

# Genetic Variability, Heritability and Expected Genetic Advance as Indices for Yield and Yield Components Selection in Cowpea (*Vigna unguiculata* (L.) Walp)

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**ABSTRACT:** In a population under selection for a metric character, gene frequencies are altered which are further modified by the mating systems employed to advance the selected genotypes. Hence, genetic variability, heritability and genetic advance studies were conducted in Ekpoma and Iyanomo locations and combined locations on eight cowpea genotypes in a randomized complete block design for grain yield and its components as well as other vegetative characters. Significant wide range of mean values were observed in all the characters evaluated various genetic indices for selection were estimated. Genotypes indicated substantial variations for all characters in each and combined locations. High broad-sense heritability percentage was observed in all characters except for pod weight character which indicated low estimate of 25.5% in Iyanomo location. The expected genetic advance as percentage of population mean (GA%) was relatively high for pod length, pod weight, seeds per pod and 100-seed weight characters in the two locations. The high significant heritability and genetic advance observed in the genotypes across locations could be exploited through improvement and selection programmes in cowpea yield character [Academia Arena, 2010;2(5):22-26] (ISSN 1553-992X).

**Keywords:** Cowpea genotype, genetic advance, heritability, selection, character.

## 1. Introduction

The magnitude of genetic variability present in base population of any crop species is pivotal to crop improvement which must be exploited by plant breeders for yield improvement. The cowpea is the most widespread economically important and genetically diverse cultivated subspecies. Because the crop is grown in diverse agro-ecological environments, variation in genetic constitution do exist among the various strains thus making it a variable species. According to Raje and Rao (2000), genetic variability is essential in order to realize response to selection pressure as the estimates of genetic parameters of variation are specific for a particular population and the phenotypic expression of the quantitative character may be altered by environmental stress that affect plant growth and development.

Heritability of a character is important for the cowpea breeder because it provides him an idea of the extent of genetic control for the expression of a particular character (Chopra, 2000). Moreover, heritability serves as a guide to the reliability of phenotypic variability in the selection programme and hence determines its success (Hamdi, 1992). However, Johnson *et al.* (1955) stated that heritability estimates together with genetic advance are more important than heritability alone to predict the resulting effect of selecting the best individuals.

Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.*, 2003).

Selection which is the retention of desired genotypes and elimination of undesirable ones is a major and important process in breeding for improvement of one or more plant attributes. In a population under selection for a quantitative character, genotypic frequencies and hence gene frequencies are altered and these changes are further modified by the mating systems that may be employed to advance the selected individuals to the next generation(s) (Chopra, 2000). Thus, the utilization of any criterion for selection is linked with high genetic coefficient of variation and estimates of heritability as the magnitudes of heritability and other genetic parameters for a character would vary from location to location (Ramachandran *et al.*, 1982).

As a result, the present investigation is aimed to evaluate variability, heritability and genetic advance of grain yield and its component characters in eight cowpea genotypes to provide necessary information that could be useful in cowpea improvement programmes aimed to improve yield character.

## 2. Materials and Methods

An investigation study was carried out at two locations – the Rubber Research Institute of Nigeria (RRIN) Iyanomo and the Teaching and Research Farm (T and RF), Ambrose Alli University, Ekpoma. Eight cowpea genotypes of diverse genetic origin viz *TVu*-1120, *TVu*-1153, *TVu*-1157, *TVu*-1242, *TVu*-16627, *TVu*-16629, *TVu*-16630 from IITA genebank, Ibadan and Ekpoma brown (*Ekp-br*) a local cultivar were used to evaluate their genetic parameters. The materials were sown out to the field in randomized complete block design (RCBD) in three replications on 12<sup>th</sup> and 28<sup>th</sup> April 2008 cropping season, respectively.

For combined locations:

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

Each entry was assigned to plots of 5m long single rows and sown at 30cm within and 60cm apart with one seed per station. Normal management practices were followed. Five plants were selected at random for data record on quantitative characters from the 3m- mid rows of each plot and replicate on plant height, leaf area index (LAI), 50% flowering, 50% maturity, pod length, pod weight, seeds per pod, 100-seed weight and grain yield.

Data were subjected to statistical analysis of ANOVA using SAS software model. Heritability estimate in the broad-sense ( $h^2 b$ ) on mean basis for each location and combined locations was used as suggested by Ekebili *et al.* (1977).

