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Full Length Research Paper

Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vigna unguiculata* (L.) Walp] accessions

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Field experiments were conducted in 2006 and 2007 to estimate genetic variability, heritability, correlations and path analysis of some reproductive characters on grain yield of 10 cowpea accessions. The experiment was laid out in a Randomized Complete Block Design (RCBD) at the research farm, University of Nigeria, Nsukka. The accessions showed significant ($p<0.05$) variability for days to 50% flowering, number of peduncles plant^{-1}, flowers plant^{-1}, pods plant^{-1}, seeds pod^{-1}, pod length, 100-seed weight and grain yield. The magnitudes of the genotypic variance of these traits were higher than the environmental variance, indicating that the genotypic component was the major contributor to total variance. Phenotypic coefficient of variation and genotypic coefficient of variation were high for the traits studied, except pod length and seeds pod^{-1}. High broad-sense heritability (63.16 - 96.74%) indicated the presence of additive gene effects. Positive correlation were found between grain yield and number of peduncles plant^{-1} (r = 0.716), flowers plant^{-1} (r = 0.776**), pods plant^{-1} (r = 0.640*) and 100-seed weight (r = 0.690*). Path analysis showed high positive direct effects of number of peduncles plant^{-1} (p = 0.94), flowers plant^{-1} (p = 1.40) and 100-seed weight (p = 1.45). Numbers of peduncles plant^{-1}, flowers plant^{-1}, pods plant^{-1} and 100-seed weight were identified as selection criteria for obtaining good parental lines in cowpea breeding programs.**

Key words: Accession, additive effects, cowpea, path analysis, variability.

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp) is one of the important food legumes in the hot-dry tropics and sub-tropics and especially, in the sub-Saharan Africa (Uarrota, 2010). Cowpea plays a substantial role by serving as a grain and vegetable crop mainly for the rural people in the East, West, South and Central parts of Africa (Mortimore et al., 1997). According to Diouf (2011), cowpea feeds millions of people in the developing world with an annual worldwide production estimated around 4.5 million metric tons on 12 to 14 million ha. Yield potential of cowpea is high, averaging 1.5 to 6 t ha^{-1} depending on genotype, though actual yields are low with annual total production ranking 8th among pulse crops (FAO, 2007).

In the context of yield enhancement, in order to have a good choice of character for selection of desirable genotypes under planned breeding programme, knowledge of the nature and magnitude of variation existing in available plant breeding materials, the association of component characters with yield and their exact contribution through direct and indirect effects are very important. Genotypic and different components of variance, heritability and genetic advance have been calculated for different yield characters in cowpea by several workers (Damarany, 1994; Uguru, 1995; Pathmanathan et al., 1997; Umaharan et al., 1997; Ubi et al., 2001; Omoigui et al., 2006) which revealed that selection was effective for

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Table 1. Meteorological data for 2006 and 2007 cropping seasons at Nsukka, Nigeria.

Weather record	Jan.	Feb.	Mar.	Apr.	May	Jun.	Jul.	Aug.	Sept.	Oct.	Nov.	Dec
2006												
Total rainfall (mm)	36.3	4.0	103.1	51.0	243.8	259.6	213.8	195.5	190.5	313.9	1.5	0
Rain days (No.)	1	2	4	5	16	16	21	19	25	19	1	0
Max. air temp (°C)	33.1	33.6	33.1	35.5	30.5	29.9	28.6	27.8	28.1	29.9	31.7	32.6
Min. air temp (°C)	23.0	23.2	22.8	23.3	21.3	21.2	21.5	20.8	21.3	21.2	18.9	17.9
Relative humidity (%)	66.5	67.8	67.6	68.2	74.4	74.9	76.8	77.4	76.7	74.8	60.8	50.0
2007												
Total rainfall (mm)	0	9.9	39.1	121.6	193.5	327.6	62.9	323.6	169.6	267.2	55.1	0
Rain days (No.)	0	1	4	8	11	16	14	17	19	18	4	0
Max. air temp (°C)	33.2	35.0	35.1	32.6	31.1	29.3	28.5	27.6	28.2	29.5	30.4	31.6
Min. air temp (°C)	20.8	22.6	23.1	22.9	21.8	21.8	21.2	21.8	21.3	20.7	21.3	20.0
Relative humidity (%)	57.5	64.3	67.1	69.2	73.9	74.8	76.9	76.9	76.9	73.8	66.2	63.1

a population with broad genetic variability and character with high heritability.

