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VARIABILITY AMONG SOME ACCESSIONS OF COWPEA (*VIGNA UNGUICULATA* L. Walp) IN NIGERIA BASED ON THE EXPRESSION OF QUANTITATIVE TRAITS

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ABSTRACT

A Field experiment was conducted to examine genetic variability, heritability, correlations and genetic advance using 10 accessions of cowpea. 13 quantitative characters of (100-seed weight, terminal leaflet length, terminal leaflet width, number of main branches, number of nodes on main stem, number of pods per peduncle, peduncle length, number of pods per plant, pod length, plant height, pod weight, number of seeds per pod and number of leaves per plant) were measured during the rainy season of 2012. Analysis of variance (ANOVA) showed significant differences among the accessions for all the traits studied except number of pods per plant which showed the highest level of coefficient of variation (CV). Genotypic and phenotypic coefficients of variation were highest for peduncle length, plant height and number of nodes. High broad sense heritability for seed weight, peduncle length, plant height, pod weight and terminal leaflet width coupled with high genetic advance as per cent of mean values, showed that the crop could be improved by selecting these characters. Positive correlations that existed among the variables implied typical association among the tested traits.

Key words: Cowpea, Variability, Heritability, Quantitative traits, Genetic Advance, Nigeria

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp), is an important food legume widely distributed throughout the tropics and sub tropics (Uarrotta, 2010), especially in sub-Saharan Africa, Asia, and Central and South America (Singh *et al.*, 1997). The wild forms are endemic to Africa (Zannou *et al.*, 2008). The cowpea is a principal source of protein for the rural and urban people (Ileke *et al.*, 2013). In Africa, the crop is grown for its young leaves and seeds which are used as meals for both rural and urban population (Zannou *et al.*, 2004). According to Diouf (2011) cowpea feeds millions of people in the developing world with annual world production estimated at 4.5 million metric tonnes on 12 to 14 million hectares. Cowpea production is unstable yearly and according to FAO (2009), world production of its dry seed is estimated to be 5.3

million tons per year. Nigeria produced 2.4 million tonnes in 2009, followed by 1.6 million tons from Niger and 105,376 tonnes from Mali. Nigeria is ranked to be the largest producer of cowpea seeds in the world worldwide (FAO, 2009). Most varieties of cowpea cultivated in Nigeria were developed from land races which are photo-periodically sensitive in addition to poor yields. Grain and fodder production from cowpea have been inconsistent due to genotypic sensitivity of the crop (Mukhtar and Singh, 2006; Umar *et al.*, 2010), poor edaphic environmental condition, excessive or inadequate moisture, inappropriate cultural practices, pests, diseases and poor genetic potentials of most varieties. Factors for improving a particular crop include understanding of the genetic potential of genotypes, stability of the desirable trait in environments and the relationship among

Table 1: List of Tested Accessions

CODES	ACCESSIONS
A1	NG/SA/DEC/07/0309
A2	NG/SA/07/1057
A3	NGB/06/0055
A4	NG/SA/07/0113
A5	NG/SA/07/1066-1
A6	NG/SA/07/0098
A7	NG/AO/11/08/0121
A8	NG/SA/07/0063
A9	NGB/06/0057
A10	NG/AO/11/08/0083

quantitative traits. Building a detailed breeding technique on these would help in selection of genotypes (Adeigbe *et al.*, 2011).

Before embarking on improvement programme on any crop species, a thorough understanding of the level of genetic variability existing for various characters is important. For yield enhancement, and choice of good characters for selection of desirable genotypes under planned breeding programme, the knowledge of nature and magnitude of variation existing among available plant materials, the association of component characters with yield and their exact contribution to yield expression are desirable. The components of variation, heritability and genetic advance have been derived for different yield characters in cowpea (Omoigui *et al.*, 2006; Mangoel *et al.*, 2012). This revealed that selection is effective for a population with broad genetic variability and characters with high heritability.

Correlation analysis serves as a useful technique and source of information which proves that selection for one character results in progress for other positively correlated characters. Correlation studies in selection programmes, is appreciable when highly heritable characters are associated with important character like yield (Bizeti *et al.*,

2004). The objectives of this study, therefore, are to estimate the genetic variability and association of characters among cowpea accessions with the intention of identifying the desirable accessions suitable for breeding programmes.

