STUDIES OF VARIABILITY AND CLUSTER ANALYSIS IN SOME ACCESSIONS OF SORGHUM [Sorghum bicolor (L.) Moench]

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Abstract

An experiment was carried out to evaluate nineteen accessions of sorghum grown for two consecutive cropping seasons of 2015 and 2016 at the Teaching and Research Farm of Crop Production Department. Federal University of Technology, Minna, Niger state. The experiment assessed variability in 19 sorghum accessions base on their morph-agronomic traits and determined yield with its component traits. A randomized complete block design with three replications was used for the experiment. Data were collected on various morph-agronomical traits and were subjected to individual and combined analysis of variance (ANOVA). Based on the result of this study, highly significant differences among most accessions were found. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) and high phenotypic and genotypic variability was observed between the nineteen sorghum accessions. Highest heritability was observed in grain yield (99 %), and the most high yielding accession was AKV11 (Kaura) with grain yield of 614g in 2015 and 514.33g in 2016. High genetic advance was recorded in grain yield and panicle length. The grouping pattern of the accessions into five clusters indicated there was significant genetic variability among the accessions of sorghum tested. The most outstanding performance accessions for grain yield are: AKV11, AKV9 and AKV14, which could be used for Sorghum improvement, programme and recommend for farmers in the Southern Guinea Zones of Nigeria.

Keywords: Sorghum, Variability, Accessions, Cluster

INTRODUCTION

Sorghum (Sorghum bicolor (L.) Moench) is a member of the grass family, poaceae, a group of flowering plants that also includes such important agricultural grains as wheat, rice, maize and sugar cane. Sorghum grain is used for animal feed in USA and India (Obilana, 2005). Sorghum is one of the most important staple food crops in Nigeria and its production surpasses all other crops (Baiyegunhi and Fraser, 2009). The leaves and grains are also used for livestock feeds and the stalks for thatching houses and making fences.

There are collections of sorghum genotypes in some research institutes and most of these collections lack information on its morphology- agronomic traits that could be used by researchers to improve sorghum production in Nigeria. However, breeding for high yield crops require information on the nature and magnitude of variation in the available materials and the relationship of yield with other agronomic characters (Ahmed et al., 2012). Grain yield in sorghum is quantitative in nature and polygenically controlled, effective yield improvement and simultaneous improvement in yield components are imperative (Ahmed et al., 2012). Selection on the basis of grain yield character alone is usually not very effective and efficient. However, selection based on its component characters could be more efficient and dependable (Bello et al., 2010). The study aimed was to determine yield with its component traits in different sorghum accession.

MATERIALS AND METHODS

Description of the study Area

The trial was conducted in 2015 and 2016 rainy seasons at the Teaching and Research Farm of Department of Crop Production, Federal University of Technology, Gidan kwano campus Minna, Niger state. The site is located in the Southern Guinea Savanna of Nigeria, with Geographical Positioning System (GPS) co-ordinates of (Latitude 9.52335N, and Longitude 6.44791E). Minna is located in the Southern Guinea Savanna agro-ecological zone of Nigeria with a mean annual rainfall of 1200mm (Adeboye et al., 2011). The rainfall which has its peaks in September and it usually begins in April and ends in the first week of October. The temperature ranges between 35 and 37.5°C, with relative humidity between 60 and 80 % in the month of July and 40 and 60 % in January.

Planting Materials

The Sorghum germplasm used in this study comprised of nineteen sorghum accessions collected from Institute for Agricultural Research (IAR) Ahmadu Bello University Zaria.

Experimental Design and Field Layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three (3) replications. The gross plot size was 4m by 2m (8m²); 5 ridges of 2m long each. The net plot size was 2.4m by 2m (4.8m²); 3 ridges of 2m long each. Gross plots were separated by a distance of 0.5m each while a distance of 1m separated one replication from the other. The total land area of 658m² was measured, ploughed, harrowed mechanically and was ridged manually. Two seeds were sown per hill and each stand was later thinned to one plant per stand.

Statistical Analysis

Data collected were subjected to analysis of variance (ANOVA) using SAS 9.1.3 software statistical package. The means were separated by Student- Newman-Keuls (SNK) test at 5 % level of significant. Genotypic and phenotypic variances, heritability and genetic advance were estimate. Cluster analysis was done using the unweight pair group method with arithmetic mean (UPGMA) analysis and dendograms were constructed using the SAHN program.

