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Heterosis and Phenolic Performance in a Selected Cross of Cowpea *Vigna unguiculata* (L.) Walp for Humid Environment Performance

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Abstract: Cowpea genotypes with explorable traits for humid environment performance remain a major concern to plant breeders. Practical breeding programme require knowledge of gene actions explorable for yield improvement. This study studied genetic variations and heterosis from a cross of landrace and cultivar parents. Four generations of 1st and 2nd filial (F_1 and F_2) and backcrosses to the parents (Bc_1 and Bc_2) were raised. About 10 traits were evaluated. Numbers of branch, seed and maturity time gave high heterotic values in the F_2, Bc_1 and Bc_2. Genetic diversity between the 2 parents accounted for differences in the heterotic performance of the traits. Genotypic variations and additive gene component (D) were high for flowering and maturity periods, branching and peduncle traits in the generations. High genetic advance complemented the high heritability estimates for same traits. Selection of these traits for cowpea yield improvement for humid environment specific performance was found reliable.

Key words: Genetic variations, landrace, cultivar, cowpea crosses, selection, environment

INTRODUCTION

Genetic and environmental requirements of cowpea varieties in the unguiculata genus are extremely diverse within regions and therefore, make breeding programmes more complex (Singh and Sharma, 1996).

To develop high yielding types for humid specific environment, inheritance pattern in the trait performance is of tremendous assistance to plant breeders. The seed yield of cowpea (*Vigna unguiculata* (L.) Walp) is determined by collective influence of both qualitative and quantitative traits and phenolic similarity between cowpea parents and its progenies depend largely on the additive dominance variance components (Aremu *et al*., 2003).

Cowpea is diploid and self pollinating with 2n = 22 (Singh, 2000). The study of the genetic parameters controlling the expression of its yield and components of yield is essential in determining the effect of such genetic parameters in enhancing the seed yield of cowpea. In the humid tropics, seed yield of cowpea is low due to unfavorable environmental conditions such as high rainfall, high disease incidence, reduced sunshine hour, poor soil fertility level etc. The choice of cowpea specific genotypes adaptable to this unfavorable environmental condition is determined by careful breeding programmes (Khattack *et al*., 2002). One of such programmes involves knowledge of the gene actions operative in both qualitative and quantitative traits and formulation of breeding techniques for combining any of such desirable traits into developing high yielding genotypes for specific environment sensitivity (Aremu *et al*., 2003).

A measure of heterotic value typifies the superiority of a hybrid over its parental lines. Researchers exploited heterotic performance in some crop species (Bhushana *et al*., 2000) discovered maximum heterotic trait performance in a single cross of cowpea lines. Intra-population improvement using a single cross of maize, maximized gain in the population perse reported better parent heterosis to be 81.6% for number of pods per plant and 20.4% for number of seeds pod in cowpea. Trait genetic variation is determined to a large extent by gene additivity. Using a land race cowpea cultivar with high genetic potential yet exploited, it is expected that such cultivar would produce better hybrids with maximum heterosis. Traits with greater magnitude of additive epistasis than dominance type are exploitable by standard hybridization and selection procedure. Selection of traits with such genetic variation would lead to meaningful breeding programme. The use of heritability estimates complemented by genetic gain (genetic advance) in

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making superior selection has proved successful (Abou Al-Fadil *et al*., 2004; De Araujo *et al*., 2002). Estimated heritability values of various agronomic traits in brome grass and discovered low heritability estimates for traits under complex genetic control using humid environments.

In the contrary, Khattack *et al.* (2002) discovered high heritability and heterosis >100% over the better parent of a single maize hybrid. This research studied genetic variations and heterotic performance from a selected cross of a landrace and cultivar cowpea types using a humid environment field plots.

MATERIALS AND METHODS

Ife-brown (P_2) cultivar cowpea parent used in this study is grown in humid ecology having brown seed coat color with smaller seed size to the land race parent (P_1) with white seed coat color and grown in savanna agro-ecology (Table 1). Both parents were sourced from each of the growing environment.

In 2007 growing season, the parents were grown in the green house to generate the first filial generation (F_1). The backcrosses (BC_1 and BC_2) were later produced using the F_1 as common parent to each of the Ife-brown and Danilla seeds, respectively. Seeds from F_1 plants were grown out to produce the 2nd filial generation (F_2).

