

Original Research Article

To Estimate Genetic variability Parameters, Correlation and Path Coefficient in Cowpea [*Vigna unguiculata* (L.) Walp]

Bhagwati Baranda*, Deva Ram Meghawal, P. P. Sharma and Hemlata Sharma

Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan)-313001, India

*Corresponding author

ABSTRACT

Genetic variability is carried out with 30 genotypes and revealed high PCV and GCV estimates were recorded for plant height (37.57% and 37.14%) and number of branches per plant (24.18 % and 24.11%) Whereas, low PCV and GCV was recorded for days to 75% maturity (2.66% and 1.14%). High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for plant height (98.00% & 75.61%), 100-grain weight (97.00% & 33.92%) and seed yield per plant (94.00% & 40.72%) indicating that these traits were mainly governed by additive gene action and are greatly influence for direct selection for genetic improvement by pedigree selection methods of heritable traits. Significant positive correlation were found between seed yield per plant at both phenotypic and genotypic level with biological yield ($r_g=0.878^{**}$ & $r_p=0.817^{**}$), harvest index ($r_g=0.393^{**}$ & $r_p=0.319^{**}$), pods per plant ($r_g=0.372^{**}$ & $r_p=0.313^{**}$), cluster per plant ($r_g=0.339^{**}$ & $r_p=0.269^{**}$) and 100-grain weight ($r_g=0.260^*$ & $r_p=0.256^*$). However, seed protein content exhibited non-significant and negative correlation at both genotypic and phenotypic level with seed yield. The highest positive direct effect on seed yield per plant was exhibited by biological yield followed by plant height, harvest index, pod length and 100-grain weight. Both correlation and path analyses indicated that biological yield per plant, harvest index, pods per plant and plant height were the major direct contributors to seed yield.

Keywords

Heritability, additive gene, path analysis, variability

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp] autogamous leguminous vegetable crop of India belongs to family leguminosae (Mackie and Smith, 1935) with a chromosome number of $2n=2x=22$ (Darlington and Wylie, 1955). It is an important versatile food crop. It is one of the most ancient crops known to man. It is native to India (Vavilov, 1949) but tropical and central Africa is also considered as secondary centre of origin where wild races are found (Ng and Marechal, 1985).

It is considered as one of the oldest legumes and referred as “Poor man’s meat” because of its high protein (20-25 %) source for human and livestock (Steele, 1972). In different parts of the world it is known as Lobia, Southern pea, Blackeye pea, Chawalie and Mulatto-Gelato. It has multipurpose use such as green pods for vegetable, seed as pulse and leaves and foliage for fodder purpose, that’s why it is an important crop of the arid and humid tropics. Cowpea has been intercropped for

long time with various other crops such as maize, wheat, millet, sorghum (Johnson, 1970).

Materials and Methods

Thirty genotypes including three check (RC-101, RC-19 and RCV-7) were evaluated in *kharif*, Each crop was sown in randomized block design with three replications keeping two rows of each genotype in a plot of 4m length in each replication with the spacing of 30×10 cm. Recommended and uniform agronomical practices was adopted.

In each replication, observation were recorded on five randomly selected competitive plants viz., Plant height (cm), Number of branches per plant, Number of pods per plant, Number of clusters per plant, Pod length (cm), Number of seeds per pod, 100-grain weight (g), Seed yield per plant (g), Biological yield per plant (g), Harvest index (%) and Seed protein content (%), whereas, Days to 50% flowering and Days to 75% maturity were recorded on plot basis.

Statistical analysis was performed on the basis of data were subjected to different statistical analysis viz., analysis of variance, magnitude of genetic variability were performed following the standard procedures, phenotypic (PCV) and genotypic (GCV) coefficients of variation were estimated as suggested by Burton (1952), heritability (broad sense) and genetic advance as followed by Allard (1960).

Analysis of variance (ANOVA)

Statistical methods by Panse and Sukhatme (1985) for all the characters. The structure of analysis of variance (ANOVA) is given in Table 3

$$\text{Mean: } \bar{X} = \frac{\sum X}{N}$$

Where,

$\sum X$ = Mean variance of i^{th} genotype
 N = Total number of genotypes

Range

The lowest and highest mean value for each character was taken as range.

