

Genetic Variability, Correlation and Path Coefficient Analysis in Seed Yield and Related Traits of Cowpea (*Vigna Unguiculata* (L.)Walp) Germplasm Accessions on High Altitude Area of Jos Plateau

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Abstract

A field experiment was carried out at Dagwom farm at National Veterinary Research Institute (NVRI) Vom, in Jos South Local Government area of Plateau state Nigeria (Lat.09^o44N, long.08^o47E, altitude 1293.2 m above sea level) in 2013 and 2014 rainy seasons, to evaluate the genetic variability, correlation and path coefficient analysis in seed yield and related traits of cowpea. The treatments consisted of eighty (80) cowpea germplasm accessions obtained from International Institute for Tropical Agriculture (IITA) Ibadan Nigeria. The experiment was laid out in a Randomized Complete Block Design (RCBD) in two replicates. The Analysis of Variance (ANOVA) showed significant difference at (P<0.01) among the entries for all the yield and related traits accessed. High phenotypic coefficient of variability (PCV) compared with genotypic coefficient of variability (GCV) coupled with low Environmental coefficient of variability (ECV) was observed for all the yield and related traits accessed. High broad sense heritability (H²B) and genetic advance (GAM (%)) was observed for the entire yield and related traits accessed except days to maturity which recorded high heritability with moderate genetic advance. Significant positive correlation was observed between grain yield and number of pod per plant (r=0.572**), hundred seed weight (r=0.504**), pod length (r=0.523**), number of secondary branches per plant (r=0.450**), number of seed per pod (r=0.431**), number of primary branches per plant (r=0.339**) plant height (r=0.285*), suggests that improving any of these characters will boost grain yield of cowpea. Path coefficient analysis showed that, number of pod per plant (P=0.65), hundred seed weight (P=0.54), number of seed per pod (P=0.29) number of secondary branches per plant (P=0.16), plant height (P=0.05)), and pod length (P=0.04) contributed directly to grain yield. The result from this study therefore revealed that hundred seed weight, number of pod per plant, number of secondary branches per plant, number of seed per pod, pod length and plant height recorded high genetic variability, heritability and genetic advance coupled with high significant genotypic correlation with grain yield and

contributed directly to grain yield. Therefore, these characters should be considered when planning hybridization programme for cowpea yield improvement.

Keywords: *Accessions, Germplasm, Cowpea, Genetic Advance, Heritability, Correlation, Path Analysis.*

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Introduction

Cowpea (*Vigna unguiculata(L.) Walp*) is a very important crop legume in Nigeria. It is a vital crop in the livelihood of both humans and animals, where it serves as a close substitute to animal protein especially to people who cannot afford animal protein due to low income and large family size. The dry leaves, stem and husk also serve as a rich source of protein for ruminant animals. Cowpea is considered as poor man's meat. They are generally rich in protein (18-25 %) and good source of mineral and vitamins (Tharanathan and Mahadevamma, 2003). Cowpea fixes atmospheric nitrogen through symbiosis with nodule bacteria (Shiringani and Shimeles, 2011). It does well and is most popular in the semi-arid regions of the tropics where other food legumes do not perform well (Sankie et al., 2012). Cowpea ranks well among neglected crops and can contribute to food security if its genetic resources are saved for utilization in breeding and improvement (Adewale et al., 2012).

More than 4.9 million tons of dried cowpea are produced worldwide with Africa producing over 5.2 million. Nigeria, the largest producer and consumer, accounts for 61% of production in Africa and 58% worldwide (IITA, 2009).

Considering the importance of cowpea to the livelihood of humans and animals, there is a need therefore to expand its cultivation to other areas of Nigeria especially the high altitude of Jos, so as to meet the nutritional requirements of the growing population in Nigeria and the world at large.

