The Pharma Innovation

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Genetic variability, correlation and path analysis studies in grain cowpea (*Vigna unguiculata* (L.) Walp subsp. *unguiculata*)

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Abstract
In the present study, 45 genotypes of cowpea were evaluated during *Kharif* 2021 and summer 2022 to assess the genetic variation and inter-relationships among ten yield and yield attributing traits at botany garden of Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad,. The analysis of variance indicated that the 45 cowpea genotypes showed highly significant differences for all studied characters. The high genotypic coefficient of variation and phenotypic coefficient of variation was observed for number of pods per plant, number of clusters per plant and number of pods per cluster. Considerable amount of genetic variability was present in the experimental material, which could be exploited for improvement of cowpea. High heritability coupled with high genetic advance for characters viz., number of clusters per plant, number of pods per cluster, number of pods per cluster, number of pods per plant, test weight and grain yield per plant indicated additive gene effects. Hence, simple selection could be effective for further improvement in these characters. Genetic correlation indicated that traits *viz.*, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, peduncle length, number of seeds per pod and test weight showed a significant positive association with grain yield per plant. Path analysis revealed that days to 50% flowering, number of clusters per plant, number of pods per plant, pod length and peduncle length showed direct positive effects on grain yield per plant at genotypic level indicating that direct selection for these traits results in an increase in yield. If the selection is made for any of these components, the improvement in seed yield could be achieved.

Keywords: Correlation, heritability, genetic advance over percent mean, GCV, PCV

Introduction
Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual, self pollinated legume belonging to family Leguminaceae with a diploid chromosome number of 2n=2x=22. It is native to Central Africa and India is considered as secondary centre of origin. In India cowpea is cultivated for food (grain), vegetables (immature green pods), and fodder purpose (Arya *et al*., 2019). This crop has tremendous adaptability to various conditions and therefore it is cultivated from north Jammu& Kashmir to south Tamil Nadu. Cowpea has been referred to as "Poor man's meat" because of its high protein content (20- 25%) (Sabale *et al*., 2018) [17]. It is considered as one of the oldest legume used as protein source for humans and livestock. It is being used as pulse in form of dry seed, immature pod and green leaf and growing twig can be utilized as vegetable. It is an important source of green as well as dry fodder. It is a drought hardy crop and responds well under irrigated conditions. Cowpea can as well be grown as intercrop with fodder sorghum, maize or pearl millet to improve the quality of fodder (Phogat *et al*., 2017) [16]. The crops like cowpea can become a valuable component in cereal based farming system as it restores soil fertility for succeeding crop. It fixes about 240kg/ha atmospheric nitrogen and leaves about 60 to 70 kg nitrogen for succeeding crop (Kumar, 2020). Therefore, being a pulse crop, it is useful to improve soil fertility (Nguyen *et al*., 2016) [14].

Globally Cowpea is cultivated in an area of 23.4 million hectares with production of 18.29 million tonnes and productivity of 637 kg ha^{-1} (Anon., 2019-20) [3]. In India Cowpea is grown in an area of 4 million hectares with the production of 2.7 million tonnes and with the productivity of 567 kg ha^{-1} (Anon., 2019-20) [3]. Karnataka accounts for 12% of area under pulses in the country and stands fourth in Cowpea among all pulses. In Karnataka the total area under Cowpea production is 62009 hectares with a production of 21311 tonnes (Anon., 2019-20) [3].

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There is need to develop varieties suitable for a specific region and use. Low and variable grain yield, seed quality and susceptibility to diseases & pests are the main constraints in cowpea production. Under such conditions genetic diversity is of great importance and plays a crucial role in focusing crop improvement. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are measured to study the variability present in the germplasm. The characters having high GCV and PCV encompass the possibility of large variation. However, it does not determine the proportion of heritable variation of the total variation present for that character. Heritability and genetic gain together would be more useful in predicting the effect of selection (Johnson *et al*., 1955) [9]. Therefore, proper understanding of these parameters is very important for efficient utilization in crop improvement programme. When heritability is coupled with high genetic advance as per cent of mean (GAM), effective progress in improvement through selection could be achieved (Ajayi *et al*., 2014) [25].

