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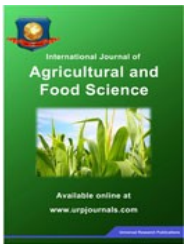

Original Article

MORPHO- GENETICS OF A LANDRACE CROSS OF COWPEA (*vigna unguiculata L. walp)* FOR HUMID ENVIRONMENT PERFORMANCE

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Abstract

Cowpea breeding programme have released varieties for dry savanna for dry savanna cowpea yield improvement. Knowledge of gene actions operative for humid environment-sensitive genotypes are explorable in practical cowpea breeding. Danilla (P_1), a land race genotype grown in dry savanna ecology and Ife-brown (P_2), a cultivar grown in dry and transitional savanna ecology respectively produced early generations of (F_1 - F_2) and backcrosses to study the inheritance pattern in 10 agronomic traits. Simple additive-dominance gene effects controlled variations in number and length of peduncles, number of pods per plant and number of seeds per pod. Additive gene effects were higher than dominant gene effects for these traits. Direct selection for seed weight and days to flowering with duplicate epistatic gene effects will not produce appreciable result in meaningful practical breeding. To breed for reduced date to flowering with weighted seed size, high genetic variance with fixed additive gene effects will be required for these traits. Peduncles and seed number traits with additive gene effect and reduced environmental effect can be exploited in practical breeding programme for producing high yielding genotypes of cowpea for humid savanna agro-ecology.

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Key words: humid savanna, gene interaction, traits, genotypes, inheritance, cowpea.

INTRODUCTION

The phenotype of any individual is the product of the combined action of the genotype and the environment (Tefera 2002). Genetic relationships arise from linkages which are in most cases pleiotropic and therefore important in meaningful crop improvement programme (Ng 1992). The seed yield of cowpea (*Vigna unguiculata (L) walp*) is determined by collective influence of both qualitative and quantitative traits. Phenolic similarity between cowpea parents and its progenies depend largely on the additive dominance variance components (Aremu *et al.,* 2003).

Cowpea is diploid and a self pollinating crop specie with 2n=22. 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.

Tefera and Peat (1997a) discovered complementary gene action on culms length, panicle weight and spikelet per panicle for *Tef* specie. Several works on the genetic studies of cowpea have been carried out. Fawole (1986) reported a single but recessive gene action controlling branching habit, while Baron and Ng (1990), gave additive gene effect for pod number and Khattack *et al* 2002, reported partial dominance for plant height at first flower for mungbean.

Table 1: Means and standard errors of cowpea characters of six generations in a cross P (Danilla) X P2 (Ife-brown).

	Generations					
Trait	P_1	P_2	F_1	F_2	BC_1	BC_2
Days to 50% flowering	55.33±0.20	36.76±0.14	49.00±0.08	52.13±0.31	53.00±0.22	42.61±0.25
Number of branches/plant	5.43±0.11	2.33±0.09	4.70±0.05	3.39±0.20	2.42±0.19	4.41±0.13
Number of peduncles/plant	18.23±0.23	11.22±0.14	19.72±0.13	17.21±0.35	19.25±0.15	15.31±0.21
Length of peduncle (cm)	42.00±0.12	28.66±0.19	45.51±0.15	35.30±0.41	31.54±0.15	15.31±0.21
Number of pods/plant	56.13±0.26	48.64±0.25	59.81±0.13	59.31±0.57	47.31±0.24	56.71±0.21
Number of seeds/pod	8.14±0.14	10.43±0.19	10.61±0.63	11.03±0.16	12.16±0.13	10.65±0.14
Days to 95% maturity	81.37±0.17	68.21±0.16	78.21±0.05	75.21±0.21	84.19±0.16	79.21±0.13
Height at flowering (cm)	40.31±0.21	31.72±0.15	33.42±0.06	33.17±0.52	37.39±0.19	39.42±0.14
Height at maturity (cm)	62.05±0.19	43.10±0.22	57.21±0.19	49.21±0.23	58.17±0.51	60.17±0.26
100 seed weight (g)	16.41±0.20	10.12±0.19	12.24±0.13	12.03±0.42	15.29±0.06	12.19±0.09
Number of plants	60	60	120	300	100	100

Table 2: Within family variance for traits in a cross Danilla X Ife-brown.