Standard error of mean

$$\text{S.Em } \pm = \frac{\sqrt{2MSe}}{r}$$

Where,

r = number of replication
 MSe = MSS due to error

Coefficient of variation (CV)

$$\text{CV (\%)} = \frac{\sqrt{MSe}}{\bar{X}} \times 100$$

Where,

MSe = Error variance
 \bar{X} = Grand total

Critical difference (CD)

$$\text{CD} = \frac{\sqrt{2EMS}}{r} \times t\text{-value}$$

t-value = table value of error difference at 5% level of significance

Where,

r = number of replications

EMS = error mean sum of squares

Estimation of genetic parameters of variation

Genotypic, phenotypic and environmental variances

Genotypic variance (σ^2_g)

$$\text{Genotypic variance } (\sigma^2_g) = \frac{(MSt - MSe)}{r}$$

Where,

MSt = Mean square due to genotypes.
 MSe = Mean square due to error.
 r = Number of replications.

Phenotypic variance (σ^2_p)

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

σ^2_g = Genotypic variance.
 σ^2_e = Mean sum of squares due to error.

Environmental variance (σ^2_e)

$$\sigma^2_e = MSe$$

Coefficient of variation

The estimation of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was done as per the formula given by Burton (1952).

$$\text{Genotypic coefficient of variation (GCV) \%} = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV) \%} = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

Where,

σ^2_p = Phenotypic variance.
 σ^2_g = Genotypic variance.
 \bar{X} = Grand mean.

Heritability in broad sense

Suggested by the Lush (1949).

$$h^2 (\%) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = genotypic variance.
 σ^2_p = phenotypic variance.
 h^2 = Heritability in broad sense.

Computation of expected genetic advance (GA)

Formula as given by Jhonson *et al.*, (1955).

$$G.A. = k \times h^2 \times \sigma_p$$

Where,

G.A. = Expected genetic advance.
 h^2 = Heritability in broad sense.
 σ_p = Phenotypic standard deviation.
 k = Standardized selection differential. Its value is a constant for a given selection intensity. It was taken as 2.06 at 5% selection intensity in present investigation.

Computation of genetic advance as percent of mean: Johnson *et al.*, (1955)

$$GAM\% = \frac{G.A.}{\bar{X}} \times 100$$

Where,

G.A. = Expected genetic advance under selection

\bar{X} = Grand mean

Estimation of correlation coefficient

The phenotypic and genotypic correlation coefficients of all the characters were worked out as per the procedure suggested by Fisher (1954) and Al-Jibouri *et al.*, (1958)

Genotypic covariance (Cov_{gxy})

$$Cov_{gxy} = (MSPg - MSPe) / r$$

Where,

MSPg = Mean sum of products due to genotypes between variable x and y.

MSPe = Mean sum of products due to error between variable x and y.

r = Number of replication.

Phenotypic covariance (Cov_{pxy})

$$Cov_{pxy} = Cov_{gxy} + Cov_{exy}$$

Where,

Error covariance (Cov_{exy}) = MSPe

r = Number of replication

Genotypic correlation coefficient (r_{gxy})

$$r_{gxy} = \frac{cov(xy)_g}{\sqrt{\sigma^2_{gx} \cdot \sigma^2_{gy}}}$$

Where,

Cov(xy)_g = Genotypic covariance between two characters x and y.

□_{gx} = Genotypic variance for character x.

□_{gy} = Genotypic variance for character y.

Phenotypic correlation coefficient (r_{pxy})

$$r_{pxy} = \frac{cov(xy)_p}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$

Where,

Cov (xy)_p = Phenotypic covariance between two character x and y.

□_{px} = Phenotypic variance for character x.

□_{py} = Phenotypic variance for character y.

Test of significance

The significance of the correlation coefficient values for (n-2) degree of freedom was done by calculating the 't' values using following formula described by Panse and Sukhatme (1985).

$$t = \frac{r}{\sqrt{(1 - r^2)}} \times \sqrt{(n - 2)}$$

Where,

't' = Calculated value of 't'.

r = Correlated coefficient between two variables.

n = Total number of observations.

Path coefficient analysis

Path coefficient is a standardized partial regression coefficient. It measures the direct and indirect contribution of independent variable on dependent variable and it allows splitting the total correlation coefficient between two variables into components of direct and indirect effects. The path coefficient analysis was carried out as per the method suggested by Dewey and Lu (1959) at both phenotypic and genotypic level.

The residual effect was computed as follows:

$$R = \sqrt{1 - \sum p_{iy}r_{iy}}$$

Where, R is the residual effect.