During the 2008 farm year, seeds of each of P_1, P_2, F_1, F_2, BC_1 and BC_2 were planted out in the research farm of Ladoke Akintola University of Technology (LAUTECH), Ogbomoso, Nigeria. A 3×3 m field plots of Randomised Complete Block Design with three replications were used for each family generation.

The inter and intra-row spaces were 45 and 30 cm, respectively. The total number of plants from the harvest area for each of the family generation is shown in Table 1. About 2 weeks after planting, insect pests were controlled using monocrotophos (Azodrin) at 4 mL/20 L of water. Weeding was done manually as at when due. Data were recorded using each individual family.

Data collection: Data were collected on days to 50% flowering, height at flowering (cm), number of branches/plant, number of peduncles/plant, length of peduncle (cm), number of pods/plant, number of seeds/pod, days to 95% maturity, height at maturity (cm) and 100-seed weight (g).

Data analysis: The observed parental F_1, F_2, BC_1 and BC_2 means and variances were calculated using Analysis of Variance (ANOVA) to determine the variations in the mean performance of the genotypes evaluated. Standard errors were used to compare trait mean performances of the hybrids and their parents. Trait heterotic performance was estimated as following the adaptation of (Bhushana *et al*., 2000) as:

$$\text{Heterosis (MP) (\%)} = (F_1\text{-MP})/\text{MP}\times 100$$

$$\text{Heterosis (BP) (\%)} = (F_1\text{-BP})/\text{BP}\times 100$$

Where:

F_1 = Performance at the first filial generation
MP = Mid-Parent value
BP = Better Parent value

Estimates of heritability in broadsense (H_B), Genetic Advance (GA) and components of variance (σ_P; σ_G^2) were obtained following the statistics outlined by (Singh and Chaudhary, 1985) i.e.,

$$\partial(_\downarrow P^\uparrow 2)=((r\sigma(_\downarrow G^\uparrow 2))+\Upsilon(_\downarrow e^\uparrow 2)) -\sigma(_\downarrow e^\uparrow 2))/\Upsilon=\frac{MS_G - Ms_e}{r}$$

and

$$\sigma_P^2 = \sigma_G^2 + \sigma_e^2 = \frac{MS_G - Ms_e + Ms_e}{r}$$

$$\frac{h_B^2 = (\sigma_g^2)}{\sigma P^2}$$

Where:

MS_G = Mean Square for genotype in ANOVA
MSe = Mean Square for error in ANOVA

Table 1: Means and standard errors in six generations of cowpea traits in a cross of cowpea (Danilla x Ife-brown)

	Generations					
Traits	P_1	P_2	F_1	F_2	BC_1	BC_2
Days to 50% flowering	55.3±0.20	36.8±0.14	49.0±0.08	52.1±0.310	50.2±0.41	48.2±0.22
Number of branches/plant	5.4±0.11	2.3±0.09	4.7±0.05	4.3±0.200	3.7±0.30	2.1±0.14
Number of peduncles/plant	18.2±0.23	11.2±0.14	19.7± 0.13	17.2±0.350	14.2±0.22	10.7±0.27
Length of peduncle (cm)	42.0±0.12	28.6±0.19	45.5± 0.15	35.3±0.410	38.3±0.19	30.1±0.32
Number of pods/plant	56.1±0.26	48.6±0.25	59.8± 0.13	50.6±0.310	50.3±0.13	49.0±0.21
Number of seeds/pod	8.1±0.14	10.4±0.19	10.6± 0.63	9.2±0.070	6.1±0.21	9.2±0.35
Days to 95% maturity	81.4±0.17	68.2±0.16	78.2±0.050	63.4±0.240	70.6±0.20	69.2±0.28
Height at flowering (cm)	40.3±0.22	31.7±0.15	33.4±0.060	41.6±0.330	41.2±0.34	33.1±0.34
Height at maturity (cm)	62.1±0.19	43.1±0.22	57.21±0.09	58.0±0.320	60.1±0.23	44.0±0.26
100- seed weight (g)	16.4±0.20	10.1±0.19	12.2±0.130	10.23±0.17	13.1±0.31	9.7±0.29

cm = centimeter: g = gramme

E = 1/3 ($\sigma P_1 + \sigma P_2 + \sigma F_1$)
D = 2 (σF_2 - σB_1 - σB_2)
H = 4(σF_2 – ½ σ_D-E)
√H/D = Degree of dominance
E = Environmental effect
D = Additive gone effect
H = Additive effect
σ_P = Variance of the genotype
σ_{P1} = Variance of first parent
σ_{P2} = Variance of second parent
σ_{F1} = Variance of first filial generationSeptember 30, 2010
σ_{B1} = Variance of first backcross
σ_{B2} = Variance of second backcross
r = Number of replicates