Correlation analysis is a handy technique which provides information that selection for one character results in progress for other positively correlated characters. The importance of correlation studies in selection programmes is appreciable when highly heritable characters are associated with the important character like yield. Correlation coefficients, although, very useful in quantifying the size and direction of trait associations can be misleading if the high correlation between two traits is a consequence of the indirect effect of other traits (Bizeti et al., 2004). Path coefficient is an excellent means of studying direct and indirect effects of interrelated components of a complex trait. Path-coefficient analysis measures the direct influence of one variable on another. Each correlation coefficient between a predictor variable and the response variable is partitioned into its component parts: the direct effect or path coefficient (a standardized partial regression coefficient) for the predictor variable and indirect effects which involve the product of a correlation coefficient between two predictor variables with the appropriate path coefficient in the path diagram (Dewey and Lu, 1959). By determining the inter-relationships among grain yield components, a better understanding of both the direct and indirect effects of the specific components can be attained (Chaudhary and Joshi, 2005). Several workers have estimated the correlation between different yield attributing characters and their direct and indirect effects on yield in cowpea (Uguru, 1996; Nakawuka and Adipala, 1999), soyabean (Malik et al., 2007; Vange and Egbe, 2009), rice (Tran Thi et al., 1999; Saif-ur-Rasheed et al., 2002) and bambara groundnut (Makanda et al., 2009; Oyiga and Uguru, 2011). The objective of the present investigation was to estimate the genetic variability, association of different characters and their direct and indirect effect on grain yield with a view to identify the accessions with best potentiality for upgrading grain yield and its component characters.

MATERIALS AND METHODS

Experimental site and materials

Two field experiments were carried out in 2006 and 2007 cropping seasons at the Teaching and Research Farm of the Department of Crop Science, Faculty of Agriculture, University of Nigeria, Nsukka. Nsukka is in the derived savannah agro-ecological zone with vegetation predominantly of grass interspersed with trees. The area is characterized by low land humid tropical conditions and has a bimodal rainfall pattern with a total annual rainfall of about 1500 mm. The relative humidity ranges from 70 to 80% while the ambient temperature ranges from 20 to 30°C during the rainy season. The weather data from the University of Nigeria, Nsukka meteorological station are presented in Table 1. The experimental materials comprised of ten cowpea accessions. Six accessions were obtained from Pankshin, Shendam and Langtang North LGAs of Plateau state, North central Nigeria (Latitude 09°26′N; Longitude 9°08′E and altitude of 282.2 m above sea level), and four accessions were obtained from Nsukka LGA of Enugu state, South-eastern Nigeria (Latitude 06°52′N; Longitude 07°24′E and altitude of 447.2 m above sea level).

The source and description of the cowpea accessions used for the study are presented in Table 2. The experimental design was a Randomized Complete Block Design (RCBD) with three replications. The experimental plot was 0.075 ha. This was ploughed and harrowed to provide a fine tilth. The experimental unit was 4 × 4 m (16 m^2). The treatment was the ten cowpea accessions. Planting was done in July of 2006 and 2007 using a 1 × 1 m intra and inter row spacing was used giving a total of 16 plants $plot^{-1}$. Plants in the two middle rows constituted the net plot and used as the sampling unit. The plots were weeded manually to keep weed pressure low. Other recommended agronomic management practices were adopted for optimum crop growth and development.

Data collection and analysis

The data collected included days to 50% flowering, number of

Table 2. Description of the cowpea accessions used in the study.

Accession	State	Village/town	Latitude and longitude	Growth habit	100-seed weight(g)	Seed size description	Seed-coat color
Bwa-Tal	Plateau	Tal-Pankshin	9°26'N 9°08'E	Decumbent	22.3	Large***	Cream
Bwa-Chip	Plateau	Chip-Pankshin	9°26'N 9°08'E	Decumbent	20.4	Large	Ash
Gag	Plateau	Tal-Pankshin	9°26'N 9°08'E	Climbing	15.9	Medium**	Black
Gazum	Plateau	Gazum	9°08'N 9°47'E	Decumbent	27.3	Large	White
Du'ut	Plateau	Shendam	8°43'N 9°30'E	Decumbent	27.4	Large	White
Jalbang	Plateau	Shendam	9°26'N 9°08'E	Decumbent	17.4	Medium	Oxblood
Akidi-ani	Enugu	Nsukka	6°52'N 7°24'E	Decumbent	11.3	Small*	Black
Akidi-enu1	Enugu	Nsukka	6°52'N 7°24'E	Climbing	11.4	Small	Black
Akidi-enu2	Enugu	Nsukka	6°52'N 7°24'E	Climbing	10.8	Small	Ash
Akidi-enu3	Enugu	Nsukka	6°52'N 7°24'E	Climbing	10.7	Small	Brown