Correlation among traits helps to simultaneously select for more than one trait of importance at a time. Yield is a complex character determined by several component characters. Hence, the knowledge of correlation between yield and its component traits is essential for yield improvement through selection programmes. Path coefficient analysis provides an effective means of partitioning the correlation

coefficients into direct and indirect effects of the component traits of yield on the basis of which crop improvement programmes can be logically devised (Vidya and Oommen, 2002) [22, 23]. Genetic variability of yield and yield contributing characters and correlation between them is basic to plan out future improvement programme in any crop. Keeping these aspects in view, the proposed study was undertaken to assess the nature and magnitude of genetic variability and association of growth, earliness, yield and quality parameters in cowpea.

Material and Method
The present study was conducted using 45 diverse genotypes of grain type cowpea. The details of the material used in the study is represented in table 1 for grain type cowpea. The sowing of the material was taken up in the botany garden of department of Genetics and Plant breeding, College of Agriculture, UAS, Dharwad following randomised complete block design with three replications for two seasons *i.e*., *kharif* 2021 and summer 2022. Each genotype was raised in 5 rows of four meter length with a spacing of 45 cm between the rows and 10 cm between the plants and all the recommended agronomic and plant protection practices were followed during cropping season to maintain the optimum plant population.

Table 1: List of Grain type Cowpea material used in the experiment

Sl. No	Genotype	Source
Germplasm Accessions		
1	EC390219	NBPGR, New Delhi
2	EC390500	NBPGR, New Delhi
3	EC 390248	NBPGR, New Delhi
4	EC390228	NBPGR, New Delhi
5	IC202918	NBPGR, New Delhi
6	IC202849	NBPGR, New Delhi
7	IC 202762	NBPGR, New Delhi
8	IC 202919	NBPGR, New Delhi
9	IC 209165	NBPGR, New Delhi
10	IC 243489	NBPGR, New Delhi
11	IC 249137	NBPGR, New Delhi
12	IC 249585	NBPGR, New Delhi
13	IC 257428	NBPGR, New Delhi
14	IC 257452	NBPGR, New Delhi
15	IC 259106	NBPGR, New Delhi
16	EC724153	NBPGR, New Delhi (obtained from IITA, Nigeria)
17	EC724157	NBPGR, New Delhi (obtained from IITA, Nigeria)
18	EC724160	NBPGR, New Delhi (obtained from IITA, Nigeria)
19	EC738126	NBPGR, New Delhi (obtained from Italy)
Released varieties		
1	C 152(Old adapted variety)	Selection from exotic collection (IARI, New Delhi)
2	RC 101(National check)	RARI, Durgapura-Jaipur, Rajasthan
3	GC 3(National check)	SDAU, Palanpur, Gujarat
4	DC 15(National and state check)	UAS, Dharwad
5	DCS 47-1(State check)	UAS, Dharwad
6	TPTC-29(State check of AP)	RARS, Tirupati, ANGRAU, AP
7	KBC 5	GKVK, Bangalore
8	KBC 6	GKVK, Bangalore
9	KBC 8	GKVK, Bangalore
10	KBC 9	GKVK, Bangalore
11	Bhagyalakshmi	KAU, Thrissur, Kerala
12	Phule CP05040	MPKV, Rahuri, Maharashtra
13	CO (CP-7)	TNAU, Tamil Nadu
Advanced breeding lines		
1	DC 16 (promising line under MLT)	UAS, Dharwad

2	DC 17 (F10 stabilized promising line)	UAS, Dharwad
3	DC 18 (F10 stabilized promising line)	UAS, Dharwad
Interspecific hybrid derivatives between Cowpea × Rice bean in F$_{10}$ generation identified for grain type		
1	F10- 36-2-1	Dept. of GPB, UAS, Dharwad
2	F10- 62-3-1	Dept. of GPB, UAS, Dharwad
3	F10- 37-2-1	Dept. of GPB, UAS, Dharwad
4	F10- 15-4-2	Dept. of GPB, UAS, Dharwad
5	F10- 34-1-2	Dept. of GPB, UAS, Dharwad
6	F10- 53-1-3	Dept. of GPB, UAS, Dharwad
7	F10- 81-1-2	Dept. of GPB, UAS, Dharwad
8	F10- 15-2-1	Dept. of GPB, UAS, Dharwad
9	F10- 46-1-1	Dept. of GPB, UAS, Dharwad
10	F10- 50-2-1	Dept. of GPB, UAS, Dharwad

For recording various observations, five competitive plants of each genotype were randomly selected from each replication. Observations were recorded on the characters, namely, days to 50% flowering, days to maturity, number of clusters per plant, number of pods per cluster, number of pods per plant, peduncle length (cm), pod length (cm), number of seeds per pod, test weight (g) and grain yield per plant (g).