MATERIALS AND METHODS

Plant materials

The 10 accessions used in this study were collected from the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Nigeria. The names of the accessions are given in Table 1.

Experimental conditions

The study was carried out at the Experimental Field of the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba-Akoko (Lat. 7° 28’N; Long 5°44’E, Altitude 423 above sea level), during the rainy season of 2012 (between 25th June and 10th November). The 10 accessions used in the study were planted on the field laid out in a Randomized Complete Block Design with three replications. Each accession was regarded as a treatment by planting unit in rows with each treatment consisting of 20 plants, totaling 600 plants in the field of a spacing of 50 by 30 cm and 1m between treatments. Weeding was done as and when required.

Data collection and analysis

Data on morphological and agronomical characters (at eight weeks after planting and at maturity respectively) were collected from 10 randomly selected plants and their means were recorded for all observations. Data for all variables measured were subjected to analysis of variance (ANOVA) to estimate the level of variability among the cowpea accessions, using SPSS Windows Version 16 (SPSS, Inc., Chicago IL). The phenotypic variation for each trait was partitioned into genetic and non-genetic factors and estimated according to the methods of Johnson *et al.* (1955) and Uguru (2005):

$$V_p = MS_g/r \dots\dots\dots eq. 1$$

$$V_g = (MS_g - MS_e)/r \dots eq. 2$$

where V_p and V_g are phenotypic variance and genotypic variance respectively; MS_g , MS_e and r are mean squares of accessions, mean square error and number of replications respectively.

To compare the variations among traits, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were

computed according to the methods of Burton (1952) and Allard (1960):

$$PCV = (\sqrt{V_p}/X) 100 \dots \text{eq. 3}$$

$$GCV = (\sqrt{V_g}/X) 100 \dots \text{eq. 4}$$

where X is the grand mean for each of the studied traits. Broad sense heritability (h^2B) was calculated according to Burton and DeVane (1953) and Allard (1960) as the ratio of the genotypic variance (V_g) to the phenotypic variance (V_p)..... eq. 5

Correlation coefficients analysis was conducted among the measured traits. Genetic advances and Duncan multiple range tests were computed among all the measured traits. Thirteen [13] quantitative traits were measured using the International Board for Plant Genetic Resources (IBPGR) cowpea descriptors. The quantitative traits are 100-seed weight (g), Terminal leaflet length (cm), Terminal leaflet width (cm), Number of main branches, Number of nodes on main stem, Number of pods per peduncle, Peduncle length (cm), Number of pods per plant, Pod length (cm), Plant height (cm), Pod weight (g), Number of seeds per pod and Number of leaves per plant.

RESULTS

The traits studied exhibited very high level of uniformity due to their low coefficient of variations (Table 2). Analysis of variance showed that the mean squares for the accessions were highly significant for all traits measured except the number of pods per plant. A wide range significant variations were observed in plant height (15.75cm to 21.41cm), peduncle length (14.22cm to 21.56cm) and seed weight (16.99g to 29.49g) (Table 2). Phenotypic variance was higher than genotypic variance in all the traits studied, similarly the phenotypic coefficients of variation (PCV) was higher than genotypic coefficient of variation (GCV) in all the traits studied, and GCV values ranged from 3.92% (number of pods per peduncle) to 30.86% (peduncle length) (Table 3). The values of PCV and GCV were low for number of pods per peduncle, number of seeds per pod, number of leaves, terminal leaflet length, pod length and number of main branches. The values of PCV and GCV were moderate for terminal leaflet width, number of nodes, pod weight, number of pods per plant and seed weight whereas PCV and GCV