*Small = <15g/100-seed weight, **Medium =15-19g/100-seed weight, ***Large = >20g/100-seed weight; (Omoigui et al., 2006).

flowers/plant, number of peduncles/plant, number of pods/plant, pod length, number of seeds/pod, 100-seed weight and grain yield. Numerical counts were made for the number of leaves/plant and number of primary branches/plant. Vine length was measured at 4, 8 and 12 weeks after planting (WAP). Days to 50% flowering was monitored as the number of days from sowing to when 50% of the plants within a plot flowered. A numerical count of the number of flowers/plant, peduncles/plant, and seeds/pod was done. One hundred seeds were weighed to obtain the 100-seed weight for each accession and grain yield plot^{-1} were weighed and extrapolated to hectare equivalent in line with standard unit of measuring grain yield (Kg/ha).

Data for all the variables measured were subjected to Analysis of Variance (ANOVA), to estimate the level of variability among the cowpea accessions, using Genstat Discovery Edition 3 (Genstat, 2007) software. The phenotypic variation for each trait was partitioned into genetic and non-genetic factors and estimated according to Johnson et al. (1955) and Uguru (2005):

$V_p=MS_g/r$; $V_g=(MS_g-MS_e)/r$; $V_e=MS_e$

Where V_p, V_g and V_e are phenotypic variance, genotypic variance and environmental variance, respectively; MS_g, MS_e and r are mean squares of accessions, mean squares error and number of replications respectively.

To compare the variations among traits, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) were computed according to the method suggested by Allard (1960) and Burton (1952):

$PCV = (\sqrt{V_p}/X)\ 100$
$GCV = (\sqrt{V_g}/X)\ 100$
$ECV = (\sqrt{V_e}/X)\ 100$

Where X is the grand mean for each of the studied traits. Broad sense heritability (h^2B) was calculated according to Burton and DeVane (1953) and Allard (1960) as the ratio of the genotypic variance (V_g) to the phenotypic variance (V_p). The correlation coefficients (r) were computed among all the measured traits using SPSS for Windows Version 16 (SPSS, Inc., Chicago, IL). Path coefficient analyses were calculated using the Analysis for Moment Structures for Windows Version 16 (AMOS Development Corp., Spring House, USA) software program to partition the correlations obtained into components due to direct and indirect effects.

RESULTS

Genetic variability

The mean squares and genetic parameters estimates of the 10 cowpea accessions averaged over two growing seasons are presented in Table 3. The analysis of variance showed that the mean squares for the accessions were highly significant for all traits measured. The phenotypic variance was partitioned into heritable (genotypic variance) and non heritable (environmental variance) components. Generally, the phenotypic variance was higher than the genotypic variance in all the traits studied. The magnitude of the genotypic variance for all the yield traits were however higher than the environmental variance (Table 3). The phenotypic coefficient of variation (PVC) and Genotypic Coefficient of Variation (GCV) were highest for 100-seed weight (41.46 and 38.47 respectively), followed by grain yield (38.55 and 36.76 respectively), number of peduncles plant^{-1} (36.96 and 32.86 respectively), number of flowers plant^{-1} (32.29 and 29.59 respectively), number of pods plant^{-1} (29.88 and 28.23 respectively) and days to 50% flowering (26.54 and 26.02 respectively). Low PVCs and GVCs were recorded for number of seeds pod^{-1} (24.11 and 20.66 respectively) and pod length (19.81 and 15.79 respectively). The Environmental Coefficient of Variation (ECV) was generally low for all traits

Table 3. Estimates of mean squares, variance components and heritability of 10 cowpea accessions averaged over two cropping seasons.

Trait	Mean	MS	σ^2_{ph}	σ^2_g	σ^2_e	PCV	GCV	ECV	H^2B (%)
Days to 50% flowering	56.67	710.07**	241.94	234.07	7.87	26.54	27.45	4.95	96.74
No. of peduncle plant^{-1}	37.50	495.74**	192.08	151.83	40.25	36.96	32.86	16.92	79.05
No. of flowers plant^{-1}	71.90	1443.86**	538.85	452.51	86.34	32.29	29.59	12.92	83.98
No. of pods plant^{-1}	46.10	534.45**	189.78	169.34	20.44	29.88	28.23	9.81	89.23
Pod length(cm)	17.49	27.33**	12.08	7.63	4.45	19.87	15.79	12.06	63.16
No. of seeds pod^{-1}	13.53	20.25**	10.64	7.81	2.83	24.11	20.66	12.43	73.40
100 Seed weight (g)	15.91	118.08**	43.15	37.47	5.68	41.46	38.47	14.98	86.84
Grain yield Kg ha^{-1}	1.49	0.93**	0.33	0.30	0.03	38.55	36.76	11.62	90.91

MS = mean squares, σ^2_{ph} = phenotypic variance, σ^2_g = genotypic variance, σ^2_e = environmental variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, ECV = environmental coefficient of variation, H^2B (%) = broad sense heritability.