Results and Discussion

Analyses of variance revealed highly significant mean of squares due to genotypes for all trait except days to 50% flowering (Table 1). It showed the considerable amount of genetic variability is present among the genotypes evaluated. In a breeding programme, quantification of genetic variability of a population is a determining factor since it reveals the genetic structure of the populations.

This result revealed that phenotypic coefficient of variation are slightly higher than genotypic coefficient of variation it showed that apparent association of two character is not only due to genotype but also favourable influence of environment. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates were recorded for plant height (37.57% and 37.14%) followed by number of branches per plant (24.18 % and 24.11%), biological yield per plant (22.85% and 21.76%) & seed yield per plant (20.96% and 20.35%) this finding as per Sharma *et al.*, (2017) except biological yield and Khan *et al.*, (2015) for primary branches per plant. Whereas, low PCV and GCV was recorded for days to 75% maturity (2.66% and 1.14%) and days to 50% flowering (5.44% and 2.32%). While low GCV and PCV were also report for days to 50% flowering as per relevant Sharma *et al.*, (2017) and Chattopadhyay *et al.*, (2014).

High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for plant height (98.00% & 75.61%), 100-grain weight (97.00% & 33.92%), seed yield per plant (94.00% &

40.72%) and biological yield per plant (90.00% & 42.00%). Moderate heritability and genetic advance as per cent of mean was observed for number clusters per plant (58.00% and 18.07 %), pods per plant (73.00% & 17.38%), pod length (64.00% & 14.14%) and seed per pod (67.00% & 16.24%). While low heritability and genetic advance was recorded for for days to 75% maturity (18.00% and 1.00%) this result supported Thorat and Gadewar (2013) for plant height & Dinesh *et al.*, (2017) for plant height, pods per plant.

Phenotypic and genotypic correlation coefficient

The result on phenotypic and genotypic correlation coefficient revealed that seed yield per plant was significantly and positively correlated with biological yield (rg=0.878** & rp=0.817**), harvest index (rg=0.393** & rp=0.319**), pods per plant (rg=0.372** & rp=0.313**), cluster per plant (rg=0.339** & rp= 0.269**), plant height (rg=0.268* & rp=0.266*) and 100-grain weight (rg=0.260* & rp=0.256*). Sharma *et al.*, (2016) also observed for number of cluster per plant, number of pods per plant, biological yield per plant, harvest index, 100-grain weight and plant height. These finding also supported by Bhardwaj *et al.*, (2014) and Kamai *et al.*, (2014) for harvest index. However, seed yield revealed that, seed protein content exhibited non-significant and negative correlation at both genotypic and phenotypic level. Seed protein content exhibited significant negative correlation with days to 75% maturity (rg= -0.462**& rp= -0.251*), plant height (rg= -0.313** & rp= -301**) and (rg= -0.276** & rp= -0.280**) but seed protein content also expressed significant correlation in positive direction at both genotypic and phenotypic level with pod length (rg=0.235* & rp=0.221*)

Table.1 Analysis of variance of various characters

Character	Days to 50% flowering	Days to 75% maturity	Plant height(cm)	Branches/plant	Cluster s/plant	Pods/plant	Pod length (cm)	Seeds/pod	Biological yield(g)	Harvest index (%)	Seed yield/plant (g)	100-grain weight (g)	Seed protein content (%)
Replication	8.71	2.31	1.84	0.42	0.09	0.21	1.56	0.20	96.94	1.52	11.45	0.12	0.09
Genotype	9.71	4.22*	2345.89**	32.41**	2.56**	6.9**	4.52**	4.67**	5650.95**	12.04**	761.10**	11.38**	2.25**
Error	5.86	2.52	18.36	0.62	0.43	0.74	0.72	0.66	193.19	2.36	14.99	0.10	0.05

*and** significant level of 5% and 1%, respectively

Table.2 Range of variation, mean, phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability (h^2 bs), genetic advance (GA) and genetic advance expressed as per cent of mean (GA%) for thirteen characters in cowpea in environment