Results and Discussion
Range and mean performance: The analysis of variance indicated that the 45 cowpea genotypes were found to be highly significant for all the characters studied (Table 2), which justified further genetic analysis of the data. Results revealed that considerable amount of genetic variability were present in the experimental material, which can be exploited for improvement of cowpea. Grand mean and range for 10 characters were observed in 45 genotypes (Table 3). Among all the characters studied, wide range of variation was observed for number of pods per plant (12.50 - 47.15) followed by grain yield per plant (31.17 – 54.52 g), days to maturity (68.00 – 90.67), days to 50% flowering (38.83 – 57.67) and peduncle length (25.75 – 38.68 cm). However, number of pods per cluster, number of clusters per plant, pod length, number of seeds per pod and test weight exhibited narrow range.

Genetic variability, heritability and genetic advance: In present investigation, the magnitude of phenotypic coefficient of variation was slightly higher than genotypic coefficient of variation for all the characters (Table 3), which revealed the less sensibility of characters to environmental factors under field conditions. The days to 50% flowering exhibited a low phenotypic coefficient of variation of 8.77% and a genotypic coefficient of variation 7.79%. This trait revealed high heritability of 78.97% and moderate genetic advance as per cent mean of 14.27%. The days to maturity exhibited a low phenotypic coefficient of variation of 8.18% and genotypic coefficient of variation of 6.81% along with high heritability value of 69.37% coupled with moderate genetic advance as per cent mean of 11.69%. Number of pods per plant showed high phenotypic coefficient of variation of 21.00% and a genotypic coefficient of variation of 18.58%. The trait revealed values of high heritability of 78.22% coupled with high genetic advance as per cent mean (33.84). The number of pods per cluster showed high phenotypic coefficient of variation of 19.66% and a high genotypic coefficient of variation of 16.24%. The trait exhibited high heritability value of 68.28% coupled with high genetic advance as per cent mean of 27.65. The number of pods per plant showed high phenotypic coefficient of variation of 28.18% and also a high

genotypic coefficient of variation of 23.12%. The trait revealed values of high heritability (67.29%) coupled with high genetic advance as per cent mean (39.06). Low phenotypic coefficient of variation (10.60%), genotypic coefficient of variation (5.42%) along with moderate heritability (26.11%) and low genetic advance as per cent mean (5.70%) were recorded for the trait. Moderate phenotypic coefficient of variation (13.08%), low genotypic coefficient of variation (10.45%) along with high heritability (63.88%) and moderate genetic advance as per cent mean (17.21%) were observed for this trait. The number of seeds per pod exhibited moderate phenotypic coefficient of variation (14.27%) and a low genotypic coefficient of variation (11.03%). This trait had high heritability (59.76%) coupled with moderate to high advance as per cent mean (17.57%). Moderate phenotypic coefficient of variation (12.56%), low genotypic coefficient of variation (10.88%), and high heritability (74.97%) with moderate genetic advance as per cent mean (19.40%), were observed for this trait. The grain yield per plant exhibited a moderate phenotypic coefficient of variation of 15.80% and genotypic coefficient of variation of 13.59% and high heritability (74%) coupled with a high genetic advance as per cent mean (24.09%). GCV along with heritability and genetic advance was identified as good estimates of genetic gain to be expected from selection on phenotypic basis. The estimates of high heritability coupled with high genetic advance, suggesting that simple selection could be done for the improvement of these traits. Above findings were supported by earlier observations Vidya *et al*., 2002 [22, 23]; Chauhan *et al*., 2003 [7]; Shashidhar *et al*., 2010 [18]; Chattopadhyay *et al*., 2014 [6]; Khanpara *et al*., 2015 [10]; Gerrano *et al*., 2015 [8]; Aliyu and Makinde (2016) [2] and Srinivas *et al*., (2017) [21].