Table 4. Correlation coefficients of days to flowering and yield components of 10 cowpea accessions averaged over two cropping seasons.

Variable	1	2	3	4	5	6	7	8
50%DF	1							
PE/P	-0.060	1						
FL/P	0.549*	0.547	1					
PO/P	-0.056	0.836**	0.662*	1				
PL	0.100	0.857**	0.655*	0.780**	1			
S/PO	-0.015	0.392	0.588	0.577	0.584	1		
100-SW	0.767**	0.110	0.603	0.001	0.099	0.144	1	
GY	-0.521**	0.716**	0.776**	0.640*	0.621*	0.333	0.690*	1

** Correlation is significant at 0.01 level of probability (2-tailed); * correlation is significant at 0.05 level of probability (2-tailed)
D50%F = Days to 50% flowering, PE/P=No. of Peduncle plant^{-1}, FL/P=No. of flowers plant^{-1}, PO/P=No. of pods plant^{-1}, PL= pod length (cm), S/PO= No. of seeds pod^{-1}, 100SW=100 seed weight (g) GY= grain yield (Kg/ha).

assessed and ranged from 4.95 to 16.92. Broad sense heritability estimates was high (Table 3) for days to 50% flowering (79.05%), number of peduncles plant^{-1} (96.74%), number of flowers plant^{-1} (83.98%), number of pods plant^{-1} (89.23%), pod length (63.16%), number of seeds pod^{-1} (73.40%), 100 seed weight (86.84%) and grain yield (90.91%).

Correlation

Simple correlation coefficients calculated among the characters averaged over two cropping seasons (years) are presented in Table 4. Significantly positive correlations were found between grain yield and number of peduncles plant^{-1} (r = 0.716**), number of flowers plant^{-1} (r = 0.776**), number of pods plant^{-1} (r = 0.640**) pod length (r = 0.621**) and 100-seed weight (r = 0.690**). Conversely, grain yield was negatively correlated with days to 50% flowering (r= -0.521*). Days to 50% flowering however, had significantly positive correlations with number of flowers plant^{-1} (r = 0.549*) and 100-seed weight (r = 0.767**). This trait also recorded a negative relationship with number of peduncles plant^{-1} (r = -0.060), pods plant^{-1} (r = -0.056) and seeds pod^{-1} (r = -0.015) (Table 4).

Path coefficient analysis

Path diagrams showing cause and effect relationships of pod yield and its components are presented in Figure 1. The direct, indirect and total effects of some reproductive traits on grain yield averaged over two cropping years are presented in Table 5. Path analysis showed the highest positive direct effect of 100-seed weight (p = 1.45). This character was followed by number of flowers plant^{-1} (p = 1.40), number of peduncles plant^{-1} (p = 0.94) and number of seeds pod^{-1} (p = 0.49). Pod length (p = -1.78), days to 50% flowering (p = -1.20) and number of pods plant^{-1} (p = -0.97) contributed negative direct effects on grain yield (Table 5).

Despite the high negative direct effects of days to 50% flowering, its indirect effects via number of flowers plant^{-1}