Trait	**P_1**	**P_2**	**F_1**	**F_2**	**B_1**	**B_2**
Days to 50% flowering	1.25	5.31	0.82	7.31	6.21	5.75
Number of branches/plant	0.48	0.49	0.63	2.06	1.62	0.96
Number of peduncles/plant	1.25	2.32	2.05	3.20	3.77	2.63
Length of peduncle (cm)	2.94	2.05	1.80	4.51	2.86	1.25
Number of pods/plant	3.74	3.31	5.91	7.42	4.27	2.17
Number of seeds/pod	0.47	0.82	0.53	2.22	1.29	1.63
Days to 95% maturity	1.63	2.21	2.49	3.47	2.93	2.21
Height at flowering (cm)	0.80	1.94	1.25	4.01	3.81	2.56
Height at maturity (cm)	2.86	4.02	2.73	1.72	2.17	1.91
100 seed weight (g)	1.03	1.22	2.03	3.21	3.01	2.33

Table 3: Joint scaling test with three parameter model m [d] [h] of Mather and Jinks (1985), for traits in a cross of Danilla X Ife-brown cowpea.

Trait	**M**	**[d]**	**[h]**	**Chi-square**
Days to 50% flowering	52.03±0.16	10.33±0.41	3.07±0.83	103.43
Number of branches/plant	2.92±0.08	0.75±0.32	-4.49±0.21	17.24
Number of peduncles/plant	18.75±0.14	2.92±0.32	-4.12±0.89	52.17
Length of peduncle (cm)	35.39±0.22	-9.76±0.12	-4.96±0.14	10.11
Number of pods/plant	52.33±0.41	-8.55±0.41	-5.08±0.31	19.51
Number of seeds/pod	14.00±0.09	0.29±0.24	-2.83±0.04	1.25
Days to 95% maturity	73.00±0.19	3.63±0.17	-7.27±1.31	148.22
Height at flowering (cm)	78.21±0.24	0.39±0.14	2.71±0.41	65.71
Height at maturity (cm)	93.83±0.13	4.21±0.22	-3.29±0.31	47.22
100 seed weight (g)	11.37±0.08	-1.11±0.21	2.71±0.41	63.27

Table 4: Estimates of genetic components of six generation means fitted to a six parameter models of Mather and Jinks (1985), Singh and Chaudhary (1985) for traits in a cross of Danilla X Ife-brown cowpea.

Trait	**M**	**D**	**H**	**I**	**J**	**L**
Days to 50% flowering	51.97±0.14	9.87±0.39	3.05±0.80	1.97±1.10	-12.63±0.71	-16.23±1.73
Number of branches/plant	2.53±0.11	-071±0.31	4.28±0.73	0.73±0.21	1.13±0.32	0.75±0.31
Number of peduncles/plant	18.71±0.04	2.70±0.32	-3.78±0.27	-2.91±0.14	6.21±0.63	-6.41±0.15
Length of peduncle (cm)	34.33±0.21	-9.70±0.11	3.93±-1.97	1.25±0.05	7.21±0.53	-16.41±0.22
Number of pods/plant	50.92±0.41	-8.13±0.36	-5.12±0.52	1.71±0.21	13.21±0.21	-12.46±0.31
Number of seeds/pod	14.21±0.07	0.18±0.21	-2.32±0.04	1.12±0.12	4.01±0.56	-3.50±0.09
Days to 95% maturity	70.89±0.20	4.03±0.35	-7.52±1.12	-3.21±0.91	-13.21±0.22	-20.83±0.43
Height at flowering (cm)	79.20±0.41	-2.01±0.19	-1.23±0.21	2.31±0.72	3.17±0.14	4.29±0.45
Height at maturity (cm)	92.91	4.20±0.21	2.17±0.17	3.17±0.44	4.21±0.21	9.33±0.75
100 seed weight (g)	11.21±0.07	-1.02±0.20	1.93±0.40	1.29±0.91	2.91±0.31	-5.43±0.63

