Variability and Inheritance of Quantitative Traits in Hybrids among Cowpea [*Vigna unguiculata* (L.) Walp] Culti-groups

Ilori, C.O.* and Adewumi, A.S.
Department of Crop Protection and Environmental Biology, University of Ibadan, Nigeria.
*Corresponding Author E-mail: *chrislori@yahoo.com*

Abstract

Inheritance of quantitative traits in F_1 and RF_1 hybrids was studied in 14 cowpea accessions representing Unguiculata, Sesquipedalis and Biflora culti-groups. Twenty-three (23) F_1 and Twenty-five (25) RF_1 hybrids were evaluated together with the fourteen (14) parental lines in a Randomised Complete Block Design (RCBD) with four replicates. Data were taken on agro-morphological quantitative traits for the parental lines, F_1 and RF_1 hybrids. Significant differences were observed for all the quantitative traits evaluated among the parents as well as among the F_1 and RF_1 hybrids and their respective parental lines. Heterosis was observed for number of branches (198.97%), cotyledonary leaf length (22.81%), number of productive peduncles (22.67%), cotyledonary leaf width (21.92%) and number of leaves (20.65%). Estimates of broad sense heritability were high for hundred-seed weight (76.69), pod length (73.22), plant height (67.98), cotyledonary leaf width (65.08), cotyledonary leaf length (60.61) and days to first ripe pod (58.81). High genotypic and phenotypic variances were obtained for plant height while the lowest phenotypic and genotypic variances were obtained for cotyledonary leaf width. Total seed weight was showed significant positive correlations with plant height (0.24), number of leaves (0.32), number of branches (0.34), number of productive peduncles (0.42), peduncle length (0.22), number of pods (0.59), pod length (0.29), number of seeds per pod (0.43) and hundred seed weight (0.19). Hybridization across cowpea culti-groups can be useful in cowpea improvement programmes as a means of generating new genotypes that are multipurpose as well as broadening genetic variability.

Keywords: Accessions, Culti-groups, Genotypic variance, Heritability, Heterosis, Phenotypic variance, Quantitative traits

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is one of the most important grain legume crop grown in sub-Saharan Africa. Cowpea plays a major role in human nutrition not only because of its good protein quality with high nutritional value but also because cowpea hay is critical for feeding animals during the dry season in many parts of West Africa. Moreover, cowpea is a valuable source of income for farmers and grain traders of this region (Timko and Singh, 2008; Diouf, 2011). Although cultivated cowpea classification was based on three groups for a long time (Westphal, 1974), it is now based on four cultivar groups: *Unguiculata*, *Sesquipedalis*, *Biflora*, and *Textilis* (Pasquet, 1998). These culti-groups are a reflection of the variability present within the cultivated cowpeas.

Cultivated species of crops are usually variable because of artificial selection under diverse environments of which cowpea is not an exception. 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). Cowpea cultivated groups exhibit significant variation in their quantitative and qualitative traits (Padulosi and Ng, 1997). The variation in these traits may be explored in breeding programmes to develop hybrids that can combine various desirable traits to meet the needs of growers as well as optimise the use of available genetic resources by breeders. Hybridization across cultivated groups thus holds promise as a means of generating new genotypes that are multipurpose as well as broadening genetic variability.

The objectives of this study therefore are:

- to evaluate the variation in the quantitative traits in hybrids among cowpea cultivar groups
- to estimate heritability, genotypic and phenotypic variances among the quantitative traits
- to estimate the relatedness (correlation) among the evaluated quantitative traits

Materials and Methods

Experimental location

The experiment was conducted at the roof top garden of the Department of Crop Protection and Environmental Biology, University of Ibadan, Nigeria which is located at latitude 7° 27' N and longitude 3° 53' E.

