

Genotypic Variability for Agronomic and Yield Characters in Some Cowpeas (*Vigna unguiculata* (L.) Walp.)

D. O. Idahosa¹ J. E. Alike² and A. U. Omoregie¹

1. Department of Crop Science, Ambrose Alli University, Ekpoma, Nigeria

2. Department of Crop Science, University of Benin, Nigeria.

E-mail: danielidahosa@yahoo.com

Abstract: Cultivated species of crops are usually variable because of artificial selection under diverse environments of which cowpea is not exception. Consequently, genotypic variability study was conducted with eight parent line cowpeas to evaluate some genetic parameters namely coefficient of variation, genetic variance and heritability estimates in the broad-sense. Per se mean performance was variable among the genotypes for all characters investigated which indicated the superiority of some parent lines. Highly significant heritability effects were observed for all characters except for 100-seed weight (42.2%) which expressed moderate heritability estimate. Days to 50% flowering, pod length, pod weight and grain yield characters showed that some levels of genetic variability existed. Consequently, progress could be made from selection and improvement for those characters. [Nature and Science 2010;8(3):48-55]. (ISSN: 1545-0740).

Keywords: Genotypic variability, genetic variance, coefficient of variation, heritability, cowpea.

1. Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is one of six major cultivated crop species of the family *leguminosae* distributed throughout the tropics (Padulosi and Ng, 1997; Pasquet, 2001). It is the second most important grain legume crop after groundnut as well as second only to cereals (Blade *et al.*, 1997). Millions of relatively poor people in developing countries in the tropics rely on it for their livelihood. This is because there is a chronic-protein deficiency in every home in virtually every developing country. Hence, it is a key staple food crop for the ever increasing population both in the rural and urban areas. Because the cowpea is native to West Africa where wild and weedy forms exist in many parts of the region (Ng and Marechal, 1985), it is one of the most variable species and genetic variability is the basis of genetic enhancement (Singh, 2003).

Cultivated species of crops are usually variable because of artificial selection under diverse environments of which cowpea is not exceptional. Moreover, genetic variability among characters is of

vital importance in selecting the desirable genotypes for breeding programmes. Parental selection for cowpea improvement requires knowledge of the likelihood of improving characters of interest based on the amount and type of genetic control of the character(s). The amount of control is influential because improvement of a character with very small genetic control relative to environmental influences will be difficult due to heritability (Ragsdale and Smith, 2003).

Heredity is generally expressed as the proportion of the observed total variability that is genetic. In other words, selection of superior genotypes is proportional to the amount of genetic variability (Obilana and Fakorede, 1981). Thus, heritability serves as a guide to the reliability of phenotypic variability in any selection programme and hence determines its success (Hamdi, 1992). As a result, the present study is targeted at estimating genotypic variability and heritability of agronomic and yield characters in eight parent line cowpea genotypes as this will assist in providing useful information in a breeding work.

2. Materials and Methods

From twenty-eight germplasm screened, eight seemingly hopeful lines based on per se performance in two earlier experiments were selected to serve as parent lines (Table 1) and used in this study. The experiment was carried out at two locations viz Rubber Research Institute of Nigeria, Iyanomo, near Benin (Lat. 6° 09' 24" , Long. 5° 31' 27" E, Alt. 304.8m) and the Teaching and Research Farm, Ambrose Alli University, Ekpoma (Lat. 6° 08' E, Long. 6° 42' N, Alt. 460m). The eight genotypes were sown to the field under rainfed condition in a randomized complete block design (RCBD) in three replicates on 12th and 28th April 2008, respectively. Plots consisted of 5m long single rows. Seeds of each entry were sown at 30cm intra- and 60cm inter-rows spacing with one seed per stand. All agronomic and plant protection practices were followed.

Data were recorded from 5 randomly selected plants from the 3m-mid rows of each replicate on plant height, LAI, days to 50% flowering, 50% maturity, pod length, pod weight, seeds per pod, seed weight and grain yield. Data were subjected to ANOVA using SAS

software model. Means separation was performed with Student-Newman-Keuls Test, coefficient of variation, genetic variance using the formula.

Pooled locations

$$\sigma^2 g = \frac{MSg - MSg \times e}{r \times \ell}$$

Where,

$\sigma^2 g$ = Genetic variance;

MSg = Mean square of genetic variance;

MSg x e = mean squares of genetic and error variances;

$r \times \ell$ = replicate by location

Broad-sense heritability for pooled data over locations was estimated as described by Ekekebil *et al* (1977). Thus, for pooled locations

$$h^2 b(\%) = \frac{\sigma^2 g}{\sigma^2 g + \frac{\sigma^2 g \times \ell}{\ell} + \frac{\sigma^2 e}{rl}} \times 100$$

Where, $\sigma^2 g$ is genetic variance; $\sigma^2 e$ is the error variance; ℓ is the locations; rl is replicate \times location; $\sigma^2 g \times \ell$ is the variance due to genotype by location.