Single location:

$$h^2 b(\%) = \frac{\sigma^2 g}{\sigma^2 g + \frac{\sigma^2 e}{r}}$$

Where  $\sigma^2 g$  is genetic variance;  $\sigma^2 e$  is error variance;  $\ell$  is location;  $r\ell$  is replicate by location;  $\sigma^2 g \times \ell$  is variance due to genotype by location and  $r$  is replication.

Genetic Advance (GA) and Genetic Gain (GG) values were determined as described by Johnson *et al.* (1955)

$$GA = \frac{\sigma^2 g}{\sigma ph} \times K$$

Where, K = 2.06 (selection differential at 10%);  $\sigma^2 g$  = genotype variance;  $\sigma ph$  = square root of phenotypic variance. Genetic gain (GA) was determined from genetic advance (GA) expressed as a percentage of the population mean ( $\bar{x}$ ).

## 3. Results and Discussion

Analysis of variance indicated significant variability for all characters in the two locations and combined locations except for plant height, leaf area index (LAI) and days to 50% maturity which revealed no significant difference.

The mean performance of all characters among the genotypes in each and combined locations (Table 1) showed that all characters were significantly influenced by location effect except for days to 50% flowering, 50% maturity and pod weight which had similar high mean values of 57.00 and 72.00 days to 50% flowering and maturity and pod weight of 2.05g (Ekpmoma location); days to 50% flowering (57.3); 50% maturity (72.67) and pod weight (2.77g)(Iyanomo location). It has been reported that the length of the

reproductive period in cowpea is very variable (Madamba *et al.* 2006). An observation of the mean values and ranges for days to 50% flowering and 50% maturity further indicated that there was no wide range of variation in the expression of the characters in the different locations as well as in combined locations. Plant height and LAI exhibited a wide range of (47.7cm–20.13cm) and LAI (2.43–0.56) in Ekpmoma location; and 102.40cm–38.33cm and LAI(5.50–1.11) in Iyanomo location which were largely influenced by location effect. The highest mean plant height in Iyanomo was 102.40cm while 47.07cm was recorded in Ekpmoma. A similar trend of high mean value of 5.50 for LAI was observed in Iyanomo when compared to 2.43 in Ekpmoma while 4.19 was recorded in the

combined locations. However, the least LAI (0.56) was observed in Ekpoma.

Significant differences were observed in yield and its component characters across the two locations as well as in combined locations (Table 1). Highest mean pod length (19.73cm), seeds per pod (16.37), 100-seed weight (14.93g) and grain yield (1723.8kg/ha) were recorded in Iyanomo than those in Ekpoma for pod length (17.97cm), seeds per pod (13.67), 100-seed weight (13.23g) and grain yield (538.5kg/ha). These data in the study suggest that the growth conditions at Iyanomo were more favourable than in Ekpoma and that differences between locations reflects differences in soil type and other environmental conditions prevalent at that time.

Estimates of heritability, genetic advance and genetic advance as percentage of the population mean are shown in Table 2. The magnitude of heritability was generally high in all characters across locations and combined locations except for pod weight and 100-seed weight which recorded low and moderate heritability effect at Iyanomo and combined locations, respectively. According to Ansari *et al.* (2004) high heritability percentage reflects the large heritable variance which may offer the possibility of improvement through selection. However, Johnson *et al.* (1955) reported that heritability estimates together with genetic advance are more important than heritability alone to predict the resulting effect of selecting the best individuals. Earlier reports had shown high broad-sense heritability for plant height in cowpea (Sharma and Singhania, 1992). An observation of heritability estimates for yield and its components in the two locations and combined locations show high heritability for LAI, days to 50% flowering and 50% maturity. High heritability for LAI was also reported by Sharma and Singhania (1992); days to 50% flowering (Tyagi *et al.*, 2000); 50% maturity (Siddique and Gupta, 1991); pod length (Roquib and Patnaik, 1997). However, low heritability estimate of 25.5% was observed in Iyanomo in this study contrary to earlier report.

Damarany (1994) and Tyagi *et al.* (2000) reported high heritability for seeds per pod. Moderate heritability estimate was obtained for 100-seed weight in combined locations. However, Tyagi *et al.*, (2000) and Gomes (2003) had reported high heritability which agrees with findings in Ekpoma and Iyanomo locations, respectively. Grain yield had high heritability which confirmed earlier reports (Fery and Singh, 1997; Tyagi *et al.*, 2000).