Source of Experimental Materials

The fourteen cultivated cowpea accessions used in this study were collected from the Genetic Resource Center of the International Institute of Tropical Agriculture, Idi Ose, Ibadan. These accessions consisted of nine accessions of the *Unguiculata* culti-group (TVu1174, TVu1490, TVu1503, TVu1596, TVu1832, TVu1840, TVu2011, TVu2159 and TVu2311), four accessions of the *Sesquipedalis* culti-group (TVu21, TVu14204, TVu15651, TVu16441) and one accession of the *Biflora* culti- group (TVu13825).

Experimental Procedures

Hybridization

Fifty two crosses (26 main crosses and 26 reciprocal crosses) were made among the culti-groups of which forty eight (48) crosses consisting of 23 main crosses and 25 reciprocal crosses were successfully generated. The F_1 and RF_1 seeds generated were dried to constant moisture content preparatory to evaluation.

Evaluation

The 23 F_1 and 25 RF_1 seeds generated from the crosses and the 14 parental lines were evaluated in a Randomised Complete Block Design (RCBD) replicated four times giving a total 248 experimental units. Two seeds were sown into 25 cm diameter plastic pots containing about 6 kg top soil and later thinned to one plant per pot 2 weeks after planting. The pots were watered to field capacity regularly and agronomic practices such as weeding were carried out at regular intervals. Cyperdiforce® (Cypermethrin 30g/L + Dimethoate 250g/L) was sprayed at the rate 1L/ha at two-week intervals to control insect pests.

Data Collection

Data was collected on the following quantitative traits: cotyledonary leaf length and width (cm), plant height at six weeks after

planting (cm), number of leaves per plant, number of main branches per plant, number of productive peduncles per plant, peduncle length (cm), days to first flowering, days to first ripe pod, pod length (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g) and total seed weight (g).

Data Analysis

Data collected on quantitative traits were analysed using the Analysis of Variance Procedure of the GENSTAT software and means were compared using Least Significant Difference at 5% level of significance.

Heterosis was estimated following the mid-parent approach using the formula:

$$\text{Mid Parent Heterosis} = \frac{F_1 - MP}{MP} \times 100$$

Where

F_1 is the mean value for both F_1 and RF_1 and

MP is the mean value of the two parents

Heritability in the broad sense was estimated following the procedures of Falconer (1989). Genotypic variance and phenotypic variance were obtained from the analysis of variance table following the procedures described by Comstock and Robinson (1985). The mean square values used for genetic analyses to estimate Phenotypic Variance and Genotypic Variance were obtained following the procedures outlined by Singh and Chaudhury (1985). Correlation coefficients among the quantitative traits were estimated following the procedures of Kashiani and Saleh (2010) at 5% level of significance.

Results

Significant differences were observed for all the quantitative traits assessed among the parental lines both within and among the culti-groups (Table 1). Among the parental lines, coefficient of variation was very high for number of branches (94.02%) and plant height (71.16%). Coefficient of variation was moderate for number of pods per plant (34.05%), hundred-seed weight (33.85%) and pod length (30.56%).

Table 2 shows the variability in the quantitative traits for the parental lines, F_1 and RF_1 hybrids. Significant differences were observed among the F_1, RF_1 and their respective parental lines for all the quantitative traits. Estimate of hybrid vigour (heterosis) was very high for number of branches (198.97%). Heterosis estimates were also significant for cotyledonary leaf length (22.81%), number of productive peduncles (22.67%), cotyledonary leaf width (21.92%), number of leaves (20.65%), number of pods per plant (18.94%) and total seed weight (13.67%). The F_1 and RF_1 also flowered earlier (-7.05% heterosis) and matured earlier (-6.51% heterosis) compared to their respective parents. Reciprocal differences were also observed for plant height, number of branches, total seed weight, cotyledonary leaf length, cotyledonary leaf width and hundred-seed weight.