Table 1. Name, pedigree and geographic origin of the eight cowpea genotypes

Entry	IITA –Prefix Genotype	Pedigree Name	Origin
1	TVu-1120	Dan-Tamanin	Nigeria
2	TVu-1153	325	USA
3	TVu-1157	53C	South Africa
4	TVu-16627	ILCA-12646	Not available
5	TVu-16629	ILCA-12648	Not available
6	TVu-16630	ILCA-12665	Not available
7	TVu-1242	53-C-82	South Africa
8	Ekp-br.		Ekpoma brown(local cultivar)

3. Results

The pooled analysis showed significant variations for location, genotypes for all characters and genotype–environment interaction for days to 50% flowering, pod length and 100–seed weight. Mean performance of the different parental lines indicated variations for all characters studied (Table 2). Highest plant height was observed in parent line *TVu*–16627 (74.73cm) followed by *TVu*–16630 (64.47cm) and *Ekp.*–*br.* (47.73cm). Similarly, *TVu*–16627 had the largest leaf area index (LAI) value of 4.19, followed by *Ekp.*–*br.* (3.81) and *TVu*–1153 (3.23). For days to 50% flowering, parent line *TVu*–16629 had longer days of 57.17 and closely followed by *Ekp.*–*br.*, *TVu*–1120 and *TVu*–1157 with 50.33, 48.17 and 45.50 days respectively. Similar trends was observed for days to 50% maturity with the longest days occurring in parent line *TVu*–16629 (73.33), followed by *Ekp.*–*br.* (68.00), *TVu*–1153 (66.00), *TVu*–1120 (65.67) and *TVu*–1157 (64.67).

Pod length also revealed significant differences among the parent genotypes. *Ekp.*–*br.* (18.85cm) had the longest pod

length and followed by *TVu*–16627 (16.83cm) while least pod length was observed in *TVu*–1242 (10.57cm). Pod weight also followed the same trend as in pod length among the genotypes. Parent line *Ekp.*–*br.* had the heaviest pod weight (2.42g) and followed by *TVu*–16627 (2.07g) while the least pod weight also occurred in *TVu*–1242 (0.88g)(Table 2). Highest mean number of seeds per pod was observed in parent line *TVu*–16629 (14.47), *Ekp.*–*br.*(13.90) and *TVu*–16627 (12.05). However, only parent genotype *Ekp.*–*br.* (13.40) had the highest seed weight. The highest grain yield (1131.1Kg/ha) as compared to other parent lines was recorded in *TVu*–16627 (Table 2).

There were large variations in coefficient of variation and genetic variance in all characters evaluated (Table 3). Highest genetic variance was found in seed yield (57977.5). In all characters, high heritability was observed except for 100–seed weight which was moderately inherited (42.2%).

Table 2: Per se mean values of nine characters in eight parent line cowpea genotypes evaluated over pooled location

Genotype	C H A R A C T E R S								
	Plant ht(cm)	Leaf Area Index (LAI)	50% Flowering	50% Maturity	Pod length (cm)	Pod weight (g)	Seeds per Pod	100- seed wt. (g)	Grain Yield (Kg/ha)
<i>TVu-1120</i>	30.7	1.57	48.17	65.67	14.35	1.19	10.13	8.97	432.8
<i>Ekp.-br.</i>	47.73	3.81	50.33	68.00	18.85	2.42	13.90	13.40	353.5
<i>TVu-1153</i>	39.10	3.23	42.33	66.00	13.47	1.27	7.45	11.75	274.3
<i>TVu-16627</i>	74.73	4.19	43.67	63.50	16.83	2.07	12.05	11.15	1131.1
<i>TVu-1157</i>	31.17	0.83	45.50	64.67	11.55	1.00	8.77	9.57	136.6
<i>TVu-16629</i>	36.57	1.39	57.17	72.33	14.2	1.98	14.47	11.02	389.2
<i>TVu-1242</i>	36.72	2.74	44.67	63.00	10.57	0.88	6.95	10.20	77.8
<i>TVu-16630</i>	64.47	2.70	43.50	62.67	13.05	1.46	10.97	9.05	203.1
Mean	45.148	2.55	46.917	65.729	1.397	1.534	10.585	10.64	375.28
LSD(0.05)	14.024	1.58	3.95	4.38	1.4	0.41	2.14	1.26	5.85

Table 3. Percentage values of coefficient of variation (CV), genetic variance (σ^2g) and heritability in broad-sense (h^2b) of nine agronomic and yield characters in cowpea genotypes over pooled locations

