

Full Length Research Paper

Heritability and Genetic Variability Analysis of Reproductive Traits in Cowpea (*Vigna unguiculata* (L.) Walp.

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The success of most crop improvement programs largely depends upon the genetic variability and the heritability of desirable traits. The magnitude and type of genetic variability help the breeder to determine the selection criteria and breeding schemes to be used for improvement purposes. A screen house experiment was carried out at Samaru, Nigeria in 1999 and 2000 dry seasons to estimate the genotypic variability of some reproductive traits and their heritability in some selected cowpea varieties. Results of the study showed that there was considerable variation among cultivars for duration of reproductive phase and rate of photosynthate partitioning. Genotypic coefficients of variation were also high for days to first flower, 100-seed weight, plant height, and harvest index. Broad-sense heritability estimate (h^2) was 98.9% for 100-seed weight, 94% for duration of reproductive phase, 84.5% for days to first flower, 83.9% for days to maturity, and 77.3% for harvest index. This information showed that there is sufficient genetic variance to warrant selection for improvement in the cowpea genotypes studied. We concluded that considerable progress in cowpea breeding could be achieved by exploiting these traits.

Key words: Cowpea, reproductive traits, variability, heritability.

INTRODUCTION

For any planned breeding programs to improve grain yield potentials of crops, it is necessary to obtain adequate information on the magnitude and type of genetic variability and their corresponding heritability. This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability for example, is used to indicate the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates also suggests the extent to which improvement is possible through selection. Briggs and Knowles (1967) put forward the view that if environmental variability is negligible

compared to genetic variability, selection will be effective in improving the character if such character with high genotypic variability and also easily measurable happened to be highly correlated with yield. This applies to cowpea where a period of vegetative growth is followed by the production of flowers and pods after which the plant dies. For example, molecular markers have been used to estimate genetic differences in gerplasm accession of soybean and other crops (Autrique et al., 1996; Johns et al., 1997; Thompson et al., 1997). Phenotypic differences may also elucidate genetic differences Autrique et al. (1996), Johns et al. (1997), and Van Beuningen and Bush (1997) used morphological, developmental, and physiological traits to create distance measures for use in examining the genetic diversity in large collection of crop genotypes. Grafius et al. (1976)

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and Grafius (1978) applied this concept to practical breeding by employing cultivar

Table 1. Origin and Description of the genotypes used for this study.

Variety	Origin	Maturity	Growth habit	100-seed wt. (g)	Seed size	Seed coat colour	Hilum
IT89KD-288	IITA	PSL	Prostrate	20.2	Large	White	Brown
1AR-1696	IAR	PSL	Prostrate	23.0	Large	White	Black
KANANNADO	IITA	PSL	Prostrate	29.3	Large	White	Brown
IAR-48	IAR	NPSE	Erect	19.5	Medium	Brown	Brown
IT88D-876-11	IITA	PSE	Erect	17.4	Medium	Brown	Brown
IT93K-452-1	IITA	NPSE	Semi-prostrate	17.0	Small	White	Black
IT88DM-345	IITA	NPSE	Erect	13.3	Small	Tan	Ringed black
176B(SAMPEA 4)	IAR	PSM	Prostrate	15.4	Medium	White	Black
Tvx-3236	IITA	NPSM	Erect	12.3	Small	Cream	Brown

NPS, Non photosensitive; PS, photosensitive; PSE, photosensitive early; IITA, International Institute of Tropical Agriculture; IAR, Institute for Agricultural Research; NPSE, non photosensitive early; PSM, photosensitive medium; and PSL, Photosensitive late.

differences in morphological traits to select genetically diverse breeding pairs.

The reproductive phase of cowpea represents the combined effects of many genetic and environmental factors. Emeberi and Obisesan (1991) working in the rainforest ecological zone under short-dayF conditions and using varieties within the same maturity group and seed size reported narrow sense heritability (h_n) of 52% for days to pod filling period. In an earlier study, Ogunbodede and Fatula (1985) reported a higher estimate of narrow sense heritability for pod length and seed size. Similarly, Dumbre et al. (1983) reported broad sense heritability estimates of 52% and 42% for maturity and pod filling period, respectively. Aryeetey and Laing (1973) also reported high heritability estimates for seeds per pod and pod length, suggesting that early generation selection for these traits will be successful.

