internode /stalk (no)	Millable canes (no)	Single stalk weight (kg)	^{o}Brix	Cane yield (t/ha^{-1})
USRI08/03	30	167	1.50	1.93	8.65	12	74	0.70	20.3	68.9
USRI08/16	23	110	1.11	2.07	6.80	11	47	0.50	19.6	58.4
USRI08/43	9	83	1.34	2.20	9.59	10	39	0.60	20.1	58.6
USRI08/46	34	141	1.52	2.40	8.67	13	53	0.83	20.4	67.5
USRI08/58	10	73	1.38	2.53	7.65	14	25	0.80	20.0	56.1
USRI08/63	24	128	1.23	1.93	8.73	14	52	0.70	20.0	71.6
USRI08/68	9	85	1.05	2.38	8.52	13	36	0.77	19.7	62.8
USRI08/80	21	126	1.58	2.10	9.18	15	46	0.67	20.4	62.5
USRI08/85	6	74	1.03	2.03	9.54	9	32	0.33	19.7	55.4
USRI08/87	15	120	1.17	1.97	8.99	12	45	0.40	19.9	63.0
Co 6806	24	60	1.36	2.57	8.70	16	52	0.97	20.4	71.0
Co 957	10	68	1.15	2.15	8.54	16	38	0.47	20.9	57.6
ILS-001	12	70	1.23	2.97	9.40	11	16	0.50	19.7	54.4
ILS-002	18	94	1.17	2.13	7.79	14	43	0.50	19.6	60.4
Local Check	25	158	1.10	1.97	8.64	11	61	0.40	20.0	8.14
Mean	18	104	1.34	2.22	8.63	12.73	43.93	0.61	20.05	61.09
Sed	4.64	27.16	0.23	0.28	0.64	1.79	23.26	0.269	0.69	9.24

Table 4: Ethanol content in sugarcane progenies and two check varieties (Ilorin, 2012).

	Brix value	pH value				
Genotype	Before fermentation	Before fermentation	After fermentation	Volume of distillate (ml)	Ethanol (%)	Kinematic viscosity of the slurry (cm3/s) @ 27^{o}C
USRI/09/03	18.5	5.0	3.6	470	15	6.1
USRI/09/16	18.5	5.0	3.5	420	10	5.4
USRI/09/43	18.5	5.2	3.4	815	8	1.1
USRI/09/46	14.0	5.3	4.3	1060	5	1.2
USRI/09/63	14.5	5.4	3.4	925	5	4.5
USRI/09/68	16.0	4.8	3.6	500	10	1.0
USRI/09/80	15.0	5.2	3.5	750	10	8.5
USRI/09/85	16.5	4.8	3.5	680	5	5.3
USRI/09/87	15.0	5.0	3.5	650	8	2.5
USRI/09/18	14.0	4.8	3.6	410	8	2.3
Mean						
ILS-001+	18.0	4.7	4.3	1390	51	2.1
ILS-002+	18.0	4.8	4.1	1460	46	5.0
Co 957+	18.0	4.8	3.5	3,200	26	6.1

+; Determination made in 2011 season.





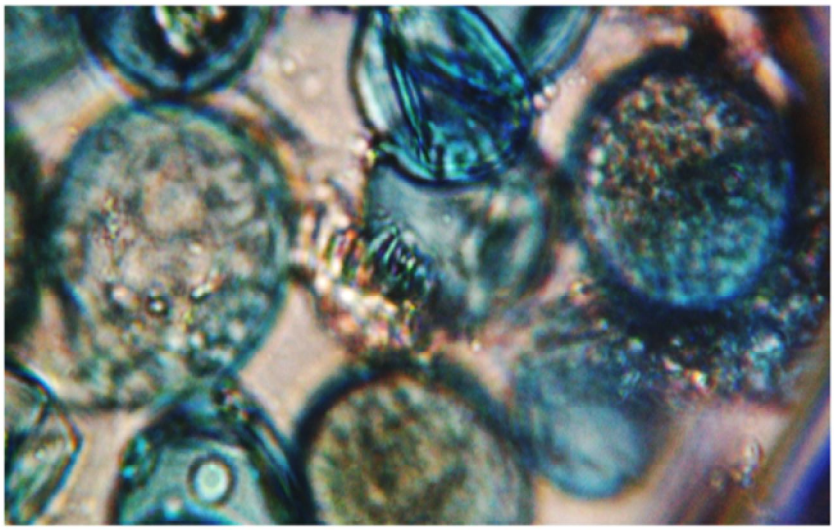


Plate 2: Different types of pollen morphology in sugarcane genotypes: inviable pollen grains (top), sulcate viable pollen grains (middle) and colpate viable pollen grains (bottom).

Plate 1: View of sugarcane juice Extractor (left), Fermenter (middle) and Distillation unit (right)

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FIELD PERFORMANCE AND SELECTION OF ADVANCED MUTANT LINES OF GINGER

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ABSTRACT

Generation of useful genetic variability in ginger through induced mutation using gamma-ray radiation was imitated at the National Root Crop Research Institute, Umudike in 2009 cropping season. The objective was to develop improved ginger varieties with high yield potentials and desirable agronomic characteristics considering the rhizome yield, oleoresin and resistance to field diseases. The generated mutant clones of ginger derived from the gamma-ray radiation have been subjected to recurrent selection based on the established selection criteria. In 2012, twenty mutant lines of M_3 generation were selected and advanced to M4 for further evaluation. Field result showed that fifteen out of twenty mutant lines at M_4 generation gave higher rhizome yields ranging from 21 tons -37 tons/ha with corresponding high percentage of oleoresin. The response of the M_4 mutant lines to diseases showed that the mutants were resistant to nematode. The mean gall index (MGI) recorded on each mutant line ranges from 0.02 -1.87. The leaf spot infestation was high in some mutant lines such as UG2-5-52, UG2-5-47, UG2-5-04, and UG1-9-01 but the severity of infestation tend to have less effect on the rhizome yield. This shows that some of the mutants are tolerant to the leaf spot disease. Fifteen promising M4 mutant lines were selected and nominated for multilocational trial to ascertain the yield stability.

Keywords: Disease, ginger, irradiation, lines, mutation, Mutants, yield

INTRODUCTION

Ginger (*Zingiber officinale* Rosc) is a monocotyledonous perennial herb in the family Zingiberaceae, grown mainly for its spicy and aromatic rhizomes. Ginger is a native of tropical south or Southeast Asia (Peter et al, 2007). It is an important tropical horticultural plant valued for it aroma, flavor and also medicinal properties. Ginger has basic antiseptic properties and is used as carminative and stimulant (Singh and Singh, 2000). It is also used as veterinary medicine (Islam et al 2008).

Ginger is an obligatory asexual species with narrow genetic base because gene introgression or recombination through hybridization is almost impossible (Iwo and Ekaette, 2010). As a result varietals development or improvement of ginger using conversional methods has become very difficult. According to Oseni (1994) improvement of any crop depends on the magnitude of genetic variability and yield related traits that can be exploited for efficient crop management and yield enhancement. Ginger being a vegetative propagated crop can be improved through induced mutagenesis. Induced mutagenesis serves as an important tool for creating usable genetic variability in crops. Genetic variability is fundamental to successful breeding program in vegetative propagated crops. The variation can occur naturally or can be induced through mutation using physical mutagens such as Gamma ray irradiation. The main advantage of mutation induction in vegetative propagated crops is the ability to change one or a few characters without changing the remaining characters in the genotype. The ultimate purpose of the Research work was to develop improved ginger varieties with high yield potentials and desirable agronomic characteristics considering the rhizome yield, oleoresin and resistance to pest and diseases. The generated mutant clones of ginger derived from the gamma-ray radiation have been subjected to recurrent selection based on the established selection criteria. In 2012, twenty mutant lines of M_3 generation were selected and advanced to M_4 for further evaluation for high rhizome yield, oleoresin and resistance to field pest and diseases.

MATERIALS AND METHODS

In 2012 cropping season, twenty promising M3 mutant lines of ginger were selected and advanced to M4 generation based on their agronomic performance. The mutant lines including the control were planted on the field in three replicates at Umudike. Each line was planted in 2-rows plot of 0.8 x 5m with inter-row and intra-row spacing of 0.4 x0.4m respectively. Mulching was carried out immediately after planting. The M4 mutant plants were evaluated using number of tillers, rhizome fingers, oleoresin contents, rhizome yield and response to pest/diseases as the selection criteria. The incidence of field diseases such as leaf spot and mean gall index (MGI) were measured using a scale of 1-5. The determination of oleoresin was carried out using the methods suggested by Onwuka, (2005)

RESULTS

The performances of the evaluated twenty mutant lines are shown in table 1. Generally the performance of the mutant lines were tremendous considering the rhizome yields. Fifteen M4 mutants' lines tend to be more promising with rhizome yields ranging from 21tons/Ha - 37tons/Ha. These conformed to earlier report by Orkwor (1983) that yields of 30-34 tons/ha are obtainable under well managed experimental farms and Purseglove (1987) reported that under improved cultivation condition, yields as high as 38 tonnes/ha can be achieved. Each of the high yielding mutant lines gave a commensurate percentage of oleoresin above the control.

The response of the evaluated advanced mutant lines to diseases showed that the mutants were resistant to nematode. The mean gall index recorded on each line was very low ranging from 0.02-1.87 except the control with 3.02 MGI. This indicated that the gamma-ray irradiation also assisted in inducing resistance gene against nematode (Table 2). Leaf spot infestation was high in some mutants such as UGII-5-52, UGII-5-47, UGII-5-04, and UGI-9-01.The severity of infection tend to have less effect on the rhizome yield of the mutants. This may be a case of tolerance to the late leaf spot.

CONCLUSION

The agronomic performance and variations in yield components observed on the developed mutant lines of ginger shows the effectiveness of induced mutation. Based on the observed variability on yield potentials and oleoresin content, fifteen M_4 mutant lines were selected and nominated for multi-locational evaluation. The multi-locational evaluation across different ecological zones known for ginger production will ascertain the yield stability of the selected mutant lines. Integration of cultivar stability with yield is important for the purpose of selecting high yielding and stable genotypes.

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Table 1. Mean values of agronomic components of improved mutant lines (M_4) of ginger

S/N	**Mutant lines**	**Number of Tillers**	**Total Rhizome Fingers**	**Oleoresin (%)**	**Rhizome yield Tons/ha**
1	UG2-5-31	21	8	7.2	33.8*
2	UG2-5-03	17	15	6.5	16.5
3	UG2-5-52	11	16	6.0	26.8*
4	UG2-5-35	12	18	6.2	27.5*
5	UG2-11-07	14	18	5.6	26.78*
6	UG2-5-48	8	17	7.0	21.6*
7	UG2-5-49	10	17	5.7	24.0*
8	UG2-5-38	18	17	5.8	23.0*
9	UG2-5-18	15	17	7.2	21.5*
10	UG2-5-22	9	16	6.1	30.0*
11	UG2-5-47	8	19	6.2	21.7*
12	UG2-5-04	17	16	6.6	17.3
13	UG2-7-24	13	19	6.0	25.0*
14	UG2-13-02	11	15	5.7	22.0*
15	UG2-7-25	10	14	5.6	37.5*
16	UG1-9-01	8	18	5.3	21.0*
17	UG1-11-10	8	17	5.4	9.8
18	UG1-5-24	14	16	6.4	18.9
19	UG1-11-03	11	17	5.2	27.0*
20	UG1-9-05	4	13	5.6	7.5
21	Control	6	9	4.5	6.5
	Mean	**11.6**	**15.6**	**6.7**	**22.3**
	SE±	**0.93**	**0.76**	**0.67**	**1.63**
	CV (%)	**36**	**21**	**45**	**32**
	.				

Key: *=The fifteen high yielding mutant lines

Table 2: Incidence of field diseases on M_4 Mutant lines of ginger evaluated at Umudike in 2012

S/N	Mutant lines	Mean Gall index	Leaf spot	Rhizome yield t/ha
1	UG2-5-31	0.03	0	33.8
2	UG2-11-03	0.45	0	16.5
3	UG2-5-52	0.15	5	26.8*
4	UG2-5-35	0.04	2	27.5
5	UG2-11-07	0.40	0	26.7
6	UG2-5-48	0.02	1	21.6
7	UG2-5-49	0.25	0	24.0
8	UG2-5-38	0.20	2	23.0
9	UG2-5-18	0.15	1	21.5
10	UG2-5-22	0.11	5	30.0*
11	UG2-5-47	0.05	5	21.7*
12	UG2-5-04	0.14	0	17.3
13	UG2-7-24	0.20	1	25.0
14	UG2-13-02	0.13	1	22.0
15	UG2-7-25	0.13	1	37.5
16	UG1-9-01	1.40	5	21.0*
17	UG1-11-10	0.67	0	9.8
18	UG1-5-24	0.93	1	18.9
19	UG1-11-03	0.67	0	27.0
20	UG1-9-05	1.87	0	7.5
21	Control	3.02	4	6.5*

Key:

*=Susceptible but tolerant to late leaf spot disease

PGB20

CHARACTERIZATION OF MINI CORE COLLECTION OF COWPEA ACCESSION FOR *STRIGA* RESISTANCE USING SSR AND AFLP-DERIVED SCAR MARKERS

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ABSTRACT
S .gesnerioides (Willd) Vatke is a major biological constraint to cowpea production in the dry Savannas of sub-Saharan Africa. Yield losses caused by *S. gesnerioides in* these regions are estimated in millions of tons annually, and prevalence of *Striga* soil infestation is steadily increasing. The use of resistant varieties remains the most economically and environmentally

friendly means of controlling the parasite. *Striga* resistance in cowpea is conferred by a single dominant gene. The lack of broad resistance is one of the biggest problems when trying to develop resistant cultivars across biotypes. Most of the cowpea cultivars with resistance to *Striga* biotypes prevalent in Nigeria were developed using B301 or lines derived from it as sources of resistance. There is therefore the need to identify additional sources of resistance other than B301 in order to ensure sustainable control of the parasite. In the present study, one hundred and ninety four mini core collections of cowpea accessions were screened for resistance to *Striga* under artificial infestation of *Striga* in the screen house using pot culture technique. Six cultivars with known *Striga* reaction were included as checks. There was high genetic variability among accessions in terms of reaction to Striga. Out of the total 194 accessions screened, only three of the accessions (Tvu-9343, Tvu-1272 and Tvu-16514) were completely and consistently free of *Striga* attachment to the cowpea root. The three newly identified accessions were characterized using three DNA markers to validate phenotypic data. Two out of the three accessions produced polymorphic bands which were different from that of B301 band size, which indicates a different resistance gene source. These new accessions are potential donor parents for breeding and pyramiding of *Striga* resistance genes(s) into single genotype for horizontal resistance.
Keywords: Maker assisted selection, FTA technology, cowpea, *Striga gesnerioides,*

INTRODUCTION

Cowpea *Vigna unguiculata* (L.) Walp is an important grain legume grown in tropical and subtropical region of the world, primarily in sub-Saharan Africa. Cowpea is of significant economic importance worldwide with 24% protein and high mineral content. The relatively high protein content of cowpea makes it an important supplement to the diet of many African people (Emechebe *et al*., 1991), who consume cereals, roots, and tubers high in carbohydrate and low in protein (Lambot, 2002). The crop provides cash income as well as fodder for livestock and is frequently intercropped with cereals where crop mixtures with cowpea are beneficial in maintaining soil fertility (Carsky *et al*., 1995; Noubissie *et al*., 2010). The estimated world cowpea production is over 12 million ha with annual production estimated at about 4.99 million tons (FAO, 2010). Out of this estimate, West and Central Africa (WECA) accounts for over 9 million ha of the area under cowpea cultivation with about 3 million tons of grain production. Nigeria is the largest cowpea producer in West Africa, accounting for about 60% of the total world production and also has the highest level of consumption, followed by Niger and Burkina Faso which produces 10% (Pereira *et al*., 2001).

Despite the importance of cowpea, its production is constrained by several biotic and abiotic stresses. Among the biotic stresses, the parasitic weed *Striga gesnerioides* (Willd) Vatke of the Orabanceae family is one of the most important constraints to its production especially in the dry savannas, where cowpea is an important crop. *S. gesnerioides* is an obligate root hemiparasite that parasitizes cowpea plants leading to severe chlorosis, wilting, stunting and even death of the susceptible host (Olmstead et al., 2001). Annual yield losses are estimated in millions of tons (Kamara *et al*., 2008). Total crop failure on susceptible host has also been reported (Hibberd *et al*., 1996). Control of *S. gesnerioides* is difficult to achieve because of the intimate association between the parasite and its host. Several control strategies have been developed for parasitic weeds including improved cultural practices, breeding using wild and cultivated germplasm as

sources of resistance, and the use of chemical control. Among these control strategies, the use of resistant cultivar is probably the most economic and efficient method to control the parasite.

Over the last two decades several improved cowpea varieties have been developed for *Striga* resistant. However, a recent study conducted by Omoigui et al., 2011in northern Nigeria showed that some varieties that were classified as resistant to *Striga* in one region were found to be susceptible when grown in another region and they speculated the existence of different races of *Striga* in Nigeria. Studies by Botanga and Timko (2006) using molecular profile identified seven different races of *Striga* that affect cowpea across West and Central Africa.
The lack of broad or horizontal resistance is a major problem when trying to develop resistant cultivars across biotypes. Most of the cowpea cultivars with resistance to *Striga* biotypes prevalent in Nigeria were developed using B301 or lines derived from it as sources of resistance. There is therefore need to identify additional sources of resistance other than B301 in order to ensure sustainable control of the parasite. The discovery of new sources of *Striga* resistant gene would not only help in improving cowpea, but will help to develop strategies for pyramiding resistance gene in cowpea. The study was initiated to screen a large germplasm collection to identify new source of resistance to cowpea *Striga* using DNA profile and convention approaches.

MATERIALS AND METHODS
This experiment was conducted in two locations (Pot culture techniques screening was conducted at IITA, Kano while the DNA analysis was carried out at the Molecular Biology Laboratory of the University of Agriculture, Makurdi).

One hundred and ninety four cowpea accessions collected from IITA genebank were used for the study. Six cultivars with known *Striga* history were included as checks. This comprised four resistant cultivars: B301, IT97K-499-35, IT03K-338-1, and three *Striga* susceptible cultivars; IT84S-2246-4S, TVx 3236, and Borno Brown (a local cultivar from Borno State),

Striga seeds were used as inoculums. .The plants were grown in plastic pots filled with a mixture of sand and top soil in a ratio 2:1 and infested with 1000 *Striga* seeds per pot. After soil infestation with *Striga* seeds, the soil was kept moist for 9 days to precondition *Striga* with seeds to ensure optimum germination. Three cowpea seeds were sown in each pot and later thinned to two plants at two weeks after planting. One gram of compound fertilizer (NPK: 15:15:15) was applied at one week after planting. The pots were watered adequately, maintained at field capacity. Weed was controlled by hand pulling to keep pots free of weeds.

Data were collected on plant height, day to *Striga* emergence, stem weight, *Striga* plant attached, *Striga* height, plant shoot weight (biomass), plant root dry weight, *Striga* count at 7 and 8 weeks after planting, *Striga* root weight and *Striga* houstorium weight. The experiment was terminated at 70 days. Pots were washed and examined for *Striga* houstorium attachment. Plants which support Striga houstorium attachment were classified as susceptible while those that were free of *Striga* houstorium attachment were classified as resistant(see Fig. 1). Data collected were analysed using the linear additive model for the CRD in SAS (Little and Hill 1999).

Fig. 1: Resistance was assessed by visual counting of emerged and underground *S. gesnerioides* haustorial attachment on the accessions and cultivars

Following morphological characterization, DNA analysis was carried out to validate phenotypic data. Genomic DNA was extracted from leaf tissue of two week- old plants using the FTA® Plant saver cards for PCR analysis using the methodology of Whatman, (2002) and Omoigui *et al.*(2009).

The secondary young leaf was excised from the plant and placed in a square of the FTA card. The leaf sample was covered with a parafilm paper and a pestle was used to press the leaf sample onto the FTA® paper until both sides of the FTA were soaked with the plant sap (Fig. 2). In circumstances where the pestle was stained by the leaf sap as a result of parafilm paper damage, a paper towel soaked in 70% ethanol was used to clean the pestle in between samples to prevent cross- contamination. The FTA cards were allowed to dry for one hour; plant material was brushed off with tissue paper. After air drying, FTA® cards were placed in a paper pouch and stored at ambient temperature in a dry location.

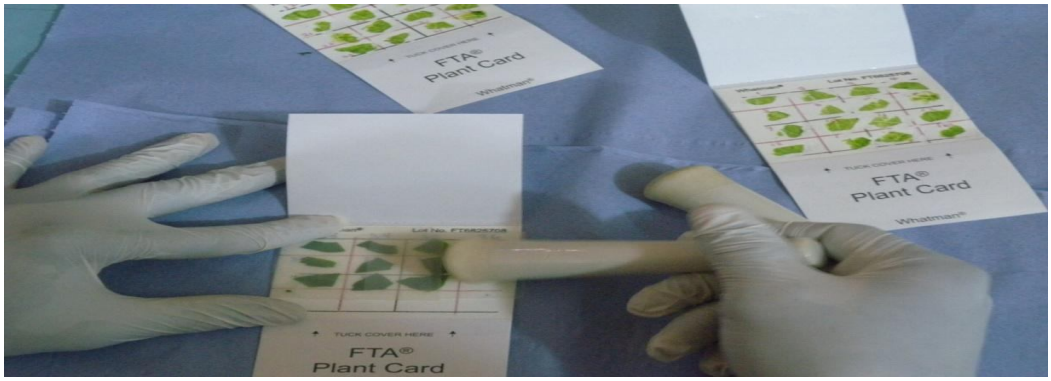


Fig. 2: Genomic DNA extraction using FTA card and a pestle to press the leaf sample onto the FTA card at IITA Lab, Kano Station

A disc from the dried FTA tissue print was removed using a clean Harris® micro- punch and the disc was placed directly into a 1.5 ml eppendorf tube. The disc was washed twice with 200 µl of 70% ethanol, and incubated for 5 min between each wash. A repeat wash with 200 µl of FTA

reagent, was incubated for 5 min at room temperature. The liquid was discarded. The tubes were inverted and drained on a paper towel tor air for approximately 1 h. After drying, the disc was transferred to a PCR tube for PCR analysis.

PCR analysis was done with 3 primers SSR-1, MahSe2 and C42B. Accupower PCR premix tube (BIONEER) was used for the PCR reaction to which 1 FTA purified disc containing the DNA sample and 16µl of water-Molecular Biology Grade (Lonza) were added.

A 10µl of the final PCR product was electrophoreses on a 2% agarose gel with ethidium bromide staining. The gels were run for approximately 1 h 20 min at 170 voltage in 1 X Tris acetic acid (TAE) buffer (45 mmol L-1 glacial acetic acid, 0.5 mmol l-1 ethylenediaminetetra acetic acid (EDTA), (pH, 8.4). 10µl of a 100bp DNA was ladder loaded in the first well for band size determination of PCR products. The ethidium bromide-stained gel was visualized on an UV transilluminator and photographed using a Polaroid camera.

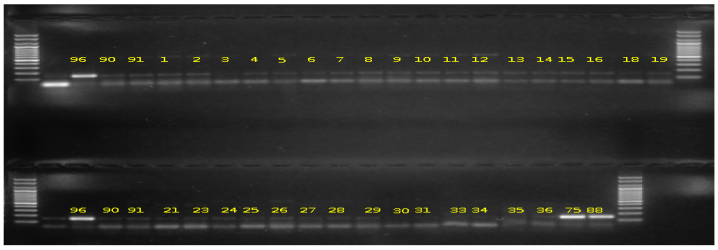
RESULTS

Out of the total 194 accessions screened, three of the accessions (Tvu-9343, Tvu-1272 and Tvu-16514) were completely and consistently free of *Striga* attachment to the cowpea root. Result from the ANOVA revealed high genetic variability among the accessions for reaction to *Striga* and other parameters measured. Among the parameters measured, plant height had the highest mean (14.08) with a range 3.0-19.5. High variability was also observed for Days to *Striga* emergence, *Striga* attachment, and *Striga* count at 56 days (Table 1). The lowest mean score was recorded for *Striga* root weight. Out of the 89 accessions characterized using DNA markers, only two showed polymorphic band (Fig. 3 and 4), while the one of the accessions (Tvu-9343) was not amplified by the marker used (Fig.3, 4).

Table 1: Mean and Range Performance of Cowpea Accessions

Character	Mean	Range
PHT@wk	14.08	3.0-19.5
STMwt	2.42	1.5 to 3.8
Dstremg	9.45	0 to 51.5
Statt	3.27	0 to 35.0
STrHT	2.4	0 to 17.35
PLRTwt	2.35	0.1 to 7.6
PLShwt	6.75	1.2to 12.5
Scnt49D	0.93	0 to 9
Scnt56	1.25	0 to 15.0
STrwt	0.25	0 to 4.55
STRhwt	0.262	0 to 2.45

PHT@3wk= Plant height at 3 week, STMwt= Stem weight, Dstremg= Days to *Striga* emergence, Statt= *Striga* attached, STrHT= *Striga*root height, PLShwt= Plant shoot weight, PLRTwt= Plant root weight, Scnt49D= *Striga* count at 49 days, Scnt56D= *Striga* count at 56 days, STrwt= *Striga* root weight and STRhuwt= *Striga* haustorium.



A section of PCR reaction products of SSR resolved in 2% Agarose gel.

Fig. 3: A section of PCR reaction products of SSR-1 resolved in 2% Agarose gel

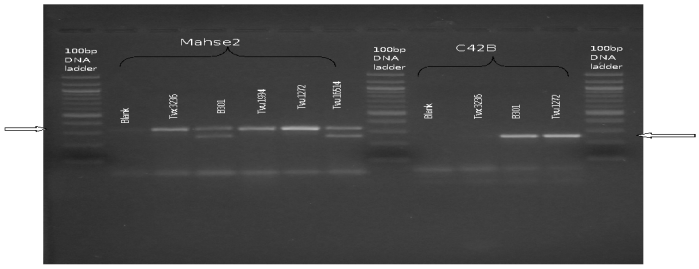


Fig. 4. PCR amplification of DNA based on the use of BIONEER Accupower PCR premix with the SCAR(marker Mahse2 and C42B) in 2% agarose gel with ethidium bromide staining.

DISCUSSION

A total of 194 accessions collected from a mini core collection of the IITA cowpea germplasm with six known genotype as checks were phenotype for resistance to *S. gesnerioides* in pot trials carried out in screen house of IITA, Kano station . Of the 194 accessions screened in the preliminary study, 89 were free from *Striga* attachment while the rest supported Striga attachment and were classified as susceptible. Out of the total of 89 accessions screened, only three of the accessions (Tvu-9343, Tuv-1272 and Tvu-16514) showed absolute resistance and were confirmed by molecular assay except Tvu-9343 that was not amplified by the markers used. The mechanism of resistance of the newly identified accessions may be antibiosis or antixenosis (non preference) that prevent the germination of the *Striga* seeds or the penetration of the host roots by the parasite radicle.

The ninety six accessions were genotyped to validate phenotypic data and determine the relationships of the resistant accessions with the existing B301 using the three DNA markers. Of the 96 accessions genotyped only two accessions (Tvu-1272 and Tvu-16514) produced polymorphic bands). It is interesting however, to note that the genotypic score did not fully agree with phenotypic score in one of the accessions (Tvu-9343). It is very likely that the three markers are not linked to the gene that confers the resistance in Tvu-9343. This result is similar to the report of Timko et al. (2013) who reported that SSR-1 marker was found in GH2284 although this cowpea accession was not resistant. Since the marker is imbedded at the C-terminal end of the RSG3- B301 gene conferring SG3 resistance, it would appear that GH2284 may have picked up mutation that rendered it susceptible. This study also corroborate with the report of (Ouedraogo J, Ouedraogo M, and Timko M P, unpublished data) which says analysis has shown that a modified version of 61R termed MahSe2 is effective in identifying resistance to *Striga* race SG3. However, this study is also slightly different with the finding of Omoigui et al (2012) who reported that MahSe2 and C42B markers indicator was quite similar with the phenotypic classification. Finally, this study could also suggest that Tvu-9343 is completely susceptible but escape phenotypic characterization. It is also interesting to note that one of the newly indentified accessions (Tvu-16514) has the same band size with the control checks B301 (Plate C and D). This is not full indicator that B301 and Tvu-16514 have the same gene that confers their resistance. This therefore, can be ascertained in two ways. First, study of their allelic relationship. The second option is the use of primers designed based on the variations observed in their nucleotide sequences at this gene region. The resistant accession amplified different band sizes indicating genetic variation or a new gene for *Striga* resistance.

CONCLUSION

This research work presents a report on the morphological and molecular characterisation of mini core collection of cowpea accession for *Striga* resistance. The study revealed that three out of 194 accessions screened, were absolutely free from *Striga* attachment on the cowpea roots. SSR-1 and SCAR markers were used to validate the phenotypic data. It was interesting to note that two of the three accessions (Tvu-1272 and Tvu-16514) produced polymorphic bands. However, the amplified bands were different from that produced by B301, which suggests that the *Striga* resistance gene(s) in the accessions may be different from resistance gene in B301. These new accessions are potential donor parents for breeding and pyramiding of *Striga* resistance genes(s) into single genotype for horizontal resistance.

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PGB21

ASSESSMENT OF GENETIC DIVERSITY IN NIGERIAN SESAME USING MORPHOLOGICAL MARKERS

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ABSTRACT
The assessment of genetic diversity among 23 sesame genotypes (*Sesamum indicum* L.) obtained from different locations in 10 states across Nigeria was carried out using evidences from qualitative, quantitative growth and pod morphological traits. The plants were grown in 2008 and 2009 at the Research Garden of the Biological Sciences Department, Kogi State University (KSU), Anyigba, Nigeria in Randomized Complete Block Design (RCBD) to characterize and evaluate the sesame genotypes. Nine qualitative, eighteen growth and eight pod attributes were studied. Data pooled on these attributes were subjected to Analysis of Variance (ANOVA) and means with significant differences were separated using the Duncan Multiple Range Test (DMRT). The results revealed that all the traits considered in this study showed significant variation among the 23 different sesame genotypes which imply that high genetic diversity exists among the 23 studied sesame accessions. Therefore, there is ample opportunity for sesame breeders to develop improved varieties from the accessions considered in this study.

Keywords: Diversity, Sesame, Qualitative, Quantitative, Pod.

INTRODUCTION

The family Pedaliaceae, according to Zavareh *et al.* (2008) consists of 16 genera and about 60 species. *Sesamum indicum* (L.) like other plants that have been domesticated for a long time, comprises many different varieties that differ considerably in size, form, growth habit, corolla colour and seed characteristics such as size, colour and composition (Weiss, 2000). Tabatabaei *et al.* (2011) reported that little is known about genetic variability of sesame in many possible hot spot. One of these hot spots is postulated to be West Africa which includes Nigeria. Recently, Ercan *et al.* (2002), Gidey *et al.* (2012), Kumar and Sharma (2011), Pham *et al.* (2010), Suhasini (2006) and Tabatabaei *et al.* (2011) investigated the genetic diversity of sesame from Turkey,

Ethiopia, India, Viatem, Dharwad and Iran respectively using morphological markers. Olaoye and Ishaq (2009) reported that information on genetic diversity among plant collections is important in understanding the course of evolution in new varieties and in selecting desirable parents for breeding. Therefore, accurate assessment of the extent of genetic diversity among Nigerian sesame accessions will be useful for hybrid development. Alege and Mustapha (2013) reported great genetic diversity among Nigerian sesame using proximate traits and recommended the use of other markers like morphological study to substantiate the extent of genetic diversity in Nigerian sesame. It is against this background that the present work was undertaken to assess the genetic diversity among 23 sesame genotypes obtained from different locations across Nigeria using morphological traits.

MATERIALS AND METHODS

Twenty three accessions of sesame, comprising 18 traditional and 5 improved accessions were collected from ten states in North-West, North-East, North-Central and South-West regions of Nigeria between the months of September to November in 2008 when farmers were expected to harvest the crop. Preliminary information on the plants was obtained from the farmers. A brief description of the sesame accessions used for this study is shown in Table 1. Field trial was conducted at the research garden of the Biological Sciences Department of Kogi State University, Anyigba, Nigeria. The 23 sesame genotypes were laid out in Randomised Complete Block Design (RCBD) with three replications for each genotype.

Thirteen qualitative, eighteen vegetative growth and eight reproductive yield (pod) attributes were studied. The descriptions of qualitative traits studied were done according to the code of International Plant Genetic Resources Institute (2004). All the linear measurements were carried out according to the method of Akinyele and Adigun (2006). Weighing was carried out according to Alege *et al.* (2011). Data pooled on the quantitative vegetative and yield characteristics were then subjected to Analysis of Variance (ANOVA) and means were separated using the Duncan Multiple Range Test (DMRT). The clustering of the 23 accessions was done by average linkage method on the 18 vegetative growth and 8 reproductive yield traits using SPSS V2 software.

RESULTS AND DISCUSSION

All the 23 sesame accessions grew developed well with virtually no clear differences between their phenotypic appearance at the research site and their place of origin. However, qualitative attributes like the habit of plant, shape and margins of the leaves on the upper and lower parts of the plants are stable among the 23 different sesame genotypes studied. In contrary, leaves on the middle part of the plants vary among the 23 sesame genotypes (table 2). This report is in agreement with the findings of Robert (2002) who reported that sesame leaves vary widely in shape and size, not only among different varieties, but also on the same plant. Traits like hairiness of the stem, colour of the stem, maturity period and flower colour to some extent vary among the 23 sesame samples. This indicates that each of the 23 sesame accessions is a distinct genotype. The qualitative attributes considered in this study did not show much variation among the 23 studied genotypes because qualitative traits are known to be controlled by single or few genes with little or no environmental influence on their expressions (Elmund *et al.* 2004).

All the 18 quantitative (vegetative) traits studied showed significant differences among the 23 sesame genotypes using Analysis of Variance (ANOVA) (table 3 and 4). This further revealed that wide genetic diversity exists among the 23 sesame accessions for improvement. This report agrees with the findings of Pham *et al.* (2010) who reported significant differences among 17 sesame varieties from different origins for all the morphological characters studied in Vietnam and China. Also, Ozkan *et al.* (2012) reported significant variations in all the morphological attributes studied on 12 local sesame genotypes from Kilis region in Turkey.

The number of loculi, number of stamens and numbers of styles were not analyzed statistically (Table 5). The result shows that there are 4 loculi in each pod for all the accessions except accession 19 which contains 6 loculi and all the studied sesame genotypes had 4 stamens and 1 style in their flowers. This indicates that the evolution of these attributes is along the same trend and they are under strong genetic control in sesame. All the 8 yield characteristics showed significant differences among the 23 sesame genotypes using Analysis of Variance (ANOVA) (Table 5). Similarly Alege *et al.* (2011) reported the existence of genetic diversity among three species of sesame for all the pod traits studied.

The sesame accessions studied were grouped into six diversity classes (table 6). Sesame accessions in the same cluster are more closely related in terms of the 18 vegetative and 8 yield characters analyzed than those accessions in different clusters. Clusters III and V were formed by 2 accessions each while clusters I, II, IV and VI were formed by 11, 4, 3 and 1 accessions respectively. Clusters V and VI comprised of the black seeded accessions (tables 1 and 5). The clustering of the black seeded accessions 20 and 22 together in the same group is in conformity with the earlier report of Alege and Mustapha (2013) for proximate composition of Nigerian sesame. Also, the grouping of accessions 11, 12, 13 and 23 together was earlier reported by Alege and Mustapha (2013) which further confirms their close genetic similarity This indicates that sesame accessions from the same adaptation zones or geographical origins in Nigeria may be closely related. Though the clustering of accessions 5, 6 and 8 together in this study contradicts the report of Alege and Mustapha (2013) where the three accessions occupied separate groups using proximate composition which indicates that genes controlling proximate traits differ from those controlling morphological characters.

Generally, clustering of all the accessions reflects geographical affinity based on origin of the accessions or place of collection (table 5) which is consistent with the report of Pham *et al.* (2010) on sesame landraces from Turkey and Gidey *et al.* (2012) on sesame landraces from Ethiopia. Varieties belonging to different clusters have maximum potential to generate variability among progenies when used in crosses for the production of hybrid sesame. Gidey *et al.* (2012) reported that crosses between parents with maximum genetic divergence would be more responsive to improvement since they are likely to produce higher heterosis and desirable genetic recombination among segregating populations.

CONCLUSION

There is high genetic diversity in Nigerian sesame to be considered for their improvement. Accessions from different geographical origin may have different genetic background. The genetic diversity reported in this study is therefore wide enough for the improvement of Nigerian sesame.

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Table 1: Origin and brief description of the 23 Sesame accessions used for the study.

Accession Numbers	Accession Names	Sample Sources (States)	Geopolitical Zones	Brief Morphological Description of Samples at their Location
1	03M	Badeggi (Niger)	North Central	Erect green stem, branched, whitish pink flower with light brown seeds.
2	E8	Badeggi (Niger)	North Central	Erect green stem, branched, whitish pink flower with light brown seeds.
3	01M	Badeggi (Niger)	North Central	Erect green stem, branched, whitish pink flower with light brown seeds.
4	02M	Badeggi (Niger)	North Central	Erect green stem, branched, whitish pink flower with light brown seeds.
5	EXSUDAN	Badeggi (Niger)	North Central	Erect green stem, branched, whitish pink flower with light brown seeds.
6	IBA I	Ibadan (Oyo)	South West	Erect green stem, branched, whitish pink flower with dark brown seeds.
7	IBA II	Ibadan (Oyo)	South West	Erect green stem, branched, whitish pink flower with light brown seeds.
8	OKE I	Okene (Kogi)	North Central	Erect green stem, branched, whitish pink flower with light brown seeds.
9	YOL I	Yola (Adamawa)	North East	Erect green stem, branched, whitish pink flower with light brown seeds.
10	MAI I	Maiduguri (Borno)	North East	Erect green stem, branched, whitish pink flower with dark brown seeds.
11	KAN III	Kano (Kano)	North West	Erect green stem, branched, whitish pink flower with white seeds.
12	KAN II	Kano (Kano)	North West	Erect green stem, branched, whitish pink flower with light brown seeds.

13	KAN I	Kano (Kano)	North West	Erect green stem, branched, whitish pink flower with light brown seeds.
14	MAK I	Makurdi (Benue)	North Central	Erect green stem, branched, whitish pink flower with light brown seeds.
15	OUT	Otukpo (Benue)	North Central	Erect green stem, branched, whitish pink flower with light brown seeds
16	ZAR I	Zaria (Kaduna)	North Central	Erect green stem, branched, whitish pink with dark brown seeds
17	ANY I	Anyigba (Kogi)	North Central	Erect green stem, branched whitish pink flower with light brown seeds
18	ANY II	Anyigba (Kogi)	North Central	Erect green stem, branched, whitish pink flower with dark brown seeds
19	OKE II	Okene (Kogi)	North Central	Erect green stem, branched, whitish pink flower with dark brown seeds
20	ILO I	Ilorin (Kwara)	North Central	Erect purple stem, branched, purple flower with black seeds.
21	ILO II	Ilorin (Kwara)	North Central	Erect purple stem, profusely branched, pink flower, black seeds
22	OFF I	Offa (Kwara)	North Central	Erect green stem, branched, pink flower, black seeds
23	JAL I	Jalingo (Taraba)	North East	Erect greenstem, branched, whitish pink flower with light brown seeds

Table 2: Qualitative Attributes of the 23 Sesame Accessions.

Accession Numbers	Plant habit	Branching Pattern	Hairness Of the stem	Stem colour	Upper leaf shape and margin	Middle leaf shape And margin	Lower leaf shape And margin	Maturity Period (days)	Flower Colour
1	Erect	Opposite	Absent	Green	LE	OSSL	OS(LOBED)	64	Whitish pink
2	Erect	Opposite	Medium	Green	LE	OSSL	OS(LOBED)	61	Whitish pink
3	Erect	Opposite	Sparce	Green	LE	OSSL	OS(LOBED)	66	Whitish pink
4	Erect	Opposite	Medium	Green	LE	OSWL	OS(LOBED)	58	Whitish pink
5	Erect	Opposite	Medium	Green	LE	OSSL	OS(LOBED)	64	Whitish pink
6	Erect	Opposite	Sparce	Green	LE	OSSL	OS(LOBED)	91	Whitish pink
7	Erect	Opposite	Medium	Green	LE	OSSL	OS(LOBED)	89	Whitish pink
8	Erect	Opposite	Medium	Green	LE	OSWL	OS(LOBED)	66	Whitish pink
9	Erect	Opposite	Sparce	Green	LE	OSWL	OS(LOBED)	71	Whitish pink
10	Erect	Opposite	Medium	Green	LE	OSWL	OS(LOBED)	78	Whitish pink
11	Erect	Opposite	Medium	Green	LE	OSWL	OS(LOBED)	56	Whitish pink
12	Erect	Opposite	Medium	Green	LE	OSWL	OS(LOBED)	62	Whitish pink
13	Erect	Opposite	Medium	Green	LE	OSSL	OS(LOBED)	54	Whitish pink
14	Erect	Opposite	Medium	Green	LE	OS(NO LOBED)	OS(LOBED)	62	Whitish pink
15	Erect	Opposite	Sparce	Green	LE	OSSL	OS(LOBED)	90	Whitish pink
16	Erect	Opposite	Sparce	Green	LE	OS(NO LOBED)	OS(LOBED)	65	Whitish pink
17	Erect	Opposite	Sparce	Green	LE	OS(NO LOBED)	OS(LOBED)	64	Whitish pink
18	Erect	Opposite	Sparce	Green	LE	OS(NO LOBED)	OS(LOBED)	68	Whitish pink
19	Erect	Opposite	Medium	Green	LE	OS(NO LOBED)	OS(LOBED)	61	Whitish pink
20	Erect	Opposite	Profuse	Purple	LE	OSWL	OS(LOBED)	74	Purple
21	Erect	Opposite	Profuse	Green	OS	OS(NO LOBED)	OS(LOBED)	71	Pink
22	Erect	Opposite	Medium	Green	OS	OS(NO LOBED)	OS(LOBED)	83	Whitish pink
23	Erect	Opposite	Medium	Green	LE	OSWL	OS(LOBED)	65	Whitish pink

KEY FOR THE QUALITATVE ATTRIBUTES :

OS-OVATE SHAPE DLEAF WITH SERRATED MARGINS LE-LINEAR SHAPED LEAF WITH ENTIRE MARGINS SERRATED MARGIN AND WEAKLY LOBED

TABLE 3: Some Quantitative Vegetative Traits for the 23 Studied Sesame Genotypes.

AC.N	PHP	NLP	NBP	NSB	SGP	NNP	LNP	RLP	FPH
1	93.24 bcd	34.80 a	5.40 abc	2.40 a	2.34 bcd	9.60 abc	12.04 defg	15.58 ab	166.86 i
2	86.24 bc	49.80 ab	3.60 abc	4.60 a	3.06 cd	9.40 abc	10.86 cdef	19.34 abc	173.38 i
3	99.34 bcdef	64.20 ab	6.40 abc	2.20 a	2.66 bcd	11.20 bcd	13.54 fg	16.28 ab	167.78 i
4	98.50 bcdef	48.80 ab	5.20 abc	2.00 a	3.12 d	10.20 bcd	15.56 g	20.32 abc	167.58 i
5	88.70 bc	45.00 ab	3.60 abc	0.20 a	2.70 bcd	12.00 bcde	12.74 efg	15.64 ab	159.14 i
6	83.94 b	48.40 ab	4.80 abc	2.00 a	2.32 bcd	10.80 bcd	11.78 def	17.40 ab	112.26 bcde
7	111.22 fg	68.20 b	7.80 cd	5.00 a	2.26 bc	12.40 bcde	11.54 cdef	17.46 ab	121.16 cdefg
8	96.82 bcdef	42.80 ab	6.80 bc	0.40 a	2.20 b	11.00 bcd	10.18 abcdef	20.90 bcd	142.20 g
9	109.10 efg	65.00 ab	5.60 abc	0.60 a	2.54 bcd	13.20 cde	9.42 abcde	16.92 ab	138.12 gh
10	91.90 bcd	48.60 ab	4.40 abc	0.60 a	2.18 b	11.80 bcde	10.82 cdef	17.64 ab	121.30 cdefg
11	98.66 bcdef	49.00 ab	2.40 a	1.20 a	2.72 bcd	10.60 bcd	13.62 fg	16.84 ab	126.60 defgh
12	92.80 bcd	40.60 ab	2.80 ab	1.20 a	2.48 bcd	10.60 bcd	13.74 fg	17.18 ab	122.80 cdefg
13	96.16 bcdef	50.80 ab	2.40 a	1.80 a	2.50 bcd	10.80 bcd	10.90 cdef	18.42 abc	132.50 fgh
14	94.26 bcde	55.40 ab	11.00 de	1.60 a	1.36 a	14.40 de	10.90 cdef	23.40 cd	108.08 bcd
15	96.58 bcdef	68.40 b	6.80 bc	5.00 a	2.36 bcd	14.00 de	11.82 def	19.46 abc	106.68 bc
16	88.68 bc	47.60 ab	3.00 ab	1.00 a	2.10 abc	6.00 a	8.66 abcd	15.16 ab	133.54 gh
17	119.12g	51.00 ab	4.00 abc	5.20 a	2.28 bc	15.40 e	9.16 abcde	19.98 abc	126.30 efgh
18	101.48 cdef	37.60 ab	3.60 abc	2.40 a	1.90 ab	8.20 ab	7.66 abc	14.70 a	108.46 bcd
19	88.72 bc	48.20 ab	2.80 ab	1.20 a	2.18 b	11.80 bcde	10.46 bcdef	18.70 abc	100.32 b
20	83.88 b	121.40 c	13.20 e	7.20 a	2.44 bcd	11.60 bcde	6.74 ab	25.94 d	114.46 bcdef
21	66.00 a	146.60 c	7.80 abc	24.40 c	2.54 bcd	10.60 bcd	6.46 a	23.62 cd	70.64 a
22	87.26 bc	146.60 c	7.80 abc	15.40 b	2.06 ab	8.80 ab	6.25 a	14.86 a	111.34 bcde
23	104.80 def	49.40 ab	3.80 abc	4.80 a	2.10 ab	8.80ab	11.40 cdef	16.98 ab	119.26 cdefg
SED	0.96	1.96	0.26	0.59	0.05	0.26	0.24	0.35	8.89

SED- Standard Error of Deviation, AC.N-Accession numbers.

Mean values with different superscripts in the same column are significantly different from one another at P<0.05

KEY: NNP-Number of nodes, PHP-Plant height, SGP-Stem girth, NSB-Number of secondary branches, FPH-Final plant height LNP-Length of internodes, NLP-Number of leaves, RLP-Root length, NBP-Number of secondary branches

TABLE 4: Quantitative Vegetative Leaf Traits for the 23 Studied Sesame Genotypes**.**

AC.N	BLL	MLL	TLL	BLB	MLB	TLB	BLA	MLA	TLA
1	7.16 ^{bc}	9.42 ^{abcde}	8.34 ^{efgh}	4.34 ^{abc}	7.02 ^{cdefg}	2.20 ^{de}	31.50 ^{abc}	66.90 ^{abcd}	18.34^{def}
2	7.44 ^{bc}	15.34 ^{g}	8.72 ^{fgh}	5.10 ^{c}	8.34 ^{fg}	1.98 ^{bcd}	38.73 ^{bc}	130.16^{e}	17.35^{bcdef}
3	7.34 ^{bc}	11.90 ^{cdef}	9.38 ^{h}	4.82 ^{abc}	7.28 ^{defg}	2.16 ^{de}	35.97 ^{dc}	86.23 ^{bcd}	20.28^{e}
4	7.68 ^{bc}	11.48 ^{cdef}	9.32 ^{gh}	5.00 ^{bc}	8.90 ^{g}	2.10 ^{cde}	38.73 ^{bc}	102.83^{de}	19.63^{ef}
5	7.70 ^{bc}	12.02 ^{cdef}	7.86 ^{defgh}	5.20 ^{c}	7.40 ^{efg}	1.74 ^{abcd}	40.20 ^{bc}	95.30 ^{cde}	13.70^{abcde}
6	7.70 ^{bc}	8.82 ^{abc}	7.10 ^{bcde}	5.22 ^{c}	5.04 ^{abc}	1.84 ^{abcd}	41.92 ^{bc}	44.52 ^{a}	11.50^{ab}
7	10.00 ^{de}	12.58 ^{efg}	6.12 ^{b}	7.34 ^{d}	6.84 ^{bcdefg}	1.68 ^{abcd}	74.26 ^{d}	86.52 ^{bcd}	10.08^{a}
8	7.24 ^{bc}	8.96 ^{abc}	8.30 ^{efgh}	4.38 ^{abc}	5.98 ^{abcde}	2.14 ^{de}	33.31^{abc}	54.26 ^{abc}	17.75^{cdef}
9	7.96 ^{bc}	12.04 ^{cdef}	7.10 ^{bcde}	5.32 ^{c}	5.40 ^{abcde}	1.20 ^{a}	44.17^{c}	65.47 ^{abcd}	8.55^{a}
10	8.42 ^{cd}	12.44 ^{defg}	8.16 ^{efgh}	5.08 ^{bc}	6.86 ^{bcdefg}	2.26 ^{de}	46.09^{c}	89.64 ^{bcd}	18.48^{def}
11	6.38 ^{bc}	11.34 ^{cdef}	7.76 ^{cdefg}	4.32 ^{abc}	7.48 ^{efg}	1.70 ^{abcd}	28.11^{bcd}	86.44 ^{bcd}	18.48^{def}
12	7.12 ^{bc}	12.10 ^{cdef}	6.94 ^{bcdef}	3.96 ^{abc}	7.48 ^{efg}	2.06 ^{cde}	28.35 ^{abc}	92.59 ^{bcde}	14.64^{abcdef}
13	7.48 ^{bc}	12.20 ^{cdefg}	7.00 ^{bcde}	4.40 ^{abc}	8.42 ^{fg}	1.82 ^{abcd}	33.07^{abc}	86.64 ^{bcd}	12.81^{abcd}
14	8.12 ^{cd}	8.92 ^{abc}	6.40 ^{bcd}	5.00 ^{bc}	6.12 ^{abcde}	1.38 ^{ab}	42.69^{bc}	52.29 ^{ab}	9.31^{a}
15	11.04 ^{e}	14.40 ^{fg}	6.20 ^{bc}	7.84 ^{d}	6.48 ^{abcdef}	1.94 ^{bcd}	86.61^{d}	93.26 ^{bcde}	12.12^{abc}
16	5.92 ^{b}	9.18 ^{abcd}	7.24 ^{bcdef}	3.52 ^{ab}	4.58 ^{a}	2.30 ^{de}	12.12 ^{ab}	43.22 ^{a}	16.86^{bcdef}
17	7.32 ^{bc}	10.12 ^{bcde}	8.80 ^{bcde}	4.64 ^{abc}	6.50 ^{abcdef}	1.74 ^{abcd}	34.44^{abc}	66.23 ^{abcd}	14.50^{abcdef}
18	7.58 ^{bc}	11.58 ^{cdef}	7.08 ^{bcde}	4.38 ^{abc}	5.14 ^{abcd}	1.68 ^{abcd}	33.96 ^{abc}	60.00 ^{abc}	12.06^{abc}
19	6.44 ^{bc}	12.02 ^{cdef}	6.34 ^{bcd}	3.90 ^{abc}	5.64 ^{abcde}	1.46 ^{abc}	25.29 ^{abc}	66.99 ^{abcd}	9.28^{a}
20	6.98 ^{bc}	10.06 ^{bcde}	6.18 ^{bc}	4.50 ^{abc}	5.96 ^{abcde}	1.38 ^{ab}	33.07 ^{abc}	60.05 ^{abc}	8.64^{a}
21	3.94 ^{a}	6.76 ^{a}	3.20 ^{a}	3.22 ^{a}	5.18 ^{abcd}	2.60 ^{e}	13.78 ^{a}	35.44 ^{a}	10.17^{a}
22	8.38 ^{cd}	7.16 ^{ab}	7.20 ^{bcdef}	4.94 ^{bc}	4.84 ^{ab}	2.34 ^{de}	42.77 ^{bc}	34.41^{a}	16.78^{bcdef}
23	6.48 ^{bc}	12.58 ^{efg}	8.78 ^{fgh}	3.90 ^{abc}	7.38 ^{efg}	1.94 ^{bcd}	26.35 ^{abc}	93.20 ^{bcde}	17.48^{bcdef}
SIG.	0.13	0.21	0.10	0.09	0.13	0.04	2.58	1.36	0.38

Mean values with different superscripts in the same column are significantly different from one another at P<0.05

KEY

MLB-Middle leaf breadth, BLA-Basal leaf area, TLA-Terminal leaf area, MLL- Middle leaf length, TLL-Terminal leaf length,

MLA-Middle leaf area, BLB-Basal leaf breadths, TLB-Terminal leaf breadth, BLL-Basal leaf length, SED- Standard Error of Deviation, AC.N-Accession numbers.

TABLE 5: Means for the Quantitative Yield Characters in 23 Sesame Accessions.

ACCESSION NO.	PV	PN	PL	PG	NS	SL	LS	100SW	NO OF LOCULI	NO OF STAMENS	NO OF STYLE
1	95.14^{fg}	39.20^{efgh}	2.02^{b}	2.08^{abc}	57.80^{abc}	1.36^{bcd}	1.28^{abc}	1.428^{hij}	4	4	1
2	75.80^{b}	38.60^{efg}	2.44^{bcdef}	2.42^{defg}	62.20^{abcdef}	1.38^{bcde}	1.33^{abc}	1.396^{efgh}	4	4	1
3	97.20^{fg}	42.00^{fghi}	2.70^{def}	2.62^{ghij}	76.60^{fgh}	1.40^{cdefg}	1.37^{bc}	1.402^{efghi}	4	4	1
4	97.04^{fg}	43.40^{fghi}	2.72^{def}	2.56^{fghi}	80.20^{h}	1.51^{i}	1.37^{bc}	1.398^{efgh}	4	4	1
5	98.60^{g}	49.00^{ghi}	2.82^{ef}	2.70^{ghij}	76.20^{fgh}	1.59^{j}	1.37^{bc}	1.458^{jk}	4	4	1
6	79.36^{bcd}	54.20^{i}	2.34^{bcd}	2.12^{abcd}	76.00^{fgh}	1.33^{b}	1.28^{abc}	1.396^{efgh}	4	4	1
7	96.60^{fg}	52.40^{hi}	2.88^{f}	2.66^{ghij}	68.20^{bcdefgh}	1.45^{gh}	1.22^{ab}	1.432^{hij}	4	4	1
8	96.46^{fg}	26.40^{bcde}	2.68^{def}	2.46^{efg}	77.60^{gh}	1.34^{bc}	1.28^{abc}	1.346^{bcd}	4	4	1
9	88.86^{defg}	22.20^{abcd}	2.50^{cdef}	2.28^{cdef}	65.40^{bcdefg}	1.35^{bc}	1.29^{abc}	1.348^{bcd}	4	4	1
10	90.58^{efg}	13.20^{ab}	2.76^{def}	2.86^{ji}	63.60^{abcdefg}	1.25^{a}	1.34^{bc}	1.408^{efghi}	4	4	1
11	82.26^{bcde}	28.20^{cde}	2.86^{f}	2.94^{jk}	73.60^{defgh}	1.41^{defg}	1.18^{a}	1.442^{ij}	4	4	1
12	88.86^{defg}	25.80^{bcde}	2.46^{bcdef}	2.56^{fghi}	68.20^{bcdefgh}	1.39^{cdef}	1.40^{c}	1.384^{defg}	4	4	1
13	92.16^{efg}	33.60^{def}	2.62^{def}	2.82^{hij}	69.80^{cdefgh}	1.35^{bc}	1.37^{bc}	1.380^{def}	4	4	1
14	63.34^{a}	21.60^{abcd}	2.88^{f}	3.22^{k}	78.00^{i}	1.58^{j}	1.34^{bc}	1.430^{hij}	4	4	1
15	88.34^{defg}	48.40^{ghi}	2.34^{bcd}	1.92^{ab}	116.60^{gh}	1.25^{a}	1.32^{abc}	1.344^{bcd}	4	4	1
16	87.48^{def}	16.40^{abc}	2.46^{bcdef}	2.62^{ghij}	72.20^{cdefgh}	1.35^{bc}	1.23^{ab}	1.424^{ghij}	4	4	1
17	88.08^{defg}	21.20^{abcd}	2.54^{def}	2.62^{ghij}	59.40^{abcd}	1.43^{efg}	1.18^{a}	1.416^{fghi}	4	4	1
18	91.64^{efg}	15.40^{abc}	2.40^{bcde}	2.40^{defg}	55.20^{ab}	1.44^{fgh}	1.35^{bc}	1.370^{cde}	4	4	1
19	92.92^{efg}	23.20^{abcd}	2.62^{def}	2.50^{efgh}	60.60^{abcde}	1.33^{b}	1.28^{abd}	1.492^{k}	6	4	1
20	88.60^{defg}	50.80^{ghi}	2.36^{bcd}	2.12^{abcd}	71.40^{cdefgh}	1.45^{gh}	1.56^{d}	1.326^{b}	4	4	1
21	86.90^{cdef}	9.60^{a}	1.32^{a}	1.84^{a}	50.40^{a}	1.49^{hi}	1.37^{bc}	1.270^{a}	4	4	1
22	91.98^{efg}	18.20^{abc}	2.06^{bc}	2.22^{bcde}	55.00^{ab}	1.33^{b}	1.37^{bc}	1.378^{cdef}	4	4	1
23	77.18^{bc}	28.00^{cde}	2.72^{def}	2.44^{defg}	75.00^{efgh}	1.43^{efg}	1.30^{abc}	1.338^{bc}	4	4	1
SED	0.67	0.87	0.03	0.021	0.90	0.10	0.004	0.01			

Mean values with different superscripts in the same column are significantly different from one another at P<0.05

KEY

PV-POLLEN VIABILITY,
PN-POD UMBER
PL-POD LENGTH
PG-POD GIRTH
NS-NUMBER OF SEEDS
SL-STYLE LENGTH
LS-LENGTH OF STAMENS
100SW-WEIGTH OF 100 SEEDS

Table 6: Grouping of the 23 sesame accessions into diversity classes.

Cluster	Number of Genotypes	Accessions
I	11	7 (IBAII), 9 (YOLI), 11 (KANI), 12 (KANI), 13 (KANI), 14 (MAKI), 15 (OTU), 17 (ANYI), 18 (ANYII), 19 (OKEII), 23 (JALI),
II	4	2 (E8), 3(01M), 10 (MAI), 16 (ZARI)
III	2	1 (03M), 4 (02M),
IV	3	5 (EXSUDAN), 6 (IBAI), 8 OKEI),
V	2	20 (ILOI), 22 (OFFI),
VI	1	21 (ILOII),

PGB22

PHYSICO-CHEMICAL AND PASTING PROPERTIES OF TUBERS IN SOME LESSER KNOWN YAMS

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ABSTRACT

Yam (*Dioscorea* spp.) serves as one of the major staple food in West Africa. The variation in physicochemical and pasting properties of yam species: *Dioscorea bulbifera* (8 varieties), *D. cayenesis* (7 varieties), *D. dumetorum* (5 varieties) and *D. esculenta* (7 varieties) were determined. Yam tubers were sampled from different yam growing regions in West Africa and processed into flour for physicochemical analysis including mineral content, dry moisture content, sugar, amylose, and starch and pasting properties. Results on the mineral content showed that potassium (7983.50-31812.68mg/100g) was the most abundant while cobalt (0.01-0.88mg/100g) was the least abundant. Starch content ranged from 77.8% (*D. bulbifera*) to 58.37% (*D. esculenta*). Amylose value ranged between 24.71% (*D. cayenensis*) and 13.96% (*D. dumetorum*). Peak viscosity ranged for 19.08-401.04RVU in the four species with *D. cayenesis* having the highest mean (241.54±56.37 RVU) while *D. esculenta* had the least (43.02±8.04 RVU). A corresponding variation in trough (15.55-164.42 RVU) and final viscosity (26.34-529.71 RVU) was observed in the studied species with *D. cayenesis* showing highest trough (109.02±12.97 RVU) and final viscosity mean values (296.94±68.37 RVU) while *D. esculenta* had the least trough and final viscosity mean value of 28.85±10.90 RVU and 42.27±9.37 RVU, respectively. This study gives an insight in the extent of intra and interspecific variation in respect to physicochemical and pasting potential of yam flours thus providing scope for improvement through breeding

Keywords: Breeding, Physicochemical, Pasting, Yam

INTRODUCTION

Yams (*Dioscorea* spp.) are a major staple food source for millions of people in the tropics especially in West and Central Africa where at least 60 million people depend on it (Hahn, 1995). Yams are also regarded as a major source of income and forms an integral part of socio-cultural life of the people (Asiedu and Sartie, 2010). Yams constitute an important source of food and income and play a major role in sociocultural life of a wide range of smallholder households. They bring flexibility to the annual cycle of food availability through several species and cultivars. The tubers have organoleptic qualities that make them preferred carbohydrate food where yams are contributing up to 350 dietary calories per person each day for millions of people in the major producing countries (Degras, 1993)

Yams fulfill a number of basic roles in the global food system, all of which have fundamental implications for meeting food requirements, increasing food security, and reducing poverty. Lack of information on the physico-chemical characteristics of the starches hinders utilization. Among the priority breeding objectives are tubers with acceptable quality, i.e. appropriate dry matter content, a good cooking texture, taste, and no oxidation (rate of enzymatic browning). The uses of starches are determined by their physical and chemical characteristics, which also vary between varieties. Physicochemical properties of yams significantly differ among genotypes (Lebot *et al*., 2005). Identification of physico-chemical variation within germplasm is essential for accelerated breeding for nutritional enhancement. Plant breeding can significantly improve the diet of the rural population through the development and distribution of varieties of yams which contain elevated levels of micronutrients. This may be a cost effective and sustainable approach to alleviating nutrient deficiencies (Boius, 2002).

We aim to study the intra and interspecific variation of the physicochemical and pasting potential of yam flours from species *D. bulbifera, D. cayenesis, D. dumetorum* and *D. esculenta*.

MATERIALS AND METHODS

Four species of yam - *D. bulbifera* (8 varieties), *D. cayenesis* (7 varieties), *D. dumetorum* (5 varieties) and *D. esculenta* (7 varieties) were used for this study (Table 1). A total of twenty-seven yam varieties were obtained from International Institute of Tropical Agriculture (IITA), Ibadan. The cultivars were originally collected different yam growing regions in West Africa (Table 1)

Yam tubers were peeled and diced into cubes and dried in an oven drier (Fisher Scientific Co. USA) at 50ºC for 72hours and then ground in a Kenwood portable mill into fine flour (250µm mesh size) and stored in airtight sample bags for further analysis. The moisture content of the samples were determined using AOAC (2005) method. In the study, iron (Fe), zinc (Zn)**,** calcium (Ca), manganese (Mn), copper (Cu), phosphorus (P), sodium (Na), magnesium (Mg), potassium (K), aluminum (Al), molybdenum (Mo), cobalt (Co), cadmium (Cd), nickel (Ni), lead (Pb) and selenium (Se) were determined using ICP-ES (2005). Reading was taken using an ‘’Inductively Coupled Plasma Atomic Emission Spectrometry (ICPAES) (Switzerland by ARL model 3580 B).

The free sugars and starch content of the samples were determined as described by Dubois *et al*. (1956). Hot ethanol was used for extraction from the sample and then centrifuged using Sorvall

centrifuge (Newtown, Conneticut, USA, model GLC-1). The supernatant was collected and used for free sugar analysis, while the residue was used for starch analysis. To the supernatant made up with distilled water, an aliquot was takenin which 5% phenol and concentrated sulphuric acid was added. The sample was allowed to cool and the absorbance read on a spectrophotometer (Milton Roy Company, USA), model spectronic 601 at 490nm wavelength. While for the starch analysis, the residue was added perchloric acid and allowed to hydrolyze. It was diluted with distilled water and filtered and the filtrate was made up to with distilled water, vortexed and ready for color development as was described for standard glucose curve preparation. This was determined using the method of Williams *et al*. (1970) was used. Absorbance (A) was read using a Spectrophotometer at 620nm wavelength. A blank was used to standardize the spectrophotometer at 620nm.

Pasting properties of the samples were determined with a Rapid Visco Analyser 3 C (RVA, model 3C, Newport Scientific PTY Ltd, Sydney, Australia) according to Ross *et al*. (1987) and Walker *et al*. (1988). Three grams (3.0g) of sample were weighed and mixed with 25ml of distilled water in a test canister. The slurry was heated from 50 °C to 95 °C with a holding time of 2 minutes followed by cooling to 50 °C with 2 min holding time. The rate of heating and cooling were at a constant rate of 11.25°C/min. Peak viscosity, trough, breakdown, final viscosity, set back, peak time, and pasting temperature were read from the pasting profile with the aid of Thermocline for Windows Software connected to a computer (Newport Scientific, 1998).

RESULTS AND DICUSSION

The value of the minerals in the yam samples are presented in Table 2. Potassium (7983.50-31812.68mg/100g) was the most abundant while cobalt (0.01-1.94mg/100g) was the least abundant of the minerals determined. Magnesium (653-1578.54 mg/100g), calcium (72.62-1095.7mg/100g) and phosphorous (216.75-506.93mg/100g) were also observed to be high in the yam samples when compared with the rest of the minerals analysed. In addition, it is worth knowing that *D. bulbifera* (accession: TDb 3058) had the highest potassium, magnesium, iron and sodium content in this study.

Table 3 shows that sugar content ranged between 1.76% for *D. cayenesis* (variety: TDc 2809) and 7.2% for *D. esculenta* (variety: TDe 3036). Starch content ranged from 77.8% (*D. bulbifera*) to 58.37% (*D. esculenta*). Amylose value ranged between 24.71% (*D. cayenensis*) and 13.96% (*D. dumetorum*). Peak viscosity ranged for 19.08-401.04RVU in the four species with *D. cayenesis* having the highest mean (241.54±56.37 RVU) while *D. esculenta* had the least (43.02±8.04 RVU). A corresponding variation in trough (15.55-164.42 RVU) and final viscosity (26.34-529.71 RVU) was observed in the studied species with *D. cayenesis* showing highest trough (109.02±12.97 RVU) and final viscosity mean values (296.94±68.37 RVU) while *D. esculenta* had the least trough and final viscosity mean value of 28.85±10.90 RVU and 42.27±9.37 RVU, respectively (Table 3).

The high moisture content could be the possible reason yam tubers are prone to microbial attack in the storage which often result to high postharvest losses. Similar range of moisture content has been reported by Osagie (1992). Similar results on the abundance of potassium in yam have been previously reported (Alinnor and Akalez, 2010; Kouassi et al. 2010; Senanayake et al. 2012).

Potassium plays an essential role in electrolyte regulation, nerve function, muscle control and blood pressure in the human body. Bellows and Moore (2013) reported adequate intake of potassium per day is 4,700 mg for males and females age fourteen through adulthood as well as pregnant women. This study revealed that yam consumption may reduce the risk of potassium deficiency in individuals.

Comparable sugar content in yam has been reported (Maziya-Dixon and Asiedu, 2003; Lebot et al. 2005). The high starch content is one of the major properties that influence the suitability of yam for different products because of its effects the textural, rheological and physiochemical characteristics of the final product. Our observation in starch agrees with the findings of Tamiru et al. (2008). Efforts will be made in future studies in understanding the nature of starch granule size and molar masses. The amylose content we observed is in agreement with previous studies of Farhat et al. (1999) and Amani et al. (2004). Consideration of amylose content during breeding is important because it imparts definite characteristics to starch (Moorthy, 1994). It is a very important parameter that influences starch pasting and retrogradation behaviour (Zhenghong et al. 2003).

Higher viscosities of paste obtained in *D. cayenensis* suggest that they can form thick paste on cooking. This can be attributed to higher swelling potentials of the starches as reported by Otegbayo et al. (2006). *D. cayenesis* forms a complex with *D. rotundata* the most preferred cultivar for pounded yam. Other species exhibited lower viscosity suggesting higher internal bonding between the starch granules. *D. cayenesis* showed highest breakdown values in viscosity. This suggest that there is less granule rupture for the starches as reported by Otegbayo et al. (2006). The variations in the physicochemical and functional properties reveal that there is scope for improvement in the long term by breeding.

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Table 1. *D. bulbifera*, *D. cayenesis*, *D. dumetorum* and *D. esculenta* species and their varieties source and **y**ear of collection

Varieties		Source country	Year
D. bulbifera			
3697	TDb	Congo	1994
1455	TDb	Gabon	1992
3079	TDb	Ghana	1992
3046	TDb	Nigeria	2003
3048	TDb	Benin	1997
3029	TDb	Togo	2002
4120	TDb	Sierra Leone	2004
3085	TDb	Nigeria	1992
D. cayenesis			
2817	TDc	CotedIvoire	1992
2790	TDc	Togo	1997
2809	TDc	Benin	1992
3839	TDc	Nigeria	2004
2815	TDc	Nigeria	1992
3935	TDc	Benin	1994
3093	TDc	Togo	1993
D. dumetorum			
3779	TDd	Nigeria	2002
4118	TDd	Togo	2004
3100	TDd	Togo	1993
3907	TDd	Nigeria	2004
3778	TDd	Nigeria	1998
D. esculenta			
4149	TDe	Guinea	2004
3035	TDe	CotedIvoire	1993
3033	TDe	Togo	1993
3041	TDe	Togo	1993
3039	TDe	Togo	1993
2786	TDe	Nigeria	2004
3036	TDe	Ghana	2002

Table 2: Mineral contents (mg/100g) of the yam flours

	Accession	Al	Fe	Zn	Ca	Cd	Co	Cu	K	Mg	Mn	Mo	Na	Ni	P	Pb	Se
1	TDb 4120	1.27	23.65	12.28	504.14	0.1	0.23	6.12	17497.92	852.69	2.06	1.3	20.95	0.06	394.19	2.42	0.8
2	TDb 3029	6.83	27.16	14.78	638.44	1.21	0.25	4.52	14770.2	950.87	3.16	0.78	55.24	1.68	387.14	27.84	3.0
3	TDb 3048	1.87	17.63	9.56	196.52	0.07	0.06	8.58	22934.78	736.95	1.29	0.02	55.86	0.04	334.78	0.61	2.5
4	TDb 3697	0.58	23.94	29.98	263.15	0.15	0.17	9.81	22318.8	823.98	1.74	0.65	42.7	0.03	435.72	0.34	1.3
5	TDb 3079	0.74	19.34	8.82	254.69	0.01	0.01	4.04	26924.54	653	1.09	0.05	37.53	0.86	340.86	1.69	1.2
6	TDb 3046	5.81	35.25	20.01	339.24	0.1	0.26	12.21	26771.48	1122.54	6.57	0.14	89.76	0.71	384.98	0.65	1.2
7	TDb 3085	1.45	35.49	20.77	490.93	0.14	0.14	12.17	31812.68	1578.54	4.43	0.39	162.57	0.01	483.38	1.21	0.9
8	TDb 1455	0.21	29.4	25.6	456	0.17	0.02	7.12	28996	1376	1.4	0.31	84.6	0.12	444	0.01	0.7
9	TDc 2817	2.44	13.15	11.14	72.62	0.1	0.13	6.39	12633.86	906.13	0.27	0.05	61.34	0.77	329.5	0.46	0.1
10	TDc 2815	1.63	15.32	11.96	362.33	0.1	0.19	5.38	14169.24	1311.08	0.47	0.35	147.55	0.45	348.03	1.09	0.7
11	TDc 2809	2.54	17.06	11	189.71	0.08	0.29	3.95	11350.48	1024.34	0.55	0.84	107.71	0.59	415.7	1.99	1.2
12	TDc 2790	8.18	11.61	9.76	171.26	0.13	0.01	0.59	7983.5	722.81	0.5	0.79	29.95	0.3	371.17	1.12	3.8
13	TDc 3839	5.74	8.46	11.62	324.26	0.21	0.33	9.29	8459.19	705.11	5.17	0.64	39.6	0.7	216.75	71.16	5.0
14	TDc 3935	1.68	25.83	17.34	1036.01	0.11	0.17	5.38	11836.68	1240.26	1.66	0.29	106.8	0.03	506.93	0.15	0.0
15	TDc 3093	1.31	19.71	19.76	392.24	0.14	0.06	2.8	12517.53	861.65	2.16	0.74	154.75	0.11	422.25	2.18	0.0
16	TDd 3100	2.66	15.9	12.41	530.27	0.07	0.09	1.79	9901.75	937.4	1.46	1.22	72.62	1.27	462.41	1.6	0.8
17	TDd 3779	1.39	19.75	16.25	235.4	0.12	0.24	7.37	16442.45	1005.72	1.96	0.8	45.21	1.21	427.5	1.97	0.3
18	TDd 4118	0.56	17.64	21.65	565.77	0.07	0.33	8.03	11590.8	1366.86	0.69	0.59	102.63	1.01	368	2.77	0.9
19	TDd 3907	1.8	25.24	16.43	1019.95	0.02	0.13	4.6	11029.44	1212.7	7.92	1.29	108.95	0.01	404.23	0.73	1.1
20	TDd 3778	1.63	15.14	18.58	1095.7	0.06	0.28	6.89	9947.26	1173.04	3.5	8.12	125.03	0.85	315.82	2.38	2.1
21	TDe 3041	1.85	19.77	15.55	286.84	0.17	0.05	4.71	14239.73	1014.45	1.51	0.27	52	1.01	454.75	1.17	1.2
22	TDe 3033	2.03	19.88	15.42	332.53	0.18	0.88	5.95	14228.83	1102.6	1.13	0.12	45.5	0.27	374.09	1.29	0.8
23	TDe 3039	0.85	21.5	17.66	343.7	0.1	0.01	4.56	16547.61	1125.19	2.09	0.33	43.77	0.16	430.1	0.12	0.8
24	TDe 3036	0.06	24.22	19.81	659.74	0.06	0.55	6.18	13493.4	1036.12	2.98	2.27	58.61	0.49	501.83	2.4	0.2
25	TDe 2786	1.67	18.22	14.19	236.92	0.05	0.02	2.4	11656.54	945.76	2.15	0.24	37.59	0.65	370.08	0.44	0.3
26	TDe 3035	0.2	17.72	12.93	295.05	0.12	0.25	4.17	9834.31	923.74	1.9	0.18	36.08	0.62	313.2	0.48	0.6
27	TDe 4149	2.31	21.96	14.46	303.2	0.08	0.14	3.69	10672.49	1022.35	2.27	0.48	40.03	0.15	404.27	1.39	0.5
	Mean	2.20	20.74	15.92	429.50	0.15	0.20	5.88	15576.35	1027.11	2.30	0.86	72.78	0.52	394.14	4.80	1.2
	Max	8.18	35.49	29.98	1095.7	1.21	0.88	12.21	31812.68	1578.54	7.92	8.12	162.57	1.68	506.93	71.16	5.0
	Min	0.06	8.46	8.82	72.62	0.01	0.01	0.59	7983.5	653	0.27	0.02	20.95	0.01	216.75	0.01	0.0
	Std	2.05	6.36	5.03	265.36	0.22	0.19	2.86	6634.34	224.76	1.85	1.53	40.78	0.46	64.40	14.24	1.2

Table 3: Mean proximate and pasting characteristics of dried yam flour

	Accession	% MC	%Sugar	% Starch	% Amylose	Peak 1	Trough 1	Breakdown	Final Visc	Setback	Peak Time	Pa Te
1	TDb 4120	7.62	5.8	63.4	21.99	110.2	112.3	9.44	142.23	53.8	7.1	93
2	TDb 3029	7.52	7.03	69.42	22.77	112.79	107.09	5.71	158.38	51.3	7	93
3	TDb 3048	7.59	5.16	60.61	23.22	90.42	77.42	13	137.75	60.33	7	94
4	TDb 3697	7.8	6.06	68.55	22.38	49.33	41.75	7.58	79.67	37.92	7	94
5	TDb 3079	7.82	6.99	74.61	21.46	101.67	91.33	10.33	153.17	61.83	7	95
6	TDb 3046	7.43	4.22	70.97	23.49	187.25	162.05	14.54	257.13	95.09	8.98	64
7	TDb 3085	7.53	3.9	77.8	23.69	97.25	74.17	10.5	119.12	45.75	8.99	94
8	TDb 1455	7.85	5.69	65.59	19.55	43.67	35.88	7.79	74.05	38.17	7	93

9	TDc 2817	6.49	4.32	76.27	16.66	355.75	164.42	191.34	462.38	297.96	4.86	64
10	TDc 2815	6.41	2.95	76.65	18.47	401.04	106.25	250.63	529.71	423.46	6.78	64
11	TDc 2809	6.44	1.76	69.26	22.19	78.5	63.25	15.25	119.17	55.92	7	94
12	TDc 2790	6.55	4.67	72.63	22.6	365.13	125.54	226.63	468.54	343	6.94	64
13	TDc 3839	6.4	4.4	71.44	24.71	187,00	120.92	66.08	191.79	70.88	4.8	89
14	TDc 3935	6.96	3.13	68.5	17	82.83	70.75	12.08	125.67	54.92	7	89
15	TDc 3093	7.46	3.33	74.25	14.69	166	112	54	181.33	69.33	4.67	88
16	TDd 3100	7.59	5.07	71.47	13.83	62.54	54.63	7.42	101.38	46.25	5.04	93
17	TDd 3779	7.58	4.74	69.72	14.36	88.09	71.04	17.05	114.38	43.34	5	94
18	TDd 4118	7.11	4.86	77.77	14.05	54.83	37.58	17.25	66.5	28.92	6.75	64
19	TDd 3907	7.03	3.33	60.65	16.41	76.5	61.5	15	96.75	35.25	5.07	95
20	TDd 3778	7.53	3.9	77.8	13.69	77.25	64.17	16.5	99.12	43.75	4.99	64
21	TDe 3041	6.99	5.69	69.26	16.02	39.79	23	16.8	32.83	9.84	4.32	63
22	TDe 3033	7.04	5.93	71.74	16.61	52	31	21	43	12	4.27	65
23	TDe 3039	7.33	6.32	71.72	15.24	19.08	15.55	3.55	25,00	9.46	4.77	93
24	TDe 3036	6.71	7.2	63.72	16.66	28.21	17.79	10.42	26.34	8.58	4.64	94
25	TDe 2786	6.76	6.45	58.37	18.47	85.29	63.63	21.67	79.33	15.71	4.5	93
26	TDe 3035	6.88	6.29	71.15	14.86	36.92	19.08	17.83	27.17	8.08	4.6	94
27	TDe 4149	6.9	2.65	75.13	14.71	39.83	31.92	7.92	44.92	13	4.66	94
	Max	7.85	7.2	77.8	24.71	401.04	164.42	250.63	529.71	423.46	8.99	95
	Min	6.4	1.76	58.37	13.69	19.08	15.55	3.55	26.34	8.08	4.27	63
	Mean	7.16	4.88	70.31	18.51	111.62	72.44	39.53	151.22	75.33	5.95	84
	Std	0.47	1.45	5.43	3.70	104.26	42.33	67.92	135.43	104.59	1.41	13
	CV%	6.58	29.79	7.73	20.00	93.40	58.43	171.81	89.55	138.85	23.65	16

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PROVENANCE VARIATION FOR MORPHOLOGICAL TRAITS AND OIL CONTENT IN *SOME* JATROPHA CURCAS *L. GERMPLASM COLLECTIONS.*

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ABSTRACT

Twenty one provenances of *Jatropha curcas* L. collected from seven states of the Northwestern Nigeria and established in a provenance trial at the Institute for Agricultural Research farm, Ahmadu Bello University, Samaru, Nigeria were evaluated using principal component analysis (PCA) to analyze their pattern of variation, determine the correlation among the morphological traits and oil content, identify the major traits responsible for the variation and suggest appropriate breeding material for the improvement of the crop. All the provenances showed highly significant variation for all the traits studied except main stem height which was significant at 5% level only. Three out of the ten principal components extracted had eigenvalue greater than one and altogether accounted for 77.07% of the total variability. Principal component 1 exhibited 34.77% while principal components 2 and 3 showed 24.48% and 17.83% variability respectively among the provenances for the traits studied. Number of fruit bunch per lateral branch, number of capsules per bunch and number of capsules per lateral branch had the highest loadings on principal component 1 indicating their significance for this component. On principal component 2, collar height and number of lateral branches were important. The third principal component however, was more related to plant height (cm) and main stem height (cm). Number of capsules per lateral branch, number of capsules per bunch, collar height and plant height are found to be the major traits responsible for the variation in the *Jatropha curcas*

provenances. Tsaki, Gwarzo and Kwanan maje provenances were identified as potential materials for the improvement of *Jatropha curcas* L. in Nigeria.