High genetic advance as percentage of population mean (Table 2) was observed for plant height, pod length, pod weight, seeds per pod and 100-seed weight in Ekpoma and Iyanomo locations except for plant height that indicated low genetic advance percentage mean in Iyanomo location. Thus, progress shoud be expected from selection between individual genotypes for these characers. Moderate progress would be expected from selection for plant height, LAI and 50% flowering in Iyanomo location.

The relative high heritability and genetic advance as percentage mean therefore showed high heritability together with high genetic advance as percentage mean for pod length, pod weight, seeds per pod and 100-seed weight in both Ekpoma and Iyanomo locations. The estimates of heritability and genetic advance as percentage mean considered together will no doubt help in drawing conclusion about the nature of gene action governing a particular character. This is due to the fact that combined study of heritability and gentic advance is more reliable in forecasting the effect of selection (Johnson *et al.*, 1955). Based on the findings, it can be concluded that selection will be effective in the test materials used in this study as revealed by the significant substantial variations among the genotypes for all the characters observed in each and combined locations. Therefore, the significant genetic variability for these characters in the genotypes over locations recorded in the test materials can be further exploited through improvement and selection programmes.

**Table 1.** Means of range values of 9 characters in cowpea genotypes evaluated at Ekpoma, Iyanomo and combined locations

LOCATION										
	Plant	LAI	50%	50%	Pod		Pod		Seeds	100-seed
	Height (cm)		Flowering	Maturity	Length (cm)		Weight (g)	per Pod	Weight (g)	(kg/ha)
<b>Mean</b>	1	2	3	4	5		6	7	8	9
Ekpoma	30.88	1.42	46.5	66.21	13.51		1.28	9.69	10.02	229.59
Iyanomo	59.42	3.69	47.33	65.25	14.70		1.79	11.45	11.25	514.9
Combined	45.15	2.55	46.92	65.73	14.11		1.53	10.59	10.64	3758.28
<b>Range Max</b>										
Ekpoma	47.70	2.43	57.00	72.00	17.97		2.05	13.67	13.023	538.5
Iyanomo	102.40	0.50	57.33	72.67	19.73		2.77	16.37	14.93	1723.8
Combined	74.73	4.19	57.17	72.33	18.85		2.42	14.47	13.4	1131.1
<b>Range Min</b>										
Ekpoma	20.13	0.56	40.00	64.33	10.50		0.74	6.5	8.03	30.2
Iyanomo	38.33	1.11	42.33	61.00	10.63		0.96	7.04	9.00	125.4
Combined	30.70	0.83	42.33	62.67	10.57		0.88	6.95	9.05	136.6

**Table 2.** Broad-sense heritability estimates ( $h^2 b\%$ ), genetic advance (GA) and genetic advance as percentage mean (GA%) of 9 characters in cowpea genotypes evaluated at Ekpoma, Iyanomo and combined locations

LOCATION										
	Plant	LAI	50%	50%	Pod		Pod		Seeds	100-seed
	Height (cm)		Flowering	Maturity	Length (cm)		Weight (g)	per Pod	Weight (g)	(kg/ha)
<b>Heritability (<math>h^2 b\%</math>)</b>	1	2	3	4	5		6	7	8	9
Ekpoma	99.8	93.9	99.1	91.6	88.1		75.4	85.4	97.9	100.0
Iyanomo	99.5	99.0	97.6	99.1	98.6		25.5	96.6	52.3	100.0
Combined	89.9	98.9	81.9	84.7	97.6		95.9	90.7	42.2	53.3
<b>Genetic Advance (GA)</b>										
Ekpoma	0.07	3.19	4.05	0.06	8.38		1.84	3.71	4.27	0.2
Iyanomo	13.64	0.50	10.10	1.37	10.06		8.96	6.04	11.83	0.0
Combined	0.002	0.05	1.60	0.62	1.90		1.73	0.58	0.41	350.0
<b>Genetic Advance as % of Mean (GA%)</b>										
Ekpoma	0.23	224.65	8.71	0.09	62.03		143.25	37.51	41.82	0.0
Iyanomo	22.96	13.55	21.34	2.10	68.44		500.56	52.61	105.16	0.0
Combined	0.004	1.96	3.41	0.94	135.71		113.07	5.48	3.85	93.3

### Acknowledgement

The authors immensely appreciate staff of IITA (Genebank Unit) Ibadan for the test materials used and the Management of Rubber Research Institute of Nigeria (RRIN), Iyanomo, for kindly providing the piece of land within its nursery field for this study to be conducted.

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Submission Date: 23/02/2010.