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Studies on genetic parameters, correlation and path coefficient analysis in cowpea

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Abstract

In the present study, 30 genotypes of cowpea were evaluated during *Kharif* season, 2017 to assess the genetic variation and inter-relationships among 17 agro-morphological characters at Directorate of Farms, CCS Haryana Agricultural University, India. The analysis of variance indicated that the 30 cowpea genotypes showed highly significant differences for all studied characters. The high genotypic coefficient of variation and phenotypic coefficient of variation was observed for biological yield per plant, followed by plant height, harvest index, number of clusters per plant, pod yield per plant, seed yield per plant, number of pods per plant, number of branches per plant, pod weight and days to 50% flowering. 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*., biological yield per plant, followed by plant height, harvest index, number of clusters per plant, seed yield per plant, pod yield per plant, number of branches per plant, pod weight, days to 50% flowering, 100 seed weight, number of seeds per pod, days to maturity and pod length indicated additive gene effects. Hence, simple selection could be effective for further improvement in these characters. Correlation analysis indicated that seed yield per plant exhibited highest and positive significant correlation with pod yield per plant, followed by number of pod per plant, number of clusters per plant, number of pods per cluster, harvest index, number of seeds per pod, number of branches per plant and pod weight. Harvest index, biological yield per plant, pod yield per plant, number of seeds per pod and number of pods per plant reflected high direct and positive effect of on seed yield. If the selection is made for any of these components, the improvement in seed yield could be achieved.

Keywords: Cowpea, Genetic advance, Genetic variability, Path analysis

Introduction

Cowpea [*Vigna unguiculata* L.Walp.] is an important indigenous African grain legume grown in places with severe weather conditions in the tropic and sub-tropic regions. It has ability to tolerate drought and fix atmospheric nitrogen which allows it to grow and improve poor soils. Cowpea is multipurpose crop. It is used at all stages of the crop for both human and animal consumption. Besides being used as pulse in form of dry seed, cowpea's immature pod and green leaf and growing twig can be utilized as vegetable. However, it is more important as the source of green as well as dry fodder. It is a good source of calories, vitamins and minerals and provides a significant amount of dietary protein (18-35%) and lysine to both humans and domestic animals. Cowpea-based food products are utilized as weaning foods for infants. Legume seeds as protein sources are used as flours in products such as baby formula or supplemental diet for preschool children, baking products, pastas or extruded products (Khalid *et al*., 2012).

Area, production and yield under cowpea cultivation for dry grain over the world were 12.6 million hectares, 5.6 million tones and 443 kg/ha, respectively. Niger, Nigeria and Burkina Faso are the first rankings in harvested area and production also (FAOSTAT, 2014). In India, cowpea is grown as sole, inter-crop, mixed-crop and in agro-forestry combinations. It is cultivated in almost half of 1.3 m ha of area occupied by Asian region. In India, cowpea is cultivated mainly in arid and semi-arid tracts of Rajasthan, Karnataka, Kerala, Tamil Nadu, Maharashtra and Gujarat. It is also grown for fodder during *Kharif* as well as summer in pockets of Punjab, Haryana, Delhi and western Uttar Pradesh along with considerable area in Rajasthan (Tiwari and Shivhare, 2016).

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). 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).

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). 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.

Materials and Methods

***Plant materials and experimental designing*:** The experimental material was comprised of 30 genotypes of cowpea (Table 1) collected from various parts of India. These genotypes were selected from the collection, available in Forage section, Department of Genetics & Plant breeding, CCS, Haryana Agricultural University, Hisar. The field experiment was carried out during *Kharif* season 2017 at Directorate of Farms, CCS Haryana Agricultural University, Hisar, Haryana, India. Geographically, Hisar is situated in the semi-arid sub-tropics at 29°10' N latitude and 75°46' E longitude with an altitude of 215.2 meters above the mean sea level.

The experiment was carried out in Random Block Design with three replications. Each genotype was sown in single row of 4 m length with a row-to-row distance 0.45 m and plant to plant spacing of 15 cm. The experimental crop was sown on 25th May, 2017. The recommended cultural and agronomic practices were followed to raise crop. During experimentation weather parameters were also recorded. The mean minimum and maximum temperature (17.3 to 40.8°C) and relative humidity (28.0-90.0%) exhibited a wide range. The highest rainfall during the crop growth season occurred in the month of June (283.8 mm).

Table 1. List of genotypes evaluated during experiment

Sr. No.	Genotype	Sources
1.	PL-3	Pant Nagar
2.	GC 1203	Gujarat
3.	PGCP 28	Pant Nagar
4.	TC 161	-
5.	RC 101	Rajasthan
6.	CPD 240	NAU, Navsari
7.	KBC 10	UAS, Bangalore
8.	CPD 29	NAU, Navsari
9.	UCP 12-007	Uttar Pradesh
10.	GC 1304	Gujarat
11.	VCP 09-019	-
12.	DC 7-15	Dharwad
13.	Chirodi	-
14.	CS 88	HAU, Hisar
15.	PTB-1	Pattampi
16.	KBC-8	UAS, Bangalore
17.	Goa Cowpea-3	Goa
18.	Pant Lobia-2	Pant Nagar
19.	DCS 47-1	Dharwad
20.	KBC-6	UAS, Bangalore
21.	GC 1207	Gujarat
22.	TPTC-29	Andhra Pradesh
23.	PCP-07-272	-
24.	TC 150	-
25.	KBC 9	UAS, Bangalore
26.	PGCP-54	Pant Nagar
27.	GC 901	Gujarat
28.	PGCP-23	Pant Nagar
29.	GC 1110	Gujarat
30.	GC-3	Gujarat

***Observation procedure*:** For recording various observations, five competitive plants of each genotype were randomly selected from each replication. Observations were recorded on the characters, namely, plant height (cm), days to 50% flowering, days to maturity, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), pod breadth (mm), pod weight (g), pod yield per plant (g), number of seeds per pod, 100 seeds weight (g), seed yield per plant (g), biological yield per plant (g), harvest index and seed protein content (%).