Key words: Principal component analysis, Provenances, Provenance trial

INTRODUCTION

Jatropha curcas L. is a species of the flowering plants in the spurge family, Euphorbiaceae containing about 170 known species (Heller, 1996). It is a rapidly emerging biofuel crop currently attracting a lot of interest and investments (Wouter, 2010). The Jatropha plant is a small tree or large shrub which can reach a height of 3-5m (Garg *et al.*, 2011) with articulated growth and a morphological discontinuity at each increment (Kumar, *et al*, 2008). It is resistant to a high degree of aridity, allowing it to be grown in deserts. The crop is used as a hedge (living fence) all over the world by farmers as it is not browsed by animals (Garg *et al.*, 2011). Jatropha has several industrial, pharmaceutical, environmental and other uses (Abubakar, 2002). The plant, because of its numerous uses has potential to generate rural employment, reclaim wasteland, earn foreign exchange, facilitate the establishment of rural based agro-industries, improve the socio-economy of rural dwellers and lead to overall development of the country (Abubakar, 2010). The seeds of Jatropha contain averagely 34.4% oil that can be processed to produce a high quality biodiesel fuel usable in a standard diesel engine (Achten, 2008). Jatropha is a new and very important crop in Nigeria. However, the crop is in its infancy as scientific evidence for elite accessions and adequate breeding work on the crop in Nigeria are lacking. In order to improve the crop for high yield and identify the best genotype for a particular location in Nigeria, provenance research will be the quickest and simplest step to start considering the size and lifespan of the crop. The objectives of this study are to; evaluate and determine the variation pattern in the *Jatropha curcas* L. provenances, determine the correlation among the morphological traits and oil content, identify the major traits responsible for the variation of the provenances and suggest potential provenances that could be used in the improvement of the crop in Nigeria.

MATERIALS AND METHODS

A survey and collection of *Jatropha curcas* L. germplasm from the Northwestern zone of Nigeria was conducted in the year 2009. Twenty one (21) accessions were collected from the seven states of the zone which spans across the Sahel, Sudan and Guinea Savannas and formed the genetic materials for this research. The states were Sokoto, Kebbi, Zamfara, Katsina, Kaduna, Kano and Jigawa. The eco-geographical characteristic of the survey area is presented in Table 1. A provenance trial was established from these collections at Samaru (11º11'N, 07º38'E) in 2009. Each accession, a representative of a provenance, contained 20±2 trees planted in single row plots of 44m long with 3m inter- and intra-row spacing each stand taken as a replication. All agronomic activities were carried out on the field in establishing the provenances.

Data were taken on ten randomly selected mother trees from each provenance. The morphological traits of the plants and seeds assessed were specifically: Plant height (cm), seed oil content, main stem height (cm), collar height (cm), collar thickness (cm),number of branches on collar, number of lateral branches, number of fruit bunch per lateral branch, number of capsule per bunch and number of capsule per lateral branch. The SAS statistical package (SAS

Institute Inc.2004) was used for all analyses, with $P< 0.05$ considered statistically significant for all tests. Analyses of variance were carried out using the GLM procedure. Mean separation was done by Duncan's Multiple Range test (DMRT).

Table 1-Ecogeographical characteristics of the survey area in the Northwestern Zone of Nigeria where *Jatropha curcas* L. germplasm were collected

State	Latitude (N)	Longitude (E)	Zone	Soil type	Climate
Kaduna	9°11'-11°22'	8°21'-7°14'	NGS, SGS	Alfisols	Tropical wet and dry
Katsina	11°23'-13°07'	7°23'-7°47'	SSS	Entisols	Tropical wet and dry
Kano	11°06'-11°58'	9°-00'-9°02'	SS	Alfisols	Hot and semi-arid
Jigawa	11°00'-11°33'	9°30'-9°34'	SSS	Alfisols	Hot and semi-arid
Zamfara	11°56'-13°07'	6°25'-6°43'	SSS	Entisols	Hot and semi-arid
Sokoto	12°03'-13°10'	5°46'-4°33'	SSS NGS	Entisols	Hot and semi-arid
Kebbi	12°05'-12°41'	4°07-4°26'	SSS	-	Hot and semi-arid

SS: Sudan Savannah, NGS: Northern Guinea Savannah, SSS: Sudano-Sahelian Savannah, SGS: Southern
Guinea Savannah. (Source; Halilu *et al* (2011))

The model used for the analysis was: $Y_{ijkl} = \mu + \gamma_k + \varepsilon_{ijkl}$

Where; Y_{ijkl} = tree$_l$ in treatment combination$_{ijk,}$ γ_k = provenance$_k$
μ = the grand mean, ε_{ijkl} = residual error

Table 2: Mean Squares for each Character

Sources of Variation	Df	MS	EMS
Replication	$(r-1)$	M_r	
Provenance	$(p-1)$	M_p	$\sigma_e^2 + r\sigma_p^2$
Error	$rp(r-1)$	M_e	σ_e^2

The contribution of each component of variance to the total phenotypic variation was calculated by equating the appropriate mean squares to the expectation of mean squares (EMS) using the method described by Singh and Chaudhary (1985) as follows:

$\sigma^2_e = M_e$

$\sigma^2_p = M_p - M_e = \sigma^2_e + r\sigma^2_p - \sigma^2_e = r\sigma^2_p$

$\sigma^2_{ph} = \frac{Mp-Me}{r} + \sigma^2_e$

Where, r = number of replications, σ^2_e = Error variance, σ^2_p= Genotypic variance, σ^2_{ph} = Phenotypic variance, M_e = Error means square, M_p = Provenance means square

Phenotypic correlation coefficients were estimated for all possible pairs of characters examined using the standard procedure suggested by Miller *et al*. (1958) and Kashiani and Saleh (2010) from the corresponding variance components using the equation: $rpxy = \frac{\sigma pxy}{\sqrt{\sigma^2 px * \sigma^2 py}}$

Where, $rpxy$ = phenotypic correlation coefficient between characters X and Y

$\sigma^2 px$ = Phenotypic variance of character x

$\sigma^2 py$ = Phenotypic variance of character y

RESULTS AND DISCUSSION

The analysis of variance for the different traits (Table 3) showed that generally, there were highly significant variation among the 21 provenances of *Jatropha curcas* for all the morphological traits studied except main stem height which showed significant difference at 0.05 level of significance only. The existence of these differences suggests the presence of considerable genetic variability among the provenances for these traits. This is most likely because these provenances were sourced from different natural environments which might have been affected by natural selection. These variations found in the morphological traits present us with a viable selection alternative at a very early stage (germplasm collection) from base seed material. This could be of use in improvement programmes especially considering the fact that the *Jatropha curcas* is a new crop in which crop breeding is still in its infancy. Provenances could be selected on the basis of distinguishable desirable traits and hybridized to obtain superior genotypes. This is in agreement with Clausen *et al.* (1948) and Wattstein (1958) who are on the view that hybrid from combining different provenances may result in hybrid vigor for many characters. This also agrees with the report of Pryor (1963) that provenance selection is the simplest and quickest means of improving trees. Traits such as high number of lateral branches, high number of capsules per lateral branch and high number of fruit bunch per lateral branch indicate high quantity of fruits and ultimately high quantity of seeds per plant. This suggests that provenances with these traits can be selected for high seed yield per plant. Highly significant

correlation was found between number of fruits bunch per lateral branch and number of capsules per bunch (r = 0.64839) and number of capsules per lateral branch (r = 0.67504). Highly significant correlation was found between plant height and main stem height (r = 0.91432). Highly significant correlation was also observed between number of lateral branches and number of capsules per bunch (r = 0.69747) and between number of capsules per bunch and number of capsules per lateral branch (r = 0.79802). Oil content has weak correlation with all the morphological traits studied except collar height and number of lateral branches which showed negative correlation with the oil content (r = -0.22377 and -0.11248 respectively). As number of lateral branches has significant correlation with number of capsules per lateral branch as well as highly significant correlation with number of capsules per bunch (Table 4), selection for one trait leads to the improvement of the other trait in the same direction. Plant height and number of lateral branches are important characters that can be looked upon as major selection indices when the objective is to incorporate *Jatropha curcas* in an agroforestry system.

Number of lateral branches and number of capsules per lateral branch have higher genotypic variances than error variances (Table 5) indicating little environmental influence in these traits. However, these traits have no any significant positive correlation with the percentage of oil in the seeds (seed oil content) as shown in Table 4 as to influence the total oil yield of the plant. Number of capsules per bunch has highly significant correlation with number of lateral branches as well as significant correlation with number of capsules per lateral branch. This indicates that plants with good branching habit tend to develop more number of capsules. This is in agreement with the work of Rao *et al.* (2008). The number of fruit bunch per lateral has highly significant correlation with the number of capsules per lateral branch and number of capsules per bunch. This result indicated that selection for any of these traits will indirectly results in high seed yield obtainable from a tree. Plant height and main stem height have highly significant correlation with each other showing that the two traits have strong association. The negative correlation observed between plant height and number of lateral branches, number of capsules per lateral branch, number of capsules per bunch and number of fruit bunch per lateral branch was in agreement with the findings of Rao *et al.*, (2008). The absence of any significant correlation between oil content and all the morphological traits is in agreement with the work of Alireza *et al*. (2012) and Freitas *et al.* (2011). However, the result is not in agreement with the findings of Rafii *et al.* (2012) and Rao *et al*. (2008). This is most likely attributable to the fact that at three years the yield of Jatropha plant has not reached its full potential.

Results from principal component analysis shows that three out of the ten principal components extracted had eigenvalue greater than one and altogether explained 77.07% of the total variability (Table 6). Principal components 1, 2 and 3 exhibited 34.77%, 24.48% and 17.83% variability respectively among the provenances for the traits under study. Principal component 1 is associated with number of fruit bunch per lateral, number of capsules per bunch and number of capsules per lateral (Table 7). Collar height (cm) and number of lateral branches were important for principal component 2. The third principal component however, was more related to plant height (cm) and main stem height (cm).

CONCLUSION

Highly significant variation was found in all the morphological traits studied except main stem height which was significant at 0.05 level of significance only. Highly significant correlations

were found between number of fruit bunch per lateral branch and number of capsules per bunch, number of lateral branches and number of capsules per bunch and between number of fruit bunch per lateral branch and number of capsules per lateral branches. The principal component analysis identified number of capsules per lateral branch, number of capsules per bunch, collar height, plant height and main stem height as the major traits responsible for the variation in the *Jatropha curcas* L. provenances (Table 7). Tsaki, Kwanan maje and Soba provenances were identified as potential materials that could be used in the improvement of *Jatropha curcas* L. in Nigeria (Table 8).

Further research towards finding alleles for maximizing all desirable traits and pyramiding them into highly productive Jatropha varieties through breeding and the use of the available techniques is recommended.

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Table 3: Mean squares from the analysis of variance for nine traits in *Jatropha curcas* Provenances established in IAR field 2012

Source	df	PH	MSH	CH	CT	BOC	LB	FBPL	CPB	CPL
Rep	9	261.85*	314.98*	1.77	109.77*	0.35	0.61	0.16	0.98	3.03**
Provenance	20	1617.48**	1102.49*	29.06**	158.84**	7.95**	8.92**	2.92**	6.91**	30.97**
Error	180	131.54	148.07	3.29	57.01	0.50	0.69	0.43	0.70	1.31
Total	209									

PH=Plant height, MSH=Main stem height, CH=Collar height, CT=Collar thickness, BOC=Number of branches on collar, LB=Number of lateral branches, FBPL=Number of fruit bunch per lateral branch
CPB=Number of capsules per bunch, CPL=Number of capsules per lateral branch

Table 4: Phenotypic correlation coefficients between morphological traits and oil content in *Jatropha curcas* L. provenances

	PH	**MSH**	**CH**	**CT**	**BOC**	**LB**	**FBPL**	**CPB**	**CPL**	**OC**
PH	1	0.91432**	0.25374	0.04288	0.11999	-0.06272	-0.15725	-0.29358	-0.33665	0.23804
MSH		1	0.1048	0.15269	0.16976	0.01194	0.01331	-0.07128	-0.13033	0.24341
CH			1	-0.68394**	-0.46698*	0.14965	-0.31988	-0.05976	-0.36122	-0.22377
CT				1	0.59044**	-0.46484*	-0.08222	-0.25681	-0.00091	0.25583
BOC					1	-0.44137*	-0.06551	-0.26149	-0.1059	0.24816
LB						1	0.42216*	0.69747**	0.50534*	-0.11248
FBPL							1	0.64839**	0.67504**	0.04764
CPB								1	0.79802**	0.03433
CPL									1	0.00905
OC										1

Table 5: Estimate of phenotypic, genotypic and error variances for morphological traits in *Jatropha curcas* L. provenances

	Provenance Means	σ^2_e	σ^2_g	σ^2_{ph}
PH	191.9	131.54	148.60	280.14
MSH	173.0	148.07	95.44	243.51
CH	9.0	3.29	2.58	5.87
CT	57.2	57.01	10.18	67.19
BOC	2.9	0.5	0.75	1.25
LB	5.4	0.69	0.82	1.51
FBPL	2.5	0.43	0.25	0.68
CPB	3.4	0.70	0.62	1.32
CPL	4.9	1.31	2.97	4.28

Table 6: Eigenvalues of the Correlation Matrix and the Proportion and Total Variance Explained by the first three Principal Components

	Eigen value	Difference	Proportion	Cumulative
Prin1	3.4767	1.0291	0.3477	0.3477
Prin2	2.4476	0.6646	0.2448	0.5924
Prin3	1.7830	0.8096	0.1783	0.7707

Table 7: Eigenvectors of Principal Components for Ten Characters in 21 *Jatropha curcas* L. Provenances

	Prin1	Prin2	Prin3
Plant Height	-.295417	0.198753	0.561951
Main Stem Height	-.188415	0.094050	0.675272
Collar Height	-.167114	0.530871	0.006323
Collar Thickness	-.091000	-.552975	0.140050
No. of Branches on Collar	-.112252	-.479458	0.238675
No. of Lateral Branches	0.394445	0.304822	0.167499
No. of Fruit Bunch per Lateral	0.433034	-.050372	0.213671
No. of Capsules Per Bunch	0.481361	0.083240	0.162208
No. of Capsules Per Lateral	0.468773	-.110308	0.135812
Oil Content	-.184008	0.140058	-.182018

Table 8: Standardized Principal component scores from the original data of 21 *Jatropha curcas* provenances from the first three principal components representing 77.07% of the variance from the original 10 characteristics

Provenance	**Prin1**	**Prin2**	**Prin3**
Bakin gada	0.605	0.208	0.457
Kakiyayi	0.516	0.92	-0.365
Soba	0.103	0.577	2.793
Gwarzo	1.447	-1.954	1.825
Rowan kanya	1.5	-1.998	1.813
Dirpindai	0.37	-0.487	-1.411
Masaya	-0.256	-1.273	-0.535
Kangire	-2.78	1.518	-1.441
Burum	2.233	2.241	0.204
Jega birni	0.008	0.308	0.575
Sabon garin dabai	-0.402	0.814	0.745
Maga	0.571	-1.445	-0.721
Kwanan maje	-3.866	2.758	0.503
Take tsaba	-0.904	1.889	-0.53
Daki takwas	-5.011	-3.633	-0.043
Pompo	0.274	0.984	-0.251
Kajiji	0.664	-1.426	-2.52
Tsaki	2.87	0.203	-2.213
Danjanku	0.483	0.423	1.1
Dankama	0.642	-0.088	1.019
Karohi	0.934	-0.538	-1.004

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PGB24

PHENOTYPIC VARIATION SHOWS 10 DISTINCT CLUSTERS OF WATER YAM (*D. ALATA*) GERMPLASM IN NIGERIA

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ABSTRACT

A pre-requisite for a sustainable *D.alata* (water yam) crop improvement in Nigeria is to understand the state of variation in the phenotypes of present collection. 163 accessions comprising of collections from different yam growing regions were evaluated using a total of 77 phenotypic descriptors. Multivariate analysis of quantitative and qualitative data resulted to 10 major distinct cluster groups with varying number of individual entries. Days to tuber emergence, stem length, internode length and waxiness contributed to 54 % of total variation. The findings suggest a narrow genetic base and buttresses that most of the collections from different regions are duplicates. Proposal for efficient utilization of the inherent genetic potentials in the cluster groups in breeding programmes complimented with more collections within and outside the country should be encouraged and vigorously pursued.

Keywords: Breeding, Genetic, Phenotype, Water yam

INTRODUCTION

Yams (*Dioscorea* spp) are economically important starch staple in tropical and sub-tropical regions of the world, particularly West Africa. *D. alata* ranks second to *D. rotundata* in terms of production and consumption in Nigeria (Orkwor, 1998). *D. alata* is the most widely distributed species in the world and has an advantage for sustainable cultivation especially when yam production seems to be on the decline as a result of high cost of production, low yields and post-harvest losses (Wireko-Manu, 2011)

Yam production has not kept pace with demand due to an ever increasing population and the lack of varieties that combine high and stable yield of good quality tubers (Olojede *et al*., 2000). Apart from these, other constraints to yam production include the occurrence of pests and diseases that cause foliar and tuber problems in field and storage (Emehute *et al.*, 1998). There is, therefore, the need to breed cultivars that are high yielding, possess disease and pest resistance, good storability and culinary quality.

The International Institute for Tropical Agriculture (IITA) Ibadan, Nigeria holds in trust collections of *D. alata* from Nigeria. This germplasm collection was set up to preserve the genetic diversity and for further use in the genetic enhancement of the crop. The diversity can introduce useful new traits and create new heterotic combinations. These in turn can contribute

to more crop yields and enhance adaptability of finished varieties by providing appropriate and useful genetic stocks for breeding program.

The objective of this study is to assess the genetic diversity among cultivars of *D. alata* germplasm collected from different parts of Nigeria using morphological descriptors

MATERIALS AND METHODS

The study was conducted in IITA yam field. One hundred and sixty three cultivars of *D. alata* were grown from tuber setts (100 g) planted on ridges spaced 1 m x 1 m apart. Each cultivar was represented by 3 plants, which were individually trained on to 2.0 m bamboo stakes when vines were 30 – 50 cm long. No fertilizer was applied and plants were irrigated during periods of dry weather. Agronomic practices were done based on recommendation of Orkwor (1998)

The plant descriptors used are those recommended by IPGRI/IITA (1997). Aerial vegetative parts were monitored and described between March and October at juvenile and adult stages. Plants were harvested after senesce. Harvested tubers were stored in a shaded yam barn and described thereafter. 77 plant characters were measured and coded for analysis.

Table 1: List of 77 morphological descriptors and number of class categories

Descriptor	Class
Young stem descriptors	
Young stem color	3
Presence of wax on young stem	2
Presence of wings on young stem	2
Presence of spine on young stem	2
Presence of colored spot on the base of spine	2
Presence of barky patches	2
Plant descriptor	
Plant type	3
Plant vigor	3
Bearing type	3
Layering habit	2
Twining habit	2
Stem height at 8 weeks after planting	3
Stem color	3
Number of internodes at first branching	4
Presence of wax on older stems	2
Presence of wings on old stem	2
Presence of hair on old stem	2
Presence of spine on old stem	2
Spine shape	3
Presence of coalescent spines	2
Presence of color spot at spine base	2
Color of spots at spine base	4
Types of pigmentation	5

Hairiness of upper lower surface	4
Leaf arrangement	3
Leaf density	4
Leaf type	2
Leatheriness of leaf	2
Onset of leafing	3
Leaf color	4
Waxiness of upper/lower leaf surface	3
Leaf shape apex	3
Distance between lobes	2
Upward folding of leaf along main vein	2
Downward arching of leaf along main vein	2
Downward arching of leaf lobes to form a cup	2
Upward arching of leaf lobes	2
Position of the widest part of leaf	3
Leaf tip length	3
Leaf tip color	3
Petiole length	3
Petiole hairness	2
Petiole spot color	3
Presence of stipule	2
Qualitative descriptors for flower characteristics	
Flowering	2
Presence of inflorescence smell	2
Sex	2
Inflorescence position	2
Number of inflorescence per plant	3
Inflorescence type	3
Average length of inflorescence	4
Number of flowers per inflorescence	3
Flower color at maturity	3
Female flower length	3
Male flower diameter	3
Fruit formation	2
Qualitative descriptors for tuber characteristics	
Tuber growth	3
Tuber maturity at emergence	3
Number of tubers per hill	3
Relationship among tubers	3
Presence of corms on tubers	2
Corm size in relation to tuber size	3
Corm ability to be separated from tuber	2
Sprouting at harvest	2
Aerial tuber formation	2

Skin color	4
Surface texture	2
Bumps on tuber	2
Skin thickness	2
Tuber shape	4
Uniformity in tuber shape	3
Place where tuber branch	3
Tuber length	2
Spiny roots at tuber surface	2
Rootlets on tuber surface	2
Wrinkles on tuber surface	2
Cracks on tuber surface	2

Seventy seven morphological characters were measured on 163 cultivars. The scores for each character were standardized to have a zero mean and unit variance. From this matrix, the correlation coefficients between every pair of cultivars were computed. In order to assess the variation among cultivars principal component analysis (PCA) were performed according to Sneath and Sokal (1973) using statistical analysis software (SAS, 2003). The dendrogram was based on the general relationship between any two units for comparison, which is expressed as a measure of dissimilarity. The Euclidean distance coefficient *d*, was used where

$$d^2jk = \sum 1 (X_{ji} - X_{ki})^2$$

j and k denote any two cultivars being compared and i denotes characters.

The plot of canonical variables of the 163 cultivars was used to establish the clustering

RESULTS

The cultivars studied were separated between a distance coefficient of 0.4 and 3. This resulted into 10 clusters. The clusters showed three distinct groups (Figure 1). Cluster 2 exhibited high coefficient distance when compared to others. Clusters 5, 9, 7 and 10 formed a distinct grouping and had majority of the entries and (Figure 2). Clusters 1, 3, 4, 6 and 8 where distinct showing a coefficient distance of between 0.4 to 0.8. Clusters that had the highest entries were 1 and 9, and both had 50 and 44 cultivars respectively. The least entries were observed in cluster 8 and 10 with both having 2 and 1 individuals respectively. Distance between cluster centroids shows that cluster 7 exhibited highest variability when compared to other clusters (Table 2)

54% of the total variation resulted from days to tuber emergence, stem length, internode length and waxiness (Table 3). Each cluster was peculiar to a specific trait though most of the traits overlapped. Cluster 2 entries showed waxiness on the stem while cluster 3 was distinct with purplish green leaf. Cluster 1 had dark green stem at maturity with cluster 4 having highly

shaped cylindrical tuber shape. Cluster 5 had dark maroon skin shape flesh while cluster 7 had irregular shaped tubers. Stem length was high in cluster 10 while days to tuber emergence were least in cluster 6. Cluster 9 gave shortest internode length while cluster 8 showed deep purplish colour of leaf margin days after sprout emergence.

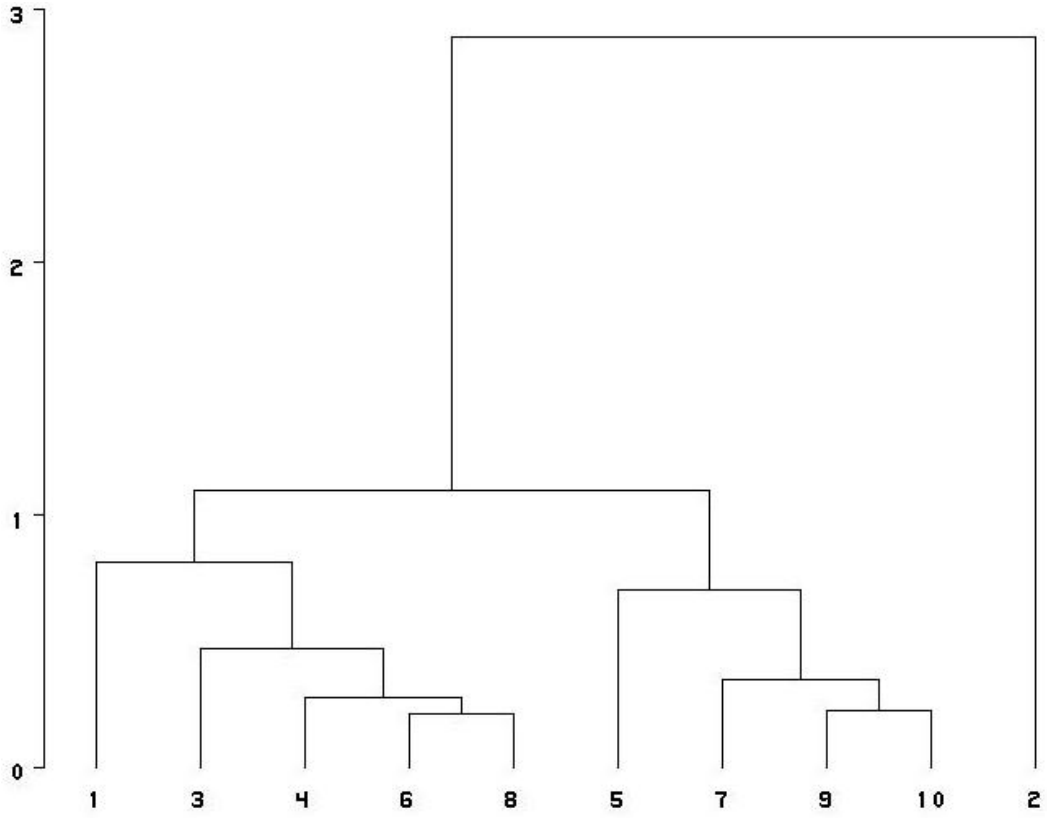

Figure 1: Dendrogram showing 10 clusters generated from 163 *D. alata* cultivars based on morphological descriptors

	1	2	3	4	5	6	7	8	9	10

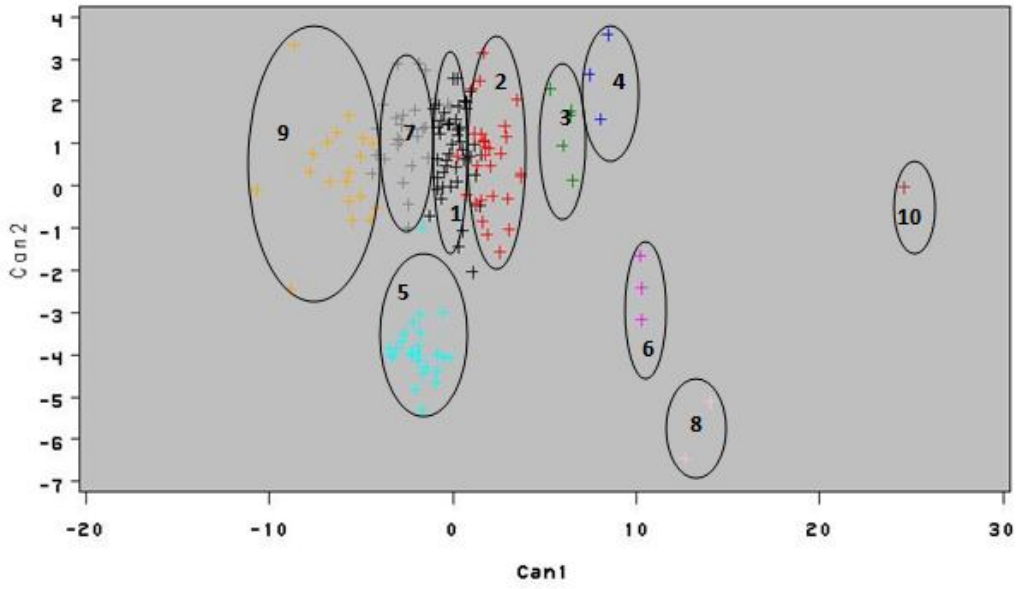

Figure 2: Plot of two dimensional canonical variables identified by clusters

1		75.78	23.24	128.41	45.45	24.57	216.87	98.59	33.84	24.49
2	75.78		53.84	54.13	34.85	57.05	141.76	24.81	42.06	52.49
3	23.24	53.84		105.96	24.44	15.01	194.33	76.13	13.05	8.17
4	128.42	54.13	105.96		85.49	109.27	88.81	31.34	94.90	105.19
5	45.45	34.85	24.44	85.49		25.18	173.37	55.48	16.64	23.90
6	24.57	57.05	15.01	109.28	25.18		197.12	79.51	19.23	15.89
7	216.87	141.76	194.33	88.81	173.37	197.12		118.72	183.22	193.52
8	98.59	24.81	76.13	31.34	55.48	79.51	118.72		65.18	74.95
9	33.84	42.06	13.05	94.90	16.64	19.23	183.22	65.18		12.61
10	24.49	52.49	8.17	105.19	23.90	15.89	193.52	74.95	12.61	

Table 2: Distance between cluster centroids

Table 3: Factor scores of 4 major characters in the first four principal component axes with the eigen-values and percent of total variation accounted for by each of the four component axes used in the ordination of 163 yam cultivars of *D. alata*

Character	Principal component axis			
	I	II	III	IV
Date to tuber emergence	0.141	-0.082	-0.111	0.030
Stem length	0.070	0.287	0.077	-0.043
Internode length	0.095	0.261	0.034	-0.116
Waxiness	-0.144	-0.029	-0.245	0.095
Eigen-value	8.138	5.228	4.184	2.684
Proportion of variation accounted	0.220	0.141	0.113	0.066
Cumulative	0.220	0.361	0.474	0.540

DISCUSSION

IPGRI/IITA (1997) was useful in assessing variation among *D. alata* cultivated in Nigeria held in trust by IITA. Seventy seven descriptors made up of qualitative and quantitative traits were effective in appraising the morphological diversity.

The information generated is vital for breeding new cultivars with novel or improved characteristics that are high yielding with good crop vigour, resistant to common pests and diseases of yams especially potty virus, leaf blight, nematodes and anthracnose as well as yam varieties that have high dry matter consumer acceptable food qualities such as pounding for fufu and friability for chewing varieties which can store well, with good tuber aesthetic qualities of shape and smooth skin. The dendrogram constructed in our study showed 10 distinct clusters of *D. alata* in Nigeria. The allelic diversity within and across the 10 clustered group can be used in breeding programmes for the development of novel cultivars. It provides basis for defining heterotic groups which are informative for reciprocal recurrent selection and for further genomic analyses.

It is obvious from our study that the genetic base of *D. alata* in Nigeria is narrow. The cultivars collected from different regions with diverse local names probably might have resulted in

duplication of most of the few available cultivars. *D.alata* is Asiatic in origin and further collection mission should target the region to avoid duplications which might be prevalent in close countries to Nigeria. There is need to maximise genetic gains by embarking on more collection.

Major contributing characters are days tuber emergence, stem length, internode length and waxiness and followed by leaf colour, colour of stem at maturity, tuber skin colour, shape of tuber and colour of leaf margin days after sprout emergence. These characters were highly discriminatory among individual cultivars and may be useful in further studies differentiating *D. alata* cultivars. Some of these descriptors have earlier been highlighted by Martin and Rhodes (1977). These traits can be used as identification keys for cultivar groups which in turn can expedite selection process.

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PGB25

GENETIC VARIABILITY OF *STRIGA GESNERIOIDES* (WILLD) IN NORTHERN NIGERIA

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ABSTRACT

Cowpea is an important grain legume crop in Sub-Saharan Africa. Its production is constrained by an obligate root parasitic weed, *Striga gesnerioides.* Crop yield losses due to this noxious weed may be up to 100% depending on the extent of damage and level of infestation. In West and Central Africa regions, seven races of *Striga* have been reported. The use of resistant cultivars seems to be the cheapest and most effective method of controlling the parasite. Several cowpea cultivars exhibiting resistance to the parasite have been developed during the last two decades. However, most resistant cultivars show a differential response when grown in different countries across West and Central Africa, suggesting that there are different races of *S. gesnerioides* within or between countries. This study was undertaken to investigate the genetic variability within and between 3 *Striga* populations collected from three different geographical zones (Borno, Jigawa, and Kano) of Nigeria, where cowpea is a major crop. Five cowpea cultivars with known history of reaction to *Striga* were used for the study. Results showed that there was no differential response of the cowpea genotypes to the *Striga* seeds collected from the three geographical areas, suggesting that there is no race variation in *Striga* population in Nigeria.

Keywords: *Striga*, genetic variability, cowpea, northern Nigeria.

INTRODUCTION

Cowpea is the most important grain legume crop in Sub-Saharan Africa. It is a staple food in more than 65 countries (Singh, 2006) due to its high nutritional value, plasticity, and ability to adapt to a wide range of environments in tropical and subtropical regions of the world. It is usually the first crop harvested before the cereal crops are ready and therefore is commonly referred to as "hungry-season crop". The fruits are consumed at all stages of growth (e.g. green pods, fresh or dry seeds) and the young leaves are often used for soups and stews [Quaye *et al*., 2009]. Cowpea is an extremely resilient crop and cultivated under some of the most extreme agricultural conditions in the world (Owolade *et al.*, 2006; Muoneke *et al*., 2012.

Nigeria and Niger each cultivate well over 4 million ha and account for more than 45% and nearly 15%, respectively of the total world production. Burkina Faso stands a distant third, with 6.1% of the world's total production (Abate *et al.*, 2012). Like most crops, cowpea growth and grain yields are greatly reduced by a variety of biotic and abiotic constraints. Among the major biotic constraints is parasitism by *Striga gesnerioides* commonly referred to as witch-weed of the

family Orobanchaceae. Witch weeds are noxious and persistent pests in farmer's fields and yield losses due to *S. gesnerioides* parasitism are extensive in the Sudano-Sahelian belt of West and Central Africa (Parker, 2009). On susceptible cultivars, yield losses can reach 100% when *S. gesnerioides* population is over 10/plant (Kamara *et al*., 2008). Omoigui *et al.* (2009) added that yield losses caused by *Striga* in the dry savanna of sub-Saharan Africa are estimated in millions of tons annually and the prevalence of the pest is steadily increasing.

The current knowledge of genetic diversity of *S. gesnerioides* has not been sufficiently evaluated relative to their wide distribution. Genetic diversity is due to hybridization, clonal variation, local adaptation and frequent colonization events. Colonization events of autogamous species formed genetically uniform populations. The genetic diversity inherent in *Striga* is extremely important for modelling its future dispersal in the light of global climate change. Limited information is available on genetic variability of *Striga* population in Nigeria.The objectives of this work is to identify whether there are different biotypes of *Striga gesnerioides* in Nigeria and to identify cowpea lines that could be resistant across the different *Striga* biotypes if ever they exist.

MATERIALS AND METHOD

The experiment was conducted in the screenhouse at the International Institute of Tropical Agriculture (IITA), Kano Station. Kano is situated at latitude 11°30'0" N, longitude 8°30'0" E in DMS (Degrees Minutes Seconds) and altitude 518 m asl and lies in the Sudan savanna agro-ecology. Cowpea genotypes were selected based on their reactions to *S. gesnerioides* in a **previous** screening in pot and field infested with *S. gesnerioides.* The genotypes are TVX-3236, B301, IT97K-499-35, IT81D-994 and VYA (Cameroun).

Clean sterilized plastic pots measuring 10 inches in diameter were filled with a mixture of top soil and sharp sand in the ratio 2:1 respectively, and infested with *Striga* seeds (0.025g about 5,000 seeds) at 5-7 cm deep. The pots were arranged in completely randomized design with three replications in the screen house. *Striga* to be used was obtained from Kano, Jigawa and Borno states. The infested soil was kept moist for 7–9 days to precondition the *Striga* seeds to ensure optimum germination, based on adopted protocol of *Striga* infestation reported by Berner *et al*. (1999). Three cowpea seeds were sown in each pot. The pots were watered adequately to field capacity and kept weed-free by hand weeding. Compound fertilizer (NPK: 15:15:15) was applied at 7 days after plant emergence. Cowpea seedlings were thinned to two plants per pot at 2 weeks after planting (WAP). The cowpea plants were observed daily in order to determine the date of flowering and *Striga* emergence.

RESULTS

The analysis of variance (ANOVA) for growth and *Striga* parameters are presented in Table 1.The cowpea genotype showed significant difference in terms of plant height and *Striga* count at 49 days after planting (DAS) ($P < 0.01$ and 0.05, respectively, Table 1). IT97K-499-35 recorded the highest mean followed by IT81D-994, while B301 recorded the lowest mean followed by VYA (Cameroun) (table 2). *Striga* count at 56 days after planting, plant shoot dry weight, plant root dry weight and *Striga* dry weight has no significant difference (table 1). Location for *Striga* seed collection has a significant effect on Striga dry weight ($P < 0.05$) but not

on growth parameters (figure 1). Genotype x location was not significant for all the parameters taken (table 1). However, few *Striga* emerged in one pot of B301 and IT97K-499-35 (Table 3). IT81D-994, which was previously identified as resistant supported *Striga* shoot when infested with *Striga* seeds collected from the three locations (Table 3).

Table 1 Analysis of variance for plant height at 3 weeks after planting, *Striga* count at 49 and 56 days after planting, plant shoot dry weight, plant root dry weight and *Striga* dry weight.

SOURCE OF VARIATION	**DF**	**MEAN SQUARES**					
		PLTHGT3	**STCNT@49**	**STCNT@56**	**SHTDRWT**	**RTDRWT**	**STDRWT**
GENOTYPE	4	66.69**	253.7*	432	22.276	56.47	3.741
STRIGA LOC	2	2.29	396.1	428.1	2.54	35.61	2.486*
GENOTYPE * ST LOC	8	14.33	66.8	119.5	3.389	8.89	1.243
RESIDUAL	15	13.37	129.3	297.9	6.314	19.75	1.54

* and **, Significant at 5% level of probability

Table 2: Effect of genotype on plant height at 3 weeks after planting, *Striga* count at 49 and 56 days after planting, plant shoot dry weight, plant root dry weight and *Striga* dry weight.

Genotype	PLTHGT3	STCNT@49	STCNT@56	SHTDRWT	RTDRWT	STDRYWT
VX-3236	2.49a	28.93ab	11.50ab	2.36a	17.33a	1.06a
B301	7.83a	23.56c	0.33b	0.00a	5.93a	0.00a
IT97K-499-35	6.64a	32.25a	0.50b	0.10a	5.39a	0.00a
IT81D-994	2.60a	29.26ab	10.00ab	1.41a	18.17a	1.49a
VYA (Cameroun)	1.43a	23.93bc	14.33a	1.71a	15.67a	1.59a

Means followed by the same letter (s) are not statistically significant using DMRT at 5% level of probability.

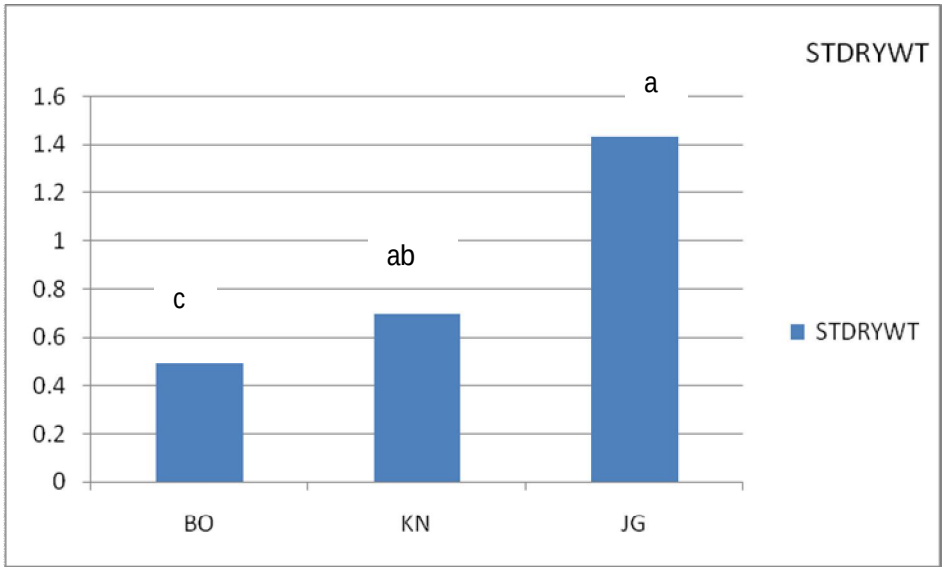

Figure 1: Effect of *Striga* location on *Striga* dry weight.

Table 3: Reaction of the cowpea genotypes to different *Striga* locations

GENOTYPE	STRIGA LOCATION			PREVIOUS STUDIES REACTION TO STRIGA
	BO	KN	JG	
TVX-3236 Susceptible to all races		S	S	S
B301 Resistance to SG 1,2,3,4		R	R	$S^{+/-}$
IT97K-499-35 Resistance to SG 1,3		R	R	S*
IT81D-994 Resistance to SG 1,3		S	S	S
VYA (Cameroun) Susceptible to all races	S	S	S	

R and **S** mean *Striga* resistant and susceptibility respectively

DISCUSSION

The cultivars TVX-3236 and VYA showed susceptibility to the *Striga* seeds collected from the three locations, which is in conformity with the previous studies by Omoigui *et al.* (2011). IT81D-994 was susceptible to *Striga* seeds collected from the three locations, which is in conformity with the work of Muranaka *et al.* (2008) who reported its susceptibility to SG3.

B301 showed resistance to *Striga* seeds collected from Kano and Borno but supported few *Striga* in one of the pots infested with *Striga* seeds collected from Jigawa State. Similar report by Mellor *et al.* (2012) indicated some *Striga* attachment on B301 root in ex vitro germination study.

Similarly, IT97K-499-35 was found to be resistant to the *Striga collected from* Kano and Borno states but it allowed some *Striga* attachments from *Striga* seeds collected from Jigawa State. This is also in conformity with the study of Omoigui *et al*. (2011), who found IT97K-499-35 supporting few *Striga* plants when tested in Borno State.

However, present results certainly do not suggest a new race, because one would have expected to observe a certain high degree of differentiation between the populations. This was clearly not the case in the *S. gesnerioides* populations studied here. The *Striga* shoots observed in B301 and IT97K-499-35 probably could have resulted from physical seed admixture, which needs further

investigation. Consequently, the results of this study do not indicate the presence of a different *Striga* race other than that race 3 of the *Striga* previously reported in Nigeria by Lane *et al*. (1996). Apparently, there is need for further investigations to confirm the claims of the present study.

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PGB26

HERITABILITY ESTIMATE IN SUGARCANE (SACCHARUM OFFICINARUM L.) GENOTYPES FOR YIELD AND YIELD COMPONENTS.

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ABSTRACT

Experiment was conducted in Sokoto State at Fadama land area, a spring behind Vice Chancellor's Quarters of Usmanu Danfodiyo University Sokoto in the Sudan Savanna agro-ecological zone of Nigeria, during 2011 and 2012 growing seasons. The experiment was laid out in a Randomized Complete Block Design (RCBD), replicated three times. Fourteen sugar cane hybrids and a local check were evaluated; twenty two parameters were taken through the procedure outlined in the IBGR/ICRISAT Sugarcane descriptor to measure each trait. The data obtained were analyzed using Analysis of variance (ANOVA), result revealed high broad-sense heritability (H^2 > 45%) in almost all the traits measured, thus result suggests that selection for these traits will be easy and as such the cultivars (those with H^2 < 45%) could be used in breeding programme for selections in favour of enhanced high cane yield, crack on stalk (20%) and growth habit (8%). All these also showed low heritability estimate and are expected not to

respond to selection easily. However negative broad-sense heritability (H^2) were observed in sprout count at two weeks after planting (-26.32 %) and total cane yield (-16.19 %). Number of stalk/stool, stalk length, stalk girth and final brix were recommended to serve as a breeding guide for selection due to their high heritability estimate.

Key words: Heritability, yield, Sugarcane, yield components.

INTRODUCTION

Sugar cane (*Saccharum officinarum* L.*)* belongs to the grass family Poaceae, and is characterized by segmented stems and blade-like leaves, and Reproduction can be by seed, or vegetatively by cutting ("setts") (Barnes, 1974). Sugarcane is a tropical plant, it has no adaptation to survive freezing and it is dependent on abundant sunlight for healthy growth (Hussain, 2001). As a tropical plant, sugarcane has a specific photosynthetic mechanism for fixing carbon into plant sugar, in this adaptation, the first product of photosynthesis is four-carbon sugar (C_4 plant) that is fixed in specialized cells in the conductive tissue (stem) of the plant (Cox *et al.,* 2000). Sugar yield being a quantitative character, is the result of various characters working together during the crop growth, which are interdependent in their development. It is, therefore, desirable to study the association between yield and yield attributing characters since this would facilitate effective selection for simultaneous improvement of one or more yield influencing components (Olaoye, 2009). The purpose of selection is to identify seedlings which are genetically superior, if that superiority is genotypic in nature, the seedlings will reproduce its value faithfully in other environments, however if on the contrary, the value is mainly environmental, thus the degree of genetic determination (DGD) which is the ratio of genotypic variance to phenotypic variance (H^2) is used to estimate yield, quality and other traits in a population (Olaoye, 2004).

Sugarcane is currently grown in over 110 countries in the world with 1,661,251,480 tonns were produced worldwide, this is harvested from 23,777,743 hectares giving a yield of 698,658kg/ha, the African total production for the year was 94,154,405 tonns harvested from 1,573,034 hectares at a yield of 59,853kg/ha, in Nigeria the total production being 1,412,070 tonns, harvested from 17,890 hectares at the rate of 196,421kg/ha (FAOSTAT, 2009). But the top fifteen Sugarcane Producing countries are Brazil 6.71 million/ha, India 4.90 million/ha, China 1.24 million/ha, Pakistan 1.03 million/ha, Thailand 1.01 million/ha, Mexico 0.68 million/ha, Colombia 0.45 million /ha, Australia 0.42 million/ha, South Africa 0.42 million/ha, Cuba 0.40 million/ha, Philippines 0.40 million/ha, United States of America 0.36 million/ha, Indonesia 0.35 million/ha Argentina 0.29million/ha and Vietnam 0.29 million/ha (FAOSTAT, 2009). The study objective was to determining broad sense heritability estimates for sugarcane characters to be used in selection for high cane yield.

MATERIALS AND METHODS

Field experiment was conducted at Fadama land, behind Vice Chancellor's Quarters of Usmanu Danfodiyo University Sokoto during 2011 and 2012 growing seasons. Sokoto is located in the Sudan Savanna agro-ecological zone of Nigeria on latitude 13^0 08 N and longitude 5^0 15 E on an altitude of about 350m above sea level (ASL). Mean annual rainfall is about 752 mm, the minimum and maximum temperatures are 26^0C and 35^0C, respectively, and relative humidity of

23-41%. The area is characterized by long dry season with cool air during hammattan (November – February), dry air during hot season from March – May followed by a short rainy season (Bello, 2006). The experiment was laid out in a Randomized Complete Block Design (RCBD), replicated three times. Fourteen sugar cane hybrids and a local check were evaluated. The hybrids were: ILS-001, USRI/08/85, USRI/08/43, USRI/08/80, CO957, USRI/08/63, USRI/08/03, USRI/08/87, USRI/08/68, ILS-002, CO6806, USRI/08/58, USRI/08/16, USRI/08/46 and local cheek **(**Yar Ilela**).** The hybrids were sourced from University of Ilorin Sugar Research Institute (USRI). One three-eyed cane sett was planted per stand and eight setts per row. The gross plot was 17m x 45m ($765m^2$), the plot had two-rows of 5m x 2m and 0.6m intra-row and 1.5m inter-row.

Composite samples from the depth of 0-15cm and 15cm-30cm were taken at random, from the experimental site. The samples were mixed in laboratory, air dried and sieved through 2mm sieve and used for physical and chemical analysis. Soil pH was determined using pH meter, and the particle size analysis was carried out using Bouyoucos hydrometer method (Bouyoucos, 1951), textural class was determined using textural triangle. Total nitrogen was determined by macro-kjeldahl digestion distillation technique Page *et al.* (1982). Available phosphorous was determined by Bray No.1 method (Bray and Kurtz, 1945), calcium, potassium, magnesium, sodium, organic carbon and cation exchange capacity (C.E.C.) using a procedure prescribed by Page *et al.* (1982). Result soil showed that the soil was clay-loam, the soil reaction was moderately acidic and organic carbon was moderate. Total N. available, P. exchangeable K. content were also moderate, CEC and exchangeable bases (Na, Ca and Mg) were moderate.

The land was prepared using hoe to make furrows on 10/11/2011. Transplanting**,** transplanting was done at an intra-row spacing of 0.6m and inter-row spacing of 1.5m. Irrigation schedule, irrigation was done weekly before the establishment of rain. Fertilizer application NPK fertilizer at 150kg of N, 60kg of $P_2 0_5$ and 90kgK_2O was applied in equal halves (at split dose) at planting and 10 weeks after planting. Weed control, pre-emergence herbicides 2,4-D amine and 2,4-D ester were used and one supplementary hoe weeding was carried out at 15 weeks after planting.
Data were collected on sprout count, sprout count was taken at two, four and six weeks after planting. Tiller count, tiller count was taken at three, six, nine and twelve months after planting. Stalk length (cm), the sample of five stalks from the net plot were used to measure the length of the stalk from the ground to the visible dewlap using a meter-rule. Number of stalks per stool, this was done by counting the number of stalks per stool from five randomly selected stools per net plot. Stalk weight (kg), five randomly selected stalks were cut at the base and each weight was taken separately per net plot, using weighing scale. Millable stalk per plot, this was taken by counting the total number of millable stalk per net plot (i.e. stalk >1.5cm diameter). Yield, the yield of the net plot area was weighed and extrapolated to kg per hectare. Refractometer brix (%), the final brix was taken before harvest, using a hand refractometer and Punch at 12 months after planting. Data obtained were analyzed using the Statistical Analysis Systems (SAS) (2003). Then the statistical model described by Bohren,*et al.*(1961) was used for the forms of general analysis of variance.

Table 1: Showing form of Analysis of Variance (ANOVA)

SOURCE OF VARIATION	df	MS	EMS
Replication	(r-1)	M3	
Genotype	(g-1)	M2	$\delta^2 g + r\ \delta^2 g$
Error	(g-1)(r-1)	M1	$\delta^2 e$
Total	g(r-1)		

Where: r = Number of replication

g =Number of genotypes

$\delta^2 g$ = Total genotypic variance among genotype

$\delta^2 e$ = error variance

$M_{3=}$Replication mean square

$M_{2=}$Genotype mean square

$M_{1=}$Error mean square

EMS= Error mean square

Broad sense heritability were estimated using the formulae described by Fehr (1987)

$$h^2 = \frac{\delta^2 g \times 100}{\delta^2 ph}$$

Where

$\delta^2 g$ =Genotypic Variance

δ^2_{Ph}= Phenotypic Variance

RESULTS

Estimate of broad- sense heritability (H^2)

The result of broad-sense heritability of all the traits measured, revealed high heritability (H^2 > 45%) for all characters under study, except for stalk crack with 20% and growth habit with very low heritability of 8%.

Table 2. Genotypic, phenotypic variance and Broad sense heritability estimates for growth and yield characters of 15 Sugarcane hybrids evaluated Usmanu Danfodiyo University, Sokoto during 2011 and 2012 growing seasons.

Traits	Genotypic variance	Phenotypic variance	Heritability (%)
Sprout count at two weeks after planting	-0.005	0.019	-26.32
Sprout count at four weeks after planting	1.61	2.02	79.7
Sprout count at six weeks after planting	3.47	4.98	69.68
Tillers count at three months after planting	31.29	41.39	75.6
Tiller count at six months after planting	500.63	733.27	68.27
Tiller count at nine months after planting	501.27	665.72	75.3
Tiller count at 12 months after planting	456.28	619.65	73.64
Number of stalks per stool	15.35	15.74	97.52
Stalk length (m)	0.21	0.22	95.45
Stalk girth (cm)	0.11	0.12	91.67
Number of internodes per Stalk	4.71	5.24	89.89
Internode length	0.000022	0.000031	70.97
Smut	0.12	0.19	63.16
Root rot	0.26	0.48	54.17
Stalk crack	0.05	0.25	20
Number of milliable cane per plot	458.21	601.08	76.23
Final brix (%)	4.18	4.53	92.27
Single stalk weight (kg)	0.05	0.08	62.5

Total Cane weight per plot	-5487.86	33888.61	-16.19
Growth habit	0.02	0.25	8

Heritability (h^2) ≥45 is significant (trait highly heritable)

Heritability (h^2) ≤45 is not significant

Heritability ≤18 (very low heritable traits)

DISCUSSION

Yield being a quantitative character, is the result of various characters working together during the crop growth which are interdependent in their development, it is, therefore, desirable to study the association between yield and yield attributing characters since this would facilitate effective selection for simultaneous improvement of one or more yield influencing components because the purpose of selection is to identify seedlings which are genetically superior, if that superiority is genotypic in nature, the seedlings will reproduce its value faithfully in other environments, however if on the contrary, the value is mainly environmental (Olaoye, 2009).

Broad sense heritability indicated that number of stalk/stool, stalk length, stalk girth and final brix had high heritability estimates thereby suggesting that, selection for them will be relatively easy. However, growth habit and crack on stalk had low heritability estimates which indicate that selection for them will difficult. For sugarcane breeding programme to be successful it is important to know which traits give the highest estimates of heritability, this is line with a research conducted by Puri, *et al*. (1982) reported that if an estimate of broad-sense heritability of a particular trait is high it indicates that environmental conditions have little impact on the phenotypic differences observed in the population.

Stalk crack and growth habit had low heritability and would not respond to selection easily, as reported by Obilana and Fakorede (1986) that, if a character is influenced by environment, its heritability would be low in a population. However negative broad-sense heritability (H^2) estimate were observed in sprout count at two weeks after planting (-26.32 %) and total cane yield (-16.19 %), this may be as a result of sampling error. This finding corroborates Gill (1968) who reported that negative heritability estimate may be due to experimental/sampling error.

CONCLUSION

High broad-sense heritability indicated that four traits namely number of stalk/stool, stalk length, stalk girth and final brix could serve as a breeding guide for selection.

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PGB27

ASSESSMENT OF PHENOTYPIC VARIATIONS IN FINGER MILLET (*ELEUSINE CORACANA*(L) GAERTN) LANDRACES FROM NORTHERN NIGERIA.

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ABSTRACT

Germplasm identification and characterization is an important link between conservation and utilization of plant genetic resources. The present study was conducted to assess the phenotypic variation/diversity of 10 germplasm accessions of Finger millet (*Eleusine coracana* (L) Gaertn) from diverse locations in the geographic region of Northern Nigeria during the 2008, 2009 and 2010 cropping seasons. Randomised Complete Block Design (RCBD) was used for a field study in two locations Gwagwalada and Keffi and field data were analysed based on phenotypic characters. Phenotypes were found to express significant diversity for plant height, 1000 seed weight, leaf length and number of tillers. The results were analysed using ANOVA model and showed that plant height in accession Ex-Kwi was significantly different from all the other nine accessions while the highest leaf length which was recorded in Ex-Riyom was significantly different ($p<0.05$) from accession Ex-Dantse. Similarly, significant variations were observed in the number and length of fingers, and 1000 seed weight across all the accessions. Cluster analyses revealed six distinct groups, with one landrace forming an independent colony. Our results suggest a high phenotypic variability which could exist among the selected morphological traits.

INTRODUCTION

In Nigeria, the finger millet plant is diverse and is popularly used without restriction in our different multi-ethnic, multi-cultural and multi-religious groups. In various regions of the world it is referred to as tamba (Nigeria), Ragi (India), Mandua Winbi (Swahili) bulo (Uganda), kurakan (Sri Lanka), fingerhirse (German) (Dewet, 1976). Epidemiological evidence showed that the plant is widespread and well adopted to diverse regions of the world. In East Africa, the plant is known to originate from Ethiopia and then spread by geographic spatial pattern to Southern African countries such as Namibia and Botswana. The plant is also well known and grows well in Asian countries such as India and China, Middle East (Gupta, *et al*, 2010).

Germplasm identification in finger millet plant is an important link between conservation and utilization of plant genetic resources. The usefulness of germplasm in the study of plant genetic resources could play an important role in the generation of new hybrids and high yielding crop varieties with disease resistant traits to cope with adverse challenges associated with biotic and abiotic stress, (Murray, *et al*. 2008).

The problem of erosion of genetic diversity of finger millet in Nigeria as a result of large-scale farming activities, urbanization and preferential land uses causes leaching, has gradually destroyed the natural vegetation and transformed the farming systems and crop cultures and this has positioned finger millet as threatened crop genetic resource (Fakrudin, *et al.,* 2004). This study was therefore conducted to assess the phenotypic properties of Nigerian finger millet crop. The phenotypic characterization could also reveal the genetic relatedness within these species. This will be useful in the conservation of new species and understanding of the genetic diversity of the finger millet crop.

MATERIALS AND METHODS

Field survey was conducted between November 2007 and February 2008. The 10 finger millet (seeds) were randomly collected from local farmers in consultation with the Agricultural Development Programme (ADP) in five states (Bauchi, Gombe, Nasarawa, Plateau and Kaduna)

and the Federal Capital Territory (FCT) Abuja, Nigeria. The Randomized Complete Block Design (RCBD) was used to plant the finger millet seeds in the three cropping seasons in 2008 in accordance with standard agricultural practices in two locations, Gwagwalada and Keffi. Each plot consisted of 2m X 3m ($6m^2$). Plant to plant spacing was maintained at 10cm in both locations. A basal dose of NPK was applied 4 weeks after planting in both locations. Fertilizer was applied at 100kg N (Nitrogen) 60kg K_2O (Potassium) and 40kg, P_2O_5 (Phosphorus) in both locations. Weeding was done at six weeks after planting in both locations. This field experiment was repeated in the two locations in the 2009 and 2010 cropping seasons using the same treatments and conditions and data were collected for all the seasons. Morphological traits such as plant height, plant width, leaf length, leaf width, number of fingers, finger length and finger width were determined and recorded in accordance with standard finger millet descriptors (IBPGR/ICRISAT, 1985). The number of days to flowering was recorded for each plot as a whole and the remaining characters were recorded on 10 randomly chosen plants per plot. The number of fingers per panicle and number of productive tillers per plant were recorded. Mature panicles or fingers were harvested, sundried and weighed to record panicle yield, and then threshed to measure grain yield.

RESULTS

Table 1 shows the pooled means of morphological traits of finger millet accessions planted in Northern Nigeria for the three cropping seasons. Plant height varied from 54.66cm in Ex-Dantse to 64.96cm in Ex-Biliri with a mean value of 59.79cm across the ten accessions. Plant width varied from 9.77cm in Ex-Andaha to 12.30cm in Ex-Tafawa Balewa with a mean of 11.07cm across all the accessions. Leaf length varied from 49.02cm in Ex- Dantse to 58.20cm in Ex-Riyom with a mean of 53.53cm across the ten accessions. Leaf width varied from 1.30cm in Ex-Tafawa Balewa to 1.94cm in Ex-Kwi and a mean of 1.51cm across all the accessions. Number of fingers varied from 73.5 in Ex-Dantse to 171.5cm in Ex-Kwi and a mean of 105.1 across the ten accessions. Finger length varied from 44.90cm in Ex-Gwagwalada to 99.25cm in Ex-Andaha with a mean of 64.80cm across the ten accessions while the finger width ranged from 2.1cm in Ex-Gura to 2.7cm in Ex-Riyom with a mean of 2.39cm across all the accessions. Number of ears varied from 16.5 in Ex-Gwagwalada to 25.5 in Ex-Kwi with a mean value of 20.15 across the accessions while 1000 seed weight varied from 150.9g in Ex-Gwagwalada to 275g in Ex-Andaha with a mean value of 200.09g across the ten accessions.

Table 1: Pooled Means of Morphological traits of finger millet Accessions grown in northern Nigeria in the three cropping seasons.

Accession	Plant Height (cm)	Plant width (cm)	Leaf Length (cm)	Leaf width (cm)	Number of Fingers	Finger length (cm)	Finger width (cm)	Number of Ears	Seed Weight (1000)g
Ex-Dantse	54.66	10.68	49.02	1.43	73.50	61.30	2.60	20.00	175.70
Ex-Riyom	60.33	12.00	58.20	1.45	79.50	79.35	2.70	19.50	185.75
Ex-Bum	56.33	11.06	55.36	1.38	81.50	60.95	2.20	21.50	190.75
Ex-Gura	59.16	11.52	50.96	1.67	132.00	64.65	2.10	19.00	183.40

Ex-Kwakwi	58.28	10.42	55	1.57	115.50	61.15	2.30	20.00	210.95
Ex-Tafawa Balewa	59.05	12.30	54.29	1.30	102.50	51.65	2.20	21.00	200.80
Ex-Biliri	64.96	11.78	54.32	1.38	77.50	54.00	2.40	19.00	180.90
Ex-Gwagwalada	60.47	10.15	53.16	1.50	85.00	44.90	2.60	16.50	150.90
Ex-Andaha	58.26	9.77	50.24	1.57	132.50	99.25	2.30	22.50	275.85
Ex-Kwi	62.50	11.39	54.15	1.94	171.50	70.90	2.50	25.50	245.75
TOTAL	567.9	110.74	535.3	15.50	1051.00	648.10	23.90	201.50	2000.0
MEAN	59.79	11.07	53.53	1.51	105.10	64.80	2.39	20.15	200.09
S.E.	3.38	0.32	3.37	0.106	3.97	5.26	0.07	1.88	3.38
LSD(0.05)	6.48	0.48	7.61	0.184	13.61	7.77	0.09	2.69	32.54
CV (%)	11.54	6.85	6.05	3.064	4.63	0.77	0.08	1.69	16.55

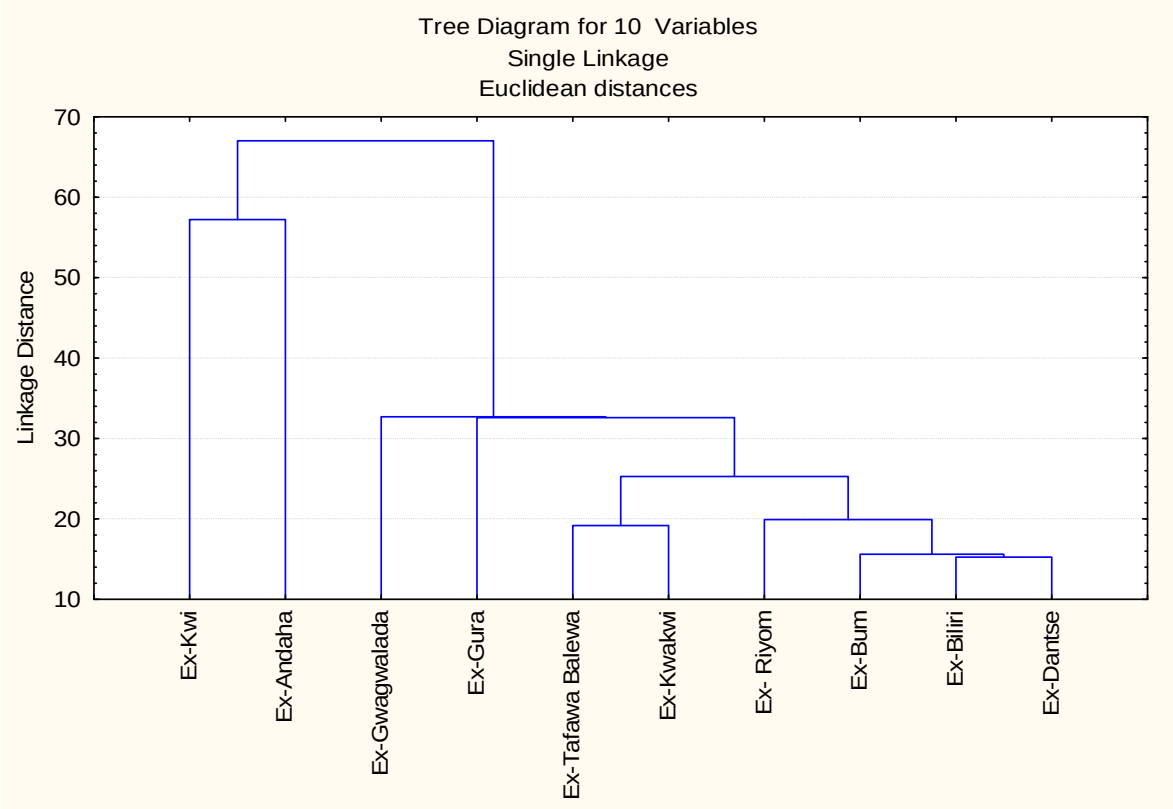

Fig 1: Dendrogram of morphological characters showing the linkages among ten accessions of finger millet grown in northern Nigeria for the three cropping seasons.

The lowest similarity was observed between Ex-Andaha and Ex-Gwagwalada (Fig.1). The dendogram showed the highest genetic similarity between the germplasms Ex-Biliri, Ex-Bum and Ex-Dantse. The population is divided into two germplasm which included a smaller subgroup comprising of Ex-Kwi and Ex-Andaha. The other subgroup contains germplasm of

Ex-Gwagwalada and Ex-Gura; Ex-Tafawa Balewa and EX-Kwakwi; Ex-Riyom, Ex-Bum, Ex-Biliri and Ex-Dantse. Phenotypic relatedness was observed between Ex-Riyom, Ex-Bum Ex-Biliri and Ex-Dantse and maximum closeness was observed in Ex-Dantse, Ex-Biliri and Ex-Bum, Ex-Riyom, Ex-Tafawa Balewa and Ex-Kwakwi Phenotypically, Ex-Tafawa Balewa, Ex-Kwakwi, Ex-Riyom, Ex-Bum, Ex-Biliri and Ex-Dantse could constitute a specie where the morphological differences amongst them are narrow or close.

DISCUSSION

Results of our assessments of 10 finger millet landraces using 9 morphological traits and weight showed significant variations across all the 10 landraces of finger millet accessions within the three cropping seasons (2008, 2009 and 2010) respectively. Our results agree with the earlier findings of Mnyenyembe and Gupta (1998) and Upadhyaya, *et al*., (2007).

Evaluation of the phenotypic characters for the different accessions showed that the phenotype could have genetic diversity for plant height, 1000 seed weight, leaf length and tillers than all the other traits assessed in this trial.

Table 2 shows the genetic variability existing in the ten accessions used in this trial. Our research concurs with Shahryani *et al.,* (2011), Garavandi and Kabrizi (2010), who established genetic diversity for plant height, 1000seed weight, spikelet in bread wheat genotypes and similar crops. Kempana and Thirumalachar (1968), and Abraham *et al.* (1989) also found significant variation for grain yield and number of productive tillers per plant. Josh and Mehra (1989) reported significant genetic variation for days to flowering and other parameters as plant height, finger length, number of fingers and phenotypic relatedness in finger millet accessions.

Upadhyaya *et al.* (2007) reported large phenotypic diversity in pearl millet germplasm especially in terms of days to flowering, plant height, total tillers and 1000-seed weight which was also observed in this work. Our findings also indicated that at the three year trials in both Keffi and Gwagwalada locations, there were accessions that could flower as early as 60 days and others as late as 120 days. Similarly, phenotypic variations were observed in plant diameter, leaf length, number of fingers, number of ears and 1000seed weight. This exhibition of significant genetic diversity observed in this report agrees with the work of Garavandi and Kabrizi, (2010) and Shahryari, *et al.,* (2011) who reported genetic biodiversity for plant height, 1000seed weight, seed number, spikelet etc in bread wheat genotypes..

Table 2: Range of variation for important morphological characters in finger millet accessions grown in Keffi and Gwagwalada, Northern Nigeria, for the 3 cropping seasons

Parameter	MIN	MAX	MEAN	VARIANCE
Time to flower (days)	60	120	97.67	11.43
Plant height (cm)	54.66	64.96	59.67±3.38	6.85
Plant diameter (cm)	9.77	12.30	11.07±0.32	6.08
Leaf length (cm)	49.00	55.30	53.50±3.37	6.05

Leaf diameter(cm)	1.30	1.94	1.51±0.11	3.06
Number of fingers	73.50	171.5	105.1±3.97	4.63
Length of fingers (cm)	44.90	99.25	64.80±5.26	0.77
Finger diameter (cm)	2.1	2.7	2.39±0.07	0.08
Number of ears	16.5	25.5	20.15±1.88	1.69
1000seed weight (g)	150.9	275.85	200.09±3.38	16.55

CONCLUSION

The objectives of this study have been modestly achieved. The results established the diversity among the morphological traits and also determined the phylogenetic diversity of the plant using cluster analysis. These results have clearly established the possibility of genetic variation and this could be useful in ascertaining evolutionary diversion which occurs whenever mutation occurs. Further studies should involve the identification of specific primers which could identify the specific loci responsible for this diversity.

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PGB28

EVALUATION OF GENETIC VARIANCE AND HERITABILITY OF AGRONOMIC AND YIELD TRAITS IN PIGEON PEA- *CAJANUS CAJAN* (L.) MILLSP. (FABACEAE)

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ABSTRACT

The selection of useful traits is necessary to achieve any breeding objective. Therefore, plot trials were carried out in research farm of the Department of Botany, University of Ibadan for two years. The study aimed at evaluating the components of genetic variance and heritability of some agronomic and yield related traits of some accessions in pigeon pea. The result showed variations in mean values of traits ranging from 0.15 ± 0.00 to 166.34 ± 1.6. Accessions CL13 and 26 produced higher seed yield per pod (0.2g) compared to other accessions. CL 26 had the highest stem length at maturity (179.5cm), while the highest number of plant per pod (85.5) was recorded for CL 29. Stem length at maturity had the highest values of the phenotypic variance, genetic variance and environmental variance. The heritability estimate of traits ranges between 54-99%.The accessions were highly significant (P<0.01) for most of the agronomic and yield related traits.

Keywords: accessions, pigeon pea, traits, heritability

INTRODUCTION

Pigeon pea *(Cajanus cajan* L.*)* is one of the most important leguminous plants with high nutritional, medicinal and economic values. It is widely used in improving the soil fertility (Olawuyi and Fawole, 2005). The leaves are used in treatment of some skin and respiratory infections, while an aqueous infusion of seeds mixed with leaves are also used in management of genetic disorder (Dhar, 1968; Owere *et al*., 2000). The breeding of pigeon pea for early and maturing traits, tolerance to drought, pests, diseases and characterization of morphological and yield related traits have been attributed to the success of this crop (Odeny, 2000; Kimani *et al*., 2000). The correlation coefficient, principal component analysis and character association of some pigeon pea genotypes have been reported (Kharif *et al*., 1973; Kimani, 2000). But the evaluation of the components of genetic variance has not been widely explored. The limited improved varieties of pigeon pea also necessitate the selection of genetically influenced yield components for germplasm improvement. Therefore, this study estimated the genetic parameters of some agronomic and yield related traits in pigeon pea.

MATERIALS AND METHODS

A field experiment was conducted at the nursery farm of the Department of Botany, University of Ibadan (latitude 7^{o} 20'N and longitude 3^{o} 54'E, 200m above sea level), Nigeria for two years (2002 and 2003). The four accessions (CL 1, CL 13, CL 26 and CL 29) evaluated in this study were the breeding products obtained from the collection maintained in the Department of Botany, University of Ibadan. The accessions were grown on the field using randomized complete block design with three replicates. Each plot consisted of three rows spaced at 0.75m between and 0.5m within rows. Two seeds from each accession were planted at 2-3 cm depth from the soil, but thinned to one three weeks after planting. Agronomic practices were duly carried out.

Data were collected on Number of days from sowing to: emergence (DSE), production of primary leaflets (DSP), production of first flower (DSF), production of first pod (DSP), number of branches at production of first flower (NBF), number of flowers (NOF), stem length at maturity (SLM), stem diameter at maturity (SDM), length of pods per plant (LPP), width of pods per plant (WPP), number of seeds per pod (NSP), seed weight per plant (SWP), pod weight per plant (PWP), number of pods per plant at maturity (NPM), Total number of pods per plant at harvesting (NPP), leaf length at maturity (LLM), leaf width at maturity (LWM) and seed weight per pod (SW). The data were subjected to analysis of variance with Statistical Analysis System package (SAS, 1999). Genetic component of variation and broad sense heritability estimates were determined according to the procedure of Johnson *et al.* (1955), Singh and Chaudhary (1985).

RESULTS AND DISCUSSION

The range, mean, standard errors of ten growth and yield traits are shown in Table 1. A wide range was observed for most of the traits. The total number of pods per plant at harvesting (NPP) had the highest range of 45- 85.5, while seed weight per pod (0.1-0.2) g was the least. The mean values of all the traits were higher than their respective standard errors. The coefficient of variation for the different traits ranged from 0.00% for seed weight per pod (SW) to 15.6% for number of seeds per pod (NSP). The stem length at maturity (SLM) and NPP showed the highest mean performance of 166.34cm and 60.63 respectively. Accessions CL13 and CL26 produced higher seed weight per pod (0.2g) compared to other accessions. CL26 had the highest stem length at maturity (179.5cm), while CL29 produced the highest number of pods per plant at harvesting. CL26 also performed best for all the traits except seed weight per plant. The lower values of coefficient of variation (CV) are indices of experimental reliability (Gomez and Gomez, 1984). The range of CV which varies from 0 to 15.6% could be attributed to high magnitude of genotypic variation found in most of the traits for different accessions.

The mean squares from the analysis of variance for agronomic traits are shown in Table 2. Highly significant differences ($p<0.01$) were observed in six traits; number of days from sowing to production of first pod (DSP), number of flowers (NOF), leaf length at maturity (LLM), leaf width at maturity (LWM), stem length at maturity (SLM) and stem diameter at maturity (SDM), but significantly different ($p<0.05$) for three traits; number of days from sowing to production of first flower (DSF), number of branches at production of first flower (NBF) and height at first flowering (HFF), while number of days from sowing to emergence (DSE) and number of days from sowing to production of secondary leaflets (DSS) did not show significant differences. The significant variations could be as a result of genetic contribution of the accessions to the yield

components. This enhances selection of best accessions with quality morphological traits, and contributes to their diversities.

The estimates of phenotypic variance, genotypic variance, environmental variance and heritability of ten yield related traits are shown in Table 3. The genotypic variances were high in stem length at maturity, number of pods per plant at maturity (NPM) and total number of pods per plant at harvesting compared to other traits. The genotypic variances were higher than the environmental variances in all the traits. The stem length at maturity had the highest value of phenotypic variance (968.70), genotypic variance (957.10) and environmental variance (11.60). The heritability of the traits ranged between 54-99%. High heritability estimates was observed for most of the traits. The SDM, NPP, NSP and length of pods per plant (LPP) had the highest heritability estimate of 99%, while seed weight per pod (SW) had the least (54%).

Higher phenotypic variance than genotypic variance could be due to the interaction of environmental components as similarly observed by Oseni and Khadir (1994) and Nguru (1995). The moderately high genotypic variance in some traits indicated that attention should be given to the improvement of traits by combining other traits to enhance greater yield. The lower values of environmental variance in the traits are an indication of little or no effect of environmental factors as similarly conforms to the findings of Abubakar and Samarawira (1989). High heritability estimates show high measure of variation which could be as a result of an additive gene effect. This enhances effective selection of desirable accession for improvement of traits as similarly reported by Pathak and Dikit (1992).

The result of mean square of eight yield related traits in Table 4 shows that five traits; NPM, NPP, LPP, NSP and SW produced highly significant ($p<0.01$) effect, while significant differences ($p<0.05$) were shown for three traits; width of pods per plant (WPP), seed weight per plant (SWP) and pod weight per plant (PWP). This is in accordance with the report of Omoigui *et al.* (2006).

CONCLUSION

From the results, highly significant effect produced by the accessions indicated genetic variability that exist for most of the agronomic and yield related traits. The components of variance and heritability estimates were models which could be considered in selection of suitable traits and accessions for yield improvement.

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Table 1: Ranges, means and coefficient of variation of growth and yield traits in pigeon pea

Traits	Range	Mean ± S.E	C.V (%)	accessions CL1	CL 13	CL 26	CL29
SLM (cm)	152- 179.5	166.34 ± 1.60	1.92	162	152	179.5	170
SDM (cm)	6.35- 7.40	6.86 ± 0.13	3.79	6.40	6.35	7.40	7.30
LPP(cm)	7.20-8.10	7.66 ± 0.10	2.61	7.20	7.60	8.10	7.75
WPP (cm)	0.85- 1.15	0.99 ± 0.04	8.10	0.85	0.95	1.15	1.00
NSP	4.60-5.50	5.00 ± 0.39	15.60	4.60	4.80	5.50	5.10
SWP (g)	0.55-1.00	0.79 ± 0.03	7.60	0.55	0.65	0.95	1.00
PWP (g)	0.60-1.10	1.03 ± 0.04	7.77	0.75	0.60	1.65	1.10
NPM	15-25	19.38 ± 1.22	12.59	15	17	25	20.5
NPP	45-85.5	60.63 ± 1.12	3.70	48	45	64	85.5
SW (g)	0.1-0.2	0.15 ± 0.00	0.00	0.1	0.2	0.2	0.1

Stem length at maturity (SLM), stem diameter at maturity (SDM), length of pods per plant (LPP), width of pods per plant (WPP), number of seeds per pod (NSP), seed weight per plant (SWP), pod weight per plant (PWP), number of pods per plant at maturity (NPM), Total number of pods per plant at harvesting (NPP) and seed weight per pod (SW)

Table 2: Mean squares of eleven agronomic traits in pigeon pea

Source of variation	df	DSF	DSP	NBF	NOF	HFF	DSE	DSS	LLM	LWM	SLM	SDM
Entries	3	1.32*	1.47**	1.41*	0.54**		1.98*	0.64^{ns}	1.04^{ns}	0.13**	0.11**	1.59**	0.13**
Error	1	0.00	0.00	0.01	0.00	0.02	0.14	0.07	0.03	0.00	0.01	0.00	
Total	4												

*, ** Significantly different at p<0.05 and p< 0.01 levels of probability respectively. Number of days from sowing to: emergence (DSE), production of primary leaflets (DSP), production of first flower (DSF), production of first pod (DSP), number of branches at production of first flower (NBF), number of flowers (NOF), stem length at maturity (SLM), stem diameter at maturity (SDM), leaf length at maturity (LLM), leaf width at maturity (LWM).

Table 3: Phenotypic, genetic variance, environmental variance and heritability of ten yield related traits in pigeon pea

Genetic parameters	**Phenotypic variance**	**genotypic variance**	**environmental variance**	**heritability (H^2b) %**
SLM (cm)	968.70	957.10	11.60	98.0
SDM (cm)	0.48	0.479	0.001	99.0
LPP(cm)	2.51	2.507	0.003	99.0
WPP(cm)	0.04	0.033	0.007	83.0
SWP(cm)	0.02	0.018	0.002	90.0
PWP(g)	0.002	0.0015	0.001	75.0
SW(g)	10.54	5.69	4.85	54.0
NSP	1.06	1.058	0.002	99.0
NPM	60.68	53.75	6.93	89.0
NPP	712.39	706.68	5.71	99.0

Stem length at maturity (SLM), stem diameter at maturity (SDM), length of pods per plant (LPP), width of pods per plant (WPP), number of seeds per pod (NSP), seed weight per plant (SWP), pod weight per plant (PWP), number of pods per plant at maturity (NPM), Total number of pods per plant at harvesting (NPP) and seed weight per pod (SW)

Table 4: Mean squares of eight yield related traits in Pigeon pea

Source of variation	df	NPM	NPP	LPP	WPP	NSP	SWP	PWP	SW
Entries	3	1.22**	1.12**	0.11**	0.14*	0.39**	0.30*	0.40*	0.10**
Error	1	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Total	4								

*, ** significantly different at $p<0.05$ and $p<0.01$ levels of probability respectively. Length of pods per plant (LPP), width of pods per plant (WPP), number of seeds per pod (NSP), seed weight per plant (SWP), pod weight per plant (PWP), number of pods per plant at maturity (NPM), Total number of pods per plant at harvesting (NPP) and seed weight per pod (SW)

PGB29

HERITABILITY ESTIMATES FOR BIOMASS PRODUCTION IN LOCAL SORGHUM (*SORGHUM BICOLOR* L. MOENCH) OF SOME SELECTED STATES IN NORTH-WESTERN NIGERIA

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ABSTRACT

Ten local Sorghum varieties were evaluated at Usmanu Danfodiyo University, teaching and research farm, Sokoto, Sokoto State during the 2010 rainy season and at Bubuche, in Augie Local Government Area, Kebbi State during the 2011 rainy season, all in North Western, Nigeria. The treatments were laid out in a Randomized Complete Block Design (RCBD) with three replications. The study revealed that high narrow sense heritability estimates of 90.67 % were observed on flag leaf area, leaf length 65.82%, straw weight 61.48%, plant height 52.95% and flag leaf length 51.54%. Leaf area index recorded 36.84% narrow sense heritability, while leaf number had 10%, 100- seed weight 15.93% and total grain yield recorded 16.24%. The study therefore indicates that selection for biomass related characters can easily be carried out among the local Sorghum germplasm of North Western, Nigeria.

Key words: Biomass; Heritability; North-Western Nigeria; Production; Sorghum,

INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench) belongs to family Poaceae (Gramineae) with Chromosome number 2n = 20 (Dogget, 1970). Origin and geographical distribution of

sorghum, in both cultivated and wild types found in north-eastern part of Africa (Biswas *et al.*, 2001). It is an important staple food crops and provide bulk of raw materials for the livestock and many agro-allied industries in the world (Dogget, 1970). An estimated 55,721,588 tonnes were produced worldwide, harvested from 40,935,896 hectares in 2010, with an average yield of 13,612 kg/ha, the African total production for the year 2010 was 211,107,724 tonnes harvested from 24,837,754 hectares at an average yield of 8,498 kg/ha. In Nigeria the total production was 4,784,100 tonnes, harvested from4,736,730 hectares at an average yield of 10,100 kg/ha (FAOSTAT, 2010).