Ntare (1992) studied the variation in reproductive period and grain yield of cowpea under high temperature condition and reported considerable variations among cultivars in the duration of reproductive period, crop growth rate and partitioning of photosynthates. Also, Ramachandran et al. (1980) working on cowpea reported that the major parts of total variation in yield for pods per plant and internodes length was largely due to genetic causes and obtained high genetic variance for days to flower and harvest. All these studies revealed that the utilization of any criterion for selection is linked with high genetic coefficient of variation and estimates of heritability. Thus, a greater understanding is needed not only of the environmental factors that interact with the genotype to influence crop reproductive development and yield but also of the genetic factors that control these characters. The knowledge of genetic variation and relationships among genotypes will help the breeders in developing appropriate breeding strategies to solve problems of low yield in cowpea.

Previous studies regarding heritability in cowpea and other crops indicate that the magnitudes of heritability and other genetic parameters for a character would vary

from location to location. Limited information is available on the nature of variability and magnitude of heritability of reproductive phase in cowpea in the moist savanna. Therefore, the objective of this study was to investigate the genetic variability and heritability of some reproductive and quantitative traits in some selected cowpea genotypes.

MATERIALS AND METHODS

Genetic materials, field, and data collection

The screen house experiments were conducted in 1999 and 2000 at the Institute for Agricultural Research, Samaru, Zaria, Nigeria (07.38° E, 11.11° N, 686 m asl). Soil type is a fine-loamy, isohyperthermic Plinthustalf; USDA taxonomy. A total of nine cowpea genotypes were used in this study. The genotypes were selected based on variability for growth habit, maturity, and seed size (Table 1). The treatments were evaluated in a completely randomized design with three repetitions. Each repetition had 27 plastic plots.

A total of 81 plastic pots (Each 228 mm in diameter, 8.6 L in volume) were used in each of the experiment. Six seeds of each of the genotypes were planted in the plastic pots filled with fresh topsoil (Composition: soil/sand mixture). The seedlings were thinned to three plants per plot at 2 weeks after planting (WAP) to maintain a population of nine plants for the three pots per genotype, which constituted a replicate. Prior to sowing, 1.0 g of compound fertilizer (15:15:15 NPK) at the rate of 100 kg/ha was incorporated into each pot. The potted plants were watered daily to field capacity using watering tank throughout the growth period of the plant.

A mixture of Karate 25 EC and Mycotrin 80 WP at the rate of 37.5 g a.i./ha and 62.5 g to 10 L of water, respectively was sprayed at 7 days interval to control flowering-and post-flowering insect pests. Weeds were controlled by hand pulling as and when necessary throughout the growing period of the crop.

The mean monthly minimum and maximum daily air temperatures and sunshine hours during the period of the experiments were taken from a nearby weather station (Table 2). Observation was recorded on days to flower, duration of reproductive period (DRP), which is the number of days from first flower appearance to pod maturity. Data were also collected on number of pods per plant, plant height at maturity, pod length, number seeds per pod, 100-seed weight, pod weight per plant harvest index and seed yield per plant. Pod filling period (PFP)

Table 2. Mean monthly minimum and maximum daily air temperature and sun shine hours from October 1999 to June 2000.

Month	Minimum temperature (°C)		Maximum temperature (°C)		Sunshine (h)	
	1999	2000	1999	2000	1999	2000
October	22.40	-	31.50	-	6.66	-
November	20.20	-	33.90	-	9.09	-
December	17.37	-	32.49	-	6.54	-
January	-	16.08	-	33.24	-	7.71
February	-	18.08	-	35.57	-	8.69
March	-	23.07	-	38.07	-	7.10
April	-	25.20	-	37.60	-	6.41
May	-	24.74	-	35.89	-	6.76
June	-	23.16	-	32.53	-	6.94

taken at 7- days interval starting from the day pod appear. The mean value of the five plants of each genotype randomly selected was used for analysis.

Statistical analysis

The mixed model analysis of variance (ANOVA) was used on entry basis for the individual traits combined across years. The SAS procedure used for the ANOVA was GLM (general linear model). The linear additive models used for individual year and for the two years combined are presented below.