Jos is located on a high altitude with a mountainous climate characterized by very low temperatures. Cowpea is a heat-loving crop which can thrive well on low lands and warm climate especially in the savannah region. It is therefore a challenge for breeders to develop new cowpea varieties suitable for cultivation in this disadvantageous area. And these can be achieved through planned breeding programs.

The first step in any breeding program is to find out if there is sufficient variability among the breeding materials for breeders to explore. Variability is the basis for selection in any crop. And that can be achieved through estimation of phenotypic and genotypic variabilities, heritability and genetic advance (Denton and Nwangburuka, 2011). Emphasized that genotypic and phenotypic coefficients of variation and heritability accompanied with genetic advance are very important parameters in improving traits.

Variability alone is not adequate to enable selection of characters of interest for further breeding work, that was why correlation was used in this study to reveal the relation between some characters and yield. Correlation, even though very important in determining the relationship between two variables, can be misleading especially when correlated with an important character like yield, since yield is a complex trait controlled by many genes and also environment. That was why path coefficient analysis was used in order to decompose the total correlations into direct and indirect effects to know which character contributed positively and directly to yield and can be selected for further improvement. Several researchers (Manggoel et al., 2012; Lesly, 2005; Alidu et al., 2013; El-Ahainy, 2012) have estimated

correlation between yield and yield contributing characters and their direct and indirect effects on cowpea and have revealed that character that has contributed positively and directly to grain yield can be selected for further work on cowpea yield improvement. That is why this research is carried out to evaluate the genetic variabilities correlation and path coefficient analysis in cowpea germplasm accessions with the objective of selecting characters of interest to be utilized in further breeding work for improving the yield potential of cowpea on high altitude area of Jos.

Materials and Methods

Experimental site location

The experiment was carried out in Dagwom farm at National Veterinary Research Institute (NVRI) Vom, Jos South Local Government Area of Plateau State (Lat.09⁰44N, long.08⁰47E. altitude 1293.2 m above sea level) during the 2013 and 2014 cropping seasons.

Experimental Materials

Eighty (80) Cowpea (*Vigna unguiculata* (L.) Walp) accessions obtained from International Institute for Tropical Agriculture (IITA) Ibadan, Nigeria, were used for this study.

Experimental Design

The experiment was laid out in a Randomized Complete Block Design (RCBD) in two replicates. Each accession was planted in a row of 30 cm long, with a spacing 70 cm x 30 cm between and within row respectively. All standard agronomic practices for cowpea were followed strictly to ensure full expression of the cowpea potentials. The crop was harvested after maturity. Matured pod were handpicked 2-3 times from each row and sun dried before post-harvest data collected.

Data Collection and Analyses

Data were collected from five (5) randomly selected plants in the mid row of each accessions on the following characters: plant establishment, plant height, days to flower initiation, days to flower termination, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pod per plant, pod length, number of seed per pod, hundred seed weight and grain yield (kg/ha). The data were subjected to analysis of variance (ANOVA) using Crop Stat Version 7.2 model software program, developed by the crop and soil science Department USA to estimate the level of variabilities among the accessions. Correlation was analysed using Genstat Discovery Edition 3 (Genstat, 2007) software program. To partition the total correlation into direct and indirect effect, Analysis for Moment Structure for Windows Version 16 (AMOS Development Corp., House USA) software program was used.

The phenotypic variation for each trait was partitioned into genetic and non-genetic factors as estimated according to Johnson *et al.* (1955). As follows:

$$\delta^2 g = \frac{MSg - MSe}{r} \delta^2 ph = \delta^2 g + \frac{MSe}{r}$$

$$\delta^2 e = \frac{MSe}{r}$$

Where $\delta^2 g$, $\delta^2 ph$ and $\delta^2 e$ are genotypic, phenotypic and environmental variances respectively while MSg, MSe and r are mean squares for accessions, mean squares error and number of replications respectively.

