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

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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 time. Results revealed that, there was wide variation among the genotypes. Genotype 11D-15-40 recorded a higher grain yield per plot (689.8g) in Kontagora while genotype 99K-57-3-2-1 recorded a higher grain yield per plot (282.7g) 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.

Keywords: Cowpea, Yield and Muli-location

INTRODUCTION

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, 2010). 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. 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. 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) 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 *et al.*, 2012).

MATERIALS AND METHOD

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. Twenty cultivars 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 used.

The experiment was laid out in a randomized complete block design (RCBD) with three replications. The plot size was 5m by 1m ($5m^2$)

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

RESULTS

Table 1. shows the mean value for phenotypic traits of 20 cowpea genotypes evaluated at Minna environment during 2017 cropping season. It was observed that, plant height was not significantly ($P \leq 0.05$) different among the genotypes. Numbers of branches ranged from 11 and 25 per plant with genotypes 12K-261 and 12K-487 produced more branches and 11D-24-40 produced fewer branches. Days to first flowering were not significantly different ($P \leq 0.05$) among genotypes. Pod length was significantly different ($P \leq 0.05$) among genotypes with IT10K-292-10 having a longer pod compared to genotype 07K-210-1-1 which recorded a shorter pod length. Number of pods per plant was significantly different ($P \leq 0.05$) among genotypes with 99K-57-3-2-1 having more pods than genotypes 04K-207-8, 09K-456 and IT10K-292-10 which recorded fewer pods. Leave area was not significantly different ($P \leq 0.05$) among genotypes. Number of seeds per pod was significantly different ($P \leq 0.05$) with genotype 12K-489 producing more seeds per pod, which is statistically similar to all of the genotypes except 07K-210-1-1 and 98K-1092-1 which had lower number lesser of seeds. Hundred grain weight was significantly different ($P \leq 0.05$) among genotypes with genotype IT10K-292-10 producing more weight and genotype 04K-207-8 and 12K-632 which recorded lower weights. Biomass weight was also significantly different. Genotype 12K-487 had a higher weight, which was statistically similar to genotype 11D-15-40, 12K-281, 12K-487, 12K-632 and TVU-408. All other were not significantly different. Total yield per plot was also significantly different with genotype 99K-57-3-2-1 having a higher yield however, genotype 10K-816-1, 11D-15-40 and IT10K-292-10 were observed to had lower yield.

Table 2. Shows the mean value for phenotypic traits of 20 cowpea genotypes evaluated at Kontogora environment during 2017 cropping. The results revealed that, Plant height was not significantly ($P \leq 0.05$) different among the genotypes at first branching, also, number of days to first flowering was not significantly ($P \leq 0.05$) different among genotypes. Number of branches were significantly ($P \leq 0.05$) different among the genotypes with 12K-689 producing more branches which is similar to all except 04K-207-8 and 07K-210-1-1 recording fewer branches. Pod length was significantly ($P \leq 0.05$) different among genotypes with 09k-480 having longer pods and IT10K-837-1 recorded shorter pods. Number of pods per plant was also significantly ($P \leq 0.05$) different among genotypes, which ranged from 7 and 23 pods per plant. Genotype IT10K-292-10 (23 pods) recorded the highest while 07K-210-1-1 (7 pods) recorded less. Leaf area was significantly different with variety 710K-292-10 having a wider leaf area which is statistically similar to most of the genotypes except for variety 11D-15-40 which recorded a lower leaf area. Number of seeds per pod was significantly different among genotypes with variety 12K-48-7 and 1710K-827-7 which had a higher number of seeds which is statistically similar to most of the genotype except for genotype 12K-632 and TVU-408 which recorded a lower number of seeds weight per pod. 100 grain weight were not significantly ($P \leq 0.05$) different among genotypes. Total yield per plot was significantly ($P \leq 0.05$) different among genotypes with 11D-15-40 having a higher yield compared to 07K-210-8 which recorded lower yield per plot. Also, biomass weight was significantly ($P \leq 0.05$) different among genotypes with 12K-487

recorded heavier biomass weight among genotypes and 04K-267-8, 07K-210-1-1, 98K-1092-1 and 100K-817-3 recording a lighter biomass weight.
Figure 1 is the result showing boxplot for Seed yield of Cowpea genotypes across the two environments. Kontagora environment recorded a higher mean performance than Minna environment. Also, the cowpea genotypes showed wider variability in Kontagora environment.