Correlation coefficient
Genotypically grain yield per plant showed a significantly strong positive correlation with number of clusters per plant (0.925), number of pods per cluster (0.756), number of pods per plant (0.929), peduncle length (0.676), pod length (0.764), number of seeds per pod (0.779) and test weight (0.693). This trait exhibited negative significant correlation with days to 50% flowering (-0.519) and days to maturity (-0.367) (Table 4).
Phenotypically this trait showed a significantly strong positive correlation with number of clusters per plant (0.643), number of pods per cluster (0.565), number of pods per plant (0.750), peduncle length (0.246), pod length (0.519), number of seeds per pod (0.505) and test weight (0.517). Further this trait showed a significant negative correlation with days to 50% flowering (-0.401) and days to maturity (-0.283) (Table 5)..

The concurrent results were reported by Aliyu and Makinde (2016) [2], Srinivas *et al*. (2017) [21] for number of clusters per plant; by Vidya and Oommen (2002) [22, 23] and Aliyu and Makinde (2016) [2], for number of pods per cluster; and by Chauhan *et al*., 2003 [7], Manggoel *et al*. (2012) [12], Chattopadhyay *et al*. (2014) [6], Meena *et al*. (2015) [13], Aliyu and Makinde (2016) [2] and Srinivas *et al*. (2017) [21] for number of pods per plant or number of seeds per pod. Days to fifty per cent flowering and days to maturity was significantly negatively correlated with grain yield per plant. It might be due to the fact that in early flowering genotypes, dry matter accumulation in seed is at faster rate than the late flowering genotypes. It also might be due to high rate of photosynthesis at early stages as compared to the reproductive stages of the plant growth which leads to high seed yield per plant in early flowering genotypes. It indicated that seed yield can be increased whenever there is an increase in characters that showed positive associations with seed yield and vice versa for characters that showed negative correlations.

Hence, characters viz., number of pod per plant, pod yield per plant, number of clusters per plant, number of pods per cluster and number of seeds per pod could be considered as criteria for selection for higher seed yield as these were mutually and directly associated with seed yield. On the contrary, genotypes showing lateness in maturing should be excluded in development high seed yield varieties.

Path analysis

The total correlation coefficient between yield and its component characters may sometimes be misleading, as it may be an over or underestimate of its association with other characters. In these cases, direct selection on the basis of correlated responses may not be fruitful. For critical evaluation, the correlation coefficient needs to be split into direct and indirect effects using path coefficient analysis, since many characters affect a given trait. Thus, the correlation and path coefficients in combination can give a better insight into the cause-and-effect relationship between different pairs of characters.

Because the grain yield of cowpea is polygenic, selecting one feature to improve yield necessarily influences the other associated traits. As a result, understanding the relationship between economic traits and yield is quite valuable. To achieve this goal, the genotypic correlations of different traits with grain yield per plant were divided into direct and indirect effects in order to give more specific information for a genetic improvement programme in grain yield of cowpea [Asha *et al*. (2021) [5] in babycorn].

The characters that were exposed to correlations were also subjected to path coefficient analysis in order to estimate the direct and indirect impacts and develop a selection criterion in this study. The results of the study are described further down. The traits such as days to 50 per cent flowering, number of clusters per plant, number of pods per plant, peduncle length and pod length exerted a positive direct effect on grain yield per plant. As a result, direct selection for these traits would be beneficial for increasing yield. The traits *viz.,* days to maturity, number of pods per cluster, number of seeds per pod and test weight, exerted negative direct effects (Table 6 and 7). This indicates that indirect selection should be practiced for these traits to improve grain yield per plant in case of cowpea. Selection would be rewarding if these traits were considered accordingly. Similar findings were obtained by the previous studies conducted by Paghadar *et al*. (2019) [15], Singh *et al*. (2020) [19] and Yadav and Rajasekhar (2019) [24].

The number of pods per plant, number of clusters per plant and peduncle length and pod length exerted the highest positive direct effects on grain yield per plant. The number of pods per plant exerted the highest positive indirect effect through the number of seeds per pod on grain yield per plant, so considering these traits accordingly while selecting the genotype for the breeding programme would be rewarding.