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

$$GCV = \frac{\sqrt{\delta^2 g}}{\bar{X}} \times 100\% , PCV = \frac{\sqrt{\delta^2 ph}}{\bar{X}} \times 100\%$$

$$ECV = \frac{\sqrt{\delta^2 e}}{\bar{X}} \times 100\%$$

Where \bar{X} is the grand mean for the studied character. The categorization of phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) and environmental coefficient of variability (ECV) was done as per the scale given by Subramanian and Memon, (1973) as follows.

<u>Category</u>	<u>Range</u>
Low	<10 per cent
Moderate	11-20 per cent
High	>20 percent

Broad sense heritability (H^2B) is the ratio of the genotypic variance to the total variance, its denotes the proportion of phenotypic variances that is due to genotypes (heritable) and is calculated according to the formula given by Henson *et al.* (1956).

$$H^2B = \frac{\delta^2 g}{\delta^2 g + \delta^2 e} \times 100\%$$

Where

$\delta^2 g$ = genotypic variance

$(\delta^2 g + \delta^2 e)$ = Phenotypic variance

Broad sense heritability (H^2B) was categorized as proposed by Johnson *et al.* (1955).

<u>Category</u>	<u>Range</u>
Low	<30 per cent
Moderate	30-60 per cent
High	>60 percent

Genetic advance is the improvement in the mean genotypic value of the selected families over the base population it is calculated in percent of mean using the formula given by Johnson *et al.* (1955).

$$GA(\% \text{ of mean}) = \frac{\delta^2 g + (k)}{\delta p \times \bar{X}} \times 100\%$$

Where

k = selection differential at 5% selection intensity k=2.06

$\delta^2 g$ = genotypic variances

δp = phenotypic standard deviation of the character

The range of genetic advance as percentage of mean for various traits was categorized as suggested by Johnson *et al.* (1955)

<u>Category</u>	<u>Range</u>
Low	<10 per cent
Moderate	11-20 per cent
High	>20 percent

Results

Genetic variability heritability and genetic advance

Analysis of variance (ANOVA) revealed highly significant difference at ($P < 0.01$) for all the yield and related traits accessed. The (ANOVA) also revealed significance accession \times season ($A \times S$) interaction for all the yield and related traits accessed except plant height Table 2.

The results of the Phenotypic coefficient of Variability (PCV), Genotypic coefficient of Variability (GCV) Environmental coefficient of variability (ECV), broad sense heritability (H^2B) and genetic advance as percent of mean GAM % for all the characters observed are presented in Table 3. Generally, the PCV were higher than GCV also the ECV was lower in magnitude compared with GCV for all the

yield and related traits accessed. High heritability H^2B with genetic advance GAM % were observed in all the yield and related traits accessed except days to maturity which recorded high heritability with low genetic advance. The highest heritability with genetic advance was observed for hundred seed weight.

Genotypic Correlation with grain yield

Genotypic correlation computed among the characters averaged over two years are presented in Table 4. Significant positive correlation was found between grain yield and number of pod per plant ($r=0.572^{**}$), pod length ($r=0.523^{**}$) hundred seed weight ($r=0.504^{**}$), number of secondary branches per plant ($r=0.450^{**}$), number of seed per pod ($r=0.431$), number of primary branches per plant ($r=0.339^{**}$) and plant height ($r=0.285^*$).

Genotypic Path Coefficient Analysis

Path diagram showing cause and effect relationship of grain yield and its related traits are presented in Figure 1. The direct, indirect and total effect of some yield and related traits on grain yield averaged over two years are presented in Table 5.

Number of pod per plant recorded the highest direct effect on grain yield its direct contribution was 0.65 out of the total genotypic correlation of 0.5746. The value of the direct contribution of number of pod per plant was higher than the genotypic correlation coefficient of this character to grain yield. It's contributed indirectly to grain yield via number of secondary branches 0.12 and plant height 0.0035.

Hundred seed weight recorded a direct contribution of 0.54 to grain yield out of the total genotypic correlation of 0.506, it contributed indirectly to grain yield via number of seed per pod was 0.0928, pod length 0.0264 and plant height 0.0105. The values of the direct effect of hundred seed weight on grain yield was higher than its total genotypic correlation to grain yield.