Character	CV	σ^2g	h^2b
Plant height (cm)	26.27	0.001	89.9
Leaf area index (LAI)	52.41	0.01	98.9
Days to 50% flowering	7.12	1.68	81.9
Days to 50% maturity	5.63	0.44	84.7
Pod length (cm)	8.37	2.21	87.6
Pod weight (g)	22.65	1.56	95.9
Seeds per pod	17.10	0.39	90.7
100-seed weight (g)	9.99	0.24	42.2
Grain yield (Kg/ha)	105.1	57977.5	53.8

4. Discussion

The present study revealed significant genotypic differences in mean plant height and LAI characters among the parent genotypes. Memon *et al.*, (2005) reported that the expression of a trait depended on its genetic control and in this case, among the parent lines used in this study. Moreover, the large variability evident among the genotypes for LAI character also revealed significant differences in mean leaf area development which may be due to increased meristematic activity which would have enhanced leaf expansion (Nalayini and Kandasamy, 2003). Previous studies had reported high heritability in the broad-sense in cowpea for plant height character (Sharma and Singhanian, 1992; Tyagi *et al.*, 2000); LAI (Roquib and Patnaik, 1990; Sharma and Singhanian, 1992). Thus, this study is in conformity with earlier findings for the characters being investigated. A negligible genetic variability was estimated for plant height and LAI indicating that environmental influence affected the expression of these characters.

Days to 50% flowering and 50% maturity revealed narrow mean differences among the genotypes studied for the characters. Earliness has been reported to

be an important agronomic character measured by such criterion as days from sowing to maturity (Fery and Singh, 1997). Parental genotype *TVu-16630* had the least number of days to reach maturity with a delay in days to 50% maturity in *TVu-16629*. In cowpea, the post flowering (maturity) is a major difference between the two maturity groups (early and late) because of the striking difference in grain-filling periods. Flowering and maturity characters showed high heritability effects. The high heritability estimates observed in this study for both characters confirmed earlier findings (Siddique and Gupta, 1991; Tyagi *et al.*, 2000). Low genetic variance for days to 50% flowering with a negligible genetic effect on days to 50% maturity was observed indicating the presence of much environmental factors in the characters expression.

The mean pod length varied widely among the genotypes. However, two parent line genotypes *Ekp.-br.* and *TVu-16627* had much longer pods when compared to others thus indicating the presence of genetic variability for the character. Thus, the study revealed some measure of genetic variance indicating that the character was genetically controlled

and could be selected for in improvement programme. High heritability was observed in this study which also confirmed earlier reports in cowpea (Siddique and Gupta 1991; Tyagi *et al.*, 2000). The per se mean performance of the different genotypes indicate some measures of different genetic constitution. Genotypes *Ekp.-br.* and *TVu-16627* were outstanding in pod weight character when compared to others. High broad-sense heritability estimate was obtained in earlier findings (Ogunbodede and Fatunla, 1985; Pathmanathan *et al.*, 1997). A relatively low estimate of genetic variance was observed for pod weight.

Mean number of seeds per pod showed substantial variability among genotypes. More seeds were produced by *TVu-16629* and *Ekp.-br.* Heritability effect was high for the character thus confirming earlier reports (Damarany 1994; Tyagi *et al.*, 2000). Low genetic variance was however noticed for seeds per pod indicating that selection for the character may not be effective. Per se mean performance showed close variations in seed weight character among the genotypes except for genotype *Ekp.-br.* which had highest seed weight. Moderate heritability value was observed for the character. However, very low genetic variability was found for seed weight character in this study.

Mean values indicated sufficient variability for grain yield among the genotypes. More grain yield was produced

by *TVu-16627*. Grain yield had been reported to vary considerably under most local conditions (Okeleye *et al.*, 1999; Remison, 2005). The reports of several investigations indicate that yield portion of cowpea plant are moderately to highly heritable under most environmental conditions. Siddique and Gupta (1991) demonstrated that additive gene effects govern seed yield. In this study, high broad-sense heritability was observed for grain yield which support previous reports (Fery and Singh, 1997; Tyagi *et al.*, 2000). Furthermore, a relatively high genetic variance was observed which suggest the possibility for selection and improvement on the character.

Conclusion

The study revealed the superiority of some lines. *TVu-16627*, *TVu-1120*, *TVu-16629* and *Ekp.-br.* thus may be selected due to their better mean performance in most of the characters for evolving high yielding genotypes of cowpea.

All correspondence should be addressed to Idahosa, D. O.