Individual year, the linear statistical model used was:

$$Y_{ijk} = \mu + \alpha_j + \beta_k + (GE)_{ij} + \epsilon_{ijk}$$

Where: Y_{ijk} = the observation made in the i^{th} genotypes on the j^{th} rep., in the k^{th} year; μ = the overall mean of the trait; α_j = the effect of the j^{th} rep; β_k = the effect of the k^{th} year; $(GE)_{ij}$ = sum of interaction terms of the genotypes and year, and ϵ_{ijk} = the residual effects.

Components of variance were estimated using the method described by Bliss et al. (1973). Variance components were obtained by equating the mean square for a source of variation to its expectation and solving for the unknown as given below:

$$\begin{aligned} \sigma_e^2 &= M_3 \\ \sigma_{gy}^2 &= M_2 - M_3 / Y \\ \sigma_g^2 &= M_1 - M_2 / ry \end{aligned}$$

Where: σ_e^2 , σ_{gy}^2 , and σ_g^2 are components of variance for error, genotype by environment interaction and genotype, respectively. M1, M2, and M3 are the observed values of the mean squares for the genotype, interaction and error, respectively (Fehr, 1987).

Heritability estimates was calculated in broad sense on entry basis using the formula suggested by Fehr (1987) given as:

$$\sigma_{g/}^2 / \sigma_{ph}^2 = \sigma_g^2 / (\sigma_{gy}^2 / ry + \sigma_e^2 / y + \sigma_g^2)$$

Where: r and y are number of repetition, and year respectively.

Genetic coefficient of variation was estimated by the formula suggested by Burton (1952) given as:

$$GCV = \sigma_g^2 \times 100$$

Where μ = mean value of the particular trait.

RESULTS AND DISCUSSION

The results of the combined analysis of variance (Table 3) showed that the mean squares for genotype were significant for all the characters studied. Large variability was observed for shoot weight, 100-seed weight, days to flower and plant height in descending order. The least range of variation was observed for pod per plant followed by pod length. As shown in Table 4, the genetic variance for number of days to first flower appearance, duration of reproductive phase, 100-seed weight and days to maturity were greater than their respective interaction and error variances, respectively. Wide ranges of difference for genetic coefficient of variation were observed for the characters studied (Table 4). The values varied from 7.3% to 44.9% for pod and shoot weight, respectively. Broad sense heritability for pod weight was the least (15.68%) while the 100-seed weight was the highest (98.9%). The results of the pod development rate showed that varietal differences exist among genotypes. The maximum seed filling rate for some of the genotypes were 21 days while others especially the large seeded types recorded 28 days. However, there was no genotype by year interaction for grain yield and many of the agronomic traits studied.

The wide ranges in the data observed for most of the traits and the significant mean square obtained have shown the presence of genetic variability for the traits studied. This indicates that these traits can be improved through breeding. Secondary traits are very valuable in selection for improved cowpea grain yield. The highly significant genotypic effect observed for days to first flower confirmed that genetic variability exist among the genotypes even though the day length was relatively shorter than the critical value needed for the photoperiodic responses.

Most of the genotypes that flowered early had shorter

Table 3. Ranges, mean and values of 'F' from estimates of variance for the various plant characters.

Character	Range of variation	Mean	Error variance	F observed
Days to first open flower	4.03-82.52	55.81	9.14	963.41**
Duration of reproductive phase	18.37-23.80	21.16	0.68	19.81**
No. of Pod per plant	3.47-6.37	4.81	0.82	13.06**
Pod weight (g)	4.57-8.95	6.97	2.13	7.09**
Pod length (cm)	12.77-15.11	13.88	0.64	4.29**
100-seed weight (g)	12.69-28.21	19.50	0.73	150.33**
Plant height (cm)	16.37-39.48	22.41	3.01	311.49**
Shoot weight per plant (g)	3.99-23.38	8.85	0.85	192.04**
Maturity	62.53-106.85	16.03	18.03	1141.98**
Harvest Index	0.17-0.47	0.39	0.002	0.06**
Seed per pod	7.00-11.37	9.15	0.79	12.36**
Yield per plant	3.78-8.08	5.83	1.06	12.01**

*, ** Significant at 5% and 1% levels of probability, respectively.