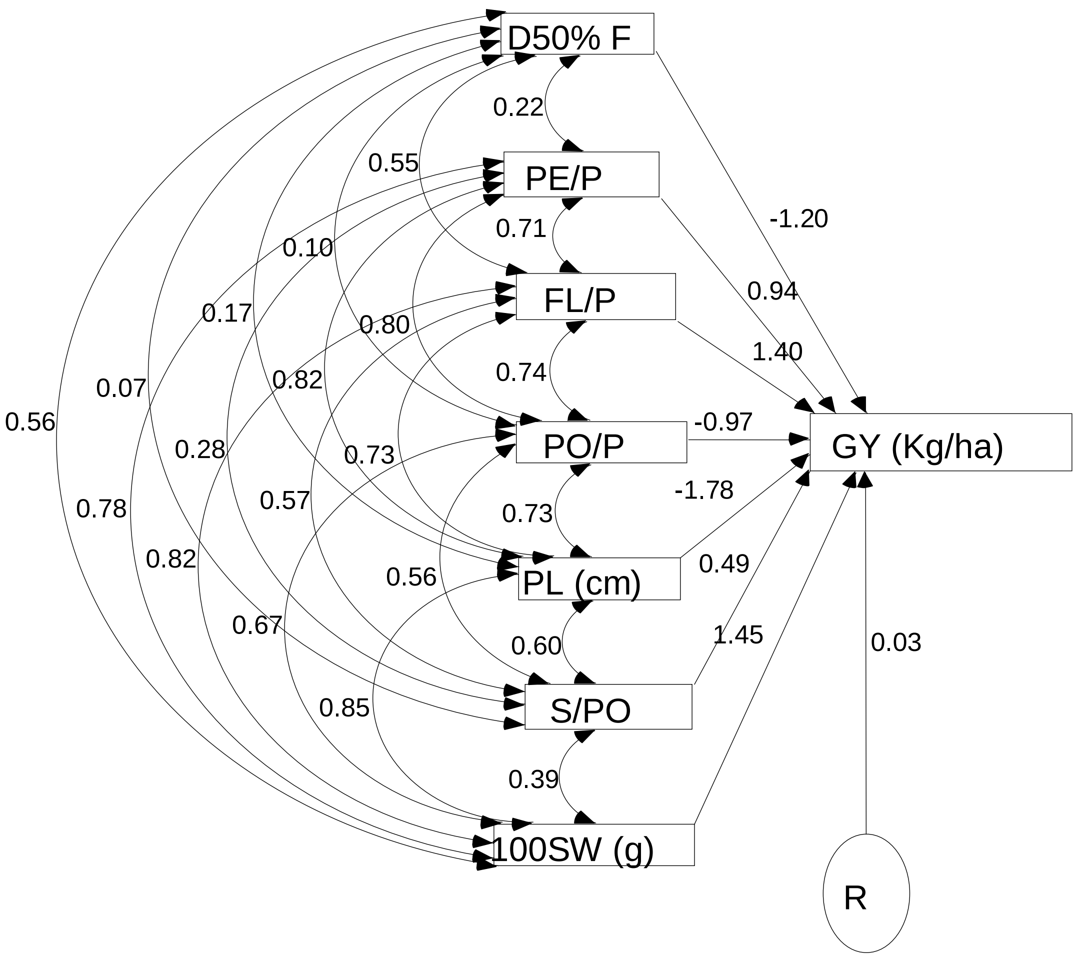

Figure 1. Path diagram representing cause and effect relationships among reproductive traits and grain yield in 10 cowpea accessions averaged over two cropping seasons. D50%F = Days to 50% flowering, PE/P=No. of peduncle plant^{-1}, FL/P=No. of flowers plant^{-1}, PO/P=No. of pods plant^{-1}, PL=Pod Length (cm), S/PO= No. of seeds pod^{-1}, 100SW=100 seed weight (g) GY= grain yield (Kg/ha).

Table 5. Path analysis showing direct and indirect influence of reproductive traits on grain yield of 10 cowpea accessions averaged over two cropping seasons.

Variable	Indirect effect to GY							Total effects		Total correlation to grain yield
	1	2	3	4	5	6	7	Direct	Indirect	
D50%F		0.21	0.77	-0.10	-0.30	0.03	0.81	-1.20	1.42	0.22
PE/P	-0.26		0.99	-0.78	-1.46	0.14	1.13	0.94	-0.24	0.70*
FL/P	-0.66	0.68		-0.72	-1.30	0.28	1.19	1.40	-0.53	0.87**
PO/P	-0.12	0.75	1.04		-1.30	0.27	0.97	-0.97	1.61	0.64*
PL	-0.20	0.77	1.02	-0.71		0.29	1.23	-1.78	2.40	0.62*
S/PO	-0.84	0.26	0.80	-0.54	-1.07		0.57	0.49	-0.82	0.33
100SW	-0.67	0.73	1.15	-0.65	-1.51	0.19		1.45	-0.76	0.69*

D50%F = days to 50% flowering, PE/P=No. of peduncle plant-1, FL/P=No. of flowers plant-1, PO/P=No. of pods plant-1, PL=pod length (cm), S/PO= No. of seeds pod-1, 100SW=100 seed weight (g).