Characters	Range		Mean	GCV (%)	PCV (%)	h^2 (Broad sense)	GA	GA as % of mean
	maximum	minimum						
Days to 50% flowering	53.00	45.66	49.17	2.32	5.44	18.00	0.99	2.01
Days to 75% maturity	68.33	63.66	66.04	1.14	2.66	18.00	0.66	1.00
Plant height(cm)	144.63	36.53	75.00	37.14	37.57	98.00	56.71	75.61
Branches/plant	20.36	8.33	13.50	24.11	24.81	94.00	6.52	48.27
Cluster/plant	8.40	5.46	6.78	11.48	15.03	58.00	1.23	18.07
Pods /plant	17.1	11.23	14.55	9.85	11.50	73.00	2.53	17.38
Pod length(cm)	16.5	11.2	13.08	8.60	10.78	64.00	1.85	14.14
Seeds/pod	15.33	10.16	11.94	9.67	11.85	67.00	1.94	16.24
Biological yield(g)	310.39	135.72	196.04	21.76	22.85	94.00	83.54	42.61
Harvest index (%)	39.46	31.8	35.21	5.10	6.72	98.00	2.81	7.97
Seed yield(g)	115.8	48.7	77.47	20.35	20.96	94.00	31.55	40.72
100-grain weight (g)	15.43	7.77	11.61	16.69	16.92	97.00	3.94	33.92
Seed protein content (%)	25.89	22.47	24.4	3.51	3.64	93.00	1.70	6.95

Table.3 Genotypic and Phenotypic correlation coefficient between seed yield per plant and other characters in cowpea

Character	D / F	Days to 50% Flowering	Days to 75% Maturity	Plant Height (cm)	Branches / Plant	Cluster/ Plant	Pods/ Plant	Pod Length (cm)	Seed/ Pod	Biological Yield/ Plant (g)	Harvest Index (%)	100-grain Weight (g)	Seed Protein Content (%)	Seed Yield/ Plant (g)
Days to 50% Flowering	G	1.000	-0.213*	-0.713**	0.059	-0.493**	-0.441*	0.412**	-0.484**	0.064	0.065	0.245*	-0.023	-0.119
	P	1.000	0.277**	-0.314**	0.092	0.038	-0.006	0.090	0.086	0.046	0.001	0.131	-0.047	-0.007
Days to 75% Maturity	G		1.000	-0.556**	-0.137	-0.110	-0.319**	0.016	-0.517**	0.267*	-0.210*	0.442**	-0.462**	-0.001
	P		1.000	-0.242*	0.048	0.139	0.046	-0.097	-0.024	0.086	-0.009	0.214*	-0.251*	0.055
Plant Height (cm)	G			1.000	-0.034	0.276**	0.328**	-0.077	0.394**	0.109	0.083	-0.227*	-0.313**	0.268*
	P			1.000	-0.031	0.228*	0.257*	-0.072	0.316**	0.095	0.060	-0.219*	-0.301**	0.266*
Branches/ Plant	G				1.000	-0.602**	-0.410**	-0.089	0.213*	-0.023	-0.172	0.243*	-0.047	-0.210*
	P				1.000	-0.401**	-0.304**	-0.073	0.213*	-0.030	-0.128	0.244*	-0.056	-0.181
Cluster/ Plant	G					1.000	0.523**	0.150	-0.155	0.372**	0.224*	-0.069	-0.152	0.339**
	P					1.000	0.344**	0.031	0.035	0.231*	0.093	-0.032	-0.127	0.269*
Pods/ Plant	G						1.000	0.162	0.152	0.139	0.529**	-0.051	0.130	0.372**
	P						1.000	0.077	0.148	0.151	0.298*	-0.041	0.100	0.313**
Pod Length (cm)	G							1.000	0.100	0.014	-0.026	0.263*	0.235*	0.066
	P							1.000	0.106	-0.021	-0.057	0.191	0.221*	-0.006
Seed/ Pod	G								1.000	-0.091	-0.066	0.059	-0.120	-0.008
	P								1.000	-0.121	-0.003	0.067	-0.101	0.012
Biological Yield/ Plant g)	G									1.000	0.187	0.400**	-0.161	0.878**
	P									1.000	0.094	0.368**	-0.146	0.817**
Harvest Index (%)	G										1.000	-0.179	0.042	0.393**
	P										1.000	-0.121	0.038	0.319**
100-grain Weight (g)	G											1.000	-0.276**	0.260*
	P											1.000	-0.280**	0.256*
Seed Protein Content (%)	G												1.000	-0.057
	P												1.000	-0.062