were high for peduncle length and plant height. These range of values of PCV and GCV for measured traits indicate a high level of genetic variability for these traits. In order to draw conclusions on the level of genetic variability, in addition to GCV values; heritability and genetic advance as per cent of mean estimates were computed. Heritability values for the studied traits ranged from 4% for number of pods per plant to 99% in seed weight (Table 3). High heritability estimate was recorded for seed weight (99%), peduncle length (96%) plant height (94%), pod weight (76%), number of pods per plant (70%) and terminal leaflet width (61%) (Table 3). High genetic advance as per cent of means were recorded for peduncle length (62%), plant height (47%), seed weight (27%), number of pods per plant (28%) and pod weight (25%); moderate for terminal leaflet width (19%), number of nodes (18%), pod length (12%) and terminal leaflet length (11%) (Table 3). The simple correlation among measured traits showed; number of pods per peduncle to be positively correlated with number of seeds per pod (0.215), peduncle length (0.252) and pod weight (0.246). Number of seeds was positively correlated with pod weight (0.654), pod length (0.485) and peduncle length (0.250). Peduncle length had positive correlation with terminal leaflet length (0.390), pod length (0.383), terminal leaflet width (0.334), pod weight (0.272) and number of leaves (0.227). Number of nodes on main stem had positive correlation with number of main branches (0.981), number of leaves (0.941), terminal leaflet length (0.309), and terminal leaflet width (0.314) and plant height (0.303). Terminal leaflet width had positive correlation with terminal leaflet length (0.747), plant height (0.403), pod length (0.353), number of leaves (0.338) and number of main branches (0.301). Terminal leaflet length had positive correlation with plant height (0.373), number of leaves (0.351), pod length (0.314) and number of main branches (0.308). Number of leaves showed positive correlation with number of main branches (0.952) and plant height (0.356). Pod length showed positive correlation with plant height (0.479) and pod weight (0.325). Number of main branches showed positive correlation with plant height (0.360) (Table 4).

Table 2: Mean values of thirteen quantitative characters among the tested cowpea accessions

Accessions	TLL (cm)	TLW (cm)	MB	NMS	PH (cm)	NL	PDL (cm)	PPD	NPP	SP	PW (g)	PODL (cm)	SW (g)
A1	12.79±0.49a	7.20±0.19a	6.60±0.35ab	6.60±0.35ab	16.44±0.11a	14.60±0.62ab	20.95±0.67e	1.27±0.12b	2.40±0.24a	8.27±0.34ab	2.90±0.11bc	12.49±0.49ab	29.46±0.43e
A2	11.83±0.38ab	7.17±0.18a	5.87±0.40a	5.87±0.40a	15.75±0.13a	12.87±0.78a	15.69±0.31bc	1.20±0.11ab	2.33±0.25a	8.73±0.37b	2.89±0.10bc	12.47±0.33ab	23.47±0.24bc
A3	12.49±0.33b	8.57±0.34c	6.93±0.32ab	6.93±0.32ab	16.50±0.09a	14.93±0.69ab	17.12±0.37d	1.13±0.10ab	2.53±0.30a	8.40±0.32b	2.86±0.09bc	12.58±0.40ab	24.10±0.63c
A4	11.83±0.32ab	7.49±0.21ab	5.93±0.34ab	5.93±0.34a	16.55±0.09a	13.93±0.37ab	17.41±0.24d	1.13±0.10ab	2.13±0.26a	8.13±0.43ab	2.74±0.11ab	12.21±0.47ab	23.44±0.11bc
A5	12.41±0.40b	7.62±0.30abc	5.73±0.60a	5.73±0.61a	16.77±0.07a	12.93±1.10a	17.18±0.29d	1.13±0.10ab	2.33±0.23a	7.93±0.30ab	2.95±0.07bc	12.25±0.45ab	21.99±0.11b
A6	11.61±0.32ab	7.53±0.24abc	6.33±0.34ab	6.33±0.35ab	18.43±0.30b	13.47±0.69ab	14.77±0.27ab	1.27±0.12b	2.47±0.29a	8.00±0.40ab	3.13±0.05c	12.35±0.46ab	29.20±1.00e
A7	12.73±0.56b	7.85±0.39abc	6.67±0.41ab	6.60±0.43ab	20.54±0.14cd	14.40±0.74ab	15.99±0.21bcd	1.13±0.10ab	2.57±0.26a	8.53±0.32b	2.30±0.03a	13.47±0.35b	17.35±0.13a
A8	10.82±0.85a	7.07±0.59a	6.80±0.60ab	6.80±0.60ab	19.52±1.40bc	14.27±1.22ab	14.22±1.05a	0.98±0.10a	2.20±0.28a	7.07±0.61a	2.95±0.21bc	11.76±0.88a	26.76±0.48d
A9	12.65±0.34b	8.10±0.33abc	7.40±0.52b	7.73±0.43b	21.41±0.12d	15.80±1.07b	16.39±0.12cd	1.07±0.10ab	2.59±0.31a	8.13±0.47ab	2.47±0.03a	13.67±0.21b	16.99±0.13a
A10	12.59±0.5b	8.47±0.36bc	6.33±0.52ab	6.33±0.52ab	18.88±0.57b	14.47±1.00ab	21.56±0.39e	1.13±0.10ab	1.93±0.18a	8.13±0.29ab	2.90±0.09bc	13.69±0.33b	26.63±0.83d
CV (%)	4.90	6.50	2.40	8.60	29.00	6.40	14.10	7.00	8.97	5.40	9.00	5.30	18.00

