PHENOTYPIC AND GENOTYPIC VARIATIONS IN COWPEA (*Vigna unguiculata* L. Walp) GENOTYPES IN NIGER STATE, NIGERIA

BY

NOMA, Annah Kumbwa
MTech/SAAT/2016/6474

DEPARTMENT OF CROP PRODUCTION
FEDERAL UNIVERSITY OF TECHNOLOGY
MINNA

OCTOBER, 2019

ABSTRACT

Cowpea production is faced with a number of constraints which results into low grain and fodder yields. The study was carried out to determine variation in yield with its component traits in different cowpea accessions. Twenty genotypes of Cowpea were evaluated in two locations (Minna and Kontagora) in a randomized completely block design (RCBD) and replicated three times. Some of the parameters that were collected include plant height at first branching, number of branches at 3,6and 9 weeks, days to first flowering and poding, pod length, leaf area and biomass weight. Results revealed that, there was wide variation among the genotypes. Genotype 11D-15-40 recorded a higher grain yield (689.8kg/ha) in Kontagora while genotype 99K-57-3-2-1 recorded a higher grain yield (282.7kg/ha) in Minna. Kontagora environment recorded a higher performance than Minna environment. However, the cowpea genotypes showed wider variability in Kontagora environment as shown by Boxplot for seed yield. Genotypes 04K-267-8, 10K-816-1, 98K-1092-1and 100K-817-3 were better in Kontagora, while genotypes 12K-261, 12K-632, TVU-408, IT10K-827-7 and 99K-57-3-2 1 in Minna as indicated by genotype plus genotype by environment interaction (GGE) biplot. From the study, cowpea would be better produced in Kontagora than Minna.

TABLE OF CONTENTS

CHAPTER ONE

CHAPTER TWO

CHAPTER THREE

CHAPTER FOUR

CHAPTER FIVE

LIST OF TABLES

Tables **Page**

LIST OF FIGURES

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background to the Study

Cowpea (*Vigna unguiculata* (L). Walp) is a dicotyledonous plant belonging to the family Fabaceae and sub-family Fabiodeae. It is grown extensively in the low lands and mid-altitude regions of Africa (particularly in dry savannah) sometimes as sole crop but more often intercropped with cereals such as sorghum or millet (Agbogidi, 2010a). Cowpea grain contains about 28.4 % protein, fat 1.9%, fibre 6.3%, thiamine 0.00074%, riboflavin 0.00042%, and niacin 0.00281%. It is also a genuine African crop for hay and forage production (Chinma *et al.,* 2008). Cowpea has been referred to as ‘poor man’s meat’ (Fall *et al.,* 2003) and its young leaves and pods contain vitamins and minerals. About 5.4 million tonnes of dried cowpea are produced worldwide, with Africa producing close to 5.2 million tonnes of cowpea. Nigeria, being the largest producer and consumer of cowpea, accounts for approximately 61% of production in Africa and 58% worldwide. Africa exports and import negligible amounts. Approximately 11 million hectares are harvested worldwide, 97% of which is in Africa. Nigeria alone harvests 4.5 million hectares yearly (FAO, 2011). The crop can be harvested in three stages: while the pods are dry, mature and green and young and green (IITA, 2009).

It was estimated that 3.3 million tonnes of cowpea dried grains were produced worldwide in year 2000. Of this, Nigeria produced 2.1 million tonnes which ranked her the world’s largest producer. This was followed by Niger and Mali with approximately 650,000 and 110,000 tonnes respectively (Adegbite and Amusa, 2008). It was also estimated that cowpea was cultivated on a total land area of 9.8 million hectares, out of which about 9.3 million hectares is found in West Africa.

Additionally, the world average yield was 337 kg per hectare while Nigeria and Niger had 417 kg per hectare and 171 kg per hectare as average yield, respectively (IITA, 2004). Though, it sounds thrilling, the unfortunate side of this reported statistics is that it is based on improved cowpea lines which have slowly reduced the genetic diversity of the landraces (Udensi *et al.*, 2012). Every stage in the life cycle of cowpea has at least a major insect pest that affects it from vegetative to reproductive stage. Aphids (*Aphis craccivora* Koch.) attack cowpea especially in the seedling stage, flower thrips (*Megalurothrips sjostedti* Trybom) attack cowpea at flowering, pod borer (*Maruca vitata* Fabricus) attack cowpea at flowering and also pod formation, numerous pod sucking bugs at poding, and the weevil (*Callosobruchus maculatus* Fabricus) attack mature cowpea in the field and during seed storage. Since cowpea is grown mainly in the dry savannah areas with no irrigation facilities, intermittent rainfall especially early in the season has adverse effects on the growth of the crop, although hampered by frost. All of these factors, singly or combined, are responsible for the low grain yield, estimated at approximately 350 kg per hectare that farmers in sub-Saharan Africa obtain from their cowpea fields (IITA, 2009).

Cowpea has the largest usable protein content of all cultivated legumes and is arguably one of the most important plant protein sources as a valuable and dependable commodity crop for farmer and grain traders (Nwosu *et al.,* 2013). With an annual worldwide estimated production of about 4.5 million metric tons, cowpea provides food for several millions of people in developing world (FAO, 2002). Cowpea is grown mostly by poor farmers in the developing countries with over 80% of the production coming from the savannas of tropical Africa. In the past decades though, advances in crop development have opened opportunities for its production in wet agro-ecologies (Nwofia e*t al.,* 2012).

1.2 Statement of the Research Problem

One of the major global challenges of the millennium is food security and how to address the phenomenon of malnutrition among the teeming and ever rising population of poor rural dwellers of the third world countries. In the wake of climate changes, fluctuating global economy and intensification of low-input agricultural production which has led to a rapid increase in soil degradation and nutrient depletion in many parts of sub-Saharan Africa, constituting serious threats to food production and food security, there is need to promote crops that could fix into global nutrient requirements. One of such crops is cowpea. Cowpea production is faced with a number of constraints which are biotic and abiotic that resulted into low grain and fodder yield. In most West African countries, development and release of improved varieties that adapts well and yield better have been slow in getting to the farmers (FAO, 2000). Development of cultivars with early maturity, acceptable grain quality, resistance to diseases and pests is necessary to overcome the ever-growing food shortage (Ehlers and Hall, 1997). Hence, there is need to generate more information on variability among the existing germplasm and cultivars and also broadening the gene pool of the crop for selection and development of more improved varieties not just in yield but with better nutritional values.

1.3 Justification of the Study

Successful conservation of germplasm largely depends on the understanding of the diversity within the species (Karuri *et al*., 2010). Germplasm with wider genetic base provides buffer and resilience against climatic and other environmental changes and ensures sustainable food security. The presence of genetic variability among crop genotypes depicts the richness of the genepool and assures plant breeders of the possibilities of combating subsequent food security crisis for the crop. Moreover, understanding the nearness and diverseness of genotypes within the same species is an important primary knowledge to guide selection and improvement in a breeding programme. In essence, diversity leads to the identification of superior genotypes which may be recommended as cultivar and identification of genotypes with desirable phenotypic traits for selection as parents for eventual breeding and improvement programmes. Cowpea comes first ahead of other arable food legumes in the sub-Sahara Africa. The recent annual global production of cowpea approximates 3.3 million tons; Central and West Africa region are the major areas of its cultivation (CGIAR, 2011). While it is chiefly a vegetable and grain crop for human who values it as a nutritional supplement to cereals and an extender of animal proteins, it provides a very safe fodder for livestock animals. Cowpea has vast utility in the food culture of both man and animal (Fang *et al*., 2007).

The study of variability and diversity in accessions of cultivated crops could provide vital information for the establishment of breeding programme, especially when intraspecific hybridization are necessary for the incorporation of new features or for mapping purposes. Assessment of genetic diversity and variability in cowpea would enhance development of cultivars for adaptation to specific production constrain. Therefore, sufficient information is necessary on genetic variability among the available germplasm to formulate and accelerate breeding programme. Previous workers have reported on genetic variability among different varieties of cowpea (Nwosu *et al.,* 2013) and a number of reports on the nutrient analysis (Mamiro *et al.,* 2011; Odedeji and Oyeleke, 2011).

1.4 Aim and Objectives of the Study

The aim of this study was to estimate the extent of genetic variability for the yield and its component traits among some selected cowpea genotypes.

The objectives were to;

i. determine yield with its component traits in different cowpea accessions.
ii. evaluate the performance of cowpea genotypes across environments and to identify better cowpea genotypes for yield trials.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin and Distribution of Cowpea

Cowpea is an ancient crop which originated in southern and central West Africa and then spread throughout Africa, Asia, the Americas, and Europe (Valenzuela and Smith, 2010).It was reported that cowpea is a native of Africa, within West Africa and particularly Nigeria (FAO, 2012). It is believed that the crop was first introduced to India during the Neolithic period (IITA, 2015) South eastern Africa is however reported as the centre of diversity of the wild *Vigna* species (Blade *et al.,* 2011). The name ‘’cowpea’’ originated from the fact that the plant was a vital source of hay for ruminant animals in South Eastern United States and other parts of the world.

However, the earliest intensive cultivation may have been by the Greeks and Romans in southern Europe in the 8th century B.C. (Tosti and Negri, 2002). South eastern Africa is however reported as the centre of diversity of the wild *Vigna* species (Blade *et al.,* 2011).

2.2 Botany of Cowpea

Cowpea (*Vigna unguiculata* (L). Walp) is an ancient grain legume crop widely grown in Africa, Asia and South America. Cowpea is used as forage and vegetable crop mainly in the tropics. Vigna was named Dominico Vigna, an Italian botanist during the first half of the 17th century, who was Professor of Botany and Director of the botanical garden at Pisa, and wrote a commentary on the works of Theophrastus. Unguiculata is from the latin word *unguiculatus*, like a fingernail (Simpson, 2010).

Vigna is broadly divided into three types, according to use: for grain, forage, or dual-purpose. *Vigna unguiculata* falls into the last type. There is a great deal of variation within the species, and there are many cultivars. It may be prostate, climbing, or semi-erect to erect (15-80cm high). The leaves are alternate, trifoliate, with petioles 5-25 cm long. The lateral leaflets are opposite and asymmetrical, while the central leaflet is symmetrical and ovate. The inflorescence is racemose, and the flowers may be white, cream, yellow, or purple (Simpson, 2010). The pods are 10-23 cm long, with 10-15 seeds per pod. The seeds are variable in size and shape, square to oblong and variously coloured, including white, brown, maroon, cream and green (Simpson, 2010).

Cowpea grows rapidly, reaching a height of 19-24 inches (48-61 cm) when grown under favourable conditions (Valenzuela and Smith, 2002). Seed shape is a major characteristic correlated with seed development in the pod. Seeds develop a kidney shape if not restricted within the pod. When seed growth is restricted by the pod, the seed becomes progressively more globular (Davis *et al*., 1991).

Cowpea is an annual, short day leguminous crop that has strong tap root and many adventitious roots in the soil surface (Agbogidi, 2010b). Cowpea grows in varied patterns, some are erect, trailing or climbing or bushy. The colour of cowpea leaves is usually dark green and the first pair of leaf is simple and opposite. The stem may be smooth or slightly hairy, and sometimes tinged with purple colouration (Perrino *et al.,* 2011).Cowpea is a self-pollinated crop with varied flowers' colour ranging from white, dirty yellow, pink, pale blue and purple. These flowers are arranged in alternate pairs (Shaw, 2012). Though, cowpea is known to be a self-pollinated crop but pollinating insects are still very necessary for two important reasons: to increase the numbers of pod set and to increase the numbers of seeds per pod (Agbogidi and Egho, 2012).

Fruits and pods of cowpea vary in size, shape, colour and texture. It may be erect, crescent in shape or coiled (Singh, 2007). The pod has 8-20 seeds on the average and seed vary considerably in size, shape and colour also. The pod length also varies between 2-12 mm and having an average weight of 5-30 g/100 seeds (Singh *et al.,* 2013). Cowpea seed shape could be globular with smooth or wrinkled seed coat.

Most root growth usually occurs within the topsoil layer, but in times of drought, cowpea can grow a taproot as long as 8 ft (243.84 cm) to reach moisture deeper in the soil profile. It is consumed by relatively rural and peri-urban people of less developed countries. Rural families derive food protein, animal feed and cash from the production of the crop. It is source of protein, a vital nutrient for healthy growth in humans and livestock. Its leaves, green pods and grain are consumed as a dietary source of protein (Ghaly *et al.,* 2010). Grain legumes have been described as one of the most important crops in many countries, providing about one-quarter of the world's dietary protein. The varietal requirements in terms of plant type, seed type, green pod color, maturity and use are extremely diverse from region to region, making breeding programs more complex than any other crop (Davis *et al.,* 2003)

2.3 Growth Requirements of Cowpea

Cowpea can be grown under rain fed conditions as well as by using irrigation or residual moisture along river or lake flood plains during the dry season, provided that the range of minimum and maximum temperature is between 28 and 30℃ (night and day) during the growing season (Dugje *et al*., 2009). Cowpea performs well in agro ecological zones where the rainfall range is between 500 and 1200 mm per year. However, with the development of extra-early and early maturing cowpea varieties, the crop can thrive in the Sahel regions where the rainfall is less than 500 mm per year. It is tolerant of drought and well adapted to sandy and poor soils (Dugje *et al*., 2009). It has little tolerance of salinity but is somewhat tolerant of soils high in aluminium. Similar to most legumes, it does not survive waterlogged or flooded conditions. Cowpea grows under a wide extreme of moisture conditions, and once established it is fairly drought tolerant (Valenzuela and Smith, 2002). In Hawaii, cowpea grows year-round at elevations ranging from sea level to 1000 ft. At higher elevations (up to 2000ft), planting should be limited to the warmer spring and summer months, according to the United State Department of Agriculture (USDA) Natural Resources Conservation Service (NRCS). However, best yields are obtained in well-drained sandy loam to clay loam soils with the pH between6 and 7.