The degree of correspondence between phenotype and genotype is measured by heritability of the trait. Statistically heritability is a regression coefficient of genotype on phenotype. Theoretically, heritability ranges from 0 to 1, but the extreme values are very rare (Ferh, 1987). A particular heritability value is for a particular trait in a particular population at a particular time. This is so because the gene frequency varies from population to population. The diversity of Sorghum expresses a wide range of heritability and adaptability to different conditions, including different genotypes from early to late maturing, dwarf to tall, loose to compacted panicles, white and red seeded and plant breeders are interested in developing cultivars with improved yield and other desirable agronomic characters. In order to achieve this goal, the breeders should determine heritability of the desirable traits for genotypes before selection (Puri, *et al*., 1982). The selection criteria may be yield, or one or more of the yield component characters. However, breeding for high yield crops require information on the nature and magnitude of variation in the available materials, relationship of yield with other agronomic characters and the degree of environmental influence on the expression of these component characters, since grain yield in sorghum is quantitative in nature and polygenically controlled, effective yield improvement and simultaneous improvement in yield components are imperative (Bello and Olaoye, 2009). Heritability is a measure of the extent to which observed phenotypic differences for a trait are due to genetic differences. There are two commonly used measures of heritability, broad-sense (H2) and narrow-sense (h2) heritability. Broad-sense heritability measures the proportion of phenotypic difference (*V*P) that is due to variation in genetic factors for a single population under the limits of the environment during the experiment. An estimate of broad-sense heritability near 1.0 indicates that environmental conditions have little impact on the phenotypic differences observed in the population; an estimate near 0.0 indicates that the environment is almost solely responsible for the differences (Puri, *et al*., 1982). Broad-sense heritability is considered to be the sum of additive variance (*V*A), dominance variance (*V*D) and interactive variance (*V*I); thus, H^2=*V*A+*V*D+*V*I. Broad-sense heritability estimates are less accurate than narrow-sense heritability ones in estimating the selection potential of quantitative traits since calculations take into account all forms of genetic variation, not just additive genetic effects. Conversely, narrow-sense heritability excludes dominance and interactive variance, leaving only additive variance; thus, H^2=*V*A=VA/VP. Narrow-sense heritability estimates are useful for predicting the phenotypes of offspring during selection procedures; the closer the heritability to 1.0, the greater one's ability to make an accurate prediction of the phenotype of the offspring based on the knowledge of parental phenotypes There are two major methods for estimating heritability; one uses correlation and regression among related individuals to estimate heritability (Puri, *et al*., 1982).

The objective of the research was to determine narrow sense heritability estimates for traits associated with biomass production in North Western, Nigeria, an area where crop cultivation have become incorporated with livestock rearing.

MATERIALS AND METHODS

Ten local sorghum landraces were evaluated during the 2010 rainy season at Usmanu Danfodiyo University, teaching and research farm, Sokoto, Sokoto State and during the 2011 rainy season at Bubuche, in Augie Local Government Area, Kebbi State, all in North-Western Nigeria. Sokoto is located in the Sudan Savanna agro-ecological zone of Nigeria on latitude 13^0 01 N; longitude 5^0 15 E and altitude of about 350m above sea level (ASL). Mean annual rainfall is about 752 mm. The minimum and maximum temperatures are 26^0 and 35^0, respectively, and relative humidity of 23-41%. The area is characterized by long dry season with cool air during Hammattan (November – February), dry air during hot season from March – May followed by a short rainy season, (Bello, 2006) and Bubuche is located in Augie local government area of Kebbi State on latitude 13^0 05 N ; longitude $4^0$12 E and altitude of 345m above the sea level, temperature ranges from 27^0-34^0 and relative humidity of 24-44% with mean annual rainfall of 6700-7600mm (Anon, 2009). The texture of the soil was loamy sand and the soil is deep, loose and well drained, chemical analysis shows that the soil is slightly acidic, low to medium in organic carbon, low total nitrogen, low exchangeable cat ions low in cat ions exchange capacity (CEC), very low available P and K Ca and Mg contents and low Bulk density.

The materials used in the study consisted of ten indigenous grain sorghum genotypes representing the types widely grown in North-Western Nigeria, which were collected by the National Center for Genetic Resources and Biotechnology (NACGRAB), Moor plantation, Ibadan, Nigeria (Table, 1).

The experiment was laid out in a Randomized Complete Block Design (RCBD) in three replications. Each pot size was 6m x 3m, 75cm as inter row spacing and intra-row spacing of 30cm and a total of 240 plants per plot after thinning were used. Before sowing, seeds were treated with Apron-plus 3g/kg seed against soil fungi and insects. Sowing was on 10^{Th} of June, 2010 and 2011. Five seeds were sown in each hole. Seedlings were thinned to three plants per hole after three weeks from sowing. Hand hoeing weeding practiced trice, the first one was two weeks after sowing and the subsequent weeding were carried out at three weeks interval.

Data were collected on days to 50% flowering (DF), plant height (PH), and leaf characteristics including leaf length (LL), leaf number (LN), leaf area index (LAI), flag leaf area (FLA) and flag leaf length (FLL). At maturity, total grain yield (TGY), 100-grain weight (HGW) and straw weight (STRAW-WT0 were recorded at both locations and during both seasons in accordance with the procedure outlined in the IBGR/ICRISAT sorghum descriptor (IBPGR and ICRISAT 1993). Leaf area (LA) per plant was calculated on the basis of the length and width of the third top leaf multiplied by the total number of leaves and a coefficient of 0.71 (Krishnamurthy, *et al.*, 1974).

Individual analysis of variance was performed for all traits on each location according to the procedure described by Gomez and Gomez (1984) for the randomized complete block design. The combined analysis of variance was done, for all traits, following the

method described by LeC lerg *et al.* (1962), based on a randomized complete block design. For mean comparison, the means were separated using Duncans Multiple Range Test (DMRT) at 0.05 level of significant, according to the procedure described by Gomez and Gomez (1984).

Phenotypic and Genotypic Variances

Phenotypic (σ^2ph) and genotypic (σ^2g) variances were estimated using individual analysis of variance as follows:

$$\sigma^2 g = \frac{M2-M3}{r}$$

$$\sigma^2 ph = \sigma^2 g + \sigma^2 e$$

Where: σ^2e: is the error variance (M3) for RCBD.

Narrow sense heritability estimate

Narrow sense heritability will be estimated using the formulae described by Fehr (1987)

$$h^2 = \frac{\delta^2 A}{\delta^2 ph}$$

Where

δ^2A = Additive Variance

δ^2_{Ph}= Phenotypic Variance

RESULTS AND DISCUSSION

High narrow sense heritability values were observed on flag leaf area (90.67%), leaf length (65.82%), straws weight (61.48%), plant height (52.95%) and flag leaf length (51.54%) (Table 5). The result suggests that selection for these traits will be easy and as such the cultivars used in the study are potentially useful in breeding programme for enhanced biomass production. Similarly leaf area index recorded 36.84% narrow sense heritability. Similar results were obtained by William *et al.* (1987), Khaliq *et al*. (2008) in their study which revealed that, characters such as plant height, days to 50% flowering, flag leaf area, flag leaf length and leaf length would respond positively to selection when selected, because of their high heritability, this also agreed with the findings of Eckebil *et al.* (1997), Totok (1997) and Biswas *et al.* (2001).

However, leaf number (10%), 100- seed weight (15.93%) and total grain yield (16.24%) heritability were not significant and would not respond to selection easily because of their low heritability estimates. Similar results were observed by Bello *et al.* (2001) and Bello *et al.* (2007), when they reported low heritability estimates of grain yield is due to the direct or indirect multiplicative effects of several yield components on grain yield. Similarly Obilana and Fakorede (1986) reported that, if a character is influenced by environment, its heritability would be low in a population in which plant environments vary widely.

CONCLUSION

High narrow sense heritability estimates were observed for flag leaf area, leaf length, straw weight, plant height and flag leaf length all of which are good determinants of biomass production. The study therefore concludes that these traits will definitely respond positively to selection, it also indicates that environmental conditions have little

impact on the traits. Breeding for high biomass production in the sorghum germplasm of North Western, Nigeria is therefore possible.

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Table1. Sorghum landraces used in the study

S/No	Name	Area Collected	Grain Colour	Major Use
1	Zago.Ex-BATSARI	Katsina State	Brown	Food
2	NG/SA/07/005	Niger State.	White	Food
3	NG/SA/07/125	Zamfara State	White.	Food
4	NGB/06/001	Kaduna State	White	Food
5	NG/SA/DEC/07/0049	Niger State	White	Food
6	NG/SA/DEC/07/0108	Niger State	White	Food
7	NG/SA/DEC/07/0213	Kaduna State	White	Food
8	NG/SA/DEC/070123	Kano State	White	Food
9	NG/SA/DEC/07/0036	Niger State	White	Food
10	EX-ARGUNGU (Kaura)	Kebbi State	Red	Food

Table 2: Narrow Sense Heritability estimate for Ten Sorghum Traits Evaluated during 2010 rainy season at Sokoto and during 2011 rainy season at Bubuche Combined.

Traits	Phenotypic variance	Genotypic variance	Narrow Sense Heritability (%)
LN	2.01	0.21	10
LL	58.05	38.21	65.82
PH	815.85	432.05	52.95
LAI	0.19	0.07	36.84
FLA	8133.7	7374.6	90.67
FLL	18.49	9.53	51.54
STRAW-WT	2.44	1.5	61.48
100-GWT	11.11	1.77	15.93
TGY	731528.42	118795.75	16.24

Heritability (h^2) ≥45 is significant (trait highly heritable)

Heritability (h^2) between 18 and 35 is nearly significant

Heritability ≤18 is not significant (lowly heritable traits)

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RELATIONSHIPS BETWEEN NORMALIZED DIFFERENCE VEGETATION INDEX (NDVI) AND OTHER TRAITS OF TROPICAL TESTCROSS MAIZE HYBRIDS UNDER DROUGHT AND WELL-WATERED CONDITIONS

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ABSTRACT

Normalized difference vegetation index (NDVI) is a nondestructive measure of green vegetation growth or aboveground biomass of a crop. NDVI may also be used to evaluate traits such as early vigor and stay green which are important for adaptation to drought stress. In the present study, the relationships between NDVI and grain yield as well as other measured agronomic and drought-adaptive traits were examined under drought stress and full irrigation conditions in a trial composed of testcross hybrids of exotic and adapted maize inbred lines. NDVI had higher correlation coefficients with grain yield under full irrigation than under drought stress, though the relationships were generally weak. NDVI had stronger association with grain yield at 8-leaf stage than at 3-leafed stage under full irrigation conditions. The R^2 values of NDVI_1 with grain yield and plant height under both irrigation treatments were ≤ 0.20. The R^2 values of NDVI_2 with grain yield were 0.31 and 0.45 under drought and full irrigation environments, respectively, while the values with plant height under drought and full irrigation conditions were 0.48 and 0.38, respectively.

INTRODUCTION

Maize breeders have identified the urgent need to improve maize productivity through the use of germplasm that have better adaptation to the climatic conditions of any particular agro-ecology. This has necessitated the growing advocacy for precision agriculture technologies as a vital component of crop breeding activities (Barker and Sawyer, 2011). Applications of new remote-sensing tools based on the use of irradiation to estimate green biomass status at field level are gaining more prominence in maize breeding. One of such devices that has been proposed for high throughput phenotyping in tropical maize adaptation under water stress (Lu et al., 2012; Araus and Hearne, unpublished) is a spectroradiometer, otherwise known as Greenseeker handheld optical sensor unit (NTech Industries, Inc., USA) which is used to measure normalized difference vegetation index (NDVI). NDVI, a numerical indicator that is useful in analyzing remote sensing measurements, has been reported to be highly correlated with grain yield in maize and other crops (Cabrera-Bosquet et al., 2011; Lu et al., 2011; Lu et al., 2012) and has been suggested as a secondary trait for evaluating maize germplasm

for drought tolerance (Hearne and Araus, unpublished). NDVI is computed using the measurements of reflectance taken in the visible region and near infrared region of the spectrum (Lu et al., 2012). The NDVI which provides a means of monitoring the vigor of the green vegetation growth or biomass was found to be proportional to the leaf area of a plant population and, therefore, a functional part of active photosynthesis which ultimately determines final grain yield (Lu et al., 2011; Lu et al., 2012). Maize hybrids or genotypes that accumulate abundant biomass under drought stress as revealed in high NDVI values at the seedling stage of the crop would be expected to produce high grain yields at harvest.

The use of NDVI as a valued trait in maize breeding for drought and low N tolerance in both temperate and tropical germplasm is presently gaining prominence (Wu et al., 2011; Lu et al., 2012; Winterhalter et al., 2012). In order to assess the value of NDVI in a new hybrid maize breeding program, this study was conducted to examine the relationships between NDVI and other measured traits of a set of newly developed testcross maize hybrids.

MATERIALS AND METHODS

A total of 41 hybrids, including 40 testcrosses and the hybrid formed by crossing two inbred line testers, were developed at Saminaka (10°40'N; 8° 77'E; altitude 730 m) in Nigeria in the main season of 2010 (Adebayo, 2012). A trial composed of the 41 testcrosses and 3 hybrid checks (Table 1) was planted under managed drought stress conditions at Ikenne on November 24 in 2010 and on November 22 in 2011. Ikenne receives little rainfall from November to March of every year, making the location suitable for conducting drought stress tolerance evaluation during the dry season. The soil at this site is eutric nitrosol (FAO classification) and the experimental fields are flat and reasonably uniform, with high water-holding capacity (Menkir et al., 2009; Badu-Apraku et al., 2010). Experiments were planted in two adjacent blocks that received different irrigation treatments. The first block (well-watered) received irrigation water throughout the life cycle of the crop whereas the second block (drought stress) received irrigation water for 28 days only, which is approximately two to three weeks before anthesis.

The blocks were separated by four ranges (each 4.25 m wide) to restrict lateral movement of water from the fully irrigated block to the drought stress block. The testcross trial was planted in each block in 4x11 alpha (0,1) lattice design with three replications. Different randomizations were used in the two treatment blocks. Experimental plot consisted of a single 4-m row spaced 0.75 m apart with 0.50 m spacing between hills. Three seeds were sown in a hill and later thinned to two plants two weeks after planting (2WAP) to attain a plant population density of 53,333 plants per hectare. Water was supplied with an overhead sprinkler irrigation system that dispenses 12 mm of water per week. Except for the different irrigation treatments, all field management practices were uniform for both the well-watered and drought stress experiments. Basal application of a compound fertilizer was done immediately after planting at the rates of 60 kg N, 60 kg P, and 60 kg K per hectare. An additional 60 kg ha^{-1} N was applied in the form of urea as top dressing four weeks later. In each trial, gramazone and atrazine were applied as pre-emergence herbicides at 5 l ha^{-1} each of Paraquat and Primextra. Subsequently, manual weeding was done to keep the trials weed-free.

Several traits were measured on plot basis in both water-stressed and fully irrigated blocks at Ikenne in 2010 and 2011 (Adebayo, 2012) but data on normalized difference vegetation index (NDVI), anthesis-silking-interval (ASI), plant height (PLHT), ear aspect (EASP), number of ears per plant (EPP), and grain yield (GY) are presented in this report. Normalized difference vegetation index (NDVI) was measured using Greenseeker Optical Sensor Unit (Ntech Industries, Inc.). Measurements were recorded at 2 and 4 weeks after planting (WAP) when the plants were at 3- and 8-leafed stages, respectively, in December 2010 and December 2011. The Greenseeker handheld optical sensor unit was installed with red sensor, red waveband centered at 650 ± 10 nm, and near infra-red (NIR) band centered at 770 ± 15 nm. The unit was held at a distance of approximately 60 cm above the canopy while each plot was traversed, starting from the beginning of the row to the end, and data were collected in log plots mode. A HP iPAQ installed with NTech capture programme for pocket PC was used to measure, compute and save NDVI directly from the Greenseeker. The device computes the NDVI according to the following formula:

$NDVI = (R_{NIR} - R_{RED})/(R_{NIR} + R_{RED})$

where R_{NIR} = the fraction of emitted NIR radiation returned from the sensed area (reflectance), and R_{RED} = the fraction of the emitted red radiation returned from the sensed area (reflectance). The data were later transferred by syncing the iPAD to a synchronized desktop computer for further processing.

Days to 50% anthesis (DTA) and days to 50% silking (DTS) were recorded as the number of days from planting to when 50% of plants in a plot had shed pollen, and had emerged silks, respectively. ASI was computed as the difference between DTS and DTA. PLHT was measured in centimeters (cm) as the distance from the base of the plant to the height of the first tassel branch. EASP was also visually rated on a scale of 1 to 5, where 1 = clean, uniform, large, and well-filled ears and 5 = rotten, variable, small, and partially filled ears. During harvesting, the total number of plants and ears were counted in each plot at the time of harvest. A cob was counted if it had at least one kernel set. EPP was then computed as the proportion of the total number of ears at harvest divided by the total number of plants harvested. All ears harvested from each plot were weighed and shelled to determine grain weight. A representative sample was taken to determine percent moisture. GY, measured in kg ha^{-1} and adjusted to 15% moisture content was calculated from grain weight and percent moisture. The following equation was used for estimating grain yield:

GY (kg ha^{-1}) = (GWT (kg)/ 3 m^2 x [(100 – MC) / (100-15] x 10,000 m^2.

where GWT = Grain weight of harvested area in kg, MC = Moisture content of grains at harvest, Moisture content for storage = 15%, 1 hectare = 10,000 m^2, Plot area (area harvested) = 3 m^2.

Analysis of variance (ANOVA) was computed for the 44 entries for each year to generate entry means adjusted for block effects according the lattice design (Cochran and Cox, 1960; Menkir et al., 2003). The pooled error mean square was calculated for each block ANOVA by dividing the sum of the error sums of square by the corresponding sum of the error degrees of freedom. Combined analysis of variance was then computed across years using the adjusted means. In the combined analysis, year, replications and blocks were treated as random effects while testcrosses were considered as fixed effects. All analyses were carried out with PROC GLM in SAS (SAS Institute, 2009) using a RANDOM statement with TEST option. Pearson's correlation coefficients were calculated using the mean values of the measured traits. Although NDVI measurements

were taken at the same periods under both irrigation treatments, the values were correlated with those of grain yield and other traits that were measured after moisture stress has been imposed in the drought stress block. Also, linear regression models were used to determine the relationships between GY and NDVI using Procedures in SAS (SAS Institute, 2009).

RESULTS AND DISCUSSION

Results of analysis of variance combined over two years (Table 2) revealed that year effect was significant for all measured traits except for EPP under both irrigation treatments and GY under well-watered conditions. Hybrids differed significantly for all measured traits under both irrigation treatments except for NDVI_1 under drought stress. Genotype x year (GxE) interaction was significant for GY under both environments and also for NDVI_1 and NDVI_2 under well-watered conditions.

Results of correlation analysis between NDVI and every other trait under both irrigation treatments are presented in Table 3. NDVI measured at 3-leaf stage had non-significant and weak associations with GY under drought stress and well-watered conditions, respectively. The relationships became stronger when NDVI was measured at 8-leaf stage. Also, NDVI taken at 3-leaf stage had positive but weak associations with plant height under both irrigation treatments. When NDVI was taken at 8-leaf stage, it exhibited a strong association with plant height under drought stress and even stronger relationship under full irrigation conditions (Table 3). The R^2 values of NDVI_1 with grain yield and plant height under both irrigation treatments was ≤ 0.20. The R^2 values of NDVI_2 with grain yield were 0.31 and 0.45 under drought and full irrigation environments, respectively, while the values with plant height under drought and full irrigation conditions were 0.48 and 0.38, respectively.

The significant and positive correlation between NDVI and grain yield in our study was in agreement with the results of several other workers (Araus et al., 2010; Islam et al., 2011; Lu et al., 2011). Though some of these workers reported a strong relationship, our finding agreed more with Lu et al. (2011) who reported a weak genetic correlation between NDVI and grain yield (0.38-0.49) in maize. A stronger relationship that existed between NDVI and grain yield under full irrigation condition when compared with what obtained under drought stress points to the predictive value of aboveground biomass for grain yield in maize under optimum growing conditions. The relationship that became stronger at 8-leaf stage (4WAP) under both irrigation regimes agreed with other results which indicated that growth stage is a deciding factor in yield forecast in maize, and that a strong relationship exit between NDVI and grain yield at 8-leaf stage (Teal et al., 2006; Islam et al., 2011). The improved relationship between grain yield and NDVI at 8-leaf stage was attributed to the maximum biomass which is accumulated later in seedling stage in cereals (Cabrera-Bosquet et al., 2011). Hybrid maize genotypes that accumulate higher aboveground biomass at the vegetative stage have the tendency of producing higher grain yield when growing conditions are optimal than when there is drought stress. In this study, less variation in GY was explained by NDVI at 8-leaf stage under full irrigation compared to what has earlier been reported in wheat and maize, respectively, when NDVI was normalized by the number of days of growth (Raun et al., 2001, Teal et al., 2006).

Table 1: Line code, abbreviated pedigree, adaptation, breeding center, and maturity of 10 exotic and 10 adapted DT inbred lines along with 2 testers evaluated in testcrosses over two years at Ikenne in Nigeria.

No.	Line code	Pedigree	Adaptation	Center	Maturity
1	EXL09	Cuba/Guad C3 F85-3-3-1-B*6	Exotic	CIMMYT	Intermediate
2	EXL11	La Posta Seq C7-F103-2-2-2-1-B*5	Exotic	CIMMYT	Intermediate
3	EXL12	La Posta Seq C7-F12-2-3-1-1-B*5	Exotic	CIMMYT	Intermediate/Late
4	EXL13	La Posta Seq C7-F152-1-1-2-1-B*3	Exotic	CIMMYT	Intermediate/Late
5	EXL18	La Posta Seq C7-F31-2-3-1-1-B*5	Exotic	CIMMYT	Intermediate/Late
6	EXL19	La Posta Seq C7-F32-2-1-1-2-B*4	Exotic	CIMMYT	Intermediate/Late
7	EXL20	La Posta Seq C7-F64-1-1-1-1-B*5	Exotic	CIMMYT	Intermediate/Late
8	EXL21	La Posta Seq C7-F64-2-6-2-2-B-B	Exotic	CIMMYT	Intermediate
9	EXL22	La Posta Seq C7-F86-3-1-1-1-B*5	Exotic	CIMMYT	Intermediate
10	EXL23	La Posta Seq C7-F97-3-1-1-2-B*5	Exotic	CIMMYT	Intermediate
11	ADL25	P43SRC9FS100-1-1-8-#1-B1-13-B1-B*7	Adapted	IITA	Intermediate/Late
12	ADL30	(TZMI501xKU1414x501)-1-4-3-1-B*7	Adapted	IITA	Intermediate/Late
13	ADL32	161-B-B-B-B-B	Adapted	IITA	Late
14	ADL33	ACR-86-8-1-2-1-1-1-B-1-B*6	Adapted	IITA	Late
15	ADL34	TZL-COMP3-C2-S2-34-4-1-2-B*6	Adapted	IITA	Late
16	ADL35	DTPL-W-C7-S2-7-1-1-1-1-B-5-B*6	Adapted	IITA	Late
17	ADL36	DTPL-W-C7-S2-1-2-1-1-5-B-1-B*6	Adapted	IITA	Late
18	ADL38	Babangoyo x MO17LPA x Babangoyo-23-4-3-4-B*8	Adapted	IITA	Intermediate/Late
19	ADL42	(GT-MAS:Gk x BABANGOYO x GT-MAS:Gk)-1-1-3-1-B*6	Adapted	IITA	Late
20	ADL48	GT-MAS:gk x 9450 x GT-MAS:gk -1-1-2-3- B*9	Adapted	IITA	Intermediate
21	1368	Across 7721 x TZSR	Tester	IITA	Intermediate/Late
22	9071	N28 x TZSR	Tester	IITA	Intermediate/Late

Table 2: Mean squares of traits from the analysis of variance combined over two years for 41 testcrosses and 3 hybrid checks under both well-watered and drought stress conditions at Ikenne in Nigeria

Source of variation	Df	[1]GY	ASI	PLHT	EASP	EPP	NDVI_1	NDVI_2
Well-watered								
Year (Y)	1	2539759	8.4**	840.0*	1.5**	0.02	0.2***	1.0***
Rep (Y)	4	1520333	1.2	1864.2***	0.2	0.004	0.004***	0.03**
Genotype	43	9050287.8***	2.6***	882.8***	0.6***	0.02**	0.001***	0.02***
Genotype x Y	43	1978806.7**	1	246.2	0.1	0.01	0.001***	0.01*
Error	156	1001839	0.8	212.7	0.1	0.01	0.0002	0.005
Drought stress								
Year (Y)	1	23218205.0***	18.2*	58157.1***	11.3***	0.001	0.02***	0.1**
Rep (Y)	4	2195454**	11.0**	1176.7**	1.1**	0.04	0.004***	0.03**
Genotype	43	1877469.6***	9.3***	1138.2***	0.8***	0.1*	0.0003	0.01**
Genotype x Y	43	914345.1**	3.0	326.6	0.4	0.04	0.0002	0.004
Error	156	543386	3.0	322.1	0.3	0.03	0.0003	0.01

*,**,*** Data significant at P < 0.05, 0.01, and 0.0001, respectively. [1]GY=Grain yield measured in kg ha^{-1}, ASI= Anthesis-silking interval (d),

PLHT=Plant height measured in cm, EASP=Ear aspect (1-5) where 1=clean, uniform, large, and well-filled ears and 5=rotten, variable,

small and partially filled ears, EPP=Number of ears per plant calculated as ratio of plants harvested to ears harvested, NDVI_1=NDVI

measured 2WAP; NDVI_2=NDVI measured at 4WAP.

Table 3: Correlation coefficients of NDVI_1 and NDVI_2 with other traits of the 41 testcrosses and 3 hybrid checks under drought stress (DS) and well-watered (WW) environments over two years at Ikenne in Nigeria.

Trait	DS		WW	
	NDVI_1	NDVI_2	NDVI_1	NDVI_2
Grain yield (kg ha^{-1})	0.26^{ns}	0.57***	0.45**	0.67***
Anthesis dates (d)	-0.32*	-0.65***	-0.30*	-0.47**
Silking dates (d)	-0.20^{ns}	0.52**	-0.22^{ns}	-0.40**
Anthesis-silking-interval (d)	0.08^{ns}	-0.04^{ns}	0.24^{ns}	0.25^{ns}
Plant height (cm)	0.35*	0.70***	0.47**	0.63***
Ear aspect (no)	-0.07^{ns}	-0.47**	-0.25^{ns}	-0.49**
Number of ears per plant	0.20^{ns}	0.43**	0.01^{ns}	0.25^{ns}
NDVI_2	0.54**	-	0.69***	-

NDVI_1=NDVI measured at 3-leaf stage 2WAP, NDVI_2=NDVI measured at 8-leaf stage 4WAP. *, **, *** Data significant at P < 0.05, 0.01, and 0.0001, respectively; ^{ns} Data not significant

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PGB31

EVALUATION OF YIELD AND YIELD COMPONENTS OF CASTOR (*RICINUS COMMUNIS* L.) GERMPLASM FROM RAIN FOREST AND SOUTHERN GUINEA SAVANNAH AGRO-ECOLOGICAL ZONES OF NIGERIA

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ABSTRACT
Forty-two castor accessions were evaluated at the Teaching and Research Farm of the University of Agriculture, Makurdi. Randomized Complete Block Design (RCBD) with three replications was used. Four-row plots of 5.5 m lengths were seeded to 11 hills of two seeds that were thinned to single stand per hill .The rows were 1m apart and the hills were spaced 0.5 m intra-row. The two middle rows of a total of 22 plants in a plot were used for observation. Variations existed from the primary to the tertiary panicles in yield components per panicle types of the germplasm. There were sequential per centage decreases in number of capsules, 100-seed weight and seed yield per panicle types from primary to penterimary panicles. Over 85% of the seed yield components each were captured from primary to quarternary panicles. From the stepwise regression analysis, secondary panicle alone fitted into the yield equation contributed 57.6% of the total seed yield. Primary to quarternary panicles yielded 88.4% of the total seed yield. This implies that investigations, in this indeterminate crop, could be terminated after the harvest of the quarternary panicles without distorting the yield trends of the crop.
Keywords: - equation, harvest, indices, panicle, regression, stepwise.

INTRODUCTION
To capture the natural variability that can be useful to breeding programmes, germplasm collection is of paramount importance. The principal justification for plant collection is to obtain natural variability that can broaden the germplasm pool for crop improvement (Bennett, 1979). Castor plant varies greatly in its growth habit; colour of foliage and stem, seed size, seed colour and seed oil content, so that varieties often bear little resemblance to each other (Weiss, 1971). Kulkarni (1959) observed that the crop has diverse variability, which could be used for genetic studies, yet not much work has been done on the genetics of the crop.

The yield characters include: panicles, capsules and 100-seed weight as well as seed yield. Panicle number is a seed yield component. The panicles are borne terminally on the main and lateral branches. They are designated as primary, secondary, tertiary, etc panicles. The main stem ends in a primary panicle, usually the longest on the plant (Weiss, 1971; Brigham, 1980). There are varietal differences in this character. Hooks *et al*. (1971) and Uguru (2000) recorded ranges of 3.1 to 7.5 and 2 to 36 panicles per plant, respectively.
Capsule number depends on the proportion of pistillate flowers on the panicle. This is a function of the variety. Uguru (2000) reported a range of 84 to 530 capsules per plant. Seed yield per plant and 100-seed weight vary with variety and with the type of panicle. Kittock and Williams (1967) reported that 100-seed weight from primary panicle was always the highest when compared to the secondary, tertiary and quaternary panicles. Similarly, Kittock and Williams (1968) reported percentage distribution of seed yield per panicle sequentially as: primary panicle, 25%; secondary panicle, 45%; tertiary panicle, 20%; quaternary panicle, 8%; and the penternary panicle, 0.5%. Weiss (1971) reported the highest seed yield per panicle for primary panicle, while successive panicles produced progressively lower seed yields. Uguru (2000) recorded ranges of 90.2 to 507.2 g for seed yield per plant and 11.92 to 51.7 g for 100-seed weight. Gobin *et al*. (2001) reported that the mean seed yield ranged as from 500 kg/hectare in India to 1000 kg/hectare in Thailand and 2500 kg/hectare under improved conditions in USA.

MATERIALS AND METHODS

A germplasm of 98 accessions, collected from the Rain Forest and Southern Guinea Savanna agro-ecological zones of Nigeria was assembled in Makurdi. From this collection, forty-two accessions were selected because they had sufficient seed for agronomic evaluation and characterization.

The forty-two accessions were evaluated at the Teaching and Research Farm of the University of Agriculture, Makurdi. Randomized Complete Block Design (RCBD) using three replications. The land was ploughed and harrowed. With a Tractor, NPK 15-15-15 compound fertilizer was broadcast before ridging at the rate of 300 kg/hectare. Four-row plots of 5.5 m lengths were seeded to 11 hills of two seeds that were thinned to single stand per hill .The rows were 1m apart and the hills were spaced 0.5 m intra-row. The two middles rows of a total of 22 plants in a plot were used for observation. Weed control was manually done four weeks after planting. The same type of fertilizer was used to top-dress after weeding at the rate of 150 kg/hectare. Data was collected on the following characters: number of capsules, 100-seed weight and seed yield by panicle type. The means of data by replicates were subjected to analysis of variance and stepwise regression analysis was carried out to determine the panicle types that fitted into the yield equation. SAS programme was used for the analyses

RESULTS

The mean square estimates of yield components in various panicle types are presented in Table 1. There was significant variation among the accessions with respect to the components from primary to tertiary panicle except for seed yield in the tertiary panicle. The number of capsules and 100-seed weight, among the accessions were highly significant ($P< 0.01$) from primary to tertiary panicle, while on other hand, seed yield recorded significant ($P<0.05$) variation among the accessions in primary and secondary panicles. The stepwise regression analysis in Table 2 revealed the relative contributions of the panicle variables in predicting the total seed yield of castor. When only the secondary panicle was fitted in the yield equation, its contribution was 57.6%. Similarly, the quaternary panicle contributed 19.5%, quaternary and primary panicles added 7.0%, whereas quaternary, primary and tertiary panicles contributed 4.3% when each was fitted along with the secondary panicle in the regression equation. In essence, from primary panicle to quaternary panicle, 88.4% of the total yield in castor was realized in this study. The regression equations are listed in Table 3 as four selection indices. The use of secondary panicle alone as a selection index would capture 57.6% of the total yield per plant, while the use of secondary and quaternary panicles together, as a selection index would capture additional 19.5% of the total yield per plant. Furthermore, the use of secondary, quaternary and primary panicles as well as secondary, quaternary, primary and tertiary panicles would capture additional 7.0 and 4.3% of the total yield per plant, respectively.

DISCUSSION

The variation that existed in the yield components studied in the castor accessions showed that castor seed yield could be improved upon through selection programmes if genetic information on how these characters are inherited is known. Similar variations were reported on yield (Hooks

et al., 1971); 100- seed weight and seed yield (Giriraj *et al*., 1973); seed yield per plant (Bhatt and Reddy, 1983); seed yield, and 100-seed weight (Bhardwaj *et al.*, 1996); 100-seed weight and seed yield (Uguru, 2000). The progressive decrease in percentage of sequential number of capsules, 100-seed weight and seed yield per panicle type from primary to penternary panicles agrees with earlier patterns reported by Kittock and Williams (1967) and percentage yield decrease in seed yield per sequential panicle type agrees with the reports of Kittock and Williams (1968) and Weiss (1971). The progressive decrease in sequential yield components might be as a result of either mouldy or abortive nature of flowers during the cloudy and high rainfall months (July to September) or some natural phenomena where panicle size decreased with more branching. The sequential decrease in yield components with more branching could be attributed to competition for photosynthates by the many numerous sites on many panicles as compared to the primary and secondary panicles, with fewer storage sites. Furthermore, this could be attributed to some environmental factors like low rainfall associated with drier months from October to December where water stress could result in poor seed filling. The formation of tertiary panicles usually coincides with this period of water stress, a possible reason for poor seed filling.

Seed yield is a complex character and it is polygenic in inheritance (Singh and Bains, 1968). Therefore, selection for seed yield *per se* may be difficult due to the low heritability of the character (Allard, 1956). However, certain characters, which may be strongly related with seed yield, may be more heritable than the seed yield. If such components are selected for, better success may be achieved in seed yield improvement

CONCLUSSION

The study revealed considerable variability in most of the castor accessions for the characters studied. The contribution to the yield components by panicle type decreased sequentially from primary to penternary panicles. The stepwise regression analysis attributed 88.4% of the variation in total seed yield to yield from primary to quaternary panicles. Therefore, harvest of yield component data could be terminated after the quaternary panicles without distortion to yield trend, thereby solving the problem of continuous harvest in the indeterminate plants.

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TABLE 2. RELATIVE CONTRIBUTIONS OF SEED OF VARIOUS PANICLES TO TOTAL SEED YIELD OF SECLECTED CASTOR ACCESSIONS

Variable	Constant	Reg.Coef.	R	R^2 Change	F
Secondary panicle	6.828	2.443	0.759	0.576	39.500
Secondary panicle	1.792	1.751	0.878	0.195	47.092
Quaternary panicle		3.342			
Secondary panicle	-1.206	1.361	0.917	0.070	47.364
Quaternary panicle		3.452			
Primary panicle		0.858			

Secondary panicle	2.933	1.099	0.940	0.043	49.093
Quaternary panicle		2.040			
Primary panicle		0.941			
Tertiary panicle		1.947			

TABLE 3. REGRESSION EQUATIONS FOR THE PANICLE VARIABLES

Panicle Variables	Regression Equations
Secondary panicle	$\hat{Y} = 6.828 + 2.443X_2 + \Sigma ij.$
Secondary and quaternary panicles	$\hat{Y} = 1.792 + 1.751X_2 + 3.342X_4 + \Sigma ij.$
Secondary, quaternary and primary panicles	$\hat{Y} = 1.206 + 1.361\ X_2 + 3.452\ X_4 + 0.858X_1 + \Sigma ij.$
Secondary, quaternary, primary and tertiary panicles	$\hat{Y} = 2.933 + 1.099\ X_2 + 2.040\ X_4 + 0.941X_1 + 1.949X_3 + \Sigma ij.$

KEY:

X_1 = primary panicle;

X_2 = secondary panicle;

X_3 = tertiary panicle;

X_4 = quaternary panicle.

TABLE 1: MEAN SQUARE ESTIMATES FOR YIELD COMPONENTS ON VARIOUS PANICLE TYPES OF SOME SELECTED CASTOR ACCESSIONS.

Sources of variation	Df	Primary panicle			*Secondary panicle*			*Tertiary panicle*			*Quaternary pa*	
		NC	SW100 (g)	SY (g)	NC	SW100 (g)	SY (g)	NC	SW100 (g)	SY(g)	NC	SW10
Rep	2	1251.38**	263.29	134.81**	768.13**	6.98	18.80	213.16**	226.00	24.96*	31.60	59.21
Entry	41	226.54**	940.55**	18.51*	213.60**	1066.29**	16.38*	57.80**	765.92**	5.49	25.35	191.0
Error ‡	82	114.94	139.96	12.07	88.09	7.62	11.42	27.59	107.12	5.14	23.13	121.3

*, ** Significant at probability levels of 0.05 and 0.01, respectively.

† Penternary panicle and above

KEY:

NC = number of capsule/panicle;

SW100 = 100 seed weight (g);

SY = Seed yield (g)/ panicle.

‡ Variations in degree of freedom (df) of error mean square for the three yield components by panicle type are as follows:

	NC	**SW100**
SY		
Primary	-5	-14
-7		
Secondary	-8	-10
-8		
Tertiary	-17	-18
-13		
Quaternary	-36	-39
-31		
Penternary	-52	-56
-5		

PGB32

DETERMINATION OF GENE ACTION OF FIVE YIELD AND YIELD RELATED CHARACTERS OF SELLECTED CASTOR ACCESSIONS IN A 5X5 DIALLEL CROSSES

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ABSTRACT
From a germplasm of castor accessions assembled for character evaluation in the University of Agriculture Makurdi Teaching and Research Farm, five selected castor accessions were crossed in all possible combinations excluding reciprocals. An evaluation trial experiment was laid out at

Akwanga and Lafia in Nasarawa State and Makurdi in Benue State. The parents and the F_1s were evaluated in a randomized complete block design of three replications. The plots were made up of three rows of 1.5 m in length spaced 1.0 m apart. The rows were sown to four hills of two seeds each, spaced 0.5 m and thinned to single stand per hill. The consistency t^2 test values for all the characters were non-significant. The regression coefficient b in all the characters has fulfilled the additive-dominance model except seed yield/hectare, which implies epistasis. The seed yield/hectare is controlled by predominantly recessive or minor-genes and is conditioned by over-dominance gene action. While the four traits partial dominance gene action. Therefore, hybrid seed production could be used to explore the over-dominancy.
Keywords: Additive-dominance, minor-genes, partial-dominance, over-dominance, epitasis.

INTRODUCTION

Hayman (1954) listed six assumptions as the basis for the application of additive-dominance model. These assumptions were re-emphasized by Allard (1956), who further stated that if the assumptions are valid, the points on the covariance (w_r)/ variance (v_r) graph are expected to fall on a line of unit slope. Where the regression line is significantly different from unit slope epitasis is implicated (Manga and Sidhu, 1979; Srivastava *et al*., 1979). The intercepts of regression lines determine the levels of dominant gene action. Where the intercept is below the origin, at origin or above the origin, the gene actions is over-dominance, complete dominance and partial dominance, respectively (Hayman, 1954; Allard, 1956; Singh and Chaudhary, 1985). The positions of the points of parental array in relation to the origin separate the parents into either dominant or recessive parents (Hayman, 1954; Allard, 1956; Singh and Chahal, 1974; Sirohi and Choudhury, 1983; Jolliffe and Arthur, 1993). However, the positions of the parental array in relation to the sides of the regression line are used to determine the additive and non-additive gene actions of the parents. Where the parent points lie above the regression line, they are said to possess additive gene action whereas those below are said to possess non-additive gene action (Manga and Sidhu, 1979; Kaw and Menson, 1983; Sirohi and Choudhury, 1983). Sirohi and Choudhury (1983) went further to add that those arrays below the regression line implicated both non-additive and epistatic gene actions. There is dearth of information in literature regarding covariance (w_r)/ variance (v_r) graphs and additive-dominance model in castor. In the light of the above, the current study is to highlight gene action using graphic method.

MATERIALS AND METHODS

From a germplasm collected from Southern Guinea Savannah and characterized in the University of Agriculture Makurdi Teaching and Research Farm, five selected castor accessions were crossed in all possible combinations excluding reciprocals. An evaluation trial experiment was laid out at Akwanga and Lafia in Nasarawa State and Makurdi in Benue State. The parents and the F_1s were evaluated in a randomized complete block design of three replications. The plots were made up three rows of 1.5 m in length spaced 1.0 m apart. The rows were sown to four hills of two seeds each, spaced 0.5 m and thinned to single stand per hill.

Observations were made on four plants of the middle row of each plot. Eleven characters viz: leaf area, leaf length, number of leaf lobes, number of nodes to primary panicle, height to primary panicle, days to 50% flowering, days to 100% flowering, 100-seed weight, seed yield/hectare and plant height.Hayman's (1954) method was adopted for covariance (Wr) and variance (Vr) estimates using the genotype means on MS Excel programme.

RESULTS

The covariance (Wr)/variance (Vr) graphical analyses are presented in Figures 1 to 5. The five yield-related characters have non-significant consistency t^2 values. The number of days to 50% flowering (D50F), number of days to 100% flowering (D100F), Number of days to maturity (NDM) and 100-seed weight (SW100) have their regression coefficient b values fulfilling the unit slope, while that of seed yield/hectare (SYH) is more than a unit slope. The four characters: D50F, D100F, NDM and SW100 have their regression lines intercepted the covariance (Wr)/variance (Vr) graphs above the origins as shown in Fig 1, 2, 3 and 4, respectively, a partial gene action. The seed yield/hectare(Fig. 5) regression line intercepted the covariance (Wr)/variance (Vr) graph below the origin, over-dominance.

Fig.1 and Fig. 2 show accession 3 closer to the origin and the rest of the accessions away from the origin, exhibited dominance and recessive gene actions, respectively. Accessions 10 and 34 are additive while accession 9 non-additive in nature. Similarly, accession 3 exhibited dominance gene action in Fig.3 compare to the rest of accessions. In the same vein accessions 10 and 6 exhibited additive gene actions while accession 9, non-additive gene action. Dominance gene actions were displayed by accessions 6 and 9 in Fig. 4 while accession 3 was recessive. The five accessions in Fig.5, are all controlled by recessive genes and non is either additive nor non-additive.

DISCUSSION

Literature citations were not available on covariance (W_r) and variance (V_r) graphical analysis in castor *per se*. However, from Hayman's (1954) assumptions, the consistency t^2 values for all the characters were non-significant. The regression coefficient b in all the characters has fulfilled the additive-dominance model except seed yield ha^{-1}. Epitasis is implicated in this character with regression coefficient b significantly different from unit slope (Manga and Sidhu, 1979; Srivastava et al., 1979). The covariance (W_r) /variance (V_r) graphic analyses have shown that l seed yield/hectare exhibited over-dominance gene action as indicated by the regression lines intercepting the W_r coordinate below the origin, while partial dominance gene action was exhibited by the rest of the characters as the regression lines intercepted the Wr coordinates above the origins (Hayman, 1954; Allard, 1956; Singh and Chaudhary, 1985). The overdominance in this trait as deduced from the W_r/V_r graphs, revealed that the characters might be controlled by dominance or non-additive gene action. This agreed, in part, with the findings of Uguru and Abuka (1998) of overdominance reported in seed yield. Regarding the positions of the parental arrays on the graphs, Ac.3 tended to have predominantly dominant genes in the characters for earliness (number of days to maturity and number of days to 50 as well as 100% flowering) by occurring towards origin of the covariance (W_r) /variance (V_r) graphs. This agreed

with the assertion of Hayman (1954), supported by Allard (1967), Singh and Chahal (1974), Sirohi and Choudhury (1983), Singh and Chaudhary (1985) and Jolliffe and Arthur (1993) that the parents were either predominantly dominant or preponderantly recessive when they occur close to or far away from the origin, respectively. Accession three (Ac. 3) possessed mostly recessive genes for 100-seed weight and seed yield ha^{-1}.

The genes controlling seed yield/hectare were mostly recessive genes, as parental points occurred far away from the origin of covariance (W_r)/variance (V_r) graph. This showed that the genes controlling seed yield/hectare were mostly recessive genes. This is an indication that the inheritance of seed yield/hectare was governed mostly by minor genes. In conclusion, hybrid seed production could be explored to capture dominant gene action existing in seed yield/hectare.

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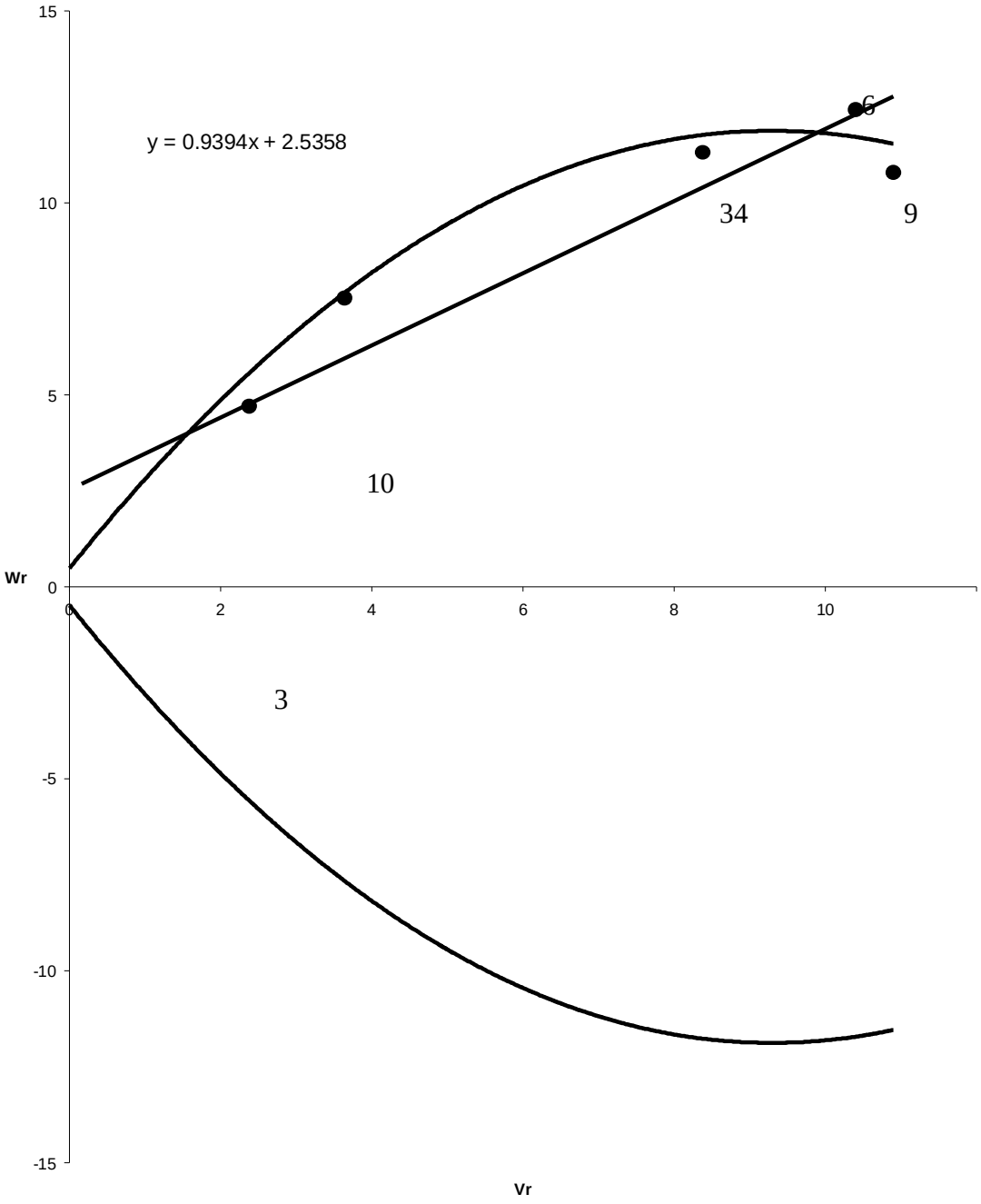
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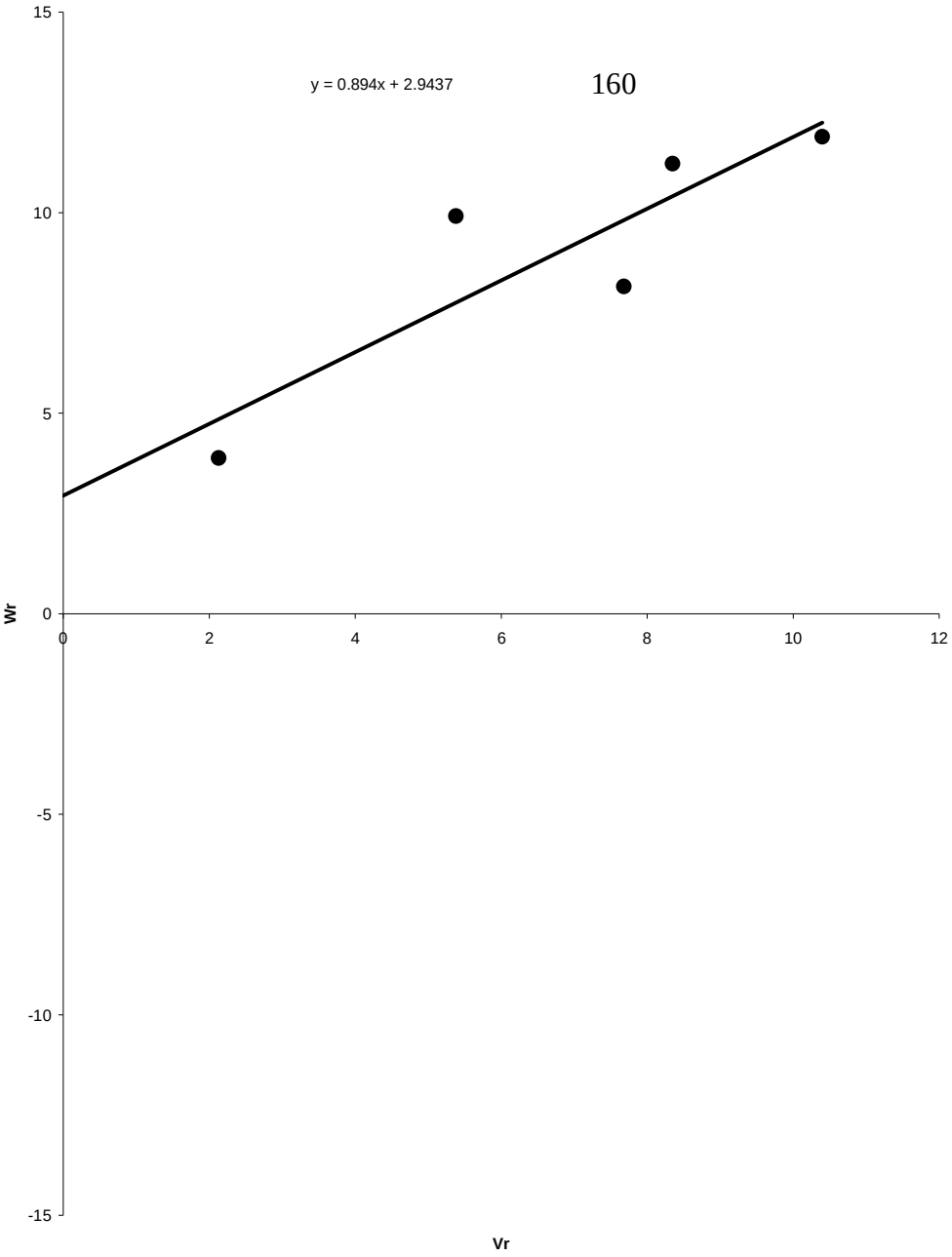
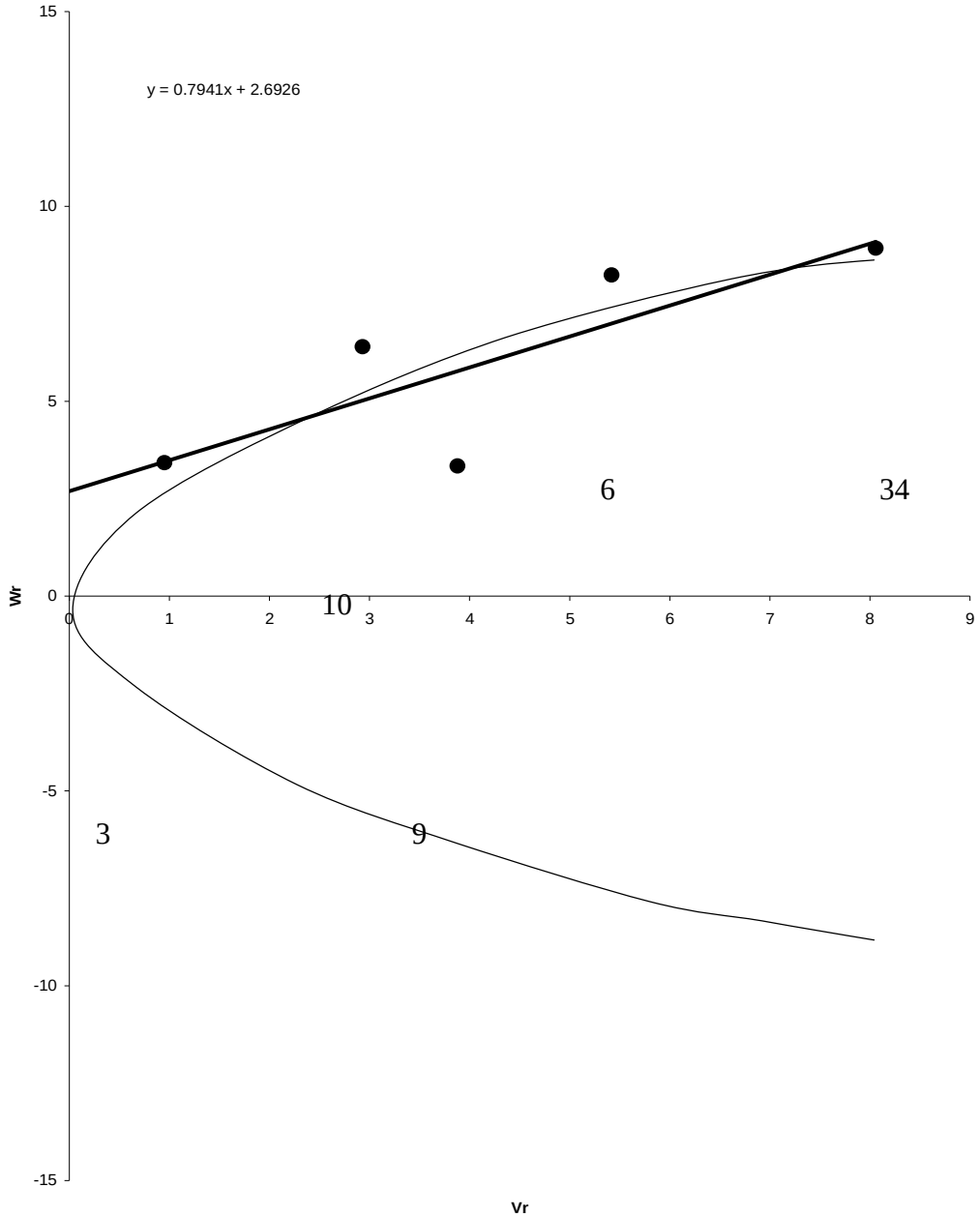


FIG. 1: COVARIANCE (W_r)/ VARIANCE (V_r) GRAPHS FOR DAYS TO 50% FLOWERING OF CASTOR IN SOUTHERN GUINEA SAVANNA OF NIGERIA.

FIG. 2: COVARIANCE (W_r)/ VARIANCE (V_r) GRAPHS FOR DAYS TO 100% FLOWERING OF CASTOR IN SOUTHERN GUINEA SAVANNA OF NIGERIA.



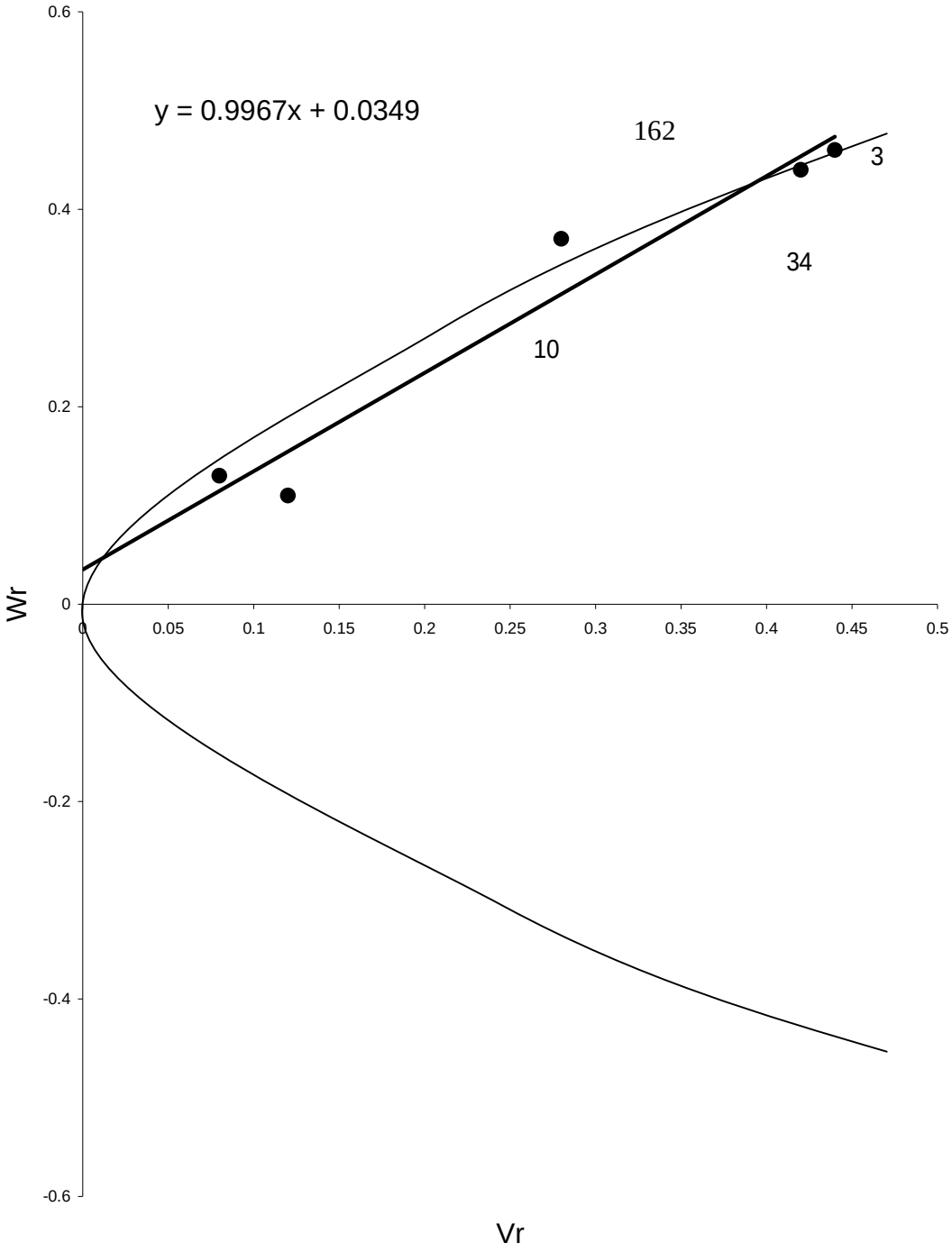


FIG. 3 COVARIANCE (W_r)/ VARIANCE (V_r) GRAPHS FOR NUMBER OF DAYS TO MATURITY OF CASTOR IN SOUTHERN GUINEA SAVANNA OF NIGERIA.

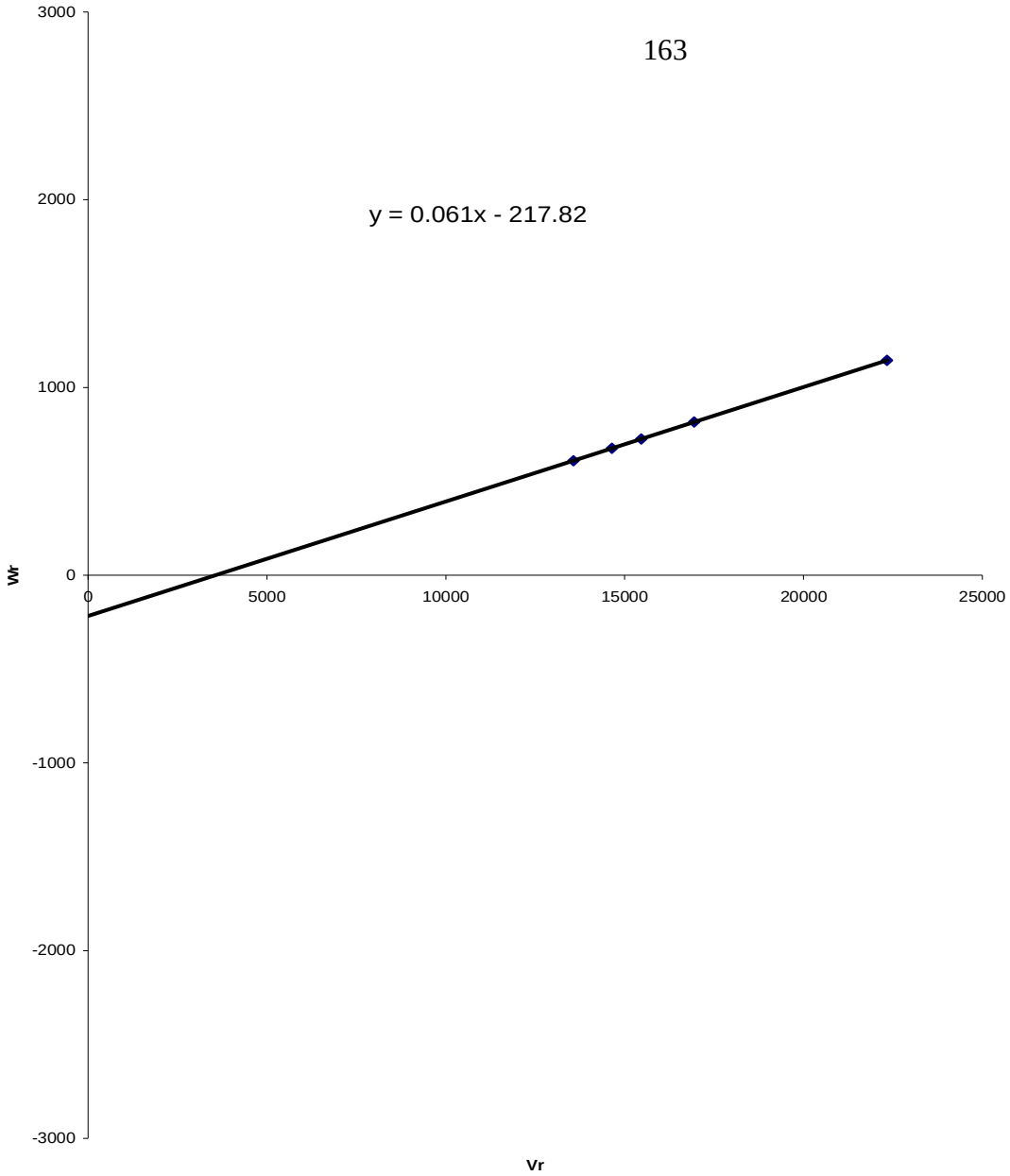


FIG. 4: COVARIANCE (W_r)/ VARIANCE (V_r) GRAPHS FOR 100-SEED WEIGHT (G) OF CASTOR IN SOUTHERN GUINEA SAVANNA OF NIGERIA.

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FIG.5: COVARIANCE (W_r)/ VARIANCE (V_r) GRAPHS FOR SEED YIELD HA^{-1} (KG) OF CASTOR IN SOUTHERN GUINEA SAVANNA OF NIGERIA.

PGB33

EFFECT OF GROUND AND UNGROUND PEPPER (*CAPSICUM ANNUM*) IN THE CONTROL OF COWPEA WEEVILS (*CALLOSOBRUCHUS MACULATUS*) AMONG SOME COWPEA VARIETIES (*VIGNA UNGUICULATA* L. WALP) DURING STORAGE.

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ABSTRACT

The effect of ground and unground pepper (*Capsicum annum*) in the control of cowpea weevils (*Callosobruchus maculatus*) among some cowpea varieties (*Vigna unguiculata* L. Walp) during storage was investigated. The treatments used were fine grounded pepper, marshed pepper and ungrounded pepper, while the five varieties of cowpea used included. Iron Beans, Small White, IAR48 (small brown), IT3629 (big white) and Ife brown. The experimental design used was a factorial laid out in Completely Randomized Design (CRD) with three replicates. The results obtained from the research indicated that there was significant difference ($p<0.05$) among the cowpea varieties and treatments used. Among the treatments, fine grounded pepper preserved cowpea best and gave the least weight reduction in the order: Small white <IAR48 (small brown) < Ife brown < Iron beans < IT3529 (big white) or (12.94g, 23.19g, 25.80g 31.66g, and 33.78) respectively and marshed peppers was next to fine grounded pepper with a weight reduction of 17.78g, 28.20g, 31.50g, 41.78g and 49.01g while ungrounded pepper gave a weight reduction of (25.75g, 32.26g, 41.62g, 49.33g and 55.27g). The relative efficiency of all these treatments showed that they can actually replace chemicals in the preservation of cowpea grains which are expensive and can cause serious environmental and health hazards to human beings.

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp*)* otherwise called the Southern pea belongs to the family leguminasae and is a crop of high value which contributes significantly to farm income and dietary protein of Africans (Ogbaji, 2002). It is a valuable warm season legume believed to have West African as its centre of origin and greatest morphological diversity (Smart *et al.*, 1985). Cultivated cowpea is an herbaceous annual belonging to the substribe phaseolinae, the tribe phasedese, the family papilionaceae (or Fabaceae) and the order Fabales.

Cowpea constitutes the cheapest source of protein for most people in the tropical world (Ogbaji and Ndam, 2002) where per capital income and consumption of animal protein are both very low (Rachie, 1985). The nutrient content of mature cowpea seed contains 24.8%, protein, 1.9% fats, 6.2% fibre, 63.6% carbohydrates, 0.00074% thiamine, 0.00042% riboflavin and 0.00281% niacin (Singh *et al.,* 1985). Cowpea also serves as a quick cover crop for erosion control and smothering of weed seeds in addition to its capacity in fixing up to 240 kg/ha to the soil after a crop cycle (Rachie, 1985). The haulms and husk of cowpea serve as roughage for livestock (IITA, 2002). It also increases soil organic content and improvement of soil structure after soil incorporation (Valenzuala, 2002). Insect infestation is a major contributor to quality deterioration of cowpea stored in warm and humid climates. Considerable physical and nutritional loss are sustained by cowpea due to the infestation by weevils and results in reduction of quality. However, most farmers and consumers of cowpea use synthetic chemicals such as organo-chlorine and residual insecticide for cowpea grain storage. The chemicals are not only expensive but can cause serious environmental and health hazards or even death to livestock and human beings. In Nigeria, multi-tactic control methods have been developed to reduce the menace of storage pest. Cultural methods entailed the manipulation of the environment to make it unfavourable weevil growth and population build up but it has limited or no remedial value in emergency situations. The use of plant materials for the protection of crops and stored commodities against insect attack has a long history (Golob and Webley, 1980). It is quite safe and promising (Jilani *et al.*, 1980). In years back, significant results have been reported with the use of botanical insecticides in treating grains meant for storage. These included the use of plant oils (Odunlami, 1992), Fagara, (*Zanthoxylum* spp) (Ogunwolu, 1996), Neem (*Azadirachta indica*) (Ivibijaro, 1983), tobacco (*Nicotiana tobacum*) (Tooley, 1971), pepper, (*Capsicum spp*) (Ivibijaro, 1983), ginger (*Zinger officinale*) (Olitodun, 2001), ash (Murdock and Babalola, 1990) and bitterleaf (*Vernorila amygdalina*). Just recently, Ogbaji and Osuman (2012) investigated and reported on the great efficiency of bitter pepper *(Capsicum annum)* in the control of cowpea weevils, *(Callosobruchus maculatus)* during cowpea storage. Another trial was therefore carried out to find out if marshing/grinding pepper will further enhance its efficiency in the control of *C. maculatus* during cowpea storage.

Therefore, the broad objective of this study was to ascertain the effect of ground and unground pepper (*Capsicum annum*) in the control of cowpea weevils (*Callosobruchus maculatus*) among some cowpea varieties (*Vigna unguiculata L. Walp*) during storage in Makurdi, a location in the Southern Guinea Agro-Ecological Zone of Nigeria.

MATERIALS AND METHOD

The experiment was conducted in the Zoology Laboratory of Benue State University, Makurdi between September and December, 2012. Makurdi, the capital city of Benue State lies between latitude $7^0$15'-7^0 45'N and longitude 8^0 15'-8^0 40'E in the Guinea Savanna vegetation Zone of Nigeria. The five varieties of cowpea were all obtained from the Benue State Agricultural and Rural Development Authority (BNARDA) Makurdi. These varieties had earlier been confirmed to do very well in the Makurdi environment (Ogbaji and Ndam, 2002). The cowpea varieties were Iron Bean, Ife Brown, Small White, IAR48 (small brown) and IT3629) (Big White). Dried chilli pepper (*Capsicum annum*) was obtained from North Bank Market in Makurdi and forty five (45) air tight plastic containers each with a depth of 7.5cm and diameter of 13cm attached

with the cover lid and one stainless pin were all obtained from the modern Market, Benue State, Makurdi. The cowpea varieties were sundried for a period of six days to enable *C. maculatus* escape. Sun drying continued until there was ceasation of reproduction of *C. maculatus* to ensure that all the immature stages had been hatched. Thereafter, perforated, undersized seeds were sorted out leaving behind the healthy seeds and all the good sorted cowpea were stored in the tight plastic containers. The weights of the containers were all measured. Each contained 500g of the cowpea seeds. Measurement was done using electric sensitive weighing balance called the Adam's scale. Each variety of cowpea had three (3) replicates and were then mixed with fifty (50) g of chilli pepper (*Capsicum annum*) which served as the treatment. 50g of each of the treatments (fine grounded state, marshed grounded state and ungrounded state), were admixtured equally to the three (3) replicates of cowpea seeds each containing 500grams in each of the containers. The cowpea seeds and pepper were mixed thoroughly to ensure uniform distribution with a pinhole perforated covered lid at the centre to enable the circulation of air and breathing of the insects. The set up was then stored in Laboratory at room temperature.

The data collection included the progressive weight loss of the cowpea varieties at two weekly intervals. The weight loss was measured using a digital sensitive weighing balance. The weights were determined as follows:

Initial Weight of cowpea = X_1g
Weight of chilli pepper + container = X_2g
Combined weight of cowpea + pepper + container = X_3g
Weight loss X_3-X_2 (g) = X_4g
Average weight loss =
Also percentage (%) weight loss = $\frac{\text{Wight loss of replicates (g)}}{X_1\text{ (g)}} \times \frac{100\%}{1}$

The experimental design used was a factorial laid out in the Completely Randomized Design (CRD) with three replicates while collected data were analyzed using Analysis of Variance (ANOVA). Treatment means were separated using Fishers Least Significant Difference at 5% level of significance.

RESULTS AND DISCUSSION

Visual observation of the cowpea varieties in the containers indicated that in the first two weeks of storage, IT3629 (Big White), Iron Beans and IAR48(Small Brown) were the first cowpea varieties to be infested by *Callosobruchus maculatus*. This was manifested by the fact that by hand feeling, the containers containing these varieties showed increased temperature rise.

Among the cowpea varieties, significant differences existed among them in their levels of resistance (Table 1). The variability in level of resistance in the cowpea varieties to *C. maculatus* attack during storage is most probably as a result of genetic differences among these lines as they were developed from different pedigrees. This result agrees with studies done by Jackai *et al.*, (1990) and Ogbaji and Osuman, (2012) who also reported genetic variability among some cowpea lines in their resistance to *C. maculatus*. In the case of the treatments used, there were also significant ($P<0.005$) differences among them. Among the treatments, finely grounded pepper performed best in the control of cowpea damage by *C. maculatus* during storage. This is most likely due to the fact that the very fine particles of pepper blocked all the available air spaces in between the cowpea seeds thereby suffocating the insects to death and also stopping the reproduction and subsequent multiplication of the insects. The significant seed weight

reduction among some of the cowpea varieties stored with the treatments may be as a result of reduced oviposition and adult emergence of *C. maculatus* occasioned by the insecticidal effect of pepper. The results corroborate earlier findings by Rhem *et al.*, (1991) who reported that the insecticidal effect of pepper fruits to *C. maculatus* was attributable to the its pungency which is as a result of the capsicum present in them which was capable of also delaying the reproduction and hence multiplication of *C. maculatus.* Schmuhener *et al.,* (1984), while working on another botanical also reported same results that the insecticidal activities of neem (*Azadiradata indica*) was a result of the presence of highly oxidized tetrapenoids, azadirachtin, salanin and other active products that posses repellant, antifectant and growth disruptive properties against various insect species particularly *C. maculatus.*

The interactive effects of the cowpea varieties and treatment on actual weight loss of cowpea seeds (Table 3) and the interactive effects of varieties and treatments on percentage weight loss of cowpea seed during storage (Table 4) were all significant. These results indicated that all the treatments used for the storage were effective but differed in their efficiency in the control of cowpea weevils (*C. maculatus)* during storage. This result also implied that with the proper combination between the cowpea varieties and the treatments, more efficiency in the control of *C. maculatus* damage will be achieved. It is therefore recommended that cowpea farmers can further enhance the already known efficiency of pepper (*Capsicum annum)* in the control of *C. maculatus* during cowpea storage by mashing/grinding the pepper. Using this method can be particularly beneficial because the pepper used has no harmful side effects, is environment friendly and the pepper used for the storage can still be destructively sampled or consumed after the cowpea storage.

ACKNOWLEDGEMENTS

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Table 1: Main Effects of Varieties and Pepper Treatments on Actual Weight Loss (grams) of Cowpea Seed During Storage

Varieties	**Weeks of Storage**					
	2	4	6	8	10	12
IAR48(big brown)	498.28	497.87	493.94	489.56	482.7	472.45
Iron bean	487.50	485.47	483.24	478.40	467.80	459.08
Ife brown	499.19	497.46	494.50	484.61	477.00	467.03
IT3629 (big white)	498.39	496.34	498.52	481.68	468.60	453.68
Small white	499.50	499.35	497.94	495.59	485.60	481.18
S.E (+ve)	0.92	0.42	0.62	1.01	7.66	1.19
C.V(%)	0.20	0.10	0.01	0.20	1.60	0.03
FLSD (0.05)	**0.89**	**0.41**	**0.61**	**0.98**	**7.37**	**1.48**
Treatments						
Fine grounded pepper	497.23	495.96	493.92	489.99	483.10	474.52
Marshed grounded pepper	496.73	495.35	492.62	486.10	478.10	466.37
Ungrounded pepper	495.77	494.58	481.81	481.81	467.80	459.15
FLSD (0.05)	**0.69**	**0.31**	**0.46**	**0.76**	**5.71**	**0.89**

Table 2: Main Effects of Varieties and Treatments on Percentage Weight Loss (%) of Cowpea Seed During Storage

Varieties	**Weeks of Storage**					
	2	4	6	8	10	12
IAR48(small brown)	0.30	0.47	1.26	2.01	3.46	5.51
Iron bean	0.34	2.91	3.33	4.33	6.45	8.16
Ife brown	0.20	0.51	1.09	2.90	4.61	6.51
IT3629 (big white)	0.30	0.73	1.41	3.67	6.28	9.38
Small white	0.10	0.19	0.41	0.88	1.82	3.81
S.E (tve)	0.01	0.12	0.41	0.22	0.11	0.19
C.V(%)	5.90	12.3	6.50	7.90	4.30	2.80
FLSD (0.05)	**0.06**	**0.11**	**0.01**	**0.21**	**0.09**	**0.18**
Treatments						
Fine grounded pepper	0.40	0.80	1.21	1.92	3.41	5.01
Marshed grounded pepper	0.70	0.96	1.50	2.74	4.38	6.75
Ungrounded pepper	0.80	1.12	1.84	3.67	5.77	8.24
FLSD (0.05)	**0.05**	**0.09**	**0.07**	**1.16**	**0.15**	**0.14**

Table 3: Interactive Effects of Cowpea Varieties and Treatments on Weight Loss (grams) of Cowpea Seeds During Storage

Varieties	**Treatments**	**Weeks of Storage**					
		2	4	6	8	10	12
IAR48(small brown)	Fine grounded pepper	499.32	498.52	496.13	493.19	486.80	476.84
	Marshed pepper	498.93	498.30	493.68	489.26	485.00	471.80
	Ungrounded pepper	496.60	496.79	492.00	486.24	476.30	467.74
Iron bean	Fine grounded pepper	488.10	486.23	483.98	481.45	473.60	468.34
	Marshed pepper	487.54	485.28	483.37	478.49	467.90	458.22
	Ungrounded pepper	486.87	484.90	482.36	475.27	461.80	450.67
Ife brown	Fine grounded pepper	499.35	498.46	496.16	491.19	486.60	476.20
	Marshed pepper	499.37	497.94	495.34	485.14	476.90	468.50
	Ungrounded pepper	498.84	496.37	491.91	477.54	467.40	458.38
IT3629(big white)	Fine grounded pepper	499.46	497.08	494.68	487.53	475.40	466.22
	Marshed pepper	498.36	496.31	492.51	482.44	463.70	450.90
	Ungrounded pepper	497.36	495.62	490.36	475.06	461.80	444.70
Small white	Fine grounded pepper	499.93	499.51	498.63	496.65	493.20	487.06
	Marshed pepper	499.40	499.34	498.20	495.18	491.90	482.22
	Ungrounded pepper	499.16	499.21	496.91	494.95	471.70	474.25
FLSD (0.05)		**0.54**	**0.70**	**1.05**	**1.69**	**1.28**	**1.99**

Table 4: Interactive Effects of Cowpea Varieties and Treatments on Percentage Loss (%) of Cowpea Seeds During Storage

Varieties	Treatments	Weeks of Storage					
		2	4	6	8	10	12
IAR48(small brown)	Fine grounded pepper	0.01	0.21	0.77	1.36	2.65	4.64
	Marshed pepper	0.20	0.74	1.31	2.17	3.00	5.44
	Ungrounded pepper	0.40	0.64	1.60	2.77	4.74	6.45
Iron bean	Fine grounded pepper	0.38	2.75	3.20	3.71	5.28	6.33
	Marshed pepper	2.50	2.94	3.33	4.34	6.42	8.36
	Ungrounded pepper	2.60	3.02	3.46	4.95	7.67	9.87
Ife brown	Fine grounded pepper	0.20	0.51	1.09	2.90	4.61	6.51
	Marshed pepper	1.10	0.31	0.75	1.37	2.67	5.17
	Ungrounded pepper	0.20	0.73	1.60	4.62	6.52	8.32
IT3629(big white)	Fine grounded pepper	0.20	0.56	1.06	2.49	4.93	6.76
	Marshed pepper	0.30	0.74	1.41	3.51	6.26	9.98
	Ungrounded pepper	0.50	0.88	1.93	4.99	7.64	11.39
Small white	Fine grounded pepper	0.00	0.01	0.26	0.67	1.52	2.59
	Marshed pepper	0.10	0.13	0.36	0.95	1.62	3.69
	Ungrounded pepper	0.20	0.33	0.61	0.01	2.32	5.15
FLSD (0.05)		**0.01**	**0.11**	**0.08**	**0.13**	**0.33**	**0.31**

PGB34

EFFECTS OF DIFFERENT PEPPER VARIETIES IN THE CONTROL OF COWPEA WEEVIL (CALLOSOBRUCHUS MACULATUS) IN SOME VARIETIES OF COWPEA (VIGNA UNGUICULATA L.WALP)

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ABSTRACT
A study was carried out to investigate the effect of some pepper varieties (*Capsicum annum*) in the control of weevils (*Callosobruchus maculates)* during cowpea storage. Three pepper varieties (hot pepper, moderately hot pepper and sweet pepper) were used for the study while the five cowpea varieties used include: Small white, Big white, IAR48, Iron beans and Aloka. The

experimental design was a Completely Randomized Design (CRD) with three replications. Results showed that there was a significant difference ($P< 0.05$) among the cowpea varieties and the treatments applied. Aloka showed the least reduction in weight loss to *Callosobruchus maculatus* indicating most resistance with 18.00g, followed by Big white 26.30g, IAR48 35.50g, Small white 42.80g and lastly Iron beans with 65.50g. Among the treatments applied, hot pepper gave the best protection against *Callosobruchus maculatus* giving overall weight reduction of 34.4g, next was moderately hot pepper 37.4g and sweet pepper with 41.1g. The interaction between cowpea varieties and treatment applied were also significant. The relative efficiency of these treatments indicated that they can be used to preserve cowpea against *Callosobruchus maculatus* during storage more so that they have no negative side effects on human health.