Table 1: Variation in quantitative traits among the parental lines in the cowpea culti-groups

Accession	Culti-group	PH (cm)	NL	CLL (cm)	CLW (cm)	DFF	DFRP	NB	NPPP	PedL (cm)	NPP	PodL (cm)	NSP	HSW	TSW
Tvu 1174	Unguiculata	18.2	7.25	5.2	3.14	36.75	52.75	0	3	18.73	4	15.73	10.17	8.45	4.67
Tvu 1490	Unguiculata	25.5	11.25	6.11	3.98	37.25	52.25	0	3.25	17.22	5.5	12.85	6.34	18.25	6.36
Tvu 1503	Unguiculata	30.7	10	6.83	4.24	39.5	56.5	0.25	2.75	22.69	3.5	12.62	7.58	16.89	3.83
Tvu 1596	Unguiculata	56.8	15.75	5.64	3.79	40.25	53.5	1.2	5.25	23.89	8	13.93	12.17	11.55	8.44
Tvu 1832	Unguiculata	52.1	16.5	6.31	3.78	36.5	52.25	1.4	5.25	23.19	7	12.09	10.17	18.69	7.34
Tvu 1840	Unguiculata	34.5	11	5.1	3.44	36	54.25	0	3.5	22.49	5	14.68	10.25	16.56	6.4
Tvu 2011	Unguiculata	27.2	10.25	5.48	3.83	39.75	54.75	1.25	3.25	17.93	5.25	12.24	11.04	12.07	5.39
Tvu 2159	Unguiculata	25.9	13	5.53	3.44	37.25	51	0.75	5	21.91	8	16.01	12.08	9.72	6.24
Tvu 2311	Unguiculata	31.1	13.75	4.73	3.79	35	56.25	0.5	3.75	24.59	7.25	12.68	11.5	11.48	6.98
Tvu 21	Sesquipedalis	29.5	18.5	8.33	4.71	35.25	52.75	0.25	2.75	19.36	4.5	23.35	7.83	24.88	7.1
Tvu 14204	Sesquipedalis	129.9	16.25	6.03	3.76	44.75	55.75	1.75	3.25	17.69	5.25	24.83	12.17	17.69	9.67
Tvu 15651	Sesquipedalis	24.5	12.25	5.58	3.46	42.25	54.25	1.2	3.25	20.85	5.25	19.56	11.67	14.25	7.24
Tvu 16441	Sesquipedalis	27.9	10.75	6.3	4.33	44.75	60.75	0.5	2	22.94	3.5	25.22	11.5	19.25	5.94
Tvu 13825	Biflora	38.6	12.75	4.73	2.88	38.5	51	0	4.75	23.42	10.5	11.26	12.42	6.78	7.64
Means		39.46	12.80	5.85	3.76	38.84	54.14	0.65	3.64	21.21	5.89	16.22	10.49	14.75	6.66
Std Error		7.50	0.82	0.25	0.13	0.86	0.69	0.16	0.27	0.68	0.54	1.32	0.52	1.33	0.40
Min		18.2	7.25	4.73	2.88	35	51	0	2	17.22	3.5	11.26	6.34	6.78	3.83
Max		129.9	18.5	8.33	4.71	44.75	60.75	1.75	5.25	24.59	10.5	25.22	12.42	24.88	9.67
CV (%)		71.16	24.03	16.06	12.72	8.31	4.80	94.02	28.07	11.95	34.05	30.56	18.44	33.85	22.32
LSD (0.05)		6.43	4.47	2.23	1.67	4.54	5.34	0.43	1.27	3.16	2.36	5.24	2.61	5.53	2.87

PH= Plant Height NL= Number of Leaves CLL=Cotyledonary Leaf Length CLW= Cotyledonary Leaf Width DFF= Days to first flower DFRP= Days to first ripe pod NB= Number of Branches NPPP= Number of Productive Peduncles per Plant PedL= Peduncle Length NPP= Number of Pods per Plant PodL = Pod Length NSP= Number of Seeds per pod HSW= Hundred Seed Weight TSW= Total Seed Weight.