Cowpea does not require too much nitrogen fertilizer because it fixes its own nitrogen from the air using the nodules in its roots. In addition, the crop fixes 80% of nitrogen for its growth demand from the atmosphere (Asiwe 2009), thereby reducing nitrogen fertilizer demand and cost for the crop. However, in areas where soils are poor in nitrogen, there is a need to apply a small quantity of about 15 kg of nitrogen as the first dose for a good crop development. If too much nitrogen fertilizer is used, the plant will grow luxuriantly predisposing the plants to attack by both pests and diseases with poor grain yield. Cowpea requires more phosphorus than nitrogen in the form of single super phosphate or SUPA. About 30 kg of P/ha in the form of supa is recommendedfor cowpea production to help the crop to nodulate well and fix its own nitrogen from the air (Dugje *et al*., 2009).

2.4 Constraints to Cowpea Production

In Nigeria, cowpea is majorly produced in the North in the savannah belt. Its yield in the South is affected by some environmental factors including rainfall hence it is seasonal. Cowpea diseases induced by species of pathogens belonging to various pathogenic groups (fungi, bacteria, viruses, nematodes and parasitic flowering plants) including insect pests of cowpea constitute one of the most important constraints to profitable cowpea production in all agro-ecological zones.

2.4.1 Biotic constraint

2.4.1.1 Cowpea Aphid-Borne Mosaic Virus (CABMV)

This is a filamentous and positive sense RNA virus with particle size of 750 mm and it induces cylindrical inclusions. The virus induces symptoms including, dark green veinal necrosis, vein-clearing, vein-yellowing, diffused chlorotic patches or intense chlorosis, blistering, stunting and severe mosaic that can eventually lead to death (Aliyu *et al.*, 2012). The trifoliate leaves may show symptoms such as yellow mosaic with or without dark green, vein yellowing, irregular vein-banding, blistering and deformation of leaves (Taiwo, 2003). Cowpea cultivar and virus strain determine the severity of infection of CABMV. The transmission of this virus could be by mechanical inoculation, seed or aphids as vectors. Example of aphids observed to be a vector is *Aphis gossypii*, which infect the crop in non-persistent manner (Taiwo and Akin, 2011).

Various scientists have reported various percentages of yield reduction. Thus, 13-87 % yield reduction caused by CABMV on cowpea crop was reported by Murphy and Biokmmowen (2009) when cowpea is naturally infected and seed yield loss of 44%

may also be recorded. But Alegbejo (2015), found that a total crop loss was observed on irrigated cowpea field in the northern Nigeria. To remedy the yield loss, Taiwo (2003) suggested close spacing, early planting and intercropping of cowpea plants with tall cereals such as sorghum, maize and millet. Alegbejo (2015) suggested planting of resistant varieties, planting of seeds free from infection of CABMV, keeping the field free from weeds and serious adhesion to quarantine measures as optimum management measures for the disease.

2.4.1.2 Cucumber Mosaic Virus (CMV)

Cucumber mosaic virus parasitizes and causes severe damage in different crop species including legume, melons squash peppers, tomatoes, cucumbers and many weeds. The virus affects both the quality and quantity and the degree of infection, is determined by the level of susceptibility of the cultivar Aliyu *et al.* (2012). CMV belongs to the member of the genus *Cucumovirus* in the family of *Bromoviridae* and it has the largest host range of any virus throughout the temperate and tropical regions of the world (Palukaitis *et al.,* 2002). It attacks more than 800 species in over 700 families of plants and it is spread naturally by more than 60 aphid species in a non-persistent manner (Palukaitis *et al.,* 2002). *Cucumber mosaic virus* is characterized by isomeric particles of 28 mm in diameter with tripartite genome. It is composed of a coat protein shell which encapsulates the single-stranded, plus-sense RNA genome. The capsid contains 180 identical protein sub-units. The RNA consists of three genomic RNAs and one or two sub-genomic RNAs (Palukalis *et al.,* 2002). The genomic RNAs are designated RNA_1 (3.3kb in length) RNA_2 (3.0kb) and RNA_3 (2.2kb) and are packaged in individual particles.

Cucumber mosaic virus replication starts with the entrance of the virus particle into the plants cell via aphid feeding on the host plants (Palukaitis *et al.*, 2002). After virion entry into the host cell, the virus particle is disassembled and the virion RNA is uncoated. Hence, host ribosomes begin to translate RNA-1, -2, -3. This translation gives rise to RNA replication. The viral replica generates negative RNA strands from the positive strand viral templates of each CMV RNAs. These negative sense RNAs strand synthesize progeny virus RNAs and RNA-4 with viral replicate. Both host and virus encoded protein may have functions during this process where translation of RNA-4 produces the coat protein. The virus appears to be the most important virus of some annual crops in Argentina, Eastern China, France, Egypt, Greece, Isreal, Italy, Japan, Poland, Spain, Sweden and in North-East of US (Tomlinson, 2005). *Cucumber mosaic virus* disease symptoms include severe mosaic, mottling, distortion of the leaves, stunting and plant death.

2.4.1.3 Cowpea golden mosaic virus

This virus has been reported in Sudan and Sahel Savanna zones of Nigeria by Alegbejo and Kashina (2001). In a similar research work carried out by Kareem and Taiwo (2011), occurrence of this virus was reported on cowpea fields in Onne, near Port-Harcourt, Rivers State, Nigeria. Symptoms include bright yellow or golden mosaic on infected leaves, leaf wrinkling and curling is apparent, plant distortion and stunting. In severe cases, the entire leaf surface turns bright yellow, malformed pods, stunted and mosaic spots may be observed. It was also observed that C*owpea golden mosaic virus* infected a lot of hosts which included cultivated cowpeas species and the wild species. The transmission of this virus is through grafting and by beetles in a persistent manner. The epidemic of this virus is said to occurring northern Nigeria in

1980s but unfortunately it was not properly studied. But it was observed that improved cowpea varieties showed lower incidence than conventional cultivars. Alegbejo and Kashina (2001) reported that less than 100 kg of cowpea seeds were harvested in one hectare. While Aliyu *et al.* (2012) reported that yield loss of 100 % in individual plant may be recorded, if infection occurs early in the season.

Planting of resistant cowpea varieties, keeping the field free of weeds and early planting practices will make escape of the high whitefly population that occur later in the season possible (IITA, 2013).

2.4.1.4 Anthracnose disease of cowpea

This disease is reported in North America, South America (Brazil), South Asia (India and Pakistan) and Africa (Nigeria, Uganda, and Zambia). It is a fungal disease caused by *Collectotrichum lindemuthianum.* It causes a major disease of cowpea (*Vigna unguiculata)* that is grown for pods, leaves and fodder. Symptoms of this disease include dark spots on the leaves, stems, petioles and fruits Taiwo and Akinjogunla (2011). The colour of the spots is tan to brown and sunken on susceptible genotypes. The occurrence of this disease is during the wet weather. The infection on the stems is more severe and more damaging than on other parts of the crop.

This disease can be prevented by cultural measures such as planting of anthracnose-resistant varieties, intercropping of cowpea with other food crops like cassava, millet, and sorghumto reduce the crop density and therefore reduce the yield reduction due to the disease infestation. The control measure of this disease can also be by cultural methods. Thus, do not plant cowpea close to already infected crops; else, the new planting cowpea will be infected at the early growth stage of the crop. This will bring about greater yield reduction.

2.4.1.5 Cowpea Yellow Mosaic Virus (CPYMV)

This virus attacks hosts containing particles which are similar in size but different in nucleic acid content. The virus can be transmitted through sap and by beetles. Symptoms caused by this virus vary from light green mottle to distinct yellow mosaic, distortion of leaf and premature death of the plant as observed by Hull (2009).

Alegbejo (2015) observed that there was yield reduction variation from 60-100% that was attributable to infection of CPYMV. Based on the epidemic potential, general severity and high susceptibility of the locally grown cowpea varieties, CPYMV is considered as one of the most important cowpea virus diseases as reported by Kareem and Taiwo (2011).

2.4.2 Abiotic constraint

2.4.2.1 High temperature

Usha and Parimal (2009) reported a temperature increase of 0.64^0C over the past 40 years and 0.97^0C over the last 72 years which implies a trend of 0.14^0C per decade. This trend postsa serious threat to cowpea production due to the fact that it changes insect pest population dynamics and this can result in sudden pest outbreak that can eventually affect cowpea production negatively.

2.4.2.2 Drought

Singh (2014) reported that cowpea require relative less amount of moisture for cultivation than many other upland crops. Singh *et al.* (2007) earlier reported that annual precipitation in the tropic has not shown any significant changes during the recent decade. However, unevenly distribution of rainfall especially during flowering and pods formation adversely affect cowpea production.

2.4.2.3 Rainfall

Rainfall distribution has changed with a trend for increase in number of heavy rainfalls. Thus, the variability in monthly rainfall distribution has made two main cultivation seasons shorter (Takahashi and Abe, 2009). Since pulses such as cowpea are mainly grown under rainfall conditions, the erratic rainfall during critical growth stages will not only expose the crop to moisture stress and excess water but also to low fertilizer use efficiency and soil erosion, thus affecting the productivity and quality of yield (Ajeigbe *et al.,* 2010).

2.5 Importance of Cowpea

Cowpea is of major importance to the livelihoods of millions of relatively poor people in less developed countries of the tropics (FAO, 2002). Islam *et al.* (2006) emphasized that all parts of the plant used as food are nutritious providing protein and vitamins. Immature peas and pods are used as vegetables while several snacks and main dishes are prepared from the grains (Bittenbender *et al.,* 1984).Egho (2009) reported that Nigeria ranks the second greatest consumer of cowpea worldwide. Among the legumes, cowpea is the most extensively consumed, distributed, grown and traded food crop, more than 50% (Agbogidi, 2010a and Ogbo, 2009). This is because the crop is of substantial nutritional and health importance to man and livestock (Agbogidi, 2010b). They form a major staple in the diet in Africa and Asian continents.Cowpea flour uses include, preparation of fried cowpea paste (*Akara*), cowpea dumplings (*Danwake)* and steamed cowpea paste (*Moin-Moin*) (Singh *et al., 2013*)The seeds make up the largest contributor to the overall protein intake of several rural and urban families hence Agbogidi, (2010b) regarded cowpea as the poor man’s major source of protein. Their amino acid complements those of cereals (Asumugha, 2002). Their mineral contents: iron and calcium are higher than that of meat, fish and egg and the iron content equates that of milk; the vitamins- niacin, riboflavin, thiamine (water soluble) and their levels compare with that found in lean fish and meat (Achuba, 2006) which make them exceptionally useful in blood cholesterol reduction. Many researchers including Adaji *et al.*(2007) have showed that daily consumption of 100-135 gm of dry beans reduces serum cholesterol level by 20%, thereby reducing the risk for coronary heart diseases by 40%. Besides its health-related benefits, beans are reasonably priced, significantly cheaper than rice or any other dietary fibre type (Ayenlere *et al.,* 2012). It is a good food security item as it mixes well with anotherrecipe (Muoneke *et al.,* 2012. It does well and most popular in the semi-arid of the tropics where other food legumes do not perform well (Sankie *et al.,* 2012). Cowpea fixes atmosphere nitrogen through symbiosis with nodule bacteria (Shiringani and Shimeles, 2011). It is an extremely resilient crop and cultivated under some of the most extreme agricultural conditions in the world (Muoneke *et al.,* 2012).

Success in breeding for cowpea depends on the genetic variability and genetic potential of the parents involved in the breeding Programme. As a legume grain, cowpea is an important source of human dietary protein and calories. The grains contain about 25% proteins and 64% carbohydrate, while young leaves, pods and peas contain vitamins and minerals (Nielson *et al,* 1997). Its high protein and lysine content make it natural supplement for high carbohydrates tubers and cereals which are common staple foods among the Sub-Saharan people. According to Geissler *et al.*(1998), malnutrition among the children in developing countries is mainly due to the consumption of cereal based meal which is bulky, high energy and anti-nutrients. Therefore, cowpea provides protein constituent of the daily diet of the economically depressed rural class, due to its potential to reduce malnutrition; it is sometimes being referred to as “poor man’s meat”. Its utilization is majorly as grain crop, vegetables and fodder for livestock (Hall *et al.,* 2003).

2. 6 Genetic Variability Studies in Cowpea

For any planned breeding programs to improve grainyield potentials of crops, it is necessary to obtain adequate information on the magnitude and type of genetic variability and their corresponding heritability. This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability for example, is used to indicate the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates also suggests the extent to which improvement is possible through selection. Briggs and Knowles (1967) put forward the view that if environmental variability is negligible compared to genetic variability, selection will be effective in improving the character if such character with high genotypic variability and also easily measurable happened to be highly correlated with yield. This applies to cowpea where a period of vegetative growth is followed by the production of flowers and pods after which the plant dies. For example, molecular markershave been used to estimate genetic differences ingermplasm accession of soybean and other crops (Thompson *et al.,* 1998). Phenotypic differences may also elucidate genetic differences Autrique *et al.* (1996), Johns *et al.*(1997), and Van Beuningen and Bush (1997) used morphological, developmental, and physiological traits to create distance measures for use in examining the genetic diversity in large collection of crop genotypes.