INTRODUCTION

Cowpea, (*Vigna unguiculata* L. Walp) belongs to the Family *Leguminosae* which is grown and consumed for its high protein content (23-25%) and contributes significantly to farm income (Ogbaji, 2002). In West and Central Africa, cowpea cultivation covers more than 8 million hectares of which Nigeria is the largest producer at 4million hectares followed by Niger with 3million (Singh and Eaglesfied,2000). From its production, rural families derive food, animal feed, and cash income. It provides nutritious grain and an inexpensive source of protein for both rural poor and urban consumers. Cowpea grain contains about 25% protein, 64% carbohydrate, 1.9% fat, 6.35% fibre as well as some of the B- vitamins (Bressani, 1985) and therefore has a tremendous potential to contribute to the alleviation of malnutrition among resource-poor farmers. It does not require a high rate of nitrogen fertilization; its roots have nodules in which soil bacteria called *Rhizobia* help to fix nitrogen from the air. Insect pest infestations are known to be the major constraints to cowpea yield and its quality.The crop is severely attacked at every stage of growth and insect pests such as cowpea aphid (*Aphis craccivora)*, flower thrips (*Megalurothrips* spp*.)* and pod sucking buds (*Anoplocnemis curvipes***).** The weevil *Callosobruchus maculatus* is the major pest that attacked stored cowpea.

Considering the importance of cowpea to world Agriculture and nutrition to man and losses in its production as a result of its destructive activities of the weevil, the need to look into ways which losses of cowpea annually can be brought to a minimal level cannot be over emphasized. The use of conventional insecticides is mostly practiced worldwide in controlling cowpea pest which pose threat to humans and environment. In Nigeria several methods of controlling stored cowpea pest has been practiced which reduces the damage done by insect pest. The use of good storage structures and use of plant materials has been effective by creating unfriendly environment thus limiting the growth of the pests. The use of plant materials to control *Callosobruchus maculatus* in stored cowpea has advantage in that it pose no threat to human compare to the use of chemicals.

Recently significant results have been reported with the use of plant materials in preventing grains from the damage done by insect pests. These included the use of neem (*Azadirachta indica*) (Ivbijaro 1983; Schuhener and Ascher 1984), dried peels of orange, Ginger leaves of onions (Ogbaji and Tyoga, 2010), Ginger, garlic and bitterleaf (Ogbaji and Osuman, 2011).

As a result, the objectives of this study were to determine the response of different varieties of cowpea to various varieties of pepper such as hot pepper, moderately hot pepper and sweet

pepper. The study will help us to know which of the treatments has a higher pesticidal effect on the cowpea against the stored cowpea weevil.

MATERIALS AND METHODS

The experiment was conducted in the Botany Laboratory of the Department of Biological Sciences, Benue State University, Makurdi. The five varieties of cowpea used were; Aloka beans, Iron beans, IAR48 (Big brown), Small white and Big white. These were all obtained from Benue State Agricultural and Rural Development Authority (BNARDA) (Plates 1 - 8). These cowpea varieties were all sorted carefully to remove perforated seeds and sundried for 7 days to allow *Callosobruchus maculatus* escape. After sundrying, the cowpea seeds were then stored in air tight plastic containers. This was laid out in a Completely Randomized Design (CRD) with three replications.

The pepper varieties used were the dried hot pepper, mild pepper and sweet pepper. All the pepper varieties were obtained from Wurukum Market. Plastic airtight containers with a transparent lid were used for the storage of the cowpea varieties. The central portion of the lid was perforated using a stainless needle. This was done to allow the entrance of air and breeding of the insects.

Using an electronic weighing balance, 50g of each dried pepper varieties (Hot pepper, moderately hot pepper and Sweet pepper) and 500g of seeds of each of the cowpea varieties were also measured and mixed together into the airtight plastic containers with three replications each. They were then stored in the Laboratory for a period of 12 weeks between August and November, 2012.

The weight of the containers was first taken and recorded and the weight of the seeds, container and pepper were also taken together. The data collected were the progressive weight loss of the cowpea varieties at two weekly intervals. The weight loss of the cowpea was determined by simple subtraction of the final weight (b) from the initial weight (a).
Initial weight of cowpea = a
Final weight of cowpea = b
Weight loss = a-b
The mean weight of the cowpea varieties was also determined at two weekly intervals.
Percentage weight loss = $\frac{(b-a)}{a} \times 100$
Data was analyzed using Analysis of variance (ANOVA) to show significance difference in response of the cowpea to the treatment applied. Treatment means were separated using Fisher's Least Significance Difference at 5% level of significance.

RESULTS AND DISCUSSION

The results obtained from the main effects of varieties and treatment on weight loss of cowpea seeds (Table 1) showed that Aloka has the least reduction in weight loss to attack by *Callosobruchus maculatus* with 18.00g followed by Big white (26.30g), IAR 48(35.50g), Small white (42.80g) while Iron beans had the highest weight reduction to attack by *Callosobruchus maculatus* during storage with a weight loss of 65.50g. In respect of the treatments applied, it was recorded that hot pepper gave the best protection against cowpea weevil giving the overall cowpea varietal a weight reduction of 34.40g, followed by mild pepper with 37.40g and then sweet pepper 41.10g. Results on the main effects of varieties and treatment on percentage weight

loss Table 2. shows similar trend to the explanation above. Aloka gave the least percentage weight loss of 3.62%, followed by Big white (5.25%) while Iron beans gave the highest percentage weight reduction of (13.22%). The treatment applied shows that hot pepper gave the best percentage protection against *Callosobruchus maculatus* during storage with 6.87%, followed by mild pepper (7.57%) and sweet pepper (8.22%). The order of performance of the treatment can be interpreted as hot pepper > mild pepper > sweet pepper. Tables 3 and 4 showed that the interactive effects of cowpea varieties and treatments on actual weight loss of cowpea seed during storage were all significant respectively.

The use of pepper plant in the control of *Callosobruchus maculatus* in this research relates to other works that has been carried out in Nigeria and Africa as a whole using plant parts in controlling *Callosobruchus maculatus* (Ogbaji and Osuman 2011; Epidi *et al.*, 2008; Udomporn 2009; Ogbaji and Tyoga 2010). From the results, Aloka has the least actual weight loss and percentage weight reduction (i.e giving the highest resistance to *Callosobruchus maculatus*) while Iron beans gave the highest actual weight loss and percentage weight loss showing its high susceptibility to *C. maculatus attack*. Resistance and susceptibility among these cowpea varieties may have been due to nature or texture of the seed coat, since it has been shown by Carlos (2004), that cowpea varies in seed coat and this plays a role in the penetration of the weevil. Also the variability in the level of weight reduction in cowpea varieties to *C. maculatus* attack during storage is most probably as a result of genetic differences among the lines as they were developed from different pedigrees. Iron beans with the highest weight reduction in this study agrees with the work of Ogbaji and Osuman (2011) which also gave the highest weight reduction when treated with different plant materials.

In the treatments applied, pepper plants is made up of chemical constituent called capsicine which gives pepper its strong taste. This varies in percentage at which it is found in pepper varieties (Tindall 1965). This capsicine tends to reduce the emergence of weevil in cowpea and the percentage composition of this capsicine determines the rate at which it will control *C. maculatus*. The result indicates that different pepper varieties have insecticidal effects but some are more efficient than others. Also the significant weight reduction in all the cowpea varieties stored with different pepper varieties may be as a result of reduced oviposition and adult emergence of *C.maculatus* This work agrees with the works of (Ebiamodon *et al.*, 2011; Epidi *et al.*,2008; Schmuhener and Ascher 1984) in which they all reported that the insecticidal effects of botanicals on the control of weevil in grains was due to the presence of toxic factors in this materials thus creating unsuitable habitat at which they can reproduce.
The results of this work has shown that pepper plant can be used as a good control measure to reduce the damage done to cowpea by *C.maculatus* . Also having shown that some pepper varieties show differences in their effectiveness to control *C.maculatus* in cowpea varieties, more efficiency will be achieved with proper combination between the cowpea varieties and the pepper varieties. It is therefore recommended that farmers across Nigeria and all over the world should adopt the method of using pepper in controlling the damage done to cowpea by *C.maculatus*. The benefits of using this method is that; it requires less skill, costs less and not hazardous to humans in comparison with the use of chemicals which when not use in correct proportion can pose great threats to human health.

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Table 1. Main Effects of Varieties and Treatments on Actual Weight loss(grams) of Cowpea seeds During Storage.

Cowpea Varieties	**Weeks of storage**					
	2	4	6	8	10	12
Small white	498.50	496.16	490.18	481.30	471.80	457.20
Big white	495.06	492.37	490.55	482.12	478.20	473.70
IAR 48	498.51	499.09	498.55	487.63	480.20	464.50
Iron beans	491.66	483.85	474.37	491.66	450.30	434.50
Aloka	498.81	498.39	495.30	490.93	489.80	482.00
S.E	0.715	2.243	1.573	2.991	4.330	6.850
F.L.S.D$_{0.05}$	**1.46**	**4.58**	**3.21**	**6.11**	**8.84**	**14.00**
Treatment						
Hot pepper	497.15	493.89	490.24	487.85	476.30	465.60
Sweet pepper	496.69	493.79	489.37	487.26	472.10	458.90
Mild pepper	495.69	494.23	489.76	485.08	473.70	462.60
F.L.S.D$_{0.05}$	**1.13**	**3.35**	**2.49**	**4.73**	**6.85**	**10.84**

Table 2. Main Effects Of Varieties and Treatments on Percentage Weight Loss (%) of Cowpea Seeds During Storage

Cowpea Varieties	**Weeks of Storage**					
	2	4	6	8	10	12
Small white	0.30	0.77	1.96	3.74	5.32	8.56
Big white	0.98	1.44	2.06	3.58	4.36	5.25
IAR 48	0.03	0.18	0.29	2.46	3.96	7.10
Iron beans	1.67	4.06	5.13	7.10	9.94	13.22
Aloka	0.25	0.32	0.94	1.37	2.99	3.62
S.E	0.12	0.20	0.30	0.58	0.90	1.39
$F.L.S.D_{0.05}$	**0.25**	**0.41**	**0.61**	**1.18**	**1.84**	**2.83**
Treatment						
Hot pepper	0.58	1.22	1.95	3.38	4.74	6.87
Sweet pepper	0.66	1.48	2.13	3.85	6.00	8.22
Mild pepper	0.70	1.37	2.15	3.73	5.20	7.57
$F.L.S.D_{0.05}$	**0.1895**	**0.3156**	**0.4746**	**0.9160**	**1.4280**	**2.1920**

Table 3. **Interactive Effects of Varieties and Treatments on Actual Weight Loss (grams) of Cowpea Seeds During Storage**

Cowpea Varieties	**Pepper Varieties**	**Weeks of Storage**					
		2	4	6	8	10	12
Small white	Hot	498.44	496.45	490.59	482.82	474.20	468.10
	Sweet	498.56	496.32	491.46	480.61	471.10	453.20
	Mild	498.51	495.72	488.48	480.46	470.00	455.20
Big white	Hot	495.63	493.22	490.88	485.04	482.00	475.90
	Sweet	495.79	493.86	492.29	488.93	486.60	483.70
	Mild	493.75	490.04	488.48	472.39	466.00	461.60
IAR48	Hot	499.74	498.66	498.08	486.46	479.40	466.40
	Sweet	499.86	499.28	499.05	489.37	482.10	467.80
	Mild	495.94	499.31	498.52	487.07	479.10	459.20
Iron beans	Hot	493.85	483.29	478.32	493.85	457.80	443.60
	Sweet	490.14	480.96	467.98	490.14	431.00	407.5
	Mild	490.99	487.31	476.82	490.99	462.00	452.40
Aloka	Hot	498.10	497.84	493.33	491.08	488.20	479.10
	Sweet	499.08	498.54	496.09	487.23	489.70	482.50
	Mild	499.25	498.78	496.49	494.47	491.50	484.50
F.L.S.D$_{0.05}$		**2.530**	**7.933**	**5.563**	**10.582**	**15.32**	**24.24**

Table 4. Interaction Effects of Varieties and Treatments on Percentage Weight Loss (%) of Cowpea Seeds During Storage.

Cowpea Varieties	**Pepper Varieties**	**Weeks of Storage**					
		2	4	6	8	10	12
Small white	Hot	0.31	0.71	1.88	3.44	5.160	7.37
	Sweet	0.29	0.74	1.71	3.88	6.44	9.35
	Mild	0.30	0.86	2.30	3.91	4.34	8.97
Big white	Hot	0.89	1.36	1.82	3.00	3.61	4.81
	Sweet	0.82	1.23	1.54	2.21	2.67	3.36
	Mild	1.25	1.73	2.80	5.52	6.81	7.69
IAR48	Hot	0.05	0.27	0.38	2.71	4.12	6.71
	Sweet	0.03	0.14	0.19	2.26	3.58	6.44
	Mild	0.01	0.14	0.30	2.42	4.18	8.15
Iron beans	Hot	1.23	3.34	4.34	5.96	8.45	11.29
	Sweet	1.97	4.98	6.40	9.66	13.80	18.51
	Mild	1.80	0.14	4.64	5.69	7.56	9.86
Aloka	Hot	0.42	0.43	1.33	1.78	2.35	4.18
	Sweet	0.18	0.29	0.79	1.22	3.51	3.51
	Mild	0.15	0.24	0.70	1.11	3.10	3.17
F.L.S.D$_{0.05}$		**0.43**	**0.71**	**0.52**	**2.05**	**3.19**	**4.90**

Plate 1 Sweet Pepper

Plate 2 Hot Pepper

Plate 3 Moderately Hot pepper

Plate 4 Iron Beans

Plate 5 Aloka

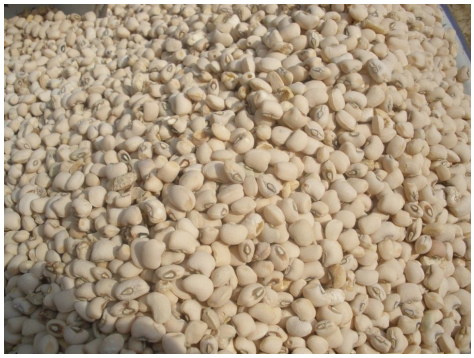

Plate 6 Big White

Plate 7 IAR48

Plate 8 Small White

PGB35

SEARCHING FOR SSR MARKERS ASSOCIATED WITH *ALECTRA VOGELII* RESISTANCE GENE IN COWPEA [*VIGNA UNGUICULATA* (L.) WALP] USING BULK SEGREGANT ANALYSIS

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ABSTRACT

The obligate root parasitic weed *Alectra vogelii* (Benth.) is one of the more formidable biotic constraints to cowpea productivity in the dry Savannas of West and Central Africa- which accounts for over 64 % of world cowpea production. This parasite causes yield losses of between70 to 100% in susceptible cultivars. The use of resistant varieties remains the environmentally friendly and economically viable means of controlling the parasite. Molecular markers have been identified that are associated with specific *Striga* resistance genes in cowpea, at present no marker has been identified for *Alectra* resistance in cowpea. The availability of molecular markers tightly linked to *Alectra* resistance genes will open up the possibility of applying MAS to cowpea improvement in breeding programmes, focused on developing elite cowpea lines that are resistance to *Alectra* . A study was designed to identify molecular markers linked to *Alectra* resistant gene using SSRs and Bulk Segregant Analysis (BSA). F_2 population of a single cross, Banjar (susceptible parent) × B301 (resistant parent) was screened for reaction to *Alectra* using pot culture technique. DNA was extracted from parental genotypes and F_2 lines at 14 DAP using FTA® plant saver cards. 50 SSR cowpea, 40 SSR rice bean and 50 SSR asparagus bean primers were used to screen DNA from B301 and Banjar for polymorphism. 20 primers were polymorphic in B301 and Banjar and these were used in the technique of BSA performed with DNA bulks of highly resistant and susceptible F_2 lines to select those that co-segregated with the resistant gene. RB16 from rice bean and CLM0356 from asparagus bean were selected and used to screen 150 F_2 lines for marker segregation, association and linkage analysis. Cluster analysis as depicted by dendogram showed a tight association (>0.75) between these markers, suggesting that these markers can be explored in MAS targeting breeding for *Alectra* resistance in cowpea.

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important food legume grown in tropical and subtropical regions of the world (Timko and Singh, 2008). It is a valuable source of protein (23%) that supplements the high carbohydrate diet of many African people (Bressani, 1985). Cowpea is widely grown in the savannas of West and Central Africa where the crop is of high importance. Nigeria is the largest producer with production estimates of over 2.3 million tons which accounts for over 50% of the total world production (Kamara *et al.*2008). Despite its importance in sub-Saharan Africa and its wide spread high potential, cowpea growth and yields are constrained by several biotic and abiotic factors (Omoigui *et al.* 2007). The more formidable biological constraints to increased cowpea productivity in West and Central Africa are attack by the witch weeds *Striga* and *Alectra* (Omoigui *et al.* 2012). *Alectra vogelii* Benth. Of the *Orobanchaceae* family) is distributed across West Africa (Riches *et al.* 1992), and in Nigeria its prevalence lies between northern Guinea savanna and Sudan savanna (Emechebe *et al.* 1991). Effect of *A. vogelii* parasitism on cowpea results in yield losses which range between 70 and 100% (Kureh *et al.* 1999), estimated in the millions of tons annually (Singh and Emechebe, 1997).

Chemical and cultural control strategies to combat the parasitic weeds are difficult and expensive and, therefore the use of host plant resistance to control the parasitic weeds (*Striga* and *Alectra)* appears to be preferable since it is affordable by resource poor farmers who lack the financial means to use high input management practices and other options (Omoigui *et al.* 2012), and environmentally friendly. Diego *et al.* (2006) have also stated that other control strategies developed for control of parasitic weeds have been without unequivocal success. However, appropriate screening and effective selection indices are needed to ensure success. Novel molecular biology techniques have been used by various researchers to identify molecular (DNA) markers linked to different traits of interest in several crop plants. In cowpea, employing these novel tools has aided the successful identification of markers linked to different race-specific *Striga gesnerioides* resistance genes (Ouedraogo *et al.* 2001; Ouedraogo *et al.* 2002). Application of molecular markers in breeding programs can help to eliminate environmental factor, allow smaller populations to be used, reduce the number of

generations needed to reach a goal and increase the accuracy of evaluations (Timko *et al*. 2007a). Over the years the integration of marker assisted selection (MAS) into *A. vogelii resistance* breeding has been hampered by the absence of molecular markers linked to the resistance gene. Therefore the objective of this work was to identify molecular (DNA) markers linked to *A. vogelii* resistance gene in cowpea using SSR mapping and Bulked segregant analysis (BSA).

The SSR technique is simple, easily reproducible, requires little quantity of moderate quality DNA and characterized by higher levels of detection of polymorphism at a given locus than other molecular marker systems (Grivet and Noyer, 1999). Also Bulked segregant analysis is a rapid procedure for identifying molecular markers in specific regions of organism's genome using a segregating population (Michelmore *et al*. 1991). Therefore, a combination of these two techniques offered a good platform for marker identification.

MATERIALS AND METHODS

F_2 progenies from a single cross between B301 and Banjar were used for this work. Genomic DNA was extracted from leaf tissue of the first trifoliate leaves of 14 days old parental genotypes along with the derived F2 population comprising 150 lines, using FTA® Plantsaver cards and made PCR ready following the procedure outlined by Omoigui *et al.* (2012) with slight modifications. 140 SSR primers used in this work were supplied by the Mike Timko laboratory of the Department of Biology, University of Virginia, USA. All PCRs were performed with *AccuPower*® PCR PreMix (Bioneer) (1 U *Top* DNA polymerase, 250 μL each of DNTPs mix, 10 mM Tris-HCl (pH 9.0), 30 mM KCl, 1.5 mM $MgCl_2$ and stabilizer and tracking dye), using a heated lid thermal cycler (Bio-Rad MyCycler™). After amplification, PCR products were separated on a 2% agarose gel stained with ethidium bromide (10mg/ml of H_20) using horizontal gel electrophoresis system (GALILEO bioscience) and viewed on a Benchtop UV Transilluminator (M-26V). Gel images were taken with a digital camera and subsequently scored prior to data analysis. DNA from parent genotypes was screened for polymorphism using 140 primers- 50 SSR primers from cowpea genome (Prefixed Cp), along with 40 SSR primers from rice bean (Prefixed RB) and 50 SSR primers from asparagus bean (Prefixed CLM), developed and proven to give amplification products in cowpea. 20 of these primers were polymorphic with respect to *Alectra* resistance and these were used for bulk segregant analysis.

DNA bulks for bulk segregant analysis were obtained from highly resistant and susceptible F2 lines. PCR was first performed using DNA extracted from the individual resistant and susceptible lines selected for bulking. Aliquot of 5 µL was pipetted from the PCR product of 5 lines into a single PCR tube to make a single bulk. This procedure was followed to construct all the DNA bulks. BSA was then performed by using primers that showed polymorphism in the parental lines to screen the DNA bulks along with the parents (B301and Banjar) as check.

RESULTS

The result of the BSA revealed two primers- RB16 from Rice bean and CLM0356 that co-segregated with the resistant gene (Plate 1). A close look at plate 1 shows the segregation integrity of primer RB16 and CLM0356. For these primers, the susceptible bulks segregated with the susceptible parent while the resistant bulks segregated with the resistant parent as shown by band movement and pattern. Whereas RB32 primer, produced similar bands with the resistant and susceptible bulks (Plate 1).

Plates 3 and 4 show agarose gel electrophoretic images of F2 lines screened with primers RB16 and CLM0356. These primers were able to discriminate between resistance and susceptibility. They were identified as likely linked to *Alectra* resistant gene based on the BSA technique. For both primers, the banding pattern showed that the resistant band sits above the susceptible band. The parents were included for ease of scoring. Homozygous resistant lines had single band and were scored 'A', while susceptible band was scored 'B' and heterozygous resistant lines had double band and were scored 'AB' (Plates 2 and 3).

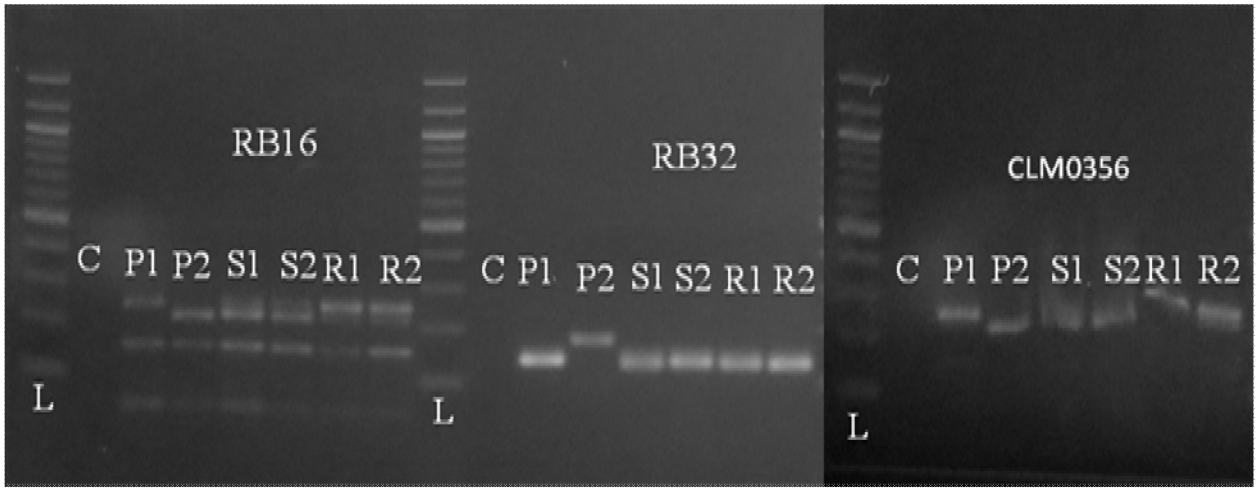

Plate 1: Sample image of agarose gel electrophoretic analysis of PCR amplified product for Bulk Segregant Analysis with Polymorphic Primers. L = 100 bp ladder, C = control without genomic DNA template, P1 = B301 (resistant parent), P2 = Banjar (susceptible parent), S1= Susceptible bulk 1, S2 = Susceptible bulk 2, R1= Resistant bulk 1, R2 = Resistant bulk 2.

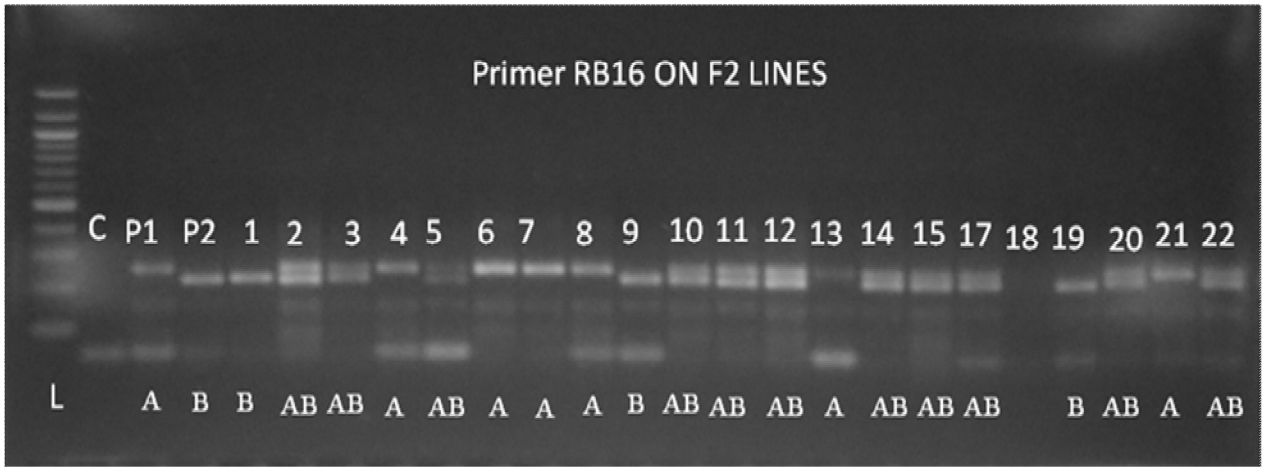

Plate 2: Sample image of agarose gel electrophoretic analysis of PCR amplified product using primer RB16 for the F2 progenies derived from B301 x Banjar. L = 100 bp ladder, C = control without genomic DNA template. P1 = B301, P2 = Banjar.

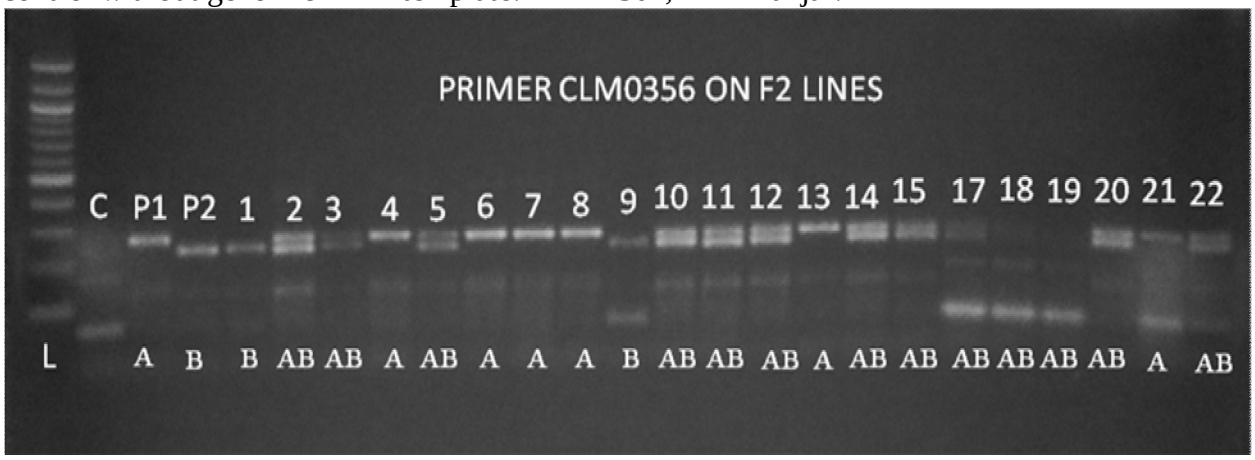

Plate 3: Sample image of agarose gel electrophoretic analysis of PCR amplified product using CLM0356 for the F2 progenies derived from B301 x Banjar. L = 100 bp ladder, C = control without genomic DNA template. P1 = B301, P2 = Banjar.

Association analysis of the segregation data of the two markers, which co-segregated with the resistant gene, was performed using the computer software (Figure 1). The cluster analysis also revealed that RB 16 and CLM0356 were close with coefficient of association of 0.75 compared with PS score with degree of association of 0.5.

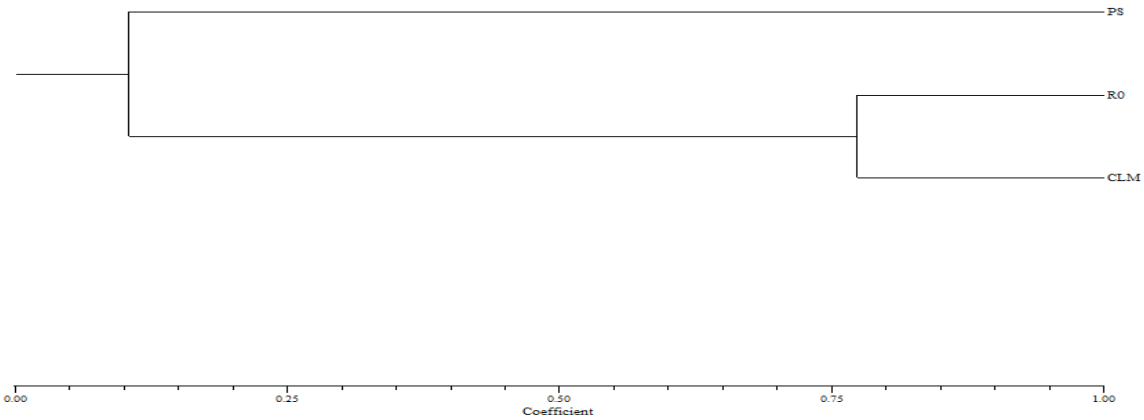

Figure 1: Dendogram showing the relationship of three cowpea markers based on segregation with *Alectra* resistance gene in an F2 population. PS=Phenotypic marker. RO= molecular marker (RB16). CLM=molecular marker (CLM0356)

DISCUSSION

The suitability of FTA PlantSaver Cards for collection, storage and recovery of cowpea genomic DNA for molecular analysis has already been reported by Omoigui *et al.*, (2001, 2012), this was also found to be suitable for analyzing bulk DNA. Electrophoretic gels stained with ethidium bromide, viewed under UV light showed clear bands with little or no smearing, which indicated that sufficient quantity of high quality DNA was trapped and retained in the FTA paper matrix. Usually 20 ng of high quality DNA is sufficient to give amplification product from PCR. The washing process to purify the DNA and make it PCR ready was efficient and contributed to the resultant high quality DNA. According to Omoigui *et al.* (2012), FTA® cards provide a simple alternative method for collection, storage and retrieval of genomic DNA for molecular study especially when operating in developing countries and regions remote from laboratory facilities.

All the 140 SSR primers screened for this work gave amplification products with cowpea genomic DNA but not all were polymorphic. Generally, SSR markers were co-dominant,

except two of the markers that were dominant. The scoring of alleles at a specific locus required careful examination of gel images particularly for F2 progeny to be able to distinguish between dominant, susceptible, and heterozygous resistant alleles**.** The ubiquitousness and even distribution of SSRs (Grivet and Noyer, 1999) is one of the advantages that have made SSR marker system attractive to scientists. In the present work, however, only 20 SSR primers out of the 140 primers screened were polymorphic with the parental lines used (B301 and Banjar). This suggests that even though B301 is a land race while Banjar is a domesticated variety, little genetic variation exists between them, hence the low level of polymorphism. This may also be a pointer that there is low level of within-specie variation in SSRs. Considering the fact that SSR primers from Asparagus and Rice bean gave amplification products in cowpea, there seems to be a conservation of SSRs in the *unguiculata* genome. This also implies that there is great potential for transferability of SSR markers between the three species (asparagus bean, rice bean, and cowpea) for molecular studies. According to Sharma (2008), microsatellite sequences are conserved over wide ranges of organisms and non-specie specific. Conservation of sequences is a factor that aids in primer design, and primers designed for a particular crop can be used for studies on another crop. The fact that SSR primers from Asparagus and Rice bean were polymorphic between cowpea genotypes with respect to *Alectra* resistance, also suggests a possible conservation of resistant gene analogues between these 3 sub-species that can be explored for identification and isolation of resistance genes.

The technique of bulk segregant analysis (BSA) is a powerful technique that has gained wide acceptance in the few years since it was first described by Michelmore *et al.* (1991). BSA which has become a popular technique in molecular breeding, has been combined with various marker systems to identify markers linked to resistance genes in sorghum (Mutengwa *et al.* 2005), apple (Yang *et al.* 1997), barley (Ardiel *et al.* 2002), wheat (William *et al.* 2002)etc. In a single study, Zhang *et al.* (2012) successfully used BSA in concert with AFLPs, SSRs, COSs, ISSRs, and TRAPs to map molecular markers linked to NIRPT a Downy mildew gesistance Gene in *Nicotiana langsdorffii*.

Previously BSA has been performed by bulking diluted genomic DNA before PCR amplification. In the present study, bulking was done after PCR amplification of DNA of individual lines selected for BSA i.e. post PCR DNA bulking. The result proved that BSA technique is a fast and reliable method for the identification of markers as it enabled the

identification 2 putative markers- CLM0356 from Asparagus bean and RB16 from Rice bean out of 20 polymorphic markers. This result also shows that post PCR bulking of DNA is a unique novel approach for BSA using DNA collected with FTA Plant Saver Card.

Cluster analysis as depicted by dendogram also showed a tight association (>0.75) between these markers and *Alectra* resistance gene showed a close linkage with the resistance gene.. Similar approach has been used to identify a range of marker–trait associations in hexaploid wheat (Roy *et al*. 2006). Hence the association of these markers with the *Alectra* resistance gene offers a unique opportunity for incorporation of marker assisted selection in local and national breeding programs to fast track breeding and delivery of *Alectra* resistant varieties.

CONCLUSION

BSA technique identified two SSR markers - CLM0356 and RB16 as closely linked marker to *Alectra* resistant gene. Cluster analysis showed a tight association between these markers and *Alectra* resistance gene. Association of these markers with the *Alectra* resistance open up the possibility of applying MAS to cowpea improvement in breeding programmes, focused on developing elite cowpea lines that are resistance to *Alectra* .

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PGB36

EVALUATION OF MORPHOLOGICAL AND MICRONUTRIENT CONTENTS OF THREE VARIETIES OF SWEET POTATO *(IPOMOEA BATATAS L.)* IN CALABAR, NIGERIA

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ABSTRACT

Morphological performance and nutrients content was evaluated in three varieties of sweet potato; TIS 87/0087, TIS 8164, and Digitate, cultivated in Calabar. Vines were planted in manually prepared beds in a complete randomized design, with three replicates. At maturity, data on morphological parameters and micronutrients composition was collected and subjected to one way analysis of variance (ANOVA). Digitate had significantly higher ($P<0.05$) vine length than TIS 87/0087 and TIS 8164. Other morphological parameters revealed no significant differences ($P>0.05$) between the cultivars. Digitate also had significantly higher ($P<0.05$) Fe, Zn, and β-carotene than TIS 8164, which had a significantly higher Mn than the other two cultivars. We conclude that on sandy-loam soil in Calabar, Digitate variety of sweet potato had higher micronutrient content than TIS 87/0087 and TIS 8164, and is thus recommended for cultivation in this geo-ecological zone, especially where increased quantity of the stated micronutrients is desired in the diet.

INTRODUCTION

The expansion of population in many countries of the world continues to place much demand for improved varieties of crops to fill the dietary needs of humans. Much of the current growth in global human populations takes place in developing nations of Africa, the Middle East, and Asia; where adequate nutrition remains a great challenge to many low income families (Diaz *et al*., 2003). Protein, vitamin, and mineral deficiencies are recognized to be at the heart of the global disease burden Black (2003). According to Frossard *et al*. (2000), vitamin A, iron, calcium, magnesium, and zinc, amongst others, are generally inadequate in the diet, and have been implicated in poor cognitive development, and lower disease resistance, especially in children. The strategy of regular in-take of pharmaceutical supplements and "nutri-fortified" canned foods, could achieve good results, but are not without notable costs; and so, are neither sustainable within many families nor on a global scale (Bouis, 2003). This has prompted much interest in utilization of techniques in crop genetics and biotechnology, in development of crops with enhanced nutrient content capacity (Raven *et al*., 2005).

Sweet potato (*Ipomoea batatas* L.) is a dicotyledonous plant belonging to the family Convolvulaceae (Tumwegamire, 2011). With an estimated annual production of 124 million tons, it is the world's 7th most important food crop, after wheat, rice, maize, potato, barley, and cassava (FAOSTAT, 2007), and is a popular staple in many countries where it is consumed by a great many folks. Nutritionally, sweet potato is rich in carbohydrate, soluble sugars, vitamins, and nutrients (Senanayake, *et al*, 2013). In Nigeria, the National Root Crop Research Institute (NRCRI), Umudike, has developed improved varieties of sweet potato,

especially those with resistance to common pests, increased starch content, and yields, amongst others.

Interest in nutrient content of staples, such as sweet potato, yam, and cassava, has increased in the intellectual and public domains; due to the realization of the fact that aside fulfilling our energy needs, staples with increased nutrient content do have a great potential in the quest for optimum nutritional status in poor families in developing countries, such as Nigeria. This forms much of the underlying rationale of this study on three varieties of sweet potato popular in Southeast Nigeria. Further justification of study is evident, in the light of the variability in nutrient content of crops grown in different geo-ecological zones; as edaphic factors such as soil physico-chemical characteristics have been known to affect performance and nutrient content of food and/or feed crops (Venuto *et al*., 2002). Much of sweet potato cultivation takes place in the "Middle belt" states of Nigeria. In the light of the aforementioned, and as G×E studies in sweet potato have reported it to be sensitive to soil/environment component (Tumwegamire, 2011), this study was conducted to determine the micronutrient content of three varieties of sweet potato, grown on sandy loam soil of Calabar, Cross River State, Nigeria.

MATERIALS AND METHODS

The three varieties of sweet potato used in this study were TIS 87/0087, TIS 8164, and Digitate; all obtained from NRCRI, Umudike, Abia State, Nigeria.This experiment was carried out in Department of Biological Science experimental farm, University of Calabar, Calabar, on a plot of land measuring 10 × 10 meters, with a general sandy-loam soil nature. The plot was divided into nine (2 × 2 m) beds; three for each sweet potato variety. Each variety was randomly assigned to three beds, where they were planted. The beds were labeled A, B, and C; for TIS 87/0087, TIS 8164, and Digitate respectively. Potato stem cuttings with length of 15-20 cm were planted, two per stand (later thinned to one) on each bed, in a slanting position, with minimum interspacing distance of 50 cm maintained. Each bed had 6 stands, giving a total of 18 replicates for each sweet potato cultivar. NPK 15:15:15 fertilizer was applied once, by ring method, three weeks after planting, and hand weeding was performed fortnightly, after every three weeks (Agbede and Adekiya, 2011).

After maturity, data were collected on leaf length, vine diameter, internodes length, leaf area, and vine length. Harvested root samples were collected bed by bed, washed, air dried and macerated, then oven dried for 6hrs at 120^{o}C. Oven dried roots were ground into a fine powder in a commercial electric blender . Laboratory analysis of micronutrients content of roots powder was performed in Department of Biochemistry, University of Calabar, Calabar, for β-carotene, iron, zinc, iodine, and manganese, according to the methods described by AOAC (1997), and absorbance read in a spectrophotometer (Jenway 6405, Essex, England). All data collected were subjected to analysis of variance (ANOVA) to check for significant differences between the cultivars at 5% probability level, and mean separation was achieved using (least significant difference) LSD.

RESULTS

Table 1 show the morphological attributes of three varieties of sweet potato cultivated in Calabar. Of all the attributes evaluated in this study, only vine length showed significant ($P<0.05$), differences between Digitate (which had the highest value) and the other two. Leaf length, leaf area, vine diameter, and internodes length revealed no significant ($P>0.05$) differences between the cultivars.

Table 1: Morphological attributes of sweet potato (*Ipomoea batatas* L.) cultivars

Parameter (cm)	TIS 87/0087	TIS 8164	Digitate
Leaf length	$6.87^{a} \pm 0.43$	$7.01^{a} \pm 0.82$	$7.13^{a} \pm 0.31$
Leaf area	$16.48^{a} \pm 0.25$	$17.30^{a} \pm 0.27$	$17.10^{a} \pm 0.33$
Vine diameter	$0.95^{a} \pm 0.06$	$0.90^{a} \pm 0.18$	$0.83^{a} \pm 0.03$
Vine length	$71.33^{a} \pm 0.26$	$66.73^{a} \pm 0.34$	$81.60^{b} \pm 0.39$
Internodes length	$3.48^{a} \pm 0.29$	$2.83^{a} \pm 0.28$	$3.10^{a} \pm 0.50$

Values are mean ± SEM. [ab]Values with the same superscript are not significantly different at 5% based on ANOVA.

Table 2 show the micronutrients content of three varieties of sweet potato cultivated in Calabar. Digitate had a significantly ($P<0.05$) higher zinc content than TIS 87/0087 and TIS 8164. TIS 8164 had significantly ($P<0.05$) lower iron content than the other two cultivars. TIS 8164 had the highest value for manganese, and this was significantly ($P<0.05$) higher than that of Digitate, and TIS 87/0087 which had the lowest. While Digitate had significantly ($P<0.05$) higher β-carotene content than TIS 8164, no significant ($P>0.05$) differences were observed in iodine content among the three cultivars.

Table 2: Micronutrients content of sweet potato (*Ipomoea batatas* L.) cultivars

Parameter (mg/100g)	TIS 87/0087	TIS 8164	Digitate
Zinc	$0.20^{a} \pm 0.02$	$0.18^{a} \pm 0.02$	$0.34^{b} \pm 0.08$
Iron	$1.66^{b} \pm 0.05$	$1.50^{a} \pm 0.03$	$1.70^{b} \pm 0.07$
Manganese	$0.10^{a} \pm 0.01$	$1.13^{b} \pm 0.09$	$0.40^{a} \pm 0.04$
Iodine	$2.61^{a} \pm 0.10$	$2.47^{a} \pm 0.31$	$2.53^{a} \pm 0.27$
β-carotene	$0.34^{ab} \pm 0.05$	$0.28^{a} \pm 0.03$	$0.41^{b} \pm 0.04$

Values are mean ± SEM. [ab]Values with the same superscript are not significantly different at 5% based on ANOVA.

DISCUSSION

The importance of micronutrients to the human body cannot be overemphasized. β-carotene is converted to vitamin A in the human body, which plays a very important role in proper vision and immune functioning, cell growth and differentiation, amongst others . Iron is an essential mineral in the synthesis of haemoglobin, the oxygen carrying pigment in blood; zinc is essential for growth, development, reproduction, sensory and immune functions, etc.; while manganese is involved in activation of enzymes. Iodine is important in metabolism and energy release rate, and deficiency can cause goiter (Cunnigham-Rundles et al., 2005; Insel *et al*., 2010). As long as metabolism is to continue optimally, dietary intake of these nutrients therefore, is a necessity.

With the exception of vine length, morphological attributes of the sweet potato varieties did not reveal significant differences between them. This means, perhaps, that these cultivars are almost equal with respect to growth attributes, in Calabar. With respect to micronutrients however, there existed significant diversity between TIS 87/0087, TIS 8164, and Digitate, going by the results of this study; Digitate performed much better than the other two, with a higher zinc and iron, as well as β-carotene. Nutrient content is yet to be associated or correlated with length of vine in sweet potato. We think therefore, that the higher vine length in Digitate, might not just yet be associated with its better performance in nutrients content; at least until sufficient experimental evidence points to such possibility; for example, by gene

linkage. This position is justifiable especially as TIS 8164 which had the shortest vine length, had significantly higher manganese content than both Digitate and TIS/870087.

Differences with genetic basis (as is supposedly the case with these cultivars) in innate attributes of plant varieties result in differences in overall plant physiology and performance, and can account perhaps, for differences in nutrient content observed in many plant cultivars, under similar environmental conditions (Høgh-Jensen et al., 2006). And even where much morphological differences were not observed, significant differences in nutrient content of plants could be noted, as is the case here; with Digitate performing better than the other two in zinc and iron content. This potential is note-worthy, from a crop genetics viewpoint.

Comparatively, and on soil with a general sandy-loam nature, in Calabar, Digitate contained higher zinc, iron, and β-carotene, than TIS 87/0087 and TIS 8164; but TIS 8164 showed a higher manganese content than the other two. All three cultivars performed equally with respect to iodine content.

CONCLUSION

Results of this study indicate that Digitate might be cultivated/consumed more, where increased quantity of micronutrients such as zinc and iron, as well as β-carotene, is an over-riding consideration; at least in Calabar and similar geo-ecological zones. As the quest for genetic improvement of local crop varieties (in features of dietary and nutritional significance) is one of continuing relevance, the results of studies such as this, in different geo-ecological zones can result in increased utility of, and benefits from, peculiar cultivars, as well as lend more impetus to local breeding programs.

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PGB37

CYTOLOGICAL EFFECTS OF THE PLANT ROOT EXTRACTS OF *TELFAIRIA OCCIDENTALIS* HOOKER FIL. ON ROOT TIPS OF *CRINUM JAGUS* (THOMPS) DANDY IN NIGERIA

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A B S T R A C T

The mitotic effects of the plant root extracts of *Telfairia occidentalis* on the root tips of *Crinum jagus* were investigated. The root extract of *Telfairia occidentalis* was used at concentrations of 0.125%, 0.25% and 0.50% respectively and was found active as inhibitor of mitosis. The results obtained showed several chromosomal abnormalities including stickiness of chromosomes (both at metaphase and anaphase), c-metaphase, lagging chromosomes and stickly bridges. The trend of the results showed that the higher the concentration of the extracts for treatment, the more inhibitory the effect of mitosis with more pronounced chromosomal aberrations. The root extract of *Telfairia occidentalis* (fluted pumpkin) was found to promote the formation of aberrant chromosomes also and this information could help in the elucidation of the mechanism of action in the light of its use as a local lethal poisoning agent in traditional medical practice. The results are discussed in the light of the possibility of using *Crinum jagus* as an alternative to *Allium cepa* and also the possibility of using the extracts of *Telfairia occidentalis* as an alternative for the rather expensive

colchicine for cytological studies. The economic potentials of the observations made are discussed.

Keywords: *Allium* cepa, chromosome, *Crinum jagus,* mitosis, *Telfairia occidentalis.*

INTRODUCTION

Telfairia occidentalis Hook. F (Cucurbitaceae). is a perennial plant with large fluted fruits. The leaves, especially the tender ones, are commonly used in the southern part of Nigeria as vegetable. The seeds are cooked and eaten as such or used in preparing soup. *Telfairia occidentalis,* commonly called fluted pumpkin is a crop of commercial importance grown across the lowland humid tropics in West Africa with Nigeria, Ghana and Sierra Leone being the major producers (Nkang *et al.,* 2003). In Nigeria, fluted pumpkin is cultivated mostly in the southern and eastern parts of the country where it is fast becoming a crop of importance for its palatable and nutritious leaves. *T. occidentalis* is a creeping vegetable shrub that spreads low across the ground with large lobed leaves and long twisting tendrils (Horsfall and Spiff, 2005). The leaves and shoots of the plant are frequently eaten as a potherb (Okoli and Mgbeogu, 1983).

In Nigeria, herbal preparations of *T. occidentalis* have been employed in the treatment of convulsion, ulcers, malaria, and anaemia (Gbile, 1988). *Telfairia* species have been found to be rich in protein (21-37%), ash (14%), fat (13%) and fibre (13%) (Akoroda, 1990). The essential amino acid contents compared favorably with those of important legumes (Asiegbu, 1987) and the high content of mineral and vitamin nutrients especially iron (Fe), magnesium (Mg) and calcium (Ca) and vitamins C and B_{12} is remarkably making the leaves potentially useful as food supplements (Adesanya, 2007). The roots are known locally as potent human poison and there are reports of their use as fish and human poison (Hutchison *et al.,* 1958). The extract from the roots, administered intraperitonally, have been found to be lethal to rats at a concentration of 10ml/kg body weight (Akubue *et al*., 1980). Again, these properties of *Telfairia occidentalis* root extract necessitated its use in mitotic studies.

The genus *Crinum* is represented by so many species as pointed out by Sharma (cited in Nwankiti, 1985). Two of these have been found in Nigeria and are classic ornamentals. They decorate both the landscape and private gardens when in bloom. Like most members of the family Amaryllidaceae, they flower by mid-dry season and bloom till the beginning of the rains in May. The two species are *C. ornatum and C. jagus* (Nwankiti, 1985). Apart from *C. octabilis* (2n = 33), 14 species investigated all had 2n = 22 (Sharma and Bhattacharya, 1956). *Crinum jagus* was used for the purpose of this study. *Crinum species* and *Allium cepa* belong to the same family Amaryllidaceae. In this research, the cytological effects of the root extracts of *Telfairia occidentalis* on the root tips of *Crinum jagus* were investigated with a view to finding some possible use of these extracts as chemicals for the modification of mitosis in much the same way as colchicine (Levan,1938). Colchicine is a very expensive drug which is not easily available for research work (Okoli and Russom, 1987).

MATERIALS AND METHODS

Bulbs of *Crinum jagus* were used as test material for this experiment. They were dug up from the Botanical garden at the University of Port Harcourt where they had been growing or were cultivated. Different sizes were selected, the smaller bulbs having smaller roots than the bigger ones which had roots many times that of *Allium cepa.* The root tips (between 1–2 cm in length from the root apex) were cut off and sectioned to produce thinner longitudinal

sections which are amenable to cytological treatments. The roots of *Telfaria occidentalis* were dug up when the plants were at anthesis in Gambi-Ama, at the University Park of the University of Port Harcourt The roots were subjected to very good washing with water as much as was necessary to remove all the attached soil and dirt. After this they were sliced to expose a greater surface area and to facilitate drying. The sliced specimens were oven-dried at a temperature between 40 ^{o}C – 60 ^{o}C. The dried materials were then crushed in a mortar to a semi-powdered form. About 200g of the crushed specimen was weighed out into the thimble of a soxhlet extractor and reflux extraction was carried out in a fume chamber. For the extraction, two solvents were used successively. Firstly was petroleum ether. This was mainly for the de-fattening of the specimen. After this, chloroform was used which effected alkaloid extraction from the specimen. It took 14 – 16 hours for complete exhaustion of the root with each solvent. The solvent was distilled off and the extract weighed. The fatty components obtained after the extraction with petroleum ether were discarded while the extract obtained after the extraction with chloroform was dried and weighed. It gave 0.12g dry weight of *Telfairia occidentalis* and from this; various concentrations of the test solution were made namely 0.8 per cent 0.4 percent, 0.2 per cent and 0.1 percent with water as the control solution.

The roots of the *Crinum jagus* were randomly selected from the bulbs and sampled by cutting them off the bulbs with a sharp razor blade. They were sliced to desirable sizes and placed in a watch glass with water. They were then treated with the test substances in vials containing about 2 mls of concentrations for 3 hours. This treatment is best from between 10.00 am and 1.00 pm in the day. This is because mitotic activities have been found to be at their best within this time of the day. After this, fixing of the roots was done in a freshly prepared 1:3 glacial acetic acid/ 95 percent ethanol (V/V) for at least 24 hours and then stored away in 70 percent alcohol under refrigeration until required. For control purposes, another group of randomly-selected roots were taken and treated with tap water instead of the test solutions after they were cut and fixation was carried out as previously described. For each period of collection, each root tip was later randomly selected for slide preparation. Hydrolysis of the fixed roots in 8 per cent HCl for about five minutes was carried out. This is to facilitate the disintegration of the middle lamella to ensure adequate staining. This treatment preceded their stabilization before squashing was done. About 2mm opaque end of the root tip was sectioned off with a sharp razor blade and used for slide preparation. For examination of mitotic chromosomes, root tips were squashed in FLP-Orcein (2g of Orcein dissolved in 100ml of solvent, containing equal parts of formic acid, lactic acid, propionic acid and water), following the method of Okoli, (1983). The materials were squashed directly by tapping with the blunt end of a ball point pen, to cause the cells to spread out properly. Slides were viewed at x400 magnification. The frequencies of mitotically dividing cells were scored by sampling portions of slides which showed unambiguity in the configurations of mitotic cells. The mitotic index was defined as the ratio of dividing cells to the total number of cells examined for each treatment (Balog, 1982). The effect of different concentrations and duration of treatment of the extract on the frequencies of the four phases of mitosis was determined. Statistical analysis was carried out to determine the correlation between the concentration of the test solution and the mitotic indices obtained. Microphotographs of chromosomal aberrations were taken from temporary slides following the method of Okoli and Russom, (1987).

RESULTS

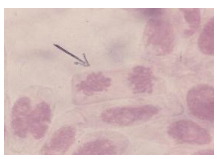
The extract exhibited a strong depressive effect on mitosis of *Crinum jagus* roots. The untreated root tips of *Telfairia occidentalis* showed mitotic index of 10.50 per cent. The treated root tips showed mitotic indices lower than those of their respective untreated counterparts. Inhibition of mitosis increased significantly with increase in the concentration of treatment solution in *Telfairia occidentalis* root extract as shown by the fact that at concentrations of 0.125%, 0.25%, and 0.50% mitotic indices of 3.2, 3.0 and 2.5 were obtained respectively. This shows a very negative correlation between the concentration of the extract and the mitotic indices produced by the observed action. Table 1 shows the mitotic effects of the root extracts of *Telfairia occidentalis* on the root tips of *Crinum jagus* while Table 2 shows chromosome aberrations of *Crinum jagus* root tip cells treated with different concentrations of *Telfairia occidentalis* root extracts scored in this experiment. Other significant observations made for the various concentrations and treatments are presented in the form of microphotographs (Figures 1).

Table 1: Mitotic effects of the root extract of *Telfairia occidentalis* on *Crinum jagus* root tips

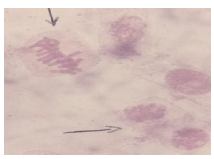
CONCENTRATION	**MITOTIC STATES**					
	Prophase	**Metaphase**	**Anaphase**	**Telophase**	**TOTAL**	**M. I**
0%	16	9	9	2	344	10.5
0.125%	2	2	2	4	309	3.2
0.25	2	2	1	5	329	3.0
0.50%	1	2	4	1	319	2.5

Table 2: Chromosome aberrations of *Crinum jagus* root tip cells treated with different concentrations of *Telfairia occidentalis* root extracts.

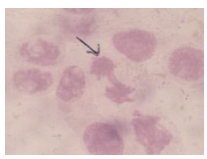
Concentrations	**Number of cells counted**	**Total dividing cells**	**Stickiness**	**C-mitosis**	**Vagrant**	**Bridges/ Fragments**	**Anaphase laggards**
Control	344	36	0	0	0	0	0
0.125%	309	10	0	1	1	0	0
0.25%	329	10	2	2	0	1	1
0.50%	319	8	3	0	1	3	2



(a)



(b)



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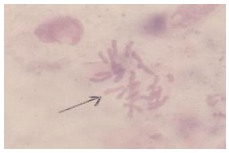

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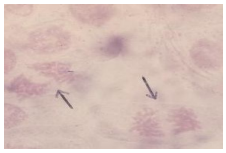

(e)

Fig. 1 Cytological effects of aqueous extracts of *Telfairia occidentalis* on *Crinum jagus* root tips.
(a) Regular anaphase in control (x400)
(b) Regular metaphase and telophase in control (x400)
(c) Anaphase bridge in.5% *T. occidentalis root* extracts (x400)
(d) C- metaphase in 0.5% *T. occidentalis* extracts (x400)
(e) Lagging chromosome in anaphase caused in 0.5% *T. occidentalis* extracts (x400).

DISCUSSION

Akubue *et al.*, (1980) reported that the root extract of *Telfairia occidentalis* exerted a lethal poisoning action in rats. Moreover, it is widely reported that the roots of *Telfairia occidentalis* is used as a human poison in the southern parts of Nigeria. In the light of the results obtained in the present study, these observations above may be due to nucleotoxic action of the extracts or the disturbance of the formation of spindle fibres during cell division which leads to chromosomal aberrations.

Stickiness and clumping of chromosomes were some of the most common effects of these extracts on the treated root tips. These abnormalities have also been reported for several extracts and chemicals already investigated (Shehab, 1979, 1980; Badr and Elkington 1982; Misra, 1982). Stickiness usually leads to the formation of anaphase and telophase bridges and these end up inhibiting meta- and cytokinesis respectively and thus hampering cell division. Stickiness might be due to the ability of the extracts to cause DNA depolymerization and partial dissolution of nucleoproteins, breakage and exchanges of the basic folded units of chromatids and the stippling of the protein covering of DNA in chromosomes (Onyenwe, C.N. University of Port Harcourt, Nigeria, personal communication).

The consistently high frequency of interphase observed in all the concentration means was expected since that stage lasts much longer than the other stages of mitosis. Even though many aberrations were observed at metaphase in high concentration of the extract, the frequency of prophase was still high enough to indicate that even the treated cells to some degree, go through prophase of mitosis normally. This observation further suggests that these extracts are potent spindle fibre inactivators and thus can supplement the use of colchicine or hydroxyquinoline in pretreating materials for mitotic studies. This is in agreement with the findings of some earlier workers (CN Onyenwe, University of Port Harcourt, Nigeria, personal communication; Ilevbare, U.K. University of Port Harcourt, Nigeria, personal communication).

Crinum jagus, which is in the same family as *Allium Cepa* (Amaryllidaceae), was used here and gave very good results which are comparable to those obtained by other researchers who have used *Allium cepa* root tips (El-Bayoumi *et al.*, (1979); Kabarity and Malallah, (1980); Nwakanma *et al.*, (2009). The results obtained here are also similar to those reported by earlier workers who have used *Crinum jagus* in other test systems (Nwakanma and Okoli, 2010). This innovation is particularly important against the background of the fact that *Allium cepa* is an edible and hence economic plant. *Crinum jagus* on the other hand is not edible and grows in the wild.

CONCLUSION

The results from this work strongly suggest that *Crinum jagus* can now be used as an alternative to the hitherto-used edible and economic plants - *Allium cepa* for cytological work. Furthermore, owing to the ability of the root extracts of *Telfairia occidentalis* to accumulate metaphase and hence inhibit mitosis, it is possible to use these extracts as an alternative for the rather expensive colchicine for cytological studies. Moreso, when after the harvest of the *Telfairia* vines for consumption, the stem and roots are often discarded as waste.

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GERMPLASM COLLECTION AND EVALUTION OF ROSELLE (*HIBISCUS SABDARIFFA* L) GERMPLASM IN NIGERIA

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ABSTRACT

In an attempt to assess the genetic diversity of Roselle (*Hibiscus sabdariffa* L) in Nigeria, a survey was undertaken to assemble the germplasm of the crop. The survey cut across 56 towns and 20 villages in 17 states including the Federal Capital Territory (FCT). 63 farmers were interviewed and 60 accessions of Roselle were collected from them. Results showed that 41.7% of these accessions were having green calyx, while 31.7% were with red calyx. On the other hand, 20.0% of the accessions possessed deep red calyx while only 6.7% were having light red and pink calyx. Collections from the North Central, North Eastern, North Western and South Western parts were observed to be replications over states, towns and villages. The highest number of Roselle accessions was collected from Kaduna state (8 accessions) followed by Niger state (6 accessions); Jigawa State (6 accessions) while FCT and Bauchi State recorded four accessions each. These results tend to suggest that these areas have the greatest diversity of this crop genetic resource in Nigeria. However, morphological as well as molecular characterizations are required to properly catalogue and characterise the Roselle accessions collected. The current results form a basis for scientific documentation of roselle germplasm in Nigeria and also a gene bank for future Roselle improvement programme in Nigeria.

Keywords: Genetic Diversity, Germplasm, Roselle Accessions, Improvement Programme

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INTRODUCTION

Roselle (*Hibiscus sabdariffa* Linn.) is a shrub belonging to the Family Malvaceae (Mahadevan *et al*., 2009; Anjah *et al*., 2012). It is thought to have originated from Asia (India to Malaysia) or Tropical Africa. The plant is widely grown in the Tropics including Caribbean, Central America, India, Africa, Brazil, Australia, Hawaii, Florida and Philippines, as a home garden crop (Mahadevan *et al*., 2009). In Sudan, it is a major crop of export, especially, in the western part where it ranks after pearl millet, and followed by *Sesamum* (Leung and Foster, 1996; Gautam, 2004). The Genus consists of about 300 species some of which are widely distributed as tropical herbs and shrubs (Heywood, 1978) or as annual erect, bushy, herbaceous sub-shrub (Amin, 2008). Some of the species include: *H. canabinus* L., *H. asper* (Hook.) F., *H. tiliaceus* L., *H. acetosella* Weiw ex Hiern, *H. scotelli* Bak. F.

The plant is about 3.5m tall and has a deep penetrating taproot system. It has a smooth or nearly smooth, cylindrical, typically dark-green to red stems (Amin, 2008; Mahadevan, *et al*., 2009). The leaves are alternate, 7.5-12.5cm long, green with reddish veins and long or short petioles. Leaves of young seedlings and upper leaves are deeply 3 to 5 or even 7-lobed and the margins are toothed. Flowers are borne singly in the leaf axils and are up to 12.5cm wide, yellow or buff with a rose or maroon eye, that turn pink as they wither at the end of the day. The typically red calyx, consist of 5 large sepals with a collar (epicalyx) of 8-12 slim, pointed bracts (or bractioles) around the base. The fruit is a velvety capsule, 2-5cm long, which is green when immature, 5-valved, with each valve containing 3-4 seeds which usually contain high percentage of oil (Rice *et al*., 1993). The capsule turns brown and splits open when mature and dry. Seeds are kidney-shaped, light-brown, 3-5mm long and covered with minute, stout and stellate hairs (Julia, 1987).

The importance of this crop cannot be over emphasized; it is used for many different purposes, the most common of which are its use as a fibre crop and the young leaves which are eaten as cooked vegetables especially with soup (Fasoyiro *et al*., 2005). The seeds are pounded into meal which is used as oily soup or sauce after roasting. Oil extracted from the seed is a substitute for castor oil while the residue is used in a fermented form as soup or cake (Aliyu, 2000).

The crop is used fresh for making wine, juice, jam, jelly, syrup, gelatin, pudding, cakes, ice cream and also dried and brewed into tea as well as flavours and carbonated soft drinks, other acidic foods, spice and used for butter, pies, sauces, tarts, and other desserts (Walford, 1984; Qi *et al*., 2005). The grinded leaves and seeds are added to curries as seasoning. Roselle contains an acid, rhubarb-like flavour. The red calyces contain anti-oxidants including flavonoids, gossypetine, hibiscetine and sabdaretine (Qi *et al*., 2005). The fresh calyces are also rich in riboflavin, ascorbic acid, niacin, carotene, Calcium, and Iron that are nutritionally important (Mahadevan *et al*., 2009), as well as, amino acids and mineral salts (Cisse *et al*., 2009).

They are also known for their unique flavour characteristics that make them appealing to taste. Roselle drink had been improved nutritionally by producing fruit-flavoured Roselle

drinks, which are richer in vitamins and minerals by addition of different fruits with higher consumption acceptability (Fasoyiro *et al*., 2004).

The crop is mainly grown as a vegetable from the savannah and semi-arid areas in Africa, while its use as a fibre crop is mostly in southern Asia. Formerly, it was traditionally cultivated in Nigeria for its leaves, seeds and stems; but is now being grown commercially for its calyces (Babatunde, 2003). Roselle is widely grown in northern parts of Nigeria, where the dried calyx is used for making a popular drink 'zobo' (Falusi, 2007).

Udom *et al*., (2001), reported that there are three common varieties of Roselle grown in Nigeria. Two of these varieties have red calyces while one has green calyces. The green variety is more predominant in the Southern parts of Nigeria while the other two red varieties are predominant in the Northern parts of this country; however, the green variety is also common in the Northern part of the country. The calyces from these varieties have a number of uses and promising prospects for industrial purposes (Alegbejo, 2000). These popular uses to which Roselle have been put had fuelled increasing demand for the crop thus, necessitating corresponding increased supply of the products. Though attempts have been made to achieve this increased supply through increased cultivation of the different varieties; the successes of such attempts have been limited by challenges ranging from unfavourable environmental conditions, as well as dwindling man-power and inadequate farming conditions. As the crop continues to play important horticultural roles in Nigeria, its improvement will surely enhance agricultural productivity, alleviate poverty and facilitate food security. But unfortunately, very little research attention has been given to the improvement of the crop. This background has made it necessary to collect and evaluate the germplasm of the crop, as a basis for research into its development and promotion as a major crop in Nigeria.

MATERIALS AND METHODS

A survey of *Hibiscus sabdariffa* (Roselle) growers was conducted in south-western, north-central, north-western and north-eastern parts of Nigeria, representing the major Roselle producing areas of the country. The survey was conducted between October 2012 and January 2013, when the farmers were expected to be harvesting the crops. The states visited were Niger, Kogi, Nasarawa, Kwara, Ekiti, Ondo, Osun, FCT, Benue, Taraba, Plateau, Kebbi, Gombe, Bauchi, Kaduna, Katsina, Jigawa, and Sokoto. Questionnaires were administered through an interpreter in some cases and samples of available Roselle accessions under husbandry were collected. The questions asked included local name of accessions, source of seed supply, yield, Roselle seed preferences, constraints to cultivation and economic importance.

The seeds were collected packed and sealed in thick paper envelopes each of which was given an accession code, local name, and locality before they were finally stored in dry containers. Ten seeds at random were selected from each of the accessions for the seed diameter. The seed diameters were measured using meter rule and the mean value was recorded as the average diameter.

RESULTS AND DISCUSSION

The survey covered 56 towns and 20 villages in 17 states including the Federal Capital Territory (FCT), Nigeria. 63 farmers were interviewed and 60 accessions of Roselle were collected (Table 1). It was observed that most of the accessions were duplicated in most of the towns and villages. The various calyx colours encountered were green, red, deep red, pink and light red (Plate 1). Results showed that 41.7% of these accessions were having green

calyx, while 31.7% were with red calyx. On the other hand, 20.0% of the accessions possessed deep red calyx while only 6.7% were having light red and pink calyx. Collections from the North Central, North Eastern, North Western and South Western parts were replicated over states, towns and villages in Nigeria. The highest number of Roselle accessions was collected from Kaduna state (8 accessions) followed by Niger and Jigawa States (6 accession each); FCT and Bauchi State on the other hand have 4 accessions each (Table1). This is an indication that these states had the greatest diversity of the crop genetic resource; it also showed that these regions might be the primary or secondary centre of origin of Roselle. This is in line with the report of Mohamed *et al*., (2012) that the genus *Hibiscus* has its centre of origin in Africa.

About 81.8% of the farmers preferred Roselle variety with dark red or red calyx because apart from having medicinal value, it is widely used in the preparations of foods and drinks. This variety is grown in commercial quantities in Jigawa, Kaduna, Bauchi, Niger States and FCT. According to Stevels (1990), Roselle plants with anthocyanin pigmentation are able to withstand the harsh environment and more tolerant than the green variety. Hence they are common in the dry zones of the areas of the production in Nigeria.

The farmers in the south-western part of Nigeria gave more priority to their starchy stable crops. 100% of them responded that they normally grow the green varieties of Roselle for vegetable. They also attend to this vegetable only when their main food crop has been established. The Roselle variety with green calyces is predominant in the south-western part of Nigeria. In view of the popularity of Roselle as a crop of considerable economic importance in Nigeria, there is a need to retain the diversity of the indigenous germplasm. A scientific morphological and molecular characterization of the materials collected is therefore necessary to ascertain the genetic diversity existing within the species in Nigeria.

Plate I: Roselle Accessions with different calyx colour. A: Accession with Green calyx; B: Accession with Light red or Pink calyx; C: Accession with Deep red calyx; D: Roselle accession with Red calyx.

Table 1: Sources and Description of Roselle Germplasm in Nigeria

S/NO	ACCESSION NUMBER	LOCAL NAME	LOCAL GOVT	STATE	CALYX COLOUR	*SEED DIAMETER
1.	NGR-OD-001	ISHAPA	IKARE	ONDO	GREEN	3.55mm

		OTATUPE				
2.	NGR-OD-002	ISHAPA	OGBESE/ AKURE	ONDO	GREEN	3.55mm
3.	NGR-OD-003	ISHAPA OLOHO	ONDO/IRELE	ONDO	GREEN	3.65mm
4.	NGR-EK-004	ISHAPA	IJERO	EKITI	GREEN	3.30mm
5.	NGR-EK-005	ISHAPA TOROMOYAN	ADO/ IJAN	EKITI	GREEN	3.65mm
6.	NGR-EK-006	ISHAPA TOROMOYAN	OMUO/ ILASHA	EKITI	GREEN	3.55mm
7.	NGR-OS-007	SAPA	IWO/ IBODE OSI	OSUN	GREEN	3.35mm
8.	NGR-OS.008	ISAPA	IKOYI/ IKIRE	OSUN	GREEN	3.35mm
9.	NGR-OS-009	ISAPA	ILAORANGUN	OSUN	GREEN	3.50mm
10.	NGR-KW-010	ISHAPA	ORO	KWARA	GREEN	3.10mm
11.	NGR-KW-011	ISHAPA	OFFA	KWARA	GREEN	3.35mm
12.	NGR-NG-012	EMAGI	BIDA	NIGER	DEEP RED	3.60mm
13.	NGR-NG-013	EMAGI	DABBAN/ LAVUN	NIGER	RED	3.35mm
14.	NGR-NG-O14	EMAGI	MOKWA	NIGER	LIGHT RED	3.30mm
15.	NGR-NG-015	AMA	BEJI/ BOSSO	NIGER	GREEN L.V	3.50mm
16.	NGR-NG-016	AMA	PAIKO/PAIKORO	NIGER	GREEN	3.45mm
17.	NGR-NG-017	YAKUWA	KONTAGORA	NIGER	PINKISH G.L	3.20mm
18.	NGR-KD-018	YAKUWA	KUBAU	KADUNA	RED	3.33mm
19.	NGR-KD-019	BARKATATA	SANGA	KADUNA	RED	3.25mm
20.	NGR-KD-020	YAKUWA	JEMA'A	KADUNA	GREEN	3.32mm
21.	NGR-KD-021	ZOBORODO	ZARIA	KADUNA	RED	3.27mm
22.	NGR-KD-022	ZOBO	CHUKUN	KADUNA	RED	3.48mm
23.	NGR-KD-023	ZOBO	KACHIA	KADUNA	RED	3.29mm
24.	NGR-KD-024	TSENG	JABA	KADUNA	GREEN	3.36mm
25.	NGR-KD-025	ZOBO	KAGARKO	KADUNA	RED	3.31mm
26.	NGR-JG-026	BAKIN ZOBO	KAZAURE	JIGAWA	DEEP RED	3.24mm
27.	NGR-JG-027	JAN ZOBORODO	GUMEL	JIGAWA	RED	3.21mm
28.	NGR-JG-028	JAN ZOBO	KAUGAMA	JIGAWA	RED	3.29mm
29.	NGR-JG-029	FARIN ZOBO	KAZAURE	JIGAWA	GREEN	3.16mm
30.	NGR-JG-030	FARIN ZOBORODO	HADEJIA	JIGAWA	GREEN	3.48mm
31.	NGR-JG-031	BAKIN ZOBO	KAUGAMA	JIGAWA	RED	3.34mm
32.	NGR-GB-032	BAKIN ZOBO	YAMALTU-DEBA	GOMBE	DEEP RED	3.31mm
33.	NGR-GB-033	BARKATA/ GWATEN	DADIN KOWA	GOMBE	GREEN	3.28mm
34.	NGR-GB-034	JAN ZOBO	KWANI	GOMBE	RED	3.41mm
35.	NGR-FCT-035	EMAGI ZURU	YABA	FCT	DEEP RED	3.80mm
36.	NGR-FCT-036	MEGI	KUCHI GORO (AMAC)	FCT	RED	4.20mm
37.	NGR-FCT-037	AMA	DAKWA (BWARI)	FCT	GREEN	2.90mm
38.	NGR-FCT-038	ECHI	ZUBA	FCT	DEEP RED	3.70mm
39.	NGR-NS-039	OGBOMWA ZOBO	EDDO (DOMA)	NASARA WA	RED	4.00mm

40.	NGR-NS-040	ECHI ZOBO	KIYI (AKWANGA)	NASARAWA	RED	3.00mm
41.	NGR-NS-041	YAKWAN MIYA	KEFFI	NASARAWA	GREEN	3.00mm
42.	NGR-PL-042	YAKUWA	JOS	PLATEAU	RED	3.90mm
43.	NGR-PL-043	YAKUWA	JOS	PLATEAU	GREEN	3.10mm
44.	NGR-BA-044	FARIN ZOBO	TORO	BAUCHI	GREEN	3.00mm
45.	NGR-BA-045	YAKUWA/BAKIN ZOB	BAUCHI	BAUCHI	DEEP RED	3.48mm
46.	NGR-BA-046	YAKUWA/JANZOBO	TORO	BAUCHI	RED	3.34mm
47.	NGR-BA-047	FARIN ZOBO	GAMAWA/KATAGUN	BAUCHI	GREEN	3.31mm
48.	NGR-BE-048	ASHWE	GBOKO	BENUE	DEEP RED	3.28mm
49.	NGR-BE-049	ASHWE	GBOKO	BENUE	RED	4.00mm
50.	NGR-BE-050	ASHWE	YANDEV	BENUE	GREEN	4.00mm
51.	NGR-TR-051	FARIN ZOBO	ARDO KOLA	JALINGO	GREEN	3.00mm
52.	NGR-TR-052	JAN ZOBO	KARIM LAMIDO	JALINGO	DEEP RED	3.41mm
53.	NGR-TR-053	YAKWA/BAKIN ZOBO	ARDO KOLA	JALINGO	DEEP RED	3.46mm
54.	NGR-KG-054	AGOLO	ANKPA	KOGI	LIGHT RED	4.00mm
55.	NGR-KG-055	AGOLO	ANKPA	KOGI	RED	4.00mm
56.	NGR-SK-056	YAKUWA	SOKOTO	SOKOTO	DEEP RED	3.29mm
57.	NGR-SK-057	JAN ZOBO	SOKOTO	SOKOTO	RED	3.16mm
58.	NGR-KT-058	YAKUWA	KATSINA	KATSINA	DEEP RED	3.48mm
59.	NGR-KT-059	YAKUWA	KATSINA	KATSINA	GREEN	3.34mm
60.	NGR-KB-061	YAKUWA	BIRNIN KEBBI	KEBBI	DEEP RED	3.31mm

Note: * Values are means of the seeds measured in millimetre**.**

Table2: Predominant calyx colours among the accessions collected

	Calyx colours				
	Green	Red	Deep Red	Others	Total
No. of Accession	25	19	12	4	60
Calyx colour (%)	41.7	31.7	20.0	6.7	100.1

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GENOTYPES X TREATMENT X CONCENTRATION INTERACTION AND CHARACTER ASSOCIATION OF MAIZE (*ZEA MAYS* L) UNDER ARBUSCULAR MYCORRHIZAL FUNGI AND *STRIGA LUTEA* LOUR

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ABSTRACT

Screen house and field experiments were carried out between 2007/08 and 2008/09 in striga endemic zones of Southern Guinea Savanna of Nigeria. The study aimed at estimating genotype x treatment x concentration x mycorrhiza interaction and to assess the characters association for four quality protein maize genotypes under striga artificial infestation and arbuscular mycorrhizal fungi inoculation. A factorial combination was laid out in 4x6x4x4 arrangements with three replications. The striga and yield related traits were evaluated according to the standard procedure. All the striga traits showed highly significant differences at the genotypic (D), treatment (C) and CxD interaction level in three locations. The striga emergence count at 8 and 10 weeks after planting (WAP), plant stand, stalk lodging and root lodging were highly significant at the concentration (A), mycorrhiza (B) and at AxB interaction level in screen house and Temidire. Where as, in Farm settlement, striga damage rating at 10 WAP were non-significant at concentration, mycorrhiza, and AxB interaction level, while stalk lodging was non-significant at the concentration level. The striga and yield related traits were highly significant at the genotype, treatment, concentration, mycorrhiza

and their interaction levels for screen house and Farm settlement, but non-significant for grain yield at AxBxCxD interaction and stalk rot at concentration level in Temidire. However, genetic improvement of traits, selection based on characters association and high yield genotype should be considered in breeding to improve maize production.

Key words: Maize genotypes, mycorrhiza, striga, traits.

INTRODUCTION

Maize is one of the world's most widely grown cereals with every part including the grains, leaves, stalks, tassels, roots of great economic value. It constitutes a major ingredient in home cooking and many industrialized food products in many regions of the world (Edmeades *et al*., 1992; Olawuyi *et al*., 2010). Several varieties of maize were grown by farmers with different combinations of desirable traits. It is important to consider selection of distinct maize varieties in breeding so as to satisfy their specific uses (Menkir *et al*., 2006).

The infestations of Striga parasitic weeds have caused a serious problem in maize production, causing large crop losses in subtropics and tropics. The incidence and severity of *Striga lutea* parasitizing maize are higher in the Southern Guinea Savanna (SGS) of Nigeria (Olakojo and Olaoye, 2003). The daily lives of 100 millions of people in Africa are negatively affected by their damaging effects (Olakojo and Kogbe, 2007; Sata *et al*., 2003). The small seed size, viability within the soil over a long period of time and prolific reproductive capacity of striga render elimination of established weeds very difficult (Parker and Riches, 1993).

Arbuscular mycorrhizal fungi (AMF) are bioinoculant and biocontrol agent which play major role in nutrient cycling, plant growth and increase productivity without harming the environment (Odebode, 2005; Olawuyi *et al*., 2012). It significantly reduced the number of *S. hermonthica* infesting a tolerant sorghum variety and improved the growth (Weber *et al*., 1993). AMF also reduced the cost of inorganic fertilizers which are expensive for farmers to afford and discourages the application of chemical herbicides, some of which are non-biodegradable and toxic to soil (Sunita *et al*., 2011; Olawuyi *et al*., 2011).

The genetics of agronomic related traits of different crops have been reported (Ajmal *et al*., 2009; Adeniji *et al*., 2011), But the interactions of maize genotypes with treatments, AMF and concentration under *S. lutea* infestation has not been studied. Also, there are paucity of information on molecular approach to establish genomic relationship among the maize genotypes and AMF. Therefore, this study aimed at investigating the effect of striga-host plant interaction on some morphological and striga-related traits in maize under infestation of *S. lutea* and AMF.

MATERIALS AND METHODS

Four maize genotypes (ILEI-OB, ART-98-SW4-OB, ART-98-SW5-OB and ART-98-SW6-OB) sourced from the germplasm collection of the Institute of Agricultural Research and Training (IAR&T) Ibadan, Nigeria was used in this study. AMF species inoculated (*Glomus mosseae, G.clarum, G.deserticola* and *Gigaspora gigantea*) were collected from soil biology unit of the department of Botany, University of Ibadan, Nigeria. They were multiplied in a screen house pot culture and identified based on spore size, hyphae, colour, different wall

types and reaction to Melzer's solution according to the standard procedure. Viable *S. lutea* seed obtained from harvested striga in IAR&T was prepared according to the method described by Berner *et al*. (1997).

Screen house trials were conducted in IAR&T, while experimental field locations at Temidire and Farm settlement, both in Eruwa are striga endemic zones in Southwestern Nigeria. The treatments were factorially combined in a 4x6x4x4 arrangement with three replications. Concentration levels represent the main plot, while infestation and genotypes represent sub-plots. A complete randomized design was used in screen house trials experiment, while randomized complete block design was adopted in the field experiments.