Table 2: Variation in quantitative traits in the parental lines, F_1 and RF_1 hybrids among cowpea culti-groups

Quantitative traits	P_1 (Mean±SE)	P_2 (Mean±SE)	F_1 (Mean±SE)	RF_1 (Mean±SE)	LSD (0.05)	Estimate of heterosis (%)	Reciprocal Difference (F_1 - RF_1)	Reciprocal Difference as % of F_1 Means
PH (cm)	36.4±6.31	44.7±6.42	34.5±2.61	26.3±2.62	3.8	-25.03	8.2	26.97
NL	12±0.62	12.7±0.33	14.2±0.83	15.6±0.71	5.2	20.65	-1.4	-9.40
CLL (cm)	5.8±0.15	5.6±0.22	7.4±0.11	6.6±0.17	1.02	22.81	0.8	11.43
CLW (cm)	3.8±0.08	3,5±0.13	4.7±0.14	4.2±0.13	0.7	21.92	0.5	11.24
DFF	37.9±0.72	40.1±0.6	34.6±0.42	37.9±0.46	3.8	-7.05	-3.3	-9.10
DFRP	54.1±0.43	53.4±0.62	48.8±0,38	51.7±0.35	3.1	-6.51	-2.9	-5.77
NB	0.53±0.1	0.44±0.12	1.6±0.2	1.3±0.2	1.8	198.97	0.3	20.69
NPPP	3.7±0.2	3,8±0.2	4.7±0.22	4.5±0.15	1.8	22.67	0.2	4.35
PedL (cm)	21.1±0.51	22.2±0.51	21.9±0.84	20.2±0.5	4.3	-2.77	1.7	8.08
NPP	5.6±0.32	7.6±0.59	8.0±0.52	7.7±0.47	3.7	18.94	0.3	3.82
PodL (cm)	15.1±0.76	17.1±1.22	15.2±0.61	15.5±0.69	2.9	-4.66	-0.3	-1.95
NSP	10.1±0.4	11.6±0.28	10.9±0.31	11.2±0.45	2.7	1.84	-0.3	-2.71
HSW (g)	14.6±0.84	12.7±1.31	14.1±0.96	12.7±0.82	3.4	-1.83	1.4	10.45
TSW (g)	6.3±0.3	7.6±0.19	8.5±0.45	7.3±0.3	3.9	13.67	1.2	15.19

PH= Plant Height NL= Number of Leaves CLL=Cotyledonary Leaf Length CLW= Cotyledonary Leaf Width DFF= Days to first flower DFRP= Days to first ripe pod NB= Number of Branches NPPP= Number of Productive Peduncles per Plant PedL= Peduncle Length NPP= Number of Pods per Plant PodL = Pod Length NSP= Number of Seeds per pod HSW= Hundred Seed Weight TSW= Total Seed Weight.

Table 3 shows the estimates of coefficients of variation, genotypic and phenotypic variances and broad sense heritability for the quantitative traits assessed in the F_1 and RF_1 hybrids and their respective parental lines. Coefficient of variation was high for number of branches (61.2%), plant height (52.7%) and total seed weight (36.4%). Genotypic variance was high for plant height, hundred-seed weight, pod length and number of leaves. Phenotypic variance was also high for plant height, hundred-seed weight, number of leaves, peduncle length, pod length and days to first flower. Cotyledonary leaf width had the lowest genotypic and phenotypic variances.

High broad sense heritability estimates were obtained for hundred seed weight (76.69%), pod length (73.22%), plant height (67.98%), cotyledonary leaf width (65.08%), cotyledonary leaf length (60.61%) and days to first ripe pod (58.81%). Moderate broad sense heritability estimates were obtained for days to first flower (49.35%), peduncle length (44.85%), number of seeds per pod (42.14%) and number of leaves (41.77%).