Department of Crop Science,
Ambrose Alli University,
Ekpoma, Edo State, Nigeria
E-mail: danielidahosa@yahoo.com
Phone: +234-805-5459-147

References

- [1] Padulosi S, Ng NQ. Origin, taxonomy and morphology of *Vigna unguiculata* [L.] Walp). In: Singh BB, Mohan Raji DR, Dashiell KE, Jackai LEN. eds. Advances in Cowpea Research 1997. IITA-JIRCAS, Ibadan, pp 1–12.
- [2] Pasquet R. *Vigna savi*. In: Mackinder B, Pasquet R, Polhill R, Verdcourt B eds. Flora zambesiaca, volume part *Phaseoleae*. 2001; Royal Botanic Gardens, Kew, pp 121–156.

- [3] Blade SF, Shetty SVR, Terao T, Singh BB. Recent developments in cowpea cropping systems research In: Singh BB, Mohan Raj DR, Dashiell KE, Jackai LEN. eds. *Advances in Cowpea Research 1997*; Pages 114–128, IITA, Ibadan.
- [4] Ng NQ, Marechal R. Cowpea taxonomy, origin and germplasm In: Singh SR, Rachie KO eds. *Cowpea Research, Production and Utilization 1985*; Chichester, John Wiley and Sons Ltd. P. 11–21.
- [5] Singh BB. What cowpea genetics tells about germplasm improvement 2003; IITA Work planning week. p19.
- [6] Ragsdale PI, Smith CW. Diallel analysis of seed set efficiency in upland cotton. In: *Proceeding Beltwide Cotton Conf. National Cotton Council 2003*; p.820, Memphis, TN.
- [7] Obilana AT, Fakorede MAB. Heritability: A treatise. *Samaru J. Agric. Res.* 1981;1(1): 72–82.
- [8] Hamdi A. Heritability and combining ability of root characters in lentil (*Lens culinaris* Medik). *Egypt J. Agric. Res.* 1992;70(1):247–255.
- [9] Ekebil JP, Ross WM, Gardner CO, Maranville JW. Heritability estimates, genetic correlations and predicted gain from S₁ progeny tests in three grain sorghum random mating population. *Crop Sci.* 1977;17:363–377.
- [10] Memon SM, Ansari BA, Balouch MZ. Estimation of genetic variation for agro-economic traits in spring wheat (*Triticum aestivum* L.). *Ind. J. Pl. Sci.* 2005;4: 171-175.
- [11] Nalayini P, Kandasamy OS. Classical growth analysis for cotton hybrids as influenced by N. levels and weed control method. *Indian J. Agric. Res.* 2003;37(4):269–273.
- [12] Sharma CD, Singhania DL. Performance of cowpea (*Vigna unguiculata* [L.] Walp.) genotypes for fodder traits. *Annals of Arid Zone* 1992;31:65–66.
- [13] Tyagi PC, Kumar N, Agarwal MC. Genetic variability and association of component characters for seed yield in cowpea (*Vigna unguiculata* [L.] Walp.) *Legume Res.* 2000;23(2):92–96.
- [14] Roquib MA, Patnaik RK. Genetic variability in grain yield and its components in cowpea (*Vigna unguiculata*). *Environment and Ecology* 1990a;8:197–200.
- [15] Fery RL, Singh BB. Cowpea genetics: a review of recent literatures. In: Singh BB, Mohan Raj DR, Dashiell KE, Jackai, LEN eds. *Advances in cowpea research, 1997*; Pages 13-29.; Copublication of IITA and JIRCAS, IITA, Ibadan, Nigeria.
- [16] Siddique AK, Gupta SN. Genotypic and phenotypic variability for seed yield and other traits in cowpea (*Vigna unguiculata* [L.] Walp.). *International Journal of Tropical Agriculture* 1991;9:144–148.
- [17] Ogunbodede BA, Fatunla T A note on the heritability of pod length and number of seeds/pod in cowpea (*Vigna unguiculata* [L.] Walp.) traits. *East Afr. Agric and Forestry J.* 1985;50: 89–100.

- [18] Pathmanathan U,,Ariyanayagam RP, Haque SO. Genetic analysis of yield and its component in vegetable cowpea (*Vigna unguiculata* [L.] Walp.) Euphytica 1997:96(2):207–213.
- [19] Damarany AM. Estimates of genotypic and phenotypic correlation, heritability and potency of gene set in cowpea (*Vigna unguiculata* [L.] Walp.) Assvit Journal of Agricultural Science 1994:25:1–8.
- [20] Okeleye K, Ariyo OJ, Olowe VI. Evaluation of early and medium duration cowpea (*Vigna unguiculata* [L.] Walp.) cultivars for agronomic traits and grain yield. Niger. Agric. J. 1999:30:1–11.
- [21] Remison SU. Arable and vegetable crops of the tropics 2005;p56. Gift-Print Associates, Benin-City.

Submission Date: 12/23/2009.