Figure 2 show the biplot for the best genotypes in each of the environment for seed yield in 2017 cropping season. 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-1092-1 and 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 1. The mean value for phenotypic traits of 20 cowpea genotypes evaluated at Minna environment during 2017 cropping season.

Genotypes	PHAFB	NB	DTFF	LA	NOSPP	NPPP	PL	100GW	BW	TYPP
04K-207-8	4.7^{a}	16^{abc}	39^{a}	17.3^{a}	8^{ab}	4^{b}	9.9^{ab}	9.4d^{e}	10.7^{b}	94.0^{abc}
07K-210-1-1	5.0^{a}	13^{bc}	38^{a}	17.1^{a}	7^{b}	8^{ab}	6.5^{b}	10.5^{abcde}	7.2^{b}	119.1^{abc}
08K-125-107	4.3^{a}	16^{abc}	39^{a}	21.4^{a}	9^{ab}	7^{ab}	10.7^{ab}	10.2^{abcde}	12.1^{b}	167.8^{ab}
08K-193-15	4.0^{a}	18^{abc}	41^{a}	10.2^{a}	10^{ab}	8^{ab}	12.3^{ab}	10.6^{abcde}	14.1^{b}	105.0^{abc}
09K-456	4.7^{a}	16^{abc}	40^{a}	15.9^{a}	11^{ab}	4^{b}	14.3^{ab}	10.3^{abcde}	15.4^{b}	105.0^{abc}
09K-480	5.3^{a}	17^{abc}	41^{a}	16.5^{a}	9^{ab}	7^{ab}	8.7^{ab}	10.7^{abcd}	17.5^{b}	92.6^{abc}
10K-816-1	4.3^{a}	16^{abc}	42^{a}	19.2^{a}	13^{ab}	5^{ab}	15.7^{ab}	11.0^{abc}	17.2^{b}	89.9^{bc}
11D-15-40	5.0^{a}	21^{ab}	40^{a}	11.0^{a}	14^{ab}	5^{ab}	16.7^{ab}	10.6^{abcd}	20.1^{ab}	61.9^{c}
11D-24-40	4.3^{a}	11^{c}	41^{a}	20.2^{a}	11^{ab}	9^{ab}	16.3^{ab}	10.8^{abcd}	19.0^{b}	127.8^{abc}
12K-261	5.0^{a}	25^{a}	48^{a}	11.6^{a}	14^{ab}	12^{ab}	13.3^{ab}	11.1^{abcd}	25.4^{ab}	202.9^{abc}
12K-487	3.7^{a}	24^{a}	47^{a}	21.2^{a}	12^{ab}	10^{ab}	15.7^{ab}	10.4^{abcde}	43.0^{a}	185.6^{abc}
12K-689	4.0^{a}	20^{abc}	36^{a}	17.2^{a}	15^{a}	5^{ab}	16.1^{ab}	9.7^{cde}	22.2^{ab}	123.8^{abc}
12K-632	4.3^{a}	17^{abc}	39^{a}	23.7^{a}	9^{ab}	8^{ab}	12.2^{ab}	9.2^{e}	25.0^{ab}	221.1^{abc}
TVU-408	5.0^{a}	21^{ab}	40^{a}	16.5^{a}	14^{ab}	9^{ab}	16.7^{ab}	10.6^{abcd}	20.5^{ab}	220.9^{abc}
IT10K-292-10	5.0^{a}	17^{abc}	40^{a}	23.4^{a}	14^{ab}	3^{b}	18.8^{a}	11.2^{a}	17.3^{b}	65.5^{c}
IT10K-827-7	4.3^{a}	19^{abc}	38^{a}	16.6^{a}	13^{ab}	7^{ab}	15.7^{ab}	10.2^{abcde}	19.0^{b}	125.5^{abc}
IT10K-837-1	5.7^{a}	13^{bc}	40^{a}	12.7^{a}	10^{ab}	9^{ab}	14.0^{ab}	10.1^{abcde}	17.3^{b}	276.1^{ab}
98K-1092-1	5.3^{a}	13^{bc}	41^{a}	12.3^{a}	7^{b}	8^{ab}	9.0^{ab}	10.6^{abcde}	11.4^{b}	141.8^{abc}
99K-57-3-2-1	4.0^{a}	18^{abc}	40^{a}	15.9^{a}	11^{ab}	13^{a}	13.2^{ab}	11.1^{ab}	13.0^{b}	282.7^{a}
100K-817-3	5.0^{a}	20^{ab}	40^{a}	15.6^{a}	14^{ab}	10^{ab}	14.7^{ab}	9.7^{bcde}	15.3^{b}	280.9^{ab}
SE±	0.1	0.6	0.5	0.9	0.5	0.6	0.7	0.1	1.6	13.6

Table 2. The mean value for phenotypic traits of 20 cowpea genotypes evaluated at Kontogora environment during 2017 cropping season.