RESULTS

Genetic Variability for Yield and Yield Components

The result of combined genetic variability for yield and yield components is shown Table 1. Genotypic and phenotypic variances, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and genetic advance for morph agronomic traits in nineteen accessions of sorghum, evaluated in 2015 and 2016 cropping seasons. Grain yield recorded the highest values of 9396.2 and 9478.48 for genotypic and phenotypic variances respectively. Days to 95 % maturity that recorded approximately equal values of 169.83 and 169.8. Panicle width recorded the lowest values of 0.19 and 0.2. Grain weight recorded the highest percentage value of 36 % for genotypic and phenotypic coefficients of variation followed by 1000 seed weight that recorded the same value of 26 %. Days to 95 % maturity recorded the lowest percentage value 9.5 % for PCV. Broad sense heritability was very high at 99 % for grain yield and days to 95 % maturity. Panicle length recorded high percentage broad sense heritability of 97 % followed by panicle width and days to 50 % flowering (95 %). The lowest estimate of broad sense heritability was recorded by 1000 seed weight at 0%. The remaining characters recorded moderate (above 40%) and high broad sense heritability above 70 % and high genetic advance in grain yield.

Table 1: Estimates of genetic variability for yield and yield components in nineteen accessions of Sorghum in Minna Southern guinea ecological zone of Nigeria for two cropping seasons of 2015 and 2016

Parameters	Mean	$\sigma^2 g$	$\sigma^2 ph$	GCV (%)	PCV (%)	$h^2 B$	GA	GAM (%)
Days to 50 % Flowering	104.12	161.2	168.11	12	12	95	23.42	22
Days to 95 % Maturity	136.98	169.83	169.84	9	9.5	99	26.57	19
Panicle Length (cm)	34.43	72.14	74.27	24	25	97	17.22	50
Panicle Width (cm)	2.61	0.19	0.2	16	17	95	0.87	33
Grain Yield (g)	267.75	9396.2	9478.48	36	36	99	198.5	74
1000 Seed Weight	28.74	57.61	57.63	26	26	0	0	0

Cluster analysis for quantitative traits of nineteen sorghum accessions evaluated during 2015 and 2016 in Minna, Southern Guinea Savanna of Nigeria

The dendogram of 2015 in Figure 1 produced three clusters; the first consisted of eleven accessions (Bukwakana, Mori, Danyana, Harju, Wagofari, Falafate, Panpara, Chakeilare, Nduvori, Yimshi and Samsorg 40). Two sub groups existed within cluster one, the first sub group consisted of seven accessions (Bukwakana, Mori, Danyana, Harju, Wagofari, Falafate and Panpara). Bukwakana and Mori, Harju and Wagofari formed a close relationship with each other. The second sub group consisted of three accessions (Chakeilare, Nduvori and Yimshi) while Chakeilare and Nduvori are closely related. Samsorg 40 appeared to be an outlier of the sub groups. The second cluster was made of seven accessions (Adamumakiwa, CSRO2, Farefare, Shawimpe, Bogfarwa, Cham and Paul Noel) Two sub groups existed, first are (Adamumakiwa, CSRO2, Farefare, and Shawimpe) Adamumakiwa and CSRO2 formed a very close relationship. Second sub group consisted of Bogfarwa and Cham that appeared closely related; Paul Noel appeared to be an outlier of the sub groups. Kaura was the only member of cluster three and appeared an outlier to other clusters.