*and ** significance levels of 5% and 1% respectively

Table.4 Genotypic and phenotypic path matrix for seed yield in cowpea

Character	D/ F	Days to 50% Flowerin g	Days to 75% Maturit y	Plant Height (cm)	Branch es/ Plant	Cluste r/ Plant	Pods/ Plant	Pod Lengt h (cm)	Seed/ Pod	Biologic al Yield/ Plant (g)	Harvest Index (%)	100- grain Weight (g)	Seed Protien Content (%)	Seed Yield/ Plant (g)
Days to 50% Flowering	G	0.085	-0.018	-0.061	0.005	-0.042	-0.037	0.035	-0.041	0.005	0.006	0.021	-0.002	-0.119
	P	0.029	0.008	-0.009	0.003	0.001	0.000	0.003	0.003	0.001	0.000	0.004	-0.001	-0.007
Days to 75% Maturity	G	-0.023	0.109	-0.061	-0.015	-0.012	-0.035	0.002	-0.056	0.029	-0.023	0.048	-0.050	-0.001
	P	0.022	0.080	-0.019	0.004	0.011	0.004	-0.008	-0.002	0.007	-0.001	0.017	-0.020	0.055
Plant Height (cm)	G	-0.262	-0.205	0.368	-0.013	0.102	0.120	-0.028	0.145	0.040	0.031	-0.084	-0.115	0.268*
	P	-0.087	-0.067	0.278	-0.009	0.063	0.072	-0.020	0.088	0.027	0.017	-0.061	-0.084	0.266*
Branches/ Plant	G	-0.015	0.035	0.009	-0.254	0.153	0.104	0.022	-0.054	0.006	0.044	-0.062	0.012	-0.210*
	P	-0.018	-0.009	0.006	-0.191	0.077	0.058	0.014	-0.041	0.006	0.024	-0.047	0.011	-0.181
Cluster/ Plant	G	0.094	0.021	-0.053	0.115	-0.191	-0.100	-0.029	0.030	-0.071	-0.043	0.013	0.029	0.339**
	P	-0.002	-0.007	-0.011	0.020	-0.050	-0.017	-0.002	-0.002	-0.012	-0.005	0.002	0.006	0.269*
Pods/ Plant	G	-0.031	-0.023	0.023	-0.029	0.037	0.071	0.011	0.011	0.010	0.038	-0.004	0.009	0.372**
	P	0.000	0.000	0.000	0.000	0.000	-0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.313**
Pod Length (cm)	G	-0.017	-0.001	0.003	0.004	-0.006	-0.007	-0.042	-0.004	-0.001	0.001	-0.011	-0.010	0.066
	P	-0.004	0.004	0.003	0.003	-0.001	-0.003	-0.042	-0.004	0.001	0.002	-0.008	-0.009	-0.006
Seed/ Pod	G	-0.034	-0.037	0.028	0.015	-0.011	0.011	0.007	0.071	-0.006	-0.005	0.004	-0.009	-0.008
	P	0.006	-0.002	0.022	0.015	0.002	0.010	0.007	0.070	-0.008	0.000	0.005	-0.007	0.012
Biological Yield/ Plant (g)	G	0.053	0.220	0.090	-0.019	0.307	0.115	0.012	-0.075	0.825	0.154	0.330	-0.133	0.878**
	P	0.035	0.065	0.071	-0.023	0.173	0.113	-0.015	-0.090	0.748	0.070	0.275	-0.109	0.817**
Harvest Index (%)	G	0.013	-0.042	0.017	-0.034	0.045	0.106	-0.005	-0.013	0.037	0.200	-0.036	0.008	0.393**
	P	0.000	-0.002	0.013	-0.028	0.021	0.066	-0.013	-0.001	0.021	0.222	-0.027	0.008	0.319**
100-grain Weight (g)	G	0.025	0.045	-0.023	0.025	-0.007	-0.005	0.027	0.006	0.041	-0.018	0.102	-0.028	0.260*
	P	0.019	0.032	-0.032	0.036	-0.005	-0.006	0.028	0.010	0.054	-0.018	0.147	-0.041	0.256*
Seed Protien Content (%)	G	-0.005	-0.107	-0.072	-0.011	-0.035	0.030	0.054	-0.028	-0.037	0.010	-0.064	0.231	-0.057
	P	-0.009	-0.046	-0.056	-0.010	-0.023	0.018	0.041	-0.019	-0.027	0.007	-0.052	0.184	-0.062

(R square= 0.9165 and Residual effect = 0.2890), (Phenotypic R2= 0.8082 and Residual effect= 0.4380)

Further, perusal of Table 3. showed that, 100-grain weight exhibited significant positive correlation with days to 75% maturity ($rg=0.442^{**}$ & $rp=0.214^{*}$), biological yield per plant ($rg=0.400^{**}$ & $rp=0.368^{**}$) and branches per plant ($rg=0.243^{*}$ & 0.244^{*}) at both genotypically and phenotypically and only at genotypic level with both pod length ($rg=0.263^{*}$) as well as days to 50% flowering ($rg=0.245^{*}$) also reported by Sharma *et al.*, (2016) revealed for number of branches per plant and Selvakumar and Ushakumari (2013) for pod length and days to maturity.