The AMF multiplied in pot culture consisted of a mixture of soil, spores and root fragments, and was applied at the rate of 12.5g, 25g and 50g per plant at the depth of 4cm in soil, while the control were the untreated plants. Viable *S. lutea* seed obtained from harvested striga in IAR&T was prepared according to the method described by Berner *et al*. (1997). 86g of striga seed was mixed with 478.6g of sieved fine sand in order to enhance uniformity. Each pot was infested with 10.4g of striga, two weeks before planting to allow pre-conditioning. Two seeds of maize were planted per 10kg plastic pot (20 cm diameter and 30cm deep) filled with sterilized soil, and each was thinned to one per pot after two weeks. Maize planted on the field was done on four-row plots of 3m x 5m. Two maize seeds were planted per hill at a spacing of 75 x 50cm under artificial infestation of about 44,000 germinable striga seed per hill. This was done 14days before the planting of maize so as to allow striga, which is endemic on the plot to condition itself to the new environment. Each entry was planted to a corresponding uninfested plot as control experiment. The corresponding uninfested plot was planted directly opposite the infested plot of about 1m in between the two. The infested plots are those inoculated with striga seeds artificially, while uninfested plots were not inoculated, but may be naturally infested by striga due to the endemic nature of the soil. All agronomic practices were duly carried out.

PCR was used to assay the specificity of primers; ARCH1311, ACAU1660, LETC 1670, GLOM1310, GLOM5.8R and GIGA 5.8R and were tested with the roots of the maize genotypes colonized by *G. mosseae*, *G. clarum*, *G. gigantea* and *G. deserticola*. Set 1 comprised the reverse specific primers (GLOM 5.8R, GIGA 5.8R) in combination with ITS1F, while set 2 contained the forward specific primers (ARCH 1311, ACAU1660, LETC1670) combined with ITS4. The primers amplify DNA fragments from 5.8S, ITS and 18S ribosomal DNA genes deduced from selected reference sequences were obtained from public data bases. A fragment of approximately 1200bp of rDNA was amplified with universal primers NS5 and ITS4. Additional reactions with single primer pairs were performed to determine which of the primers showed a true positive reaction so as to obtain sufficient products for subsequent restriction analysis.

Data recorded for striga related parameters, growth, agronomic and yield characters of maize include;. Striga damage ratings, striga emergence count, plant stand, stalk lodging, root lodging, plant height, grain yield, field weight Data were analyzed with Statistical Analysis System SAS(1992) to compute analysis of variance (ANOVA) using General Linear Model, while means were separated using DMRT test at 5% level of probability.

RESULTS

The result of Table 1 shows that priming sites tested were found to match the respective primer sequences of colonized fungi on maize genotypes. *G. mosseae* gave true positive reaction + with GLOM1310, weak positive reaction (+) with GLOM 5.8R and too weak positive (++) reaction with GIGA 5.8R. All the forward specific primers ARCH1311, ACAU1660, LET1670, (control) produced negative reactions with all the AM Fungi (Table 4). Only *G. clarum*, for ILE1-0B showed true positive reactions with GLOM 5.8R and GLOM1310 primers, while *G. gigantea* colonizing ILE1-0B, ART-98-SW4-0B, ART-98-SW5-0B and ART-98-SW6-0B produced true positive reactions with GIGA5.8R primer. LETC 1670 primer was found to produce true positive reaction with *G. deserticola c*olonizing ILE1-0B, ART-98-SW4-0B, ART-98-SW5-0B and ART-98-SW6-0B maize genotypes. *G. mosseae* and *G. clarum* colonizing ART-98-SW4-0B, ART-98-SW5-0B and ART-98-SW6-0B maize genotypes also produced true positive results with GLOM5.8R and GLOM1310 primers compared to *G. deserticola* and *G. gigantea* (Table 1). Similar observation was reported by Redecker *et al*. (1997) and Redecker (2000).

There were highly significant differences ($P< 0.05$) in growth and yield performance of maize genotypes under striga and mycorrhizal interactions (Table 2). Highest plant height of (117.85cm and 133.67cm) at 8WAP and 10WAP was produced by ART-98-SW5-0B maize genotype under the inoculation of *G. clarum*, while uninoculated (control) was the least for ILE1-0B genotype (66.95cm and 70.17 cm) at 8WAP and 10WAP respectively (Table 2). The grain yield and field weight were highest in ART-98-SW5-0B genotype inoculated with *G. clarum* (4.25 t/ha and 54.9 t/ha) respectively, while the lowest yield was produced by uninoculated (control) (1.5l t/ha and 18.56t/ha). There are wide variations among the genotypes for these agronomic characters. The genotype and treatment effects were highly significant ($P<0.01$) for striga emergence count, striga syndrome rating at 8WAP and 10WAP, Plant stand, stalk lodging and root lodging in all the locations. In screen house (Table 3) and Temidire Eruwa (Table 4) evaluations, first and second order interactions of concentration x genotypes (AxD), concentration x treatment (AxC), concentration x mycorrhiza (AXB), mycorrhiza x genotypes (BxD), mycorrhiza x treatment (BxC), concentration x treatment x genotypes (AxCxD), concentration x mycorrhiza x genotypes (AxBxD), concentration x mycorrhiza x treatment (AxBxC), mycorrhiza x treatment x genotypes (BxCxD), concentration x mycorrhiza x treatment x genotype (AxBxCxD) interactions were highly significant ($p<0.05$) for striga emergence count at 8WAP and 10WAP, plant stand, stalk lodging and root lodging except striga syndrome rating at 8WAP and 10WAP at ($P< 0.01$). The treatment x genotype (CxD) interaction was significant for all the striga related traits in Tables 3 and 4.

In farm settlement, the first and second interactions of treatment x genotype (CxD) and mycorrhiza x genotype (BxD) differed significantly from one another with respect to striga syndrome rating at 8WAP and 10WAP, plant stand, stalk lodging and root lodging, while concentration x mycorrhiza (AXB) was significant for striga syndrome rating at 8 WAP, striga emergence count at 8 WAP and 10WAP, plant stand, stalk lodging and root lodging. Treatment x genotype (CxD) interaction was also significant ($P\leq0.05$) for striga syndrome rating at 8WAP and 10WAP, plant stand, stalk lodging and root lodging while, the interaction was not significant for striga emergence count at 8WAP and 10WAP (Table 5). Mycorrhiza x treatment (BxC) interactions was significant for plant stand, stalk lodging, striga count 8WAP and root lodging, while interactive effects of concentration x genotype (AxD), concentration

x treatment (AxC) concentration x treatment x genotype (AxCxD), concentration x mycorrhiza x genotype (AxBxD), concentration x mycorrhiza x treatment (AxBxC), mycorrhiza x treatment x genotype (BxCxD) and concentration x mycorrhiza x treatment x genotype (AxBxCxD) were significantly different for plant stand, stalk lodging and root lodging (Table 5). The concentration (A) of inocula in Eruwa farm settlement was significant for striga emergence count at 8WAP and 10WAP, plant stand, root lodging, and striga syndrome rating at 8WAP, while the influence of mycorrhiza was significantly different ($P<0.05$) for all the striga related characters except striga syndrome rating at 10 WAP (Table 5).

DISCUSSION

The positive response of ILE1-0B to *G. clarum*, showing true positive reactions with GLOM 5.8R and GLOM1310 primers confirms the excellent performance of *G. Clarum* as similarly observed by Redecker *et al*. (1997) and Olawuyi *et al.* (2010). LETC 1670 primer which was also found to produce true positive reaction with *G. deserticola c*olonizing ILE1-0B, ART-98-SW4-0B, ART-98-SW5-0B and ART-98-SW6-0B maize genotypes *c*onfirms its performance. Reduction in plant height of ILE1-OB and ART-98- SW4-OB could be associated with striga infestation as similarly reported by Olakojo *et al*. (2001) and Badu-Apraku *et al*. (2008) on other maize varieties. The highly significant level of both treatment and genotype effects recorded for most of the traits considered contributed to good yield components in all the three locations as earlier reported by Olakojo *et al.* (2001) and Olakojo (2004), while significant differences in genotypic interactions could be an indication of high genetic diversity in their backgrounds.

However, the positive influence of the mycorrhiza fungi and combination of all factors in the treatment also contributed to the performance of striga and yield related traits especially in Temidire which seems to be the most endemic area of striga infestation in the study. The effects of concentration solely or in combined interactions with other factors were not significant for striga damaged ratings in screen house and Temidire compared to Eruwa field experiment.

CONCLUSION

For genetic improvement of traits, selection based on characters association and high yield genotype should be considered in breeding to improve maize production.

Table 1: Variability in maize as influenced by AMF and specificity of primers assayed by nested PCR.

Maize genotypes	AM fungi	ARCH1311	ACAU1660	LETC1670	GLOM5.8R	GLOM1310	GIGA 5.8R
ILE 1 -0B (+)(+)	*G. mosseae*	-	-	-	(+)	+	
	G. clarum	-	-	(+)	+	+ (+)	
	G. gigantea	-	(+)	-	(+)	+ (+)	
	G. deserticola	(+)	-	+	(+)	- (+)(+)	
ART-98.SW 4-0B (+)	*G. mosseae*	-	-	-	+	+	
	G. clarum	-	-	(+)	+	+ (+)	
	G. gigantea	-	(+)(+)	-	(+)(+)	(+) +	
	G. deserticola	(+)	-	+	(+)	-	

(+)(+)						
ART-98.SW 5-0B (+)	*G. mosseae*	-	-	-	+	+
	G. clarum	-	-	(+)	+	+
(+)						
	G. gigantea	-	(+)	-	(+)	(+)
+						
	G. deserticola	(+)	-	+	(+)	-
(+)						
ART-98.SW 6-0B (+)	*G. mosseae*	-	-	-	+	+
	G. clarum	-	-	(+)	+	+
(+)						
	G. gigantea	-	(+)	-	(+)	(+)
+						
	G. deserticola	(+)	-	+	(+)	-
(+)						

Reactions were counted positive when products of the expected size were consistently present. All forward primers were tested in combination with ITS4, the reverse primers (R) with ITS1F.

(+) weak positive reactions, + positive reactions, **(+)(+)** two weak positive reactions

Table 2 Growth and yield performance of maize genotypes as influenced by mycorrhiza species.

Mycorrhiza species	Maize Genotypes															
	ILE 1-0B				**ART-98-SW4-0B**				**ART-98-SW5-0B**				**ART-98-SW6-0B**			
	Plant (cm) 8WAP 10WAP	**Height**	**Grain Yield (t/ha)**	**Field Weight (t/ha)**	**Plant (cm) 8WAP 10WAP**	**Height**	**Grain Yield (t/ha)**	**Field Weight (t/ha)**	**Plant (cm) 8WAP 10WAP**	**Height**	**Grain Yield (t/ha)**	**Field Weight (t/ha)**	**Plant (cm) 8WAP 10WAP**	**Height**	**Grain Yield (t/ha)**	**Field Weight (t/ha)**
Glomus mosseae	84.82d 101.26a	92.30d 111.12a	2.13d 3.00a	35.75d 39.97a	89.21d 108.46a	108.61d 117.23a	2.80b 3.15a	38.12d 40.91	110.35c 117.85a	112.21d 125.43c	3.30d 4.25a	43.45d 54.91a	102.32d 112.52a	117.93d 122.44a	3.10c 3.43a	40.18d 44.63a
Glomus clarum	88.36c 95.48b	96.30s 103.62b	2.84c	37.35c	93.72c 102.87b	113.75c	2.92b	39.85c	113.28b	128.46b 83.54e	3.52c	44.88c	106.75c	106.75c	3.23b	41.84c
Gigaspora gigantea	66.95e	70.17e	2.91b	37.84b	68.47e	114.29b	3.05a	40.11b	114.72b		3.85b	45.88b	110.94b	110.94b	3.36b	42.50b
Glomus deserticola																
Control			1.51e	18.56e		75.02e	1.55e	20.35e	75.17d		2.00e	25.87e	71.88e	71.88e	1.88d	22.95e

Each value is the mean for 3 replicates. Means with the same letter in the same column are not significantly different at P< 0.05 using Duncan's Multiple Range Test

(DMRT).

WAP-Weeks after planting

Table 3: Interactions of Genotype x Treatment x concentration on striga related characters in maize genotypes as influenced by mycorrhiza fungi under striga infestation in screen house experiment

Source of variation	df	Striga damage rating 8WAP	Striga damage rating 10WAP	Striga emergence count 8WAP	Striga emergence count 10WAP	Plant stand	Stalk lodging	Root lodging
Replicate	2	1.98	2.54	12.35	10.69	25.00	16.65	20.34
Concentration (A)	2	0.01^{ns}	0.02^{ns}	71.41**	53.95**	1.63**	4.52**	11.04**
Mycorrhiza (B)	3	0.02^{ns}	0.03^{ns}	22.48**	17.46**	21.74**	34.35**	34.47**
Treatment (C)	5	21.47**	27.29**	70.31**	66.02**	42.79**	24.52**	27.34**
Genotype (D)	3	5.93**	7.62**	37.06**	32.07**	74.99**	49.95**	61.03**
A X D	6	0.05^{ns}	0.07^{ns}	2.74**	1.03**	1.44**	1.47**	0.89**
A XC	10	0.01^{ns}	0.01^{ns}	3.25**	4.76**	3.23**	2.05**	3.21**

A X B	6	0.01^{ns}	0.01^{ns}	47.48**	38.20**	1.83**	1.29**	2.22**	1.56**
C X D	15	0.81**	1.28**	7.37**	6.40**	4.31**	2.16**	3.43**	
B X D	9	0.06^{ns}	0.06^{ns}	1.28**	1.39**	2.71**	5.57**	2.45**	
B X C	15	0.01^{ns}	0.01^{ns}	2.45**	1.64**	3.75**	1.76**	0.57**	
A X C X D	30	0.01^{ns}	0.01^{ns}	0.52**	0.35**	0.50**	0.58**	0.50**	
A X B X D	18	0.05^{ns}	0.07^{ns}	0.50**	0.83**^{s}	0.92**	0.69**	0.61**	
A X B X C	30	0.01^{ns}	0.01^{ns}	1.23**	1.20**	0.89**	1.70**	0.79**	
B X C X D	45	0.01^{ns}	0.02^{ns}	0.45**	0.78**	0.83**	0.79**	0.73**	
A X B X C XD	86	0.01^{ns}	0.02^{ns}	0.27**	0.34**	0.58**	0.75**	0.46**	
Error	566	0.19	0.25	0.08	0.03	0.00	0.00	0.00	
Total	849								

*, ** significant at P≤ 0.05 and P≤ 0.01 respectively

ns non – significant at P≤ 0.05 and P≤ 0.01 respectively

WAP Weeks after planting

Table 4: Interactions of Genotype x Treatment x concentration on striga related characters of maize genotypes as influenced by mycorrhiza fungi under striga infestation in Temidire Eruwa

Source of variation	df	Striga damage rating 8WAP	Striga damage rating 10WAP	Striga emergence count 8WAP	Striga emergence count 10WAP	Plant stand	Stalk lodging	Root lodging
Replicate	2	2.05	2.61	10.46	9.32	11.81	14.96	10.45
Concentration (A)	2	0.01^{ns}	0.03^{ns}	1.39**	1.29**	2.82**	1.39**	0.14**
Mycorrhiza (B)	3	0.01^{ns}	0.03^{ns}	22.34**	17.49**	13.92**	11.32**	7.04**
Treatment (C)	5	21.96**	27.96**	60.56**	65.44**	25.79**	25.94**	30.44**

Genotype (D)	3	6.15**	7.84**	31.37**	27.96**	35.42**	42.48**	31.34**	
A X D	6	0.06^{ns}	0.08^{ns}	0.41**	1.33**	0.41**	1.23**	0.09**	
A XC	10	0.01^{ns}	0.01^{ns}	0.45**	0.78**	1.87**	0.74**	0.87**	
A X B	6	0.01^{ns}	0.02^{ns}	0.55**	0.28**	1.28**	0.90**	0.62**	
C X D	15	0.84**	1.29**	7.67**	6.29**	5.34**	4.27**	6.22**	
B X D	9	0.06^{ns}	0.08^{ns}	2.20**	2.11**	1.54**	2.81**	1.71**	
B X C	15	0.01^{ns}	0.01^{ns}	5.04**	5.19**	3.48**	1.17**	1.98**	
A X C X D	30	0.01^{ns}	0.02^{ns}	0.28**	0.40**	0.76**	0.65**	0.48**	
A X B X D	18	0.06^{ns}	0.08^{ns}	0.32**	0.25**	0.51**	0.88**	0.78**	
A X B X C	30	0.01^{ns}	0.01^{ns}	0.32**	0.42**	1.17**	0.98**	0.73**	
B X C X D	45	0.01^{ns}	0.02^{ns}	0.79**	0.85**	0.73**	0.68**	1.16**	
A X B X C XD	90	0.01^{ns}	0.02^{ns}	0.24**	0.34**	0.56**	0.60**	0.74**	
Error	576	0.19	0.25	0.00	0.00	0.00	0.00	0.00	
Total	863								

*, ** significant at P≤ 0.05 and P≤ 0.01 respectively

ns non – significant at P≤ 0.05 and P≤ 0.01 respectively

WAP Weeks after planting

Table 5: Interactions of Genotype x Treatment x concentration on striga related characters in maize genotypes as influenced by mycorrhiza fungi under striga infestation in farm settlement Eruwa.

Source of variation	df	Striga damage rating 8WAP	Striga damage rating 10WAP	Striga emergence count 8WAP	Striga emergence count 10WAP	Plant stand	Stalk lodging	Root lodging
Replicate	2	1.728	1.893	1.087	0.870	5.320	5.821	2.677
Concentration (A)	2	1.038*	0.177 ns	4.37**	3.52**	0.66**	0.09ns	0.39*

Mycorrhiza (B)	3	3.124**	0.238 ns	9.67**	8.30**	6.55**	5.51**	6.52**	
Treatment (C)	5	24.553**	25.459**	2.78**	1.78**	5.48**	3.99**	3.55**	
Genotype (D)	3	5.185**	5.68**	3.24**	2.61**	15.96**	17.46**	8.03**	
A X D	6	0.05 ns	0.02 ns	0.07 ns	0.10 ns	0.35*	0.60**	0.18*	
A XC	10	0.14 ns	0.12 ns	0.07 ns	0.07 ns	0.43*	0.38**	0.99**	
A X B	6	0.96*	0.20 ns	9.16**	9.56**	1.61**	0.92**	0.35*	
C X D	15	0.85**	0.97**	0.27 ns	0.34 ns	0.86**	0.90**	1.23**	
B X D	9	0.73*	0.87*	0.26 ns	0.42 ns	0.93**	0.68**	0.77**	
B X C	15	0.35 ns	0.12 ns	0.60*	0.38 ns	1.10**	0.99**	0.86**	
A X C X D	30	0.02 ns	0.02 ns	0.07 ns	0.10 ns	0.36**	0.12*	0.30**	
A X B X D	18	0.05 ns	0.02 ns	0.24 ns	0.31 ns	0.21*	0.30**	0.34**	
A X B X C	30	0.13 ns	0.14 ns	0.21 ns	0.15 ns	0.55**	0.51**	0.33**	
B X C X D	45	0.12 ns	0.22 ns	0.08 ns	0.15 ns	0.43**	0.54**	0.32**	
A X B X C XD	86	0.02 ns	0.01 ns	0.10 ns	0.12 ns	0.26**	0.24**	0.20**	
Error	566	0.21	0.25	0.28	0.24	0.08	0.08	0.07	
Total	849								

*, ** significant at P≤ 0.05 and P≤ 0.01 respectively

ns non – significant at P≤ 0.05 and P≤ 0.01 respectively

WAP Weeks after planting

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VARIABILITY PATTERN OF MORPHOLOGICAL TRAITS AMONG *SOLANUM MACROCARPON* L ACCESSIONS.

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ABSTRACT

Morphological variation was investigated among 13 accessions of *Solanum macrocarpon* L. *sourced* from Africa and Asia, to quantify variation, identify traits of high discriminatory ability and donor parents for single or multiple traits and best performer for enhancement and commercialization. Field experiments took place during 2009 thorough 2010. Two methods of multivariate analyses (Principal Component Analysis and Cluster analysis) were used to analyze the data set. The first principal component axis showed maximum variability and depicts high variation for receptacle pigmentation (purple). Ordination on the biplot and grouping on the phylogenetic tree correspond to moderate variability and phenotypic plasticity in this specie, and geographic heterogeneity. Receptacle pigmentation (purple) contributed to cluster constellation. There was no association between accessions and geographical origin. Pigmentation (purple) and fruit colour distribution (stripped) could be used by potential (plant breeders and seed companies) as morphological markers in breeding works. High heritability and heterosis should be expected in hybridization in favour receptacle pigmentation and fruit colour distribution (stripped) traits.

Keywords: *Solanum macrocarpon*, Receptacle pigmentation, Ordination, Diversity, Cluster analysis,

INTRODUCTION

The common name eggplant includes three closely related cultivated species that belong to subgenus Leptostemonum: *Solanum melongena* L., brinjal eggplant or aubergine, *Solanum aethiopicum* L., scarlet eggplant; and *Solanum macrocarpon* L., gboma eggplant (Daunay *et al.*, 2001a). The latter two species result by domestication process that occurred in Africa, starting from two wild ancestors, *Solanum anguivi* and *Solanum dasyphyllum*, (Lester, 1998; Lester and Niakan, 1986). *S. macrocarpon* (2n = 24) (Gboma eggplant) is classified in the section Melongena; series Macrocarpa Bitter, it is cultivated widely throughout tropical Africa, especially in humid regions. The glabrous leaves are important green vegetables, and fruits are consumed fresh. Many cultivars are robust, perennial with deeply lobed leaves; other cultivars from West Africa are smaller and much branched with smaller and often simple leaves and young shoots (Shippers, 2000). Fruits ranged from 3 to 12 cm in diameter, spherical or depressed, usually green, whitish or purple or with lighter markings when ready for eating, but at physiological ripeness they turn yellow or orange or brown, and the surface may crack (Duanay et al., 2001a, b).

In diversity studies some morphological characters are more useful than others. Heywood (1967) had noted that for a morphological trait to be of taxonomic importance they should meet at least

four criteria: (1) they should vary less within the supposed group than between groups; (2) they should be genetically controlled; (3) their exposure should not be significantly modified by environment; and (4) characters examined should exhibit a pattern that correlates with the pattern of variation of other characteristics. Genetic architecture of a population is generally believed to be the result of breeding system, gene flow within and between population, and prolonged selection by various natural and artificial forces. Assessment of genetic diversity in germplasm collections provides information useful for both germplasm management and breeding. It helps to identify new genetic recombination, select inbred parents for maximum heterotic response and identify materials that should be maintained to preserve maximum genetic diversity (Thormann and Osborn, 1992). These allow for establishment of core, nonredundant germplasm collections and help to guide future germplasm collection efforts.

S. macrocarpon is indigenous to Africa and has no known incompatibility with the norms and belief of communities where it is grown. It is consumed fresh with spices or boiled in stews. The importance of this crop makes it imperative to understand how much morphological variation exist within this specie and how variation could assist in conservation strategies and use in crop breeding through identification of promising accessions for enhancement and variety development. Multivariate analyses (Principal component analysis and cluster dendogram) have been used widely to measure diversity in the germplasm collections, and to assess the relative contribution of characters to total variability in germplasm collection (Baatout, 1995). A significant feature of this model is that it enables researchers to use specific attributes in gene pool for crop improvement. In this study we evaluated the extent of genetic variability among accessions of *S. macrocarpon* based on morphological traits and identify best performing accessions as donor parents for single and multiple traits

MATERIALS AND METHODS

Entries evaluated comprised of 13 accessions of *S. macrocarpon* from locations in Africa and Asia, maintained in the gene banks of AVRDC (The World Vegetable Center), Taiwan and French Institute for Agricultural Research, (INRA) Monifavet, France. The genetic stocks are homogenous for most genetic attributes. Field experiments took place at the research field of Horticultural Training Research Institute (HORTI) Arusha (Lat. 4.8°S long 3.7°E; Alt. 1290 m) with annual rainfall of 700 to 1000 mm. Soil type was clay loam with a pH of between 6.0 and 6.5. Experimental plots were laid out in a randomized complete block design with three replications. Each plot consisted of a double row plot of 7 m long and 0.75 m between rows. Seedlings were raised in multipot seedling trays for four weeks, thereafter transplanted to the sides of the ridges at 0.45 m between plants. Plants were fertilized with NPK (20-10-10) at the rate of 90 kg N/ha, 45 kg P_2O_5/ha and 45 kg K_2O/ha. Urea fertilizer was applied at the rate of 120 kg N/ha in three splits, that is, one week after transplanting, at flowering and three weeks thereafter. Ridomil WP (fungicide) was sprayed against damping off in the field at the rate of 20 g/15 L of water 12 days after transplanting. Selecron EC (insecticide) was applied 2 weeks after transplanting at the rate of 20 ml/20 L of water to control insects. The experiment was furrow-irrigated every two days for the first two weeks after transplanting, then once a week thereafter. Weeding was carried out manually and frequently with hoes to maintain weed-free plots. Every parts of the plant were sampled at all stages of growth, presumably because different parts of the genome affect different suites of traits at different times. Two-state qualitative traits, for example, presence or absence of pubescence/ prickles was coded as binary. Ordered multistate

qualitative traits were coded as series of discrete states. Morphological scoring was done according to the AVRDC and biodiversity descriptors with modifications. Traits were scored at flowering, during this time maximum development of vegetative parts ought to have taken place (Purseglove, 1972; Karamura and Karamura, 1995). Morphological traits were measured on fifteen plants (five plants per replicate). Traits related to colour (pigmentation gene) was scored using the standard Royal Horticultural Society colour chart. Data was submitted for two methods of multivariate analyses (Principal component analysis (PCA) and cluster analysis), using PROC-PCA procedure of SAS (1998). Dendogram was constructed, based on distance matrix, using the average linkage between group methods often aptly called unweighted pair group method of analysis (UPGMA), with squared euclidean phenotypic distance option ward's (Sokal and Michener, 1958) as grouping criteria, using SPSS version 16. 0.

RESULTS

The pattern of variation among accessions of *S. macrocarpon* returned 6 out of 17 principal axes to have recorded eigenvalues greater than 1.0. The first to third principal component axes had eigenvalue greater than 2.0 and altogether accounted for 68% of variation (Table 1). The first principal component axis had high eigenvalue (5.08) and accounted for 30% of total variation, it depicts primarily variation associated with receptacle pigmentation, which marked moderate and positive loading charged on leaf and petiole pubescence, the latter contributed negatively to variability on PC1. Other traits, flower (Plate 1), sepal and peduncle pigmentation recorded equal weights.. The second principal component axis illustrated that pigmentation on the leaf vein and leaf midrib recorded negative coefficients, though positive on PC1. While stem pigmentation and fruit apex shape showed moderate and positive weights on PC2. Interestingly, half of the total variability observed among the population was explained by PC 1 and 2 The third principal component axis accounted for additional 15% of variation unexplained by PC1 and 2, and showed high contribution of petiole pigmentation, seed colour and fruit colour at commercial ripeness to variability on this axis. They recorded moderate and positive weights, though negatively related to fruit colour distribution. The fourth principal axis explained additional 8% of the total variation, and showed discriminatory power of fruit colour at commercial ripeness and fruit colour at physiological maturity.

The biplot of PC1 by 2 (Figure 1) showed the ordination of 13 accessions of *S. macrocarpon* into four quadrants, the first quadrant accommodated four accessions (accessions 55, 53, 54 and 47) sourced from Ghana, Zimbabwe, Mauritania and Burkina Faso. With exception of accession 55 which contributed moderately to dispersion in the first quadrant, other entries showed very low contribution. Ordination in this quadrant is sequel to discriminatory ability of receptacle pigmentation. Four accessions (accessions 50, 45, 51 56) were ordered into the second quadrant, and are fairly equal distant from one another, the spread of accessions in this quadrant showed discriminatory power of leaf lobbing and leaf mid rib pigmentation. Two accessions (accessions 46 and 56) from unknown location and Cameroun are located in the third quadrant, ordination in this quadrant is associated with discriminatory power of petiole pigmentation and fruit colour at physiological maturity (Plate 2). In the fourth quadrant accession 57 was widely separated from the others, traits of discriminatory power in the fourth quadrant are fruit apex shape; fruit colour at commercial ripeness and stem pigmentation.

Morphological traits were important in the assignment of entries into three distinct clusters at 20% distance (Figure 2). The phylogenetic tree showed that first and second clusters had 5 and 4 members each, while cluster 3 comprised 4 accessions. Cluster 1 was divided into two sub clusters ('a' and 'b'), sub cluster 'a' comprised accessions 53 and 54, accessions 50 and 51 to sub cluster 'b', they are tightly grouped and linked to accessions 52. Members of cluster 1 are related for purple pigmentation on the petiole, sepals, peduncle, flower colour and fruits colour (purple) at commercial ripeness. On the other hand, accessions 50 and 51 are characterized by strong leaf lobbing, pigmented (purple) leaf vein and petiole. In addition to that, fruits are characteristically cream with uniform distribution at commercial harvest. The second cluster comprised 4 accessions; accessions 47 and 48 are most related for lobed leaves and non-pigmented petiole, pigmented sepals (purple), pigmented fruits (purple) at commercial ripeness and circular fruits. In general members of second cluster are similar for cream fruits at commercial ripeness and are fairy grooved fruits. The third cluster comprised accession 56 and 57; they are similar for pigmented petiole (purple) and non-pigmented sepals, receptacle, peduncle and circular fruits. The spread of accessions in the biplot is consistent with groupings on the phylogenetic tree for accessions 45 and 55, 51 and 52, 47 and 48, and 56 and 57.

DISCUSSION

Within *S. macrocarpon* receptacle pigmentation showed high discriminatory ability, this observation mirrored conclusion reached by Lester and Niaken (1998) and Prohens et al. (2005). This trait could be of importance to curators to focus on greater part of their collection for this trait. In addition, plant breeders and seed companies may use this trait as morphological marker during selection purposes. Ordination on the biplot and grouping on the phylogenetic tree correspond to low and moderate variability and phenotypic plasticity in this specie. Low variability among *S. macrocarpon* lends weight to findings reported by Bukenya and Hall (1987) and Polignano et al. (2009) based on agronomic and fruit quality traits. A low variability among *S. macrocarpon* may be associated with genotypic difference and environmental factors. In another study Bukenya and Caraso (1994) noted that accessions of *S.macrocarpon* are less morphologically diverse compared to *S. aethiopicum* and *S. melongena*. Grouping on the phylogenetic tree displayed geographic heterogeneity, entries from same or close geographical locations are dispersed among others. The lack of clustering according to geographic provenance implied that accessions from different locations in Africa and Asia are not significantly different. A similar trend was recorded among Uganda, Indonesia and European *Solanum scabrum* (Olet, 2004). Variability and similarity among *S. macrocarpon* beyond geographical limit is similar to previous reports of Polignano et al. (2009). For selection purposes emphasis should be at the population level rather than geographical location. Phenotypic plasticity was evident among accessions in this specie; this is consistent with overlapping morphological traits. In this investigation twelve accessions were sourced from Africa and one accession (accession 45) from Malaysia, though the latter grouped with accession 55 from Ghana. There is a possibility that seeds of accession 45 might have been transported from West Africa during the transhumance trade in the 19th century or during exchange of germplasm between Africa and Asia. However, molecular marker technique (AFLP and SSR) may be required to substantiate this finding..

Reference to the grouping on the phylogenetic tree, accessions 53 and 54 showed relatedness for brown seed colour, cream fruit colour at commercial harvest, pigmented (purple) stem and receptacles and violet petals. These accessions could be selected as donor parents for single or multiple traits in any breeding program, and as morphological marker for intellectual property

right. On the other hand strong leaf lobbing, violet petals and grey seed colour were best in accessions 50, 51 and 52. Accessions 47 and 48 showed cream seed colour, this in contrast to accessions 53 and 54. Accessions 45 and 55 are related for brown seed colour and non-pigmented stem and receptacle; they could be selected as a donor parent for these traits. Still in cluster 3, accessions 46 and 49 had green fruit epidermis at commercial ripeness; they turned orange in colour at physiological maturity. Fruit pigmentation (orange) is a noticeable trait (among *S. macrocarpon)* that showed differences within *Solanum* species (Collonnier et al., 2001; Kashyap et al., 2003; Nothmann, 1986; Daunay et al., 2001b; Frary et al., 2007). The colour differences in the fruit epidermis is basically due to two color pigments' and their effects on appearance are controlled by more than one gene (Nothmann, 1986; Frary et al., 2007). Pigmentation (purple) on the receptacle contributed to cluster constellation. In addition to receptacle pigmentation (purple), fruit colour distribution (stripped) are located in different clusters, high heritability and heterosis should be expected in subsequent generations provided intraspecific hybridization was conducted targeting these traits. This study demonstrated discriminatory power of receptacle pigmentation (purple) and ability to delimiting accessions in the specie for morphological characterization and conservation.

Plate 1. Flower pigmentation pattern in *S. macrocarpon*

Plate 2: Variation for fruit colour at commercial harvest (green, cream, purple) and physiological maturity (orange or brown) and fruit cross section among *S. macrocarpon.*

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Table 1: Eigen values, variation and vectors for the first six principal components axes for 17 morphological traits among 13 accessions of *Solanum macrocarpon* in Tanzania

Traits	Prin 1	Prin 2	Prin 3	Prin 4	Prin 5	Prin 6
Stem pigmentation	0.17	0.39	0.02	0.02	-0.04	0.41
Leaf pubescence	**-0.34**	0.07	0.08	0.11	0.51	0.03
Leaf lobbing	0.20	-0.14	0.25	-0.36	0.44	0.12
Leaf vein pigmentation	0.12	**-0.46**	0.13	0.07	0.05	0.18
Leaf mid rib pigmentation	0.13	**-0.43**	0.02	-0.04	-0.06	0.42
Petiole pigmentation	-0.11	-0.13	**0.54**	-0.10	-0.08	-0.24
Petiole pubescence	**-0.34**	0.07	0.08	0.11	0.51	-0.03
Flower pigmentation	0.31	0.04	0.14	0.19	0.17	-0.28
Sepal pigmentation	**0.34**	0.20	-0.01	0.12	0.14	0.43
Receptacle pigmentation	**0.36**	0.13	0.11	0.23	0.21	0.22
Peduncle pigmentation	**0.34**	0.03	0.25	0.03	0.27	-0.33
Fruit apex shape	-0.10	**0.34**	0.09	-0.10	-0.06	0.12
Fruit colour at commercial ripeness	-0.18	0.10	**0.39**	0.43	-0.20	0.09
Fruit colour at physiological maturity	-0.13	-0.31	-0.08	0.51	-0.009	0.13
Fruit cross section	**0.30**	0.26	-0.20	-0.11	0.04	-0.08
Fruit colour distribution	0.17	0.02	-0.33	0.48	0.22	-0.27
Seed colour	0.15	0.20	0.44	0.17	-0.12	0.07
Eigen value	5.09	3.77	2.62	1.63	1.29	1.04
Proportion	0.30	0.22	0.15	0.10	0.07	0.06
Cumulative (%)	0.30	0.52	0.68	0.77	0.85	0.91

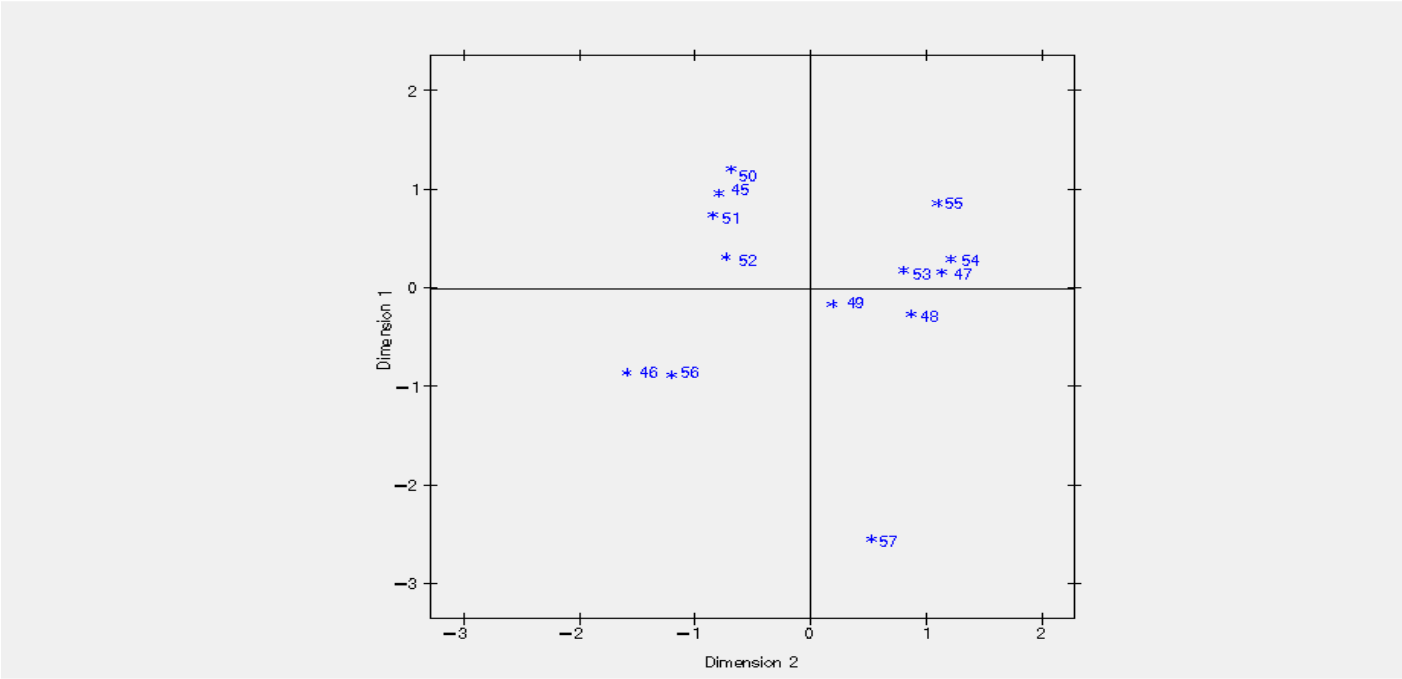

Figure 1: Plot of the first two principal components axes showing spatial distribution of 13 accessions belonging to *Solanum macrocarpon* based on morphological descriptors

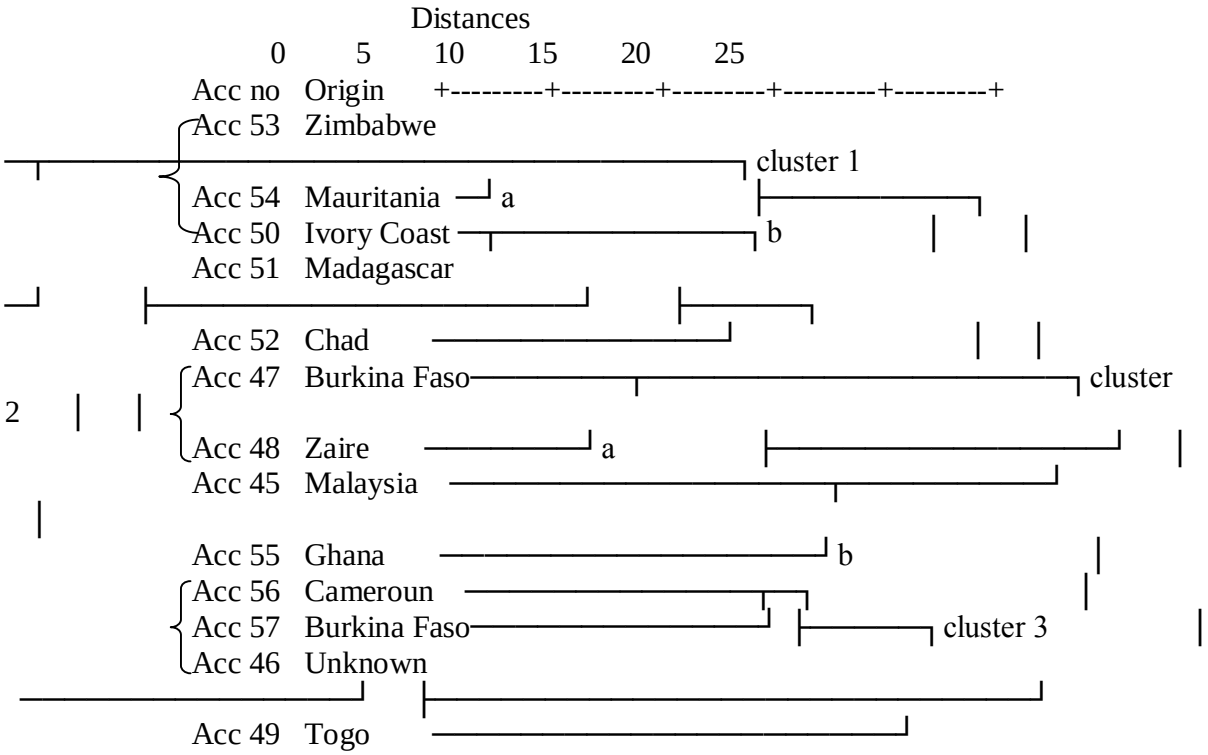

Figure 2: Phenogram produced for the 13 accessions from Solanum macrocarpon derived from UPGMA clustering of correlation coefficients for 17 morphological descriptors by squared Euclidean distance and Ward's method

PGB42

CHARACTERIZATION OF FOUR NIGERIA SESAME (SESAMUM INDICUM L.) LANDRACES USING AGRONOMIC AND MORPHOMETRIC TRAITS

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ABSTRACT
A field experiment was carried out to characterize four sesame landraces EX, Ex Sudan, Boroko local and NCRIBEN 01M in humid guinea savanna of north central Nigeria, between August and October 2012 to ascertain the diversity of the landraces using multivariate analysis. Plant height at flowering (PHF), Plant height at maturity (PHM), Height at first branch (H1B), Height at first pod (H1P) and Plant length (PL) showed significant ($P<0.001$) correlation with each other. The principal component analysis show that the first three principal component explained about 87.24% of the total variation with Height at first branch 99% , height at first pod 99%, plant height at flowering 98%, plant height at maturity 98%, number of day to maturity 95%, leave length 94% and pod length 93% as characters that contribute significantly to variations found in the sesame variaties, indicating a high variation among the sesame landraces.These collections represent a rich diversity in form and can aid selection and improvement.

Keywords: Sasame, morphology, agronomic traits, principal component, variation.

INTRODUCTION

Sesame is known to be the most ancient oil seed crop dating back to 3050-3500 BC (Bedigian and Harlan, 1986: Furat and Uzun, 2010). It is grown in tropical and subtropical areas of the world. It can set seed and yield well under fairly high temperature, it can grow in stored soil moisture without rainfall and irrigation. But continuous flooding or severe drought adversely affect sesame plants and resulted in low yield (Mensah *et al.,* 2009). Another major cause of poor yield of sesame is due to low yielding cultivars. Development of improved plant cultivars is restricted by mainly limited genetic variability. Due to narrow genetic pool it is not possible to restructure the sesame crop. It has been suggested that sesame cultivation under such degradable condition has caused serious genetic erosion for yield, where selections within the local varieties fails to respond favorably to high input managements.

Sesame is an important crop to Nigeria agriculture, it is quite extensively cultivated, it yields in relatively poor climatic condition, and it is widely used within Nigeria and is an important component of Nigeria's agricultural exports (Abubakar *et al.,* 1998). It is however, given little attention and there are relative few companies involved in the trade. As a smallholder crop, often intercropped with others, the extent of cultivation is poorly known and there is little information

on yields or productivity. For the most part the surplus crop is commercialized bulked up and exported with minimal processing limited to dry and cleaning (Azeez and Morakinjo, 2011).

The organic market for sesame is rapidly expanding. Therefore, there is the need to exploit the potential of the forest savannah transition zone for the production of improved sesame variety (Balusamy *et al.*, 1996). Since its introduction to Nigeria after the Second World War, it has been regarded as a crop of significant important compared to groundnut and other cash crop for export. (Adeyemo and Ojo, 1993).

In Nigeria, sesame is widely grown in the northern and the central part of the country as a minor crop. Since 1974, it has developed from being a crop of negligible importance to the one of the major cash earner in it area of production (viz; Nasarawa, Borno,Gombe, Benue, Kogi, Kano, Jigawa, Plateau, Yobe, Katsina state as well as the FCT Abuja (Abubakar *et al.*, 1998).
The objective of the study was to assess the phenotypic variability and traits associated with the diversity of the sesame landraces

MATERIALS AND METHODS

The four landraces were collected from National Cereal Research Institute (NCRI) Baddegi Niger State. Some of these landraces are grown by local farmers in Nigeria. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications during 2012 cropping season (July to December). The cultivated area is situated at 8˚32˙N, 8˚18˙E. It has a tropical climate with moderate rainfall (annual mean rainfall of 1100 – 1300), the temperature ranges from 20^{O} to 34^{O}. Data were collected on the plot basis; Number of days to flowering (NDF): number of days from planting to 50% flowering. Number Of days to maturity (NDM): number of days from sowing to the day when at least 50% plants had one brown pod. Plant height at flowering (cm) (PHF): height from ground level to the peak of the stem when the plant is at 50% flowering. Plant height at maturity (cm) (PHM): height from ground level to the peak of the stem. Number of pods/plant (NPP): 5 plants were picked at random per plot, number of pods counted and the average calculated. Number of branches/plant (NBPP): determined by counting number of branches on the stem. Height to 1st branch (H1B): height from ground level to the 1^{st} branch on the stem. Height of 1^{st} pods (H1P): height from ground level to the 1^{st} pods on the stem. Weight of pods/plant (g) (W0P): 5 plants were picked at random per replicate, their pods were removed, weighed and the average was calculated. Leaf length (cm) (LL): the length of five leaves from the top of the plant was measured in centimetres at peak flowering stage. 1000 seed weight (g) (1000SW): 1000 seeds per replicate was counted and weighed. Seedling length (SL): Five normal seedlings were selected at random from germination. The length between the collar region and the tip of primary shoot was measured as shoot length and the length between the collar region and the tip of primary root was measured as root length seedling length = shoot length + root length. Pod length (PL): The length of five pods from top of the Plant were measured at maturity.
First, the univariate normality was checked for 13 traits of each landrace using rank it plots. Inter correlations among traits evaluated by correlation analysis. The resulting 13 x 13 correlation was used as input for the PCA to remove the effects of scale (Johnson and Wichern, 1998). SPSS.2004 statistical package was used for the analysis of correlation and PC.

RESULTS AND DISCUSSION

Correlation analysis showed that many pairs of characters were correlated in these population (Table 1.), plant height at flowering was positively correlated with plant height at maturity (r = 0.97**), height to 1st branch (r = 0.98**), height to 1st pod (r = 0.98**), weight of pod (r =

0.74**), pod length (r = 0.89**) and ngatively corelated with number of days to flowering(r = -0.71), number of days to maturity (r = -0.94), number of pods per plant (r = -0.63) and number of branches per plant (r = -0.92). Most morphometric traits were positively correlated.This is similar to what Ercan *et al*. (2002) reported in India sesame germplasm. Some negative ccorrelation coefficients of seed yield (1000SW) and yield components observed in this study is contrary to reports of (Khan *et al*., 2001; Uzun and Cagirgan, 2001 and Sumathi *et al*., 2007). Suggesting the variability in the germplasm used.

Table 1.Correlation coefficient between morphological and agronomic traits of the sesame genotypes

	PHF	PHM	H1B	H1P	NDF	NDM	NPP	NBPP	1000SW	WOP	LL	SL
PHM	.97											
H1B	.98	.98										
H1P	.98	.98	.98									
NDF	-.71	-.74	-.72	-.73								
NDM	-.94	-.95	-.95	-.95	.73							
NPP	-.63	-.63	-.57	-.63	.44	.73						
NBPP	-.93	-.92	-.92	-.93	.62	.88	.69					
1000SW	-.13	-.12	-.05	-.07	-.03	.08	.40	-.09				
WOP	.74	.76	.72	.71	-.59	-.73	-.50	.32	.31			
LL	.14	.20	.23	.22	-.29	-.18	-.89	-.12	.25	.37		
SL	.59	.50	.53	.56	-.42	-.49	-.16	-.48	.38	.25	-.66	
PL	.89	.88	.90	.90	-.72	-.80	-.65	-.89	-.12	.62	.09	.06

PHF=Plant height at flowering,PHM=Plant height at maturity, H1B=Height at first branch,H1P=Height at first pod, NDF=Number of days to flower, NDM=Number of days to maturity, NPP=Number of pod per plant, NBPP=Number of branch per plant, 1000SW=1000 seed weght, WOP=Weight of pod, LL=Leave length , SL=Seedling length , PL=Pod length

Table 2. Principal Component Analysis of sesame landrace using morphological traits .

	PC1	PC2	PC3
Eigene value	8.492	1.599	1.251
Cumulative proportion of variation	65.319	12.298	9.623
Total variation	65.319	77.617	87.241
Characters	**Eigenvectors**		
PHF	.982	-.021	.011
PHM	.983	-.034	.073
H1B	.986	.053	.078
H1P	.986	.034	.046
NDF	-.768	-.060	-.202
NDM	-.949	.003	-.076
NPP	-.682	.478	.199
NBPP	-.939	.021	.022
1000SW	-.102	.904	.213
WOP	.747	-.125	.376
LL	.153	.170	.937
SL	.572	.648	-.413
PL	.932	.026	-.109

PHF=Plant height at flowering,PHM=Plant height at maturity, H1B=Height at first branch,H1P=Height at first pod, NDF=Number of days to flower, NDM=Number of days to maturity, NPP=Number of pod per plant, NBPP=Number of branch per plant, 1000SW=1000 seed weight, WOP=Weight of pod, LL=Leave length , SL=Seedling length , PL=Pod length

Multivariate analysis of the sesame landraces (Table2.) reveals that the first three principal components had eigen values greater than one and cummulatively accounted for 87.24% of the variation.The first PC accounted for 65.32% total variation. The second PC account for 12.3% and the third accounted for 9.62 % of the total variation.The cummulative variation of the three PC accounted for 87.24%. The high degree of variation in the first three PC axes is an indication of high degree of variation in these landraces. This is similar to the findings of (Furat and Uzun, 2010).

There are no guidelines to determine the significance or importance of a coefficient, that is, Eigen-vector (Düzyaman, 2005). However higher coefficients for a certain trait indicate the relatedness of that trait to respective PC axes (Sneath and Sokal, 1973). The variation in PC1 was mainly associated with most of the traits except seed length, leave length and 1000 seed weight, in PC2 seed length and 1000 seed weight were mainly associated while PC3 was associated with leave length . The Principal component analysis shows that plant height at flowering and maturity, height at first branch and at first pod, number of days to maturity, number of branch per plant and 1000 seed weight were among the most important descriptors which accounted for the highest phenotypic variation expressed in this germplasm collection. These descriptors were therefore found to be most useful for studying the variability of populations. It is suggested that the use of these characters will save considerable amount of time for identification of sesame germplasm.

CONCLUSION

This study provides a morpho-agronomic based classification of genetic diversity that can help breeders understand the genetic structure of Nigerian sesame landraces. The germplasm represents a valuable source of genetic diversity that is expected to be highly useful for future breeding programs. The success in genetic improvement of the crop, however, depends on the availability of genetic resources and their diversity.

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PGB43

EFFECTS OF SEED SIZE ON WEEVILS *(CALLOSOBRUCHUS MACULATES F.)* DAMAGE DURING STORAGE OF COWPEA *(VIGNA UNGUICULATA* L.WALP)

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ABSTRACT

The effects of seed size on *Callosobruchus maculatus* damage during storage of Cowpea(*Vigna unguiculata* L.walp) was investigated. The five cowpea varieties used were Aloka, Ife brown, Iron beans, Big white and Big brown. These cowpea varieties varied in size from small, medium and big size. The experimental design used was a factorial laid out in Completely Randomized Design (CRD) with three replicates. Results obtained showed that there was significant difference ($P<0.05$) in the cowpea. Among the cowpea varieties, Aloka was the least susceptible to *C. maculatus* attack with weight loss of 4.87%, the next was Ife brown with 5.79% then big brown with 9.88%, followed by Iron Beans with 10.81% and lastly Big White with 11.65%. The response of these cowpea to *C. maculatus* attack also showed that seed size significantly contributed to varietal resistance as cowpea varieties with small seed sizes (Aloka and Ife brown) were found to be more resistant to *C.maculatus* attack than the medium seed size (Big white and Iron Beans) and Big seed size (Big Brown). The result of this research has indicated that small seeded varieties of cowpea are more resistant to *C. maculatus* attack during storage and therefore can be stored by cowpea farmers over a longer period of time.

Keywords: Damage, Effect, Size, Storage, Weevils.

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp) is a pulse crop that can be grown successfully in extreme environments such as high temperatures, low rainfall and poor soils with a few inputs. Subsistence farmers in the semi-arid and sub-humid regions of Africa are the major producers and consumers of cowpea. Cowpea grain is important to the incomes of resource poor farmers as well as to the nutritional status and diets of people in West and East Africa, Latin America and the Carribean basin (Shazia *et al.,* 2006). (*Vigna unguiculata* L. Walp) has been cultivated in many countries for many centuries. It is one of the important food legume crops in the tropical and subtropical regions covering Asia, Africa, Southern Europe, Central and South America (Motshwari *et al.,* 2011). Cowpea is a crop of high valve which contributes significantly to farmers' income and dietary protein of Africans (Ogbaji and Usman, 2011). There are different varieties of cowpea all of which are essential component of cropping systems in drier regions and marginal areas of the tropics and sub-tropics. It is a drought tolerant and warm weather crop well adapted to the drier regions where other food legumes do not perform well. It fixes atmospheric nitrogen through its root nodules and grows well in poor soils with more than 85% sand low organic matter and levels of phosphorous (Motshwari *et al.,* 2011). Cowpea is a major vegetable source of protein for human consumption especially in Africa. Its seeds contain about 25% protein, making it extremely valuable in areas where many people cannot afford protein foods such as meat and fish. Cowpea is a unique dietary protein source for poor people, since this protein is one of the cheapest (Sankie *et al.,* 2012). In West Africa, cowpea is consumed in many forms, young leaves, green pods and green seeds as vegetables whereas the dry seeds are used in a variety of food preparations. The green and dry haulms are fed to livestock particularly in dry seasons when animal feed is scarce.

Despite its above outlined great importance in tropical regions, cowpea yield potential and seed quality is often reduced by insect pest damage. One of the major destructive post harvest pests of cowpea worldwide is the cowpea weevil (*Callosobruchus maculatus*). The cowpea seed beetle, *C. maculatus* is a cosmopolitan pest of stored grain legumes especially cowpeas (*Vigna unguicalata* L. Walp) in the tropics and subtropics. Severely damaged seeds are disfigured with egg covers and riddled with adult exit holes, and consequently have reduced weight and poor germiability (Ofuya, 2010).

According to FAO study, World-wide cowpea loss in store approximates 10% of all stored grain, i.e. 13 million tonnes of grain lost due to insects or 100milion tones to failure to store properly. To these effects, there is every need to study the effects of seed size on weevil damage during storage.

MATERIALS AND METHODS

The experiment to determine the effect of seed size on *Callosobruchus maculatus* in the storage of cowpea was conducted in the Zoology Laboratory of Benue State University Makurdi, Nigeria between August and December, 2012.

The five cowpea varieties used were; Aloka, IAR48 (big brown), IT362 (big white), iron Beans and IT84E-124 (Ife brown). These were all obtained from Benue Agricultural and Rural Development Authority, Makurdi (BNARDA). These varieties had earlier been confirmed to grow and yield very well in the Makurdi environment (Ogbaji and Ndam, 2012).

The cowpea varieties were sun dried one week to allow the larvae in the seeds mature and escape. Undersized and perforated seeds were handpicked and discarded. Transparent plastic containers were also bought and used for the study. The plastic containers were perforated using needle to allow adequate aeration and to prevent intrusion of any other living organisms. The plastic containers were then weighed using a digital sensitive weighing balance. 500g of each of the cowpea varieties were weighted and stored in the containers.

The experimental design used was a factorial laid out in a Completely Randomized Design (CRD) with 3 replicates.

The data collected was the progressive weight loss of the cowpea varieties at two weekly intervals. The weight loss was measured using a sensitive weighing balance.

The percentage weight loss was calculated as follows:

Initial weight of cowpea and container = a

Final weight = b

Weight loss = a-b

Percentage weight loss = weight loss / initial weight x 100/1 = a-b/a x100/1

RESULTS AND DISCUSSION

Results on the 100 seed weight (g) of the cowpea varieties used for the investigation showed significant differences ($P<0.05$) in their sizes (Table 1). This is most probably due to the inherent genetic differences among them as the varieties were developed from different pedigrees. Many researchers such as Jackai and Asante (2003), Ogbaji and Osuman (2012), Jason and Charles (2003) had earlier studied and reported on the genetic variability among different cowpea lines. Results of the study also indicated significant differences and variation in the levels of resistance/tolerance among the different lines to *C. maculatus*. Small/medium sized lines were more resistant to the insects when compared with the big sized lines in their actual weight losses during storage (Table 2) indicating inverse relationship between big seed size and resistance to *C. maculatus* damage. The same results were also obtained in the overall percentage seed weight losses at the final duration of the cowpea seed storage (Table 3). Small sized seeds like Aloka had the least overall percentage weight reduction of 4.8%, followed by medium seed sized variety of Ife brown (5.79%) while the highest percentage weight loss was obtained from the big white (11.65%) which had earlier been classified as big seeded (Table 1). The results obtained here is most probably due to the fact that the small/medium sized varieties were more compact together during storage and hence blocked most of the air spaces among them. The lack of air spaces suffocated the adult *C. maculatus* insects to death and thereby presented the reproduction and multiplication of the insects. The results obtained here are in complete agreement with studies by Ogbaji and Tyoga (2010), Jason and Charles (2003); Shazia et al, (2012) Temesgen and Waktole (2008); among other studies. For example, Jason and Fox (2003) reported that the female *C. maculatus* insects were less ready to lay eggs on small seeded variaties of cowpea while Temesgen and Waktole (2008); among other studies. For example, Jason and Fox (2003) reported that the female *C. maculatus* insects were less ready to lay eggs on small seeded varieties of cowpea while Temesgen and Waktole (2008) reported that small seeded varieties were hard and too compact for *C. maculatus* insects and also contained less moisture and were

therefore more resistant to the weevils attack as the insects preferred to starve to death instead of feeding on them. Similarly, Jason and Charles (2003) in their research showed that surface area seed size of cowpea was important oviposition stimuli for *C. maculatus* with the insects demonstrating greater preference for large seed size i.e. the big seed sized varieties.

Based on the results of this study, it is therefore concluded that small seeded cowpea varieties resist *C. maculatus* attack during storage more than the large seeded ones. Cowpea farmers may therefore make use of this vital information during their cowpea storage practices.

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Table 1: 100 Seed weight (g) of the Different Cowpea Varieties.

Varieties	Weight	Seed Size Classification
Aloka	14.66	Small
Big white	26.81	Medium
Big brown	33.43	Big
Ife brown	16.56	Small
Iron Bean	27.70	Medium
FLSD (0.05)	**3.15**	

Table 2: Main Effects of Cowpea Varieties on Actual Weight Loss (grams) of Cowpea Seed during Storage.

Varieties	Weeks of Storage					
	2	4	6	8	10	12
Aloka	499.53	496.02	491.40	483.90	478.10	475.70
Iron Beans	497.03	485.99	477.20	470.40	457.20	415.90
Ife Brown	498.19	493.56	486.60	483.60	476.50	445.00
Big Brown	499.66	498.32	487.90	473.20	462.80	460.60
Big White	499.55	495.71	478.60	473.50	456.50	441.80
FLSD (0.05)	**2.18**	**3.497**	**9.68**	**9.69**	**10.13**	**11.18**

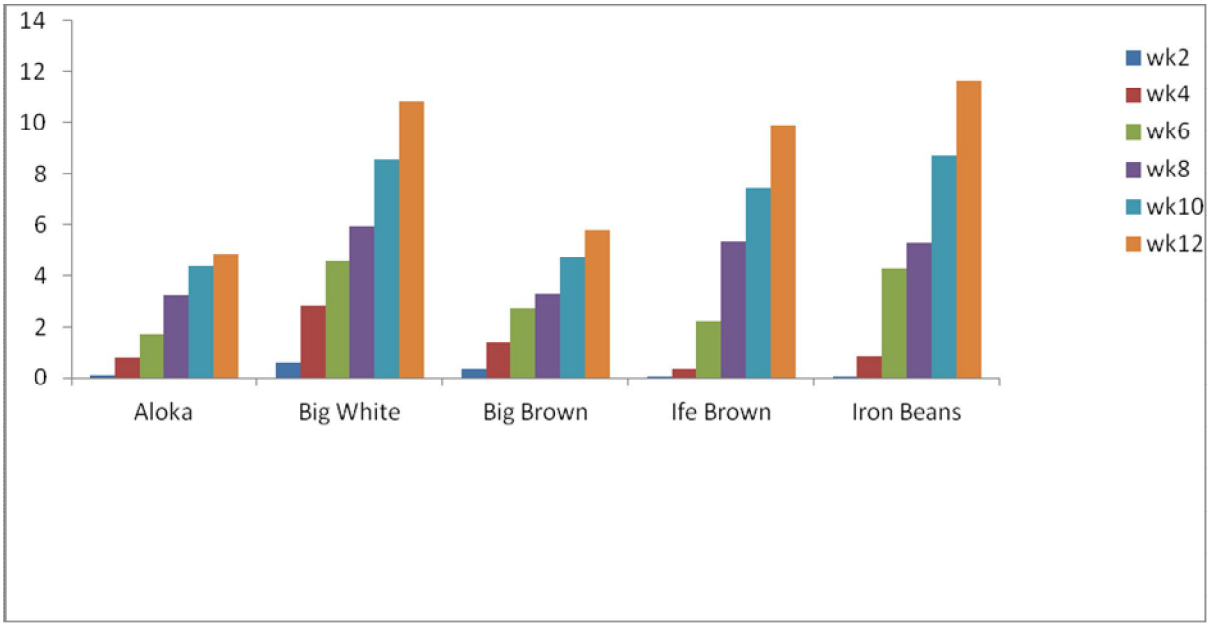

Fig. 1: Effects of Variety on Percentage Weight Loss of Cowpea to *Callosobruchus maculatus* During Storage.

Table 3: Main Effects of Varieties on percentage Weight Loss (%) of Cowpea Seed during storage.

Varieties	Weeks of Storage					
	2	4	6	8	10	12
Aloka	0.10	0.80	1.72	3.22	4.37	4.87
Iron Beans	0.60	2.80	4.56	5.91	8.55	10.81
Ife Brown	0.36	1.39	2.68	3.27	4.70	5.79
Big Brown	0.07	0.34	2.43	5.35	7.43	9.88
Big White	0.09	0.86	4.27	5.30	8.69	11.65
FLSD (0.05)	**0.03**	**0.69**	**1.94**	**1.96**	**2.01**	**2.17**

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PGB44

EFFECT OF SEED COLOUR ON WEEVIL DAMAGE (*CALLOSOBRUCHUS MACULATUS*) ON COWPEA (*VIGNA UNGUICULATA* L.WALP)

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ABSTRACT

A field experiment was carried out to investigate the effect of cowpea seed colour on weevil damage (*Callosobruchus maculatus*) during storage. The cowpea varieties used for the study were Aloka, IAR48, Big white (IT3629), Ife brown (IT845E-124) and iron beans. Selection of the cowpea varieties was based on their contrasting colours. The experimental design used was a factorial laid out in a Completely Randomized Design (CRD) with three replications. Storage was at room temperature. Results obtained showed significant differences ($P<0.05$) in the weight losses during storage indicating varietal differences in their susceptibility/ resistance to *Callosobruchus maculatus* during storage but not colour related. Aloka had the least resistance to *Callosobruchus maculatus* attack during storage and subsequently gave the highest percentage weight reduction of 15.4%. Next was Ife Brown with 11.3%, followed by Big White 10.9%, Iron Beans and lastly Big Brown with the highest resistance and least percentage weight reduction of 6.2%. However, cowpea seed colour did not affect infestation by *Callosobruchus maculatus* in storage. The discovery that cowpea colour does not play any significant role in the resistance/susceptibility of cowpea varieties to *Callosobruchus maculatus* during storage is a vital information to cowpea farmers in their effort to enhance food security in Nigeria.

Keywords: Cowpea, Colour, damage, effect.

INTRODUCTION

Cowpea (*Vigna unguiculata* L .Walp), a warm season annual herbaceous legume is one of the most ancient crops known to man. It is of African origin and is widely grown in Africa with Nigeria and Niger predominating. Cowpea has a number of common names, including Crowder pea, black eyed pea, southern pea, lubia, niebe, coupe or frijole (Bressiani , 1985).

Cowpea is an important legume in West and Central Africa, providing an inexpensive source of protein for both the Urban and Rural poor. According to Bressiani (1985), cowpea contains23-25% protein, 50-67% carbohydrates,1.9% fats, 6.35%fibre and small percentage of b-vitamins such as folic acid, thiamine, riboflavin and niacin as well as some micronutrients such as iron, calcium and zinc(IITA,2001). The seed coat can either be smooth or wrinkled and of various colours including: white, cream, green, buff, red, brown and black. Seed may also be speckled, mottled or blotchy. In fresh form, the young leaves and immature pods are used as vegetables, while the grains are utilized in a wide variety of local dishes. The relative composition of carbohydrates and richness in protein make them important components of the food ration of humans particularly where there is insufficient protein of animal origin; a typical situation in many tropical developing countries (Singh and Rachie, 1985).despite cowpea being a popular and nutritionally important crop in many parts of the tropical world, it is very susceptible to insect infestation both in the field and in storage; though the greatest damage occurs in storage (Murdock *et al*., 1997). The principal storage pest of cowpea grains in sub Saharan Africa is the cowpea beetle (*Callosobruchus*

maculatus), commonly called weevil (Taylor, 1981). Weevils cause characteristic holes in cowpea affecting seed weight and viability while enabling the introduction of pathogenic fungi and bacteria into the seed. More so, it should be noted that infestations by cowpea by *Callosobruchus maculatus* (on the field and in storage) causes both quantitative and qualitative losses (Shade *et al*., 1990).

Research in Uganda and many parts of Africa have shown that there is variability in cowpea damage by *Callosobruchus maculatus* but did not determine if the differences were due to seed colour. Hence, the objective of the study was to assess and compare the response of five different cowpea varieties with contrasting seed colour to the cowpea weevil (*Callosobruchus maculatus)* damage during storage.

MATERIALS AND METHODS

The experiment was conducted at the Botany Laboratory of the Benue State University, Makurdi, between August and November 2012. The five untreated cowpea varieties used were Aloka, Big Brown, Big White, Iron Beans, and Ife Brown. They were obtained from the National Cereals Research Institute (NCRI) Yandev substation in Benue State, Nigeria. The different varieties of cowpea were sundried for two weeks to allow the escape of *Callosobruchus maculatus* and were then sorted out by hand picking to remove undersized and perforated seed/grains. Sun drying continued so as to achieve cessation of reproduction of the weevil and also ensure that all the immature stages had been hatched. Equal quantity (500g) of seeds of each of the cowpea varieties were measured with a digital sensitive weighing balance and put into airtight plastic containers. Each variety had three replicates which were stored at room temperature in the laboratory. The weight loss was measured using the digital sensitive weighing balance. The data collected were a progressive weight loss of the cowpea varieties at two weekly intervals.

Percentage weight loss was calculated as follows:

$Initial\ weight\ of\ cowpea\ and\ container = a$

$Final\ weight = b$

$Weight\ loss = c$

$$\%\ weight\ loss = \frac{weight\ loss}{initial\ weight} \times 100$$

i. e. $\frac{a-b}{a} \times 100$

Collected data were analyzed using Analysis of Variance (ANOVA). Treatment means were separated using Fishers Least Significant Difference (FLSD) at five percent level of significance.

RESULTS AND DISCUSSION.

Results showed that the susceptibility/resistant of the cowpea varieties; Aloka, Big Brown, Big White, Ife Brown and Iron Beans to *C. maculatus* were statistically significant among the cowpea varieties. Aloka with mottle colour showed the highest weight reduction while big brown variety with dark brown colour showed the least weight reduction indicating more resistance to *C. maculatus* during storage (Table 1).

The percentage weight loss of the cowpea seeds at various weeks of storage also showed significant differences among the varieties (Table 2) and followed the same trend as above.

On a comparative scale however, Big Brown was the least susceptible with actual weight loss/ percentage weight loss of 31g and 6.2% respectively while Aloka was the most susceptible with an actual weight loss/ percentage weight loss of 76g and 15.4% respectively (Fig 1 and Table 2).

The highest weight loss implied the least resistant and none of the five cowpea varieties was observed to be completely resistant to *Callosobruchus maculatus* attack.

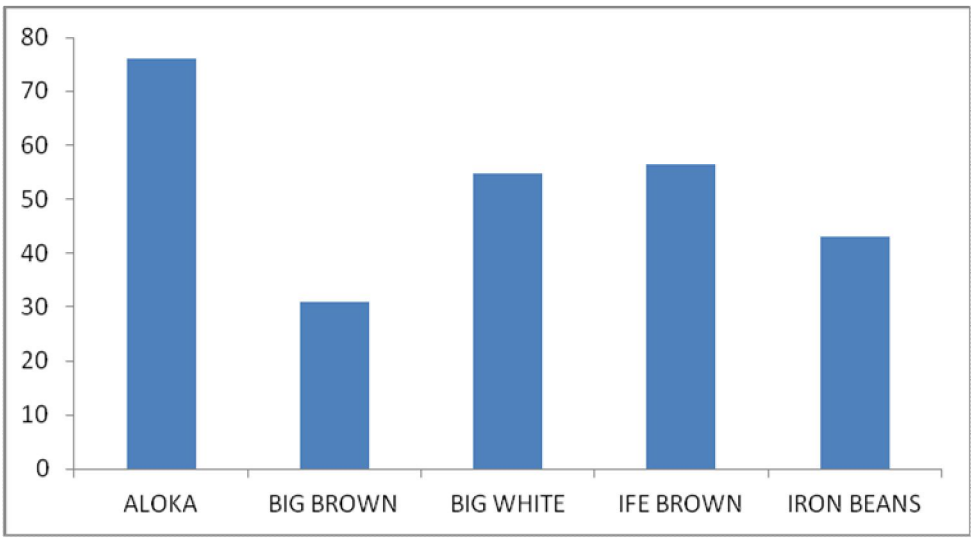

Fig 1: Actual Weight Loss of Cowpea Varieties at the end of the Experiment.

Cowpea seeds possess certain characteristics such as the nature and hardness of the seed coat which make them suitable for oviposition by *Callosobruchus maculatus.* In general, varieties with smooth seed surface are preferred for oviposition by *Callosobruchus maculatus* compared to wrinkled varieties with rough seed surface. (Patil and Jadhav, 1985; Asiedu *et al*, 2000). The weight and volume of the seed are two factors responsible for oviposition preference (Patil and Jadhav, 1985). Hardness of the seed is due to the chemical composition of the seed coat (Friends, 1981), which has an effect on the ability of *Callosobruchus maculatus* to invade the seed (Asiedu *et al.*, 2002). Differences in seed coat colour have been associated with differences in the chemical composition of leguminous plant seeds. The chemical compounds found in the seed coat of leguminous plants include tannins, lignin, non-tannins and polyphenolic compounds. The concentration of these compounds may differ depending on the level of colour pigmentation in the seed coat (Asiedu *et al.*, 2002). Nozzolio *et al.*, (1989) reported that coloured seed coats contained 15 times more lignin than the white seed coats. Morrison *et al.*, (1995), observed twice more lignin in pigmented ones. Lignin has the function of cementing and anchoring cellulose fibres together. It therefore gives mechanical rigidity to plants and also protects them against chemical, physical and biological attacks. In addition to tannins, lignin offers resistance to microbial and other attacks (Friends, 1981).

With respect to colour variation, Big brown and Ife- brown, are both dark brown, Aloka is mottle, Big white and Iron beans are all white varieties. In this research, both Big brown and Ife brown had same colour although Ife brown was much more susceptible than Big brown. However, Morrison *et al.* (1995) reported high lignin and tannin levels in the pigmented cowpea varieties. High lignin level which confers rigidity was not indicative of resistance

since these pigmented varieties recorded relatively high levels of susceptibility. This suggests that other factors besides seed coat thickness affect resistance of cowpea to insect infestation. According to Borchers *et al*. (1947) the presence of trypsin inhibitors in leguminous seeds affect the ability of the bruchids to digest proteins contained in the seed. Thus, what confers resistance to a variety should be an intrinsic property that combats development even after *Callosobruchus maculatus* oviposition. Of the five varieties of cowpea studied Big Brown recorded the longest developmental period and the least susceptibility. This might be due to the fact that the food material in Big Brown could not be utilized efficiently, thus retarding the development of *Callosobruchus maculatus* as found by Allotey and Oyewo (1993) on soybean Glycin max (L) Merr.

It is important to note however that none of the five cowpea, varieties studied was immuned to *Callosobruchus maculatus* attack. This finding agrees with that of Singh and Rachie (1985) who reported that only one cowpea variety, TVu2027, has been found to have a high level of seed resistance to *Callosobruchus maculatus* .Gatehouse *et al*, (1979) also reported that TVu2027 has a higher level of trypsin inhibitor compared to other varieties and this may be the main factor conferring resistance and not seed colour.

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Table 1: Actual Weight Loss of Cowpea Seeds at Various Weeks of Storage

	Weeks of Storage							
Varieties	**2**	**4**	**6**	**8**	**10**	**12**	**14**	**16**
Aloka	497.40	496.04	492.39	485.20	471.10	452.60	436.20	423.20
Big Brown	498.93	498.69	494.58	491.60b	486.30	478.80	73.70	469.00
Big White	498.95	494.46	492.48	473.30	463.5	455.40	449.50	445.40
Ife Brown	497.70	497.34	496.01	489.30	474.10	461.10	450.70	443.60
Iron Beans	499.47	495.43	490.75	483.30	79.20	469.60	463.30	458.90
FLSD (0.05)	**1.72**	**5.43**	**5.80**	**16.70**	**29.32**	**35.35**	**39.85**	**31.84**

Along the columns, if the difference between two treatment means is greater than the FLSD value, then those treatments aresignificantly different from each other.

Table 2: Percentage Weight Loss of Different Cowpea Varieties during Storage.

Weeks of Storage								
Varieties	2	4	6	8	10	12	14	16
Aloka	0.52	0.79	1.52	2.95	5.78	9.48	12.80	15.40
Big Brown	0.21	0.26	1.08	1.68	2.74	4.25	5.30	6.20
Big White	0.21	1.11	1.50	5.33	7.29	8.92	10.10	10.90
Ife Brown	0.44	0.53	0.80	2.14	5.18	7.78	9.90	11.30
Iron Beans	0.11	0.91	1.85	3.34	4.15	6.08	7.30	8.20
FLSD (0.05)	**0.37**	**1.09**	**1.16**	**3.33**	**5.86**	**7.08**	**7.97**	**8.35**

Along the columns, if the difference between two treatment means is greater than the FLSD value, then those treatments are significantly different from each other.

PGB45

CLASSIFICATION OF REGISTERED CROP VARIETIES IN NIGERIA

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ABSTRACT

Crop varieties registered and published in 2009 were assembled into categories based on the recommending institution in order to determine the contribution of the various categories into the pool of registered varieties in Nigeria. The highest contribution of varieties was recorded in institutions that have restricted crop mandate at 384 varieties compared to those who enjoy academic freedom at 7 varieties. The implications of these results are discussed.

INTRODUCTION

The development of new varieties may provide a breeder with several opportunities such as conservation of germplasm, exchange of germplasm, new experimental procedures, publication of papers, registration/release of new varieties etc. Each of these opportunities has benefits to the breeder with registration/release of varieties as a step that makes the new varieties available to farmers, as coordinated by the National Committee on Registration and Release of Crop varieties, Livestock breeds and Fishery (NCRRCLF). The national committee has a technical subcommittee for crops (TSC), which considers requests for registration/release of crop varieties and recommends to the NCRRCLF for possible ratification, certification and publication (NACGRAB, 2004).

Crop varieties presented to the TSC, may be registered but not released. Such varieties are often of restricted circulation and are typical of materials presented by companies for their use or among their out-grower farmers only. Most often, materials presented by public institutions, when registered and released will be in public domain.

The NCRRCLF, on registration of crop varieties, publishes an updated compendium of registered/released varieties (NACGRAB, 2009). The objective of this study is to evaluate registration of crop varieties, by various institutions, in Nigeria using the 2009 edition of NCRRCLF.

MATERIALS AND METHOD

Institutions that presented the crop varieties registered and published in 2009 were listed and categorized as follows:

A. Research Centres that have clearly defined mandate: these are mainly research institutes that have restricted mandate. Examples are institutes defined as the National Agricultural Research Institutes - NARI (Shaib et al, 1997) and a few under the Consultative Group on International Agricultural Research. It is noteworthy that some institutes classified as NARI are affiliated to Universities.

B. Universities: these are either the agricultural universities or faculties of agriculture of multidisciplinary universities. These institutions virtually enjoy academic freedom in agricultural research.

C. Mandate of some agencies may not be clear. These may be the old institutions that were involved in agricultural research before stratification into the present structure of

agricultural research and training in Nigeria. Examples may be the moribund Federal Department of Agricultural Research and Northern Nigeria Ministry of Agriculture and Natural Resources. Some agencies are foreign collaborators whose mandate cannot be well classified due to inadequate information.

Mean number of varieties registered by each of these groups was calculated and evaluated using mean separation.

RESULTS AND DISCUSSION

The range of registered varieties was one to ninety nine with a total of 427 varieties (Tables 1 and 2). Among categories, the group with restricted mandate (Category A) had the highest figure at 384 varieties, followed by the non-classified group (Category C) at 36 varieties and lastly the group enjoying academic freedom (Category B) with 7 varieties (Table 2). On the basis of mean, registration of varieties was 11.29 for Category A, which was significantly different from means obtained for Categories B and C at 2.33 and 3.60 varieties respectively (Table 2). Within the Category A, institutes that are not affiliated to universities registered 212 varieties and 172 varieties for those affiliated to universities (Table 3).

These results suggest that institutions with restricted mandate have higher tendency to drive their breeding work to the point of registration of varieties compared to institutions that have academic freedom. The case of category B may be that the phase of research which leads to paper publication is more attractive. It may also be that the last phase of on-farm trials, which is a prerequisite for registration of varieties, is expensive and institutional support for it may not be available. In this case, Category B institution may seek the assistance of the Category A institution that has the national mandate for the crop. Grants from agencies may also be available for farmer focused trials.

It is noteworthy that the potential to publish and also register varieties is there for Categories A and B without compromising any aspect as evident in publications of breeders in Category A (Omokhafe and Nasiru, 2005) with high number of registered clones as well as the commendable effort of Faculties of Agriculture of Obafemi Awolowo University, Ile-Ife and Ahmadu Bello University, Zaria (Table 1). In conclusion, breeders are encouraged to strike a balance between paper publication and registration of new varieties.

ACKNOWLEDGEMENT

Authors are grateful to the NCRRCLF for consistent compilation of registered crop varieties in Nigeria. The effort of agencies that presented crop varieties for registration is hereby acknowledged. The National Centre for Genetic Resources and Biotechnology, Ibadan, which provides the secretariat for NCRRCLF is recognized for effective coordination. The support of the Executive Director and Management of Rubber Research Institute of Nigeria (RRIN) for participation of RRIN in activities of the NCRRLF is appreciated.

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Table 1. Number of crop varieties released by various institutions in Nigeria as at 2009

S/No.	Institution Name**	Category*	Varieties
1.	IAR, Samaru	A1	99
2.	IITA, Ibadan	A2	44
3.	FDAR/NCRI, Badeggi	A2	31
4.	NCRI, Badeggi	A2	25
5.	NIHORT	A2	25
6.	IITA, Ibadan/IAR, Samaru	A1	21
7.	IAR&T, Ibadan	A1	20
8.	NRCRI, Umudike	A2	14
9.	RRIN, Benin City	A2	14
10.	CRIN, Ibadan	A2	12
11.	FDAR	C	10
12.	NRCRI, Umudike/IITA	A2	10
13.	IITA/IAR&T, Ibadan	A1	9
14.	MRP/IITA	A2	8
15.	Florida Experimental Station	C	7
16.	NIFOR, Benin City	A2	6
17.	IAR, Samaru/ABU, Zaria	B	5
18.	ILRI, Ibadan/NAPRI, Zaria	A1	5
19.	IAR, Samaru/ICRISAT, Kano	A1	5
20.	ICRISAT, Kano/IAR, SAmaru	A1	5
21.	LCRI, Maiduguri	A2	4
22.	ILRI, Ibadan	A2	4
23.	NCRI, Badeggi/IITA, Ibadan	A2	4
24.	WICSBS	C	4
25.	Sugar cane breeding Institute, Coimbatora, India	C	4
26.	Premier Seed Nig. Ltd.	C	3
27.	FDAR/Moor Plantation	C	2
28.	ILRI, Kano/ICRISAT, Kano/IAR, Samaru	A1	2
29.	WARDA, Ibadan/IITA, Ibadan	A2	2
30.	IAR, Samaru/NCRI, Badeggi	A2	2
31.	USRI, Ibadan	C	2
32.	NCRI, Umudike/RMRDC, Abuja/IITA, Ibadan	A2	2
33.	IAR&T/Moor Plantation	A1	2
34.	NBPLC	C	2
35.	IAR&T, Ibadan/Faculty of Agric., O.A.U.	B	1
36.	Faculty of Agric., O.A.U.	B	1
37.	Northern Region Ministry of Agric & Natural Resources	C	1
38.	NCRI, Badeggi/WARDA	A2	1
39.	LCRI, Maiduguri/ ICRISAT, Kano	A2	1
40.	IITA, Ibadan/WARDA, Ibadan/ NCRI, Badeggi	A2	1
41.	Sugar cane Breeding Institute Compos, Brazil	C	1
42.	LCRI, Maiduguri/Saskawa Global 2000/IAR, Samaru	A1	1
43.	NRCRI, Umudike/RMRDC, Abuja	A2	1
44.	IITA, Kano/IAR, Samaru	A1	1
45.	IAR&T/IITA/NCRI, Badeggi	A1	1

46.	ILRI, Maiduguri/IAR, Samaru	A1	1
47.	NCRI/WARDA	A2	1

*A: Institutions with clearly defined mandate;
A1: Institutions with clearly defined mandate but affiliated to universities;
A2: Institutions with clearly defined mandate that are not affiliated to universities;
B: Institutions that enjoy academic freedom (e.g. Universities);
C: Institutions of unknown status of mandate
**: Source of acronyms: NACGRAB, 2009

Table 2. Mean number of varieties registered by categories of institutions

	No. of		Mean no.
Category*	Institutions	varieties	of varieties
A	34	384	11.29a
B	3	7	2.33b
C	10	36	3.60b
Total	47	427	9.09a

*A: Institutions with clearly defined mandate;
B: Institutions that enjoy academic freedom (e.g. Universities);
C: Institutions of unknown status of mandate
**: Means followed by different letters are significantly different at p = 0.05 (t-test)

Table 3. Mean number of varieties registered by institutions with clearly defined mandate

	No. of		Mean no.
Split category*	Institutions	Varieties	of varieties
A1	13	172	13.23
A2	21	212	10.10
Total	34	384	11.29

*A1: Institutions with clearly defined mandate but affiliated to universities;
A2: Institutions with clearly defined mandate that are not affiliated to universities;

Table 3: 100 Seed weight (g) of the Different Cowpea Varieties.