Grafius *et al.* (1976) and Grafius*et al.*(1978) applied this concept to practical breeding by employing cultivar differences in morphological traits to select geneticallydiverse breeding pairs.The reproductive phase of cowpea represents thecombined effects of many genetic and environmentalfactors. Emeberi and Obisesan (1991) working in therainforest ecological zone under short-day flowering conditionsand using varieties within the same maturity group andseed size reported narrow sense heritability of 52%for days to pod filling period. In an earlier study,Ogunbodede and Fatula (1985) reported a higher estimate of narrow sense heritability for pod length andseed size. Similarly, Dumbre *et al.* (1983) reported broad sense heritability estimates of 52% and 42% for maturity and pod filling period, respectively. Aryeettey and Laing(1973) also reported high heritability estimates for seedsper pod and pod length, suggesting that early generation selection for these traits will be successful. Ntare (1992) studied the variation in reproductive period and grain yield of cowpea under high temperature condition and reported considerable variations among cultivars in the duration of reproductive period, crop growth rate and partitioning of photosynthates.

Also, Ramachandran *et al.* (1982) working on cowpea reported hat the major parts of total variation in yield for pods per plant and internodes length was largely due to genetic causes and obtained high genetic variance for days to flower and harvest. All these studies revealed that the utilization of any criterion for selection is linked with high genetic coefficient of variation and estimates of heritability. Thus, a greater understanding is needed not only of the environmental factors that interact with the genotype to influence crop reproductive development and yield but also of the genetic factors that control these characters. The knowledge of genetic variation and relationships among genotypes will help the breeders in developing appropriate breeding strategies to solve problems of low yield in cowpea.

The success of any breeding program depends on the ability to determine germplasm diversity and genetic relationships among breeding materials. Genetic diversity is an invaluable aid in crop improvement and the choice of parents is of paramount importance in any breeding program. Assessment of a large number of inbreds for genetic diversity is of utmost importance. Crop genotypes are composed of different crop forms including inbred or pure line hybrids, landraces, wild races, germplasm, accessions, cultivars or varieties. These crop genotypes have wide and diverse origin and genetic background known as genetic diversity. Genetic diversity studies therefore are a step wise process through which existing variations in the nature of individual or group of individual crop genotypes are identified using specific statistical method or combination of methods (Warburton and Crossa, 2000; Aremu, 2005; Christini *et al.*, 2009). It is expected that the identified variations would form a pattern of genetic relationship useable in grouping genotypes. Genetic diversity identifies parental combinations exploitable to create segregating progenies with maximum genetic potential for further selection, as proven by Liu *et al*. (2000), Dje *et al*. (2000), and Aremu *et al.*(2007). Genetic diversity exposes the genetic variability in diverse populations and provides justification for introgression and ideotype breeding programmes to enhance crop performance.

Mostafa *et al.*(2011) postulated that genetic diversity studies provides the understanding of genetic relationships among populations and hence directs assigning lines to specific heterogeneous groups useable in identification of parents and hence choice selection for hybridization. Choice of parent has been identified to be the first basic step in meaningful breeding programme (Aremu *et al.,* 2007; Rahim *et al.,* 2010). Furthermore, the choice of parent selection in diversity studies is valuable because it is a means of creating useful variations in subsequent progenies.

Understanding the inter and intra specie genetic relationships as provided by diversity studies has proven to increase hybrid vigour and reduce or avoid re-selection within existing germplasm. It is worthy of note that existing cultivar populations have narrow genetic bases, hence the need for creating variability within and among cultivars using genetic diversity methods. Abe *et al,* (2015) conducted field experiments during 2011 and 2012, to estimate the level of phenotypic variability among a collection of 25 cowpea genotypes. The phenotypic traits revealed that differences among genotypes were highly significant for all traits. The first five principal components showed 79.30% of the total variability among the genotypes. Pod length, leaf area, leaf area index and number of seeds per plant contributed mainly to PC1 and leaf number, plant height, dry biomass and fresh biomass contributed mainly to PC2. Cluster analysis of the phenotypic traits resulted in five distinct groups of genotypes. The phenotypic traits therefore provide a useful measure of genetic distances among the cowpea genotypes and will enable the identification of potential parental materials for future breeding efforts.

2.7 Cowpea Improvement in Nigeria

According to Queiroz (2001), genetic improvementprograms in the last decade gave rise to a significant increase in cowpea yield by the development of cultivars that meet consumers' expectations. The wide genetic variability in the species made this possible.On this background, estimates of geneticparameters that determine the variability available in populations is fundamental (Gomes and Lopes 2005). Lopes *et al.*, (2001) used estimates of the genetic variation coefficient to quantify variability in cowpea genotypes and stated considerable diversity; the highest value of all traits was found for grain yield 19.44 and 23.90 %, respectively. Generally speaking, the study of interrelations between traits aims to improve genotypes for a whole trait set simultaneously, rather than for separate traits only. The interrelations reveal how the improvement of one trait can cause alterations in others. Information on these relations is particularly important when the selection of a trait is hampered by low heritability and/or to problems of measurement and identification. Studies on correlations with cowpea (Bezerra *et al.,* 2001, Lopes *et al.,* 2001) have tried to interpret the results and obtain support to work out adequate improvement strategies.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Location

The trial was conducted at the Teaching and Research Farm of Crop Production Department, Federal University of Technology, Minna (Latitude 9.52335°N and Longitude 6.44791°E), and at the Research Farm of Federal College of Education, Kontagora, (Latitude N 10°24’10.7964” and Longitude E 5°28’22.8”), both in Niger State which are located in the Southern Guinea Savannah and Northern Guinea Savannah agro-ecological zone of Nigeria respectively.

3.2 Source of Cowpea Seeds

20 lines of cowpea, 04K-267-8, 07K-210-1-1, 08K-125-107, 08K-193-15, 09K-456, 09K-480, 10K-816-1, 11D-15-40, 11D-24-40,12K-261,12K-487, 12K-489, 12K-632, TVU-408, IT10K-292-10, IT10K-827-7, IT10K-837-1, 98K-1092-1, 99K-57-3-2-1 and 100K-817-3 were obtained from the International Institute of Tropical Agriculture (IITA), Kano, Nigeria.

3.3 Experimental Design and Field Layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The plot size was5m by 1m (5m^2); 1 ridge, each 5 m long, plots were separated by a distance of 0.5m along each accession, while a distance of 1m separated one replication from the other. The total experimental area was 30m by 18m which gave 540m^2.

3.4 Cultural Practices

3.4.1 Land preparation

The field was cleared, ploughed, harrowed and ridged. The field was laid out and each replicate contained 20 ridges of 5m long; each cultivar that was used was evaluated in a ridge. The intra row spacing of 0.23m along the ridges was used.

3.4.2 Sowing and weed management

Two seeds per stand was sown which was later thinned to one plant per stand at one week after sowing. Manual weeding using hoe was carried out regularly to control weeds in the field.

3.4.3 Insect pest management

In all the categories, D-D Force (cypermethrin plus Dimethoate) insecticide was applied at flower bud formation, flowering and at pod initiation at the rate of 1.5kg ai/ha using a knapsack sprayer (cooper Pegler) to control insect pest population.

3.5 Data Collection

The following growth and yield data were collected:

3.5.1 Plant height at first branching (cm)

This was carried out immediately the plant started branching. Plant height was taken from the base of the plant to the terminal bud using a meter rule from the tagged plants.

3.5.2 Number of branches per plant

This was taken at 3, 6 and 9 weeks after sowing. It was determined by visual counting of the branches from the tagged plants.

3.5.3 Number of days to first poding

It was taken from sowing date to the date the pod forms on the tagged plants.

3.5.4 Number of days to first flowering

It was taken from the sowing date to the time the flower initiate on the tagged plants.

3.5.5 Leaf area (cm)

This was done by measuring the leaf length and width of the tagged plants and then multiplying by 0.9134 (Oliveira *et al*., 2008) the leaf area factor of cowpea.

3.5.6 Number of pods per plant

This was determined by counting all the pods harvested from the tagged plants.

3.5.7 Average pod length (cm): This was determined using a meter rule to measure the pods harvested from the tagged plant and average calculated.

3.5.8 Pod weight per plant (g)

This was determined by weighing the total pods harvested from each tagged plant using an electronic weighing balance.

3.5.9 Number of seeds per pod

This was determined by counting the number of seeds in each of the pods from the tagged plants.

3.5.10 Seed weight per pod (g)

This was done by weighing the seeds from each pod of the tagged plants using an electronic weighing balance.

3.5.11 100 grain weight (g)

This was carried out by weighing 100 grains from the plants using an electronic weighing balance.

3.5.12 Grain yield per hectare kgha^{-1}

This was done by weighing the pods from each plot using an electronic weighing balance.

3.5.13 Biomass weight (g)

Plants were removed using hoe to uproot the whole plant, they were then weighed using an electronic weighing balance.

3.6 Data Analysis

Data on the various traits were subjected to individual and combined analysis of variance (ANOVA) using statistical analysis system (SAS). The means wasseparated by Duncan's Multiple Range Test (DMRT) at 5% level of significant. G and E interaction was conducted using Breeding Management System Software (BMS).

In order to understand genotypic variability among different traits measured, the genetic variance components were also estimated using the functions suggested by Gana (2016):

Genetic variance (σ^2_g) = $MS_g - MS_e/r$

where MS_g = mean squares of genotype, MS_e = mean squares of error, and r = number of replications,

Phenotypic variance (σ^2_p) = $\sigma^2_g + MS_e$

Genotypic coefficient of variation (GCV) = $(\sqrt{V_g}/X)100$

Phenotypic coefficient of variation (PCV) = $(\sqrt{V_p}/X)100$

where X is the grand mean for the phenotypic traits, V_g = genotypic variance, and V_p = phenotypic variance, and

Broad-sense heritability (h^2) = $(\sigma^2_g/\sigma^2_p)100$.

Genetic Advanced (GA) = $I\ h^2Vp$ where, I = selection intensity 5% (2.06)

CHAPTER FOUR

4.0 RESULTS

4.1 Phenotypic Variation in Plant Height at First Branching and Number of Branches at 3, 6 and 9 WAS of Cowpea Genotypes in Kontagora

Plant height was not significantly (P≤0.05) different among the genotypes at first branching. Also, number of branches was not significantly (P≤0.05) different among genotypes at 3 weeks after sowing. At 6 weeks after sowing, the genotypes showed significant (P≤0.05) difference,12K-487 had more branches which is statistically similar with most of the genotypes with exception of 04K-207-8,09K-456and 07K-210-1-1. Number of branches were significantly (P≤0.05) different among the genotypes at 9 weeks after sowing with 12K-689 producing more branches which is similar to all other with the exception of 04K-207-8 and 07K-210-1-1 that produced fewer number of branches as shown in (Table 4.1).

Table 4.1: Phenotypic variation in plant height at first branching and number of branches in cowpea genotypes in Kontagora

Genotypes	PHAFB	3WAS	6WAS	9WAS
04K-207-8	5.0^{a}	5.3^{a}	12.3^{bc}	15.7^{b}
07K-210-1-1	5.3^{a}	5.0^{a}	10.3^{c}	14.3^{b}
08K-125-107	4.3^{a}	5.3^{a}	14.7^{abc}	18.3^{ab}
08K-193-15	4.7^{a}	8.3^{a}	16.7^{abc}	20.3^{ab}
09K-456	5.0^{a}	7.3^{a}	12.7^{bc}	19.7^{ab}
09K-480	5.7^{a}	6.3^{a}	14.7^{abc}	17.3^{ab}
10K-816-1	3.7^{a}	6.0^{a}	14.0^{abc}	18.7^{ab}
11D-15-40	3.7^{a}	8.7^{a}	15.0^{abc}	20.0^{ab}
11D-24-40	4.3^{a}	5.7^{a}	16.3^{abc}	21.0^{ab}
12K-261	4.7^{a}	8.7^{a}	16.3^{abc}	20.3^{ab}
12K-487	4.3^{a}	8.7^{a}	23.3^{a}	23.0^{ab}
12K-689	4.3^{a}	9.3^{a}	22.7^{ab}	26.3^{a}
12K-632	4.7^{a}	6.0^{a}	15.3^{abc}	20.0^{ab}
TVU-408	4.3^{a}	9.0^{a}	22.7^{ab}	23.0^{ab}
IT10K-292-10	5.0^{a}	8.3^{a}	18.3^{abc}	21.3^{ab}
IT10K-827-7	5.3^{a}	8.7^{a}	20.0^{abc}	24.7^{ab}
IT10K-837-1	5.7^{a}	6.7^{a}	14.3^{abc}	21.0^{ab}
98K-1092-1	4.0^{a}	7.7^{a}	15.3^{abc}	22.0^{ab}
99K-57-3-2-1	6.0^{a}	7.3^{a}	15.3^{abc}	19.3^{ab}
100K-817-3	3.3^{a}	8.0^{a}	18.0^{abc}	24.0^{ab}
SE±	0.2	0.3	0.7	0.7

Means followed by the same letter(s) within a set of treatment column are not significantly different at P≤0.05 using DMRT; SE= Standard error
PHAFB = Plant Height at first Branching, WAS= Weeks After Sowing.