Number of seeds per pod showed significant positive correlation at both genotypic and phenotypic level with plant height ($rg=0.394^{**}$ & $rp=0.316^{**}$) and number of branches per plant ($rg=0.213^{*}$ & $rp=0.213^{*}$), however, revealed significant correlation in negative direction with days to 75% maturity ($rg= -0.517^{**}$) and days to 50% flowering ($rg= -0.484^{**}$) also reported by Sharma *et al.*, (2016), Diriba Shanko *et al.*, (2014) and Selvakumar and Ushakumari (2013).

Table 3 further revealed number of pods per plant exhibited significant positive correlation with number of clusters per plant ($rg=0.523^{**}$ & $rp= 0.344^{**}$) and plant height ($rg=0.328^{**}$ & $rp=0.257^{*}$) at both genotypic and phenotypic level whereas, number of branches per plant exhibited significant negative correlation ($rg= -0.410^{**}$ & $rp= -0.304^{**}$). However, both characters i.e. days to 75% maturity ($rg= -0.319^{**}$) and days to 50% flowering ($rg= -0.441^{**}$) exhibited significant positive correlation at both genotypically and phenotypically similar result was also reported by Meena *et al.*, (2015) significant negative correlation with days to 50% flowering as well as days to maturity, Diriba

Shanko *et al.*, (2014), Nancee *et al.*, (2015) and Sapar and Javia (2014).

Number of clusters per plant exhibited significant negative correlation with number of branches per plant at both genotypic and phenotypic level ($rg= -0.602^{**}$ & $rp= -0.401^{**}$) and only at genotypic with days to 50% flowering ($rg= -0.493^{**}$). However, with plant height ($rg=0.276^{**}$ & $rp=0.228^{*}$) at both genotypic and phenotypic in negative association. Selvakumar and Ushakumari (2013) they revealed for plant height.

Path coefficient

Direct and indirect attribution of component character towards the yield was analyzed using only the genotypic correlation. In present study path coefficient analysis was carried out for seed yield per plant and its component trait at genotypic level. This result revealed that in general the genotypic direct as well as indirect effects were slightly higher in magnitude as compared to corresponding phenotypic direct and indirect effects. The highest positive direct effect on seed yield per plant was exhibited by biological yield (0.825) followed by plant height (0.368), seed protein content (0.231), harvest index (0.200), days to 75% maturity (0.109), pod length (0.109), 100-grain weight (0.102) and days to 50% flowering (0.085), however, negative direct effect on seed yield per plant were contributed through number of branches per plant (-0.254) followed by number of clusters per plant (-0.191) and pod length (-0.042) as per Madhavi *et al.*, (2014), Selvakumar and Ushakumari (2013) and Diriba shanko *et al.*, (2014).

Considerable maximum positive indirect effect on seed yield per plant via 100-grain exhibited biological yield (0.330) via number of pods per plant showed by plant

height (0.120) followed by biological yield (0.115), harvest index (0.106) and number of branches per plant (0.104) and via number of clusters per plant through biological yield per plant (0.307) followed by number of branches per plant (0.153), plant height (0.102) as well as via number of branches per plant through number of clusters per plant (0.115) similar result was reported by Sharma *et al.*, (2016), Meena *et al.*, (2015), Madhavi *et al.*, (2014) and Diriba Shanko *et al.*, (2014).

Above result revealed that biological yield, harvest index, number of pods per plant and 100-grain weight also showed positive and strong correlation with seed yield per plant and were considered to be the most important yield contributing characters. Therefore, due emphasis should be placed on these characters while breeding for high grain yield in cowpea.

This result revealed that phenotypic coefficient of variation are slightly higher than genotypic coefficient of variation. High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for plant height 100-grain weight and seed yield per plant indicating that these traits were mainly governed by additive gene action and are greatly influence for direct selection for genetic improvement The present study revealed that genotypic and phenotypic positive correlation much emphasis should give on biological yield per plant, harvest index, 100-grain weight, seeds per pod and clusters per plant. Hence, improving one or more traits could result in high seed yield in cowpea.

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