Table 3: Coefficients of Variation, Genotypic and Phenotypic Variances and Broad Sense Heritability estimates for the quantitative traits studied on the F_1 and RF_1 and the parental lines

Quantitative traits	Coefficient of Variation (%)	Genotypic Variance (σ^2G)	Phenotypic Variance (σ^2P)	Broad Sense Heritability (H^2B)
PH	52.7	19.98	28.88	67.98
NL	25.7	9.77	23.39	41.77
DFF	7.4	7.25	14.69	49.35
DFRP	4.3	6.84	11.63	58.81
NB	61.2	0.51	2.21	23.08
CLL	10.7	0.89	1.32	60.61
CLW	11	0.41	0.63	65.08
NPPP	29.5	0.59	2.25	26.22
PedL	14.7	7.95	17.96	44.85
NPP	36	4.13	11.22	36.81
PodL	13.5	12.06	16.47	73.22
NSP	17.6	2.68	6.36	42.14
HSW	17.6	18.95	24.71	76.69
TSW	36.4	1.71	9.38	18.23

PH= Plant Height NL= Number of Leaves CLL= Cotyledonary Leaf Length CLW= Cotyledonary Leaf Width DFF= Days to first flower DFRP= Days to first ripe pod NB= Number of Branches NPPP= Number of Productive Peduncles per Plant PedL= Peduncle Length NPP= Number of Pods per Plant PodL = Pod Length NSP= Number of Seeds per pod HSW= Hundred Seed Weight TSW= Total Seed Weight

Table 4: Relationships among quantitative traits evaluated in the F_1 and RF_1 hybrids and the parental lines

Traits	DFF	PH	NL	NB	DFRP	NPPP	LP	CLL	CLW	NPP	LPP	NSP	HSW	TSW
DFF	1.00													
PH	0.04	1.00												
NL	-0.01	0.17*	1.00											
NB	-0.08	0.01	0.60*	1.00										
DFRP	0.68*	0.02	-0.03	-0.13*	1.00									
NPPP	-0.19*	0.12	0.55*	0.42*	-0.26*	1.00								
PedL	-0.11	0.05	-0.02	-0.06	-0.16*	0.20*	1.00							
CLL	-0.36*	0.02	0.05	0.18*	-0.39*	0.07	-0.05	1.00						
CLW	-0.41*	-0.01	-0.05	0.07	-0.36*	0.003	-0.07	0.79	1.00					
NPP	-0.09	0.07	0.37*	0.22*	-0.26*	0.60*	0.24*	-0.07	-0.16	1.00				
PodL	0.0002	0.24*	0.08	0.15*	0.09	-0.10	-0.08	0.36	0.30	-0.25*	1.00			
NSP	0.10	0.17*	0.23*	0.19*	-0.06	0.17*	0.23*	-0.18	-0.25	0.33*	0.15*	1.00		
HSW	-0.15*	0.14*	0.01	0.09	0.09	-0.11	-0.12	0.43	0.44	-0.33*	0.65*	-0.34*	1.00	
TSW	-0.19*	0.24*	0.32*	0.34*	-0.27*	0.42*	0.22*	0.17	0.10	0.59*	0.29*	0.43*	0.19*	1.00

*Significant ($P \leq 0.05$)

DFF= Days to first flower PH= Plant Height NL= Number of Leaves NB= Number of Branches DFRP= Days to first ripe pod NPPP= Number of Productive Peduncles per Plant PedL= Peduncle Length CLL= Cotyledonary Leaf Length CLW= Cotyledonary Leaf Width NPP= Number of Pods per Plant PodL = Pod Length NSP= Number of Seeds per pod HSW= Hundred Seed Weight TSW= Total Seed Weight.

Table 4 shows the correlation coefficients among the quantitative traits studied. Total seed weight showed significant positive correlation with plant height (0.24), number of leaves (0.32), number of branches (0.34), number of productive peduncles (0.42), peduncle length (0.22), number of pods (0.59), pod length (0.29), number of seeds per pod (0.43) and hundred seed weight (0.19). Total seed weight also showed significant negative correlation with days to first flower (-0.19) and days to first ripe pod (-0.27). Hundred seed weight showed significant negative correlation with days to first flower (-0.15), number of pods per plant (-0.33) and number of seeds per pod (-0.34) but showed significant positive correlation with plant height (0.14) and pod length (0.65). Number of seeds per pod showed significant positive correlation with plant height (0.17), number of leaves (0.23), number of branches (0.19), number of productive peduncles (0.17), length of peduncle (0.23), number of pods (0.33) and length of pod (0.15). Plant height had significant positive correlation with number of leaves (0.17), pod length (0.24), number of seeds per pod (0.17), hundred-seed weight (0.14) and total seed weight (0.24).