4.2 Phenotypic Variations in Number of Days to First Flowering, Number of Days to First Poding, Average Pod Length and Numbers of Pod Per Plant in Cowpea Genotypes at Kontagora

Number of days to first flowering and number of days to first poding was not significantly (P≤0.05) different among the genotypes (Table 4.2). Average pod length was significantly (P≤0.05) different among the genotypes with 09k-480 having longer pods which is statistically similar to 04K-267-8, 07K-210-1-1, 08K-125-107, 08K-193-15, 09K-456, 10K-816-1, 11D-15-40, 11D-24-40, 12K-489, 12K-632, TVU-408, IT10K-837-1 and 100K-817-3. Followed by 11D-24-40, 12K-261,IT10K-292-

10,98K-1092-1 and 99K-57-3-2-1 , IT10K-837-1 produced shorter pods. Number of pods per plant was also significantly ($P \leq 0.05$) different among the genotypes. IT10K-292-10 had more pods which is statistically similar with 09K-456, 09K-480, 10K-816-1, 11D-15-40,12K-261,12K-487, 12K489, TVU-408, IT10K-827-7, IT10K-837-1, 99K-57-3-2-1 and 100K-817-3, followed by 11D-24-40 and 98K-1092-1. 04K-267-8, 07K-210-1-1, 08K-125-107, 08K-193-15, and12K-632 produced fewer pods.

Table 4.2: Genotypic variations on number of days to first flowering, number of days to first poding, average pod length and numbers of pod per plant in cowpea genotypes at Kontagora

Genotypes	DTFF	DTFP	APL	NPPP
04K-207-8	39^{a}	45^{a}	13.1^{abc}	8^{c}
07K-210-1-1	38^{a}	43^{a}	13.7^{abcd}	7^{c}
08K-125-107	40^{a}	47^{a}	13.5^{abcd}	11^{c}
08K-193-15	41^{a}	49^{a}	14.4^{abcd}	10^{c}
09K-456	40^{a}	46^{a}	14.8^{abcd}	15^{abc}
09K-480	40^{a}	48^{a}	17.5^{a}	14^{abc}
10K-816-1	42^{a}	49^{a}	13.8^{abcd}	21^{ab}
11D-15-40	41^{a}	49^{a}	13.6^{abcd}	15^{abc}
11D-24-40	41^{a}	48^{a}	11.5^{cd}	13^{bc}
12K-261	38^{a}	46^{a}	12.2^{cd}	15^{abc}
12K-487	38^{a}	45^{a}	12.3^{cd}	14^{abc}
12K-689	36^{a}	44^{a}	14.7^{abcd}	15^{abc}
12K-632	39^{a}	47^{a}	14.9^{abcd}	11^{c}
TVU-408	37^{a}	43^{a}	14.2^{abcd}	14^{abc}
IT10K-292-10	39^{a}	48^{a}	12.2^{cd}	23^{a}
IT10K-827-7	37^{a}	44^{a}	17.2^{ab}	17^{abc}
IT10K-837-1	41^{a}	48^{a}	10.4^{d}	13^{abc}
98K-1092-1	41^{a}	49^{a}	11.6^{cd}	12^{bc}
99K-57-3-2-1	41^{a}	49^{a}	12.2^{cd}	15^{abc}
100K-817-3	40^{a}	48^{a}	12.2^{abc}	16^{abc}
SE±	0.5	0.5	0.3	0.7

Means followed by the same letter(s) within a set of treatment column are not significantly different at $P \leq 0.05$ using DMRT; SE= Standard error

DTFF = Days to first flowering, DTFP = Days to first poding, APL = Average pod length, NPPP = Number of pods per plant.

4.3. Phenotypic Variations in Pod Weight Per Plant, Number of Seeds Per Pod, Seed Weight Per Plant and Leaf Area of Cowpea Lines at Kontagora.

The results in table 4.3 showed that, Pod weight was significantly (P≤0.05) different. llD-15-40 produced heavier pods compared to 07K-210-1-1 which produced lesser heavier pods. Leaf area was significantly different, IT10K-292-10 produced a wider leaf area though statistically similar to most of the genotypes with the exception of 08K-193-15 and 11D-15-40 that produced smaller leaves. Number of seeds per pod was significantly (p≤0.05) different among the genotypes, 2K-48-7 and IT10K-827-7 had a higher number of seeds and statistically with every other genotype with the exception of 12K-632 and TVU-408 which had fewer number of seeds per pod. However, seeds weight per pod recorded significant (p≤0.05) different among the genotypes. 12K-487 produced heavier seed, though statistically similar with most of the genotypes with the exception of 08K-125-107 and TVU-408 that had lesser heavier seeds. 04K-207-8, 07K-210-1-1, 69K-456, 12K-632, 98K-1092-1 and 100K-817-3 were statistically similar.

Table 4.3: Phenotypic variations in pod weight per plant, number of seeds per pod, seed weight per plant and leaf area in cowpea genotypes atKontagora

Genotypes	PWPP	LA	NSPP	SWPP
04K-207-8	21.2^{bc}	18.2^{ab}	9^{ab}	2.8^{bcd}
07K-210-1-1	14.4^{c}	19.2^{ab}	11^{ab}	2.8^{bcd}
08K-125-107	16.8^{bc}	22.0^{ab}	9^{ab}	2.2^{d}
08K-193-15	24.3^{abc}	11.7^{b}	9^{ab}	3.3^{ab}
09K-456	26.8^{abc}	16.7^{ab}	9^{ab}	2.3^{cd}
09K-480	25.3^{abc}	17.4^{ab}	11^{ab}	2.9^{abcd}
10K-816-1	36.0^{abc}	21.3^{ab}	11^{ab}	2.9^{bcd}
11D-15-40	50.9^{a}	11.3^{b}	11^{ab}	3.0^{abcd}
11D-24-40	24.1^{abc}	20.3^{ab}	11^{ab}	3.1^{abc}
12K-261	37.1^{abc}	12.3^{ab}	12^{ab}	3.3^{ab}
12K-487	29.8^{abc}	22.7^{ab}	14^{a}	3.7^{a}
12K-689	23.9^{abc}	21.4^{ab}	12^{ab}	3.4^{ab}
12K-632	27.4^{abc}	19.7^{ab}	8^{b}	2.8^{bcd}
TVU-408	33.5^{abc}	17.9^{ab}	7^{b}	2.2^{d}
IT10K-292-10	33.3^{abc}	27.7^{a}	11^{ab}	3.0^{abc}
IT10K-827-7	36.1^{abc}	19.2^{ab}	14^{a}	3.4^{ab}
IT10K-837-1	19.5^{bc}	12.9^{ab}	12^{ab}	3.1^{abc}
98K-1092-1	18.8^{bc}	13.6^{ab}	9^{ab}	2.8^{bcd}
99K-57-3-2-1	28.4^{abc}	15.8^{ab}	12^{ab}	3.0^{abc}
100K-817-3	39.0^{ab}	15.9^{ab}	12^{ab}	2.8^{bcd}
SE±	1.6	0.9	0.4	0.1

Means followed by the same letter(s) within a set of treatment column are not significantly different at $P \leq 0.05$ using DMRT; SE= Standard error

PWPP = Pod weight per plant, LA = Leaf Area, NSPP = Number of seeds per pod, SWPP = Seeds weight per pod.

4.4 The Mean Values of Hundred Grain Weight, Biomass Weight and Grain Yield of Cowpea Genotypes Evaluated at Kontagora.

The result showed that, hundred grain weight were not significantly ($P \leq 0.05$) different among all the genotypes. However, biomass weight was significantly ($P \leq 0.05$) different among the genotypes, 12K-487 had heavier biomass. 04K-207-8, 07K-210-1-1, 98K-1092-1 and 100K-817-3 produced less heavy biomass. Grain yield per hectare was significant ($P \leq 0.05$) different among the genotypes, 11D-15-40 produced a higher yield, followed by 12k-261 while genotype 07K-210-1-1 produced a lower yield (Table 4.4).

4.5 Phenotypic Variation in Plant Height at First Branching and Number of Branches at 3, 6 and 9 WAS of Cowpea Genotypes at Minna

The results in table 4.5 indicated that plant height was not significantly ($P \leq 0.05$) different among the genotypes. Numbers of branches at 3 weeks after sowing was significantly ($P \leq 0.25$) different among the genotypes with 09K-456 and 10K-816-1 producing more branches which is statistically similar with every other genotype except genotypes 12K-698, TVU-408 and IT10K-292-10 which produced fewer branches. At 6 weeks after sowing, genotype 12K-261 produced a higher number of branches which is statistically similar with every other genotype except for genotypes 07K-210-1-1 and 11D-15-40 which produced fewer branches. At week 9 after sowing, genotypes 12K-261 and 12K-487 produced more branches and was statistically similar to most of the genotypes, 07K-210-1-1, IT10K-807 and 98K-1092-1 were statistically similar and produced few branches but more than 11D-24-40 which produced most fewer branches.

Table 4.4: Phenotypic variations in hundred grain weight, biomass weight and grain yield of cowpea genotypes at Kontagora.

Genotypes	100GW(g)	BW (g)	GY (kg/ha)
04K-207-8	10.9^{a}	13.3^{b}	634.67^{ghi}
07K-210-1-1	11.6^{a}	13.8^{b}	431.20^{ij}
08K-125-107	11.3^{a}	19.8^{ab}	502.80^{hij}
08K-193-15	11.1^{a}	24.2^{ab}	728.67^{fg}
09K-456	10.9^{a}	23.8^{ab}	810.00^{fg}
09K-480	11.6^{a}	20.1^{ab}	865.03^{def}
10K-816-1	11.3^{a}	24.5^{ab}	1175.15^{bc}
11D-15-40	11.3^{a}	23.3^{ab}	1558.47^{a}
11D-24-40	11.2^{a}	27.8^{ab}	722.20^{fgh}
12K-261	10.8^{a}	32.1^{ab}	1365.87^{ab}
12K-487	10.2^{a}	47.2^{a}	893.43^{def}
12K-689	10.4^{a}	24.8^{ab}	719.10^{fgh}
12K-632	10.8^{a}	29.3^{ab}	822.77^{efg}
TVU-408	11.5^{a}	17.6^{ab}	1038.63^{cde}
IT10K-292-10	10.8^{a}	26.9^{ab}	1185.33^{bc}
IT10K-827-7	10.4^{a}	29.1^{ab}	1081.53^{cd}
IT10K-837-1	11.1^{a}	21.6^{ab}	644.73^{ghi}
98K-1092-1	11.6^{a}	13.5^{b}	387.53^{j}
99K-57-3-2-1	11.8^{a}	16.5^{ab}	716.30^{fgh}
100K-817-3	10.3^{a}	15.5^{b}	902.67^{def}
SE±	0.1	1.9	57.78

Means followed by the same letter(s) within a set of treatment column are not significantly different at $P \leq 0.05$ using DMRT; SE= Standard error

100 GW = One hundred grain weight, BW = Biomass weight, GY = Grain yield

Table 4.5: Phenotypic variation on plant height at first branching and numbers of branches at 3, 6 and 9weeks after sowing at Minna.

Genotypes	PHAFB	3WAS	6WAS	9WAS
04K-207-8	4.7^{a}	3.0^{ab}	7.0^{ab}	16.3^{abc}
07K-210-1-1	5.0^{a}	2.3^{ab}	5.3^{b}	13.0^{bc}
08K-125-107	4.3^{a}	3.0^{ab}	5.7^{ab}	16.0^{abc}
08K-193-15	4.0^{a}	2.7^{ab}	8.3^{ab}	18.3^{abc}
09K-456	4.7^{a}	3.3^{a}	6.0^{ab}	16.3^{abc}
09K-480	5.3^{a}	2.7^{ab}	8.3^{ab}	17.3^{abc}
10K-816-1	4.3^{a}	3.3^{a}	8.3^{ab}	16.3^{abc}
11D-15-40	5.0^{a}	2.3^{ab}	5.3^{b}	20.7^{ab}
11D-24-40	4.3^{a}	3.0^{ab}	6.3^{ab}	11.0^{c}
12K-261	5.0^{a}	3.0^{ab}	10.0^{a}	24.7^{a}
12K-487	3.7^{a}	3.0^{ab}	9.0^{ab}	23.7^{a}
12K-689	4.0^{a}	2.0^{b}	8.3^{ab}	19.7^{abc}
12K-632	4.3^{a}	2.3^{ab}	6.3^{ab}	17.0^{abc}
TVU-408	5.0^{a}	2.0^{b}	7.3^{ab}	20.7^{ab}
IT10K-292-10	5.0^{a}	2.0^{b}	7.7^{ab}	16.7^{abc}
IT10K-827-7	4.3^{a}	2.7^{ab}	7.7^{ab}	18.7^{abc}
IT10K-837-1	5.7^{a}	3.0^{ab}	7.7^{ab}	12.7^{bc}
98K-1092-1	5.3^{a}	2.7^{ab}	7.0^{ab}	13.3^{bc}
99K-57-3-2-1	4.0^{a}	2.7^{ab}	8.3^{ab}	17.7^{abc}
100K-817-3	5.0^{a}	3.0^{ab}	8.3^{ab}	20.0^{ab}
SE±	0.1	0.1	0.3	0.6

Means followed by the same letter(s) within a set of treatment column are not significantly different at $P \leq 0.05$ using DMRT; SE= Standard error

PHAFB = Plant Height at First Branching, 3, 6 and 9 WAS = Weeks After Sowing

4.6 Phenotypic Variations in Number of Days to First Flowering, Number of Days to First Poding, Average Pod Length and Numbers of Pod Per Plant in Cowpea Genotypes at Minna

Days to first flowering and days to first podding were not significantly different ($P \leq 0.05$) among the genotypes. Average pod length was significantly different ($P \leq 0.05$) among the genotypes. IT10K-292-10 produced longer podwhich is statistically similar with every other genotype with the exception of 07K-210-1-1 which produced shorter pod. Number of pods per plant was significantly different ($P \leq 0.05$) among genotypes with 99K-57-3-2-1 having more pods, though statistically similar with every other genotype except for 04K-207-8, 09K-456 and IT10K-292-10 which recorded fewer pods.