Varieties	Weight	Seed Size Classification
Aloka	14.66	Small
Big white	26.81	Medium
Big brown	33.43	Big
Ife brown	16.56	Small
Iron Bean	27.70	Medium
FLSD (0.05)	**3.15**	

Table 4: Main Effects of Cowpea Varieties on Actual Weight Loss (grams) of Cowpea Seed during Storage.

Varieties	Weeks of Storage					
	2	4	6	8	10	12
Aloka	499.53	496.02	491.40	483.90	478.10	475.70
Iron Beans	497.03	485.99	477.20	470.40	457.20	415.90
Ife Brown	498.19	493.56	486.60	483.60	476.50	445.00
Big Brown	499.66	498.32	487.90	473.20	462.80	460.60
Big White	499.55	495.71	478.60	473.50	456.50	441.80
FLSD (0.05)	**2.18**	**3.497**	**9.68**	**9.69**	**10.13**	**11.18**

Table 5: Main Effects of Varieties on percentage Weight Loss (%) of Cowpea Seed during storage.

Varieties	Weeks of Storage					
	2	4	6	8	10	12
Aloka	0.10	0.80	1.72	3.22	4.37	4.87
Iron Beans	0.60	2.80	4.56	5.91	8.55	10.81
Ife Brown	0.36	1.39	2.68	3.27	4.70	5.79
Big Brown	0.07	0.34	2.43	5.35	7.43	9.88
Big White	0.09	0.86	4.27	5.30	8.69	11.65
FLSD (0.05)	**0.03**	**0.69**	**1.94**	**1.96**	**2.01**	**2.17**

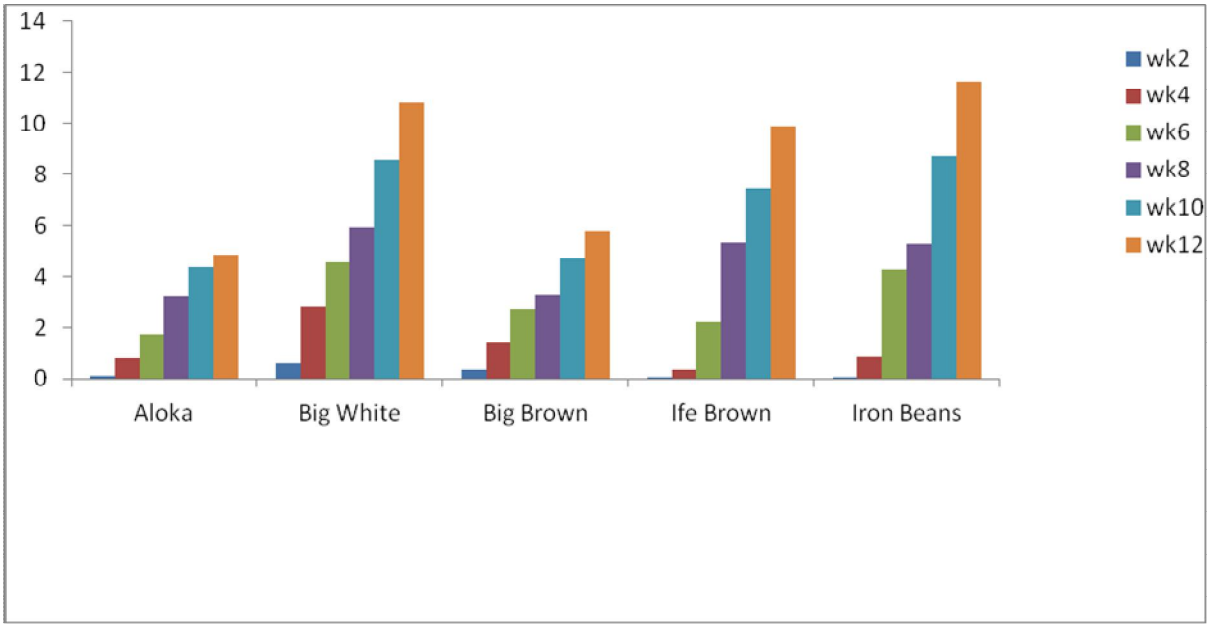

Fig. 1: Effects of Variety on Percentage Weight Loss of Cowpea to *Callosobruchus maculatus* During Storage.

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GENETIC DIVERSITY OF POLLEN MORPHOLOGY AND POLLEN PRODUCTION OF *CORCHORUS OLITORIUS* USING DIFFERENT CONCENTRATIONS OF STRONG HYPOCHLORITE SOLUTION.

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ABSTRACT

Mutations were induced in *Corchorus olitorius* using sodium hypochlorite. The *Corchorus olitorius* seeds were treated with 0%, 25%, 50% and 75% solution of sodium hypochlorite so as to assess their effects on pollen viability, pollen production and pollen diameter. Results showed that the pollen parameters were significantly different ($p \leq 0.05$). It was observed that as the concentrations of sodium hypochlorite increases, the values of pollen viability, pollen production and pollen diameter also increased. This may essentially affect productivity positively. Therefore, sodium hypochlorite could be used to induced genetic variability in the pollen of *Corchorus olitorius,* and this could be exploited for the improvement of the crop in Nigeria.

KEY WORDS: Corchorus olitorius, Sodium hypochlorite, Pollen parameters, and Genetic variability

INTRODUCTION

Corchorus is a genus of about 40-100 species of flowering plants in the family Malvaceae, native to tropical and subtropical regions throughout the world .The plants are usually annual herbs, reaching a height of 4 m, unbranched or with only a few side branches and is an erect woody herb, usually 0.5 - 1.2m high but may reach up to 2.5 m in cultivation and growing as tall 4m (14Ft).The leaves are alternate, simple, lanceolate, 5-15 cm long, with an acuminate tip and a finely serrated or lobed margin. The flowers are small (2-3 cm diameter) and yellow, with five petals; the fruit is a many-seeded capsule. It thrives almost anywhere, and can be grown year-round. The local names of *Corchorus olitorius* in English are jute plant and bush okra,In many West Africa Countries, the crop is referred to names similar to keren keren like krin krin, crain crain or kelen kelen. Some Nigerian names for the crop include ewedu in Yoruba, ahuara in Igbo, malafiya and ayoyo in Hausa. (Akoroda, 2008).

Corchorus leaves are consumed in the cuisines of various countries. It has a mucilaginous texture, similar to okra, when cooked, the seeds are used as a flavouring, and a herbal tea is made from the dried leaves. The leaves of *Corchorus* are rich in betacarotene, iron, calcium, and vitamin C. The plant has an antioxidant activity with a significant α-tocopherol E. However, despite all the tremendous benefits of jute to world economy, its diversity and uses are under threat in Nigeria due to low yield. There is an urgent need as stressed to redesign the ongoing breeding strategy to improve the yield of such economic plant (Roy *et al*; 2006).

Sodium hypochlorite solution is poisonous for water organisms and plants. It is mutagenic, very toxic and corrosive in nature. The aim of this research is to study the effect different concentrations sodium hypochlorite solution on the pollens viability, pollen diameter and pollen production of *Corchorus olitorius*. Pollen studies is widely used in convectional plant breeding, tissue culture, plant biotechnology and pollen is used in cultivated plants to increase crop yield which is ultimate goal of most plant breeding programme (Beadle,2009). Nigeria has a great potential for the production of C*orchorus olitorius* for domestic and export market and due nutritional value and economical importances. The yield of the crop is still critically low as compared to other vegetable crops. Increased production of the crop is hampered by several factors one of which is inavailability of improved seed. But unfortunately, there has been little research efforts on the crop therefore this research is designed to look at the effect different concentrations of sodium hypochlorite on the pollen parameters (David,2010).

METHODOLOGY

The study was carried out at experimental field, Centre for Preliminary and Extra- mural studies Federal University of Technology, Minna, Niger State in North central Nigeria between July – November 2012. The area is located within longitude $6^0$33'E and 9^0 37', and the climate is tropical, with mean annual temperature, relative humidity and rainfall of 30.20^0, 61.00% and 1334mm respectively. The vegetation is a typical Guinea Savannah type consisting majorly of grassland with scattered trees (Olayemi *et al*.,2009).

MATERIALS

One Kilogram of *Corchorus olitorius* seeds were obtained from the National Institute of horticulture, (NIHORT) Ibadan, the seeds were kept separately in envelopes and tied in white polythene bags. Healthy seeds were pre-soaked in distilled water by floatation method and treated were with different concentrations (0%, 25%, 50% and 75%) of sodium hypochlorite solution.

The planting of the seeds was done using the completely randomized block design. Ten seeds were grown in each five litre size of pots filled with rich loamy soil and thinned to two per pot in two weeks after planting. A total of sixteen pots per block used with three replicates and the pots were kept in the experimental field of the Centre for Preliminary and Extra –Moral Studies, Federal University of Technology, Minna, Niger State and nurtured to maturity.

The pollen production test was carried out using the method described by Mehmet. Twenty flower buds for each treatment were used in the study. The flower buds were divided into two groups, each group containing anthers from five flower buds in small vial bottles. The anther were thoroughly crushed with a glass rod and then 1ml distilled water was added into each vial bottle. A drop was placed on a two counting area containing Thoma (haemocytometric) slide (0.1mm in depth) to where a special cover slip was replaced. The pollens were placed on randomly chosen four large squares in each counted area with two replicates representing each group of flowers in vials (Mehmet, 2011). The average pollen grain amount per flower:

(P/F) = Pollen count x $1000mm^3$/ $0.1mm^3$/5 flowers

IKI (0.5g iodine (I) and1g Potassium iodide (KI)) solution was prepared by dissolving I and KI in 100ml distilled water (Eti *et al* 1996). The pollen viability counts were made within few minutes in light microscope after pollens were placed on IKI solution. The pollen grains stained Dark brown in colour were counted as viable while those with a light pinkish colour or not stained at all were considered non-viable. Two microscope slides were used for each treatment. Approximately 300 pollens were counted in each slide. Pollen viability test was performed the same day when the flower buds were collected (Eti *et al* 1996*)*. Pollen viability percentage was gotten using the formular

$$\text{Pollen viability percentage} \quad \frac{\text{No of viable pollens}}{\text{No. of pollens counted}} \times 100$$

For each treatment, flowers were randomly sampled and used to determine the amount of pollen produced and pollen diameter were determined by eye piece gravicle . Numbers of pollen grain per flower will be determined using hemacytometric methods (Eti, 1996). The amount of pollen per anther will be determined using following formular

$$Pa = P_{f,} / A_F$$

where PA is the number of pollen grain per anther

pf is the number of pollen grain per flower

A_F is the number of Anther per flower

The data collected were subjected to Analysis of variance (ANOVA) using statistical analysis was used to test the significance of the effects of the different concentrations of sodium hypochlorite solution on pollen per flowers, pollen viability and pollens diameter. It showed that the pollen parameters (i.e were significantly different ($p \leq 0.05$). Analysis of variance was used to explain the relationship between the different concentration and the number of pollens produced per flower, percentage viability, anther per flower and viable pollen grain.

RESULTS AND DISCUSSION

The result recorded on the effect of sodium hypochlorite on pollen produced per flower , anther per flower, pollen diameter, viable pollen grains and non –pollen grains in different concentrations of *Corchorus olitorius* is represented in Table 1 below.

Result of pollen parameters on effect of different concentrations of sodium hypochlorite solution in *corchorus olitorius.*

KEYS: PPF – pollen produced per flower, AFP –anther per flower, PD – pollen diameter, VPG – viable pollen grain, and NPG – non –pollen grain

TABLE 1

Concentrations (%)	PPF	AFP	PD	VPG	NPG
0	384952.38^{d}	80.33^{d}	0.0559^{d}	90.47^{d}	24.30^{d}
25	151190.48^{a}	30.24^{a}	0.0355^{c}	86.72^{c}	15.24^{c}
50	211428.57^{b}	42.29^{b}	0.0315^{b}	85.22^{b}	13.86^{b}
75	299285.71^{c}	59.86^{c}	0.0312^{a}	76.07^{a}	09.96^{a}

From Table 1, for PPF is the highest value was recorded at 0% (384952.38).This value is statistically significant and different from all other values. Also, the lowest value was at 25% concentration value (151190.48) was significantly different from all other concentrations. The PPF Values obtained indicated that as the concentrations increases PPF values tend to increase.

For AFP is the highest number of anther per flower was observed at 0% (80.33) and lowest concentration value (30.24) of anther per flower with higher anther per flower were statistically significantly different. There was consistency in the trend of the anther per flower. The highest number of pollens diameter in PD was also observed at 0% (0.0559mm) followed by 75% concentration (0.0355mm) . In 50% concentration (0.0315) and 25% concentration (0.0312)

values are closely related respectively was significantly different. There was consistency in the trend of the number of anther per flower in *Corchorus olitorius.*

For VPG, there was a corresponding increase in viable pollen grains with increasing in different concentrations, although the 25% concentration had the lowest number of pollens per flower (76.07 pollens grains). All the number of viable pollen grains in all the concentrations used is statistically significant alike. For NPG, the highest value was observed at 0% (24.30) and the lowest value was at 25% concentration (9.96), these values was significantly different from all other concentrations. The NPG values observed indicated that as the concentrations increases as well as NPG value increases. The ANOVA results for all the parameters studied (PPF, AFP, PD, VPG and NPG) showed a significant different in Table 1 above.

The significant differences observed in pollen produced per flower, anther per flower, pollens diameter, viable pollen grains and non – viable pollen grains in all the different concentrations of sodium hypochlorite solution used in this study is an indication that sodium hypochlorite can be used to induce genetic variability in the plant. The changes produced by sodium hypochlorite solution could play a significant role in the improvement of the crop. The use of sodium hypochlorite solution in this study could have induced genetic variation which favoured pollen parameters. The concentration at 0% showed the highest value for all the pollen parameters which is likely to be more productive than other concentration in the plants. This result is in line with the results of Ashri (2008) and Kumar *et al* (2003)who observed that jute plant proved less sensitive to chemical mutagens mainly ethyl methane sulphonate.

The significant differences observed in the pollen viability test may be due to the fact that the pollen viability of the control were generally high hence there was significant increase in pollen viability induced by sodium hypochlorite. The high pollen viability is in line with the result of Falusi (2006) who observed that pollen viability were high in two species of Sesame, *Sesamum indicum* and *Sesamum radiatum* which is similar to *Corchorus olitorius.*

CONCLUSION

This study has established the following:

(a) Sodium hypochlorite has the ability to induce genetic variability in *corchorus olitorius* which can serve as a basis for selection for plant breeders.
(b)Sodium hypochlorite can also be used to improve the pollen diameter and pollen production in *Corchorus olitorius*.

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INTROGRESSION OF ALLELES FROM MAIZE LANDRACES TO IMPROVE DROUGHT TOLERANCE IN AN ADAPTED GERMPLASM

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ABSTRACT

Maize (Zea mays L.) landraces in the northern Guinea savanna and Sudan savanna in West and Central Africa appear to have some drought adaptive traits. This study was initiated to assess the level of improvement in grain yield and other agronomic traits achieved under drought stress (DS) and in multiple locations (ML) after introgression of alleles from maize landraces into an elite maize variety (AK9443-DMRSR) via backcrossing. Six backcross (BC) populations together with recurrent parent (AK9443-DMRSR), a commercial hybrid (Oba Super2), and an improved variety (TZLCOMP4C1) were evaluated under DS and full irrigated (FI) conditions during the dry seasons of 1999 and 2000, as well as in seven ML trials. No significant differences were observed among genotypes for grain yield and most of the traits measured under DS and FI. Significant differences were recorded among genotypes for grain yield and other agronomic traits measured in ML trials. Drought stress reduced grain yields of the BC_1F_2 populations by 64% and recurrent parent by 71%. In ML trials, at least half of the populations were better than recurrent parent. The top three BC_1F_2 populations produced more grains than the recurrent parent (258 – 360 kg/ha) and Oba Super2 (555–657 kg/ha) with introgression of only 25% genome of the landraces. Our study demonstrated that backcross procedure was able to transfer a quantitative trait of grain yield of an elite recurrent parent into maize landraces. Additional backcross generations are needed for improved performance of the BC_1F_2 populations in water stressed environments.

INTRODUCTION

Farmers in drought prone areas frequently report low grain yields for improved varieties, as the varieties produced may not have been specifically developed for drought tolerance. The farmers are usually wary of adopting un-adapted varieties to minimize the risk of crop failure under adverse conditions. New varieties targeted to drought affected areas should combine adaptation to drought stress with high yield potential to allow them to compete with elite varieties under optimum conditions (Bidinger et al., 1994). Progress in the development of drought tolerant varieties depends on sources of alleles for improved performance under drought stress. The choice of source population plays a critical role in a breeding program because it determines the frequency of desirable alleles at the onset of selection (Hallauer, 1991). Drought tolerance alleles from drought tolerant source germplasm can be transferred to adapted germplasm by backcrossing using either conventional methods or marker assisted selection (Edmeades *et al.*, 1997a). Dudley (1982) suggested that at least one backcross to recurrent parent would enhance the probability of transferring favourable alleles from donor to recurrent parent. The resulting populations containing alleles derived from diverse sources should thus be evaluated under controlled drought stress and in multiple locations to assess incorporation of drought tolerance alleles.

Landrace varieties represent a reservoir of highly adapted genotypes that form essential components of sustainable agriculture. Blum and Sullivan (1986) suggested that landraces of sorghum (*Sorghum bicolor* L.) and pearl millet (*Pennisetum glaucum*) collected from drought affected environments could possess unique physiological attributes for drought tolerance that may not be present in elite varieties that are not exposed to drought. Although landraces of maize have not been used extensively by breeders because of their low yields and other undesirable traits, they can serve as sources of desirable alleles to enhance performance of adapted germplasm under drought stress (Beck *et al*., 1997). Introgression of alleles from local varieties into adapted germplasm could also be beneficial to widen the germplasm base and combine high yield potential with good levels of drought tolerance. Evidence from previous studies (Badu-Apraku *et al.*, 1997) in WCA indicated that the probability of obtaining drought tolerance in a population is significantly greater when the source population from which it was derived also has a high level of drought tolerance.

The poor agronomic performance and narrow adaptability of improved maize varieties have been formidable obstacles for farmers seeking to grow elite maize cultivars in the northern Guinea Savanna and Sudan Savanna of WCA. A study was initiated at the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, to investigate the extent to which drought tolerance from landraces could be effectively introgressed into elite germplasm of maize. The first step was to collect the maize landraces germplasm, which was done by the Maize Association of Nigeria (MAAN) in collaboration with IITA through a farm-level survey of maize activities throughout the country in the early 1990s, during which over 400 farmers' varieties were collected. Analysis of the response of the varieties to the challenge of the maize streak virus infection showed that many of the collections, particularly those obtained from locations far from IITA-Ibadan, were truly landraces (Fakorede et al., 2003). The objective of the present study was to assess the level of improvement in yield potential and other agronomic traits of backcross (BC) populations containing alleles derived from six landrace accessions under water stress and favourable conditions.

MATERIALS AND METHODS

More than 400 maize accessions collected by MAAN in collaboration with IITA across Nigeria were evaluated for streak virus and abiotic stresses at IITA. After preliminary evaluations, Menkir and Akintunde (2001) selected 20 of the landraces, screened them under water stress, and identified six of them as potential sources of alleles for drought tolerance. They observed that the six landraces expressed good levels of drought tolerance and recommended their use to expand the genetic base of adapted elite germplasm. The six landraces were collected from Jigawa, Kano, Katsina, and Yobe States in northern Nigeria. Characteristics of the environments in which these landraces were grown are provided in Table 1. Rainfall in these states is highly variable, with the main growing season starting late and ending early, depending on the north-south movement of the intertropical convergence zone (ITCZ). The six landraces were crossed to the elite OPV, AK9443-DMRSR, and the resulting F1s were backcrossed once to the same elite recurrent parent to generate backcross (BC_1F_1) populations. The six BC_1F_1 populations were then advanced to F_2 by selfing to produce BC_1F_2.

Table 1. Some pertinent information for the six maize landraces and recurrent parent used in producing backcross populations

Local accessions	Location	Latitude	Longitude	Altitude (m)	Temperature (C^o) Min	Max	Annual rainfall (mm)
JigawaAccNo.4(Y)	Jigawa	12^o N	9^o 45' E	376	18	35	688
JigawaAccNo.11	Jigawa	12^o N	9^o 45' E	376	18	35	688
KanoAccNo.10	Kano	11^o 30' N	8^o 30' E	530	19	33	907
KatsinaAccNo.3	Katsina	12^o 15' N	7^o 30' E	547	19	33	819
YobeAccNo.2	Yobe	12^o N	11^o 30' E	372	17	33	619
YobeAccNo.3(Y)	Yobe	12^o N	11^o 30' E	372	17	33	619
AK9443-DMRSR†	IITA-Ibadan	7^o 30' N	3^o 54' E	215	22	31	1294

† Adapted open pollinated adapted variety used as recurrent parent in backcrossing.

Source: GIS unit –IITA, Ibadan. The temperature range and mean annual rainfall were obtained from gridded climate surface (1951-2005) produced by University of East Anglia UK.

The BC1F2 populations along with their recurrent parent, an improved variety (TZLCOMP4C1), and a single cross commercial hybrid (Oba Super2) were arranged in a randomized complete block design (RCBD) with three replications and evaluated at Ikenne ($6^o52'$ N, $3^o43'$ E, altitude 60 m) under water stress (DS) and well watered (FI) conditions during the dry seasons (December – March) of 1999 and 2000. Planting was done during the first week of December each year. Each entry was planted in a pair row plot 3 m long, with 0.75 m spacing between and 0.25 m spacing within rows. Two seeds were planted in a hill and thinned to one plant after emergence. In both trials, two border rows were planted with a common check. A sprinkler irrigation system was used to supply sufficient water every week to all treatments in the two blocks during the first five weeks (35 days) after planting. Thereafter, FI block continued to receive irrigation every week until physiological maturity, whereas irrigation was withdrawn in the DS block to create drought stress at flowering and grain filling stages. Apart from the targeted water stress, all other management practices were the same for the two irrigation treatments.

The same BC_1F_2 populations, together with their recurrent parent and two checks, were also evaluated in multiple locations (ML) during the main rainy season (June – October) to assess their yield potential under random drought at Bagauda (11◦50′ N, 8◦36′ E, altitude 448 m), Ikenne, Saminaka (10◦25′ N, 8◦41′ E, altitude 762 m), and Zaria (11◦7′ N, 7◦43′ E, altitude 639 m) in 2000, and only at Ikenne, Saminaka, and Zaria in 2001. In each location, a RCBD with

four replications was used. Each entry was planted in four rows plot, 5 m long, with 0.75 m spacing between rows and 0.5 m spacing between hills within a row. Three seeds were planted per hill and thinned to two plants after emergence. Number of border rows and population density were the same as in the DS and FI trials. In all trials, a compound fertilizer was applied at the rate of 60 kg N, 60 kg P, and 60 kg K ha^{-1} at the time of sowing. An additional 60 kg N ha^{-1} was applied as top dressing four weeks later. Gramoxone (paraquat: 1, 1'-dimethyl-4,4'-bipyridinium) was applied at 5 L ha^{-1} to control weeds. Subsequently, manual weeding was done to keep the trials free of weeds.

Days to anthesis and silking were recorded as the number of days from planting to when 50% of the plants in a plot were shedding pollen and had emerged silks, respectively. Plant and ear heights were measured as the distance from the base of the plant to the height of the first tassel branch and the node bearing the upper ear, respectively. Ears aspect was scored on a scale of 1 to 5, where 1 = well filled ear with uniform grain colour and 5 = poorly filled ear with varied grain colours. All ears harvested from each plot were shelled and used to determine percentage grain moisture and grain weight. Grain yield adjusted to 15% moisture was computed from the shelled grain weight. Data from DS, FI, and ML trials were analyzed separately, using a mixed model in SAS (SAS Institute, 2002), considering all effects as random except genotypes.

RESULTS AND DISCUSSION

Under WS as well as WW, none of the sources of variation had significant effect on grain yield (Table 2). In the ML, environment significantly affected all the traits (Table 3). The variance among varieties was significant for all the traits, except number of ears per plant.

Variety x environment interaction was significant only for days to anthesis and silking (Table 3). The lack of significant differences among genotypes for grain yield and other agronomic traits under DS and FI could be attributed to large mean error variance for these traits.

Table 2. Mean performance from analysis of variance of backcross populations involving maize landraces as non-recurrent parents tested under water stress and well watered treatments for two years

Source	DF	Days to anthesis (day)	Days to silking (day)	Plant height (cm)	Ear height (cm)	Ear aspect (1-5)[a]	Grain yield (kg/ha)
				Drought stress			
Year	1	50.1***	140.2***	462.3	606.7*	5.15***	1509
Rep (Year)	4	2.6**	2.4	19.6	42.3	0.68*	87316
Variety	8	2.0**	1.4	314.0	275.3*	0.46	173585
Variety x Year	8	0.7	2.2	86.9	115.1	0.21	121707
Error	32	0.4	1.5	161.7	104.3	0.26	118890
				Full Irrigation			
Year	1	0.7	1.2	5221.5**	109.8	0.02	192413
Rep (Year)	4	0.8	0.5	876.9	354.4	0.28	487301
Variety	8	3.0**	1.9**	878.1*	550.0*	0.29	1153566
Variety x Year	8	1.0*	0.9	410.9	152.2	0.14	641235
Error	32	0.4	0.6	364.2	191.4	0.15	706737

*, **, *** significant at 0.05, 0.01 and 0.001 probability levels, respectively
[a] Ear aspect on a scale of 1 to 5, where 1 = clean, well-filled ear, and 5 = ear with undesirable features

These results indicated that the BC_1F_2 populations performed similar to their recurrent parent, a commercial single-cross hybrid, and an elite variety under water stress and well watered conditions throughout the growing season. Because the G x E mean squares in the ANOVA were not significant for grain yield under DS and FI conditions, the BC_1F_2 populations appeared to have maintained their performance regardless of the variation in the environmental factors in these ecologies.

Table 3. Mean performance from analysis of variance of backcross populations involving maize landraces as non-recurrent parents tested in seven environments in Nigeria

Source	DF	Days to anthesis (day)	Days to silking (day)	Plant height (cm)	Ear height (cm)	Ear aspect (1-5)[a]	Grain yield (kg/ha)
Environment (E)	6	589.4***	956.2***	19248.2***	3330.9***	1.51***	122026857***
Rep (E)	21	1.9**	2.0**	470.9**	222.6	0.09	710783
Variety (V)	8	14.1***	14.6***	2415.4***	1331.6***	0.08	1850683**
V x E	48	1.3*	1.9**	196.4	123.3	0.16**	679342
Error	168	0.9	1.0	201.1	171.3	0.08	574169

*, **, *** significant at 0.05, 0.01 and 0.001 probability levels, respectively
[a] Ear aspect on a scale of 1 to 5, where 1 = clean, well-filled ear, and 5 = ear with undesirable features

However, differences in yield potential became obvious in ML trials conducted during the rainy season, typically of farmers' field conditions, indicating that the BC_1F_2 populations possess alleles for yield potential expressed under random drought conditions (Table 4). It is apparent that these BC_1F_2 populations have combined productivity traits of the elite recurrent parent and traits for drought tolerance as well as other good characteristics of the landraces. These results suggested that the donor landraces had favourable alleles for drought tolerance, which may not have been present in their elite recurrent parent.

Means of the six BC_1F_2 populations, AK9443-DMRSR, Oba Super2, and TZLCOMP4C1 under DS and FI are presented in Figure 1. All the BC_1F_2 populations performed essentially the same as the recurrent parent and the two checks for grain yield and other agronomic traits under DS and FI. On average, drought stress reduced grain yields of the BC_1F_2 populations by 64% and the recurrent parent by 71%. The grain yields of Oba Super2 and TZLCOMP4C1 were also reduced by 67% and 73%, respectively. Under DS conditions, the three top populations (BC_1F_2: 1, 2, and 3) took the same number of days to reach anthesis as their elite recurrent parent. They also showed relative yield advantage (ranging from 290 to 481 kg/ha) over Oba Super2 and TZLCOMP4C1 under DS conditions. Two of the top four populations (genotype 1 and 4) involved landraces collected from Jigawa State, which is characterized by rainfall varying from

600 to 700 mm and high temperatures (35 C^o) during the cropping season. Perhaps this and similar ecologies should be surveyed for more landraces with adaptive alleles to drought. Blum and Sullivan (1986) reported that races of sorghum and pearl millet evolved in dry regions within a range of annual rainfall of 200–700 mm were more drought-tolerant than races that evolved in areas with 800–1,100 mm of rainfall.

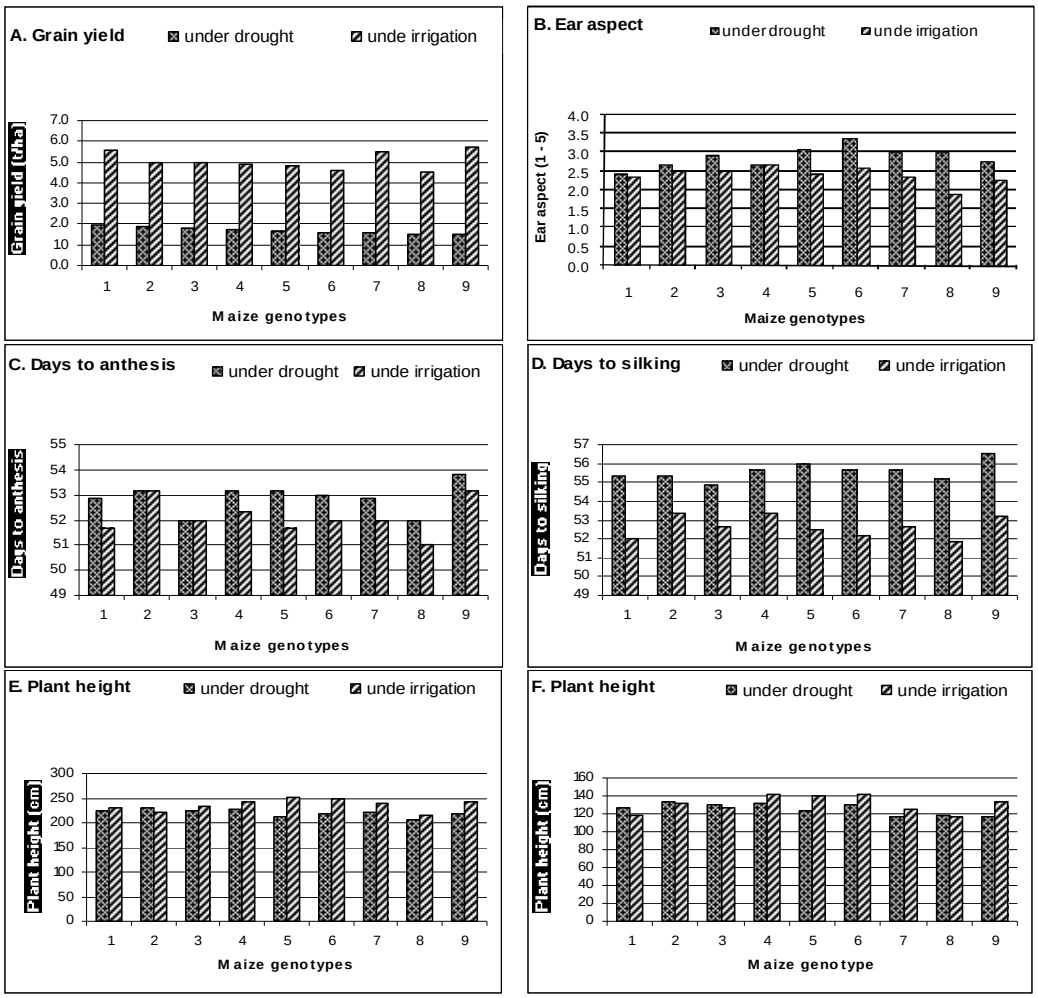

Figure 1. Means of grain yield (A), ear aspect (B), days to anthesis (C), days to silking (D), plant height (E), ear height (F) of six BC_1F_2 populations (genotypes 1 – 6), recurrent parent (genotype 7), and two checks (genotype 8, single cross hybrid; and 9, open pollinated variety) evaluated under drought stress and full irrigation averaged over two years.

Considering the diversity of origin of the six landraces used in this study, our results suggested that the potential exists for combining favourable alleles from landraces and elite varieties in developing varieties and parental lines of hybrids with superior performance under water stress. Albrecht and Dudley (1987) introgressed alleles from an exotic maize composite into adapted one and found that BC_1-F_2 had good performance as compared to the recurrent parent. Our data indicated that BC_1F_2 populations were similar in grain yield and other agronomic traits to the

elite recurrent parent under DS and FI, suggesting that favourable quantitative traits not only from the elite parent but also from the landraces have been integrated into a new population. The increase in grain yield recorded in the top three of the six BC_1F_2 populations in multiple agro-ecologies with introgression of only 25% of the genome of the maize landraces may further be enhanced by one or more generations of backcrossing to the elite recurrent parent.

Table 4. Mean performance of backcross populations involving maize landraces as non-recurrent parents evaluated in seven environments under random drought

Variety	Grain yield (kg/ha)	Days to anthesis (day)	Days to silking (day)	Plant eight (cm)	Ear eight (cm)	Ear aspect (1-5)[a]
(AK9443DMRSR)2xYobeAccNo.2	5079	57	59	231	119	2.6
(AK9443DMRSR)2xJigawaAccNo.4(Y)	5035	57	59	234	128	2.5
(AK9443-DMRSR)2xJigawaAccNo.11	5022	57	58	238	125	2.4
(AK9443-DMRSR)2xKatsinaAccNo.3	4902	57	59	226	117	2.5
(AK9443-DMRSR)2xKanoAccNo.10	4813	57	59	232	121	2.6
(AK9443-DMRSR)2xYobeAccNo.3(Y)	4705	58	59	243	129	2.5
AK9443DMRSR	4918	57	59	230	115	2.6
OBA SUPER2	4550	57	59	212	109	2.4
TZLCOMP4C1	5213	59	60	229	117	2.5
Mean	4915.2	57.2	59.0	230.6	120.1	2.5
LSD ($p<0.05$)	514.6	1.5	1.7	24.1	20.9	ns

ns = not significant at p = 0.05 level

[a] Ear aspect on a scale of 1 to 5, where 1 = clean, well-filled ear, and 5 = ear with undesirable features

It was particularly striking that under several multilocation trials, the top three BC_1F_2 populations were equal in yield to the productive variety (TZLCOMP4C1), while the other three BC_1F_2 populations produced about the same levels of grain yield as the two checks. Among the top three BC_1F_2 populations, (AK9443-DMRSR2xJigawaAccNo.11) which ranked top under DS, ranked second and third in ML trials. The improved yield performance observed across ML could be attributed to similarity in frequencies of favourable alleles for grain yield present in the recurrent parent and the donor parents transferred into BC_1F_2 populations. The ML trials reported in this study were conducted in the agro-climatic zones, including rainforest, northern Guinea savanna, and the semi-arid Sudan savanna, which are the major agro-ecologies of sub-Saharan Africa. A modest increase in grain yields (at least 100 kg/ha) of farmers' improved local varieties would be an incentive, particularly for farmers growing maize in semi-arid ecologies of northern Guinea Savanna and Sudan Savanna in WCA.

CONCLUSION

Our study demonstrated that selection of the donor parents under water stress and their use to develop BC populations can be effective for exploitation of potentially useful alleles of drought tolerance hidden in local maize landraces to improve performance of elite maize germplasm. The top three BC_1F_2 populations identified in this study may offer opportunities for increasing gains

from selection. These populations could be subjected to additional backcrossing and recurrent selection under controlled drought stress to further increase the frequency of favourable alleles of drought tolerance and grain yield, mainly with additive effects. The resulting BC populations can be invaluable sources of varieties and parental lines of hybrids that combine drought tolerance with high yield potential for further testing under water stress and in multiple locations.

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INDUCED MUTATION FOR IMPROVED YIELD ASSOCIATED TRAITS IN SESAME (*SESAMUM INDICUM* L.)

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ABSTRACT

Artificial induction of mutation through the applications of various concentrations of colchicine on sesame (*Sesamum indicum* L.) was carried out with the aim of improving some agronomic traits that are of economic interest. Seeds of sesame (*Sesamum indicum* var. *Ex-Sudan*) were treated at five different colchicine concentrations (0.1Mm, 0.5mM, 1.0mM, 2.0mM and 0.0mM as control) for two mutant generations (M_1 and M_2). The results obtained following colchicine treatment in all the mutant generations revealed highly significant improvements ($P \leq 0.01$) in the desirable agronomic characters among the mutants such as the percentage germination (1 WAP), seedlings height, root length, height at maturity, number of leaves/plant, leaf area, number of pods/plant and number of seeds/pod with decrease in colchicine concentrations. However, the seedlings height and number of seeds/pod in M_2 increased significantly ($P \leq 0.05$) with decrease in the colchicine concentrations. But no significant difference was found in the effect of the mutagen on germination percents (2 WAP) of the M_1. Colchicine was therefore found to induce beneficial mutation in sesame by improving some of its agronomic traits. We therefore recommended the use of lower concentrations of colchicine (0.1mM and 0.5mM concentrations) for improving sesame agronomic traits that are of significant interest.

Key words: Agronomic Traits, Colchicine, Ex-Sudan, Mutation.

INTRODUCTION

Sesame (*Sesamum indicum*) commonly called beniseed in Nigeria belongs to the plant family *Pedaliaceae* (Purseglove, 1968; Pham *et al*., 2011; Abu *et al*., 2012). The name sesame is used in literature worldwide. It is mentioned in the old Hebrew and Egyptian scripts and the ancient Sanskrit literature. Some of the earliest references to sesame culture were made by the ancient Greek writers Theophrastus (4th century B.C.) and Solon (7th century B.C.) (Yermanos *et al*., 1964). It is also known as "simsim" in East Africa, "Till" in India and "Gingely" in Sri-Lanka. The Hausa, Ibo and Yoruba major tribes of Nigeria called it "Ridi", "Ekuku" and "Isasa" respectively. Other tribes in Nigeria also have names for it (Abu *et al*., 2011, Busari *et al*., 2005). Oplinger *et al*. (1990) indicated it to be highly prized oilseed crop in Babylon and Assyria about 4,000 years ago. It is ranked as sixth most important oilseeds crops in the world (Olowe *et al*., 2010). Sesame is therefore an important oil seed crop which has been cultivated in tropical and subtropical areas of Asia and Africa since 3050-3500 B.C (Bedigian and Harlan, 1986; Mondal

et al., 2010). Sesame is one of the most important oil-seeds crops that were of African origin (Bedigian, 2003). A member of the family Pedaliaceae, sesame is grown all over the world for its leaf (Mann *et al.*, 2003) used as vegetable and oily seeds (Burkill, 1997). Sesame oil is a source of vitamins, minerals and proteins (Pamplona-Roger, 1999).

Nigeria is among the major sesame exporting countries (Weiss, 1971) exporting 50,000 tons of sesame annually (FAO, 2010). But despites all the tremendous benefits of sesame, its cultivation and uses are not up to expectations. This is due to decreased in price coupled with high agronomic in-puts needed for its cultivation that are attributable to lack of high yielding varieties. More so, the cultivation of improved varieties is limited due to insufficient variety information. The farmers continue to grow local varieties with low yields. These constraints contributed immensely to the decline in sesame production in Nigeria. Therefore, efforts are needed to improve sesame varieties in order to meet the needs of the world's growing population.

Mutation (a change in genetic material of an organism) induced both in seeds and vegetatively propagated crops are of scientific and commercial interest to improve both the growth and yield parameters of economic plants. It provides raw materials for the genetic improvement of economic crops (Adamu *et al.*, 2004). It facilitates the isolation, identification and cloning of genes which would ultimately help in designing crops with improved yield, increased stressed tolerance, and longer life span and reduced agronomic in-puts (Ahloowalia and Maluszynski, 2001). Induced mutations facilitate the development of improved varieties at a swifter rate (Maluszynski, 1990). Besides the vital roles in plant breeding programs, induced mutations have been used to induce beneficial genetic modification that is utilized in improving yield components of various crops. Although various mutagens are known to induce mutation in plants, this research made use of colchicine (a poisonous alkaloid from autumn crocus plant (*Colchicum autumnale*) on sesame (*Sesamum indicum* L. *var. Ex-Sudan)* to improve the quantitative traits that are of agronomic interest.

MATERIALS AND METHODS

The research was conducted in the Botanical Garden of the Department of Biological Sciences, Ahmadu Bello University Zaria (Lat11^{0}N, Long 7^0 42^{1}E) in 2007 and 2008 growing seasons. The seeds of sesame (*S. indicum* L. *Var*. *Ex-Sudan*) were obtained from the Jigawa State Agricultural and Rural Development Authority (JARDA) Ringim. The seeds were treated at five different colchicine concentrations including control (0.1mM, 0.5Mm, 1.0mM, 2.0mM and 0.0mM) via soaking for four hours and washed thoroughly in running water for an hour. The treated seeds were sown in a plot with three blocks in a Randomized Complete Block Design (RCBD) with three replications. All cultural practices followed the protocols described in the Kano State Agricultural and Rural Development Authority (KNARDA) crop production guide (2005). Data were collected from the percentage germinations One Week After Planting (1WAP) and Two Weeks After Planting (2 WAP), seedlings height, root length, height at maturity, number of leaves/plant, leaf area, number of pods/plants, and number of seeds/pods. Analysis of Variance was used to analyze the data obtained, while Duncan's Multiple Range Test was used to separate the treatment means.

RESULTS

The results obtained for the analysis of variance in the M_1 generation following treatment of the sesame seeds with various colchicine concentrations revealed highly significant difference ($P \leq 0.01$) in almost

all the selected agronomic traits except on the germination percents in two weeks after planting (Table 1).

Table1: M_1 Mean Squares for the Effects of Colchicine on Sesame Agronomic Traits

Sources of Variation	Df	% Germination (1 WAP)	% Germination (2 WAP)	Seedlings Height (cm)	Root Length (cm)	Height at Maturity (cm)	Number of Leaves / Plant	Leaf Area (cm^2)	Number of Pods/Plant	Number of Seeds/Pod
Blocks	2	4.01**	0.02^{ns}	18.66**	11.85**	85.96**	18.70^{ns}	33.36**	5.85**	21.10^{ns}
Concentration	4	9.70**	0.48^{ns}	243.60**	8.02**	528.00**	334.34**	391.53**	61.73**	473.49**
Error	208	0.38	0.39	1.67	0.80	9.88	8.60	40.01	0.56	29.23

Keys: ns= No significant difference * = Significant difference ($P \leq 0.05$)
**= Highly significant difference ($P \leq 0.01$)

The mean effects of the mutagen on the agronomic traits of sesame are presented in Table 2. The result showed that 96-100% of the mutants germinated after one week of planting, but after two weeks, 77.83-88.83% of the mutants were found to be germinated. Similarly, the mutants at seedlings stage attained a mean height of 33.54-36.85 cm, with a root length of 6.33-7.10 cm. More so, the mutants attained a mean height of 76.33-82.67 cm at matured stage. Furthermore, the mutagen increased the number and size of the leaves from 17 to 25 leaves and 39.67cm^2 to 56.00 cm^2 respectively. Similarly, the pods number and seeds produced in each pod increased among the mutants from 3 to 5 pods with 57-67 seeds/pod. The effects of the mutagen increase with decrease in its concentration.

Table 2: M_1 Mean Effects of Different Colchicine Concentrations on Sesame

Concentration	% Germination (1WAP)	% Germination (2 WAP)	Seedlings Height (cm)	Root Length (cm)	Height at Maturity (cm)	Number of Leaves/ Plant	Leaf Area (cm^2)	Number of Pods/ Plant	Number of Seeds/ Pod
0.0 mM	86.67^{c*1}	72.17^{a}	30.31^{e}	5.67^{c}	60.33^{c}	17.40^{d}	39.67^{e}	3.00^{e}	50.67^{c}
0.1 mM	100.00^{a}	88.83^{a}	36.85^{a}	7.10^{a}	82.67^{a}	25.40^{a}	56.00^{a}	5.40^{a}	66.67^{a}
0.5 mM	100.00^{a}	83.33^{a}	35.71^{b}	7.00^{a}	81.33^{a}	23.00^{b}	53.33^{b}	4.27^{b}	60.00^{ba}
1.0 mM	95.50^{b}	77.83^{a}	34.43^{c}	6.67^{ba}	78.00^{ba}	21.80^{b}	51.00^{c}	3.73^{c}	58.33^{b}
2.0 mM	95.50^{b}	77.83^{a}	33.54^{d}	6.33^{b}	76.33^{ab}	20.00^{c}	49.00^{d}	3.40^{d}	57.33^{b}
MEAN	95.53	79.99	34.17	6.55	75.73	21.52	49.80	3.96	58.60
.S.E±	2.47	2.82	1.11	0.26	4.01	1.35	5.57	0.42	2.56

N.B: *[1] Means within the columns with the same letter(s) are not significantly different ($P \leq 0.05$)

However, the results from the analysis of variance of the M_2 generation following treatment of sesame seeds with different colchicines concentrations are presented in Table 3. The result indicated highly significant difference ($P \leq 0.01$) in the effect of different colchicine concentration on the selected agronomic traits of sesame; except in the seedlings height and number of seeds/pod where the effect is significant ($P \leq 0.05$).

Table 3: M_2 Mean Squares for the Effects of Different Colchicine Concentrations on Sesame Agronomic Traits

Sources of Variation	Df	% Germination (1 WAP)	% Germination (2 WAP)	Seedlings Height (cm)	Root Length (cm)	Height at Maturity (cm)	Number of Leaves/Plant	Leaf Area (cm^2)	Number of Pods/Plant	Number of Seeds/ Pod
Blocks	2	1.07^{ns}	0.72^{ns}	2489.40**	71.00**	112453.00**	39918.10**	73765.40**	13442.00**	8615.10**

Concentration	4	4.81**	1.38^{ns}	43.63*	7.00**	1357.60**	7342.80**	4416.30**	1200.00**	287.90*
Error	208	0.32	0.62	9.97	0.99	55.51	135.37	293.80	51.04	87.85

Keys: ns= No significant difference * = Significant difference (P≤0.05) **= Highly significant difference (P≤0.01)

However, the M_2 generation results of the mean effect of different colchicine concentration on the selected agronomic traits of Ex-Sudan are presented in Table 4. The results revealed that, 93-98% of the mutants germinated after one week of planting which reduced to 68.83-73.33% after two weeks. The mutants were found to attain a mean seedlings height of 17.13-18.20 cm. The mutants' roots were found to be 5.48-5.70 cm deep with a mean height of 72.87-82.93 cm at maturity. More so, the mutants produced large number of leaves which are bigger than those of the controls. Similarly, the mutants produced large number of pods that produced large number of seeds than the controls. The effect of the mutagen is concentration dependent and decreases with increase in concentration.

Table 4: M_2 Mean Effects of Different Colchicine Concentrations on Variety *Ex-Sudan*

Concentration	% Germination (1 WAP)	% Germination (2 WAP)	Seedlings Height (cm)	Root Length (cm)	Height at Maturity (cm)	Number of Leaves/ Plant	Leaf Area (cm^2)	Number of Pods/ Plant	Number of Seeds/ Pod
0.0 mM	84.50^{c*1}	76.67^{a}	14.93^{b}	4.90^{c}	65.73^{d}	41.13^{c}	41.07^{d}	13.33^{c}	40.47^{b}
0.1 mM	97.83^{a}	68.83^{b}	18.20^{a}	5.70^{a}	82.93^{a}	72.60^{a}	66.47^{a}	26.40^{a}	45.53^{a}
0.5 mM	95.50^{ba}	71.17^{a}	16.47^{ba}	5.95^{a}	75.60^{b}	68.27^{a}	52.13^{cb}	25.80^{a}	45.87^{a}
1.0 mM	95.50^{ba}	73.33^{ba}	17.13^{a}	5.60^{ba}	73.27^{cb}	61.47^{b}	53.27^{b}	19.67^{b}	45.47^{a}

2.0 mM	93.33[b]	72.17[b]	14.27[b]	5.48[b]	72.87[c]	58.53[b]	50.47[c]	18.67[b]	48.53[a]
MEAN	93.33	72.43	16.20	5.53	74.08	60.40	52.48	20.77	45.17
S.E±	2.33	1.28	0.72	0.17	2.76	5.41	4.66	2.42	1.30

N.B: *[1] Means within the columns with the same letter(s) are not significantly different ($P \leq 0.05$)

DISCUSSION

Artificial induction mutation technique has provided the development of new genotypes with desirable agronomic traits. The results obtained in this research implied that colchicine at various concentrations can improve quantitative traits of sesame. The increased mean germination percent after one week of planting due to colchicine revealed the effects of the mutagen in the germination process. This was in agreement with the findings of Ulmalkar *et al.* (1998) who reported high germination percentages in *Capsicum annum* due to Sodium Azide treatment but was in contrast to the work of Bird and Neuffer (1988) who reported reduction in the germinating rates in plants treated with mutagen. Germination been one of the critical stages required by sesame for its optimal growth as reported by Uzo (1998) was improved through the use of colchicines mutagenesis. Chemical mutagenesis through the application of colchicines increases the germination potentiality of sesame seeds; probably by stimulating the rates of enzymatic activities, facilitating the water absorption capacity of the seeds, by turning-on the genes responsible for controlling the seeds germination or by a combination of both. More so, the mean increase in height and roots length of sesame induced by colchicine at both seedlings and matured stages were due to the alteration of their genome integrated by environmental signals as reported by Uno *et al.* (2001); probably by increasing the rates of cellular division and expansion at their meristematic regions. This was in agreement with the findings of Hoballah (1999) who reported increased in plant heights of sesame due to mutagenesis; but was in contrast to the findings of Anandakumar and Sree-Rangasamy (1995) who reported decreased in plant height due to induced mutation in rice.

Leaves attributes such as size and number were also improved by colchicine. Increased leaf area in the sesame mutants was in agreement with the findings of Maluszynski *et al.* (2001) who reported increase in leaf area among *Zea mays* mutants. The increase in leaf area provides an increase in the surface area for gaseous ex-change which has considerable effect on the process of photosynthesis (Lockhart *et al.*,1996). The mutagen stimulated growth of the cells of the lamina causing its remarkable expansion. This finding was in agreement with that of Nura *et al.*(2011) who reported increase in the number of leaves among jute mutants due to chemical mutagenesis.

The mean increase in the number of pods produced per plant in sesame was in agreement with the work of Hoballah (1999) who reported increase in the number of capsules per plant among sesame mutants. Similarly, Ulmalkar *et al.* (1998) reported induced variability in number of seeds/pod in *Capsicum annum* due to induced mutation sodium azide. This was also similar to the work of Lonnig (1982) who discovered similar result among X-rays induced mutants of pea.

CONCLUSION

Artificial induction of mutation using colchicines was found to have beneficial effects on sesame. It was concluded that artificial induction of mutation through the application of different concentrations of colchicine improves the quantitative traits of sesame that are of economic interests.

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MORPHOLOGICAL EVALUATION OF SESAME (*SESAMUM INDICUM*) GERMPLASM FROM FIVE STATES IN NORTHERN NIGERIA

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ABSTRACT

Twelve accessions of Sesame (*Sesamum indicum* L.) germplasm, collected from five states of northern Nigeria (Kaduna, Niger, Nassarawa, Kogi, and Benue) were evaluated for morphological characteristics during the cropping season of 2012 at the experimental field of the Department of Biological Science, Federal University of Technology, Minna using a Randomized complete Block Design (RCBD). Data WAS collected for Plant height, Length of petiole, No of leaves/plant, Number of branches per plant and the Leaf surface Area per plant. While accessions NG01 showed the highest plant height at 2 weeks after planting, accessions KG01 and NA01 showed the least although all these were not significantly different. Several of the accessions were identified as showing good attributes for characters such as number of leaves and numbers of branches which are also yield indicators for both grain and oil. These accessions are potential candidates for further selection and breeding objectives. The results achieved therefore can be used for improvement of sesame in the north central part of Nigeria.

Keywords: Accessions; Morphological characteristics; Germplasm; *Sesamum indicum* L.

INTRODUCTION

Sesame (*Sesamum indicum*) is an annual plant which is considered one of the most important and oldest oil crops that belong to the Pedaliaceae family (Noorka *et al.*, 2011). It is considered to be the oldest oil seed plant and has been under cultivation in Asia for over 5000 years (Bist *et al.*, 1998). The crop has early origins in East Africa and in India. Today, India and China are the world's largest producers of sesame, followed by Myanmar, Sudan, Uganda, Nigeria, Pakistan, Tanzania, Ethiopia, Guatemala and Turkey(Nayar and Mehra, 1970; Bedigian, 2003).

World production fluctuates due to local economic, crop production disturbance and weather conditions. In Vietnam, sesame is known as the king of oil seeds due to the high oil content (50 – 60%) of its seed. It is widely cultivated as an oil crop in tropical and subtropical climate and it is mostly grown under moisture stress with low management input by small holders (Cagrgan, 2006). Numerous wild relatives occur in Africa which is believed to be its origin and a small number in India (Baydar, 1999). In Nigeria, it is often referred to as beniseed and it is widely used and very popular in parts of north, where it is mostly grown.

The seeds which yield half of their weight in oil are most commonly used in soups while the young leaves are used as soup vegetable while the stem and oil extracts are used in making local soups. Traditionally, the seeds are roasted and mixed together with roasted groundnut or used as soup thickening condiment. (Falusi and Salako, 2001). According to Kobayashi *et al.*, (1990), 36

species have been identified out of which 22 are found in Africa, 5 in Asia, 7 in both Africa and Asia, and one species each in Crete and Brazil. There are three cytogenetic groups of which 2n=26 consist of the cultivated *S. indicum* along with *S. alatum, S. capense, S.schenckii, S.malabaricum;* 2n=32 consist of *S.prostratum, S.laciniatum, S. angolense*. *S.angustifolium*, while *S. radiatum, S. occidentale, S.schinzianum* belong to 2n=64. In spite of the presence of wide range of variability, selection within the local genotypes and hybridization had not resulted in a considerable achievement towards sesame improvement. However, germplasm exploration has the potential to increase sources of variability that would provide more genetic diversity for sesame improvement.

MATERIALS AND METHODS

The sesame (*Sesamum indicum* L.) germplasm accessions used in this study were collected from local farmers in the growing regions in collaboration with the Agric. Development Project (ADP) of six states of Northern Nigeria namely Kaduna, Niger, Kogi, Benue, and Nassarawa, of Nigeria. The materials were laid out in a randomized complete block design with thirty (36) pots per block replicated three times, making a total of 108 pots. Ten seeds were planted per pot (i.e. five per hole in a pot).Three weeks after planting; each pot was thinned to two plants per pot.

Data was collected for the following characters: Plant height at 2, and 4weeks after planting and at maturity, distance from ground level up to the terminal bud on main axis of a plant in cm using a metre rule, Number of branches per plant, Length of petiole(cm) using a metre rule, Leaf surface area in cm^2, Survival rate at 21 days after planting rated as percentage.

Table 1: Description and sources of sesame germplasm materials

S/N	Accession Number	Local name	source	seed colour	colour of flower	Seed lgth (mm)
1	KD	Riddi	kafanchan/Kaduna	white	white	3-3.5mm
2	NG-01	Anufi	paiko/Niger	light brown	white	2-2.5mm
3	NG-02	Ishwa	saminaka/Niger	light brown	white	3 mm
4	NG-03	Esso	katcha/Niger	light brown	white	2-3mm
5	NG-04	Anufi	mayaki/Niger	Black	white	2-3mm
6	NA-01	Riddi	keffi/Nassarawa	creamy white	purple	2-3mm
7	NA-02	Riddi	keffi/Nassarawa	Brown	NIL	2-3mm
8	NA-03	Riddi	Doma/Nassarawa		white	white 2-3mm
9	BE-01	Ishwa	Guma/Benue	white	white	2mm
10	BE-02	Ishwa	Guma/Benue	Creamy white	white	3-3.5mm
11	KG-01	gogori	Akogu/Kogi	Creamy white	purple	3 mm
12	KG-02	gogorigo	okpereke/Kogi	light brown	white	2-3mm

Table 2: Means of plant height of sesame accessions collected

Accessions	plant Height (cm)		
	2wks	4wks	6wks
KD	4.41 ± 1.05^{ab}	17.89 ± 4.75^{a}	59.13 ± 16.34^{cd}
NG-01	4.71 ± 1.49^{a}	16.97 ± 5.44^{ab}	56.16 ± 15.73^{cd}
NG-02	2.50 ± 0.69^{ef}	16.74 ± 4.99^{ab}	63.40 ± 21.84^{bc}

NG-03	4.11 ± 0.77^{ab}	13.76 ± 4.40^{bc}	54.37 ± 16.62^{cd}
NG-04	2.32 ± 0.79^{f}	7.65 ± 3.63^{f}	46.40 ± 13.72^{e}
NA-01	1.94 ± 1.13^{f}	8.3 ± 2.70^{ef}	73.27 ± 4.86^{ab}
NA-03	3.75 ± 0.84^{bc}	11.90 ± 6.68^{cd}	48.90 ± 14.49^{cd}
BE-01	3.13 ± 0.74^{de}	12.67 ± 4.09^{cd}	75.10 ± 9.56^{a}
BE-02	3.49 ± 1.01^{cd}	11.54 ± 3.96^{cd}	48.90 ± 10.94^{de}
KG-01	2.09 ± 0.7^{ef}	11.02 ± 2.79^{de}	61.50 ± 15.36^{c}
KG-02	3.45 ± 0.92^{cd}	14.67 ± 3.41^{ab}	58.27 ± 17.78^{cd}

*Values are mean±SD. Means followed by the same letter(s) within the same row do not statistically differ at the 5% level according to DMRT, analyzed for the Accessions collected

Table 3: Means of some morphological parameters of sesame accessions

Accessions	Length of petiole	No of leaves/plant	No of branches plant	Leaf surface Area
KD	1.42 ± 0.56^{ab}	59.00 ± 29.35^{bc}	4.00 ± 1.89^{a}	20.33 ± 6.01^{ab}
NG-01	1.54 ± 0.57^{a}	52.00 ± 16.34^{bc}	3.00 ± 1.16^{ab}	18.77 ± 4.12^{ab}
NG-02	1.32 ± 0.56^{ab}	65.00 ± 31.04^{b}	2.00 ± 0.98^{bc}	19.43 ± 6.42^{ab}
NG-03	1.24 ± 0.33^{ab}	52.00 ± 25.45^{bc}	3.00 ± 1.57^{ab}	17.67 ± 6.42^{ab}
NG-04	1.12 ± 0.27^{b}	34.00 ± 17.95^{d}	1.00 ± 1.26^{d}	13.40 ± 4.97^{d}
NA-01	1.24 ± 0.42^{ab}	96.00 ± 32.88^{a}	4.00 ± 1.38a	16.83 ± 5.39^{ab}
NA-03	1.13 ± 0.40^{b}	40.00 ± 16.45^{cd}	1.47 ± 1.59^{cd}	15.53 ± 8.53^{bc}
BE-01	1.17 ± 0.47^{a}	51.00 ± 16.62^{bc}	2.00 ± 0.79^{bc}	14.40 ± 5.72^{cd}

BE-02	1.48 ± 0.60^{ab}	39.00 ± 15.84^{d}	1.93 ± 1.48^{c}	15.22 ± 6.99^{cd}
KG-01	1.20 ± 0.51^{a}	52.00 ± 26.30^{bc}	2.18 ± 1.19^{bc}	18.17 ± 5.31^{ab}
KG-02	1.21 ± 0.41^{ab}	52.00 ± 17.50^{bc}	2.00 ± 1.00^{bc}	20.67 ± 7.06^{a}

*Values are mean±SD. Means followed by the same letter(s) within the same row do not statistically differ at the 5% level according to DMRT, analyzed for the Accessions collected

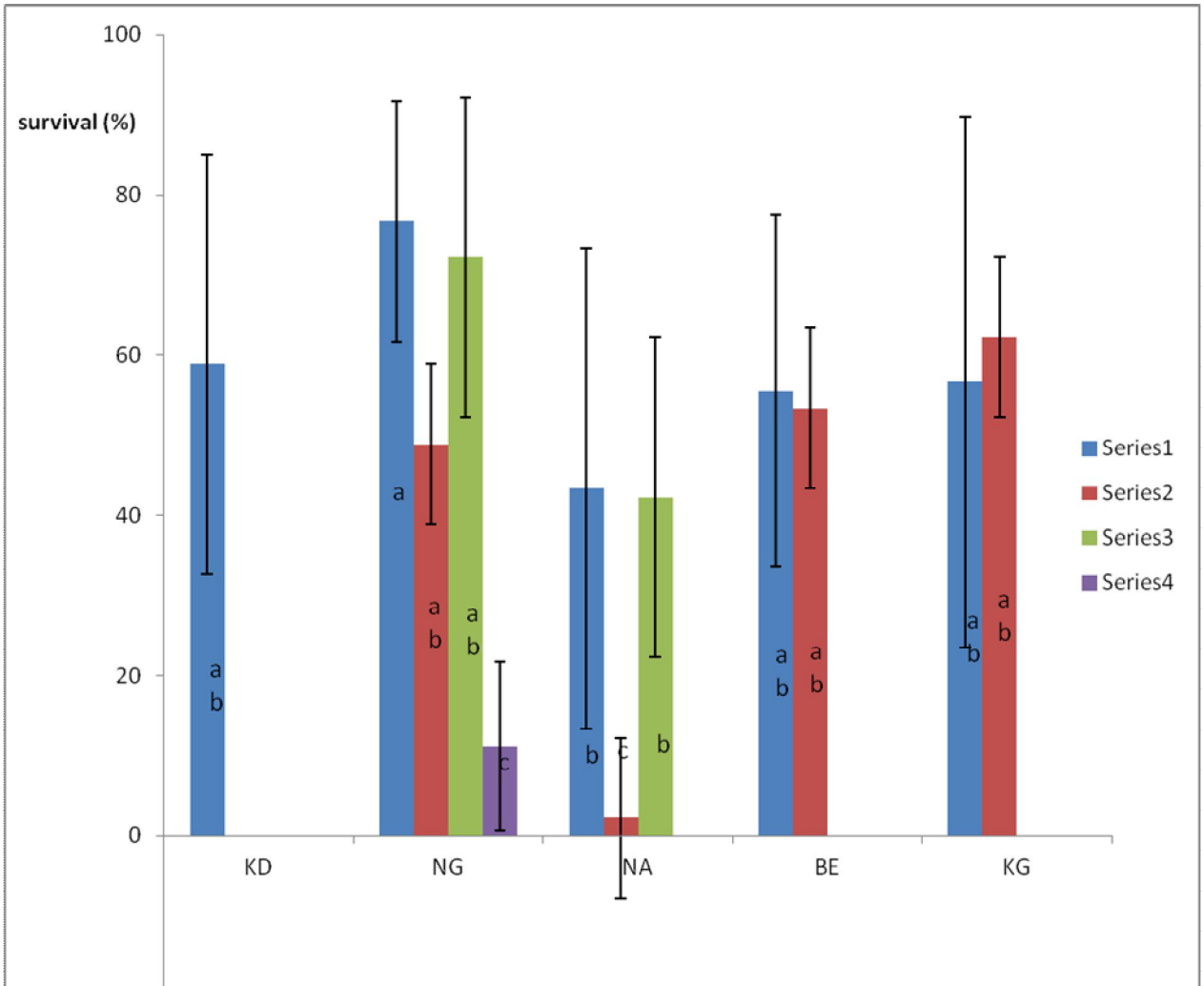

Fig.1: survival percentages (%±SD) of the different Accessions Collected

RESULTS AND DISCUSSION

In the present investigation, different quantitative characters were studied to estimate the variations in all the Sesame accessions collected. Parameters such as plant height, length of petiole, number of leaves per plant, number of branches per plant, leave surface area and survival percentage were studied. The Accession , NG01 showed the highest plant height (4.71) at 2 weeks after planting while the least was KG01 (2.32), and NA01 (1.94) respectively, no significant differences were observed between KD and NG-03 with their means (4.41) and (4.11). There were no significant differences among the Accessions ($p<0.05$) level of significant statistically (Table 2). At 4^{th} week (Table 2), the highest plant height was recorded at KD (17.89) followed by NG-01 (16.97) and NG-02 (16.74) and KG-02 (14.67) while the least was observed at NG-04 (7.65) but there are no significant differences among the other accessions at ($p<0.05$) level of significance. However, at 6^{th} week, (maturity), there were statistical differences observed where the highest plant height was recorded at BE-01 (75.10) while the least was observed at NG-04 (46.40) although there were no significant differences among KD (59.13) NG-01(56.16), NA-03 (46.90) and KG-02 (58.20) at ($p<0.05$), significant level, respectively.(Table 2).

The length of petiole showed that NG-01 had the highest mean with petiole length of (1.54) followed by NG-04 (1.12) and NA-03 (1.13), although there were no significant differences statistically at $p<0.05$ level of significant level in other Accessions Table 3. The accession with the highest number of leaves was observed at NA-01 (96.00) followed by NG-02 with the mean (65.00) and there are no significant differences statistically among the remaining accessions at ($p<0.05$) significant level (Table 3). The Accession NA-01 and KD had the highest number of branches both having the mean 4.00, the least values for the number of branches was observed in the Accession NG-04 (13.40) although there were no significant differences statistically at ($p<0.05$) significant level among the remaining Accessions (Table 3).

The Result showed that KG-02 had the highest leaf surface area with the mean (20.67a) and the least was observed from NG-04 (13.40d) but no significant difference was observed among the remaining accessions at ($p<0.05$) level of significance(Table 3). The percentages of all the accessions were taken. The accession NG01 had the highest percentage survival of 76.7% and the accession NA02 and NG04 had the lowest survival percentage of 2.2% and 11.11% respectively, although there were no statistical differences at $p<0.05$ level of significant but they were different from all other accessions. However, the accession NA03 and NA01 were different from all other accessions but they are not statistically different at $p<0.05$ with respect to their survival percentage of 42.22% and 43.33% respectively. In addition, the Accessions NG02,

BE02, BE01, KG01, KD, KG02 and NG03 are not statistically different at $p<0.05$ level of Significant Fig 1. The range of variations observed in some morphological parameters among the studied accessions like in plant height, number of leaves/plant is in conformity with (Alege *et al.*, 2013). Alege *et al.,* 2013 studied the morphological, proximate and mineral responses of sesame to different nutrient sources and observed that only four out of the eleven morphological traits studied showed significant differences across nutrient sources. These attributes are plant height, number of leaves, stem diameter, and number of pod per plant. He concluded that these four attributes are not under strong genetic influences and soil fertility status affects the expression of these morphological traits because according (Akinyele and Temikotan, 2007). The factors that may bring about variation in the original genome structure of a species include geographical isolation, chromosome aberration, infection and variation in edaphic factors. Variations brought about by infections and edaphic factors result in temporary phenotypic differences and as soon as the infections and variation in soil conditions are addressed, the differences usually fade away.

E. T. Blay *et al.,* (1999), also studied morphological and agronomic characterization of some tomato *(Lycopersicon esculentum)* germplasm in Ghana, They observed variations in plant height among eight accessions collected and that plant height ranged from 28.8 to 41. 8 cm. They concluded that plant height and other vegetative growth were suppressed probably due to the harsh environmental conditions during the growth period. This is also in line with the work of Messiaen (1992) who reported that tomato plant height may vary up to 2m tall. Seymus Furat and Bulent Uzun (2010), also studied agro-morphological characters for the assessment of genetic diversity in sesame (*Sesamum indicum*) and observed that there were variations in morphological characters such as plant height, number of fruiting branches, and other morphological characters. They reported that these characters also revealed a large genetic diversity and that the accessions with a wide range of variation for agronomic characters had potential to determine the best genotypes for different environments. Toan Duc Pham *et al*., (2010) also studied morphological evaluation of sesame varieties from different origins in Vietnam and Cambodia. They showed a positive relationship between plant heights, numbers of branches and seed production and concluded that the results achieved could be used for improvement of sesame varieties in various regions. These results were in agreement with previous observations of Varisai and Stephen (1964), Gupta and Gupta (1977), Pathak and Dixit (1992) that reported a positive relationship between plant height, and other morphological parameters.

CONCLUSION

The study on twelve sesame accessions collected from North central zones using evidence from morphological parameters indicated that genetic variability exists among Nigerian sesame. The diversity could mainly be attributed to diverse agro-climatic conditions in the different regions. Accessions from different regions were sometimes closely related and accessions from the same region had different genetic background. The intraregional diversity could be as a valuable source as interregional diversity for sesame improvement. The germplasm represents a valuable source of genetic diversity that is expected to be highly useful for future breeding programs.

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SOME MORPHOLOGICAL AND REPRODUCTIVE CHARACTERS IN *PHASEOLUS VULGARIS* L. AFTER TREATMENT WITH DOSES OF SODIUM AZIDE

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ABSTRACT

Four doses of sodium azide (0.1M, 0.04M, 0,03M and 0.02M) were used to induce mutation in the seeds of three varieties of *Phaseolus vulgaris* to study response to induced mutation as well as creating additional variability among genotypes of the crop using a randomized complete block design.The following parameters were studied; plant height, number of nodes, number of leaves, leaf length, leaf breadth, pod length, number of pods per treatment, number of pods per peduncle and 100 seed weight. Significance was tested at 0.05 level of significance.The red

kidney 0.02M showed the highest mean number of nodes among the red kidney treatments, but pinto 0.02M and 0.03M showed the highest mean number of nodes all in week 6.The pinto 0.02M showed the highest mean values for height in both weeks 4 and 6. Navy 0.1M on the other hand showed the least mean values for heights among the treatments. At week 6 all the pinto treatments surpassed the pinto control. All the navy treatments showed reduced leaf lengths and leaf breadth. Leaf length in the red kidney 0.03M and 0.02M performed better than the red kidney control. All the pinto treatments showed increased leaf lengths.The navy and red kidney treatments showed reductions in their number of trifoliate leaves in week 6. The pinto on the other hand showed all the pinto treatments increased in their mean number of trifoliate leaves except the pinto 0.1M which performed below the control in week 6. Apart from pinto 0.02M which showed the highest mean pod length, all the other pinto treatments performed lower than the pinto control. Navy and red kidney treatments had reductions in their mean number of pods per treatment, the pinto treatment had pinto 0.03M, 0.04M, 0.02M perform better than the pinto control. navy 0.1M had the least number of pods.

INTRODUCTION

Phaseolus is the most important legume worldwide for direct human consumption (Gepts, 2001) and a major protein and mineral source (Blair *et al.,* 2007). It is a herbaceous annual which is highly variable in terms of morphology (Purseglove, 1974) hence, its numerous names are based on its use, growth habits or morphology. Erect bushy or twining types are observed (Liamngee, 2006) and germination is the epigeal type (Raven, *et al.*, 1992). The leaves are alternately arranged and divided into three oval acuminate and entire leaflets. The leaves are trifoliate, petiolate and stipulate. The young leaves are used as a vegetable. The flowers are zygomorphic and can be white pink or purple. Phaseolus is grown for its immature edible pods which show colourations of green purple, yellow and black, for the dry ripe seeds and to a lesser extent for the green shelled beans (Nasser, *et al.*, 2010).

The medicinal uses of *Phaseolus vulgaris* are numerous and include a mild diuretic effect and contains a substance which reduces blood sugar especially in the unripe pods. Also there is research evidence that the regular consumption of beans reduces significantly blood cholesterol levels and lowers the risk of heart disease by about 22% (Rosa *et al.,* 1998). Also a bean diet has significantly reduced the risk for chronic diseases such as coronary heart disease, diabetes mellitus, obesity and cancer (Geil *et al.,* 1994).

The alteration of gene sequencies may be targeted or non targeted disruptions (Tierney *et al.,* 2005). This variations could be in increased yield, enhanced fitness in the ability to resist pest or disease, and to successfully endure both biotic and abiotic stress. Usually, both sporophytic (vegetative) and gametophytic(reproductive) parts of the plant of concern could be treated with the mutagen (Jain, 2010). Even though seeds have shown better results. The genetic modifications of plants using various methods have been going on for well over 80 years. This is loosely known as genetic engineering and it is critical for the understanding of the functions of genes and also the biological nature of DNA damage and repair. It has been demonstrated that genetic variability could be induced through mutations and it’s practical value in plant

improvement programmes well established (Kulthe, *et al.*, 2011), as a result a large number of plants useful to man have a developed by mutation breeding

Sodium azide acts by producing metabolites which initiate base substitutions (Alqurainy, *et al.*, 2009). The proteins hereafter produced does not have the same function as the original one (Alqurainy, *et al.*, 2009). The effect of sodium azide as mutagen on legumes and especially *Phaseolus vulgaris* have been properly documented. It was used to successfully generate useful economic traits such as days to maturity, number of pods per plant and number of seeds per plant amongst others in *Cicer arietenum* (Kulthe, *et al.*, 2011), in groundnut (Mensah, *et al.*, 2007) and many other crops. Considerable breeding work has already been done on *Phaseolus vulgaris* seeking to by various breeding tools express various genes of interest already contained in the genome of the plant. It is a self pollinating and posses limited variability. Because of its small genome, its genetic variation has become easily exhausted. Creating desired genes where and when they are needed has become the breeder's most viable option. This study was therefore designed to study the response of the plant to induced mutation while creating additional variability among genotypes of the crop.

MATERIALS AND METHODS

This study was conducted at the Mista-Ali Fadama Experimental site located on the outskirts of Jos, the Plateau state capital. The area has a mean annual temperature 26.81^0c and a mean annual relative humidity of 82.29%, it is elevated above sea level by 1,220m and it is aligned along longitude $8^0$53'E and latitude $9^0$57'N (Obigbesan, 1978).

The seeds used for this study were cultivars of *Phaseolus vulgaris* identified with respect to their colour, shape and size of seeds were obtained from local seed merchants. They were tagged as follows: Variety 1 (V_1) = pinto (black in colour),Variety 2 (V_2) = Red Kidney (red in colour) and Variety 3 (V_3) = Navy (white in colour). The experiment was laid out in a randomized complete block design using a plot size of 14.8m X 8.5m, divided into three blocks. Each block had 1 row of 15 plots making a total of 45 plots for the three blocks. Four doses of the mutagen were applied in the following concentrations; Dose 1(D_1) = 0.1M, Dose 2 (D_2) = 0.02M, Dose 3(D_3) = 0.03M, Dose 4 (D_4) = 0.04M, Control(D_0) = No treatment.

There were twelve treatment combinations and the experimental site was neatly cleared out and the beds raised for planting of seeds. The seeds were planted 15 per plot, in 3 rows and 5 columns on the 12th of November, 2012. The seeds planted to a depth of 2.5m (Purseglove, 1974). The whole experimental site was weeded on week 4 and week 8. The plants were sprayed with insecticides on the 46th and 47th Days After Planting (DAP) to kill insect pests. The plants were watered 3 times weekly till harvest.

Pinto, Red kidney and Navy *(Phaseolus vulgaris)* seeds were pre-soaked in distilled water up to ten times their volume, according to their varieties for 6 hours. While they were soaking, the mutagen solutions were prepared for four doses (D_1 = 0.1M, D_2 = 0.02M, D_3 = 0.03M, D_4 =

0.04M) for each of the 3 varieties. After soaking, the seeds were air dried for 20 minutes then soaked in the mutagen solutions according to their varieties for 11/2 hours. After the treatment time was over (11/2hours) the seeds were washed under running water for 30 minutes and immediately taken to the field for planting.

The heights of 6 randomly selected plants were measured. The measurement been from the ground to the highest plant part above the ground were taken with an inextensible string and related to a metre rule to obtain a numerical value in centimetres. The number of nodes of 6 randomly selected plants was counted for each treatment and the results recorded. All the leaves for six randomly selected plants, for each treatment were counted for all the treatments and their results were recorded. The length of the terminal leaflet of the trifoliate leaf at the fourth node was measured for six randomly selected plants per treatment at the seventh week after planting. The results were recorded. The breadth of the terminal leaflet of trifoliate leaf at the fourth node was measured for six randomly selected plants per treatment at the seventh week after planting. The results were recorded. The length of pods for 6 pods of 5 randomly selected plants per treatment were measured and the results recorded. The total number of pods on 5 randomly selected plants for each treatment were counted and the results recorded.

The number of pods on three peduncles were counted for 5 randomly selected plants per treatment. The results were recorded. One hundred randomly selected seeds were weighed on an electronic balance to determine the 100 seed weight of each treatment. This was done three times for each treatment to obtain a mean value which was recorded.