Table 2: Analysis of variance for yield and yield attributing traits in diverse genotypes of grain type Cowpea

Sources of variation	Degrees of freedom	MSS									
		Days to fifty percent flowering	Days to maturity	Peduncle length	Pod length	No. of Pods per plant	No. of Seeds per pod	No. of Pods per cluster	No. of Clusters per plant	Test weight	Grain yield per plant
Replications	2	10.70	12.30	19.35	0.06	13.13	0.19	0.14	2.21	1.00	20.45
Genotypes	44	54.22**	101.01**	18.23**	9.70**	146.93**	9.70**	0.60**	27.50**	4.06**	108.38**
Checks	4	20.69	77.40**	6.65	23.65**	358.20**	23.65**	0.98**	30.43**	1.38*	148.37**
Error	88	4.42	12.96	8.85	1.54	20.49	1.78	0.08	2.33	0.41	11.36

* Significant at 5% level of probability ** Significant at 1% level of probability

Table 3: Estimation of components of genetic variability for yield and yield attributing traits in diverse genotypes of grain type Cowpea

Character	Mean	Range		Vg	Vp	GCV (%)	PCV (%)	h^2_{bs} (%)	GAM
		Minimum	Maximum						
Days to fifty percent flowering	52.27	38.83	57.67	16.60	21.02	7.79	8.77	78.97	14.27
Days to maturity	79.50	68.00	90.67	29.35	42.31	6.81	8.18	69.37	11.69
No. of Clusters per plant	15.59	10.72	22.93	8.39	10.72	18.58	21.00	78.22	33.84
No. of Pods per cluster	2.56	1.77	3.80	0.17	0.25	16.24	19.66	68.28	27.65
No. of Pods per plant	28.09	12.50	47.15	42.15	62.64	23.12	28.18	67.29	39.06
Peduncle length (cm)	32.65	25.75	38.68	3.13	11.98	5.42	10.60	26.11	5.70
Pod length (cm)	15.78	11.66	19.08	2.72	4.26	10.45	13.08	63.88	17.21
No. of Seeds per pod	14.73	10.61	18.03	2.64	4.42	11.03	14.27	59.76	17.57
Test weight (g)	10.15	7.75	12.57	1.22	1.63	10.88	12.56	74.97	19.40
Grain yield per plant (g)	41.83	31.17	54.52	32.34	43.70	13.59	15.80	74.00	24.09

Table 4: Genotypic correlation coefficients of yield and yield attributing traits among 45 diverse genotypes of grain type Cowpea

Characters	Days to fifty percent flowering	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Peduncle length	Pod length	Seeds per pod	Test weight	Grain yield per plant
Days to fifty percent flowering	1.000	0.793 **	-0.527 **	-0.383 **	-0.487 **	-0.417 **	-0.279	-0.273	-0.512 **	-0.519 **
Days to maturity		1.000	-0.310 *	-0.160	-0.232	-0.351 *	-0.139	-0.141	-0.439 **	-0.367 *
Clusters per plant			1.000	0.783 **	0.846 **	0.594 **	0.785 **	0.798 **	0.747 **	0.925 **
Pods per cluster				1.000	0.811 **	0.748 **	0.583 **	0.596 **	0.712 **	0.756 **
Pods per plant					1.000	0.409 **	0.754 **	0.762 **	0.648 **	0.929 **
Peduncle length						1.000	0.380 *	0.382 **	0.731 **	0.676 **
Pod length							1.000	1.019 **	0.580 **	0.764 **
Seeds per pod								1.000	0.598 **	0.779 **
Test weight									1.000	0.693 **
Grain yield per plant										1.000

* Significant at 5% level of probability ** Significant at 1% level of probability

Table 5. Phenotypic correlation coefficients of yield and yield attributing traits among 45 diverse genotypes of grain type Cowpea

Characters	Days to fifty percent flowering	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Peduncle length	Pod length	Seeds per pod	Test weight	Grain yield per plant
Days to fifty percent flowering	1.000	0.577 **	-0.409**	-0.338 **	-0.418 **	-0.094	-0.2058 *	-0.216 *	-0.401 **	-0.396 **
Days to maturity		1.000	-0.234 **	-0.138	-0.195 *	-0.218 *	-0.116	-0.114	-0.283 **	-0.281 **
Clusters per plant			1.000	0.530 **	0.712 **	0.319 **	0.535 **	0.523 **	0.555 **	0.643 **
Pods per cluster				1.000	0.632 **	0.206 *	0.466 **	0.452 **	0.455 **	0.565 **
Pods per plant					1.000	0.230 **	0.570 **	0.564 **	0.549 **	0.750 **
Peduncle length						1.000	0.074	0.075	0.327 **	0.246 **
Pod length							1.000	0.977 **	0.345 **	0.519 **
Seeds per pod								1.000	0.326 **	0.505 **
Test weight									1.000	0.517 **
Grain yield per plant										1.000