The direct contribution of number of seed per pod to grain yield was $P=0.29$, it's recorded a highest indirect contribution to grain yield via hundred seed weight 0.162, pod length 0.0276, and plant height 0.016. The character recorded a total genotypic correlation of 0.4076 to grain yield.

The direct contribution of number of secondary branches per plant to grain yield was 0.16 out of the total correlation of 0.4507, it contributed indirectly to grain yield via number of pod per plant 0.4875, number of seed per pod 0.0261, pod length 0.0008 and plant height 0.005.

Pod length recorded a direct contribution of 0.04 to grain yield. Its contributed indirectly to grain yield via hundred seed weight 0.3564, number of seed per pod 0.2001 and plant height 0.0185. Pod length recorded a total genotypic correlation of 0.5285 to grain yield.

The direct contribution of plant height to grain yield was 0.05, its contributions to grain yield was highest via hundred seed weight 0.1134 then number of seed per pod 0.0928, number of pod per plant 0.0455, pod length 0.0148 and number of secondary branches per plant 0.016. Plant height recorded a total genotypic correlation of 0.2866 to grain yield.

Number of primary branches per plant only contributed indirectly to grain yield via number of pod per plant 0.2925 number of secondary branches per plant 0.1136, number of seed per pod 0.0135 plant height 0.0812 pod length 0.0104 and hundred seed weight 0.0054. The character recorded a total genotypic correlation of 0.3466 to grain yield.

Table 1. Meteorological data for 2013 and 2014 cropping seasons at Vom Jos South Local Government area of Plateau State Nigeria

Weather Record	Total Rainfall(mm)		Rain days		Max. air Temp °C		Min. air temp °C		R.H (%)	
	2013	2014	2013	2014	2013	2014	2013	2014	2013	2014
August	273.6	256.1	16	17	24	24	18	17	84	79
September	277	279	15	19	26	26	18	17	78	71
October	88.9	76.4	7	6	28	28	15	20	51	54
November	0	0	0	0	32	31	13	13	34	38
December	15.2	0	1	0	29	28	13	14	36	32

Source: National Root Crops Research Institute Potato Programme Vom Jos south Plateau state

Table 2. Combined analysis of variance for twelve traits of cowpea on high altitude area of Jos plateau state Nigeria

Traits	MS accessions	MS season	(A X S)
Plant establishment (%)	1317**	813.1**	*
Plant height (cm)	69.37**	56.56 ^{NS}	NS
Days to flower initiation	120.6**	203.2*	*
Days to flower termination	155.0**	845.0**	**
Days to maturity	112.8**	732.1**	**
Number of primary branches per plant	3.37**	2.19 ^{NS}	**
Number of secondary branches per plant	7.45**	7.93 ^{NS}	**
Number of pod per plant	36.61**	145.4**	**
Pod Length (cm)	21.40**	15.56**	**
Number of seed per pod	14.30**	63.51**	**
100 Seed weight (g)	13.79**	4.26**	**
Grain yield (kg/ha)	114360**	691943**	**

MS =Mean squares, * =significant at $p < 0.05$, **=significant at $p < 0.01$, NS= not significant

Table 3. Phenotypic Genotypic Environmental Variances, Heritability and Genetic Advance for twelve traits of Cowpea (*Vigna unguiculata* (L.) Walp) averaged over two years on high altitude area of Jos Plateau state Nigeria.