(p = 0.77) and 100-seed weight (p = 0.81) were positive. Similarly the indirect effects of pod length and number of pods plant^{-1} on grain yield via number of flowers plant^{-1} (p = 1.02) number of peduncles plant^{-1} (p = 0.77) and 100-seed weight (p = 1.23) were significantly high and positive. The indirect effects of number of pods plant^{-1} on grain yield via number of flowers plant^{-1} (p = 1.04), number of peduncles plant^{-1} (p = 0.75) and 100-seed weight (p = 0.97) were also high and positive (Table 5).

DISCUSSION

The highly significant difference in mean squares implied that there is discernable evidence of inherent genetic variability among the cowpea accessions with respect to days to 50% flowering, number of peduncles plant^{-1}, number of flowers plant^{-1}, number of pods plant^{-1} pod length, number of seeds pod^{-1}, 100 seed weight and grain yield.

The result of the variance components in this study showed that the phenotypic variance was higher than the genotypic variance in all the traits studied. The magnitude of the genotypic variance for all the yield components were however higher than the environmental variance. This result is in accord with the report of several authors (Damarany, 1994; Umaharan et al., 1997; Ubi et al., 2001; Omoigui et al., 2006) in cowpea. The low environmental influence observed compared to genetic factors suggests that the traits may be under genetic control rather than the environment, hence improvement can be achieved through selection (Vange and Egbe, 2009; Oyiga and Uguru, 2011).

The minimum magnitudinal differences in GCV and PCV coupled with low ECV for all the traits studied implied that the traits are mostly governed by genetic factors with little role of environment in the phenotypic expression of these characters. Thus, selection of these traits on the basis of the phenotypic value may be effective. Nausherwan et al. (2008) reported that polygenic variation may be phenotypic, genotypic or environmental and the relative values of these three types of coefficients give an idea about the magnitude of the variability.

Broad sense heritability refers to the ratio of heritable variance to total variance. In a narrow sense, heritability is defined as the ratio of additive genetic variance to total variance. Broad sense heritability estimates in this study were generally high for all the traits studied. The heritability values obtained in this study are within the values reported from several published studies in cowpea (Damarany, 1994; Fery and Singh, 1997; Umaharan et al., 1997; Nakawuka and Adipala, 1999; Ubi et al., 2001; Omoigui et al., 2006; Adeyanju and Ishiyaku, 2007), Mungbean (Khan, 1985; Makeen et al., 2007) and bambara groundnut (Adeniji et al., 2008; Oyiga and Uguru, 2011). According to Ubi et al. (2001), heritability estimates along with genetic advance are more useful in predicting the resultant effect for the selection of the best individuals from a population. High broad sense heritability values indicated the predominance of additive gene action in the expression of these traits and can be improved through individual plant selection (Vange and Ojo, 1997; Makeen et al., 2007; Rashwan, 2010).

The significantly positive relationships between grain yield and number of peduncles plant^{-1}, number of flowers plant^{-1}, number of pods plant^{-1} and pod length agrees with an earlier study on cowpea by Leleji (1981) who reported a positive correlation of 0.88 for pods plant^{-1} and 0.66 for seeds pod^{-1} with grain yield. The positive association between grain yield and yield attribute is also in accord with an earlier study on character association in cowpea by Uguru (1996). The author implicated pods plant^{-1} and seeds pod^{-1} as the major yield determining traits.

The vegetative phase of the plant has been found useful in allowing for the development of optimum canopy necessary for high yield (Ishiyaku and Singh, 2003). The linear relationship between days to flowering and these yield traits is therefore not out of place; since increase in days to flowering allows for proper development of the vegetative part leading to production of more number of peduncles plant^{-1}, flower plant^{-1} and other yield traits. The inverse relationship in this study is however, at variance with the report of a recent study on some floral traits and their implication on pod and seed yield in bambara groundnut (*Vigna subterrenea* (L.) Verde) conducted by Oyiga et al. (2010). The authors reported significant positive correlations between seed weight and number of pods plant^{-1} with some floral traits.

Partitioning of the total correlation into direct and indirect effects would provide actual information on the contribution of traits and thus form the basis for selection to improve grain yield. The high direct effects of number of flowers plant^{-1}, number of peduncles plant^{-1} and 100-seed weight on grain yield in this study suggests that these traits are good yield enhancing indices. However, the indirect effects of these traits on grain yield via days to 50% flowering, pod length and number of pods plant^{-1} were negative. According to Izge et al. (2006) higher indirect values could most likely be neutralized in most cases by negative indirect effects via other characters and this can lead to their low and non-significant genotypic correlations with total yield. In this regards, selection for such characters may not enhance yield improvement.