Discussion

This study revealed significant differences in the quantitative traits evaluated in the parents both within and among the culti-groups as well as among the parents, F_1 and RF_1 hybrids. The significant differences both within and among the culti-groups reflect the variability in the quantitative traits evaluated. The hybrids were also observed to have better performance for some traits when compared to their parents suggesting their superiority over their parental lines. This shows prospects of further improvements in the progenies through selection in subsequent generations which may be further exploited in improvement programmes. Estimates of heterosis being high for number of branches,

cotyledonary leaf length, number of productive peduncles, cotyledonary leaf width, number of leaves, number of pods per plant, total seed weight, days to first flower and days to first ripe pod could possibly be due to overdominance. According to Dhaliwal *et al.,* (2002) transgressive gene segregation leads to increase in hybrid vigour.

The reciprocal differences observed for some of the traits may be due to the influence of cytoplasmic or maternal genes or an interaction between nuclear and cytoplasmic genes. Manggoel and Uguru, (2012) also observed reciprocal differences in the hybrids between day-neutral cowpea genotypes and day-sensitive cowpea genotypes.

The high genotypic and phenotypic variances obtained for plant height, hundred-seed weight, pod length, number of leaves, hundred-seed weight, peduncle length and days to first flower suggests a good prospect of making selections for new cultivars using these traits as selection indices. These traits, with the exception of days to first flower, also have significant positive correlations with total seed weight. This suggests good prospects of using these traits for making selections for higher seed yields among the progenies of the hybrids among the culti-groups.

High broad sense heritability estimates were obtained for hundred seed weight, pod length, plant height, cotyledonary leaf width, cotyledonary leaf length, days to first ripe pod and days to first flower. This suggests that the expression of these traits are influenced more by genetic factors than environmental factors. Previous studies had also reported high heritability in the broad sense in cowpea for plant height (Omoigui *et al.,* 2006). High broad sense heritability estimates obtained for days to first ripe pod, pod length and moderate broad sense heritability obtained for number of seeds/pod was earlier reported by Tyagi *et al.,* (2000) and Ansari *et al.* (2004). High heritability estimates reflect the large heritable variance which offers the possibility of improvement through hybridization and selection.

Significant positive correlations recorded between total seed weight and most of quantitative traits indicate possible gains from selection when hundred seed weight, number of seeds per pod, number of pods per plant, pod length, number of productive peduncles, peduncle length, plant height, number of leaves and number of branches are used as selection indices. This agrees with the observations of Lopes *et al*., (2001) and Mehrani, (2002), who analyzed different traits of cowpea and also found significant and positive correlations between pod length, hundred seed weight and grain yield. Romanus *et al*., (2008) also reported significant and positive correlation between pod length, number of seeds per pod and yield of seven cowpea lines. The significant positive correlations observed between stem height and some other yield determining traits suggests that plant height may influence the ability of the plant to intercept sunlight which enhances the photosynthetic ability of the plant. This may increase the amount of assimilates generated at the podding stage resulting in higher total seed weight.

Conclusion

The results of this study have revealed that hybridization across cowpea culti-groups can be useful in cowpea improvement programmes. Some hybrids in the First Generation and Reciprocal First Generation were observed to perform better in some of the evaluated quantitative traits and these hybrids can be further selected in producing new genotypes with better performance in terms of fodder and grain yields.

The results from this study also revealed that the evaluated quantitative traits such as plant height, number of leaves, number of branches, number of productive peduncles, peduncle length, number of pods, pod length, number of seeds per pod, hundred seed weight, days to first flower and days to first ripe pod can be explored as selection indices in cowpea improvement programmes to select desirable parental lines and hybrids across cowpea culti-groups.