* Significant at 5% level of probability ** Significant at 1% level of probability

Table 6: Direct and indirect effects of different yield attributing traits on yield per plant at genotypic level in diverse genotypes of grain type Cowpea

Characters	Days to fifty percent flowering	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Peduncle length	Pod length	Seeds per pod	Test weight	Correlation coefficients of yield attributing traits with yield per plant
Days to fifty percent flowering	0.413	-0.106	-0.229	0.562	-0.916	-0.537	-0.069	0.143	0.219	-0.520 **
Days to maturity	0.327	-0.134	-0.135	0.236	-0.437	-0.452	-0.035	0.074	0.188	-0.367 *
Clusters per plant	-0.218	0.041	0.434	-1.147	1.593	0.766	0.195	-0.418	-0.320	0.925 **
Pods per cluster	-0.158	0.022	0.340	-1.464	1.526	0.964	0.145	-0.312	-0.305	0.756 **
Pods per plant	-0.201	0.031	0.367	-1.187	1.882	0.527	0.187	-0.399	-0.278	0.929 **
Peduncle length	-0.172	0.047	0.258	-1.096	0.771	1.287	0.094	-0.200	-0.313	0.676 **
Pod length	-0.115	0.019	0.340	-0.853	1.419	0.489	0.248	-0.534	-0.248	0.764 **
Seeds per pod	-0.113	0.019	0.346	-0.873	1.434	0.492	0.253	-0.524	-0.256	0.778 **
Test weight	-0.211	0.059	0.324	-1.042	1.221	0.941	0.144	-0.314	-0.428	0.693 **

Residual effect = -0.24

* Significant at 5% level of probability ** Significant at 1% level of probability

Table 7: Direct and indirect effects of different yield attributing traits on yield per plant at phenotypic level in diverse genotypes of grain type Cowpea

Characters	Days to fifty percent flowering	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Peduncle length	Pod length	Seeds per pod	Test weight	Correlation coefficients of yield attributing traits with yield per plant
Days to fifty percent flowering	0.002	-0.063	-0.053	-0.034	-0.202	-0.002	-0.038	0.020	-0.026	-0.396 **
Days to maturity	0.001	-0.109	-0.031	-0.014	-0.094	-0.005	-0.021	0.011	-0.018	-0.280 **
Clusters per plant	-0.001	0.026	0.131	0.053	0.343	0.007	0.099	-0.050	0.036	0.643 **
Pods per cluster	-0.001	0.015	0.069	0.099	0.305	0.004	0.086	-0.043	0.029	0.565 **
Pods per plant	-0.001	0.021	0.093	0.063	0.482	0.005	0.105	-0.054	0.035	0.750 **
Peduncle length	0.000	0.024	0.042	0.020	0.111	0.022	0.014	-0.007	0.021	0.246 **
Pod length	0.000	0.013	0.070	0.046	0.275	0.002	0.185	-0.093	0.022	0.519 **
Seeds per pod	0.000	0.012	0.068	0.045	0.272	0.002	0.180	-0.095	0.021	0.505 **
Test weight	-0.001	0.031	0.072	0.045	0.265	0.007	0.064	-0.031	0.064	0.517 **

Residual effect = 0.38

* Significant at 5% level of probability ** Significant at 1% level of probability

Conclusions

The present investigation indicated the wide variation, coupled with high heritability and genetic advance as percent of mean, which exists in different characters of germplasm of cowpea. It offers potential to evolve cowpea varieties through simple breeding methods. The improvement of seed yield in cowpea could be achieved on the basis of selection of various characters like pod yield per plant, number of pod per plant, number of clusters per plant, number of pods per cluster number of seeds per pod and test weight which were positively correlated with grain yield per plant. In addition, path analysis's results revealed high positively direct and indirect effects on grain yield related characters viz., pod length, number of clusters per plant, number of seeds per pod and number of pods per plant. Therefore, to obtain high seed yield, one should consider these characters in cowpea breeding programme.

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