Genotypes	PHAFB	NB	DTFF	LA	NOSPP	NPPP	PL	100GW	BW	TYPP
04K-207-8	4.7^{a}	16^{b}	39^{a}	18.2^{ab}	9^{ab}	8^{c}	13.1^{abc}	10.9^{a}	13.3^{b}	317.6^{abc}
07K-210-1-1	5.0^{a}	14^{b}	38^{a}	19.2^{ab}	11^{ab}	7^{c}	13.7^{abcd}	11.6^{a}	13.8^{b}	216.1^{c}
08K-125-107	4.3^{a}	18^{ab}	40^{a}	22.0^{ab}	9^{ab}	11^{c}	13.5^{abcd}	11.3^{a}	19.8^{ab}	251.4^{bc}
08K-193-15	4.0^{a}	20^{ab}	41^{a}	11.7^{b}	9^{ab}	10^{c}	14.4^{abcd}	11.1^{a}	24.2^{ab}	364.6^{abc}
09K-456	4.7^{a}	20^{ab}	40^{a}	16.7^{ab}	9^{ab}	15^{abc}	14.8^{abcd}	10.9^{a}	23.8^{ab}	401.9^{abc}
09K-480	5.3^{a}	17^{ab}	40^{a}	17.4^{ab}	11^{ab}	14^{abc}	17.5^{a}	11.6^{a}	20.1^{ab}	379.7^{abc}
10K-816-1	4.3^{a}	19^{ab}	42^{a}	21.3^{ab}	11^{ab}	21^{ab}	13.8^{abcd}	11.3^{a}	24.5^{ab}	540.3^{abc}
11D-15-40	5.0^{a}	20^{ab}	41^{a}	11.3^{b}	11^{ab}	15^{abc}	13.6^{abcd}	11.3^{a}	23.3^{ab}	689.8^{a}
11D-24-40	4.3^{a}	21^{ab}	41^{a}	20.3^{ab}	11^{ab}	13^{bc}	11.5^{cd}	11.2^{a}	27.8^{ab}	361.3^{abc}
12K-261	5.0^{a}	20^{ab}	38^{a}	12.3^{ab}	12^{ab}	15^{abc}	12.2^{cd}	10.8^{a}	32.1^{ab}	555.9^{abc}
12K-487	3.7^{a}	23^{ab}	38^{a}	22.7^{ab}	14^{a}	14^{abc}	12.3^{cd}	10.2^{a}	47.2^{a}	446.7^{abc}
12K-689	4.0^{a}	26^{a}	36^{a}	21.4^{ab}	12^{ab}	15^{abc}	14.7^{abcd}	10.4^{a}	24.8^{ab}	359.8^{abc}
12K-632	4.3^{a}	20^{ab}	39^{a}	19.7^{ab}	8^{b}	11^{c}	14.9^{abcd}	10.8^{a}	29.3^{ab}	411.4^{abc}
TVU-408	5.0^{a}	23^{ab}	37^{a}	17.9^{ab}	7^{b}	14^{abc}	14.2^{abcd}	11.5^{a}	17.6^{ab}	502.9^{abc}
IT10K-292-10	5.0^{a}	21^{ab}	40^{a}	27.7^{a}	11^{ab}	23^{a}	12.2^{cd}	10.8^{a}	26.9^{ab}	499.3^{abc}
IT10K-827-7	4.3^{a}	25^{ab}	37^{a}	19.2^{ab}	14^{a}	17^{abc}	17.2^{ab}	10.4^{a}	29.1^{ab}	540.9^{abc}
IT10K-837-1	5.7^{a}	21^{ab}	41^{a}	12.9^{ab}	12^{ab}	13^{abc}	10.4^{d}	11.1^{a}	21.6^{ab}	293.2^{bc}
98K-1092-1	5.3^{a}	22^{ab}	41^{a}	13.6^{ab}	9^{ab}	12^{bc}	11.6^{cd}	11.6^{a}	13.5^{b}	282.6^{bc}
99K-57-3-2-1	4.0^{a}	19^{ab}	41^{a}	15.8^{ab}	12^{ab}	15^{abc}	12.2^{cd}	11.8^{a}	16.5^{ab}	425.1^{abc}
100K-817-3	5.0^{a}	24^{ab}	40^{a}	15.9^{ab}	12^{ab}	16^{abc}	12.2^{abc}	10.3^{a}	15.5^{b}	585.0^{ab}
SE±	0.1	0.7	0.5	0.9	0.4	0.7	0.3	0.1	1.9	24.2