4.7 Phenotypic Variations in Pod Weight Per Plant, Number of Seeds Per Pod, Seed Weight Per Plant and Leaf Area in Cowpea Genotypes at Minna

Result in Table 4.7 shows that, Pod weight per plant was significantly different (P≤0.05) among the genotypes. 12K-261 produced heavier pods which was similar to most of the genotypes with the exception of 09K-456, 09K-480, 10K-816-1, 11D-15-40, 11D-24-40, IT10K-292-10 and IT10K-827-7 that produced pod with lesser weight. Leaf area was not significantly different (P≤0.05) among the genotypes. Number of seeds per pod and seed weight per pod was significantly different (P≤0.05) among the genotypes. 12K-489 produced more seeds and had higher grain weight, which in turn was statistically similar with all other genotypes with the exception of07K-210-1-1 and 98K-1092-1 respectively that produced lesser number of seeds and grain weight.

Table 4.6: Phenotypic variations on number of days to first flowering, number of days to first poding, average pod length and numbers of pod per plant in cowpea genotypes at Minna

Genotypes	DTFF	DTFP	APL	NPPP
04K-207-8	39^{a}	46^{a}	9.9^{ab}	4^{b}
07K-210-1-1	38^{a}	44^{a}	6.5^{b}	8^{ab}
08K-125-107	39^{a}	47^{a}	10.7^{ab}	7^{ab}
08K-193-15	41^{a}	48^{a}	12.3^{ab}	8^{ab}
09K-456	40^{a}	46^{a}	14.3^{ab}	4^{b}
09K-480	41^{a}	48^{a}	8.7^{ab}	7^{ab}
10K-816-1	42^{a}	50^{a}	15.7^{ab}	5^{ab}
11D-15-40	40^{a}	48^{a}	16.7^{ab}	5^{ab}
11D-24-40	41^{a}	48^{a}	16.3^{ab}	9^{ab}
12K-261	48^{a}	47^{a}	13.3^{ab}	12^{ab}
12K-487	47^{a}	45^{a}	15.7^{ab}	10^{ab}
12K-689	26^{a}	45^{a}	16.1^{ab}	5^{ab}
12K-632	39^{a}	48^{a}	12.2^{ab}	8^{ab}
TVU-408	40^{a}	44^{a}	16.7^{ab}	9^{ab}
IT10K-292-10	40^{a}	48^{a}	18.8^{a}	3^{b}
IT10K-827-7	38^{a}	48^{a}	15.7^{ab}	7^{ab}
IT10K-837-1	39^{a}	48^{a}	14.0^{ab}	9^{ab}
98K-1092-1	41^{a}	49^{a}	9.0^{ab}	8^{ab}
99K-57-3-2-1	40^{a}	48^{a}	13.2^{ab}	13^{a}
100K-817-3	39^{a}	49^{a}	14.7^{ab}	10^{ab}
SE±	0.5	0.5	0.7	0.6

Means followed by the same letter(s) within a set of treatment column are not significantly different at $P \leq 0.05$ using DMRT; SE= Standard error

DTFF = Days to first flowering, DTFP = Days to first poding, APL = Average pod length,NPPP = Number of pods per plant.

Table 4.7: Phenotypic variations in pod weight per plant, number of seeds per pod, seed weight per plant and leaf area of cowpea genotypes at Minna

Genotypes	PWPP	leave area	NSPP	SWPP
04K-207-8	12.9^{ab}	17.3^{a}	8^{ab}	2.5^{ab}
07K-210-1-1	9.9^{ab}	17.1^{a}	7^{b}	2.2^{b}
08K-125-107	11.5^{ab}	21.4^{a}	9^{ab}	2.7^{ab}
08K-193-15	11.0^{ab}	10.2^{a}	10^{ab}	2.9^{ab}
09K-456	7.0^{b}	15.9^{a}	11^{ab}	2.8^{ab}
09K-480	5.1^{b}	16.5^{a}	9^{ab}	2.7^{ab}
10K-816-1	5.8^{b}	19.2^{a}	13^{ab}	3.5^{ab}
11D-15-40	4.1^{b}	11.0^{a}	14^{ab}	3.6^{ab}
11D-24-40	8.5^{b}	20.2^{a}	11^{ab}	2.9^{ab}
12K-261	24.6^{a}	11.6^{a}	14^{ab}	3.8^{ab}
12K-487	12.4^{ab}	21.2^{a}	12^{ab}	3.1^{ab}
12K-689	9.6^{ab}	17.2^{a}	15^{a}	3.9^{a}
12K-632	14.1^{ab}	23.7^{a}	9^{ab}	2.8^{ab}
TVU-408	14.9^{ab}	16.5^{a}	14^{ab}	2.3^{ab}
IT10K-292-10	3.9^{b}	23.4^{a}	14^{ab}	3.5^{ab}
IT10K-827-7	8.4^{b}	16.6^{a}	13^{ab}	3.1^{ab}
IT10K-837-1	18.4^{ab}	12.7^{a}	10^{ab}	2.7^{ab}
98K-1092-1	9.5^{ab}	12.3^{a}	7^{b}	2.2^{b}
99K-57-3-2-1	18.8^{ab}	15.9^{a}	11^{ab}	3.1^{ab}
100K-817-3	18.7^{ab}	15.6^{a}	14^{ab}	3.3^{ab}
SE±	0.1	0.9	0.5	0.1

Means followed by the same letter(s) within a set of treatment column are not significantly different at $P \leq 0.05$ using DMRT; SE= Standard error

PWPP = Pod weight per plant, LA = Leaf Area, NSPP = Number of seeds per pod, SWPP = Seeds weight per pod.

4.8 Phenotypic Variations in Hundred Grain Weight, Biomass Weight and Grain Yield of Cowpea Genotypes at Minna

There was significant difference ($P \leq 0.05$) among the genotypes evaluated for hundred grain weight. The result indicated that IT10K-292-10 had more grain weight which was similar statistically to most of the genotypes, with the of100K-817-3, 12K-489, 04K-207-8 and 12K-632 that produced lesser weights. Biomass weight was also significantly different, 12K-487 produced heavier biomass, which was similar statistically to11D-15-40, 12K-281, 12K-487, 12K-632 and TVU-408. All others produced lesser biomass. There existed significant (P≤0.05) difference in grain yield per hectare among the genotypes with 99K-57-3-2-1 produced a higher yield, though statistically similar to IT10K-837-1, 11D-15-40 produced lower grain yield.

Table 4.8: Phenotypic variations in 100grain weight, biomass weight and grain yield of cowpea genotypes at Minna

Genotypes	100GW(g)	BW(g)	GY (kg)
04K-207-8	9.4d^{e}	10.7^{b}	232.00^{fgh}
07K-210-1-1	10.5^{abcde}	7.2^{b}	272.93^{efg}
08K-125-107	10.2^{abcde}	12.1^{b}	386.07^{cde}
08K-193-15	10.6^{abcde}	14.1^{b}	264.40^{fg}
09K-456	10.3^{abcde}	15.4^{b}	259.35^{fg}
09K-480	10.7^{abcd}	17.5^{b}	185.13^{gh}
10K-816-1	11.0^{abc}	17.2^{b}	219.00^{fgh}
11D-15-40	10.6^{abcd}	20.1^{ab}	123.70^{h}
11D-24-40	10.8^{abcd}	19.0^{b}	324.07^{def}
12K-261	11.1^{abcd}	25.4^{ab}	405.50^{bcd}
12K-487	10.4^{abcde}	43.0^{a}	261.00^{fg}
12K-689	9.7^{cde}	22.2^{ab}	174.10^{gh}
12K-632	9.2^{e}	25.0^{ab}	478.00^{bc}
TVU-408	10.6^{abcd}	20.5^{ab}	441.20^{bcd}
IT10K-292-10	11.2^{a}	17.3^{b}	130.00^{h}
IT10K-827-7	10.2^{abcde}	19.0^{b}	250.60^{fg}
IT10K-837-1	10.1^{abcde}	17.3^{b}	688.33^{a}
98K-1092-1	10.6^{abcde}	11.4^{b}	226.20^{fgh}
99K-57-3-2-1	11.1^{ab}	13.0^{b}	702.27^{a}
100K-817-3	9.7^{bcde}	15.3^{b}	518.60^{b}
SE±	0.1	1.6	31.69

Means followed by the same letter(s) within a set of treatment column are not significantly different at P≤0.05 using DMRT; SE= Standard error
100 GW = One hundred grain weight, BW = Biomass weight GY = Grain yield

4.9 Correlation Matrix for Quantitative Traits of 20 Cowpea Genotypes in Kontagora and Minna

The result of correlation analysis between growth and yield attributes of some cowpea genotypes in Kontagora and Minna in 2017 are shown in Tables 4.9 and 4.10 respectively. At Kontagora, plant height at first branching correlated negatively and was significant to seed yield. Days to first flowering, days to first podding and hundred grain weight correlated negatively to seed yield, all the remaining growth and yield attributes correlated positively and was significant with number of pods per plant (r=0.4884**). The strongest relationship between growth attributes was recorded between days to first podding and days to first flowering (r=0.9234) and average pod length and days to first flowering (r=0.9234**) which were also significant.

In Minna, with the exception of hundred grain weight which correlated negatively, all the growth and yield attributes correlated positively with grain yield and was significant with number of pods per plant (r=0.7683**). The strongest relationship between growth attributes was between days to first flowering and days to first podding (0.8428**) which was significant.

Table4.9: Correlation matrix between growth and yield attributes against grain yield of some cowpea genotypes in 2017 in Kontagora

Correlation	PHFB	NB9WAS	DTF	DTP	PL	NPPP	LA	100GW	BW	GY
PHFB	1									
NB9WAS	-0.1515	1								
DTF	0.0085	-0.2341	1							
DTP	-0.0198	-0.1108	0.9234	1						
PL	0.2076	0.1165	0.9234**	-0.0545	1					
NPPP	-0.2911	0.3009**	-0.0889	0.0105	0.0515	1				
LA	0.1287	-0.0418	-0.1349	-0.0657	0.1765	0.2005	1			
100GW	0.2387	-0.1999	0.2422	0.2047	-0.0149	-0.0466	-0.0356	1		
BW	0.071	0.1349	-0.1087	-0.1243	0.0538	0.1069	0.0858	-0.2466	1	
GY	-0.02838	0.164	-0.0526	-0.0093	0.2316	0.4884**	0.1026	-0.0522	0.2219	1

PHFB = Plant Height at First Branching, NB9WAS = Number of Branching at 9 weeks after sowing, DTP = Days to Flowering, DTP = Days to Podding, PL = Pod Length, NPPP = Number of pods per plant, LA = Leave Area, 100GW = 100 Grain weight, BW = Biomass Weight, GY = Grain Yield. * = Significant ($p \leq 0.05$), ** = Highly Significant ($p \leq 0.01$).

Table 4.10: Correlation matrix between growth and yield attributes against grain yield of some cowpea genotypes in 2017 in Minna

Correlation	PHFB	NB9WAS	DTF	DTP	PL	NPPP	LA	100GW	BW	GY
PHFB	1									
NB9WAS	-0.1563	1								
DTF	0.3425**	-0.1383	1							
DTP	0.3196**	-0.0452	0.8428**	1						
PL	-0.0861	0.0527	0.0019	-0.0716	1					
NPPP	0.0166	0.2445*	0.1854	0.1768	-0.0505	1				
LA	0.0179	0.0204	-0.0633	-0.0139	-0.1462	0.0327	1			
00GW	0.0026	0.0362	0.1683	0.1183	0.0642	0.161	0.0679	1		
BW	-0.0407	0.3195*	-0.2513	-0.1931	0.0123	0.0311	0.1934	-0.0375	1	
GY	0.0283	0.143	0.1595	0.1199	0.0247	0.7683**	0.0444	-0.0492	0.0759	1

PHFB = Plant Height at First Branching, NB9WAS = Number of Branching at 9 weeks after sowing, DTP = Days to Flowering, DTP = Days to Podding, PL = Pod Length, NPPP = Number of pods per plant, LA = Leave Area, 100GW = 100 Grain weight, BW = Biomass Weight, GY = Grain Yield. * = Significant (p≤0.05), ** = Highly Significant (p≤0.01).

4.10 Sensitivity and Stability across Environments

The sensitivity and stability for seed yield from cowpea genotypes across the twoenvironments in 2017 cropping season is shown in table 4.11. Genotypes that were least sensitive were the most stable genotypes in both environments. This implies that genotype 12K-632 was the most stable among genotypes and genotype 100K-817-3 the least stable across the environments.

4.11 Boxplot for Seed Yield from Cowpea Genotypes across the Environments

The boxplot for seed yield across the two environments is shown in figure4.1. Kontagora environment recorded a higher mean performance than Minna environment. However, the cowpea genotypes showed wider variability in Kontagora environment.