RESULTS

Table 1: Some Morphological Characters of M_1 *Phaseolus vulgaris* Plants

Number of Nodes for week 4	**Means**	**Number of Nodes for week 6**	**Mean**	**Heights(cm) for week 4**	**Means**	**Heights(cm) for week 6**	**Means**
Navy 0.02M	2.33[a]	Red kidney 0.04M	0.00[a]	Navy 0.1M	12.00[a]	Navy 0.1M	19.50[a]
Red kidney 0.1M	2.50[a]	Red kidney 0.1M	3.50[ab]	Red kidney 0.03M	12.12[a]	Red kidney 0.03M	20.75[a]
Red kidney 0.02M	4.71[b]	Red kidney 0.03M	4.00[abc]	Red kidney 0.04M	13.50[a]	Red kidney 0.04M	23.25[ab]
Red kidney 0.03M	5.00[bc]	Navy 0.1M	5.00[abc]	Red kidney 0.1M	14.50[a]	Red kidney 0.1M	24.00[ab]
Red kidney	5.00[bc]	Pinto 0.1M	5.22[abc]	Red kidney	15.00[a]	Red kidney	26.00[a]

0.04M			d	0.02M		0.02M	b
Navy 0.1M	5.50^{bcd}	Navy 0.04M	9.16 abcd	Navy 0.02M	15.75^{a}	Red kidney control	30.35^{a} bc
Navy 0.04M	5.83^{bcd}	Navy 0.03M	9.25^{abc} d	Navy 0.04M	16.16^{a}	Navy 0.04M	42.33^{a} bc
Pinto 0. 04M	6.44^{bcd}	Pinto 0.04M	9.44^{abc} d	Navy control	18.80^{a} b	Navy 0.02M	46.75^{a} bc
Navy 0.03M	6.62^{bcd}	Navy control	10.06^{a} bcd	Red kidney control	19.07^{a} b	Navy control	50.23^{b} cd
Pinto 0.03M	6.66^{bcd}	Red kidney control	11.21^{b} cd	Navy 0.03M	19.87^{a} b	Pinto control	52.16^{b} cd
Navy control	6.87^{bcd}	Pinto control	12.05^{b} cd	Pinto 0.03M	24. 16^{bc}	Navy 0.03M	52.22^{c} d
Pinto 0.1M	7.00^{cd}	Red kidney 0.02M	12.57^{b} cd	Pinto 0.04M	24.44^{b} c	Pinto 0.03M	64.50^{d} e
Red kidney control	7.14^{cd}	Pinto 0.03M	14.44^{b} cd	Pinto 0.1M	24.94^{b} c	Pinto 0.1M	65.77^{d} e
Pinto control	7.33^{d}	Navy 0.02M	14.88^{c} d	Pinto control	25.22^{b} c	Pinto 0.04M	68. 94de
Pinto 0.02M	7.66^{d}	Pinto 0.02M	16. 33^{d}	Pinto 0.02M	30.72^{c}	Pinto 0.02M	91.38^{c}

***** *Mean(s) followed by the same letters are not significantly different from each other*

Some Morphological Characters of M_1 *Phaseolus vulgaris* Plants (Cont'd)

Leaf length(cm)	**Means**	**Leaf Width(cm)**	**Means**	**Number of trifoliate leaves for wk 4**	**Means**	**Number of trifoliate leaves for wk 6**	**Means**
Navy 0.02M	3.50^{a}	Red kidney 0.1M	3.25^{a}	Red kidney 0.1M	0.50^{a}	Red kidney 0.1M	3.00^{a}
Red kidney 0.1M	4.50^{a}	Navy 0.02M	3.25^{a}	Red kidney 0.04M	2.33^{ab}	Red kidney 0.03M	7.50^{ab}
Navy 0.1M	4.75^{ab}	Navy 0.1M	4.75^{ab}	Red kidney 0.03M	3.00^{abc}	Red kidney 0.0M	8.33^{abc}

Navy 0.03M	7.37^{bc}	Navy 0.04M	5.50^{abc}	Navy 0.03M	3.00^{abc}	Navy 0.1M	9.00^{abcd}
Navy 0.04M	7.41^{bc}	Navy 0.03M	5.62^{bc}	Navy 0.1M	3.50^{abcd}	Red kidney 0.02M	10.71^{abcde}
Red kidney 0.04M	8.16^{cd}	Red kidney 0.04M	6.33^{bc}	Red kidney 0.02M	3.75^{abcd}	Navy 0.03M	11.57^{abcd}
Navy control	8.55^{cd}	Red kidney 0.03M	6.50^{bc}	Navy 0.02M	5.00^{bcde}	Navy 0.04M	12.00^{abcde}
Pinto control	8.77^{cd}	Red kidney control	6.71^{bc}	Pinto 0.02M	6.00^{cde}	Navy 0.02M	14.44^{bcde}
Red kidney control	9. 17^{cd}	Navy control	6.90^{bc}	Navy control	6.00^{cde}	Pinto 0.1M	15.66^{bcde}
Pinto 0.1M	9.46^{cd}	Pinto control	6.95^{bc}	Pinto 0.03M	6.500^{cde}	Pinto control	16.41^{bcde}
Red kidney 0.03M	9.75^{cd}	Pinto 0.04M	7.30^{d}	Pinto control	6.61^{cde}	Red kidney control	16.56^{bcde}
Pinto 0.03M	10.50^{d}	Pinto 0.03M	7.46^{d}	Navy 0.04M	6.66^{de}	Pinto 0.02M	16.77^{bcde}
Pinto 0.04M	10.75^{d}	Pinto 0.02M	7.65^{d}	Pinto 0.1M	6.70^{de}	Pinto 0.04M	19.05^{cde}
Red kidney 0.02M	10.83^{d}	Red kidney 0.02M	7.66^{d}	Pinto 0.04M	7.00^{de}	Pinto 0.03M	19.61^{de}
Pinto 0.02M	10.95^{d}	Pinto 0.1M	7.72^{d}	Red kidney control	7.85^{e}	Navy control	20.25^{e}

***** *Mean(s) followed by the same letters are not significantly different from each other*

Table 2: Some Yield Related Traits of M_1 *Phaseolus vulgaris* Plants

Pods per peduncle	**Means**	**Pod lengths(cm)**	**Means**	**Seeds per pod**	**Means**	**Pods per treatment**	**Means**	**100 seeds weight**	**Means**
Pinto 0.1M	1.00^{a}	Red Kidney 0.03M	10.83^{a}	Pinto 0.1M	5.50^{a}	Navy 0.1M	8.66^{a}	Navy 0.03M	14.94^{a}
Red kidney 0.1M	1.00^{a}	Red Kidney 0.02M	11.56^{ab}	Pinto 0.04M	5.50^{a}	Red kidney 0.1M	11.66^{a}	Navy 0.04M	15.26^{a}
Red kidney	1.00^{a}	Navy	11.70^{a}	Pinto	5.60^{a}	Red kidney	34.00^{a}	Navy 0.1M	15.3

0.02M		0.03M	b	control	b	0.03M	b		7[a]
Red kidney 0.04M	1.00[a]	Red kidney 0.04M	12.20[b c]	Pinto 0.02M	5.66[a b]	Navy 0.02M	39.00[a b]	Navy 0.02M	16.91[b]
Navy 0.1M	1.00[a]	Red kidney 0.1M	12.33[b cd]	Pinto 0.03M	5.73[a bc]	Red kidney 0.02M	39.33[a b]	Redkidney0.04M	19.19[c]
Navy 0.02M	1.00[a]	Red kidney control	12.76[b cde]	Navy 0.04M	6.17[a bcd]	Navy 0.04M	40.66[a b]	Redkidney 0.1M	19.27[c]
Navy 0.03M	1.00[a]	Pinto 0.1M	13.04[c de]	Red kidney 0.03M	6.39 [bcd]	Red kidney 0.04M	54.00[a b]	Navy control	19.33[c]
Pinto 0.03M	1.03[a]	Navy 0.04M	13.10[c de]	Navy 0.03M	6.50[c d]	Navy 0.03M	63.00[a b]	Redkidney control	19.50[c]
Pinto 0.02M	1.03[a]	Navy control	13.23[c de]	Navy control	6.75 [d]	Navy control	171.66[abc]	Redkidney0.03M	20.31[cd]
Navy control	1.03[a]	Pinto 0.04M	13.43[c de]	Red kidney 0.1M	6.78 [d]	Red kidney control	205.00[bcd]	Redkidney0.02M	21.56[d]
Pinto 0.04M	1.04[a]	Navy 0.02M	13.45[c de]	Red kidney control	6.86 [de]	Pinto 0.1M	277.33[cde]	Pinto 0.02M	38.37[e]
Red kidney 0.03M	1.05[a b]	Pinto 0.03M	13.50[c de]	Navy 0.1M	7.57[e f]	Pinto control	331.33[cde]	Pinto 0.03M	39.46[e]
Navy 0.04M	1.06[a b]	Navy 0.1M	13.50[d e]	Navy 0.02M	7.83[f]	Pinto 0.02M	361.66[de]	Pinto 0.1M	41.23[f]
Pinto control	1.15[a b]	Pinto control	13.80[e]	Red kidney 0.02M	7.85[f]	Pinto 0.04M	376.66[de]	Pinto 0.04M	41.30[f]
Red kidney control	1.20 [b]	Pinto 0.02M	13.82[e]	Red kidney 0.04M	7.95[f]	Pinto 0.03M	391.33[e]	Pinto control	43.42[g]

***** *Mean(s) followed by the same letters are not significantly different from each other*

DISCUSSION

In the navy treatment, navy 0.02M had the least mean number of nodes in the week 4. By week 6, it had the second highest mean number of nodes, next to pinto 0.02M. The navy treatments generally showed a reduction in their number of nodes as all of them performed below the navy control. This reduction in the number of nodes in the navy treatments could be due to the decrease in heights observed in the treatment as a result of the doses of sodium azide. In the week 6, navy 0.02M surpassed the navy control in the number of nodes. All the red kidney treatments also showed a reduction of the mean number of nodes in the week 4. In the week 6, the red kidney 0.02M surpassed the red kidney control even though the difference was not significant.

In the pinto treatments, the Pinto 0.02M surpassed the pinto control in height for both week 4 and week 6 and also showed the highest mean values for heights for both weeks. The navy 0.1M on the other hand showed the lowest mean values for heights for both week 4 and 6.In week 4, only the pinto 0.02M showed a statistically significant and positive shift over the pinto control. By the week 6, all the other pinto treatments (pinto 0.03M,0.1M, pinto 0.04M, pinto 0.02M) surpassed pinto control with pinto 0.02M showing the highest gains in height. Kulthe, *et al.*, (2011) also reported that at 0.02% of sodium azide, *Cicer arietenum* showed significant and positive increase in heights. This increase in heights could be due to the increase in the rates of cellular division and expansion at their meristematic regions (Nura, *et al.,* 2011).

Apart from week 4 where Navy 0.02M showed the maximum reduction in height, all the navy treatments were all next to only red kidney 0.1M showing maximum reduction in heights without the control. Kulthe, *et al.,* (2011) also observed that maximum reduction in seedling heights was obtained when sodium azide was used, comparatively. This suggests that sodium azide may be used in the reduction in heights of certain varieties. Reduced seedling height at higher mutagenic concentrations may occur due to gross injury caused at cellular level either due to acute chromosomal aberrations or gene controlled biochemical processes or both (Kulthe, *et al.,* 2011).

All the navy treatments showed reduced leaf lengths. In the red kidney treatments, red kidney 0.03M and red kidney 0.02M performed better than the control. All the pinto treatments showed positive increase in their leaf lengths.In the leaf breadth all the pinto treatments also showed positive and significant shifts. This may suggest that sodium azide can be used in successfully increasing the leaf size and of the pinto variety of *Phaseolus vulgaris.*
The navy treatments also all showed reductions in their leaf breadths. It may be recalled that all the navy treatments also showed reductions in their leaf lengths. Thus the use of sodium azide to reduce leaf size in the navy variety of *Phaseolus vulgaris* where necessary may yield good results.

Leaf length or width is usually associated with leaf area which is important for photosynthesis. Generally, a larger leaf area corresponds to more exposure to sunlight which means more photosynthetic activity in the plant for the production of more plant food. The number of trifoliate leaves reduced for each of the red kidney treatments, the red kidney control showing the highest mean number of trifoliate leaves in week 4. Red kidney 0.1M, 0.04M and 0.03M were the least of the treatments with respect to their mean leaf numbers in week 4. By week 6, the treatments with the least mean number of leaves did not change. Nevertheless, Navy control now had the highest mean number of leaves for week 6.
All the red kidney treatments also showed a reduction in their number of leaves in week 6. The navy treatments also performed less than navy control, while all the pinto treatments performed better than the pinto control except pinto 0.1M which showed a mean number of leaves slightly lower than the pinto control all in week 6. Generally the mutagen was effective in reducing the number leaves per treatment. This was corroborated by Mensah, *et al.*, (2007) when he reported that in his study on the effects of sodium azide and colchicine treatments on morphological and yield traits of sesame seeds that the number of leaves per plant indicated significant reductions at higher doses.

The effect of sodium azide on the treatments was clearly minimal. The highest mean number of pods per peduncle was 1.20 produced by red kidney control, closely followed by pinto control with 1.15 mean numbers of pods per peduncle. The least mean number of pods per peduncle was produced by pinto 0.1M. The difference between the highest and the lowest mean number of pods per peduncle was not greater than 1. It may therefore be concluded that sodium azide did not affect significantly the number of pods per peduncle in treatments of *Phaseolus vulgaris*.

Pinto 0.02M showed the highest mean length followed closely and also not statistically different from pinto control. Navy 0.1M performed better than navy control. Navy 0.02M also performed better than the navy control even though not significantly. All the red kidney treatments showed reduced pod lengths. Red kidney 0.03M was observed to have the least mean pod length. All the pinto treatments were observed to have reduced pod lengths except in pinto 0.02M which performed better than the control, even though not statistically.

Both Navy and Red kidney treatments had drastic reductions in their mean number of pods per treatment (Roopa, *et al.,* 2011). The pinto treatment had pinto 0.03M, 0.04M and pinto 0.02M showing higher mean number of pods then pinto control. Navy 0.01M had the lowest mean number of pods while pinto 0.03M had the highest. The mutagen was effective in reducing the number of pods per treatment in navy and red kidney varieties (Roopa, *et al.,*2011) as it can be observed that the highest doses for both varieties (Navy 0.1M and Red kidney 0.1M) are the observed to have the lowest number of pods per treatment. The pinto treatment however did not follow this trend. The worst performing pinto treatment (pinto 0.1M) performed better than all the navy and red kidney treatments. It is clear that at 0.1M, sodium azide reduces the number of pods that can be produced from all the three varieties. However, the pinto treatments unlike the other treatments had some treatments significantly performing better than the pinto control.

The pinto treatments all had their mean number of seeds per pod decreased significantly below the control. Navy 0.1M and navy 0.02M showed significantly higher mean number of seeds per pod. In the red kidney treatments, red kidney 0.02M and red kidney 0.04M performed better than the control, significantly. The highest mean number of seeds per pod was produced by red kidney 0.04M (7.95) closely followed by red kidney which produced 7.85 mean seeds per pod. The pinto 0.1M showed the lowest mean number of seeds per pod, significantly performing below the pinto control.

CONCLUSION

The observations from the verifications of this study indicate that sodium azide has a significant effect on the morphological and reproductive characters of *Phaseolus vulgaris*. however the doses used as treatments in this study were only weakly mutagenic without a buffer. The treatment doses induced the most useful mutations in the pinto treatments and were most lethal in the red kidney and navy treatments.

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CENTRE OF DIVERSITY OF TETRACARPIDIUM CONOPHORUM

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ABSTRACT

Walnut, Tetracarpidium conophorum(Mull.Arg) Hutch and Dalziel (now Pluckennetia conophora Mull. Arg) is from family Euphorbiaceae and is commonly referred to as African walnut. Tetracarpidium conophorum is found in Nigeria and Cameroon while Coula edulis (family olacaceae) which is also referred to as African walnut is found in Congo, Gabon and Liberia. The greatest diversity of *Tetracarpidium conophorum* exist in Southwest Nigeria especially in Ondo,Osun, Oyo,Ogun and Lagos states.Though they are found in other parts of Nigeria. Based on our knowledge from Vavilov, the origin of Tetracarpidium conophorum is South-West Nigeria.Most of the indigenous knowledge about planting, management, harvesting, and uses are found in these areas.

INTRODUCTION

Walnut, *Tetracarpidium conophorum* (Mull. Arg) Hutch and Dalziel (now *Pluckennetia conophora* (Mull .Arg)) is from the family Euphorbiaceae and is commonly called Africa walnut (GRIN 210, Babalola 2012). Although, walnut is a common name for small flowering plants that are important for the nuts and timber most of them produce (Ayoola etal 2011). Walnut comprises such families as Juglandaceae (English walnut), Euphorbiaceae (Africa walnut) and Olacaceae (African walnut). Each family has its own peculiar characteristics but they have some things in common such as the nuts. Juglandaceae is mostly found in the South East Europe, to Japan and more widely in the New World. *Tetracarpidium conophorum* is found in Nigeria and Cameroon while *Coula edulis* (family olacaceae) which is also referred to as African walnut is found in Congo, Gabon and Liberia (Wikipedia 2008; Ayoola et al 2011).

MATERIALS AND METHODS

Exploration and farm visit have been conducted in the areas at one time or the other. Information about the areas and *Tetracarpidium conophorum* were also gathered from the people from the areas.

Nikoli Ivanovich Vavilov stands in the forefront of contributors to our knowledge of global dispersal of crop plants and their wild relatives (Allard 1960). Vavilov proposed that the Centres of origin of species coincide with the areas where the greatest diversity exists in the species (Allard 1960).Whether or not such areas where the largest diversity exists are actually Centres of origin or only topographically or otherwise suited for the preservation of variation has little practical concern for plant explorations (Allard 1960). Vavilov also recognized the secondary Centres of origin and was careful to point out that valuable forms are found far removed from the primary area of origin (Allard 1960).

J. R. Harlan, during a plant exploration trip to turkey in 1948, was impressed with the tremendous plant diversity found in small areas.

These areas Harlan referred to as microcenters since plant evolution appeared to proceed from them at a more rapid rate than in other areas, particularly larger geographic regions. These micro- centers seemed to offer an excellent opportunity, not only to collect valuable types, but also to study evolution of cultivated types experimentally (Allard 1960).
If our knowledge gained from Nikoli Ivanovich Vavilov and J. R Harlan is anything to go by, the Centre of diversity of *Tetracarpidium conophorum* is South West Nigeria i.e Lagos, Ogun, Oyo, Ondo, Ekiti and Osun states in Nigeria. However not only that there are diversity of *Tetracarpidium conophorum* found there, but much indigenous knowledge about planting, management, harvesting and uses are found in these areas. The fruit is known as Awusa or Asala in these areas. These are Yoruba speaking states.

Tetracarpidium is a perennial shrub climber found in moist forest zones of South West Nigeria. It is cultivated principally for the nuts that are cooked and consumed as snacks along with boiled corn (Oke 1995; Edem et al, 2009; Babalola 2012). This is just like African plums (*Dacryodes edulis*). Both African walnut and African plums are boiled and consumed as snacks along with boiled corn.The two become ripe for harvest around the time of early maize season in Nigeria between April- July of the year. A bitter taste is usually observed upon drinking water immediately after eating the nuts (Ayoola et al.2011). However, apart from boiling, just like African plums, the people in this centre of diversity do roast walnut also for consumption though this is usually practiced by children.

Tetracarpidium conophorum is usually planted in cocoa plantation in these areas. The farmers version of cocoa plantation in these areas contain banana, plantation, guava, citrus species, oil palm, bitter kola, yellow yam, white yam called " dagidagi", *Theumatococcus daniella*, cocoyam, kolanut, sometimes Irvingia(bush mango), cashew tree, *Vernonia armygdlina* and mango but cocoa tree normally constitute more than 80% of the plantation. The plant of *Tetracarpidium conophorum* is normally planted under a tree that is not much of economic importance on these farms (Babalola 2012). The reason is that this support tree apart from providing strong support for the heavy weight of climber when fully established on the crown of the tree, walnut takes over the crown of the tree which is used as support. The walnut therefore competes for sunlight with the "host tree" and also affects fruiting of the host tree (Babalola 2012). The farmer therefore do not normally use cocoa tree, or kolanut tree or citrus tree as the support .If the walnut "stray" to the top of cocoa tree or kola nut tree, the farmers normally prunes the branches or destroy the walnut shrub completely. The shield or canopy formed by the walnut in cocoa plantation increased the humidity in the cocoa farm which is already a problem in cocoa plantation and reduce the penetration of sunlight which is highly essential in cocoa plantation. This leads to increased activity of *Phytophtora palmivora* and *Phytophtora infestans* (the fungi) that cause black pod disease of cocoa.

Over 80% of the farm in these areas are owned by men, however about 20% of the women also own cocoa farm. However, these women acquired the ownership either by inheritance of the plantation from their late father or late husband or by purchase of the plantation. Many of the women were not the ones who established the cocoa plantation.

However, it is the women and children that gather the fruits of walnuts that drops at maturity (Babalola 2012). The larger percentages of fruits are normally allowed to rotten before removing the seeds. The removal is done by knife and cutlass (Babolola 2012) but preferably narrow sharp knife for easy removal. The gathered fruits many at times are sold uncooked to "large scale

gatherers" who purchased in large quantities from house to house to go and sell to retailers. The retailer normally boils the seed and packaged them in nylon usually four for #20.00 or six for #50.00 as of year 2013, depending on the size of the seeds and the place of hawking or sale. The farmers do not harvest the fruit from the shrub. It is the believe of the farmers that once you start harvesting the fruit from the top of the tree, it will start aborting the immature fruits once the fruits reach the stage in subsequent years. The physiology behind this is not known.

Walnuts are considered to be an herb in traditional Chinese medicine. They are said to tonify kidneys, strengthen the back and knees, moisten the intestines and move stool. It is believed to stop asthma and is prescribed to be taken between bouts of asthma, but not for acute asthma. It is used as a constipation cure (Ayoola et al 2011).The bark is used in tea as laxative and chewed for toothache. It helps to prevent and control high blood pressure (Ajaiyeoba and Fadare 2006; Babalola 2012). The leaf juices are also used for the treatment of prolonged and constant hiccups (Onyenuga 1997; Ayoola 20011). However, in these centers of diversity the raw uncooked fruit is also eaten to serve as first aid for the cure of snake bites. Also, walnut must be consumed within two days after it has been cooked or else it will develop fowl odour and process of decay will start which make the product unfit for sale or consumption (Babalola 2012). However, the people in these areas normally roast any leftover on wire mesh after two days if not sold. However, these roasted products are normally consumed by the family of the marketers because they are not fit for sale any longer. At this point the fruit turn brown instead of white color and fruit is no longer brittle as it used to be if consumed fresh after boiling. Also, it must be noted that during consumption the hard shell are removed, followed by splitting of the seeds and embryo is normally removed before consumption. The people in these centres call the emryo removed as "oju iku" meaning "death eye". Also, it should be mentioned that in these centre of diversity various walnut trees have different sizes of fruits. However, from the same tree, though the normal thing is for the fruits which are in pods to contain four seeds in shell separated by thin layer of the pods, but some pods contain three seeds, some contain two seeds, while some contain one. The fifth seeds in some cases are small and not fully developed and cannot be eaten.

Also in these centers of diversity, those who hawk the cooked seeds in villages in trays normally group the seeds on broken shells of cracked palm kernels or sands, probably to drain water from shells of walnuts to slow the process of decay and development of foul odor that render it inconsumable.

Farmers sometimes also prefer to plant walnut close to the hedge of their farms where they have land mark that demarcate their plantations from their neighbors probably because of the shade it creates on the farm.

These centers of diversity in Nigeria where walnut is known in Yoruba language as Awusa or Asala include Afijio Local Government Areas in Oyo state, Ogbomosho areas, Ido Local Government Areas in Oyo state. Odeda Local Government areas in Ogun state, Ajebo areas in Ogun state. Also, in Osun state, it include Ikire, Apomu, Ile-Ife areas, Iyanforogi, Abata Egba, Aye Koka, Aba Joshua, Yekemi, Amodo, Ale-Amodu, Oke-Aba, Idi-Ogun Arode, Idi-Ako, Atere, Ilaka, Aye Oba, Okerenbete, Adereti, Garage Olode, Omifunfun, mefoworade, Aba Ijesa, Onigbodogi etc. In Ondo state, it include Ondo town, Ajue, Bagbe, Lasia, Asewele Korede, Asewele Oja, Omifon, Odigbo, Ale otu, Ore, Sifawu village. Also it includes Oko Oba, Emure, Ise-Ekiti in Ekiti state.

CONCLUSION

However, with the increased rate of deforestation and urbanization and due to the life span of the walnut, the answer to preservation of the genetic diversity is extensive exploration and collection program devoted to the assembling of as much of the germplasm and diligent maintenance of ex-situ genebanks of the material once they are collected (Allard 1960). Work will commence earnestly on conservation of the diversity if funds are available during next harvesting season.

Cameroun is probably the secondary center of diversity of *Tetracarpidium conophorum*.

Fig. 1

Fig. 2

Fig. 3

Fig. 4

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HYBRID VIGOUR AND GENETIC CONTROL OF SOME QUANTITATIVE TRAITS OF TOMATO (*LYCOPERSICON ESCULENTUM*)

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ABSTRACT

The parental lines and the F_1 generation of domesticated tomato (*Lycopersicon esculentum*) namely; Petomech, Grosso and Insulata obtained from Naples, Italy and *Lycopersicon pimpinellifolium* (the wild parent) were evaluated at the Teaching and Research Farm of the Department of Crop Science, University of Nigeria, Nsukka. The experiment was laid out in a randomized complete block design with three replications. Data were collected on; number of flowers/truss (NFT), number of trusses/plant (NTP), number of fruits/truss (NFRT), number of fruits/plant (NFP), fruit yield (FY), and average fruit weight (AFW)**.** Better Parent Heterosis (BPH) of the traits was estimated for the hybrids, genetic variances, gene effects and heritability of the traits were also estimated. The result of the BPH showed that the cross, W x P had the highest positive BPH of 358.36 % in fruit yield. The highest negative BPH of -95.59 % was recorded for the hybrid, W x G in average fruit weight while the hybrid, In x G had the lowest negative BPH of -16.27% in average fruit weight. Additive gene action and additive x additive gene action (*aa)* were significantly in control of three crosses, W x P, W x In and W x G in fruit yield. Additive variance was higher than dominance variance in fruit yield for all the hybrids having the wild as one of its parents such as in W x In (7925.091), W x In (3610.39) and W x P (9728.06). Hybrids with wild as one of its parent as, W x G, W x In, and W x P had the highest narrow sense heritability in fruit yield (59.15 %, 51.69 %, 59.88 %, respectively). High level of epistasis controlled some of the quantitative traits and hybridization was effective in developing new tomato cultivars with heterotic effects in the fruit yield.

Keywords: hybrids, heterosis, gene effect, genetic variance and heritability

INTRODUCTION

The domestication and improvement of crops through breeding has been highly effective in concentrating allelic variation that confers useful characteristics for cultivation and consumption (Osborn *et al.*, 2007). The objectives of hybridization in breeding self- pollinated crops, is to combine in a single genotype genes that are found in two or more different genotypes (Allard, 1960). The ability to use a particular wild relative depends on the recovery of progeny from the

initial and subsequent crosses of tomato with the wild source, although all species can be crossed with tomato, the ease of success varies greatly (Osborn *et al*., 2007).

Hybrid tomato usually produces higher yield, they generally matures earlier and more uniformly (Shankara *et al.,* 2005). Hybrid plants are usually heavy producers, and they combine the character of the parent plants. Many hybrids have better fruit quality and disease resistance. Resistance genotype should also possess other desirable economic traits to make them viable at commercial level (Kumar *et al.,* 2009). Previous studies have suggested that increasing genetic distances (variability) between parents, increases heterosis (Moll *et al*., 1965; Mechinger, 1999).

Choudhary *et al.* (1965) emphasized the effective utilization of heterosis to step up tomato production. Heterosis can be expressed when the parents of a hybrid have different alleles at a locus and there is some level of dominance or epistasis among the alleles (Falconer and Mackay, 1996). It has been suggested that plant yield is a multiplicative trait that integrates variation from several other traits and therefore it may be expected that the trait would exhibit higher level of heterosis (Williams, 1959). Allard (1960) observed that the beneficial effect of crosses appear immediately in the F_1 exhibiting heterosis. When parents differ considerably in type, the yields of the hybrids will be, with fewer exceptions, substantially greater than those of the better parent (Allard 1960; Hossain *et al.,* 1982). The increased yield of hybrids could be as a result of high yielding parents selected for hybridization (Courtney and Peirce, 1979). Sharma *et al.* (2001) observed negative better parent heterosis in average fruit weight. Generation mean analysis (Mather & Jinks, 1982) is a useful technique that gives the estimation of main genetic effects such as additive, dominance and their allelic interactions involved in the expression of quantitative traits. The prevalence of any of the genetic effects will largely determine an effective breeding method for further development of new cultivars. El- Agamy *et al*. (1975) had suggested maximum progress in new cultivar development using pedigree selection in traits where non – additive gene effect is prevalent where as hybridization will be effective in traits dominated by dominance and epistatic gene effects. The need to develop tomato genotypes that will replace the existing exotic and landrace types that are either not adaptable or poor in quality motivated this study. The objective of this research was to develop new tomato genotypes expressing heterosis in fruit yield and quality and investigate the genetic control of the main quantitative traits controlling fruit yield in tomato. This information will be very useful in the development of new cultivars with improved fruit quality and highly adaptable to the environment by tolerance to the prevalent high temperature, rainfall and disease infestations.

MATERIALS AND METHOD

The experimental materials used for the study were three parental lines of domesticated tomato (*Lycopersicon esculentum*) namely; Petomech, Grosso and Insulata obtained from Naples, Italy and *lycopersicon pimpinellifolium* (the wild parent) obtained from Mbu in Isi- Uzo Local Government Area of Enugu state. A 4 x 4 diallel analysis using Griffing's 1956 model 1 method 2 was employed to produce 6 F_1 hybrids. The parental lines and the F_1 hybrids were evaluated at the Teaching and Research farm of the Department of Crop Science, University of Nigeria, Nsukka. The experiment was laid out in a randomized complete block design with three replications. Each replication and plot was separated by a 1 meter wide path. Well cured poultry manure was broadcast at the rate of 10 ton/ha a week before transplanting. Transplanting was done at one month after planting with a spacing of I m x 0.6 m. NPK 20:10:10 was applied at the

rate of 300kg/ha one month after transplanting. Weeding and all cultural practices were carried out as at when due. The parents were evaluated along with the hybrids on the following traits; number of flowers/truss (NFT), number of trusses/plant (NTP), number of fruits/truss (NFRT), number of fruit/plant (NFP), fruit yield (FY), average fruit weight (AFW)**.** Heteriosis was estimated as better parent heterosis (BPH) as put forth by (Allard, 1960; Uguru 2005) as follows;

$$BPH = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Where $\overline{F_1}$ is the mean of hybrid,

$\overline{BP}$ is the mean of the better parent

Test of significance was done as described by Kumar *et al*. (2011):

$$\text{CD} = \sqrt{\frac{2me}{r}} \times t$$

t= t tabulated at 5% probability;

r=number of replications

me = error mean square

2= a constant

Components of the generation means were evaluated using Hayman (1958) model as explained by Singh and Chaudhary (1985) as follows;

$$a = \overline{B_1} - \overline{B_2}$$

$$d = \overline{F_1} - 4\overline{F_2} - \left(\frac{1}{2}\right)\overline{P_1} - \left(\frac{1}{2}\right)\overline{P_2} + 2\overline{B_1} + 2\overline{B_2}$$

$$aa = 2\overline{B_1} + 2\overline{B_2} - 4\overline{F_2}$$

$$ad = \overline{B_1} - \left(\frac{1}{2}\right)\overline{P_1} - \overline{B_2} + \left(\frac{1}{2}\right)\overline{P_2}$$

$$dd = \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{B_1} - 4\overline{B_2}$$

t value of effect = $\frac{effect}{SE\ of\ effect}$

a = additive mean

d= dominance effect

aa = additive x additive

ad = additive by dominance

dd = dominance x dominance

$\overline{B_1}$ = mean of backcross to parent 1

$\overline{B_2}$ = mean of backcross to parent 2

$\overline{P_1}$ = mean of parent 1

$\overline{P_2}$ = mean of parent 2

$\overline{F_1}$ = mean of First filial generation

$\overline{F_2}$ = of mean second filial generation

SE= standard error

The estimate of the genetic variances of the quantitative traits was determined using the variance estimate method as described (Acquaah, 2007; Uguru, 2005).

$m = \overline{F_2}$

$\text{Ve} = \frac{P_1 + P_2 + F_1}{3}$

$\text{Va} = 2F_2 - (BC_1 + BC_2)$

$\text{Vd} = \frac{\left(\left(BC_1 + BC_2 - F_2 - \left(P_1 + P_2 + F_1\right)\right)\right)}{3}$

$\text{Vp} = \text{Ve} + \text{Va} + \text{Vd}$

$\text{Vg} = \text{Va} + \text{Vd}$

$\text{H b} = \frac{Vg}{VP} \times 100$

$\text{Hns} = \frac{Va}{Vp} \times 100$

Where;
Ve = environmental Variance
Va = additive variance
Vd= dominance variance
Vp= phenotypic variance
Vg= genotypic variance
Hb= broad sense heritability
Hns = narrow sense heritability
The variances of the parental lines, F_1, F_2, BC_1 and BC_2 population was used in determining the additive variance, dominance variance, genotypic variance, phenotypic variance, environmental variance, and heritability.

RESULTS

Estimates of Better Parent Heterosis (BPH) of the agronomic, yield, yield component traits showed that, negative BPH was recorded in number of flowers/truss gave for all the crosses with W x G having the lowest negative value of –35.6% while G x P had lower negative BPH value of -4.82 % (Table 1). The cross, In x G had higher BPH of 19.42 % and 14.56 % in number of trusses/plant, and fruits/truss, respectively than all the hybrids. The hybrid, In x P had the lowest negative BPH in number of fruits/plant (-23.52 %). The cross, W x P had the highest positive BPH of 358.36 % in fruit yield. All the hybrids had negative BPH in average fruit weight. The highest negative BPH of -95.59 % was recorded for the hybrid, W x G for average fruit weight while the hybrid In x G had the lowest negative average fruit weight of -16.27%.

The result of the genetic effects of the agronomic, yield and yield traits of the tomato varieties studied showed that, significant additive gene effect was shown in W x P, W x In and W x G for number of flowers/truss (Table 2a). The cross, W x P, had significant *ad* gene action in number of flowers/truss. Dominance x dominance (*dd*) gene action was recorded in In x G, In x P, G x P and W x In in number of flowers /truss. Additive gene action was significant in the crosses, In x G, W x P, W x In and W x G (Table 2a). *aa* gene effect was also significant in In x G, In x P, W x P, W x In and W x G in number of trusses/plant. The crosses, W x P, W x In, W x G had

significant additive gene effects on the trait (Table 2a). *dd* gene effects was significant in all the crosses with the exception of In x P. Significant *ad* effect showed in W x P in number of fruits/truss. It was observed that additive gene action was significant in four cross combinations including; In x G, W x P, W x In and W x G in number of fruits/plant (Table 2b). Significant *aa* gene effect was recorded in In x P, W x P and W x In. Also, the crosses, In x P, W x P, W x In and W x G had significant *ad* effects in number of fruits/plant. In average fruit weight, the cross, G x P had significant additive gene effect while *aa* gene effect was significant in W x G cross for average fruit weight (Table 2b). Additive gene action was found to be significant in three crosses, W x P, W x In and W x G. (Table 2b). Additive x additive *aa* gene action was also significant in W x P, W x In and W x G crosses.

A decomposition of phenotypic variance into additive, dominant and component were carried out for the different crosses (Tables 3- 8). Additive variance was higher than dominance variance in fruit yield for all the hybrids having the wild as one of its parents that is W x In (7925.091), W x In (3610.39) and W x P (9728.06). Dominance variance was higher than the additive variance in fruit yield for hybrids of two exotic parents such as In x P (2725.24), In x G (3676.97) and G x P (2272.85). Fruit yield had the highest environmental variance than all the traits in all the hybrids studied. Hybrids with wild as one of its parent (W x G, 59.15%; W x In, 51.69%, and W x P; 59.88 %) had higher narrow sense heritability in fruit yield. The other hybrids had low narrow sense (< 50) heritability in fruit yield.

DISCUSSION

The magnitude of heterosis depends on the accumulation of favourable dominant alleles in the F_1 population. Negative BPH that occurred in all the crosses in number of flowers/truss, and number of fruits/plant could be as a result of long distance in the traits between the exotic and the wild parent. However, the results are in agreement with the findings of Sharma *et al.* (2001) who observed negative heterosis in number of fruits/plant in tomato. In fruit yield, high positive BPH was recorded in all the crosses having the wild as the mother plant (Pistillate parent) probably because the wild had transferred traits for high yield to such crosses. When parents differ considerably in type, the yields of the hybrids will be, with fewer exceptions, substantially greater than those of the better parent (Allard 1960; Hossain *et al.*, 1982). Tolerance of the wild traits to high temperature and rainfall pattern of the study area coupled with high components of yield are good indicators of higher yield in the wild variety. Also the increased yield of hybrids could be as a result of high yielding parents selected for hybridization (Courtney and Peirce, 1979). Hence, the dominance of such traits of the wild in all the crosses where the wild was the mother parent indicated the presence of maternal effect and BPH for fruit yield. This result is in conformity with the report of Dharmatti *et al.* (2006) who showed a positive BPH for fruit yield in tomato. Earlier, Sharma *et al.* (2001) had reported a negative BPH in fruit yield of tomato hybrids. The negative BPH recorded in the average fruit weight for all the crosses studied showed that none of the crosses had fruit weight that was bigger than the better parent. This could be attributed to the dominating effect of the small fruit size over the larger fruit size. This is in agreement with Sharma *et al*. (2001) who observed negative BPH in average tomato fruit weight.

Narrow sense heritability is of great importance to the breeder. This is because it is the ratio of additive variance to total variance. Additive variance is the variance that causes resemblance among relatives (Acquaah, 2007). The high narrow sense heritability (>50) recorded in fruit

yield of W x G, W x In and W x P showed that these traits are highly heritable and should be selected for further studies in those crosses. This result is in conformity to the findings of Ghosh *et al.* (2010) who recorded high heritability and high genetic advances in trusses/plant, fruits/plant, branches/plant, fruits/truss, fruit weight, and yield/plant of tomato hybrids. Wide levels of variation in broad sense heritability and narrow sense heritability in number of trusses/plant, fruit yield and average fruit weight in the crosses involving the exotic alone, In x P and G x P as well as exotic by wild is suggestive of higher environmental influence in the performance of such traits than other ones

Phenotypic variance was higher than the genotypic variance in all the traits showing that there was an interaction of the traits with the environment. However, the low environmental variance in most of the traits suggests that the differences observed were mainly genetic. Traits high in narrow sense heritability and genetic variance indicated that they are controlled mainly by additive genes that are heritable and thus transferred from one generation to another. Such additive inheritance have been reported by Causse *et al*. (2003) in some traits in hybrids between large-fruited and cherry tomato fruit lines.

Positive and significant additive gene effects occurred in all the crosses that had the wild as one of its parent in number of flowers/truss, trusses/plant, fruits/truss, and fruits/plant. These traits are therefore highly heritable. This agrees with Gamble (1962) that gene effect is positive if better performing inbreds are used as P_1. In number of fruits/plant, *aa* and *ad* were significant in crosses between the wild and an exotic. Dominance x dominance effects was significant in all the crosses except in number of fruits/truss in In x P. This result is in agreement with Zdravkovic *et al*. (2011) who reported *dd* interaction in fruit weight. In fruit yield, additive, *aa* were significant in all the crosses between wild and an exotic parent. This showed that these traits can be fixed for possible selection of promising genotypes at early generation. Average fruit weight that showed significant epistatic, additive x additive effect in only a cross (W x G) with wild as parent is suggestive of the expression of linkage drag from the wild variety small fruit size that dominated the F_1. The wild variety is intended to transfer genes for resistance to disease, adaptability to environmental conditions and high fruit number/plant. It goes on to transfer as well as the genes that reduces the fruit size and that quality affects the fruit size of the F_1 not minding the fruit size of the better parent, even though the F_1 in most crosses gave higher fruit yield. The prevalence epistatic, additive x additive, and additive x dominance gene control in the crosses with wild as a parent in number of fruits/plant could be the expression of high level of fruit number on a plant in the wild which tends to dominate the exotic variety.

CONCLUSION

Better parent heterosis which is of great importance to farmers was found to be higher in crosses having the wild as the pistilate parent, (W x G, W x P and W x In) for fruit yield. Hence, our findings show that the wild tomato variety is a good donor of genes for improvement of quantitative traits and yield in tomato. Also high narrow sense heritability was recorded in these hybrids for these trait. High narrow sense heritability and genetic variance observed in some traits indicated that they are controlled mainly by additive genes that are heritable and thus transferred from one generation to another. The high level of epistasis in the control of number of fruits/plant in those crosses with hybrid vigour in fruit yield indicated that the trait was very important in determining high yield and hybridization was effective in developing new tomato cultivars with heterotic effects in fruit yield

Table 1: Estimates of the Better Parent Heterosis (BPH) of the agronomic, yield and yield component traits of the F_1 hybrids of tomatoes used for the study

Variety	NFT(%)	NTP(%)	NFRT(%)	NFP(%)	FY(%)	AFW(%)
In x G	-14.03	19.42	14.56	-23.52	36.02	-16.27
In x P	-33.93	17.65	-30.93	-4.61	60.00	-37.06
W x In	-32.72	-54.14	-19.65	-61.51	215.38	-90.82
W x P	-7.95	-51.01	12.94	-38.19	358.36	-84.71
W x G	-35.60	-53.70	-25.45	-67.99	71.91	-95.59
G x P	-4.82	-19.08	-40.91	-56.18	-33.33	-61.49
std error	0.53	1.58	0.39	2.51	1.78	15.11
$Cd_{(P=0.05)}$	1.12	3.31	0.83	5.28	0.51	31.74

NFT = number of flowers/truss; NTP = number of trusses/plant; NFRT= number of fruits/truss; NFP= number of fruits/plant; FY= fruit yield; AFW= average fruit weight; In x P= Insulata x Petomech; In x G= Insulata x Grosso; W x G= wild x Grosso; W x In = Wild x Insulata; W x P= Wild x Petomech; G x P= Grosso x Petomech; cd= critical difference

Table 2a: Gene effects of the agronomic, yield and yield traits of the crosses used in diallel analysis of the tomato crosses used for study.

Traits	Crosses	m	*a*	*d*	*aa*	*ad*	*dd*
NFT	In x G	3.24	-0.49	-15.50	-3.85	0.01	7.88*
	In x P	4.38	-1.61	-21.72	-6.32	-0.59	9.13*
	G x P	3.92	-0.18	-19.92	-2.53	0.34	7.21*
	W x P	6.25	4.13*	-34.69	1.43	1.51*	5.59
	W x In	6.37	3.84*	-34.27	-3.46	0.20	7.87*
	W x G	5.69	3.53*	-31.39	-0.73	0.39	5.52
NTP	In x G	6.88	2.65*	-39.69	5.44	2.31*	3.18
	In x P	6.61	2.44	-39.11	8.61	2.86*	1.11
	G x P	10.46	-1.76	-58.02	-7.47	-0.99	9.49
	W x P	27.67	65.93*	-196.65	93.48	14.12*	-61.25
	W x In	27.64	64.59*	-196.07	89.15	12.35*	-60.46
	W x G	26.06	65.97*	-187.83	93.71	13.39*	-62.94
NFRT	In x G	1.33	0.15	-4.14	-3.15	0.25	7.65*
	In x P	2.28	-1.01	-9.93	-3.24	0.13	7.49
	G x P	2.49	-1.19	-11.07	-4.03	-0.16	7.71*
	W x P	5.33	3.45*	-28.22	-0.42	1.55*	7.53*
	W x In	5.08	3.49*	-25.83	-4.37	0.46	9.29*
	W x G	5.02	3.21*	-25.63	-4.42	0.27	8.97*

NFT = number of flowers/truss; NTP = number of trusses/plant; NFRT= number of fruits/truss; m = F_2 mean; *a* = additive effect; *d* = dominant effect; *aa* = additive x additive effect; *ad* = additive x dominant effect; *dd* = dominance x dominance effect; In x P= Insulata x Petomech; In x G= Insulata x Grosso; W x G= wild x Grosso; W x In = Wild x Insulata; W x P= Wild x Petomech; G x P= Grosso x Petomech;

Table 2b; Gene effects of the agronomic, yield and yield traits of the crosses used in diallel analysis of the tomato crosses used for study.

Traits	Crosses	*m*	*a*	*d*	*aa*	*ad*	*dd*
NFP	In x G	2.13	0.90*	-9.80	-1.26	0.35	5.96
	In x P	3.41	-0.03	-18.70	4.32*	1.92*	3.52
	G x P	2.45	-2.06	-13.35	2.18	0.44	2.70
	W x P	37.06	551.44*	-539.70	1039.95*	200.64*	-634.68
	W x In	35.03	471.75*	-527.60	876.81*	118.99*	-634.84
	W x G	43.15	445.23*	-567.65	805.35*	91.93*	-617.50
FY	In x G	2.85	0.86	-14.84	1.73	1.14	4.54
	In x P	85.03	0.95*	-14.57	2.23	1.28*	4.32
	G x P	2.06	0.28	-11.21	2.34	0.32	2.31
	W x P	4.39	24.13*	-27.50	45.37*	19.51	-2.36
	W x In	3.27	18.39*	-21.57	34.86*	13.45	-3.95
	W x G	4.32	13.40*	-27.12	23.92*	8.76	-2.40
AFW	In x G	74.52	-16.16	-452.95	32.24	8.29	-11.66
	In x P	43.35	10.77	-259.05	-3.75	-2.83	2.10
	G x P	49.98	34.01*	-316.65	29.46	-4.04	-33.54
	W x P	6.03	-16.37	-43.00	16.61	-0.52	-13.64
	W x In	5.28	-29.34	-52.85	46.56	0.11	-42.34
	W x G	5.78	-54.39	-79.80	93.26*	-0.49	-90.24

NFP= number of fruits/plant; FY= fruit yield; AFW= average fruit weight; m = F_2 mean; *a* = additive effect; *d* = dominant effect; *aa* = additive x additive effect; *ad* = additive x dominant effect; *dd* = dominance x dominance effect; In x P= Insulata x Petomech; In x G= Insulata x Grosso; W x G= wild x Grosso; W x In = Wild x Insulata; W x P= Wild x Petomech; G x P= Grosso x Petomech.

Table 3: Estimates of the Variance components, Broad and Narrow sense heritability of the cross between Insulata and Petomech (In x P)

Traits	Ve	Va	Vd	VP	VG	Hbs	Hns
NTP	1.19	5.71	6.18	13.09	11.89	90.84	43.61
NFT	0.39	0.69	0.14	1.22	0.83	67.42	56.28
NFRT	0.22	0.58	0.31	1.10	0.89	80.17	52.42
NFP	0.89	0.90	0.06	1.85	0.96	51.96	48.79
FY	76.96	1894.78	2725.24	4696.98	4620.02	98.36	40.34
AFW	11.74	84.99	114.09	210.83	199.08	94.43	40.31

Ve= environmental variance; Va= additive variance; Vd= dominance variance; VP= phenotypic variance; Vg= genotypic variance; Hbs= broad sense heritability; Hns= narrow sense heritability; NFT = number of flowers/truss; NTP = number of trusses/plant; NFRT= number of fruits/truss; NFP= number of fruits/plant; FY= fruit yield; AFW= average fruit weight

Table 4: Estimates of the Variance components, Broad and Narrow sense heritability of the cross between Insulata and Grosso (In x G)

Traits	Ve	Va	Vd	VP	VG	Hbs	Hns
NTP	0.99	3.469	4.93	9.39	8.39	89.42	36.94
NFT	0.35	0.22	0.19	0.77	0.416	54.39	28.50
NFRT	0.08	0.05	0.06	0.19	0.11	57.89	26.54
NFP	0.62	0.53	0.14	1.29	0.68	51.93	40.87
FY	20.09	3623.19	3676.97	7320.25	7300.16	99.73	49.49
AFW	15.29	281.27	368.83	665.39	650.09	97.70	42.27

Ve= environmental variance; Va= additive variance; Vd= dominance variance; VP= phenotypic variance; Vg= genotypic variance; Hbs= broad sense heritability; Hns= narrow sense heritability; NFT = number of flowers/truss; NTP = number of trusses/plant; NFRT= number of fruits/truss; NFP= number of fruits/plant; FY= fruit yield; AFW= average fruit weight.

Table 5: Estimates of the Variance components, Broad and Narrow sense heritability of the cross between Wild and Grosso (W x G)

Traits	Ve	Va	Vd	VP	VG	Hbs	Hns
NTP	4.71	46.76	80.66	132.14	127.43	96.44	35.39
NFT	0.76	0.61	0.39	1.76	1.00	56.91	34.86
NFRT	0.22	0.46	0.27	0.95	0.73	76.91	48.28
NFP	4.65	153.62	364.75	523.01	518.36	99.11	29.37
FY	190.38	7925.09	5282.43	13397.91	13207.53	98.58	59.15
AFW	0.89	1.33	0.86	3.08	2.19	71.14	43.41

Ve= environmental variance; Va= additive variance; Vd= dominance variance; VP= phenotypic variance; Vg= genotypic variance; Hbs= broad sense heritability; Hns= narrow sense heritability; NFT = number of flowers/truss; NTP = number of trusses/plant; NFRT= number of fruits/truss; NFP= number of fruits/plant; FY= fruit yield; AFW= average fruit weight.

Table 6: Estimates of the Variance components, Broad and Narrow sense heritability of the cross between Wild and Insulata (W x In)

Traits	Ve	Va	Vd	VP	VG	Hbs	Hns
NTP	3.48	52.05	68.34	123.87	120.39	97.19	42.02
NFT	0.26	0.52	0.32	1.10	0.84	76.11	47.46
NFRT	0.21	0.18	0.19	0.58	0.37	64.21	30.77
NFP	12.80	89.90	88.88	191.58	178.78	93.32	46.93
FY	226.39	3610.39	3146.72	6983.49	6757.11	96.76	51.69
AFW	1.47	1.20	0.91	3.58	2.11	58.95	33.51

Ve= environmental variance; Va= additive variance; Vd= dominance variance; VP= phenotypic variance; Vg= genotypic variance; Hbs= broad sense heritability; Hns= narrow sense heritability; NFT = number of flowers/truss; NTP = number of trusses/plant; NFRT= number of fruits/truss; NFP= number of fruits/plant; FY= fruit yield; AFW= average fruit weight.

Table 7: Estimates of the Variance components, broad and narrow sense heritability of the cross between Wild and Petomech (W x P)

Traits	Ve	Va	Vd	VP	VG	Hbs	Hns
NTP	6.69	45.57	83.83	136.09	129.40	95.08	33.49
NFT	0.38	0.52	0.35	1.26	0.88	69.73	41.57
NFRT	0.41	0.66	0.15	1.22	0.81	66.27	54.02
NFP	10.99	186.85	146.24	344.08	333.09	96.81	54.31
FY	23.56	9728.06	6495.48	16247.09	16223.54	99.86	59.88
AFW	1.92	3.19	3.39	8.49	6.58	77.44	37.57

Ve= environmental variance; Va= additive variance; Vd= dominance variance; VP= phenotypic variance; Vg= genotypic variance; Hbs= broad sense heritability; Hns= narrow sense heritability; NFT = number of flowers/truss; NTP = number of trusses/plant; NFRT= number of fruits/truss; NFP= number of fruits/plant; FY= fruit yield; AFW= average fruit weight.

Table 8: Estimates of the Variance components, broad and narrow sense heritability of the cross Grosso x Petomech (G x P).

Traits	Ve	Va	Vd	VP	VG	Hbs	Hns
NTP	1.81	5.38	5.79	12.98	11.17	86.06	41.42
NFT	0.33	0.49	0.19	1.01	0.68	67.41	48.28
NFRT	0.15	0.21	0.31	0.66	0.51	77.08	31.18
NFP	0.45	3.65	6.94	11.04	10.58	95.88	33.02
FY	169.71	2199.62	2272.85	4642.18	4472.47	96.34	47.38
AFW	5.19	35.99	92.14	133.33	128.13	96.10	26.99

Ve= environmental variance; Va= additive variance; Vd= dominance variance; VP= phenotypic variance; Vg= genotypic variance; Hbs= broad sense heritability; Hns= narrow sense heritability; NFT = number of flowers/truss; NTP = number of trusses/plant; NFRT= number of fruits/truss; NFP= number of fruits/plant; FY= fruit yield; AFW= average fruit weight.

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APPLICATION OF CRY1AB/AC BT STRIP FOR SCREENING OF RESISTANCE FOR MARUCA VITRATA IN COWPEA

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ABSTRACT

Maruca vitrata is a significant constraint to cowpea production in most cowpea growing areas of sub-Saharan Africa. Yield losses caused by *M.vitrata* in these regions are estimated in millions of tons annually and the prevalence of *M. vitrata* infestation is steadily increasing. Recombinant DNA technollogy have led to development of some cowpea lines with *Maruca* resistance as well as other important agronomic traits but it is time-consuming and difficult to screen for the resistant trait especially in the segregating populations using conventional screening techniques, which will lead to delay in the development of *Maruca* resistant cowpea varieties. The use of allele-based selection tool will make it easier to select plant traits and reduce the time needed to develop new *Maruca* resistant cowpea varieties. In this study, the efficacy of using *Cry1Ab/Ac Bt* strip for detecting *Maruca* resistant transgene in transgenic cowpea was systematically investigated for the first time through field derived progenies. The results showed that the *Cry1Ab/Ac Bt* strip was effective for detecting the presence of the resistant gene in cowpea genome. *Maruca* resistant plants were successfully screened from the segregating cowpea plants and the genetics of the gene was monitored. The *Cry1Ab/Ac Bt* strip was found to be suitable for genetic analysis of the *Maruca* resistant transgene in cowpea. This study has demonstrated the precision of using *Cry1Ab/Ac Bt* strips as a screening tool of transgenic lines containing *Cry1Ab* gene, this has an importance in the hybridization programme where genotypes having *cry* gene can be distinguished at seedling stage at lesser time, with the potential of putting the breeding process on a fast track and increase the efficiency of breeding activities.

Key Words: *Bacillus thuriengiensis, Cry1Ab/Ac Bt* strips, transgenic cowpea, *Maruca vitrata*

INTRODUCTION

Cowpea *(V. unguiculata L. Walp)* is considered the most important food grain legume in the dry savannas of tropical Africa (NGICA, 2002). It is the most important indigenous African legume for both home use and as a cash crop and especially important for the Sahel because of its drought tolerance (Kushwaha *et al.*, 2004). It is rich in quality protein and has energy content almost equivalent to that of cereal grains, it is a good source of quality fodder for livestock and also provides cash income (Davis *et al.*, 1991). Nearly 200 million people in Africa consume the crop (AATF, 2010; NGICA, 2002). Cowpea is consumed in many forms; the young leaves, green pods, and green seeds are used as vegetables, dry seeds are used in various food preparations, the haulms are fed to livestock as nutritious supplement to cereal fodder and being a fast growing crop, cowpea curbs erosion by covering the ground, fixes atmospheric nitrogen, and its decaying residues contribute to soil fertility (Singh *et al.*, 2002).

The overall productivity of its existing traditional genotypes are low due to their prominent susceptibility to insect pests (Darshana *et al.*, 2007) and among the most damaging insects are aphids, flower thrips, cowpea pod borer, pod sucking bugs and the cowpea weevils (Darshana *et al.*, 2007). The cowpea pod borer *(Maruca vitrata)* is a serious lepidopteran pest that inflicts severe damage to cowpea on farmers' fields (Figure 3). In severe infestations, yield losses of between 70–80% have been reported (AATF, 2010). Control through spraying with insecticide has not been fully adopted by farmers due to the prohibitive costs, causing resource-poor farmers to opt for cheaper but more toxic alternatives that impact their health (AATF, 2010).

Breeding for insect resistance with the aid of phenotypic selection is time consuming, laborious and relatively expensive (Xu and Crouch, 2008). In addition, most crops have a high level of heterozygosity that makes visual selection difficult but selection based on allele composition will avoid this problem (Ibitoye and Akin-Idowu 2010). Ability to select breeding progeny early at the seedling stage is another advantage of using allele-based selection tools (Ibitoye and Akin-Idowu 2010). The number of plants that are needed to be maintained in a crop breeding programme can be reduced by eliminating progenies that do not carry the desirable allele at the seedling stage, saving space, time, labor and other resources (Ibitoye and Akin-Idowu 2010). The present study was designed and conducted in order to understand the efficacy of using *Cry1Ab/Ac Bt* strips for detecting *Maruca* resistant transgene in transgenic cowpea through field derived progenies.

MATERIALS AND METHODS

The Research was conducted under the confined field trial site (CFT) between July, 2011 to August, 2012 at the Institute for Agricultural Research (IAR), Samaru-Zaria, Nigeria. Two genetically engineered cowpea lines: transgenic cowpea line TCL-709 and TCL-711, and three non-transformed cowpea genotypes: IT97K-499-35, IT93K-693-2 and IT86D-1010, were used in this study. Data were collected as scores of *Cry1Ab Bt* strip kits.

To establish the potency of *Cry1Ab*/*Ac Bt* strips as a screening tool for *Maruca* resistant transgene, the inheritance of *Cry1Ab* gene was monitored with the aid of *Bt* strips in filial generations. The transgenic cowpea lines TCL-709 and TCL-711 along with three non-transgenic genotypes: IT97K-499-35, IT93K-693-2 and IT86D-1010 (the original parent of the transformed lines having the same genetic architecture except the *Cry1Ab* gene) were crossed using biparental mating as described by Sharma (2006) to generate F_1 population. Some F_1 seeds were advanced to second filial generation (F_2) populations by self pollination. The following six combinations of crosses were produced; IT97K-499-35 x TCL-709, IT97K-499-35 x TCL-711, IT93K-693-2 x TCL-709, IT93K-693-2 x TCL-711, IT86D-1010 x TCL-709 and IT86D-1010 x TCL-711.

The parents, F_1 and F_2 generations were evaluated under field conditions during the 2012 cowpea growing season at CFT Samaru-Zaria between June to August, 2012. The trial was planted using randomized complete block design with three replications. The plant to plant and row to row spacing was kept at 30cm by 75cm respectively. The plot size was 3m x 5m for all entries except F_2 plants which were 6m x 5m. No insecticidal spray against lepidopteran insects was applied.

The screening was carried out with the aid of *Cry1Ab/Ac Bt* strips to check for the presence of *Cry1Ab* gene in the genetic populations (P_1, P_2, F_1, and F_2) of transgenic cowpea. Detection of *Cry1Ab* Proteins on cowpea involved assaying plant leaves for expression of the *Cry1Ab* gene. A quick *Bt* strip test was used to confirm the expression of the *Cry1Ab* protein in cowpea transgenic lines. This was achieved by placing leaf discs in test tubes containing buffer and then slowly inserting *Bt* strips into the buffer. Then, formation of a single line in the test tube proved that the test was working while the appearance of a second lower line showed that *Cry1Ab* protein was present (Envirologix, 2008). Figure I and II illustrates a typical type of *Cry1Ab Bt* strip test. In these plates, the appearance of two lines on the test membrane indicates the presence of the *Cry1Ab Bt gene*, while the appearance of only the top (control) line indicates a negative response.

The plants were screened with the aid of *Cry1Ab/Ac Bt* strips and the transfer of *Cry1Ab* gene from a transgenic cowpea plant to a non- transgenic cowpea plant was checked. The number of positive and negative plants indicating presence and absence of the transgene respectively, were taken to infer the behaviour of the transgene whether dominant or recessive and establish the efficacy of the *Cry1Ab/Ac Bt* strips.

Adequate sample size was taken from each F_2 family and analyzed with the aid of *Cry1Ab/Ac Bt* strips. Since the gene is expected to segregate in F_2 generations, the plants were clearly classified as *Cry1Ab*–positive or *Cry1Ab*-negative regarding the *Cry1Ab* expression where *Cry1Ab* positive plants indicates resistance to *M. vitrata* while *Cry1Ab* negative plants indicates susceptibility to *M. vitrata*. Envirologix (2008) procedures for *Cry1Ab*/Ac *Bt* strip test was carefully followed. The data was subjected to chi-square goodness of fit test against the Mendelian ratio 3:1 for the F_2 generations (Kiani *et al.,* 2009).

Data recorded for the genetic segregation of *Cry1Ab* transgene were analyzed with the help of chi-square (X^2) goodness of fit test, to determine whether the observed data conforms to the expected Mendelian 3:1 ratios for F_2 segregating populations of each cross. The following

formula was used using a *Proc Frequency* for a chi-square test of goodness of fit by Mcdonald (2009).

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

Where: O = Observed value, E = Expected value and $\sum$ = Summation.

RESULTS

The results of the six set of F_1 plants analyzed with the aid of *Cry1Ab Bt* strips to study the efficacy of *Bt* strips for detecting the transgene's presence through transmission and expression of the transgene have been given in (Table 1). It was found that all the F_1 plants were positive to *Cry1Ab Bt* strip test. It thus means that the gene was successfully transferred from *Bt* lines to non-*Bt* lines and the *Cry1Ab Bt* strips were potent as detecting tool for the target gene.

The results are shown in Table 2. The results reveal that Mendelian segregation ratios (3:1) existed in all the six cross combinations for the F_2. The F_2 populations of these crosses segregated into plants with positive and negative *Cry1Ab* gene indicating the presence and absence of the *Maruca* resistant gene respectively, with a good fit to the Mendelian ratio of 3:1 with non significant Chi-square values (X^2) for F_2 plants of the following crosses; IT97K-499-35 x TCL-709 (X^2 = 0.18 ; P = 0.67), IT97K-499-35 x TCL-711 (X^2 = 0.15, P = 0.70), IT93K-693-2 x TCL-709 (X^2 = 0.22 ; P = 0.64), IT93K-693-2 x TCL-711 (X^2 = 0.31 ; P = 0.58), IT86D-1010 x TCL-709 (X^2 = 0.26 ; P = 0.61), IT86D-1010 x TCL-711 (X^2 = 0.0041 ; P = 0.95) in (Table 2). This has demonstrated the potency of the *Bt* strips for detecting the presence of the transgene in the segregating populations of transgenic cowpea crosses. The strip screening clearly grouped the F_1 plants as resistant plants just like the transgenic parents and the segregating progenies of F_2 were seen clearly behaving as hypothesized into 3:1 Mendelian test ratio.

DISCUSSION

The genetic segregation and pattern of inheritance of *Cry1Ab* gene in the genetically modified cowpea were monitored in six crosses of cowpea involving transgenic and non-transgenic lines. In the present study, the segregation of *Cry1Ab* gene was found to be in Mendelian fashion in all the six cowpea crosses, the results indicated that the resistant trait was controlled by a single dominant gene in the crosses that were examined. The transgenic lines carried the dominant gene

while the recessive allele resides in the susceptible genotypes. In the F_1 generation studies, the *Cry1Ab* gene was found to be successfully transferred from transgenic to non-transgenic and it was dominant. These results are in agreement with earlier research works on genetically modified *Bt* crops with *Cry1Ab* transgene: *Cry1Ab* transgene is inherited as single dominant gene, in *Bt* corn where the *Cry1Ab* conferred resistance to stem borer (*Ostrinia nubilalis*) (Murenga *et al.,* 2012), in *Bt* Rice containing resistant gene to striped stem borer (*Chilo suppressalis*) (Kiani *et al*., 2009, Wang *et al*., 2012), in crosses of transgenic Rojolele Rice (Sulistyowati *et al.,* 2008) and in *Bt* Cotton where Khan (2008) and Zhang *et al*., (2000) studied the inheritance and segregation of foreign *Bt* (*Bacillus thuringiensis* toxin) and tfdA genes. The ability to obtain 3:1 segregation in F_2 generations using the *Cry1Ab Bt* strips means that these tests could be employed for wide-scale studies in the field to enhance cowpea breeding for resistance to *Maruca vitrata*.

The results obtained here indicate that it is possible to use this technology to select for *Maruca* resistant genotypes in cowpea. Similar results have been reported in other crops (corn, soybean, cotton and canola) using *Bt* strips technology to select plants carrying *Cry1Ab* transgene (Stave, 2002; USDA/GIPSA 2006) and had proven to be effective in detecting the presence of the transgene in these crops. *Cry1Ab Bt* strip tests for genetically engineered crops are currently being used on a large scale in the United States to manage the sale and distribution of grains that are genetically transformed (Stave, 2002). In several of these applications, it is important to get a result rapidly in the field, and in these situations strip tests are particularly useful.

Using the *Cry1Ab Bt* strips, the screening were done at seedling stage with good precision, this saves time and resources. The use of *Cry1Ab Bt* strips as a screening tool of transgenic lines containing *Cry1Ab* gene is strongly recommended, this has an importance in the hybridization programme where genotypes having the transgene can be distinguished at seedling stage at lesser time. The benefits of this technology have important implications for improving the efficiency of the characterization of cowpea genotypes for resistance to *Maruca* in the laboratory, especially when working in remote areas and in developing countries where access to laboratory facilities, chemicals, and equipment for PCR procedures are limiting. The *Cry1Ab Bt* strip test was found to be the most suitable in order to rapidly analyze large number of plants in lesser time and to differentiate between the two groups. Elite and promising plants can be faithfully screened and

selected at seedling stage particularly during the development of backcross population, aimed towards development of transgenic cowpea varieties. Results obtained from *Bt* strips sampled materials were effective and reproducible in our hands from the six F_2 populations used. The studies described here that the *Bt* strips screening offers a simple, sensitive and specific tool appropriate for identifying *Maruca* resistant transgene. We conclude that the application of this technology has the potential to significantly enhance the *Maruca* resistant cowpea breeding program, and the efficiency of breeders to speed-up the process of developing and deploying *Maruca* resistant cowpea varieties to farmers. This study demonstrates that *Bt* strip is an effective, economic and sensitive method for sampling and identifying resistant cowpea plants using leaf tissues.

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Table 1: Detection of *Cry1Ab* gene in Parents and F_1 populations of transgenic cowpea

Genotype	No. of Plants Tested	Positive	Negative	Expected ratio
TCL-709	50	50	0	1:0
TCL-711	50	50	0	1:0
IT97K-499-35	25	0	25	0:1
IT93K-693-2	25	0	25	0:1
IT86D-1010	25	0	25	0:1
IT86D-1010 x TCL-709	23	23	0	1:0
IT86D-1010 x TCL-711	23	23	0	1:0
IT97K-499-35 x TCL-709	30	30	0	1:0
IT97K-499-35 x TCL-711	28	28	0	1:0
IT93 693-2 X TCL-709	25	25	0	1:0
IT93 693-2 X TCL-711	23	23	0	1:0

Positive: *Cry1Ab* gene is present i.e. resistant to *M. vitrata*, Negative: *Cry1Ab* is absent i.e. susceptible to *M. vitrata*

Table 2: Detection of *Cry1Ab* gene in F_2 populations of transgenic cowpea crosses

Cross (Female x Male)	No. of Plants Tested	Positive	Negative	Expected ratio	Chi-square	DF	Prob.(ns=not significant at p=0.05)
IT86D-1010 x TCL-709	105	81	24	3:1	0.26	1	0.61^{ns}
IT86D-1010 x TCL-711	81	61	20	3:1	0.004	1	0.95^{ns}
IT97K-499-35 x TCL-709	89	65	24	3:1	0.18	1	0.67^{ns}
IT97K-499-35 x TCL-711	111	85	26	3:1	0.15	1	0.70^{ns}
IT93 693-2 X TCL-709	75	58	17	3:1	0.22	1	0.64^{ns}
IT93 693-2 X TCL-711	131	101	30	3:1	0.31	1	0.58^{ns}

Positive: *Cry1Ab* gene is present i.e. resistant to *M. vitrata,* Negative: *Cry1Ab* is absent i.e. susceptible to *M. Vitrata*

Figure 1**:** *Cry1Ab/1Ac Bt* strips showing positive, negative and invalid result (Envirologix, 2008)

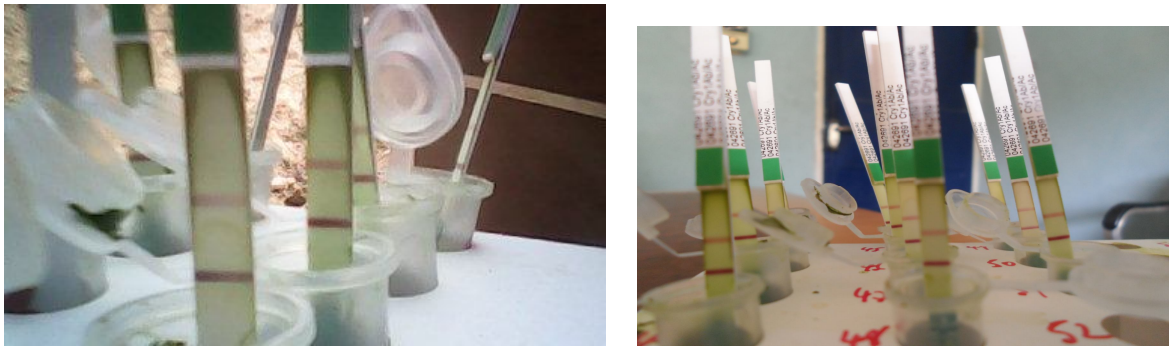

Figure 2: *Cry1Ab/1Ac Bt* strips in test tubes showing positive results (Field Result 2012)

Figure 3: Showing larvae and Adult *Maruca vitrata* (Legume Pod Borer) pest

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CHARACTER RELATIONSHIP AND GENETIC CORRELATION FOR SELECTING CHARACTERS FOR TUBER DRY MATTER YIELD IMPROVEMENT IN WHITE YAM (*DIOSCOREA ROTUNDATA*).

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ABSTRACT

Yam is an important tuber crop in Nigeria where yield potential and quality attribute have not been fully exploited due to limited breeding efforts and poor knowledge on the inheritance of some of its agronomic traits. A study was conducted at the Western experimental field of National Root Crops Research Institute - Umudike, Abia State, Nigeria to evaluate 12 hybrid yam genotypes at the stage of Uniform Yield Trial (UYT) developedthrough intra-specific crosses using three landraces of Dioscorea rotundata as checks. The specific objective was to determine the character correlation and genetic relationship for selecting characters for improving tuber dry matter yield. The experiment was carried out to achieve the following specific objectives using a two factor experiment in RCBD. The result of genetic inter-character association detected that pearson moment correlation coefficient was defective for selecting genetically stable traits for character improvement. Multi-regression analysis projected number of days to male flower buds emergence (46.83%) and number of days to female flower buds emergence (15.12%), as the traits exerting the greatest influence on tuber dry matter yield. These traits have high heritability estimates, high genotypic coefficient of variation and genetic advance. The genes controlling the traits are positively linked/coupled on the same chromosome and are inherited together. The characters are genetically stable over the years and contributed to the observed genetic variations.

Keyword: character, genetic relationship, selection, tuber dry matter yield, genetic stability.

INTRODUCTION

The yam plant is a monocotyledonous and annual herbaceous plant. It has long climbing stems which wind themselves around supports. A single plant produces between one and five tubers of varying shapes, each may weigh up to 5kg. The yams are the most important staple food crops in West Africa (Ekpe *et al*, 2005) except for cereals (Coursey, 1967, Onwueme, 1978). White

yam (*Dioscorea rotundata* Poir) is a prestigious and most preferred carbohydrate staple for peoples of the tropics particularly in West Africa and the Caribbean (FAO, 1998).

Future increases in yam output will have to rely on higher yield and necessitate that constraints to production be tackled (Manyong *et al*, 2001). Since tubers could be eaten boiled, roasted, fried, mashed or pounded to provide important energy, variability in *D. rotundata* is almost the only avenue through which local farmers and consumers can obtain yams of their desired traits. It is believed that selection of resultant hybrid genotypes with higher tuber dry matter yield and appealing tubers will contribute to high yielding genotypes of *Dioscorea rotundata* for commercial production. Therefore the focus of this Study is character relationship and genetic correlation for selecting characters for tuber dry matter yield improvement. The specific objectives include**:** to select the character(s) that contributed to tuber dry matter yield of the intra specific hybrids of *Dioscorea rotundata*, and to select the character(s) that genetically linked to the tuber dry matter yield and genetically stable over the years

MATERIALS AND METHODS

The experiment was laid out in a randomized complete Block Design (RCBD) with 6 replicates. Each of the 15 yam genotypes were each cut into setts with a mean weight of 40g from each genotype. Each genotype was planted in each plot measuring 2.0 by 2.25$m^{2.}$ Spacing on the ridges was 45cm within the row and 100cm between the ridges giving a total of 10 yam plants per plot, 150 yam plants per block or replicate and 900 yam plants for the 6 blocks or replicates. A total of 15 yam genotypes were used in the experiment. Bonds were made to check erosion and separate the plots from one another. The experiment was carried out in two cropping seasons with the first season crop established on April 16th 2009 and the second season crop established on April 20th 2010.

The yam plants were individually staked with approximately 2 meters high bamboo stake for support and for adequate exposure to sunshine for photosynthesis as well as for easy observation and data collection. The experimental fields were kept weed-free manually with hand hoes. No applications of herbicides or pesticides were carried out. Four hundred kilogram of NPK 20:10:10 per hectare of fertilizer was applied eight weeks after planting in each plot using band method. All other agronomic practices were according to the farmer's management practice.

The data collected were on Number of upright shoots that emerged from plant base, Plant height, measured from the plant base to the top of the main vine, Number of leaves, Number of primary branches, Leaf area obtained by grid method (Roderick, 1978), Leaf area index (Watson, 1982, Roderick, 1978).

$$LAI = \frac{\text{leaf area per plant}}{\text{Land area covered by plant}}$$

at 2, 4 and 6 months after planting (MAP).

Days to tuber physiological maturity, all were collected at 2, 4 and 6 months after planting (MAP). Fresh tuber yield per plant calculated at harvest. Number of tubers per plant, Tuber dry matter obtained by measuring 100g of fresh tuber from each plot, dried in a ventilated oven at 80^{o}C for hours until a constant weight is obtained to determine their dry matter yield. Crop growth rate obtained according to Radford (1967) and a Roderick (1978). The formula employed for calculation is:

$$CGR = \frac{\log W_2 - \log W_1}{P\,(T_2 - T_1)}$$

Where CGR= Crop Growth Rate, W_2= Final dry weight of plant, W_1= Initial fresh weight of plant, T_1= Initial time, T_2 = Final time, P= ground area on which W_2 and W_1 were estimated.

Analysis of variance was used to analyze Tuber dry matter yield and other yield component characteristics. Linear model for the analysis was: Xij = Ui + Bi + Ej + Ti + Tjk + Et Where Xij = value of Observation, Ui = common mean , Bi = block effect, Eji = Varietal effect, Ti = Year effect, Tjk = Year x varietal effect, Et = error term.

Simple Correlation Coefficient (Pearson Moment Product Correlation Analysis) was used to determine the relationships between: Tuber dry matter yield and other plant characters. The formula use for the calculation was $r^{12} = \frac{\sum x_1 x_2}{\sqrt{(\sum x_1)(\sum x_2)}}$

Where r^{12} = the correlation between character x_1 and x_2, $\sum x_1 x_2$ = the covariance between character x_1 and x_2, $(\sum x_1)$ = the variance of character x_1, $(\sum x_2)$ = the variance of character x_2 ,

Determination of genotypic coefficient of variation and phenotypic coefficient of variation was estimated using the following formula suggested by Burton (1952), Warwick and Legate (1981), Kumar *et al* (1985), Sharma (2004), Jawahar (2006) and Rangeswamy (2010).

Estimation of genotypic coefficient of variability:

$$GCV = \sqrt{\frac{VG \times 100}{X \quad 1}}$$

Estimation of phenotypic coefficient of variability:

$$PCV = \sqrt{\frac{VP \times 100}{X \quad 1}}$$

Where VG = Genotypic Standard deviation. VP = Phenotypic Standard deviation, X = Grand mean of the character under consideration, Genotypic and phenotypic variations were used to determine real heritable differences and environmental (non-heritable) factors.

Estimation of Heritability (in broad sense) according to Warwick and Legate (1981) and Sharma (2004) was used to estimate the heritability of all the characters.

$$h_{bs} = \frac{VG}{VP} \times \frac{100}{1}$$

Where h_{bs} = Heritability in broadsense, VG = Genetic variance, VP = Phenotypic variance

Estimation of genetic correlations was done using the following formulae by Sharma (2004) and Rangaswamy (2010).

Genotypic correlation (rg) =

$$\frac{Covg\,(x_1 \cdot x_2)}{\sqrt{(Varg\ x_1)\,(Varg\ x_2)}}$$

(ii) Phenotypic correlation (rp) =

$$\frac{Covp\,(x_1 \cdot x_2)}{\sqrt{(Varp\ x_1)\,(Varp\ x_2)}}$$

This was used to determine characters that are repeatable from year to year and whether the characters under consideration were linked on the same chromosome or located far apart on the same chromosome or they are located on different chromosomes.

Multiple Regression Analysis according to Li (1981) was used to determine the degree of contribution of each of the plant characters to Tuber dry matter yield. The following linear model was used = a + b1 x $_1$+ b_2x_2+b_3x_3+b_4x_4 ---b_nx_n + ei, Where Y = dependent plant character, a = intercept (constant), b_1 = regression coefficient, X_n = plant characters under consideration

RESULTS AND DISCUSSION

The analysis of variance showed high significant (P<0.01) and significant (P<0.05) genotypic differences for all the characters that were evaluated in each season, indicating substantial variations in plant characters among the yam genotypes. There were non-significant (P>0.05) differences in certain plant characters indicating lack of variability in the plant characters. However, the variability exhibited by the plant characters contributed to the variations in mean performance of the tuber dry matter yield of the yam genotypes. The overall performance of a crop in any environment depends on the variability in the genetic constitution of the genotypes and its inter-character relationship.

The result of the Correlation of plant characters with tuber dry matter yield and other plant characters in each of the years 2009 and 2010 are presented in Table 1. Tuber dry matter yield positively and significantly (P<0.01) correlated with number of leaves in both years (r = 0.244** in 2009 and r = 0.291** in 2010), and number of branches in both years (r = 0.324** in 2009 and r = 0.325** in 2010). Selection and improving on these characters will increase the tuber dry matter yield. If the branching of the yam plant is improved, it will increase the number of leaves significantly. Higher number of leaves will lead to higher photosynthetic efficiency of the yam crop and this will influence the dry matter accumulation of the yam tuber. Also, tuber dry matter yield positively and significantly correlated with leaf area index (r = 0.342** in 2010) and crop growth rate (r = 0.261**) in 2009. These two traits could be selected for the improvement of tuber dry matter yield in yam plants. Developing yam crops with large canopy (leaf area index) will lead to increasing planting distance of the yam plant.

The positive correlation of crop growth rate and tuber dry matter yield indicated that developing yam plants with increased number of leaves and rapid growth rate due to high dry matter accumulation will enable the crop escape diseases and pests and subdue weeds. The rapid dry matter accumulation will be stored in the tubers for high yield. Tuber dry matter yield positively and significantly (P<0.01) correlated with number of days to tuber maturity (r = 0.261**) in 2009 suggesting that as the number of days to tuber physiological maturity increases, more carbohydrates are partitioned to the underground sink (tuber). This character could be selected for the improvement of tuber dry matter yield of the yam plants. Tuber dry matter yield positively and significantly correlated with number of days to male flower buds emergence and number of days to female flower buds emergence (r = 0.392**) in 2010. Number of days to male flower buds emergence and number of days to female flower buds emergence according to Onwueme (1978) is the time for carbohydrate excess for the yam plant. This excess carbohydrate is partitioned both to the sink (tuber) and to the leaf -axils for flower bud formation and for flowering. T his trait could be selected for the improvement of tuber dry matter yield. Tuber dry

matter yield in both years positively and significantly (P<0.01) correlated with fresh tuber yield in both years (r = 0.271** in 2009 and r = 0.365**), suggesting that this character could be selected for the improvement of tuber dry matter yield.

The results in Table 2 are the estimation of genetic parameters for character selection. According to Falconer (1981) high genotypic coefficient of variation, high heritability estimate, high genetic advance and positive genetic correlation (Jawarha,2006) were used to select characters for further improvement. These genetic parameters were used for selecting characters for the improvement of tuber dry matter yield of the yam crop. According to Ibe (1998), heritability below 20% will not give the desired result.

Genetic correlation is the association between the genotypic and the phenotypic variation of the characters under consideration (Table 3). The phenotypic correlation determined the interaction between the gene and the environment while the Environmental correlation determined the influence of the environment on the genotypes. The phenotypic and genotypic correlations observed among the plant characters in this study indicated an inherent association between them. The phenotypic correlation incorporates both genotypic and environmental correlations. If environmental correlation coefficients were lower than phenotypic correlation coefficients, phenotypic correlation coefficients would be good index of genotypic correlations coefficients. This is in accord with falconer (1981) who reported that two major causes of correlations between characters were genetic and environmental (genetic plus environment = phenotype).

The positive high significant genotypic and phenotypic correlation between tuber dry matter yield per plant with plant height, leaf area and crop growth rate in 2009 suggested that these traits had genetic correlation with tuber dry matter yield indicating a correlated response which indicated that the characters are being controlled by the same gene or different genes located close to each other on the same chromosome, this could be concurrently selected for tuber dry matter improvement. The genetic correlation between tuber dry matter yield and plant heights was an indication where a gene controls two characters. In 2010, the positive high significant genotypic and phenotypic correlation of tuber dry matter yield per plant with number of days to physiological tuber maturity, number of shoots, plant height, number of leaves, number of branches, number of days to male flower buds emergence and number of days to female flower buds emergence also suggested that these plant characters genetically correlated with tuber dry matter yield per plant (Table 3). It also suggested that these traits could simultaneously improve tuber dry matter yield per plant. It was also observed in 2009 that there were high significant positive genotypic correlation between tuber dry matter yield per plant and number of days to male flower buds emergence and number of days to female flower buds emergence per plant. Also in 2010, there were high positive significant genotypic correlations between tuber dry matter yield and leaf area. These indicated a correlated genetic response that needed favourable environmental conditions to express the phenotype (which is the visible characteristics of an organism resulting from the interaction between its genetic make-up and the environment).

The negative significant genotypic correlation exhibited by tuber dry matter yield with number of shoots per plant in 2009 and number of nodes per plant in 2010 showed that these plant characters are under the influence of environmental factors, and cannot be used for the improvement of tuber dry matter yield. The genes controlling these traits were repulsive and

were located on different chromosomes. These plant characters since they were not genetically correlated could not be repeatable (Tables 3) Also, tuber dry matter yield per plant had significant genotypic correlation with plant height (length of main vines), leaf area, number of days to male flower buds emergence, number of days to female flower buds emergence, number of nodes and crop growth rate in either or both years. The implication of this observation is that these characters had the most significant influence on fresh tuber yield and tuber dry matter yield. These characters significantly and genotypically correlated with one another, and by implication selection for any of these characters will lead to a correlated response. (That is, if one character that is genetically correlated is selected, invariably other genetically correlated characters will be selected. This will ultimately lead to increase in yield, and consequent yield status will be repeatable over the years. At the genetic level, Jawahar (2006) reported that such positive significant genotypic (genetic) correlation occurs due to coupling phase of linkage. Indicating that these two different characters can be controlled/influenced by the genes located close on the same chromosomes. As mentioned by Jawahar (2006) genes do not come mixed individually during the process of reproduction, they came "linked" with other genes in the DNA.