RESULTS AND DISCUSSION

Generation means and their respective standard errors showed trait means of days to flower, number of branch, length of peduncle, number of pods/plant and plant height to be closer to the mean of the larger parent (P_1) (Danilla) (Table 1).

The generations had more seed number with reduction in their weights from their, respective pods following the pattern of the smaller cultivated parent (Ife-Brown).

All the generations matured earlier than the landrace parent. Heterotic pattern arising from the mid and better parents are shown in Table 2. Mid and better parent heterotic values in the F_1 and F_2 were positive for number of branch, number of pods, number of seeds per plant and days to maturity.

The backcross to the better parent (Bc_1) demonstrated positive heterosis for branch number, maturity time and plant height for the F_1 and F_2 generations. Plant height at flower and maturity time recorded negative but significant heterosis for both the mid and better parent in the F_1 and F_2 generations.

Genotypic variance were moderately high for flowering and maturity period, number of branch, length of peduncle and number of pods per plant (Table 3). These traits also recorded high heritability and selection index. Moderate but low genotypic variances were recorded for seed number (38.4%) and seed weight 36.2 with heritability values equally moderate 47.5 and 39.7%, respectively.

Phenotypic variances were high for number of peduncle (67.5), height at maturity (52.4) and seed weight (40.2). Gene effect at the dominance level was high even as the additive gene effects (D) were higher than the dominant component for all the traits (Table 4). Only number of peduncles per plant recorded higher dominant gene effect (31.1). The degree of dominance (√H/D) for the traits were less than unity except (√H/D) for number of peduncles which recorded >1C° of dominance.

Flowering and plant height traits in the cross of cowpea in this experiment indicated transgressive segregation towards over dominance. This is as a result of the hybrid trait mean values being larger than the landrace better parent. According to Dhaliwal *et al*. (2002), transgressive gene segregation leads to increase in vigor. The resultant generations also produced more branches and carried more pods than the cultivated smaller parent, though the backcross to this smaller parent (BC_2) produced fewer branches with reduced number of pods.

The reduction in seed weight within the generations is compensated for by having more seeds from the pods. Therefore, the choice of using a landrace cowpea parent (Danilla) from dry agro-ecology to improve the performance of a cultivated parent (Ife-brown) in the humid agro-ecology is worthwhile. Humid environment have peculiar cowpea diseases such as fungi attack, pod boring insects, flower sucking bugs etc. That the peduncles arising from the generations are longer than that of the smaller parent and therefore carry the pods far above the plant canopy is indicative of breeding for disease free genotypes in the humid environment.

Table 2: Trait mid-parent and better parent heterosis and standard error in a crossof cowpea (Danilla x Ife-brown)

	F_1		F_2		BC_1		BC_2	
Traits	MP	BP	MP	BP	MP	BP	MP	BP
Days to 50% flowering	150.3±0.20	161.3±0.50	14.5±0.30	5.4±0.20	-0.2±0.40	-0.2±0.20	0.01±3.0	-0.1±0.8
Number of branches/plant	211.1±4.20	130.5±6.10	3.7±0.05	5.4±4.10	3.2±0.20	0.2±0.10	-0.5±3.10	-0.5±1.8
Number of peduncles/plant	29.2±3.60	40.3±8.30	1.2±0.40	6.2±0.50	2.2±1.40	-0.03±0.7	-0.6±3.10	-0.3±1.4
Length of peduncle (cm)	61.4±10.1	100.7±9.40	1.0±2.50	-15.0±1.40	-2.7±1.10	0.7±0.90	-0.02±1.9	-0.1±1.9
Number of pods/plant	80.5±13.2	110.2±10.2	-51.8±4.10	-1.4±10.3	-0.4±2.30	-0.04±0.2	-0.06±2.4	-0.2±1.2
Number of seeds/pod	100.4±0.20	150.6±19.7	33.2±1.40	2.2±1.70	-2.1±1.00	0.03±0.8	0.01±2.1	-0.18±1.4
Days to 95% maturity	130.4±15.0	73.2±0.30	2.5±1.50	0.8±0.70	0.07±0.5	0.04±1.2	-0.08±0.1	-0.15±2.1
Height at flowering (cm)	-88.1±0.21	73.2±0.20	-1.2±0.60	4.4±0.20	1.7±1.30	8.1±2.40	-0.06±3.0	-0.02±1.1
Height at maturity (cm)	-70.8±0.40	-47.1±050	1.4±0.30	0.7±0.50	1.1±0.70	0.1±0.20	-0.17±3.3	-0.31±0.9
100 seed weight (g)	250.3±9.20	46.9±3.20	1.3±1.30	-3.3±1.70	1.1±0.20	-1.5± 0.8	0.21±1.0	-0.4±1.7