Means followed by the same alphabet within a column are not significantly different from one another at $P \leq 0.05$ using Duncan Multiple Range Test (DMRT)

CV = coefficient of variation, Values are means of measurements \pm S.E.

PDL= peduncle length, TLL= terminal leaflet length, TLW= terminal leaflet width, MB= number of main branches, PPD= number of pods per peduncle, NMS= number of nodes on main stem, NPP= number of pods per plant, SP= number of seeds per pod, PW= pod weight, PH= plant height, PODL= pod length and NL= number of leaves, SW= seed weight.

Table 3: Mean, GCV, PCV, heritability and genetic advance as per cent of mean for thirteen characters of ten cowpea accessions

Character	Mean	VP	VG	PCV (%)	GCV (%)	GAM (%)	h ² (%)
Plant height	18.08	19.14	17.89	24.20	23.39	46.59	93.47
No of main branches	6.48	1.38	0.34	18.18	9.03	9.22	24.64
Pod weight	2.81	0.21	0.16	16.19	14.13	25.42	76.19
Pod length	12.69	2.23	1.13	11.74	8.29	12.25	50.67
Seed weight	23.94	5.19	5.09	9.52	9.42	26.77	98.95
Number of Leaves	14.17	4.10	0.39	14.30	4.41	2.80	9.51
Terminal leaflet length	12.17	2.02	0.89	11.70	7.75	10.59	44.10
Terminal leaflet width	7.71	1.41	0.86	15.40	12.03	19.35	60.99
No of nodes	6.49	1.77	0.77	20.50	13.52	18.35	43.55
No of pods/plant	2.34	0.20	0.14	19.11	16.10	27.56	70.00
Peduncle length	17.13	29.03	27.94	31.45	30.86	62.36	96.25
No of seed/pod	8.13	1.00	0.22	12.30	5.77	5.57	22.00
No of pod/peduncle	1.14	0.05	0.002	19.61	3.92	1.62	4.00

VG: Genotypic variance; VP: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h²: Heritability; GAM: Genetic advance as per cent of mean

Table 4: Correlation co-efficient of thirteen quantitative characters of ten cowpea accessions

Variables	PH	MB	PODW	PODL	SW	NL	TLL	TLW	NMS	NPP	PEDL	SP	PPD
PH	1.000												
MB	0.360**	1.000											
PODW	0.185*	0.165*	1.000										
PODL	0.479**	0.146	0.325**	1.000									
SW	-0.211	0.450	0.460	-0.430	1.000								
NL	0.356**	0.952**	0.164*	0.199*	0.037	1.000							
TLL	0.373**	0.308**	0.133	0.314**	0.042	0.351**	1.000						
TLW	0.403**	0.301**	0.182*	0.353**	0.087	0.338**	0.747**	1.000					
NMS	0.302**	0.981**	0.158	0.159	0.037	0.941**	0.309**	0.314**	1.000				
NPP	0.146	0.116	0.016	0.022	-0.019	0.157	0.570	0.490	0.122	1.000			
PEDL	0.141	0.137	0.272**	0.383**	-0.014	0.227**	0.390**	0.334**	0.133	-0.008	1.000		
SP	0.180*	0.129	0.654**	0.485**	-0.071	0.149	0.188*	0.116*	0.143	-0.210	0.250**	1.000	
PPD	-0.008	-0.48	0.246**	0.038	-0.008	-0.030	0.183*	0.076	-0.054	0.126	0.252**	0.215**	1.000

** . Correlation is significant at the 0.01 level (2-tailed).

* . Correlation is significant at the 0.05 level (2-tailed).