Traits	GCV(%)	PCV(%)	ECV(%)	H ² B(%)	GAM(%)
Plant establishment (%)	60.39	64.81	23.57	86.78	115.90
Plant height (cm)	31.28	37.76	25.15	68.65	53.43
Days to flower initiation	11.99	13.23	5.48	82.20	22.30
Days to flower termination	11.27	11.78	3.44	91.46	22.20
Days to maturity	8.24	8.77	2.98	88.51	15.98
Number of primary branches per plant	42.96	46.93	19.13	83.43	80.66
Number of secondary branches per plant	33.30	39.71	21.60	70.51	57.60
Number of pod per plant	41.34	47.82	23.91	74.86	73.63
Pod Length (cm)	24.47	25.49	7.01	92.40	48.56
Number of seed per pod	19.37	20.91	8.06	85.03	36.72
100 Seed weight (g)	37.59	38.03	8.66	97.76	96.50
Grain yield (kg/ha)	54.10	62.57	31.41	74.79	96.40

GCV=Genotypic coefficient of variability, PCV=Phenotypic coefficient of variability, ECV=Environmental coefficient of variability, H²B (%) =Broad sense heritability, GAM =Genetic advance as percentage of mean.

Table 4. Genotypic Correlation coefficient of yield and related traits of Cowpea (*Vigna unguiculata* (L.) Walp) on high altitude area of Jos plateau averaged over two cropping seasons.

TRAITS	PE	PLH	DFI	DFT	DM	NPB	NSB	NPPP	POL	NSPP	100SW	GY
PE	1	.144	-.041	.021	-.068	.234*	.088	.126	.020	.021	-.188	-.076
PLH		1	.119	.128	.135	.271*	.98	.068	.371**	.318**	.210	.285*
DFI			1	.907**	.663**	.411**	.138	-.092	.151	-.024	.110	-.029
DFT				1	.775**	.347**	.007	-.148	.116	-.079	.130	-.097
DM					1	.139**	-.081	-.165	.098	-.110	.179	-.064
NPB						1	.708**	.453**	.262	.278*	.006	.339**
NSB							1	.775**	.019	.090	-.195	.450**
NPPP								1	-.067	-.042	-.196	.572**
POL									1	.693**	.656**	.524**
NSPP										1	.302**	.431**
100SW											1	.504**
GY												1

*significant at P= 0.05. ** significant at P= 0.01

PE= Plant establishment, PLH= Plant height, DFI= Days to flower initiation DFT= Days to flower termination DM= Days to maturity NPB=Numbers of primary branches plant⁻¹, NSB=Number of secondary braches plant⁻¹, NPPP=numbers of pod per plant, POL=Pod length, NSPP=Numbers of seed pod⁻¹, 100SW=Hundred seed weight, GY=Grain yield (Kg ha⁻¹).

Table 5. Genotypic path coefficient analysis showing direct and indirect effects of yield and related traits on grain yield of eighty (80) cowpea accessions averaged over two years on high altitude area of Jos plateau

Variables	PLH	NPB	NSB	NPPP	POL	NSPP	100SW	Total genotypic correlation to grain yield.
PLH	0.05	-0.0459	0.016	0.0455	0.01 n48	0.0928	0.1134	0.2866*
NPB	0.0135	-0.17	0.1136	0.2925	0.0104	0.0812	0.0054	0.3466**
NSB	0.005	-0.1207	0.16	0.4875	0.0008	0.0261	-0.108	0.4507**
NPPP	0.0035	-0.0765	0.12	0.65	-0.0028	-0.0116	-0.108	0.5746**
POL	0.0185	-0.0442	0.0032	-0.0455	0.04	0.2001	0.3564	0.5285**
NSPP	0.016	-0.0476	-0.0144	-0.026	0.0276	0.29	0.162	0.4076**
100SW	0.0105	-0.0017	-0.032	-0.13	0.0264	0.0928	0.54	0.506**

Where: values bold are the direct effect to yield (path coefficient)

Other values are indirect effects via different pathways except the genotypic correlation with yield.