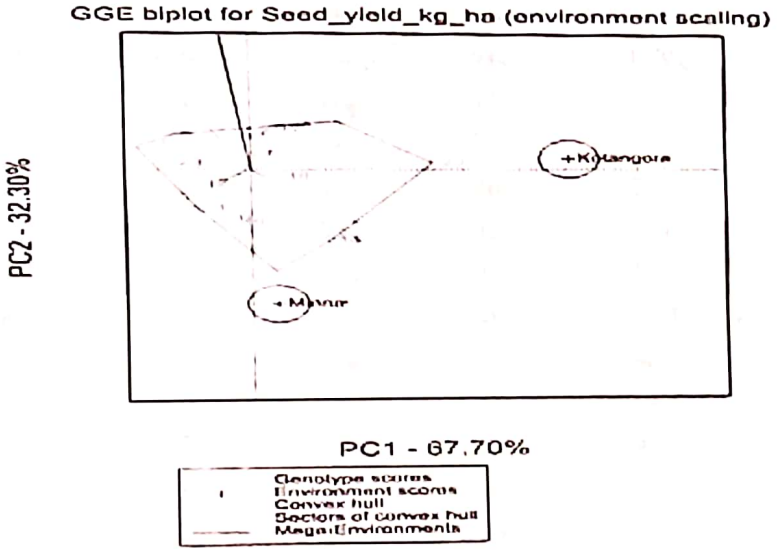

Figure 2. Genotype plus genotype-by-environment interaction (GGE) biplot sectors for seed yield (environment scaling) in 2017 cropping season.

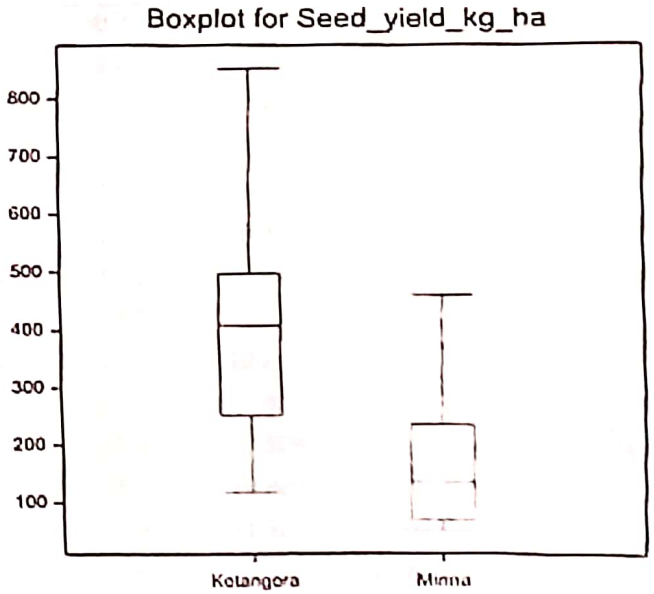

Figure 1. Boxplot for seed yield (kg ha^{-1}) from cowpea genotypes in 2017 cropping season across environments

DISCUSSION

The results from this studied indicated a 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 [illegible] flowering for variety 'Oloyin'. Furthermore, Ishiyaku and Singh (2003) reported a range of 36 [illegible] 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 (17.5 cm) and IT10K-292-10 (18.8 cm) 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) in IT10K-292-10 in Minna and (10.2 g) in 12K-487 to (11.8 g) in 99K-57-3-2-1 in Kontogora environment. This result was similar to those of Egbe *et al.*, (2010). 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 was recorded in genotype 12K-487 in both locations. This might be due to the large size of the leaves and number of branches. This indicated that this genotype showed 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.

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 possessing favourable vegetative traits and these genotypes 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 area. These lines are recommended for further evaluation across environments.

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