4.12 G*G*E Biplot

The biplot for the best genotypes in each of the environment for seed yield in 2017 cropping season is presented in Figure 4.2. The polygon view of the genotype plus genotype by environment interaction (GGE) biplot displays the best genotypes in each environment and it is a summary of the genotype by environment pattern of a multi-locational yield trial. Kontagora was one environment with 04K-267-8, 10K-816-1, 98K-1092-1and 100K-817-3 as the best genotypes in this environment. The best genotypes for Minna environment were 12K-261, 12K-632, TVU-408, IT10K-827-7 and 99K-57-3-2-1. The remaining genotypes contained in the sectors without environment were not the highest yielding genotype at any environment.

Table 4.11: Sensitivity and stability of genotypes across the locations

Genotype	Mean	Sensitivity
12K-632	446.8	–0.130
IT10K-827-7	262.9	–0.064
12K-261	302.7	–0.009
99K-57-3-2-1	327.8	0.076
07K-210-1-1	101.1	0.147
12K-489	228.5	0.244
08K-125-107	183.6	0.363
IT10K-837-1	187.1	0.419
09K-456	132.0	0.675
IT10K-292-10	162.4	0.737
TVU-408	479.5	0.815
98K-1092-1	329.4	1.158
12K-487	269.9	1.239
09K-480	242.0	1.468
11D-24-40	252.7	1.698
04K-267-8	324.7	1.762
08K-193-15	268.4	1.919
11D-15-40	285.0	1.991
10K-816-1	337.6	2.541
100K-817-3	519.6	2.950

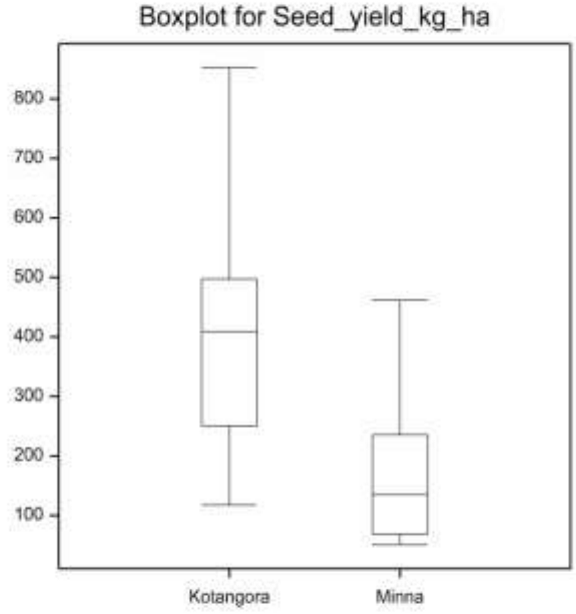

Figure 4.1: Boxplot for seed yield (kg ha^{-1}) from cowpea genotypes in 2017 cropping season across environments

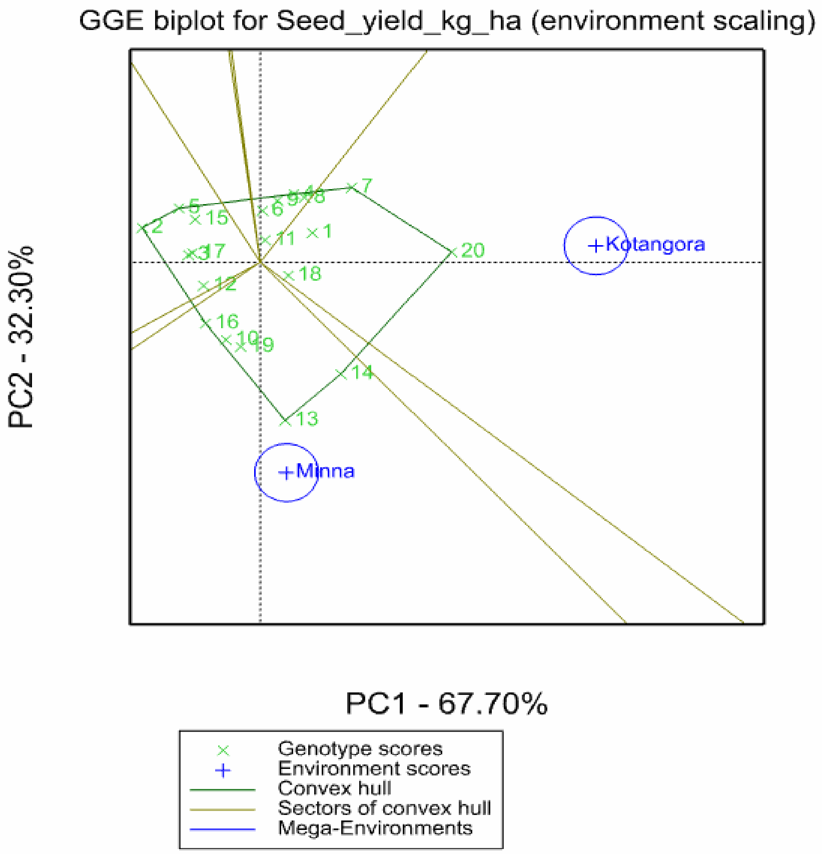

Figure 4.2: Genotype plus genotype-by-environment interaction (GGE) biplot sectors for seed yield (environment scaling) in 2017 cropping season)

1=04K-267-8, 2=07K-210-1-1, 3=08K-125-107, 4=08K-193-15, 5=09K-456, 6=09K-480, 7=10K-816-1, 8=11D-15-40, 9=11D-24-40, 10=12K-261, 11=12K-487, 12=12K-489, 13=12K-632, 14=TVU-408, 15=IT10K-292-10, 16=IT10K-827-7, 17=IT10K-837-1, 18=98K-1092-1, 19=99K-57-3-2-1

20=100K-817-3

4.13. Principal Component Analysis of 16 quantitative characters in cowpea genotypes

In the present study the principal component analysis revealed that only the first four eigenvectors had eigenvalues larger than one. These cumulatively explained 63.58 % of the total variation among the genotypes considering all of the quantitative traits (Table 4.10). The first principal component (PC1) alone explained 27.45 % of the total variation, mainly due to variation in number of branches, number of pods per plant and grain yield. Leaf area, number of seeds per pod, 100 grain weight and biomass weight contributed relatively equal loadings to PC1. Characters that contributed more strongly to PC2 and PC3, which accounted for 15.98 % and 11.71 % of the total variation, were pod length and number of seeds per pod respectively. The traits biomass weight and number of branches contributed positively also to the variation in PC2 while plant height, days to first flowering and 100 grain weight contributed relatively positively to PC3. Hundred grain weight and leaf area had the highest positive loadings to PC4, which contributed 8.43 % of the total variation under this study.

Table 4.12: Contribution of individual trait of the first five component axes to variation in cowpea genotypes

VARIABLES	PC1	PC2	PC3	PC4
PH	-0.0340	-0.1027	0.2438	-0.3332
NB	0.3170	0.1812	0.0613	-0.2769
DTF	-0.0496	-0.5625	0.2588	-0.1156
DTP	-0.0916	-0.4699	0.3920	-0.0223
PL	-0.0542	0.3065	0.5597	0.1976
NP/PL	0.3903	-0.1091	0.0373	0.2405
LA	0.0425	0.0505	-0.0959	0.6779
NS/PD	0.0126	0.3873	0.5516	-0.0630
100GW	0.1283	-0.2164	0.2788	0.4519
BW	0.2968	0.2826	0.0771	-0.0551
GY	0.4274	-0.1403	-0.0346	0.0589
% Variance	27.45	15.98	11.71	8.43
Cumulative %	27.45	43.43	55.15	63.58
EigenValues	3.5689	2.0774	1.5228	1.0956

PH= Plant Height, NB= Number of branches, DTF= Days to Flowering, DTP= Days to Poding, PL= Pod length, NP/PL= Number of pod / plants, LA= Leaf Area, NS/PD= Number of Seed/Pod, 100GW= 100 Grain Weight, BW= Biomass Weight, GY= Grain Yield

4.14 Estimation of Genetic Variance Components of 11 Characters Measured at Kontagora and Minna

The means estimate of genotypic and phenotypic variance, environmental variance, genotypic coefficients of variation (GCV) and phenotypic coefficient of variation (PCV) and broad sense heritability expressed as percentage of means in Kontagora Minna (Table 4.13 and Table 4.14 respectively). In Kontagora, result showed that the phenotypic variances were generally higher than the genotypic variances in all the characters studied. The highest genotypic and phenotypic variances in all the characters considered were recorded in yield (35639.83 and 65634.03), respectively. Similarly, high genotypic and phenotypic variances were observed in biomass weight (111.03 and 351.23) respectively. Environmental variance recorded low percentage in most of the parameters except for yield (9998.07) and biomass weight (80.07). The PCV generally ranged between 9.53 % for 100 grain weight and 80.78 % for biomass weight respectively. Equally, the GCV ranged between 4.45 % for days to first flowering and 45.42 % for biomass weight. However, heritability in broad sense estimate varied from 14.29 % for days to first flowering and 62.22 % for plant length.

In Minna, result showed that the phenotypic variances were generally higher than the genotypic variances in all the characters studied. The highest genotypic and phenotypic variances were recorded in yield (12158.03 and 21389.23), respectively. also, high genotypic and phenotypic variances were observed in biomass weight (116.70 and 270.60) respectively. Environmental variance recorded low percentage in most of the parameters except for yield (3077.07) and biomass weight (51.30). The PCV generally ranged between 9.36 % for days to first podding and 94.66 % for grain yield. Equally, the GCV ranged between 3.32 % for days to first flowering and 71.37 % for grain yield. Heritability in broad sense estimate varied from 10.06 % for days to first flowering and 59.46 % for 100 grain weight.

Table 4.13: Estimation of genetic variance components of 11 characters measured at Kontagora

Variable	σ^2g	σ^2p	σ^2e	GCV %	PCV %	H^2 %
PH	0.92	2.77	0.62	20.89	36.20	33.29
NB	16.00	37.00	7.00	26.67	40.55	43.24
DTF	3.23	22.63	6.47	4.55	12.04	14.29
DTP	6.50	25.10	6.20	5.45	10.71	25.90
PL	8.23	13.23	1.67	20.94	26.55	62.22
NP/PL	37.10	63.80	8.90	43.82	57.46	58.15
LA	33.00	94.80	20.60	32.09	54.39	34.81
NS/PD	7.90	15.10	2.40	26.52	36.66	52.32
100GW	0.50	1.10	0.20	6.43	9.53	45.45
BW	111.03	351.23	80.07	45.42	80.78	31.61
GY	35639.83	65634.03	9998.07	44.82	60.82	54.30

PH= plant height, NB= number of branches, DTF= days to flowering, DTP= days to podding, PL= pod length, NP/PL= number of pod / plants, LA= leaf area, NS/PD= number of seed/pod, 100GW= 100 grain weight, BW= biomass weight, GY= grain yield, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, H^2=broad sense heritability, σ^2g = genotypic variance, σ^2p = phenotypic variance, σ^2e = environmental variance

Table 4.14: Showing estimation of genetic variance components of 11 characters measured at Minna

Variance	σ^2g	σ^2p	σ^2e	GCV %	PCV %	H^2 %
PH	0.43	1.83	0.47	14.01	28.81	23.64
NB	11.33	19.63	2.77	36.59	48.16	57.72
DTF	1.73	17.23	5.17	3.32	10.48	10.06
DTP	3.90	19.50	5.20	4.18	9.36	20.00
PL	22.73	49.03	8.77	35.32	51.87	46.36
NP/PL	13.13	33.43	6.77	47.68	76.08	39.28
LA	30.87	77.77	15.63	33.07	52.49	39.69
NS/PD	14.87	29.37	4.83	34.12	47.96	50.62
100GW	0.73	1.23	0.17	8.23	10.68	59.46
BW	116.70	270.60	51.30	59.68	90.88	43.13
GY	12158.03	21389.23	3077.07	71.37	94.66	56.84

PH= plant height, NB= number of branches, DTF= days to flowering, DTP= days to podding, PL= pod length, NP/PL= number of pod / plants, LA= leaf area, NS/PD= number of seed/pod, 100GW= 100 grain weight, BW= biomass weight, GY= grain yield, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, H^2 =broad sense heritability, σ^2g = genotypic variance, σ^2p = phenotypic variance, σ^2e = environmental variance

CHAPTER FIVE

5.0 DISCUSSION, CONLUSION AND RECOMMENDATIONS

5.1 Discussion

Understanding of the genetic variability of cowpea is significant to design and hasten conventional breeding programmes. Collection, characterisation and assessment of available cowpea germplasm, quantification of the magnitude of diversity and classification into groups facilitate identification of genetic variability that enables breeders to select traits of interest for an improvement programme. Information on the nature and degree of genetic diversity would assist plant breeders in choosing the best genotypes as parents for hybridisation (Abe *et al.,* 2015).The results from this study indicated level of variation among cowpea genotypes. This variation revealed a large scope for breeding and provided the necessary information for the selection of useful traits for use in the cowpea improvement programme. It was observed that genotypes 12k-689, 07K-210-1-1, 04K-207-8, 08K-125-107, IT10K-827-7,TVU-408 and 12K-632 were the first to flower, within a range of 36 to 48 days. This early flowering might be attributed to inherent genetic variation as well as prevailing environmental factors, such as temperature and soil conditions.