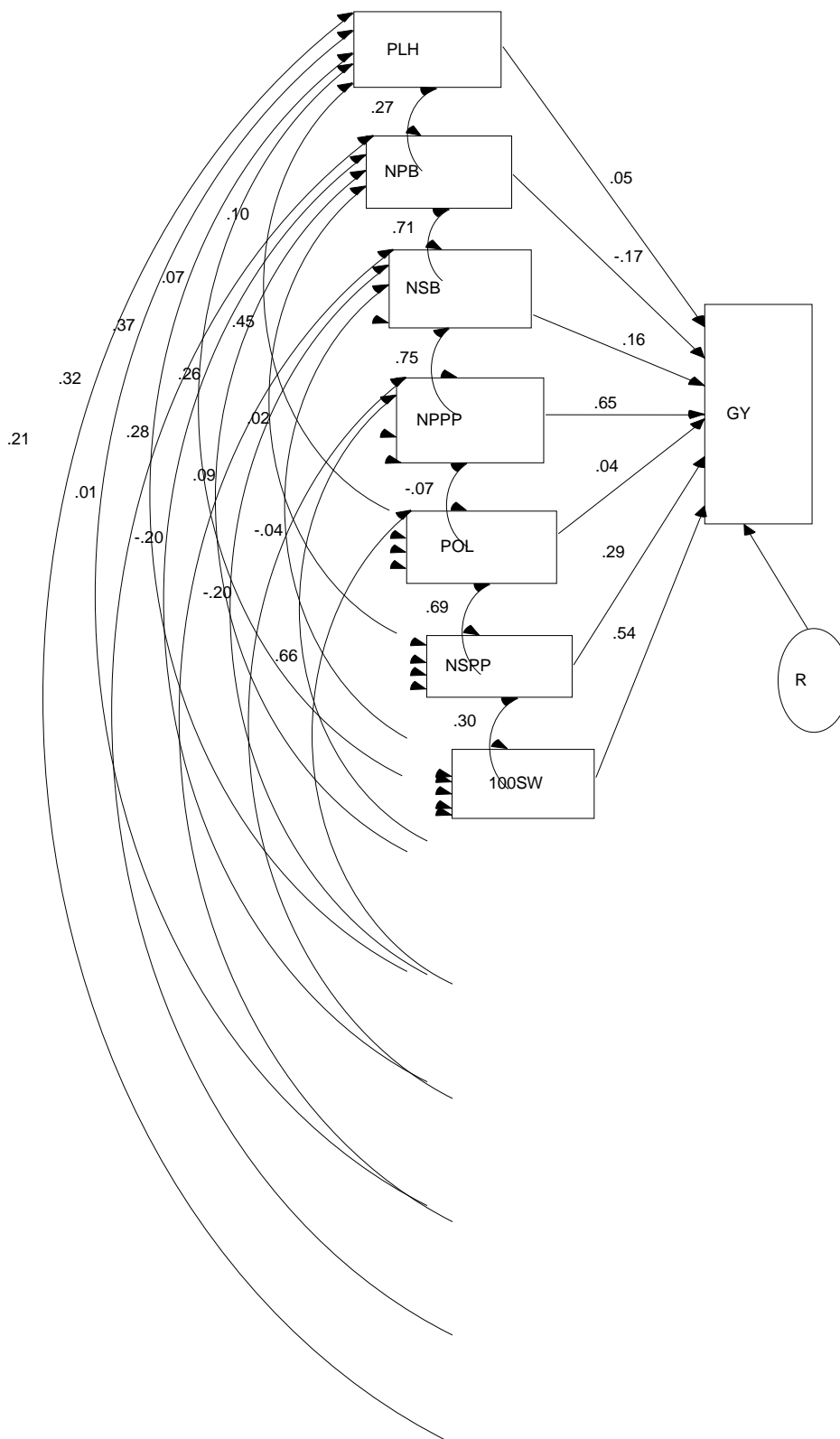


Figure 1. Path diagram showing the cause and effect relationship of yield and related traits of eighty (80) cowpea accessions averaged over two years

(Single-headed lines indicate the path coefficients, Double-headed lines indicate the genotypic correlation between traits, PLH=Plant height, NPB=primary branches plant⁻¹, NSB= # secondary braches plant, NPPP=# pod per plant POL=Pod length, NSPP=# seed pod⁻¹, 100SW=100 seed weight, GY=Grain yield (Kg ha⁻¹).