Number of tubers per plant and number of branches per plant had a positive significant association (product moment correlation) with fresh tuber yield in spite of their insignificant genotypic (genetic) correlation with fresh tuber yield and tuber dry matter yield per plant. Characters that were not genetically correlated will not be repeatable over the years (ie characters that are not genetic). This demonstrates the defects of selecting only on the basis of inter-character correlation using pearson product moment coefficient as such selection may not produce the desired result which may be very disappointing.

Tuber dry matter yield was being positively influenced by number of branches, days to male flower buds emergence and days to female flower buds emergence. Considering the association of fresh tuber yield per plant with tuber dry matter yield per plant, fresh tuber yield per plant appears to be the most reliable index of tuber dry mater yield per plant.

Wallace (1974) reported that tuber size contributed to most difference in tuber dry matter yield. Therefore, emphasis should be placed on percent tuber dry matter when selecting for high yielding yam genotypes. According to Thambura and Muthunisnan (1976) to get higher yields in sweetpotato, number of roots (which contribute to fresh yield) is the most important yield component which must be improved with reduction of number of leaves.

The multiple regression linear analysis identified the characters that contributed to tuber dry matter yield were number of days to male flower buds emergence (25.31% in 2010), number of days to female flower buds emergence (8.17% in 2010), number of leaves (38.90% in 2010), number of branches (0.02%in 2010), leaf area (7.63% in 2010), number of tubers (2.69% in 2009 and 0.13% in 2010) and fresh tuber yield (74.44% in 2009 and 2.79 in 2010) (Tables 4 and 5).

In this study, selection criteria (Table 6) for characters for the improvement of tuber dry matter yield were based on high heritability estimates, high genotypic coefficient of variation, high genetic advance and positive significant genetic correlation (Burton, 1952; John *et al.*, 1955; Warwick and Legate, 1981; Jawahar, 2006). The multiple regression linear analysis(Tables 4a

and 4b) therefore strengthens the suggestions that while breeding yam genotypes for higher tuber dry matter yields, attention to number of days to male flower buds emergence, number of days to female flower buds emergence, number of nodes, crop growth rate, number of leaves, number of branches, leaf area, number of tubers, and fresh tuber yield should be of utmost importance. If selection of characters is carried out to deliberately increase tuber dry matter yield, these characters should selected and improved to some extent. However, for the characters to be genetically stable and repeatable over the years, the characters must be genetically correlated. Therefore, the following characters were selected for the improvement of tuber dry matter yield per plant: number of days to male flower buds emergence (25.31%) in 2010, number of days to female flower buds emergence (13.67% in 2009 and 8.17% in 2010), crop growth rate (3.27% in 2009 and 4.50% in 2010), number of leaves 31.56% in 2009 and 38.90% in 2010), leaf area 7.63% in 2010, fresh tuber yield 2.79% in 2010 and number of nodes 3.35% as the factors exerting the greatest influence directly upon tuber dry matter yield. For their effect to be effective they must be genetically correlated to enable their effect be repeatable over the years.

Since heritability estimates in broad sense (h^2_{bs}) represent the proportion of heritable variation in the total phenotypic variation is large, number of days to male flower buds emergence (26.37%) in 2009, and 91.94% in 2010), should be selected. Selection of this character for tuber dry matter yield might be highly reliable. Also selected were: number of days to female flower buds emergence (39.00% in 2009 and 99.36% in 2010)(Table 6). These two characters had high heritability estimates, high genotypic coefficient of variation and genetic advance, and were significantly and genetically correlated (rg) and were selected to significantly improve the tuber dry matter yield of the yam genotypes over the years (Table 6).

CONCLUSION

Therefore, to deliberately increase tuber dry matter yield, number of days to male flower buds emergence and number of days to female flower buds emergence should be selected. The traits selected have reliable selection criteria and would be repeatable over the years. The genes controlling the traits are linked/coupled with other genes and were located on the same chromosome and contributed to the observed genetic variations. Selection of characters based on Pearson product moment correlation will be defective if the characters are not genetically correlated. The characters may not be repeatable over the years.

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Table1: Product moment Correlation of Tuber dry matter yield and other yield component character

Plant character	2009	2010
Tuber dry matter yield x no, of days to tuber maturity	r =0.261**	
Tuber dry matter yield x number of leaves		r= 0.244**
Tuber dry matter yield x number of branches		r = 0.324**

Tuber dry matter yield x leaf area index		r =0.324**
Tuber dry matter yield x number of male flower emergence		r = 0.350**
Tuber dry matter yield x number of days to female flower bud emergence		r = 0.392**

Table: 2 Estimation of genetic parameter

character	year	Phenotypic Coefficient of variation %	ggenotypic Coefficient of variation %	Heritability in broadsense %	Genetic advance %
Tuber dry matter yield	2009	23.41	15.69	19.93	2.25
	2010	22.9	16.56	52.44	2.83
Number of days to maturity	2009	0.58	0.22	14.04	6.74
	2010	1.93	0.50	6.65	3.40
Plant height	2009	11.72	6.26	28.57	20.06
	2010	12.70	6.37	25.18	5.49
No. of leaves	2009	25.42	11.70	21.19	670.03
	2010	18.40	6.28	11.64	274.24
Leaf area	2009	0.01	0.00	1.83	39.80
	2010	0.02	0.00	5.22	66.27
Leaf area index	2009	60.33	58.75	94.83	65.36
	2010	34.45	33.69	95.61	95.61
Days to male flower buds emergence	2009	140.13	71.96	26.37	75.65

	2010	54.26	52.03	91.94	94.46
Days to female flower buds emergence	2009	45.00	53.00	39.00	41.60
	2010	72.20	71.65	99.36	15.45
No.of nodes	2009	12.63	2.85	5.11	65.10
	2010	87.85	13.42	2.33	55.04
No.of stamen	2009	139.98	135.80	94.12	62.00
	2010	120.51	114.84	90.81	65.00

Table 3: Characters that have positive genetic correlation with tuber dry matter yield and other plant characters

Plant characters	2009		2010	
	Genetic Correlation (rg)	Phenotypic Correlation(rp)	Genetic Correlation (rg)	Phenotypic Correlation(rp)
Tuber dry matter yield x plant height	rg=0.243*	0.432*		
Tuber dry matter x leaf area	rg=0.471**	0.890*		
Tuber dry matter x crop growth rate	rg= 0.615*	0.811*		
Tuber dry matter x no. of days to tuber maturity			0.291*	0.132**
Tuber dry matter x no. of shoots			0.189**	0.112**
Tuber dry matter x no. of leaves			0.144*	0.040**
Tuber dry matter x no. of branches			0.145*	0.741**
Tuber dry matter x days to male flower buds emergence			0.258*	0.113**

Table: 4 Multiple regression between tuber dry matter yield per plant and other component characters in 2009.

Plant characters	Regression symbol	constant (intercept)	B-Coefficient	VR	R	R^2
Stand count at harvest	X1	0.199	0.00	0.00	0.00	0.00
No. of shoots	X2		-0.189	2.559**	0.036	3.23
Plant height	X 3		-0.035	-0.0428*	0.001	0.09
No. of leaves	X 4		0.126	1.643*	0.016	1.43
No. of branches	X5		-0.114	1.036*	0.013	1.17
Leaf area	X6		-0.114	-1.487*	0.013	1.17
Days male flower buds emergence	X7		0.174	2.051**	0.030	2.69
Days to female flower buds emergence	X8		0.046	0.505ns	0.002	0.18
No. of nodes	X9		0.067	0.847*	0.004	0.36
Crop growth rate	X10		0.068	0.909*	0.005	0.45
Days to tuber maturity	X11		0.008	0.101ns	0.001	0.18
N0.of tubers	X12		0.175	2.297**	0.031	2.69
Leaf area index	X 13		0.002	0.016ns	0.00ns	0.00
Fresh tuber yield	X14		0.911	2.461**	0.830	74.44
No. of staminate spike flowers	X15		-0.092	-1.018*	0.008	0.72
No. of pistillate spike flowers	X16		-0353	1.531*	0.125	11.21

Table: 5 Multiple regression between tuber dry matter yield per plant and other component characters in 2010.

Plant characters	Regression symbol	constant (intercept	B-Coefficient	VR	R	R^2
Stand count at harvest	X1	-11.696	0.000	0.000*	0.000	0.00
No. of shoots	X2		-0.096	-1.320*	0.009	0.04
Plant height	X 3		-0.395	-2.461*	0.156	0.66
No. of leaves	X 4		3.026	1.572**	9.157	38.90
No. of branches	X5		0.073	1.138	0.005	0.02
Leaf area	X6		1.340	5.570*	1.796	7.63
Days male flower buds emergence	X7		-0.827	-4.798*	0.684	2.91
Days to female flower buds emergence	X8		2.441	1.690*	5.958	25.31
No. of nodes	X9		1.387	12.089**	1.924	8.17
Crop growth rate	X10		0.888	4.998*	0.789	3.35

Days to tuber maturity	X11		1.029	7.790	1.059	4.50
N0.of tubers	X12		0.008	0.101	0.000	0.00
Leaf area index	X 13		0.175	2.297*	0.031	0.13
Fresh tuber yield	X14		0.810	2.562*	0.656	2.79
No. of staminate spike flowers	X15		0.656	9.948	0.430	1.83
No. of pistillate spike flowers	X16		-0.942	-3.914*	0.887	3.77

Table 6: Primary Trait (Tuber dry matter yield) and selection criteria

Plant characters	R^2		Heritability %		Genotypic coefficient of variation		Genetic advance		Genetic correlation
	2009	2010	2009	2010	2009	2010	2009 2010		
Days to male flower buds emergence	2.69	25.31	26.37	91.94	71.96	52.03	75.65	94.46	rg
Days to female flower buds emergence	0.18	8.17	39.00	99.36	153.00	171.65	41.60	15.45	rg
No. of nodes	0.36	3.35	5.11	2.33	2.85	13.42	65.10	55.04	rg
Crop growth	0.45	4.50	24.39	22.55	37.97	32.73	9.02	2.21	rg

rate									
No.of leaves	1.43	38.90	21.19	11.64	11.70	6.28	67.03	27.24	-
No. of branches	1.17	0.02	54.67	47.09	15.62	12.02	16.06	13.34	-
Leaf area	1.17	7.63	1.83	5.22	0.00	0.00	39.80	6.27	rg
No. of tubers	2.69	0.13	93.97	14.22	48.54	6.24	10.15	1.93	-
Fresh tuber yield	74.44	2.79	26.67	26.64	14.92	14.94	1.97	2.02	-

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EVALUATION OF YIELD PARAMETERS OF SOME PEPPER (*CAPSICUM SPP*) LAND RACES IN NIGER STATE

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ABSTRACT

Ten accessions of Pepper (*Capsicum spp*) landraces collected from the growing local Governments of Niger state (Tafa, Zungeru, Bida, Munya, Paiko, Mokwa, Chanchaga, Kontagora, Gwada,) were characterized and evaluated for yield parameters during the growing season of 2012 at the Department of Biological sciences experimental field using a Randomized Complete Block Design (RCBD). The aim of this study was to evaluate the performance of the accession entries on yield parameters. The results showed that the pepper landraces were significantly different ($p<0.05$) for No of Flowers/plant, No of Fruits/plant, No of seeds/fruit, weight of Fruit/plant and Fruit length respectively. The landraces were found interesting for their yield parameters and could serve as potential candidates for future breeding programmes.

Keywords: *Capsicum spp*, Yield parameters, Landraces, Breeding

INTRODUCTION

Pepper is a member of the family *Solanaceae* and the genus *capsicum.* The primary centre of diversity was Mexico, but secondarily Gauatemala (Ado, 1990). Distribution of pepper is wide spread especially in tropical and subtropical ecologies including America, either as wild or cultivated forms (Ado, 1990). Nigeria happens to be the largest producer of pepper in Africa covering about 50% of total African production. A total of about 100-200,000 ha is being assigned to pepper production annually in Nigeria (Ado, 1988). In 1983, FAO estimate of pepper production in Nigeria stood at 695,000 metric tons from a total area of about 77,000 ha. Consumption of pepper in Nigeria accounts for about 40% of average daily in-take either in soup, or as condiments for flavouring and colouring of meats, fish and other food materials. In

addition, *Capsicum* is a rich source of vitamins A and C (Ascorbic acid) (Gill, 1992; Ado, 1999).The genus consists of over one hundred (100) species and even more botanical varieties (Ado, 1999; Falusi, 2007); including five domesticated species namely: *Capsicum annum, C. frutescens,C. baccatum, C. chinense*and *C. pubescens*; all believed to have originated from the New World (Mcleod*et al*., 1982; Bosland, 1994). Pepper is generally called ata (yoruba), ose (Igbo), borkonu (Hausa), yaka (Nupe), etc.

Yield improvement programmes of pepper have indicated that some genotypes performed better than the other under certain environmental conditions (Mattei *et al.*, 1971).In another evaluation, trials conducted earlier revealed that a considerable variation exists in the Pepper Germplasm. This variability will be useful in pepper improvement programmes especially for yield and fruit quality. Niger state has been known to be one of the producing states of pepper in Nigeria. Despite being one of the leading producing states, the yield obtained by the farmers is far from their inputs (Anonymous, 1980), thus this research is designed to study, collect and characterize the land races of pepper in Niger state.

MATERIALS AND METHODS

This study was carried out at the experimental garden; Centre for Preliminary and Extra-mural Studies, Federal University of Technology, Minna, Niger State, Nigeria.

The fruits were collected fresh directly from local farmers during harvest from some of the local governments growing Pepper in Niger state Tafa, Zungeru, Bida, Munya, Paiko, Mokwa, Chanchaga, Kontagora, Gwada). After collection, their seeds were removed, dried and enveloped then labeled with their accession numbers accordingly and kept in a cool and dry place before planting. The experiment was arranged in a Randomized Complete Block Design (RCBD)

The following data were taken during the period of study: fruit length in (cm) using meter rule, fruit weight in (g), Number of fruit per plant, Number of seeds per fruit and Number of flowers per plant. Analysis of Variance (ANOVA) was used to analyze the data and Least Significant Difference (LSD) was used to separate the means. The results are represented in Table 1 below.

RESULTS AND DISCUSSION

The yield parameters were investigated during the period of study to estimate the variations in all the ten (10) pepper accessions collected, (Table 1). Pepper accessions differed significantly from one another ($p<0.05$) with respect to No of flowers/plant, No of fruits/plant, No of seeds/fruit, weight of fruit/plant and fruit length. With respect to the Number of flowers/plant, the accession MK2 had the highest with the mean (95.90) while the lowest was from Gwada with the mean (27.80) but there were no statistical differences among the remaining accessions statistically at (0.05). The number of fruit/plant was also recorded, where the accession TA had the highest mean with (30.40) and the lowest was observed from PA, MK1 and CH. With the means 9.70, 10.50, and 10.00 and they were not significant statistically (0.05). The Number of seed/fruit was found to be the highest from CH (116.50) which was statistically different from all other Accessions and the lowest from MK2, KT, MU, and BD and are statistically the same but are different from all other accessions. The highest weight of fruit was observed from BD (63.41) followed by (51.93) but there were significant differences among the remaining Accessions at ($P<0.05$) level of significant. The fruit length was also recorded and the Accessions ZU, PA, KT

and MK2 were statistically different the same although they are different from all other accessions, however the highest fruit length was from BD. The statistical differences observed in fruit length is in agreement with the findings of Adetula and Olakojo (2006) who studied Genetic characterization and evaluation of some pepper (C*apsicum frutense*) and observed significant differences among fruit positions, calyx margin, fruit length and fruit width respectively. Eshbaugh *et al*. (1983) also recognized 20-30 species in the genus out of which four were domesticated species. And observed that Fruit weight, though not statistically different, varied markedly among the pepper accessions with a range of 14.6 to 58.5.

TABLE 1:

SAMPLE	NO OF FLOWER PER PLANT	NO OF FRUITS PER PLANT	NO OF SEEDS PER FRUIT	WEIGHT OF FRUIT	FRUIT LENGTH
TA	56.10 ± 13.63^{ab}	30.40 ± 4.24^{e}	76.80 ±4.11^{ab}	32.25 ± 1.39^{c}	1.03 ± 0.08^{a}
ZU	67.80 ± 12.9^{bc}	20.40 ± 3.65^{bed}	106.60 ±11.45^{bcd}	40.66 ± 2.22^{e}	5.47 ± 0.22^{b}
BD	38.90 ± 6.29^{ab}	14.90 ± 1.71^{ab}	90.60 ± 58^{abcd}	63.41 ± 2.15^{g}	6.57 ± 0.21^{c}
MU	54.40 ± 13.50^{ab}	24.90 ± 4.81^{cde}	89.30 ± 4.01^{abcd}	17.50 ± .72^{a}	0.92 ± .12^{a}
PA	43.60 ± 7.08^{ab}	9.70 ± 1.61^{a}	108.00 ± 12.31^{cd}	38.35 ± 2.61^{de}	5.89 ± .23^{b}
MK1	44.10 ± 8.22^{ab}	10.50 ±1.42^{a}	74.20 ± 5.46^{a}	24.29 ± 1.30^{b}	1.33 ± 0.16^{a}
CH	39.20 ± 5.96^{ab}	10.00 ± 1.47^{a}	116.50 ± 18.56^{d}	16.98 ± 1.17^{a}	0.90 ± 0.11^{a}
KT	47.50 ± 8.85^{ab}	15.90 ± 3.09^{abc}	102.40 ± 7.60^{abcd}	51.93 ± 2.84^{f}	5.98 ± 0.19^{b}
GW	27.80 ± 4.69^{a}	13.10 ± 2,04^{de}	78.30 ± 6.34^{abc}	34.37 ± 1.84^{cd}	1.02 ± 0.08^{a}
MK2	95.90 ± 17.72^{c}	28.20 ± 4.33^{de}	101.00 ± 7.67^{abcd}	42.86 ± 1.43^{e}	5.76 ± 0.24^{b}

Values are means of ten replicate ± standard error of mean.

Values with the same superscript alphabets in a column are not significantly different at PL 0.05

CONCLUSION

From the study, accessions Mk2, Zu and Bd were identified as good sources for pepper improvement programme, for higher yield and fruit quality improvement.

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A REVIEW OF THE ADVANCES IN COTTON BREEDING TECHNIQUES

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ABSTRACT

The breeding achievements in cotton could be viewed from the perspectives of traits such as yield, earlinesss and fibre quality. Conventional and unconventional techniques are introduced in selection of these desired traits. Old techniques used include: Plant introduction, pureline selection, mass selection, pedigree method, bulk method, single seed descent method, backcross method, heterosis breeding, polyploidy breeding and distant hybridization. New technologies include mutation breeding, biochemical and molecular assisted breeding, genetic engineering and marker assisted selection have been used to realize these objectives. Efforts have been made in cotton genome research, especially development of genomic resources and tools for basic and applied genetics, genomics and breeding research. These resources and tools include different types of DNA markers such as restriction fragment length polymorphism, random amplified polymorphic DNA, Amplified fragment Length Polymorphism, resistant gene analogues (RGA), sequence related amplified polymorphism (SRAP), simple sequence repeats or microsatellites, DNA marker based genetic linkage maps, quantitative trait loci and genes for the artificial chromosome (BAC) and plant transformation– competent binary (BIBAC) libraries.

Key words: Advances; breeding; conventional; unconventional; genetics

INTRODUCTION

Cottons are not only a world's leading textile fiber and oilseed crop, but also a crop that is of significance for oil, energy and bio-energy production (Zhang *et al*., 2008). Although cottons are native to tropics and subtropics naturally, including the Americas, Africa and Asia, they are cultivated in nearly 100 countries. India, China, USA, and Pakistan are the top four cotton growing countries, accounting for approximately 2/3 of the world's cotton. (http://www.ers.usda.gov/Briefing/Cotton/trade.htm).

According to the Food and Agriculture Organization (FAO) of the United Nations (http://www.fao.org), the cotton planting area reached about 35 million hectares and the total world's cotton production had a record of about 23 million metric tons in 2004/2005. Cotton products include fibers and seeds that have a variety of uses. Cotton fibers sustain one of the world's largest industries, the textile industry, for wearing apparel, home furnishings, and medical supplies, whereas cottonseeds are widely used for food oil, animal feeds, and industrial materials (such as soap). Cottonseed oil is ranked fifth in production and consumption volume among all vegetable oils in the past decades, accounting for 8% of the world's vegetable oil consumption. The business stimulated by cotton is hundreds of billion dollars in the world. In the USA alone, for instance, the annual cotton business revenue exceeds $120 billion (Anon. 1999). Moreover, nearly a billion barrels of petroleum worldwide are used in every year to synthesize artificial "synthetic" fibers. Further improvement of cotton fibers in yield and quality will replace or significantly reduce the consumption of fossil oil for synthetic fiber production, thus being saved for energy

production. Finally, cottonseed oil, the main by-product of cotton fiber production, could be potentially used as biofuel.

Classical Breeding approach

Advancements in Seed Breeding

In the beginning, adapting to the introduced materials from other countries was the common practice globally. Then, production of new cultivars was started by emphasizing on selection and hybridization. Principal objectives of the cotton breeding program are improvement of yield and fiber quality, precocious, adaptation for specific regional conditions and resistance to pest and diseases. Lint yield and fiber quality have always been the primary importance to the breeders because the major profit is usually realized from maximizing yield. Because of the global phenomenon of climate change, rains set abnormally in most parts of the world and this limits the vegetation period. Consequently, earliness is considered one of the most important features of cotton cultivars. Earliness enables the cotton crop to develop during periods of more favorable moisture and to be harvested before damage from unfavorable weather conditions. In the 1970/80's, bacterial blight was the most common cotton disease in Nigeria causing substantial yield loss. Cotton research breeding programs focused on developing cotton cultivars tolerant to bacterial blight. This resulted in development of varieties such as Samcot 8-13 with higher levels of resistance to bacterial blight. In other parts of the world, a lot of projects were carried out to develop new cotton varieties not only to maintain or improve yield and fiber quality to levels acceptable to the spinners, but also to improve colored cotton, resistance to major insect pests and pathogens.

Utilization of certified seeds

Nowadays, it is a common practice in most parts of the cotton producing countries of the world to renew all of the cotton seeds every year. The rate of certified seeds utilization has rapidly increased. Farmers are using seeds which are delinted, high quality, and high germination rate and to which insecticides were applied in recent years. Moreover, delinted seeds utilization has decreased hoeing and thinning costs. The major innovation in variety development is the private sector involvement in breeding.

Glandless Cotton

Gossypol, which is a chemical substance normally present in cotton plants and seeds, limits cotton seed consumption as food and feed. Cottonseed and cottonseed meal are widely used as

protein supplements in animal feed. Gossypol is the major problem to use cottonseed meal in the livestock industry as animal feed. The glandless cotton is normal cotton without gossypol. Breeding studies still continue to develop better glandless cotton varieties.

Modified backcross is a tentative method for combining the effect of intermating and backcrossing. It may be efficient in breaking the negative correlation between the economic characters of cotton cultivars. Some results were obtained in the transference of Okra leaf and frego bract traits into a high yielding cultivar of Cotton, Xu-Zhou 142 by modified backcross. This method seems to be with an obvidus effect on increasing the lint yield and reducing the contradictory relations between yield and early maturity of cotton. Besides, there might be a change of direction in the correlation between yield and disease resistance of cotton. The coefficient of correlation was change from negative value into a slightly positive one.

Advancements in seed breeding using biotechnology

Recently, biotechnology is used in cotton breeding. Sometimes very limited success has been achieved using classical breeding methods; for example a variety resistant to wilting disease caused by a soil-borne fungus (*Verticillium dahliae*) could not be developed by classical

breeding methods. This disease causes 20% reductions in cotton yield in Turkey. Currently, there is no variety that combines high yield, superior fiber qualities and verticillium resistance. The use of molecular markers and genome mapping in plant breeding and genetics has opened new directions for cotton improvement.

Advances in cotton genomic research

According to Zhang *et al.* (2008), genome research has been demonstrated to be promising for continued and enhanced crop plant genetic improvement. Therefore, efforts have been made in cotton genome research, especially development of genomic resources and tools for basic and applied genetics, genomics, and breeding research. These resources and tools include different types of DNA markers such as restriction fragment length polymorphism (RFLP), randomly amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), resistance gene analogs (RGA), sequence-related amplified polymorphism (SRAP), simple sequence repeat (SSR) or microsatellites, DNA marker-based genetic linkage maps, QTLs and genes for the traits important to agriculture, expressed sequence tags (ESTs), arrayed large-insert bacterial artificial chromosome (BAC) and plant-transformation-competent binary BAC (BIBAC) libraries, and genome-wide, cDNA-, or unigene EST-based microarrays. Efforts are also being made to develop the genome-wide, BAC/BIBAC-based integrated physical and genetic maps, and sequence the genomes of the key cotton species. However, compared with other major crops, such as rice, maize, and soybean, the genome research of cottons is far behind, mainly due to the limited funds allocated to the species.

DNA Markers and Molecular Linkage Maps

As in most plant species, the early application of DNA markers in cotton genomic research has been in the form of RFLPs. It is, therefore, not surprising that the first molecular linkage map of the Gossypium species was constructed from an interspecific G. hirsutum G. barbadense F_2 population based on RFLPs [23]. The map contained 705 loci that were assembled into 41 linkage groups and spanned 4,675 cM. This map later was further advanced by Rong *et al.* (2004), that comprised 2,584 loci at 1.74-cM intervals and covered all 13 homeologous chromosomes of the allotetraploid cottons, representing the most complete genetic map of the Gossypium to date. Many of the DNA probes of the map were also mapped in crosses of the D-genome diploid species G. trilobum G. raimondii Rong *et al.* (2004) and the A-genome diploid species G. arboreum G. herbaceum (Desai, et al.,2006). Detailed comparative analysis of the relationship of gene orders between the tetraploid AD-subgenomes with the maps of the A and D diploid genomes has revealed intriguing insights on the organization, transmission and evolution of the Gossypium genomes.

Application of Genomic tools in Cotton Genetic Improvement

One of the major goals of genome research is to use the genomic tools developed to promote or assist continued crop genetic improvement. In cottons, the development of the genomic resources and tools has allowed addressing many significantly scientific questions that are impossible to do so before. These include, but not limited to, construction of genome-wide genetic maps ,identification and mapping of genes and loci controlling traits underlying qualitative and quantitative inheritance, determination of mechanisms of cotton genome evolution, and identification and determination of genes that are involved in cotton fiber initiation, elongation, and secondary cell wall biogenesis. The genomic resources and tools could be used to promote or facilitate cotton genetic improvement in numerous ways. Marker-assisted selection (MAS) is likely one of the most important and practical

applications at present time and in near future. The MAS technology could offer many potential benefits to a breeding program. For instance, DNA linked to a gene of interest could be utilized in early generation of breeding cycle to improve the efficiency of selection. This approach has a particular advantage when screening for phenotypes in which the selection is expensive or difficult to perform, as is the case involving recessive or multiple genes, seasonal or geographical considerations, and late expression of the phenotype. However, application of MAS in cotton breeding programs is still in its infancy as the major effort of cotton genome research in the past has been on the development of genomic resources and tools for the eventual goal of enhanced cotton genetic improvement.

Fiber quality

Zhang *et al.* (2003) used a *G. anomalum* introgression line 7235 with good fiber quality properties to identify molecular markers linked to fiber-strength QTLs. A major QTL, QTLFS1, was detected at the Nanjing and Heinan field locations (China) and College Station, Texas, (USA). This QTL was associated with eight markers and explained more than 30% of the phenotypic variation. QTLFS1 was first thought to be mapped to chromosome 10, however, further study showed that this QTL was located on LGD03 [67]. Guo *et al*. (2003)] showed that the specific SCAR4311920 marker could be applied to large-scale screening for the presence or absence of this major fiber strength QTL in breeding populations. The DNA markers tightly linked to this QTL could be useful for developing commercial cultivars with enhanced fiber length properties (Shen *et al.*2005). Wang *et al.* (2006) identified a stable fiber length QTL, qFL-D2-1, simultaneously in four environments in Xiangzamian. The high degree of stability suggests this QTL might be particularly valuable for use in MAS programs. Chee *et al.* (2005)] dissected the molecular basis of genetic variation governing 15 parameters that reflect fiber length by applying a detailed RFLP map to 3,662 BC_3F_2 plants from 24 independently derived BC_3 families utilizing G. barbadense as the donor parent. The discovery of many QTLs unique to each trait indicates that maximum genetic gain will require breeding efforts that target each trait. Lacape *et al.* (2005) performed QTL analysis of 11 fiber properties in BC_1, BC_2, and BC_2S_1 backcross generations derived from the cross between G. hirsutum "Guazuncho " and G. barbadense "VH8." They detected 15, 12, 21, and 16 QTLs for length, strength, fineness, and color, respectively, in one or more populations. The results showed that favorable alleles came from the G. barbadense parent for the majority of QTLs, and cases of co-localization of QTLs for different traits were more frequent than isolated positioning. Taking these QTL-rich chromosomal regions into consideration, they identified 19 regions on 15 different chromosomes as target regions for the marker-assisted introgression strategy. The availability of DNA markers linked to G. barbadense QTLs promises to assist breeders in transferring and maintaining valuable traits from exotic sources during cultivar development.

Cytoplasmic male sterility

In cotton, cytoplasmic male sterility conditioned by the D8 alloplasm (CMS-D8) is independently restored to fertility by its specific D8 restorer (D8R) and by the D2 restorer (D2R) that was developed for the D2 cytoplasmic male sterile alloplasm (CMS-D2). Zhang and Stewart (2001) concluded that the two restorer loci are nonallelic, but are tightly linked with an average genetic distance of 0.93 cM. The D2 restorer gene is redesignated as Rf1, and Rf2 is assigned to the D8 restorer gene. The identification of molecular markers closely linked to restorer genes of the cytoplasmic male sterile could facilitate the development of parental lines for hybrid cotton. Guo *et al.* (1998) found that one RAPD marker fragment, designated OPV-15(300), was closely linked with the fertility-restoring gene Rf1. Zhang and Stewart (2004) identified RAPD markers linked to the restorer gene and, furthermore, converted the three RAPD markers into reliable and genome-specific sequence tagged site

(STS) markers. Liu *et al.* (2003) determined that the Rf1 locus is located on the long arm of chromosome 4. Two RAPD and three SSR markers were identified to be closely linked to the Rf1 gene. These markers are restorer-specific and should be useful in MAS for developing restorer parental lines. Yin *et al.* (2006) further constructed a high-resolution genetic map of Rf1 containing 13 markers in a genetic distance of 0.9 cM. They constructed a physical map for the Rf1 locus and enclosed the possible location of the Rf1 gene to a minimum of two BAC clones spanning an interval of approximately 100 kb between two clones, designated as 081-05K and 052-01N. Work to isolate the Rf1 gene in cotton is now in progress.

Resistance to diseases and insect pests

Breeding for disease resistance is of great importance in cotton breeding program. To facilitate analysis, cloning, and manipulation of the genes conferring resistance to different pathogens, including bacteria, fungi, viruses, and nematodes, He *et al*. (2004) isolated and characterized the family of nucleotide-banding site-leucine-rich repeat (NBS-LRR)-encoding genes or resistance gene analogues (RGAs) in the Upland cotton cv. Auburn 634 genome. Genetic mapping of a sample (21 genes) of the RGAs indicated that the gene family resides on a limited number of the cotton AD-genome chromosomes with those from a single subfamily tending to cluster on the cotton genetic map and more RGAs in the A subgenome than in the D subgenome. Of the 16 RGAs mapped, two happened to be comapped with the cotton bacterial blight resistance QTLs previously mapped by Wright *et al*. (1998). Since nearly 80% of the genes (40 genes) cloned to date that confer resistance to bacteria, fungi, viruses, and nematodes are contributed by the NBS-LRR gene family, the cotton RGAs of the NBS-LRR family have provided valuable tools for cloning, characterization, and manipulation of the resistant genes to different pathogens and pests in cottons. Root-knot nematodes (RKN), Meloidogyne incognita, can cause severe yield loss in cotton. Wang *et al.* (2006) identified one SSR marker CIR316 on the linkage group A03 tightly linked to a major RKN resistant gene (rkn1) in the resistant cultivar G. hirsutum "Aacla NemX." In a companion study, a bulked segregant analysis (BSA) combined with AFLP was used to identify additional molecular markers linked to rkn1 (Wang and Roberts, 2006). An AFLP marker linked to rkn1 designated as GHACC1 was converted to a cleaved amplified polymorphic sequence (CAPS) marker. These two markers have potential for utilization in MAS. Shen *et al*. (2006) identified RFLP markers on chromosome 7 and chromosome 11 showing significant association with RKN resistance from the Auburn 634 source, a different source of resistant germplasm than Acala NemX. The association was further confirmed by detection of a minor and a major dominant QTL on chromosomes 7 and 11, respectively, using SSR markers. Ynturi *et al*. identified two SSR markers which together accounted for 31% of the variation in galling index. The marker BNL 3661 is mapped to the short arm of chromosome 14 while BNL 1231 to the long arm of chromosome 11. The association of two different chromosomes with RKN resistance suggests at least two genes are involved in resistance to RKN.

Bacterial blight caused by the pathogen Xanthomonas campestris pv. malvacearum (Xcm) is another economically important disease in cotton. Wright *et al*. (1998) and Rungi *et al.* (2002) both used mapped RFLP markers to investigate the chromosomal location of genes conferring resistance to the bacterial blight pathogen. The mapping data suggest that the resistance locus segregates with a marker on chromosome 14 known to be linked to the broad-spectrum B12 resistance gene originally from African cotton cultivars. AFLPs and SSRs were also used to search for novel markers linked to the Xcm resistance locus to facilitate introgression of this trait into G. barbadense through MAS.

CONCLUSION

A significant amount of genomic resources and tools has been available in cottons though cotton genomics research is far behind those of other major crops such as rice, maize, wheat, and soybean. These resources and tools have allowed identifying and mapping many genes and QTLs of importance to cotton fiber quality, fiber yield, and biotic and abiotic stresses and addressing several significant questions to plant biology in general and to cotton in particular. Nevertheless, many efforts are needed to further develop the resources and tools and to make the tools readily usable in applications in order to fully and effectively use them in cotton genetic improvement and biology research. In particular, the following areas of cotton genomics research should be emphasized.

(i) Development of whole-genome BAC/BIBAC-based, integrated physical maps of cottons. There is no whole-genome, robust BAC/BIBAC-based, integrated physical/genetic map that has been developed for cottons. The maps should be developed for at least two species of Gossypium. One is the Upland cotton that produces 90% of the world's cotton whereas the other is G. raimondii, the species having the smallest genome among all Gossypium species, thus likely having highest density of genes. This research is emphasized because it has been proven in model and other species, including Arabidopsis, rice, Drosophila, human, mouse, and chicken, that whole-genome integrated physical/genetic maps provide powerful platforms and "freeways" for many, if not all, modern genetics and genomics research ;development of the integrated physical maps will allow rapidly and efficiently integrating all existing genetic maps, mapped genes and QTLs, and BAC and BIBAC resources and cotton unigene ESTs, and accelerate the efficiency and reduce the cost of research in all areas by manifold.

(ii) QTL fine mapping. Many genes and QTLs that are important to cotton fiber yield fiber quality, and biotic and abiotic stresses have been genetically mapped, but two problems are apparent. The first one is that almost all of the QTLs were mapped using F_2, BC_1, or early segregating generations in a single or a limited number of environments. Since quantitative traits are readily subjected to environmental variation, the mapping results using the early generations in a single or a limited number of environments would vary from experiments to experiments. The other problem is that the genetic distances between DNA markers and most of the QTLs are too far to be used for MAS. Therefore, it is of significance to fine map the QTLs using large and advanced generation or homozygous populations, such as RILs and DHs, in multiple environments, and closely linked DNA markers, for which advantage of integrated physical maps could be taken. In addition to accurate mapping of the QTLs and development of DNA markers that are well-suited (closely linked and user-friendly) for MAS, fine mapping is also an essential step toward the final isolation of the QTL genes by map-based cloning (Zang, 2007). The isolated genes are not only the sources for molecular breeding via genetic transformation, but also the most desirable for marker development for MAS because there is no recombination between the gene and its derived marker.

(iii) Sequencing of one or more key cotton genomes. While it is costly using the current sequencing technology, whole-genome sequencing is a most-efficient method to discover and decode all cotton genes and provides a most-desired and most-fine integrated physical and genetic map of the cotton genome. Comparative genomics studies demonstrated that the gene contents and orders are highly conserved among the genomes of Gossypium species even they are significantly different in genome size (Desai *et al.* 2006 and Rong *et al*.2004). Based on this result, G. raimondii is an excellent choice to be sequenced because it has the smallest genome among all Gossypium species though it is not cultivated. If an integrated physical map is available for the major cultivated cotton, G. hirsutum, that has a three-fold larger genome than G. raimondii, the sequence information of G. raimondii could be readily

transferred to the cultivated cotton by using the BAC end sequences of its integrated physical map as anchors.

(iv) ESTs from nonfiber and nonovary tissues and fibers at the secondary cell wall deposition stage. As shown above, the number of cotton ESTs available in GenBank has been increased significantly in the past few years; however, the distribution of the ESTs among tissue sources are extremely biased. The numbers of ESTs from both nonfiber/nonovary tissues and fibers at the secondary cell wall deposition stage (15–45 dpa), particularly after 20 dpa, are especially small. The former set of expressed genes, despite of not directly contributing to fiber yield and quality, is of significance to fiber yield and quality, whereas there is no doubt that the later set of expressed genes directly contribute to the fiber strength.

(v) Profiling and identification of genes involved in individual biological processes and conditions with emphasis on those involved in fiber development. Development and availability of cDNA- or unigene EST-based microarrays have provided unprecedented opportunities for research of molecular biology, functional genomics, and evolutionary genomics, however, cotton research in these regards are very limited. Identifying and characterizing genes that are involved in the processes of fiber development, plant growth and development, and biotic and abiotic stresses will greatly facilitate our understanding of underlying molecular basis of these processes in cottons, and thus, enhance breeders' ability to cotton genetic improvement.

(vi) Translating the gene activities or expressions at different tissues and stages into fiber yield and fiber quality, thus assisting in cotton breeding. The genes that are involved in fiber initiation (Wu *et al*. 2006), elongation (Arpat *et al*, 2004), and secondary cell wall deposition have been identified from several genotypes of cottons, but it is unknown about what the up- or down regulation, or active expression of fiber genes at a developmental stage and organ means to final fiber yield and/or quality. For instance, does the active expression of a gene at fiber elongation stage in fiber suggest longer fibers? Studies in this regard are essential to use the gene expression data in cotton germplasm analysis and breeding.

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PGB64

ASSESSMENT OF CONSUMPTION, UTILIZATION AND NUTRIENT COMPOSITION OF SPICES CONSUMED IN NORTH CENTRAL NIGERIA

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ABSTRACT

This study evaluated the consumption pattern and nutrient composition of local spices used by households of North Central Nigeria. A total of 150 respondents (68 adult males and 82 adult females) were interviewed using structured questionnaires in their native homes; and samples of spices commonly consumed in the area analysed for nutrient composition. Spices available and commonly consumed by the households include clove, cinnamon, basil leaf, black pepper, Ethiopian pepper, garlic and ginger. Ginger and garlic were the most commonly consumed. Most of the households (57.3%) valued these spices for their

flavouring properties while about 25.3% of the households valued them for medicinal uses and the rest 17.3% valued them mostly for preservative properties. Also the type and quantityof spice being used for food flavouring usually dependent mostly on the type of food being prepared. The spices were rich in most food nutrients, including protein, fats and oil, fibre and ash. The high fibre, oil and ash contents are good indication of their being good source of phytochemical antioxidants, vitamins and minerals. These spices are thus excellent sources of nutrients and valued, consumed and utilized by the people.

Key words: Consumption, utilization, nutrient composition, spices.

INTRODUCTION

A spice is a dried seed, fruit, root, bark or leaf or vegetative substance used in nutritionally insignificant quantity as a food additive for the purpose of flavour, colour or as a preservative that kills harmful bacteria or prevents their growth (Musa and Haydar, 2004). Different spices and herbs have different degrees of nutrients or nutrient composition (Udeala, 1980). Spices add flavour, relish, or piquancy to foods. Spices consist of rhizomes, barks, leaves, roots, flowers, fruits, seeds and other parts of the plant while herbs are leaves of low-growing shrubs. Common spices include parsley, thyme, scent leaves, rosemary, savory, sage and celery leaves (Parry, 1969).

Spices are indispensable components of cuisines used as accessory foods mainly for flavouring food to improve palatability (Okafor, 1987; Okigbo, 1997). Spices have been defined by the Food and Drug Administration as aromatic vegetable substances used for seasoning of food and from them no portion of any volatile oil or other flavouring principle has been removed and are free from artificial colouring matter, adulterants and impurities (Farrel, 1990; Dorant and Brandt, 1993). Spices are used in small quantities and their contribution to nutrient intake is very minimal but many are rich in food nutrients, including protein, carbohydrate, fibre and minerals (Nielson, 2002). Spices are rich sources of vitamins, especially vitamin A, C, and B, protein and mineral such as calcium, sodium, potassium and iron. Spices of international trade used globally include sweet and red pepper, cinnamon, mustard, nutmeg, marjoram, oregano, black pepper, ginger, garlic, rosemary, thyme and basil leave (Kramlich et al.,1973).

In addition to adding flavour to foods and beverages, spices are valued for their nutritional, antioxidant, antimicrobial, insect repellant and medicinal properties (Farrel, 1990). Spices are used as flavour enhancers because of their health-protective phytochemicals which can help to fight cancer and other degenerative diseases. Spices have tremendous importance in being used as ingredients in food, alcoholic beverages, medicine, perfumery, cosmetics, colouring and also as ornamental plants (Sharma, 2005). Spices when added to food can also lead to complex secondary effects such as salt and sugar reduction, improvement of texture and extension of shelf life. The basic effects of Spices in food and confectionary could be for flavouring, aroma, deoxidizing, colouring and/or preservation. Spices make food and confectionary more appetizing and palatable (Ravindran *et al.*, 2002).

Nigeria is endowed with many edible plants many of whose fruits and vegetable are used as spices in many traditional homes. However many Nigerians do not value spices and ignore

their uses as food ingredients. Evidences have shown that many of these Nigerian spices apart from their regular flavouring effects also improve nutrient content and shelf life of food. Many are health promoting. This study was therefore poised to examine availability, food uses and nutrient composition of commonly existing spices in North central Nigeria. The study will be of great benefit to the society at large in providing information about availability and nutrient composition of spices in the area for more practical application in homes and industries.

MATERIALS AND METHODS

The data for this study were obtained from a sample survey of 150 households in Lafia, Nasarawa State of North central Nigeria between August and November, 2010. The survey was designed to gather general information on the socio-economic status, availability and consumption patterns of spices among households, for example, types, occurrence and frequency of utilization of spices in the study area. The target population for the survey was adults of ages 20 years and above with varied bio data. The subjects' sex, age distribution, religion, educational qualification and working experience were used as the criterion for their socio-economic status.

Samples of spices commonly consumed in the area were also collected from the respondents and analysed for nutrient composition.

Chemical analysis of spices: Each of the spice sample was milled into a homogenous blend. Moisture, crude protein, crude fat, crude fibre and ash contents were determined in duplicates by the method of the Association of Official Analytical Chemists (AOAC, 2000). Moisture was determined as the loss in weight after heating 2g subsample of each spice in a vacuum oven at 105^{OC} for 4h. Nitrogen was determined by wet digestion analysis of the micro Kjelhdal method, and nitrogen was multiplied by 6.25 to estimate crude protein content (Pearson, 1976). Crude fat was estimated by exhaustive extraction of a subsample (5g) of each of the spices with petroleum ether (boiling point, 40- 60^{OC}) using a soxhlet apparatus. The fat-free extract after ether extraction was digested alternatively with $1.25MH_2SO_4$ and with 1.25% NAOH under specified conditions. The loss in weight on ignition of the residue at 600^{OC} was reported as crude fibre content while the remainder was reported as the ash content. After wet-digestion of a subsample (5g), Calcium was determined using atomic absorption spectrophotometer (AAS) while Phosphorus was determined using the Vanadomolybdate method (AOAC, 2000)

RESULTS AND DISCUSSION

Demographic Characteristics of the respondents

Table 1 below shows that 54.7% of the respondents were females while 45.3% were males. Majority of the respondents fall within the age range 40 years and above and were followed by those of 30–39years (21.3%) and 20-29 years (12.0%). The table also show that about 60.0% of the respondents were Muslims while 40% of them were Christians. Thus the people were predominantly Muslims and Christians intermingling freely among each other. The education attainment of the people range from zero education (illiteracy) (14.7%),

primary school (58.7%), secondary school(20%) and higher institution (6.7%) and 14.7% that have been to secondary school, tertiary institution and never been to school respectively.

Table 1: Demographic characteristics of the respondents

Variable	Frequency	Percentage
Sex		
Male	68	45.3
Female	82	54.7
Total	**150**	**100**
Age of respondents		
20-29	18	12.0
30-39	32	21.3
40 and above	100	66.7
Total	**150**	**100**
Religion		
Christianity	60	40.0
Islam	90	60.0
Total	**150**	**100**
Level of education		
Never been to school	22	14.7
Primary school	88	58.7
Secondary school	30	20.0
Tertiary Institution	10	6.7
Total	**150**	**100**
Years of experience		
Less than 1-5years	38	18.7
6-11years	84	56.7
12years and above	38	25.3
Total	**150**	

Commonly available and frequently consumed spices

Table 2 shows the list of commonly available and utilized spices in the area. In all, 7 spices, including cloves, cinnamon, basil leaf, black pepper, Ethiopian pepper, garlic and ginger were very popular among the respondents. However, ginger and garlic were more frequently used by most of the respondents. These spices were used as food ingredients in soups, sauce, meal and meat. Ginger and garlic ranked high in utilization because of their high demand in spicing smoked and grilled meat and fishes which are very popular in the area. Ginger and garlic were also claimed to increase the shelf life of meat and local beverages such as" kunu zaki" (a popular cereal based drink of the locality).

Table 2: Spices available and frequency of utilization in the study area

	Occurrence		**Utilization**	
	Freq.	**%**	**Freq.**	**%**
Names of spices				
Clove (Kalipari)	6	4.0	10	6.7
Cinnamon (Fasokori)	8	5.3	4	2.7
Basil leaf	8	5.3	16	10.7
Black pepper (Masoro)	6	4.0	41	28.0
Ethiopian pepper (kimfer)	8	5.3	12	8.0
Garlic (Tarfarnwa)	43	28.7	27	18.0
Ginger (Chitta)	71	38.2	39	25.9
Total	**150**	**100**	**150**	**100**

Uses of Spices among respondents

Table 3 shows that more than half (57.3%) of the respondents use spices regularly mainly for flavouring purposes. Out of the 150 respondents interviewed, only 17.3% use spices for preservative purposes while 25.3% use spices for medicinal purposes. It is evident that most of these people do not recognize or do not understand the preservative effects of spices in food. Predominantly spices are used to give flavor, aroma and taste in food and this is in agreement with Parry (1969) who opined that spice and herbs are used to give flavor, aroma and taste in food. Interestingly, 25.3% of the respondents indicated that they use spices for medical purposes which agrees with that of Ravindran *et al* (2002) who showed that spices and herbs possess antimicrobial and pharmaceutical properties. These people should be made to realize the importance of spices as flavouring, preservation and medicinal ingredients.

Table 3: Recognized functions and application of spices by respondents

Variables	Frequency of Applications	Percentage
Preservative purpose	26	17.3
To give aroma, flavour and taste in food	86	57.3
Medical purpose	38	25.3
Total	150	100

Table 4 summaries the most popular reasons and the influencing factors why people use spices in the area. Seasons or ceremonies, type of food prepared and sometimes health condition of the consumers determine the extent and the type of spice to use if at all in food preparations. The type of food prepared most frequently determines the type and quantity of spice to be used as indicated by their responses (56%). About 25.3% of the respondents agree that their choice of spice dependent on the health condition of the consumers and health promoting effect of the particular spice.

Table 4: Reasons for using and factors influencing choice and uses of spices in food

Reasons	**Frequency**	**Percentage**
flavouring	28	18.7
Aroma enhancing	30	20.0
Preservation	26	17.3
Flavoring, aroma enhancing and preservation	66	44.0
Total	150	100
Influencing factors	**Freq .of influence**	**Percentage**
Ceremonies	28	18.7
Type of food consumed	84	56.0
Health promoting	38	25.3
Total	150	100

Nutrient composition of the commonly consumed spice in the study area

The moisture content of the spice samples ranged from 7.95% for cinnamon to 14.11% for garlic. Ginger had 12.34% while black pepper had 11.92% and basil leaf had 10.76% of moisture. Ethiopian pepper had moisture content of 10.98%. most of the spices except ginger and garlic with moisture content higher than 12% are most likely to be shelf stable at ambient condition with little or no microbial growth. However both ginger and garlic in this study are likely to be susceptible to high load of bacteria and mould on long term storage. The spices were high in crude protein, crude fibre, lipid and ash. Protein contents ranged from 6.75% for cinnamon to 25.40% for garlic. Clove had 16.39% crude protein while basil leaf had 16.64% crude protein. Crude fibre ranged from 7.69% in basil leaf to 41.06% in cinnamon while lipid content ranged from 2.36% in cinnamon to 17.73% in ginger. The high content of crude fibre is a good indication of likely high presence of most health-promoting phytochemicals while the high lipid contents are likely to be good source of fat- soluble vitamins and natural anti-oxidants in the spices (Hirasa and Takemasa, 1998). The spices were also high in ash content, indicating likely high presence of most vital minerals as indicated in calcium and phosphorus contents of these spices. These spices are therefore good source of most food nutrient; thus apart from their flavouring, preservative, and medicinal effects, they could also be sourced for adequate nutrient intakes.

Table 5: Nutrient Composition of spices commonly consumed in the study area

(Weight (g) per 100 grams of sample)

Sample	Moisture	Crude Protein	Crude Fibre	Lipids	Ash	Digestible Carbohydrates	Calcium	Phosphorus
Cloves	8.79	16.39	26.11	6.21	6.93	35.57	1.47	0.21
Cinnamon	7.95	6.75	41.06	2.36	7.89	33.99	0.79	0.23
Scent leaf	10.76	16.64	7.69	2.77	6.55	46.29	1.31	0.19
African black pepper	11.92	7.22	37.58	6.11	7.49	29.77	1.51	0.18
Ethiopian black pepper	10.98	11.05	36.42	10.43	4.52	26.55	0.65	0.16

Ginger	12.34	10.45	26.19	17.73	13.05	20.24	0.45	0.44
Garlic	14.11	25.50	13.31	14.22	6.43	30.82	1.17	0.52

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MORPHOLOGICAL DIVERSITY OF ACHA (FONIO) (*Digitaria exilis* and *Digitaria iburua*) GERMPLASM AND EVALUATION OF GENETIC VARIATIONS USING RAPD-PCR TECHNIQUES IN NIGERIA

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ABSTRACT

This study evaluated thirty-five Acha or Fonio (*Digitaria* spp) accessions for morphological and genetic characterization in order to unlock genetic potential of each variety for breeding purposes. The accessions were planted in plots measuring 2m by 3m, and replicated three times in a randomized complete block design. Data were collected using a $1m^2$ quadrant across plots in determining some morpho-agronomic parameters. RAPD

protocol was used in the molecular classification of the accessions. Data obtained was analyzed statistically using ANOVA, correlation and cluster analysis. Morphological variations and growth performance of the accessions were observed to have an influence on grain yield. Jakah variety had the highest yield of 176.24kg/plot which differed significantly ($p<0.05$) with other accessions while morphological features of peduncle length, internodes length, spikelet per panicle number and plant height were observed to have positive correlation ($P<0.05$) with grain yield. Also negative correlation was observed ($P<0.05$) between days to 50% flowering and grain yield, portraying an inverse relationship between the two. On the other hand, morphology and molecular cluster analysis gave different number of clusters which was indicative of the need to use the two techniques for classification of fonio in Nigeria. Therefore the study has established the existence of diversity in morphological/ traits of Acha accessions. Also, the study has also confirmed the use of RAPD-PCR in unraveling the phylo-genetic diversity of Acha accession.

Keywords: accessions, breeding, genetic diversity, phylogeny, morpho-agronomic

INTRODUCTION

Acha (*Digitaria exilis* Kipp. Stapf and *Digitaria iburua* Stapf) is probably the oldest African cereal. It is sometimes considered as "a small seed with a big promise" provides food early in the season when other crops are yet to mature for harvest (Ibrahim, 2001). Acha grains are the tastiest and most nutritious of all grains (NRC, 1996) and is said to contain 7% crude protein, which is high in leucine (19.8%), methionine and cystine of about (7%) and valine (5.8%) (Temple and Bassa, 1991). It forms the staple food in some of the producing areas where it is processed into various kinds of menus (Kwon-Ndung *et al*., 2001). In Nigeria, about 70,00 metric tons of the crop is produced annually (CBN, 1998) and that the economic returns of Acha when computed showed that it is profitable to grow the crop compared to other crops like rice, sorghum and cowpea (Dauda and Luka, 2003). Though the crop has been completely neglected in the past (Kwon-Ndung and Misari, 1999), it is now considered as an important crop for improvement as a cultivated species (Ibrahim, 2001, Morales-Payan *et al*., 2002).

In Africa, Acha is known as a savannah plant, which does not prosper in soils with salinity problems. It has low water demands, and survives strong droughts (Harlan 1993; Hilu *et al.,* 1997). According to Kwon-Ndung *et al.,* (2001), the existence of different types of varieties under cultivation was a common feature in Kaduna and Plateau States where the highest numbers of Acha accessions in Nigeria have been assembled. The adult plant reaches about 50 cm in height, and flowering usually occurs about 6 to 8 weeks after emergence.

Bees are known to visit the flowers and apparently play a role in flower fertilization. There are many cultivars with varying periods of maturity of 90-130 days (Purseglove, 1975).

Markers are identifiable DNA sequences found at specific location of the genome and transmitted by the standard laws of inheritance from one generation to the next. There are many different kinds of molecular markers including restriction fragment length polymorphisms (RFLPs), random amplified polymorphic DNA (RAPDs), amplified fragment length polymorphisms (AFLPs), microsatellites, and single nucleotide polymorphisms (SNPs) (Kumar *et al.,* 2009). At present, among several molecular approaches employed to assess genetic diversity and relationship in plant species, RAPD (random amplified polymorphic DNA) analysis is the simplest and least laborious method. The information on genetic diversity and relationship within and among crop species is essential for the efficient utilization of plant geneti resource collections (Irwin *et al*., 1998). Diversity studies have been carried out in the Ethiopia/Eritrea area, which, like most areas, is threatened by loss of landraces due to introduction of improved varieties from elsewhere (Edossa, *et al*., 2010). Evaluating germplasm diversity can help to identify landraces with the greatest novelty and thus are most suitable for rescue or incorporation into crop improvement programs. There is paucity of information in the area of morphological characteristics of Acha and the genetic diversity. Therefore, there is need for evaluation of some Acha or Fonio accessions for morphological and genetic characterization in order to unlock genetic potential of each variety for breeding purposes. This study aimed at investigating this and developing potential diagnostic tools through PCR analysis.

MATERIALS AND METHODS

The thirty five Acha accessions were obtained from the out station of the National Cereals Research Institute, (NCRI) Badeggi, Niger State, located in Riyom, Jos. Plateau State. The field work was done at the Research and Experimental plot of the Plant Science & Biotechnology Unit of the Department of Biological Science Nasarawa State University, Keffi (8^0 32^1N 8^0 18^1E). The molecular procedure was done at the Biotechnology Laboratory of the Science and Technology Complex (SHESTCO) and Nigerian Institute of Science Laboratory Technology (NISLT) Samonda, Ibadan. The accessions were planted in plots measuring 2m by 3m and replicated three times in a randomized complete block design (RCBD). The trial was planted by uniform broadcasting of weighted seeds across plots. Hand weeding was done at 6, 10 and 30 weeks after planting (WAP) and basal application of fertilizer was carried out at 3 WAP using 20kg N per hectare, 30kg P_20_5/ ha and 30kg K_20/ha. Morpho-agronomic descriptions such as, physical characteristic of seed, germination percentage, days to 50% flowering, tiller number per plant, leaf area, peduncle length, internode length, days to maturity, grain yield, spike number per panicle and plant height at harvest were determined by collecting data

using a $1m^2$ quadrant across plots. The data were subjected to statistical analysis using Duncan Multiple Range Test procedure to separate the cluster means. For genetic characterization, a total of thirty five accessions of Acha were grown in the screen house in polythene bags containing topsoil. Young leaves were harvested from 3weeks old seedlings, put in a sealable plastic bag, labeled properly and were used immediately for DNA extraction following the methods of Dellaporta *et al*., (1983). The extracted pure Acha DNA was quantified using spectrophotometer before PCR analysis to obtain required concentration for the research work. PCR amplification was performed according to Arunyawat (1997), using primers synthesized by Operon Technologies (USA).

RESULTS

Variations in the physical characteristics of *Digitaria* spp accessions seed in this study showed that the thirty five accessions have three main colours; White, Brown and Light Brown. Ampios, Napas, Kin, Gong-a-randong, Chun-hoss 1, Jakah, Munsung, Suhn, Napiya, Sha'alak, Dinat, Jipel, Gotip, Shalak, Tsala, Gopantor and Gwabi seed were of white colour. Gindiri 1, Kureep, Sheng, Tishi, Lalaku, Gindiri 2, Nkpwos, Ndat, Namuruk, Nashileng and Badama had light brown coloured seed while Chun-hoss 2, Chisu, Nding, Gong-halla, Chunpyeng, Npyeng and Maan seed were brown in colour while seed weights for all the accessions ranged between 0.013g and 0.093g. The morphology of the growing sections (Table 1) showed that there are variatzions in the tiller number, plant height, peduncle length, Internodes length, spikelet number per panicle, and leaf area among all the accessions.

Table 1: Morphological Variations of Growing Sections of *Digitaria* spp

NO	ACCESSION	Tiller no/plant	Peduncle length (cm)	Internode length (cm)	Spiklvet no/pannicle	Leaf area (cm)
1	AMPIYOS	19.00^{cde}	33.15^{m}	5.00^{mno}	4.00^{efg}	13.18^{c}
2	CHUN-HOSS 2	10.00^{klm}	32.72^{m}	5.00^{mno}	8.00^{ab}	11.66^{c}
3	GINDIRI 1	21.00^{c}	38.66^{i}	5.66^{klm}	4.00^{efg}	11.15^{c}
4	CHISU	21.00^{c}	29.43^{pq}	5.66^{klm}	4.00^{efg}	13.18^{c}
5	NDING	4.00^{o}	31.32^{mn}	3.70^{opq}	4.00^{efg}	12.65^{c}
6	KUREEP	18.00^{de}	29.23^{q}	4.33^{nop}	4.00^{efg}	12.67^{c}
7	SHENG	13.00^{hijk}	38.71^{i}	3.50^{pq}	3.00^{g}	10.64^{c}
8	NAPAS	19.00^{cde}	42.43^{g}	3.07^{q}	5.00^{cdef}	10.64^{c}
9	GONG-HALLA	14.00^{ghi}	32.40^{no}	5.52^{lmn}	6.00^{bcde}	9.12^{c}

10	TISHI	11.00^{jkl}	35.77^{l}	4.53^{mno}	4.00^{efg}	12.16^{c}
11	KIN	14.00^{ghi}	31.70^{no}	3.50^{opq}	4.00^{efg}	9.12^{c}
12	CHUNPYENG	20.00^{cd}	30.99^{o}	4.50^{mno}	5.00^{cdef}	12.16^{c}
13	NPYENG	13.00^{ghij}	29.18^{p}	4.50^{mno}	4.00^{efg}	12.16^{c}
14	MAAN	15.00^{fgh}	29.44^{q}	5.00^{mno}	4.00^{efg}	12.16^{c}
15	GONG-A-RANDONG	11.00^{jkl}	27.72^{r}	5.33^{mno}	4.00^{efg}	9.12^{c}
16	LALAKU	13.00^{ghij}	39.46^{hi}	4.66^{mnop}	5.00^{defg}	12.16^{c}
17	GINDIRI 2	18.00^{de}	50.03^{i}	4.50^{mno}	5.00^{fg}	13.68^{bc}
18	NKPWOS	15.00^{fghi}	35.46^{l}	4.33^{nop}	6.00^{bcde}	11.66^{c}
19	NDAT	17.00^{ef}	36.54^{k}	4.66^{mnop}	4.00^{efg}	12.67^{c}
20	NAMURUK	20.00^{cd}	40.10^{h}	5.51^{jklm}	4.00^{efg}	13.69^{bc}
21	CHUN-HOSS 1	14.00^{ghi}	39.80^{h}	5.52^{jklm}	5.00^{cdef}	13.18^{c}
22	JAKAH	20.00^{cd}	38.00^{j}	6.66^{hijk}	7.00^{ab}	3.04^{d}
23	MUNSUNG	21.00^{c}	47.96^{d}	6.66^{hijk}	7.00^{ab}	2.03^{d}
24	SUHN	9.00^{klm}	47.44^{e}	6.33^{ijkl}	7.00^{ab}	1.52^{d}
25	NAPIYA	8.00^{mn}	37.86^{jk}	7.66^{efgh}	5.00^{cdef}	3.02^{d}
26	SHA'ALAK	7.00^{n}	27.43^{r}	6.70^{ghij}	5.00^{cdef}	1.52^{d}
27	NASHILENG	18.00^{de}	35.45^{l}	11.06^{b}	8.00^{a}	10.39^{c}
28	DINAT	12.00^{ijk}	37.43^{k}	8.33^{def}	7.00^{ab}	3.04^{d}
29	JIPEL	10.00^{klm}	43.66^{f}	13.00^{a}	8.00^{a}	10.14^{c}
30	GOTIP	29.00^{a}	51.15^{a}	9.63^{bc}	7.00^{ab}	23.83^{a}
31	SHALAK	13.00^{ghij}	48.62^{cd}	8.66^{de}	7.00^{ab}	23.83^{a}
32	TSALA	15.00^{fghi}	51.34^{ab}	7.52^{efg}	7.00^{ab}	19.77^{a}
33	GOPANTOR	15.00^{fg}	48.89^{cd}	9.33^{cd}	6.00^{bcde}	19.27^{ab}
34	BADAMA	27.00^{a}	30.84^{o}	7.33^{fghi}	5.00^{cdef}	10.65^{c}
35	GWABI	24.00^{b}	49.00^{c}	12.26^{a}	7.00^{ab}	19.77^{a}
	Overall Mean	15.83	37.92	6.1	5.31	6.91
	SE of x	5.47	7.41	2.68	1.79	3.74

Growth and yield performance of *Digitaria spp* used for this experiment are shown in Table 2. The germination percentage of 14 days after planting ranged between 20.44% and 94.62% in all accessions. The lowest day to 50% flowering occurred in Dinat (77.15) accession while the fastest day to 50% flowering was

observed in Npyeng (91.53).). In addition, value of day to 50% flowering observed in Kureep (91.17), Chunpyeng (91.26), Npyeng (91.53), Maan (91.19), Gong-a- randong (91.19) and Lalaku (91.46) were significantly different with the one obtained in Npyeng accession. This showed that Npyeng variety got to flowering stage earlier than the other accessions. Also, days to maturity of the accession were relatively close; this ranged between 113 days in Jipel and 128 days in Npyeng, Maan and Lalaku accessions. On the contrary, the plant height ranged between 54.00cm and 131.66cm in Gong-halla and Tsala varieties respectively. There was significant difference in the plant height of Tsala and other accessions. However, grain yield was on ebb in most of the accessions. The highest 176.24 kg of yield was recorded in Jakah accession while the lowest occurred in Maan (0.93kg) accession. The lowest yield observed in Maan accession was not significantly different with the yield obtained from Gong-halla (2.90kg), Tishi (1.51kg), Kin (2.10kg), Npyeng (1.85kg), Gong-a-randong, Lalaku (2.42kg), Nkpwos (0.96kg) and Ndat (1.34kg).

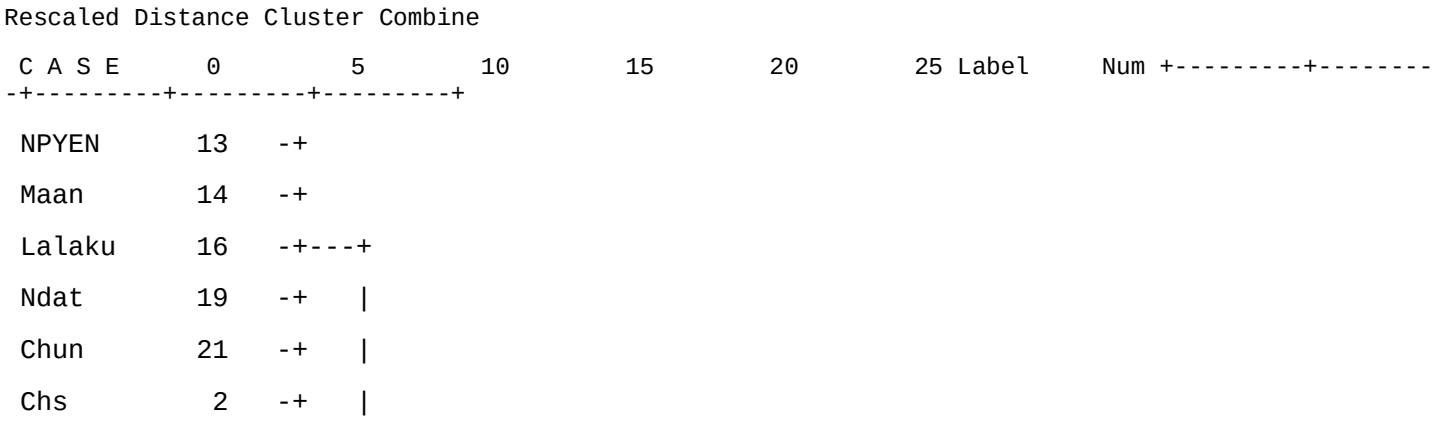
Table 2: Growth and yield traits of various Acha accessions

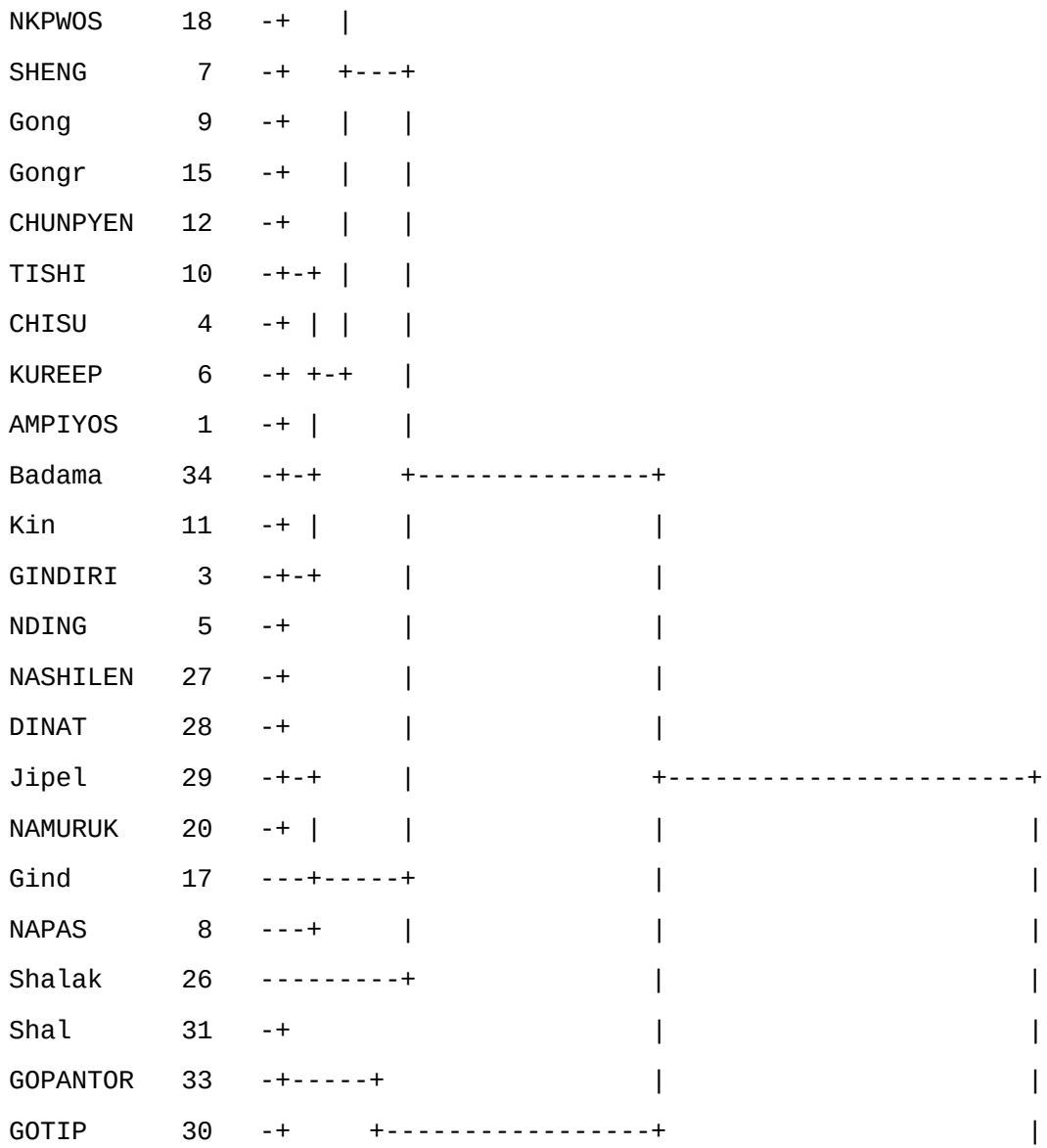
NO	ACCESSION	Germ% 14Days After Planting	Days to 50% flowering	Days to maturity	Plant height (cm)	Grain Yield (kg)
1	AMPIYOS	80.62^{cd}	77.42^{cd}	115.00^{f}	67.66^{i}	5.33^{opq}
2	CHUN-HOSS 2	40.40^{h}	83.92^{b}	123.00^{cde}	67.33^{i}	5.87^{o}
3	GINDIRI 1	59.60^{f}	77.42^{cd}	115.00^{f}	72.33^{h}	13.96^{m}
4	CHISU	59.85^{f}	84.15^{b}	123.00^{cde}	56.66^{klm}	15.92^{m}
5	NDING	70.52^{e}	84.25^{b}	121.00^{e}	67.00^{i}	15.14^{m}
6	KUREEP	70.28^{e}	91.17^{a}	127.00^{ab}	58.33^{kl}	6.06^{o}
7	SHENG	50.85^{g}	84.25^{b}	121.00^{e}	75.00^{gh}	4.42^{opqr}
8	NAPAS	40.60^{h}	84.11^{b}	124.00^{bcde}	100.40^{d}	9.56^{n}
9	GONG-HALLA	51.16^{g}	84.59^{b}	126.00^{abcd}	54.00^{m}	2.90^{qrs}
10	TISHI	60.94^{f}	84.56^{b}	124.00^{bcde}	57.00^{klm}	1.51^{rs}
11	KIN	71.63^{e}	77.18^{cd}	115.00^{f}	57.00^{klm}	2.10^{rs}
12	CHUNPYENG	50.36^{g}	91.26^{a}	127.00^{ab}	57.00^{klm}	4.85^{opqr}
13	NPYENG	31.01^{i}	91.53^{a}	128.00^{ab}	55.66^{klm}	1.85^{rs}
14	MAAN	30.05^{i}	91.19^{a}	128.00^{a}	58.66^{k}	0.93^{s}
15	GONG-A-RANDONG	50.75^{g}	91.19^{a}	127.00^{ab}	54.33^{lm}	2.50^{rsq}
16	LALAKU	33.14^{i}	91.46^{a}	128.00^{a}	57.00^{klm}	2.42^{rs}
17	GINDIRI 2	41.31^{h}	77.42^{cd}	115.00^{f}	95.66^{e}	35.17^{i}
18	NKPWOS	40.79^{h}	83.95^{b}	123.00^{cde}	75.33^{gh}	0.96^{s}
19	NDAT	30.93^{i}	91.61^{cd}	126.00^{abc}	75.66^{gh}	1.34^{s}
20	NAMURUK	40.45^{h}	84.34^{b}	121.00^{e}	77.66^{g}	30.83^{j}
21	CHUN-HOSS 1	30.22^{i}	90.01^{a}	127.00^{ab}	74.66^{gh}	5.43^{op}
22	JAKAH	70.79^{e}	84.42^{b}	122.00^{de}	76.00^{gh}	176.24^{a}
23	MUNSUNG	50.63^{g}	84.24^{b}	122.00^{cde}	112.66^{c}	122.41^{b}
24	SUHN	31.10^{i}	84.63^{b}	124.00^{bcde}	100.66^{d}	84.87^{c}
25	NAPIYA	30.84^{i}	84.01^{b}	121.00^{e}	76.00^{gh}	80.26^{d}
26	SHA'ALAK	21.03^{j}	77.65^{cd}	115.00^{f}	56.66^{klm}	49.40^{f}

27	NASHILENG	30.64^{i}	77.65^{cd}	115.00^{f}	84.66^{f}	33.49ij
28	DINAT	20.44^{j}	77.15^{cd}	115.00^{f}	77.00^{g}	33.85^{i}
29	JIPEL	31.89^{i}	76.84^{d}	113.00^{f}	85.00^{f}	19.79^{l}
30	GOTIP	81.32^{c}	78.05^{cd}	115.00^{f}	120.66^{b}	33.26^{ij}
31	SHALAK	89.87^{b}	76.37^{d}	114.00^{f}	112.66^{c}	40.51^{h}
32	TSALA	87.75^{b}	78.72^{c}	114.00^{f}	131.66^{a}	72.22^{e}
33	GOPANTOR	81.76^{c}	77.55^{cd}	114.00^{f}	113.33^{c}	42.41^{g}
34	BADAMA	78.61^{d}	77.83^{cd}	115.00^{f}	62.66^{j}	5.06^{opq}
35	GWABI	94.62^{a}	78.64^{c}	115.00^{f}	112.00^{c}	25.15^{k}
	Overall Mean	50.57	82.8	119.80	77.07	28.23
	SE of x	20.13	5.50	5.50	21.85	38.10

Correlation coefficient of morphological and growth parameters of *Digitaria* Species with the grain yield showed highly significant negative correlation (-0.198) existing between Grain Yield and Days to 50% Flowering ($P<0.05$). It implied an inverse relationship between the grain yield and Days to 50% Flowering while, 14 days after planting, Tiller Number Per Plant, Leaf Area, Peduncle Length, Internode Length, Days to Maturity, Spikelet/panicle Number, as well as Plant Height had no significant correlation with the grain yield ($P<0.05$).

Based on the morphological data obtained in the studies of thirty five accession of Acha, the phylogeny relationship grouped the accessions into twelve distinct races as shown in fig. 1. Npyeng and Maan accessions formed distinct race of Acha plant based on their growth and yield parameters. The other 32 accessions have related phylogeny trait and can be traced to be of the same descent. The RAPD analysis showed that a total of 10 RAPD OPERON primers were screened using thirty five (35) of the Acha lines. Out of these, only eight of the primers showed polymorphisms with all the thirty five line. The dendogram of the DNA cluster variations of all the thirty-five accessions are shown in fig. 2 below.


Rescaled Distance Cluster Combine
C A S E 0 5 10 15 20 25 Label Num
NPYEN 13
Maan 14
Lalaku 16
Ndat 19
Chun 21
Chs 2


NKPWOS 18
SHENG 7
Gong 9
Gongr 15
CHUNPYEN 12
TISHI 10
CHISU 4
KUREEP 6
AMPIYOS 1
Badama 34
Kin 11
GINDIRI 3
NDING 5
NASHILEN 27
DINAT 28
Jipel 29
NAMURUK 20
Gind 17
NAPAS 8
Shalak 26
Shal 31
GOPANTOR 33
GOTIP 30

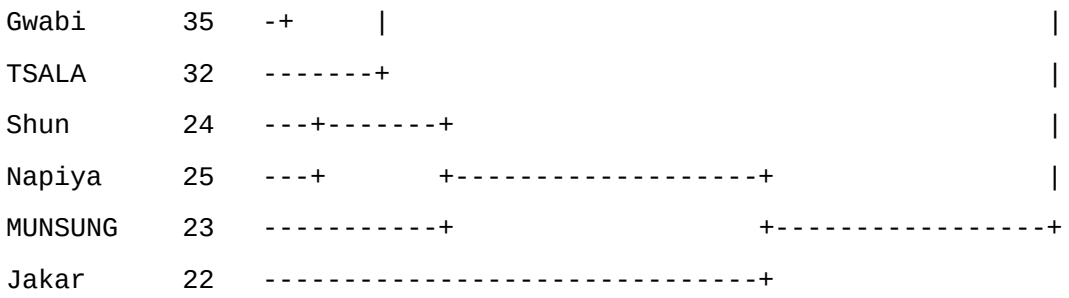


Fig. 1 Hierarchical Clusters Dendrogram of *Digitaria* Species Morphological Variations in Nigeria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0.75
1.00
Coefficient

Fig. 2: Dendrogram of DNA Cluster Variations of *Digitaria* Species in Nigeria

KEY: 1.AMPIYOS, 2. CHUN-HOSS 2, 3.GINDIRI 1, 4. CHISU, 5. NDING, 6. KUREEP, 7. SHENG, 8. NAPAS, 9. GONG-HALLA, 10. TISHI, 11. KIN, 12. CHUNPYENG, 13. NPYENG, 14. MAAN, 15. GONG-A-RANDONG, 16. LALAKU, 17. GINDIRI 2, 18. NKPWOS, 19. NDAT, 20. NAMURUK, 21. CHUN-HOSS, 22. JAKAH, 23. MUNSUNG, 24. SUHN, 25. NAPIYA, 26. SHA'ALAK, 27. NASHILENG, 28. DINAT, 29. JIPEL, 30. GOTIP, 31. SHALAK, 32. TSALA, 33. GOPANTOR, 34. BADAMA, 35. GWABI

DISCUSSION

The smallness of the size of all the Acha accessions examined in this study conform with the report of Acha being a small seed with big promise (NRC, 1996; Ibrahim 2001). This portrays Suhn accession as having potential to contribute to serve as additional food source for human and their livestock. Morphological difference of the various accessions in terms of growth sections performance can be associated with the pedigree of each accession as well as the response of the Acha varieties to environmental and ecological variables. Dinat accession had better adaptation to the growing climatic condition of the locality; as it had delayed germination and got to 50% flowering earlier than other accessions; this is in line with Ibrahim (2001) findings that Acha has capacity to survive when other grains are yet to mature.

Higher negative correlation of days to 50% flowering with grain yield implies that the days to 50% flowering had influence in the performance of Acha in Nigeria. Thus, the lower the number of day to 50% flowering, the higher the grain yield while the relative negativity of leaf area with grain yield also portray an inverse relationship between the two. On the other hand, growth factors such as peduncle length, Internodes length, spikelet/panicle number and plant height with relatively positive correlation can be ascribed to have slight influence on grain yield. Lower yield of Acha accessions recorded confirmed earlier reports on the plant (CBN, 1998; Cruz, 2004). This could be linked with call for identification of accessions with high yield that can be adopted for improvement program in Nigeria (Kuta *et al.*, 2003). Jakah accession with the highest yield can be adopted for such program.

The resultant eight morphoclusters obtained from the cluster analysis of the thirty five accessions conform to classification of *Sorghum* based on morphological differences (Appa-Rao and Prasada-Rao, 1996; Dje and Ater, 1998). Also, the use of genetic features in identifying the phylogeny relationship of plant was established with the engagement of the RAPD-DNA procedure (Hashizume and Sato, 1993; McDonald *et al.*, 1995; Zhang and Kubelik, 1997). The polymorphism of Acha plant was shown with the banding of eight primers with the

plants extracted DNA. This confirms the reliability of use of molecular marker with small quantity of DNA for plant identification (Welsh & McClelland, 1990; Williams *et al.*, 1990; Cheng and Chang, 1997). Contradiction that occurred in the morphology and molecular dendrogram plots with Chun-Hoss I forming a distinct morphoclusters in the morphology cluster analysis might be attributed to the influence of environmental conditions on phenotypes of crops (Sakdren *et al.*, 1994). The dendrogram plot of molecular classification gave multilinked single group, thus, showing that all accessions were of the same descent.

Conclusively, based on the findings of this study, the use of only morphologic features in classifying Acha does not give the same result with the engagement of molecular techniques. However the study has established the existence of diversity in morphological/ traits of Acha accessions. Also, the study has also confirmed the use of RAPD-PCR in unraveling the phylo-genetic diversity of Acha accession. The study identified the accessions that have the potential to be adopted in Acha selection and improvement programmes. It is hereby recommended that Jakah accession with the highest yield should be improved by crop breeders. Other varieties with closer morphology and yield variables to Jakah can also be adopted in improvement program. Classification of the crop in the country should involve the use of both morphology and molecular techniques. Also, further studies can be done on the nutritive values of these accessions in order to identify the accessions with the best nutritive elements.

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