Ige *et al.,* (2011) reported 39 days to 50 % flowering for variety ‘Oloyin’. Furthermore, Ishiyaku and Singh (2003) reported a range of 36 to 42 days to 50% flowering for two cowpea cultivars and attributed this to be controlled by a single dominant gene in cowpea. The values obtained for the number of pods per plant was similar to that reported by Egbe *et al.,*(2010) in different cowpea cultivars. This indicated a higher yield potential for this genotype.

Genotype 09K-480 and IT10K-292-10 were observed to have the longest pod length compared with all other genotypes in Kontogora and Minna respectively. Variation in pod length might be due to genotype, environment, and the interaction of genotype and environment. Moreover, Egbe *et al.* (2010) reported pod lengths of 8.95 to 20.17 cm, and Idahosa *et al.,* (2010) reported pod lengths of 10.57 to 18.85 cm, which are within the range of findings of the current investigation. Hundred seed weight ranged from 9.2 g in 04K-632 to 11.2 g at IT10K-292-10 in Minna and 10.2 g in 12K-487 to 11.8 g in 99K-57-3-2-1 at Kontogora environment. This result was similar to those of Abe *et al.,* (2015). Also, Idahosa *et al.,* (2010) found hundred-seed weight ranged from 8.97 to 13.40 g for eight cowpea lines. The highest fresh biomass weight for above ground biomass that was recorded in genotype 12K-487 in both locations might be due to the large size of the leaves and number of branches. This indicated good performance in terms of vegetative growth characteristics and could be well suited for use as a leafy vegetable, fodder or dual-purpose cowpea genotype.

Genotype by environment interaction (GGE) biplot displays the best genotypes in each environment and it is a summary of the genotype by environment pattern of a multi-locational yield trial. In Kontagora environment, genotypes 04K-267-8, 10K-816-1, 98K-1092-1 and 100K-817-3 were the best genotypes and yielded optimally while the best genotypes for Minna environment were 12K-261, 12K-632, TVU-408, IT10K-827-7 and 99K-57-3-2-1 in grain yield.The positive association between a pair of phenotypic traits indicate that selection of desirable quantitative traits will have simultaneous positive effects on other traits, which would help breeders to improve both characters at the same time. Selection of highly associated traits, such as number of pods per plant and grain yield, days to 50 % flowering and days to poding, and days to 50 % flowering and pod length, are important traits that can be improved in the cowpea improvement programme.Similar study carried out by Abe *et al*., (2015) which reported strong positive and highly significant (p<0.01) correlation between pod length and number of seeds per pod.Selection is effective when magnitude of variability in the breeding population is enough (Muhammad *et al.,* 2015).The information obtained from a principal component analysis assists breeders in identifying phenotypic traits that contribute great genetic variation among genotypes for selection of potential parents for crossing blocks for the traits of interest.PC1 and PC2 explained the most variation among the genotypes, revealing a high degree of association and interrelationships among the traits studied.

5.2 Conclusion

This study has revealed that there is sufficient variability among the 20 genotypes which can be exploited for use in the cowpea improvement programme for the phenotypic traits of interest. Genotypes 12K-487 was identified to possess favourable vegetative traits and it could be used as parents when breeding for leafy vegetable or for fodder production. Similarly, genotypes 04K-267-8, 10K-816-1, 98K-1092-1 and 100K-817-3 in Kontogora and genotypes 12K-261, 12K-632, TVU-408, IT10K-827-7 and 99K-57-3-2-1 in Minna location were associated with desirable grain yield characteristics and are suitable parental lines for improvement of grain production in such areas. These lines are recommended for further evaluation across environments

5.3 Recommendations

Based on the results of the study, it is recommended that;

1. For large scale cowpea production, Kontagora may be considered in order to ensure high yield and effective production
2. Genotypes 04K-267-8, 10K-816-1, 98K-1092-1 and 100K-817-3 could be evaluated in Kontagora environment and genotypes 12K-261, 12K-632, TVU-408, IT10K-827-7 and 99K-57-3-2-1 evaluated in Minna environment for yield evaluation trials

REFERENCES

Abe, S.G., Patrick, O. A., Willem S.J., Van Rensburg, & Sunette, M. L. (2015). Genetic Variability in Cowpea (*Vigna unguiculata* (L.)Walp) Genotypes. *South African Journal of Plant and Soil* 5, 23-25

Achuba, F. I. (2006). The effect of subletethal concentration of crude oil on the growth and metabolism of cowpea (*vigna unguiculata*) seedlings. *The Environmentalist,* 21(1), 17-20.

Adaji,M. J., Olufala, O. O.,& Aliyu, L. (2007). Effect of intra-row spacing and stand density on the growth and yield of cowpea (*vigna unguiculate* (L.) Walp). *African Journal of plant science,*12, 47-71.

Adegbite, A.A.& Amusa, N. A. (2008). The major economic field diseases of cowpea in the humid agro-ecologies of South-Western Nigeria. *African Journal of Biotechnology,*7, 4706-4712.

Agbogidi, O. M. & Egho, E. O (2012). Evaluation of eight varieties of cowpea (*Vigna unguiculata* (L.) Walp) in Asaba agro-ecological environment, Delta State, Nigeria *European Journal of Sustainable Development,* 1(2), 303-314.

Agbogidi, O. M. (2010a). Screening six cultivars of cowpea (*Vigna unguiculata*(L.) Walp) for adaptation to soil contaminated with spent engine oil *Journal of Environmental Chemistry and Ecoloxicology*. 7, 103-109.

Agbogidi, O. M. (2010b). Response of six cultivars of cowpea (*vigna unguiculata*(L.) Walp) to spent engine oil. *African Journal of Food Science and Technology* 1(6), 139-142.

Ajeigbe, H. A., Singh, B. B., Musa, A., Adeosun, J. O., Adamu, R. S & Chikoye, D. (2010). Improved cowpea – cereal cropping system: cereal – double cowpea system for the Northern Guinea Savanna Zone Available from http://www.iita.org/c /document library/ Retrieved 26th April, 2015.

Alegbejo, M. D & Kashina, B. D (2001). Status of legume viruses in Nigeria. *Journal of Sustainable Agriculture,* 18(1), 55-69.

Alegbejo, M. D. (2015). Virus and virus like disease of cowpea in Nigeria Zaria, Nigeria, *Ahmadu Bello University press,* 12, 89-91.

Aliyu, T. H., Balogun, O. S., & Kumar, L. (2012). Survey of the symptoms and viruses associated with cowpea (*Vigna unguiculata* (L).) in the Agroecological zones of Kwara State, Nigeria. *Ethiopian Journal of Environmental Studies and Management,* 5(4), 613-619.

Aremu, C. O. (2012). Exploring Statistical Tools in Measuring Genetic Diversity for Crop Improvement, Genetic Diversity in Plants, Prof. Mahmut Caliskan (Ed.), In Tech, Available from: http://www.intechopen.com/books/genetic-diversity-in-plants/exploring-statistical-tools-in-measuring-genetic diversity-for-crop-improvement.

Aremu, C.O. (2005). Diversity selection and genotypes Environment interaction in cowpea unpublished Ph.D Thesis. University of Agriculture, Abeokuta, Nigeria. P. 210

Aremu, C.O., Adebayo, M.A., Oyegunle, M., & Ariyo, J.O. (2007). The Relative Discriminatory Abilities Measuring Genotype by Environment Interaction in Soybean (*Glycine max*). *Agricultural Journal*. 2(2), 210-215

Arogundade, O., Balogun, O. S., Shokalu, O., & Aliyu, T. H. (2010). Influence of *Cowpea mottle virus* and *Cucumber mosaic virus* on the growth and yield of six lines of soybean (*Glycine max* L. Merrril). *Journal of Agricultural Science*. 2, 72–78.

Asiwe, Jan (2009). Insect Mediated Outcrossing and Geneflow in Cowpea (*vigna unguiculata* (L.) Walp). Implication for Seed Production and Provision of Containment Structures for GT Cowpea. *African Journal of Biotechnology*. 8(2), 226-230.

Asumugha, V. U. (2002). Sensory and functional properties of dry vegetable cowpea product (akara). *In*: ubbanu, C. N., Eke, O. S. & Uzomah, A. (eds.). proceedings of the 26th Annual Conference of the Nigerian Institute of Food Science and Technology (NIFST) held at the Federal University of Technology, Owerri, Imo State between 4th and 8th of November, 2002. (pp 66-67).

Autrique, E., Nachit M. M., Monneveux, P., Tanksley, S. D., & Sorrells, M. E. (1996). Genetic diversity in durum wheat based on RFLPs, morphological traits, and coefficient of parentage. Crop Science. 36, 735-742.

Ayenlere, A. E., Mohammed, A. B., Dutse, F., Abdullahi, M. & Mohammed, L. A. (2012). An assessment of the economics of maize-cowpea cropping system in Ogun area of Kwara State, Nigeria. *Biological and Environmental Sciences Journal for the tropics* 9(1), 39-43.

Bezerra, A. A. C., Anunciação Filho,C. J., Freire Filho, F. R. & Ribeiro V. Q. (2001) Inter-relação entre caracteres de feijão-caupi de porte ereto e crescimento determinado. Pesquisa Agropecuária Brasileira 36, 137-142.

Bittenbender, H. C., Barret, R. P. & Indire-Lauvsa, B. M. (1984). Beans and cowpeas as leaf vegetables and grains legumes. Monograph No. 1 Bean/cowpea

Collaborative Research Support Programme. Michigan State University, East Lansing. (pp 25-28).

Blade, S. F., Shetty, S. V. R., Terao, T. & Singh, B. B. (2011). Recent developments in cowpea cropping systems research. in Singh, B.B., Mohan Raj, D. R., Dashiell, K. E. & Jackai, L. E. N. (Eds.) *Advances in Cowpea Research.*Ibadan, Nigeria. *International Institute of Tropical Agriculture* and *Japan International Research Center for Agricultural Sciences*. 2, 11-17.

Brigges, F. N. & Knowles P. F. (1967). Introduction to plant Breeding. Renihold Publishing Cooperation New York Amsterdam, London Burton GW (1962). Quantitative Inheritance in grasses In: *Proceedings of the Sixth International grassland Congress* 1, 277-283.

CGIAR. (2011) Consultative Group on International Agricultural Research http://www.cgiar.org/impact/research/cowpea.html [Accessed 23 April, 2011].

Chima, C. E., Alomede, I. C. & Emelife, I. G. (2008). Physicochemical and functional properties of some Nigeria cowpea varieties 7(1), 186-190.

Christine, Joshua, H., William, A. & Stacy, A. (2009). Genetic diversity of creeping bentgrass cultivars using SSR markers. *International Turfgrass Society Research Journal*. 11, 80-110.

Davis, D. W., Oelke, E. A., Oplinger, E. S., Doll, J. D., & Hanson, C. V. (2003). Variability in yield and yield related traits in cowpea landraces. Biological Science 55, 124-128.

Davis, D. W., Oelke, E. A., Plinger, E. S., Doll, J. D., Hanson, C. V.& D. H. Putnam (1991), Cowpea Alternative Field Crops manual. http://www.hort.purdue.edu/newcrop.

Dje, Y., Hevretz, M., Letebure, C. & Vekemans, X. (2000). Assessment of genetic diversity within and among germplasm accessions in cultivated sorghum using microsatellite marked *theory of Applied Genitics*. 100, 918-925.

Dugje, I. Y., Omoisui, L. O., Eketeneme F. & Kamara A. Y. (2009). Farmers Guide to Cowpea Production in West Africa. (pp 46-48).

Dumbre, A. D., Deshimukh R. B.& Paddy A. P. (1983). Variability in Cowpea. Geotype, the Mcharashtra Agricultural University 8(1), 85-88.

Egbe, O. M., Alibo, S. E. & Nwueze, I. (2010). Evaluation of some extra-early-and early-maturing cowpea varieties for intercropping with maize in southern Guinea Savanna of Nigeria. *Agriculture and Biology Journal of North America* 1, 845–858.

Egho, E. O. (2009). Control of major insect pests of cowpea *Vigna unguiculata*(L.) Walp using Conventional and Non-Conventional Chemicals. A PhD Thesis submitted to the Department of Agronomy, Delta State University, Asaba Campus. 224.

Ehlers, J. D. & Hall, A. E. (1997). Cowpea (*Vigna unguiculata* (L.) Walp), *Field Crops Research*. 53, 187-204.

Emeberi, L. C.& Obisesan, I. O. (1991). Duration of Specific Development Stages in Cowpea (*Vigna unguculata* (L.) (Walp). Heritability and Relationship to Yield. *Journal of Genetics and Breeding* 45, 81-86.

Fall, L., Diouf. &Fall, M. A. (2003). Genetic diversity in cowpea (*Vigna unguiculata* (L.) Walp) varieties determined by ARA and RAPD techniques. *African Journal of Biotechnology* 2 (2), 48-50.

Fang, J. Chao, C. T. Robert, P. A.Ehler. J. D. (2007). Genetic diversity of cowpea [*Vigna unguiculata* (L.) Walp.] in four West African and USA breeding programs as determined by AFLP analysis, *Genetic Resource Crop Evolution* 54, 1197-1209.

FAO (2002). *World Agriculture*: *towards 2015/2030*. Summary report, Rome.