According to Khattack 2002, traits with greater magnitude of additive × additive (i) type of epistasis than dominance × dominance (j) can be exploited by standard hybridization and selection procedures. This study therefore examined the gene actions operative in some cowpea traits using a cultivar and a land race parents of contrast environments and to identify explorable traits for humid environment breeding.

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 seedcoat 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) family. 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 second 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. 3m×3m field plots of Randomised Complete Block Design with three replications were used for each family generation. The inter and intra-row spacing was 45cm and 30cm respectively. The total number of plants from the harvest area for each of the family generation is detailed in Table 1. Two weeks after planting, insect pests were controlled using monocrotophos (Azodrin) at 4mls per 20 litres of water. Weeding was done manually as at when due. Data were recorded from each individual family. Data were collected on days to 50% flowering, height at flowering, 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).

The observed parental F_1, F_2, BC_1 and BC_2 means and variance were used to estimate mid-parent mean (m), Additive (d) and Dominance (h) gene effects, using Joint scaling test model with three parameters of Mather and Jinks (1985) assuming that epistatic gene effects were important for the traits. When the genetic variations observed in some traits were not adequately explained using the Joint scaling test, the interaction terms (i, j and h) were then included following the method of Mather and Jinks (1985). Components of genetic variance of Singh and Chaudhary (1985) were used to estimate the non-interacting parameters of the components. The model fitting was carried out using the IML procedure of SAS (2000 - 2005).

RESULT AND DISCUSSION

The trait mean values for Danilla (land-race larger parent) were larger except for number of seeds per pod. This justifies the use of a landrace with explorable genetic potential as first parent (P_1) even though the cultivated Ife-brown (smaller parent), flowered and matured earlier **(Table 1)**. The F_1 means for most traits fell within the parents range. Mean values for number of branches, peduncles, and length of peduncle per plant fell closer to that of the larger parent at the F_2 and BC_2 generations. This indicates dominance towards the larger parent. Betterstill, the mean values for number of pods per plant at the F_2 generation and number of seeds per plant were higher than that of the larger parent even as the mean values for number of seeds per pod and days to maturity were egually higher than that of the larger parent when backcrossed (BC_1).This indicated transgressive segregation towards overdominance and therefore places Danilla a better choice as parent in breeding for increased seed yield. Also, selection for more seed number even in the early generation of F_2, will be an added advantage. According to Tefera (2002), using a cross of Alba and Gea lamie tef plants, gene action was recorded to be overdominance for length of first and second basal culm internodes in the F_1 and F_2 mean values.

Within family variance values for the traits were higher in the BC_1 generation than in the BC_2 **(Table 2)**. This exposes the use of a landrace parent sourced from dry savanna ecology, to be of practical advantage in improving the yield of cowpea for specific adaptation to humid environment. According to Ogunbayo et al. (2007); Guei and Traore, (2001), landraces are good sources of unique genes for stress tolerance, high yield stability and adaptability and genetic dynamism. Using the joint scaling test, and weighted least square means with three parameter model of Mather and Jinks (1985), number of seeds per pod, length of peduncle and number of branch per plant were controlled by additive-dominance gene effects **(Table 3)**. Increased numbers of days to flowering and maturity as well as weight of seeds were controlled by dominance (H) gene effect. The simple additive-dominance model was not adequate in explaining the variation of the traits with high chi square values of ($P < 0.05$) and therefore extended to a six parameter model including three interaction terms additive-additive (i), additive-dominance (j), and dominance × dominance (L) terms **(Table 4)**. Number and length of peduncles, number of pods and number of seeds per plant respectively, showed a satisfactory fit with five-parameter model (m), (d), (h), (i) and (L) by dropping (j) which had very little genetic effect. Tefera (2002,) reported opposite signs of (h) and (L) gene effects to indicate duplicate gene action. This is true for number of branches, height at flowering and days to 50% flowering. Therefore, practical manipulation of those traits for cowpea specific environment yield improvement may be difficult especially at the early generation of F_2 and BC_2. To achieve success in breeding for reduced flowering and maturity dates would require that the genetic variance be high and the interaction effect fixed (Aremu *et al* 2003). Singh *et al.* (1997), in his findings, using inbred lines of pea, reported duplicate epistatic effect for number of pod and plant