The values of direct effect of number of flowers plant^{-1}, number of peduncles plant^{-1} and 100-seed weight were higher than the value of correlation coefficient of this character with grain yield. Therefore, direct selection through these traits would be effective. The high positive indirect effects of number of pods plant^{-1} via number of flowers plant^{-1}, number of peduncles plant^{-1} and 100-seed weight neutralized its high negative direct effect resulting to a high total correlation to grain yield, thus, direct selection through pods plant^{-1} would also be effective. Such similar results have been reported in cowpea (Singh, 1974; Uguru, 1995; Nakawuka and Adipala, 1999); Soyabean (Bizeti et al., 2004; Malik et al., 2007; Vange and Egbe, 2009) and bambara groundnut (Makanda et al., 2009; Oyiga and Uguru, 2011) which confirmed our results. That number of peduncles plant^{-1} had significantly high positive indirect effects on grain yield via number of flowers plant^{-1} is consistent with the fact that increased in the number of peduncles plant^{-1} result in a corresponding increase in the number of flowers plant^{-1}.

Within in the range of materials used in this study, there exist substantial genetic variability and heritability in the character studied to warrant selection in the cowpea accessions for improvement. The level of genetic variability observed for different traits would be useful for breeding varieties of cowpea for high yield. The high genetic variance components and heritability estimates couple with significantly positive correlations and high direct effects of number of flowers plant^{-1}, number of peduncles plant^{-1}, pods plant^{-1} and 100-seed weight on grain yield, these traits were identified in this study and could be listed in selection criteria for good parental lines in a cowpea breeding program.

REFERENCES

Adeniji OT, Peter MJ, Bake I (2008). Variation and interrelationship for pod and seed yield characters in bambara groundnut (*Vigna subterrenea*) in Adamawa State. Nig. Afr. J. Agric. Res., 3 (9): 617-621.

Adeyanju AO, Ishiyaku MF (2007). Genetic study of earliness in cowpea cowpea [*Vigna unguiculata* (L.) Walp] under screen house condition. Int. J. Plant Breed. Genet., 1: 34-37.

Allard RW (1960). Principles of plant breeding. New York; John Wiley and Sons Inc. 485 pp.

Bizeti HS, deCarvalho CGP, deSouza JRP, Destro D (2004). Path Analysis under Multicollinearity in Soybean. Agron. J., 47(5): 669-676.

Burton GW (1952). Quantitative inheritance in grasses. Proceedings of the 6th International Congress, 1: 277-283

Burton GW, DeVane EM (1953). Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agron. J., 45:478-481.

Chaudhary RR, Joshi BK (2005). Correlation and Path Coefficient Analyses in Sugarcane. Nepal Agric. Res. J., 6: 24-28.

Damarany AM (1994). Estimates of genotypic and phenotypic correlation, heritability and potency of gene set in Cowpea [*Vigna unguiculata* (L.) Walp.]. Assuit J. Agric. Sci., 25: 1-8.

Dewey DR, Lu KH (1959). A correlation and path coefficient analysis of components of crested wheatgrass seed production. Agron. J., 51: 515-518.

Diouf D (2011). Recent advances in cowpea [*Vigna unguiculata* (L.) Walp.] "omics" research for genetic improvement. Afr. J. Biotechnol., 10(14): 2803-2819.

FAO (2007). FAOSTAT. Food and Agriculture Organization of the United Nations, Rome, Italy.

Fery RL, Singh BB (1997). Cowpea genetics, a review of recent literature. In: *Advances in cowpea research*. B.B. Singh, D.R. Mohan Raj K.E. Dashiell and L.E.N. Jackai (eds.) Copublication of IITA and JIRCAS. IITA, Ibadan, Nigeria, pp 13-29.

Ishiyaku MF, Singh BB (2003). Inheritance of shortday-induced dwarfing in photosensitive cowpea. Afr. Crop Sci. J., 9(2): 1-8.

Izge AU, Kadams AM, Gungula DT (2006). Studies on character association and path analysis of certain quantitative characters among parental lines of pearl millet (*Pennisetum glaucum*) and their F_1 hybrids in a diallel cross. Afr. J. Agric. Res. 1(5): 194-196.

Johnson AW, Robinson HF, Comstock RE (1955). Estimates of genetic and environmental variability in soyabean. Agron. J., 47: 314-318

Khan IA (1985). Correlation and path coefficient analysis of yield components in mung bean (*Phaseolus aureus* Roxb.). Bot. Bull. Academia Sinica, 26: 13-20.

Leleji OI (1981). The extent of hybrid vigour for yield and yield components in cowpea (*Vigna unguiculata* (L.) Walp) in the Savana region of Nigeria. Nig. J. Agric. Sci., 3(2): 141-148.