cm= centimeter; g = gramme

Table 3: Phenotypic variance genotypic broad sense heritability $(H_B)^2$ and genetic advance (GA) of traits measured in a cross of cowpea (Danilla x Ife brown)

Traits	σ^2_P	$\sigma\Sigma^2_P$	HB	G_A
Days to 50% flower	44.2	59.7	69.3	95.60
Number of branch/plant	41.2	51.3	78.7	54.71
Number of peduncle/plant	67.5	10.2	23.4	19.10
Length of peduncle/plant	37.2	41.1	61.2	43.20
Number pods/plant	38.1	42.7	73.6	54.70
Number of seeds/plant	48.2	38.4	47.5	50.70
Days to 95% maturity	18.3	48.2	26.6	12.60
Plant height at flower	20.2	12.5	6.3	31.00
Plant height at maturity (cm)	52.4	52.3	41.3	53.10
100 seed wt (g)	40.2	36.2	39.7	10.60

cm = centimeter: g = gramme

Table 4: Additive (D), dominance (H) and Degree of dominance (√H/D) components for the traits in a cross of cowpea (Danilla x Ife brown)

Components	Days to 50% flower	No. of branch/plt	No. of peduncle/plt	Peduncle/ plt (cm)	No. of pods/plt	Length of no. of seeds/plt	Days to 95% maturity	Plant height flower (m)	Plant height maturity (cm)	Seed weight (g)
H	4.80	9.10	31.10	4.30	8.70	21.40	12.60	17.40	17.40	16.70
D	30.00	37.80	19.80	52.80	24.00	39.00	33.60	24.20	55.00	47.80
(√H/D)	0.40	0.51	1.25	0.29	0.60	0.74	0.61	0.85	0.56	0.59

Plt = Plant; cm = centimeter; g = gramme

The consistent high heterosis demonstrated by the segregating generations for branching, seed and time of maturity traits suggest the existence of superior segregates with dominant favorable genes for productivity using the humid environment. This result agrees with the findings of where plant height and panicle branches gave positive heterosis using tef specie.

High heterosis was also reported by Bhushana *et al.* (2000) and Tefera and Peat (1997). The differences in the heterotic values among the traits in the segregating generations could be attributed to the genetic diversity between the landrace and cultivar parents used in the crosses.

Saleh *et al.* (2002) discovered genetic diversity using 10 crosses of maize inbred lines. The negative but significant heterosis recorded for plant height across the generations predisposes gene for tallness in cowpea to be dominant and can equally be favored during selection.

The high genotypic variation for flowering and maturity period, number of branch, pods per plant and peduncle length is a demonstration of the high genetic variation in the expression of these traits and that environmental influence is minimal on the performance of these traits.

The moderately high heritability and genetic advance values for these traits also confirm the reliability in the choice to improve cowpea yield for humid environment performance. Knowledge of gene action with quantitative traits is important in enhancing yield improvement for environment sensitive varieties. That dominance component (H) was not zero is a pointer to the fact that the traits were not dominant at all loci but partial. All the traits exhibited partial dominance by recording additive components (D) to be higher than dominant components. These findings equally agree with the study of Saleh *et al.* (2002) who reported partial dominance for plant height and pod maturity for mungbean. Tefera (2002) reported additivity to increase amount of genotypic superiority available for future breeding programme.

The high additive gene effect for these traits is highly informative and that manipulation of genes controlling would produce appreciable results especially for humid sensitive environment.

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