PDL= peduncle length, TLL= terminal leaflet length, TLW= terminal leaflet width, MB= number of main branches, PPD= number of pods per peduncle, NMS= number of nodes on main stem, NPP= number of pods per plant, SP= number of seeds per pod, PW= pod weight, PH= plant height, PODL= pod length and LN=number of leaves, SW= seed weight.

DISCUSSION

The mean square values among the studied traits differed significantly except for number of pods per plant; this suggests inherent genetic variability among the cowpea accessions. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits studied; this implies the combination of environmental and genetic factors. Similar results have been reported by other researchers in vegetable crops, roselle and cowpea respectively (Vijayan, 2005; Ibrahim and Hussein 2006, Adewale *et al.*, 2010 and Adeigbe *et al.*, 2011).

Peduncle length, plant height and number of nodes showed the highest values of phenotypic and genotypic coefficient of variations, this indicates the presence of broad genetic base among the accessions for these characters rather than environmental (Kaushik *et al.*, 2007; Adewale *et al.*, 2010). The moderate genotypic coefficient of variation observed in traits like seed weight, number of pods per plant, pod weight, number of nodes and terminal leaflet width show the presence of moderate variability among the genetic stock studied (Vijayan, 2005). These results agreed with those of Adewale *et al.* (2010) for seed weight and number of pods per plant in cowpea (Manju and Streelathalkumary, 2002) for seed weight in chilli pepper. The low genotypic coefficients of variation observed in traits like number of main branches, pod length (cm), terminal leaflet length (cm), number of seeds per pod, number of leaves per plant and number of pods per peduncle show that these characters may be responsive for improvement through selection (Vijayan, 2005). The closeness of phenotypic and genotypic coefficients of variation with respect to the characters studied, suggest partial environmental effect on these characters and this may make selection for them effective.

Moderate to high heritability in almost all the traits studied shows that the traits are less influenced by environmental effects, which makes them effectively transmitted to the progeny. For heritability estimates to be reliable, it must be accompanied by high genetic advance (Ibrahim and Hussein, 2006). High estimates of

heritability in peduncle length, seed weight, plant height, pod weight, number of pods per plant and terminal leaflet width, coupled with their high genetic advance as percent of mean (GAM) indicate additive gene effects, and suggest that effective progress in improvement through selection could be achieved for yield. These results are in agreement with several workers on other crops (Munshi and Behera, 2000; Vijayan, 2005; Ibrahim and Hussein, 2006). Moderate heritability coupled with moderate genetic advance as percent of mean (GAM) observed in terminal leaflet length and number of nodes indicate that fair degree of improvement could be achieved for these traits through selection (Amarchand *et al.*, 1990; Vijayan, 2005). Number of seeds per pod, number of leaves per plant and number of peduncles showed low heritability and GAM, indicating that the traits are highly influenced by environmental effects, a condition which may make selection for them ineffective.

The positive correlations among the measured characters obtained in this study would be of interest for breeding objectives. The study also identified that a group of accessions, namely; A1, A2, A3, A6, A7, A9 and A10, were different from others in some important characters such as high number of seeds per pod, pod length, plant height, seed weight and number of pods per plant. These accessions can be used for further cowpea improvement programmes through cross breeding.

It is concluded that high level of genetic variability based on the observed traits among the tested accessions would be useful for breeding varieties of cowpea with high yield. Therefore, high heritability estimates and genetic advance as percent of mean (GAM) coupled with positive correlations in various characters should be taken into consideration during selection for higher yield in cowpea.

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