The high significant difference exhibited for all the yield and related traits accessed Table 2, indicated the existence of sufficient genetic variability among the cowpea accessions and a scope of improvement in cowpea. our result agreed with the earlier findings by Lesly, (2005) who reported sufficient variability for all the characters observed in this study, (Manggoel *et al.*, 2012) also reported significant variability for days to 50% flowering, number of peduncle per plant, number of flowers per plant, number of pod per plant, pod length, number of seed per pod, hundred seed weight and grain yield. This confirmed our result. The significant interaction between accession \times season suggests non-adaptability of the tested accessions to the high altitude of Jos since their performance was not stable across the season.

The phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were higher than the environmental coefficient of variability (ECV) for all the yield and related traits accessed suggests that those characters are mostly controlled by genetic factor with a little environmental influences on the expression of these characters, thus selection for these traits on the basis of phenotypic value may be effective. Our results agreed with earlier findings by several researchers on cowpea (Manggoel *et al.*, 2012, Oyiga and Uguru, 2011). This confirmed the study results.

High heritability and genetic advance attributed to high additive gene effect was observed for all the yield and related traits accessed in this study, except Days to maturity which recorded high heritability with moderate genetic advance. These Suggests mass selection breeding method as a means of improving those traits.

The significant positive correlation between grain yield and plant height, number of primary branches per plant, number of secondary branches per plant, number of pod per plant, pod length, number of seed per pod, hundred seed weight. Suggests that improvement in any of these character will lead to increase in grain yield of cowpea. Our results agree with earlier finding by (Lesly, 2005) who reported significant positive genotypic association of seed yield with hundred seed weight, seed per pod, pod length, number of pod per plant, number of primary branches per plant also (Igbal *et al.*, 2003) reported high significant positive correlation of grain yield with number of pod per plant and hundred seed weight. (Fana *et al.*, 2004) also reported significant positive correlation of grain yield with number of pod per plant. These confirmed our results.

Path coefficient analysis indicated that, number of pod per plant, hundred seed weight, number of seed per pod, number of secondary branches per plant, plant height and pod length exerted a positive direct effect on grain yield. The highest direct effect on grain yield was recorded by number of pod per plant followed by hundred seed weight. Suggests that these traits are good yield enhancing indices. our result agrees with the reports of (Manggoel *et al.*, 2012) who reported direct positive effect of hundred seed weight on grain yield of cowpea, (Kutty *et al.*, 2003) also reported positive direct effect of number of pod per plant on grain yield in cowpea. However, number of primary branches per plant contributed

negatively to grain yield even though it shows positive significant genotypic correlation with grain yield, its significant correlation might be as a result of indirect contributions of other characters. These therefore suggests that direct selection for yield improvement of cowpea based on number of primary branches will lead to loss in grain yield of cowpea.

Conclusion

From the result of the two years' trials involving eighty (80) cowpea accessions on high altitude area of Jos plateau the Analysis of Variance (ANOVA) revealed high significant variability at $P < 0.01$ for all the yield and related traits accessed. The phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were higher than the environmental coefficient of variability (ECV) for all the yield and related traits accessed. A high heritability coupled with high genetic advance attributed to high additive gene effect was observed for all the yield and related traits accessed in this study, except Days to maturity which recorded high heritability with moderate genetic advance. There was also significant positive correlation between grain yield and plant height, number of primary branches per plant, number of secondary branches per plant, number of pod per plant, pod length, number of seed per pod and hundred seed weight. Path coefficient analysis showed that, number of pod per plant, hundred seed weight, number of seed per pod, number of secondary branches per plant, plant height and pod length exerted a positive direct effect on grain yield.

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