The dendogram of 2016 also produced three clusters (figure 2), the first cluster consisted of fourteen accessions Adamumakiwa, Farafara, Shawimpe, Bogfarwa, Panpara, CSRO2, Paul Noel, Cham, Bukwakana, Wagofari, Falafate, Harju, Danyana and Mori. Three sub groups existed in this cluster, sub group one are; Adamumakiwa, Farafare and Shawimpe. Farefare and shawimpe appeared to be closely related. In Sub group two (Bogfarwa, Panpara, CSRO2, Paul Noel and Cham), there existed two closely related relationships in this sub group between Bogfarwa and Panpara, CSRO2 and Paul Noel while Cham formed an outlier to the sub group. In Sub groups three, there existed two close relationships, Bukwakana and Wagofari, Falafate and Harju. While, Danyana joined the group, Mori appeared an outlier to the sub group. The second cluster consisted of four accessions (Chakeilare, Nduvori, Yimshi and Samsorg 40). Chakeilare and Nduvori appeared to be closely related, while Yimshi joined the group and Samsorg 40 appeared to be an outlier to the group. Kaura was the only member of cluster three and an outlier to other clusters.
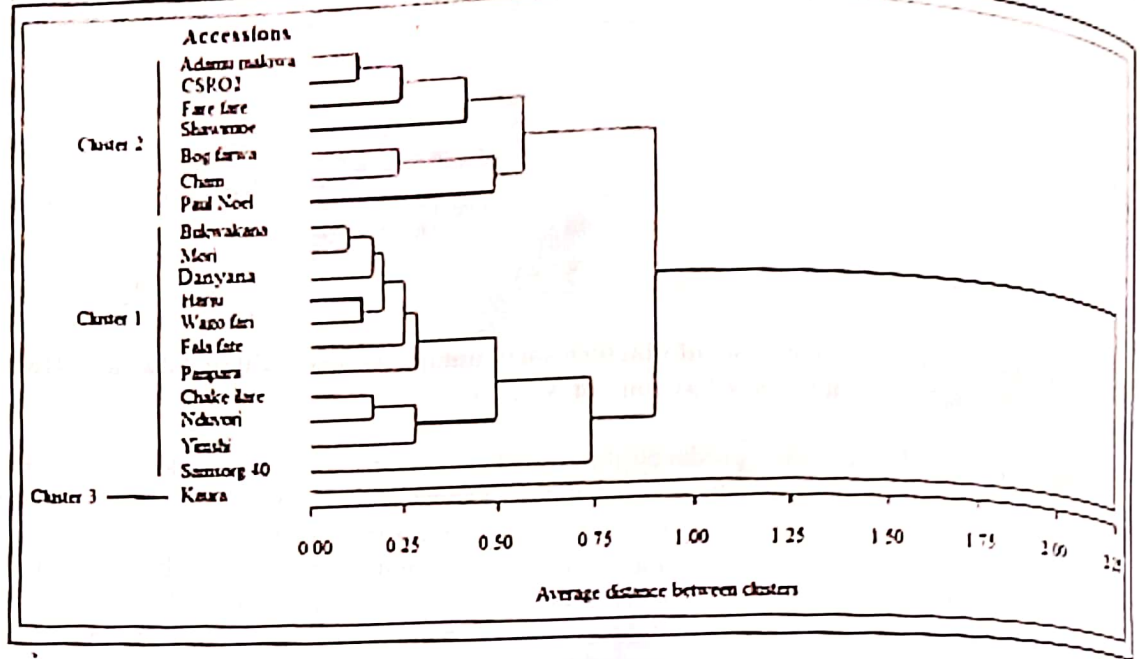
Figure 1: Dendogram of the relationship among Sorghum accessions based on their growth and yield parameters in 2015 cropping season, depicted by Unweight Pair Group Method with Arithmetic (UPGM
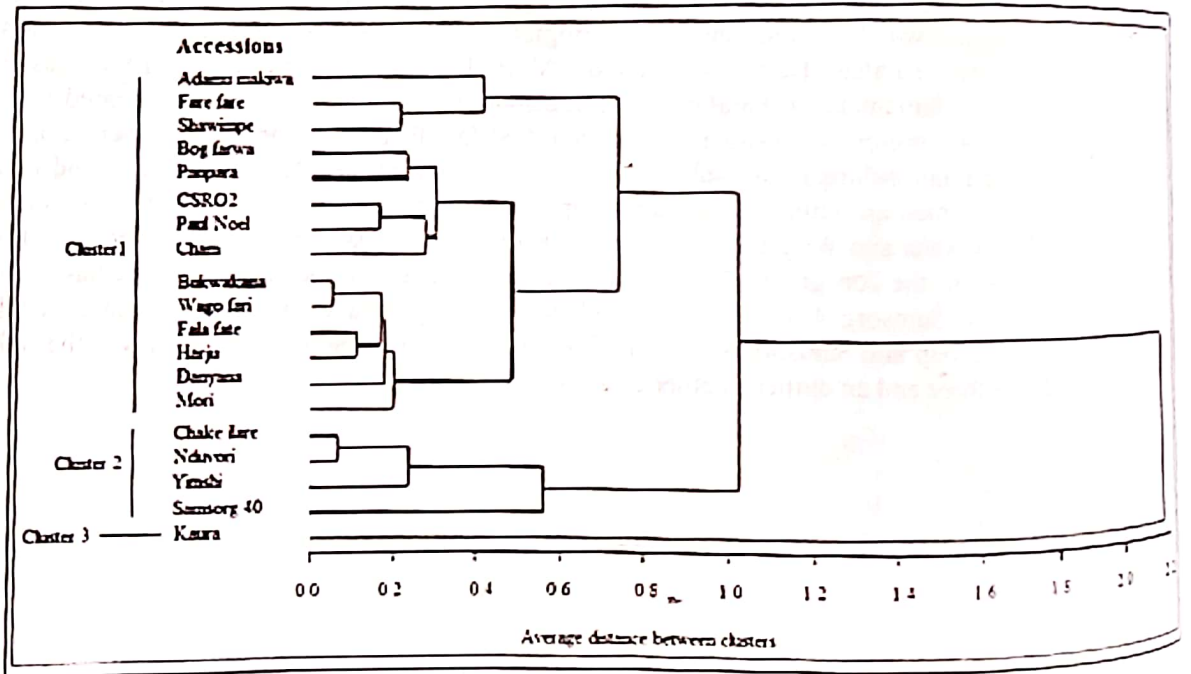