Table 4. Estimate of genetic variance (σ_g^2) genotype \times year interaction (σ_{gy}^2) variance, phenotypic variance (σ_{ph}^2) and error variance (σ_e^2) for 13 reproductive characters of some cowpea genotypes, Samaru, Nigeria 1999 and 2000.

Characters	(σ_{ph}^2)	(σ_g^2)	(σ_{gy}^2)	(σ_e^2)	h^2_b (%)
Days to first open flower	149.69	126.41	65.26	9.14	84.78
Duration of reproductive phase	3.26	3.06	0.25	0.68	77.51
No. of Pod per plant	0.59	0.19	0.76	0.82	19.25
Pod weight per plant(g)	1.66	0.26	3.12	2.13	49.02
No. of seed per pod	1.63	1.125	1.56	0.80	75.82
Pod length (cm)	0.66	0.45	0.32	0.65	42.94
100-seed weight (g)	24.98	24.70	0.48	0.73	96.19
Plant height (cm)	45.03	30.77	41.29	3.01	88.58
Shoot dry weight per plant (g)	26.65	15.80	32.11	0.86	90.33
Maturity	177.56	149.01	76.62	18.03	79.98
Yield per plant	1.52	0.38	2.89	1.06	51.68
Pod development rate	0.086	0.055	0.048	0.030	64.33

reproductive phases than the late flowering ones, especially when the temperatures were warmer (36.4°C / 21.9°C). Also, the large seeded prostrate cultivars like the *Kananado* had longer reproductive periods but exhibited no yield advantage over the medium seed size genotype. This suggests that seed size is not influenced by the duration of reproductive phase; rather it is governed by other genetic factors. Therefore, it could be suggested that the longer reproductive period observed for small medium seeded cowpea types was probably due to poor pod establishment and photosynthate partitioning. This observation is in agreement with the earlier reports showing that the poor ability of some genotypes to assimilate carbon and nitrogen during reproductive period and to partition large gains of these into pods limit cowpea yield (Jacquinot et al., 1967; These results indicate that there is sufficient genetic variability within the genotype to warrant selection. This finding also provided some insight into the possible sources of large

GCVs associated with some traits in the evaluation. Generally, large GCVs may be caused by small means relative to large error terms, or vice versa. In this study, proportion of total variation attributable to the error variance was relatively small.

The moderate-to-large genetic variance and heritability obtained in the present study suggest that substantial residual genetic variability is still available to ensure good progress from further selection for duration of reproductive phase, which in turn will lead to increase in grain yield. High heritability estimates (h^2) was obtained for 100-seed weight, duration of reproductive phase, days to first flower appearance, maturity, and harvest index. The results of the present study corroborate those of Raamachandran et al. (1980), Seekamar et al. (1984) and Fehr (1987). These authors also reported high heritability for these traits.

The genetic coefficient of variation and heritability were high for days to maturity and harvest index. This

suggests that selection for these characters would be effective for further selection and improvement. Duration for reproductive phase had a high heritability but the genetic coefficient of variation was low. This indicates that though, the character is highly heritable, its improvement through early generation selection may not give the desired results.

The low genetic coefficient of variation and heritability obtained for grain yield per plant is not particularly surprising since yield is a product of many complex characters. Therefore, direct selection for grain yield improvement may not be possible, but through indirect selection of other secondary traits may be feasible. However, the low genetic coefficient of variation and heritability obtained for pods per plant and pod weight per plant are at variance with those of Ogunbodede and Fatula (1985) who reported high broad sense heritability for these traits.

Within the range of materials used in this study, there exist substantial genetic coefficient of variation and heritability in the characters studied to warrant selection in the genotypes for further improvement. The level of genetic variability observed for different characters would be useful for breeding varieties of cowpea for high yield. The high heritability estimates obtained for days to first flower, duration of reproductive phase, 100-seed weight, days to maturity and harvest index suggests that these characters are highly heritable and therefore the traits can be easily transferred from parent to offspring. Secondary traits are very valuable in selection for improved cowpea grain yield. The result of the present study revealed that longer duration of reproductive phase would not necessary translate to high yield advantage but that genotypes with moderate period for this trait and combined with high efficiency of assimilate partitioning would result in higher grain yield.

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