FAO (Food and Agriculture Organization) (2012). FAOStat Gate Way http:// faostat.fao.org/site/ Retrieved 24/05/2018

FAO. (2000). The state of food insecurity in the world (SOFI) Rome. Italy: FAO-UN. www.fao. org/FOCUS/E/SOFI00/sofi001-e.htm Accessed on March 12th, 2014.

FAOSTAT. (2011).Food and Agriculture Organization. *Bulletin of Tropical Legume*

Geissler, P.W., Mwaniki, D.L., Thiong'o, F., Michaelsen, K. F. & Friis, H. (1998). Geophagy, iron status and anemia among primary school children in Western Kenya,*Tropical Medicine and International Health*. 3(7), 529-534.

Ghaly, A. E., Alkoalk, F. N., & Hall, A. E. 2010. Extraction of protein from common plant leaves for use as human food and Applied Science. 7(3), 323-334.

Gomes, RLF & Lopes ACA (2005) Correlations and path analysis in peanut. *Crop Breeding and Applied Biotechnology* 5, 105-112.

Grafius, J. E., Thomas R. L.& Bernard J (1978) Multiple characters and correlated response. Crop Science, 18, 931-934.

Grafius, J. E., Thomas, R. I.& Bernard, J (1976). Effect of parental component complementation on yield and components of yield in Barley. Crop Science 16, 673-677

Hall, A. E., Cisse, N., Thiaw, S., Elawad, H. O. A. & Ehlers, J. D. (2003). Development of cowpea cultivars and germplasm by Bean/Cowpea CRSP, *Field Crop Research*. 82,103-134.

Hull, R. (2009). *Comparative plant virology,* California, USA. Second edition. Elsevier Academic Press. (pp 20-28).

Idahosa, D. O., Alika, J. E. & Omoregie, A. U. (2010). Genetic variability, heritability and expected genetic advance as indices for yield and yield components selection in cowpea (*Vigna unguiculata* (L.) Walp). Academia Arena 2(5), 22–26.

Ige, O. E., Olotuah, O. F., & Akerele V. (2011). Floral biology and pollination ecology of cowpea (*Vigna unguiculata* (L.) Walp). Modern Applied Science 5, 74–82.

IITA (International Institute of Tropical Agriculture) (2015). *Cowpea production in Nigeria Available at https://agronigeria.ng>Research.*

IITA (International Institute of Tropical Agriculture). (2013). Research highlights Ibadan.Hull, R (2009). *Comparative plant virology,* California, USA. Second edition. Elsevier Academic Press.

International Institute of Tropical Agriculture (IITA) (2004). Crops and farming system www.iita.org.crop/cowpea.htm.

International Institute of Tropical Agriculture (IITA) (2009). Cereal and legume system www.iita.org.cms/details-present-details-asp.

Ishiyaku, M. F. & Singh, B. B. (2003). Genetics of juvenile phase in cowpea (*Vigna unguiculata* (L.) Walp.). *Journal of Food, Agriculture and Environment* 1, 133–136.

Islam, S., Cowmen, R. C.& Ganer, J. O. (2006). Screening for tolerance of stress temperature during germination of twenty- five cowpea (*Vigna unguiculata* (L.)Walp) cultivars. *Journal of Food, Agriculture and Environmental* 4(2), 189-191.

Johns, M. A., Skrotch, P. W., Neinhusis, J., Hinrichsen, P., Bascur, G., &Munoz-Schick, C. (1997). Gene pool classification of common bean landrances from Chile based on RAPD and morphological data. Crop Science 37, 605-619.

Kareem, K. T., & Taiwo, M. A. (2011). Interactions of viruses in cowpea: Effects on growth and yield parameters. *Virology Journal*, 4(1), 234-240.

Karuri, H. W., Ateka, E. M., Amata, R., Nyende, A. B., Muigai, A. W. T., Mwasame, E., Gichuki, S. T. (2010) Evaluating diversity among Kenyan sweet potato genotypes using morphological and SSR markers, *International Journal of Agricultural Biotechnology*, 12, 33–38.

Liu, S., Cantrell, R. G., Mccarty, J. C., & Stewart, M. D. (2000). Simple Sequence Repeat Based Assessment of Genetic Diversity in Cotton Race Accessions. *Crop Science.* 40, 1459-1469.

Lopes, A. C. A., Freire Filho F. R., Silva R. B. Q., Campos F. L. & Rocha M. M. (2001). Variabilidade e correlações entre caracteres agronômicos em feijão-caupi (*Vigna unguiculata*). Pesquisa Agropecuária Brasileira 36, 515 – 520.

Mamiro, P.S., Mbwaga, A.M., Mamiro, D. P., Nmanri, A.W. & Kinabo, J.L. (2011).Nutritional quality and utilization of local and improved cowpea varieties in some regions in Tanzania, *African Journal of Food, Agriculture, Nutrition and Development*. 11(1), 4490-4506.

Mostafa, K., Mohammad, H. & Mohammad, M. (2011).Genetic diversity of wheat genotype baspdon cluster and principal component analyses for breeding strategies. *Australian Journal of Crop Science.* 5 (1), 17-24.

Muhammad, Z. A., Muhammad, S. M., Hidayatullah, B., Abdul, W. S., Faiz, H. P., Abdul, R. C. & Karim, B. S. (2015). Genetic Variability, Coefficient of Variance, Heritability and Genetic Advance of Some *Gossypium hirsutum* L. Accessions. *Journal of Agricultural Science*; 7(2), 1916-9760 Published by Canadian Center of Science and Education

Muoneke, C. O., Ndukwe, O. M., Umana, P. E.,Okpara, D. A. & Asawalam, D. O. (2012). Productivity of vegetables cowpea (*Vigna unguiculata* (L.) Walp) and maize (*zea mays* L.) intercropping system as influenced by component density in a tropical zone of southeastern Nigeria *International Journal of Agricultural Research and Development* 15(1), 835-847.

Murphy, J. F. & Biokmmmowen, K. L. (2009). Synergistic disease in pepper caused by the mixed infection of *Cuucumber mosaic virus* and *Pepper mottle virus.* Phytopathology, 96, 240-247.

Nielson, S., Ohler, T. & Mitchell, C. (1997). Cowpea leaves for human consumption: production, utilization and nutrient composition. In: Singh, S.R. and Rachie, K.O. (eds.). Cowpea researches, production and utilization. Wiley, New York. (pp 145-162).

Ntare, B. R. (1992). Variation in reproductive efficiency and yield of cowpea under high temperature condition in a sahelian environment, Euphytica 59, 27-32.

Nwofia, G. E., Nwanebu, M & Agbo, C. U. (2012). Variability and inter-relationship between yield and associated traits in cowpea (*Vigna unguiculata* L. Walp) as influenced by plant population, *World Journal of Agricultural Sciences.* 8(4), 396-402.

Nwosu, D. J., Olatunbosun, B. D., & Adetiloye, I. S. (2013). Genetic variability, heritability and genetic advance in cowpea genotypes in two agro-ecological environments,*Greener Journal of Biological Science*. 3(5), 202-207.

Odedeji, J. O. & Oyeleke, W.A (2011). Proximate, physiochemical and organoleptic properties of whole and dehulled cowpea seed flour (*Vigna unguiculata*), *Pakistan Journal of Nutrition*. 10(12), 1175-1178.

Ogbo, E. M. (2009). Effects of diesel fuel contamination seed germination of four crop plants- *Arachis hypogaea, Vigna unguiculata, Sorghum bicolor* and *Zea mays*. *African Journal of Biotechnology* 8(20), 250-253.

Ogunbodede, B. A., & Fatula, T (1985). A note on the heritability of pod length and number of seeds per pod in cowpea (*Vigna unguiculata* (L.) (Walp). traits. *East African Agricultural and Forestry Journal.* 50, 89-100.

Oliveira, F. A., Medeiros, J. F., Miranda, N. O., M. K. T. Lima., C. J. S., & Galvao, D. C. (2008). Mathematical Model to Estimate Leaf Area of Cowpea. Unpaginated.

Owolade, O. F., Akande, M. O., Alabi, B. S. & Adediran, J. A. (2006). Phosphorus level effects on brown blotch disease, development and yield of cowpea. *World Journal of Agricultural Science* 2(1), 105-108.

Palukaitis, P., Roossinck, M. J., Dietzgen, R. G., & Francki, R.I.B. (2002). *Cucumber mosaic virus*. *Advances in Virus Research*, 41, 281-341.

Perrino, P. G., Laghetti, P. L., Spagnoletti Zeuli, & Monti, L. M. (2011). Diversification of cowpea in the Mediterranean and other centers of cultivation. Genetic Resources and Crop Evolution 40, 3, 121-132.

Queiroz, M. A. (2001). Melhoramento genético no Brasil: Realizações e perspectivas. In: Nass L. L., Valois A. C. C., Melo I. S. andValadares-Inglis M. C. E. (eds.) Recursos Genéticos e Melhoramento – Plantas. Fundação M. T., Rondonópolis, 2-28.

Rahim, M.A., Mia, A. A, Mahmud, F., Zeba, N. & Afrin, K. (2010). Genetic variability, character association and genetic divergence in Murgbean plantation 3,1-6.

Ramachadran, C., Peter, K. V.& Gopalakrishnan, P. K. (1982). Variation in selected varieties of cowpea (*Vigna unguculata* (L.) (Walp). Agric. Res. Karale 18(1), 94-97.

Sankie, L., Addo-Bediako, K. O. & Ayodele, V. (2012). Susceptibility of seven cowpea (*Vigna Unguiculata* (L.) Walp) cultivation to cowpea beetle

(*Callosobruchus macullatus*). *Agricultural Science Research journals,* 2(2), 65-69.

Shaw, M. (2012). 100 Most Protein Rich Vegetarian Foods*Smarter Fitter Blog*. Retrieved 28/07/2015.

Shiringani, R. P. & Shimeles, H. A. (2011). Yield response and stability among cowpea genotypes at three planting dates and test environments. *African Journal of Agricultural Resources* 6(4), 3259-3263.

Simpson, D. (2010).*Vigna Unguiculata* (L.)Walp. Alternative Field Crops Manual. Cowpea. D. W. Davis, E. A. Oelke, E. S. Oplinger, J. D. Doll, C. V. Hanson and D. H. Putnam Departments of Horticultural Science, Agronomy and Plant Genetics, Center for Alternative Plant and Animal Products, Minnesota Extension Service, University of Minnesota, St. Paul, MN 55108. Department of Agronomy, College of Agricultural and Life Sciences and cooperative Extension Service, University of Wisconsin-Madison, WI 53706, July, 1991.

Singh, B. B. (2014). *Cowpea: The food legume of the 21st century*. U. S. A. *Crop Science Society of America.*

Singh, B. B., Mohan, D. R., Dashiell, K. E. & Jackai, L. E. N. (2007). *Advances in Cowpea Research,* Ibadan Nigeria, International Institute of Tropical Agriculture.

Singh, B., Ajeigbe, H. A., Tarawali, S. A., Fernandez-Rivera, S & Abubakar, M. (2013). Improving the production and utilization of cowpea as food and fodder. *Field Crops Research.* 84, 169–150.

Taiwo, M. A. & Akinjogunla O. J. (2011). Cowpea viruses: Quantitative and qualitative effects of single and mixed viral infections. *African Journal of Biotechnology,* 5(19), 1749-1756.

Taiwo, M.A. (2003). Viruses infecting legumes in Nigeria case history. 365-380. Hughes, J. A. and Odu, B. O. *Plant Virology in Sub-Sahara Africa. Proceeding of a conference organized by IITA, 4*-8 June, 2011, IITA, Ibadan. Nigeria. 589.

Takahashi, R. & Abe, J (2009). Soybean maturity genes associate with seed coat pigmentation and cracking in response to low temperatures. *Crop Science,* 49, 1657- 1662.

Thompson, J. A., Nelson R. L.& Vodkin L. O. (1998). Identification of diverse soybean germplasm using RAPD markers. Crop Science. 38, 1348-1355.

Tomlinson, P. (2005). *Cucumber mosaic virus*. *Advance in Virus Research*, 41, 281 – 348.

Tosti, N. & Negri, V. (2002). Efficiency of three PCR-based markers in assessing genetic variation among cowpea (*Vigna unguiculata* (L.) Walp) landraces. Genome 45(2), 268-275.

Udensi, E. A., Edu, E. V., Ikpeme, J. K., Ebiwgai, & Ekpe, D. E. (2012). Biometric Evaluation and Yield Performance Assessment of Cowpea (*Vigna unguiculata* (L.) Walp). Landraces grown under lowland races lowland tropical conditions. *International Journal of Plant Breeding and Genetics*, 6, 47-53.

Usha, M. & Parimal S. (2009). Effects of Climate Change on Plant Pathogens. *Crop Science Society of America,* 14(4), 124-129.

Valenzuela & Jody S. (2002). Cowpea Sustainable Agriculture Green Manure Crops Departments of Tropical Plant and Soil Sciences and Natural Resources and Environmental Management 2002.

Valenzuela, H. & Smith, J. (2010). Cowpea. Honolulu, Hawaii. *College of Tropical Agriculture and Human Resources. University of Hawaii at Monoa,* 274.

Van Beuningen, L. T. & Bush, R. H. (1997). Genetic diversity among North American spring wheat cultivars: 1. Analysis of the coefficient of parentage matrix. Crop Science. 37, 570-579.

Warburton, M. & Crossa, J. (2000). Data analysis in the CIMMYT. Applied Biotechnology Center for fingerprinting and Genetic Diversity Studies. CIMMYT, Mexico.