Acknowledgement

The authors are grateful to Dr. O.A. Oyatomi and the Genetic Resources Centre of the International Institute of Tropical Agriculture, Ibadan for providing the cowpea accessions used for this study.

References

Birky, C.W. (2001).The inheritance of genes in mitochondria and chloroplasts: laws, mechanisms and models. *Annual Review of Genetics* 35: 125-148.

Dhaliwal, M.S., Kaur, A. and Singh, S. (2002). Genetic analysis and correlations involving populations derived from *L. esculentum* X *L. pimpinellifolium* crosses of tomato: *Journal of Genetics and Plant Breeding* 56: 345-352.

Diouf, D. (2011). Recent advances in cowpea [*Vigna unguiculata* (L.) Walp.] "omics" research for genetic improvement. *African Journal of Biotechnology* 10: 2803-2810.

Manggoel, M. and Uguru, M.I. (2012). Evidence of Maternal Effect on the Inheritance Flowering Time in Cowpea [*Vigna unguiculata* (L.) Walp] *International Journal of Plant Breeding and Genetics*, 6: 1-16.

Mehrani, P. (2002). Genetic diversity in local and exotic pea (*Pisum sativum L.*) germplasm for morphological traits and SDS-PAGE markers. *M. Phil Dissertation* Quaid-e-Azam University, Islamabad.

Omoigui, L.O. Ishiyaku, M. F., Kamara, A.Y., Alabi, S. O. and Mohammed, S.G. (2006). Genetic variability and heritability studies of some reproductive traits in cowpea (*Vigna unguiculata* (L.) Walp). *African Journal of Biotechnology*, 5(13): 1191-1195.

Othman, S. A., Singh B. B. and Mukhtar, F.B. (2006). Studies on the inheritance pattern of joints, pod and flower pigmentation in cowpea [*Vigna unguiculata* (L.) Walp]. *African Journal of Biotechnology*, 5(23): 2371-2376.

Padulosi, S. (1993). Genetic diversity, taxonomy and ecogeographic survey of the wild relatives of cowpea (*V. unguiculata*). *Ph.D. Thesis*. University Catholique Lovain-la-Neuve.

Padulosi, S. and Ng, N.Q. (1997). Origin, taxonomy and morphology of *Vigna unguiculata* (L.) Walp. In: Singh, BB, DR Mohan-Raj, KE Dashiell and LEN Jackai. (Eds). Advances in Cowpea Research. Co-publication of IITA and JIRCAS, IITA Ibadan.

Pasquet, R. S. (1998) Morphological study of cultivated cowpea *Vigna unguiculata* (L) Walp: importance of ovule number and definition of CV Gr Melanophthalmus. *Agronomie* 18:61-70.

Pasquet, R. S. (1999). Genetic relationships among subspecies of *Vigna unguiculata* (L.)Walp. Based on allozyme variation. *Theoretical and Applied Genetics* 98:1104–1119.

Romanus, K.G., Hussein, S. and Mashela, W. P. (2008). Combining ability analysis and association of yield and yield components among selected cowpea lines. *Euphytica* 162: 205-210.

Timko, M.P. and Singh, B.B. (2008). Cowpea, A Multifunctional Legume. In: Genomics of Tropical Crop Plants (Moore PH and Ming R, Eds.). Springer Science & Business Media, New York, 227-258.

Tyagi, P.C., Kumar, N. and Agarwal, M.C. (2000). Genetic variability and association of component characters for seed yield in cowpea (*Vigna unguiculata* [L.] Walp.) *Legume Research,* 23(2) : 92–96.

Vaillancourt R.E. and Weeden N.F. (1992). Chloroplast DNA polymorphism suggests a Nigerian center of domestication for the cowpea, *Vigna unguiculata* (Leguminosae). *American Journal of Botany* 79: 1194–1199.

Westphal, E. (1974). Pulses in Ethiopia: their taxonomy and agriculture significance. Agricultural Research Reports 815. Centre for Agricultural Publishing and documentation, Wageningen.