Figure 2: Dendogram of the relationship among Sorghum accessions based on their growth and yield parameters in 2016 cropping season, depicted by Unweighted Pair Group Method with Arithmetic (UPGMA) mean

DISCUSSION

Crop improvement activities through breeding are aimed at boosting the genetic potential for yield. Selection based on yield alone is not effective. Therefore breeders select for high yield indirectly through yield association and highly heritable characters after eliminating environmental components of phenotypic variation (Tadele and Assefa, 2012). It is therefore important to get information on both genotypic and phenotypic coefficients of variation to know about the heritability of a character. The information on phenotypic coefficient of variation and heritability was helpful at predicting the possible genetic advance by selection for the character. Knowledge of cluster assisted in grouping the accessions selection indices.

There were differences in most of the characters investigated which indicated the presence of wide range of variability, and in agreement with (Khandelwal et al., 2015) that reported similar result of high significant differences in the characters of 224 genotypes investigated. Jain and Patel (2016) studied 32 sorghum genotypes for yield and yield component traits reported existence of diversity in nine quantitative traits among the genotypes. The phenotypic coefficient of variability (PCV) was higher than genotypic coefficient of variability (GCV) for most of the traits investigated except for days to 50 % flowering and grain yield that both PCV and GCV maintain the same values. High (PCV %) and (GCV %) were observed in some of the characters studied. (Khandelwal et al., 2015) studied 224 genotypes of sorghum for genetic parameters and characters association among yield components, the result revealed that phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the traits investigated. For grain yield similar high broad sense heritability was reported by Jain and Patel (2012) who also found similar high heritability investigated in 102 land races of forage sorghum for 50 % flowering and other components. The clustering pattern showed that there was significant genetic variability among the accessions of sorghum tested, that means the presence of excellent opportunity to bring about improvement through hybridizing accessions from different clusters and assemble desirable traits with higher hetrotic potential.

It was discovered that most of the traits with positive relationship also have high heritability. Therefore characters like grain weight, days to 50 % flowering, days to 95 % maturity, length, panicle length and panicle width that have high heritability could be used in selection programme. Therefore for selecting plants for higher yield, days to 50 % should be considered. Cluster analysis provided an opportunity in the classification of accessions and identification of the subset of accessions having difference between yield and yield components.

CONCLUSION

The information about components of variance, broad sense heritability, genetic advance, cluster analysis in respect of sorghum yield and yield contributing traits obtained could be used as guide for the improvement of sorghum. It can also help farmers to select productive and profitable accessions. The most outstanding performance accessions for grain weight are AKV11 (kaura), followed by AKV9 (shawimpe) and AKV14 (farefare)

RECOMMENDATION

The following accessions; AKV11, AKV9 and AKV14 were recommended for Sorghum improvement programme and farmers in Southern guinea ecology of Nigeria.

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