Makanda I, Tongoona P, Madamba R, Icishahayo D, Derera J (2009). Path analysis of bambara groundnut pod yield components at four planting dates. Res. J. Agric. Biol. Sci., 5(3): 287-292

Makeen KA, Garard J, Arif J, Singh KA (2007). Genetic variability and correlations studies on yield and its components in mungbean (*Vigna radiata* (L.) wilezek). J. Agron., 6: 216-218.

Malik MFA, Ashraf M, Qureshi AS, Ghafoor A (2007). Assessment of genetic variability, correlation and path analyses for yield and its components in soybean. Pak. J. Bot., 39(2): 405-413.

Mortimore MJ, Singh BB, Harris F, Blade SF (1997). Cowpea in Traditional Cropping Systems. In: Advances in Cowpea Research, Singh, B.B., D.R. Mohan Raj, K.E. Dashiell and L.E.N. Jackai (Eds.). IITA and JIRCAS, Hong Kong, pp 99-113.

Nakawuka CK, Adipala E (1999). A Path coefficient analysis of some yield component interactions in cowpea. Afr. Crop Sci. J., 7: 327-331.

Nausherwan NN, Ghulam MS, Khalid M, Qamar S, Akhtar S (2008). Genetic variability, correlation and path analysis studies in garden pea (*Pisum sativum* L.). J. Agric. Res., 46(4): 333-340.

Omoigui LO, Ishiyaku MF, Kamara AY, Alabi SO, Mohammed SG (2006). Genetic variability and heritability studies of some reproductive traits in cowpea [*Vigna unguiculata* (L.) Walp.]. Afr. J. Biotechnol., 5(13):1191-1195

Oyiga BC, Uguru MI (2011). Genetic Variation and Contributions of Some Floral Traits to Pod Yield in Bambara Groundnut (*Vigna subterranea* L. Verdc) under Two Cropping Seasons in the Derived Savanna of the South-East Nigeria. Inter. J. Plant Breed., 5(1): 58-63.

Oyiga BC, Uguru MI, Aruah CB (2010). Studies on the floral traits and their implications on pod and seed yields in bambara groundnut [*Vigna subterrenea* (L.) Verdc]. Aust. J. Crop Sci., 4(2): 91-97.

Pathmanathan U, Ariyanayagam RP, Haque SO (1997). Genetic analysis of yield and its components in vegetable cowpea [*Vigna unguiculata* (L.) Walp.] Euphytica, 92(2): 207-213.

Rashwan AMA (2010). Estimates of some genetic parameters using six populations of two cowpea hybrids. Asian J. Crop Sci., 2: 261-26.

Saif-ur-Rasheed M, Sadaqat HA, Babar M (2002). Inter-relationship among grain quality traits in rice (*Oryza sativa* L.). Asian J. Plant Sci., 1(3): 245-247.

Tran Thi NHTQK, Tan PS, Hiraoka H (1999). Path-coefficient analysis of direct-seeded rice yield and yield components as affected by seeding rates. Japan International Research Center for Agricultural Sciences, Tsukuba, Ibaraki, Japan. pp. 104-110.

Uarrota VG (2010). Response of cowpea (*Vigna unguiculata* [L.] Walp) to water stress and phosphorus fertilization. J. Agron., 9: 87-91.

Ubi EB, Mignouna H, Obigbesan G (2001). Segregation for seed weight, pod length and days to flowering following cowpea cross. Afr. Crop Sci. J., 9(3): 463-470.

Uguru MI (1995). Heritable relationships and variability of yield and yield components in vegetable Cowpea. Afr. Crop Sci. J., 3(1): 23-28.

Uguru MI (1996). Correlation and Path-Coefficient analysis of major yield components in vegetable Cowpea [*Vigna unguiculata* (L.) Walp.]. Proc. 14th HORTSON Conference, Ago-Iwoye, 1-4 April, 1996.

Umaharan P, Ariyanayagan RP, Haque SQ (1997). Genetic analysis of yield and its components in vegetable cowpea [*Vigna unguiculata* (L.) Walp.]. Euphytica, 7: 207-213.

Vange T, Egbe MO (2009). Studies on Genetic Characteristics of Pigeon Pea Germplasm at Otobi, Benue State of Nigeria. World J. Agric. Sci., 5(6): 714-719.

Vange T, Ojo AA (1997). Variability and Heritability estimates of yield and yield components in some Nigeria lowland rice genotypes. Inter. Rice Res. Notes (IRRN), Phillipines. 22: 3-6.