Table5: Components of genetic variance for additive (D), dominance (H), direction of dominance (F), environmental (E), degree of dominance ($H/D^{1/2}$) for traits in a cowpea cross of Danilla X Ife-brown.

Genetic component	Days to 50% flowering	Number of branches	Number of peduncles	Length of peduncles (cm)	Number of pods/plant	Number of seeds	Days to 95% maturity	Height at flowering (cm)	Height at maturit (cm)	100 seed weight (g)
D	9.28	-1.04	4.62	0.86	4.10	1.86	-5.98	13.42	19.78	21.37
H	42.41	4.32	17.97	44.48	30.63	11.35	13.36	8.20	10.31	7.42
F	1.88	-0.41	1.05	1.97	1.94	-0.13	-0.97	2.31	1.37	1.93
E	48.52	5.53	17.70	20.60	40.30	0.67	2.11	91.30	38.30	14.20
$H/D^{1/2}$	1.74	1.88	1.44	0.84	2.48	2.47	1.50	0.52	1.22	1.03
Hb	89.16	72.43	82.00	89.34	76.60	87.29	67.31	49.20	6.27	30.14
Hn	35.56	25.84	40.05	67.12	18.72	21.48	31.77	53.70	28.10	72.30

height. Complementary gene effects were observed for number and length of peduncles per plant, number of pods per plant and number of seeds per pod. According to Tefera and Peat (1997); Mather and Jinks (1982), gene interaction is complementary when *h* and *L* components have same sign.

The effect of these complementary gene effects on these traits is such that yield improvement via peduncle length and number alone will not produce success in yield improvement until pod and seed number traits are equally incorporated into the breeding programme. This finding is important in that developing cowpea genotype specifically for humid tropic environment requires that the peduncles are long and above the plant canopy, so as to withstand the high relative humidity peculiar to humid environment and thus, prevent and or reduce fungal disease incidence.

The adequacy of additive-dominance model was further tested by partitioning the variations to show allelic or non-allelic relationship (Table 5). Dominance (H) components being greater than zero confirmed that the traits were not dominant at all loci but epistatic. However, plant height and seed weight exhibited partial dominance by having *D* values greater than *H* and the direction of dominance towards the larger parent (Danilla). khattack et al 2002, using mungbean discovered high value of *D* type of epistasis to be greater than *H* component for pod bean number and flower initiation. Also Dhaliwal at al. (2002), in the genetic analysis of tomatoe using contrasting parents discovered additivity in pulp weight.The high additive gene component exhibited by peduncle traits in this study agrees with the findings of khattack et al, (2002) and confirm the explorable potential in the choice of these traits for standard hybridization and selection procedure towards improving cowpea yield, even in the wet environment, where cowpea is naturally not favoured for good yield performance, due to high fungal disease attack.

CONCLUSIONS

This research reveals high family variance at F_2 and backcrosses using a landrace parent source with high trait performance. Selection for number of pod and peduncle per plant; number of seed per pod at the early generation of F_2, would produce achievable success as landrace crop type are potential sources of genes for crop improvement for wide environment adaptation. Number and length of peduncle per plant and number of seed per pod and pod per plant are controlled by complementary gene action. Therefore, cowpea yield improvement in humid environment is possible when these traits are simultaneously incorporated into the breeding programme.

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