***Statistical analysis*:** It was carried out according to Panse and Sukhatme (1967) for analysis of variance;

Burton (1952) for calculation of GCV, PCV; Johnson *et al*. (1955) for heritability and genetic advance; Al-Jibouri (1958) for correlation coefficient; Dewey and Lu (1959) for path analysis.

Results and Discussion

***Range and mean performance**:* The analysis of variance indicated that the 30 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 17 characters were observed in 30 genotypes (Table 2). Among all the characters studied, wide range of variation was observed for plant height (41.60-546.40 cm), followed by biological yield per plant (55.56-443.89 g), days to 50% flowering (43.00-103.33), days to maturity (71.33-129.33), pod yield per plant (12.78-74.89 g), number of pods per plant (16.66-65.33), seed yield per plant (8.67-47.78 g), number of clusters per plant (10.00-40.27), 100 seed weight (6.20-13.10 g), pod length (9.93-16.10 cm) and harvest index (0.06-0.33). However, number of pods per cluster, pod breadth, number of seeds per pod and seed protein content exhibited narrow range.

The variations are helpful in the selection of superior and desired genotypes for further improvement and exploitation through selection, hybridization and combination breeding. The wide and exploitable variations in different cowpea germplasm were observed earlier (Singh and Verma, 2002; Jain *et al*., 2006; Sharma *et al*., 2008; Gerrano *et al*., 2015; Khandait *et al*., 2016; Nguyen *et al*., 2016; Harveen *et al*., 2018). The genetic relationship among all the 30 cowpea genotypes based on Euclidean distance was presented in the dendrogram (Fig 1). Similar relationship was also reported in *Brassica juncea* by Yadav *et al*. (2013).

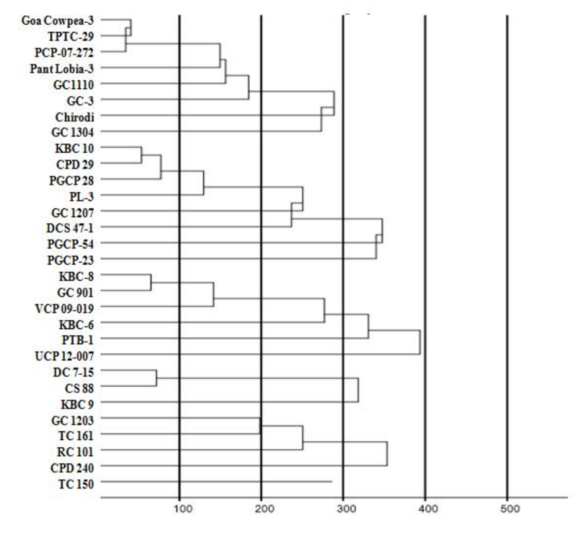

Fig 1. Dendrogram representing genetic relationship among cowpea genotypes based on Euclidean distance

Table 2. Variability, heritability and genetic advance as per cent of mean for 17 traits in 30 genotypes of cowpea

Trait	Range		GCV	PCV	h^2bs	Genetic	GAM
	Min	Max	(%)	(%)	(%)	advance	
Plant height (cm)	41.60	546.40	49.09	49.31	99.11	311.43	100.68
Days to 50% flowering	43.00	103.33	20.82	21.11	97.36	27.44	42.33
Days to maturity	71.33	129.33	14.84	15.14	96.03	27.23	29.95
Number of branches per plant	3.53	8.20	22.69	23.59	92.51	2.63	44.96
Number of clusters per plant	10.00	40.27	37.94	38.30	98.10	16.94	77.40
Number of pods per cluster	1.70	3.23	11.73	16.97	47.79	0.41	16.71
Number of pods per plant	16.66	65.33	32.96	34.87	89.33	24.33	64.17
Pod length (cm)	9.93	16.10	13.91	14.48	92.27	3.64	27.52
Pod breadth (mm)	5.30	8.97	10.50	11.46	84.04	1.44	19.83
Pod weight (g)	0.84	1.87	21.78	22.37	94.85	0.59	43.70
Pod yield per plant(g)	12.78	74.89	34.08	36.01	89.57	29.49	66.45
Number of seeds per pod	7.00	13.85	18.21	19.95	83.31	3.41	34.24
100 seeds weight (g)	6.20	13.10	19.06	20.25	88.60	3.63	36.96
Seed yield per plant (g)	8.67	47.78	33.60	34.72	93.62	17.79	66.97
Biological yield per plant (g)	55.56	443.89	59.24	59.49	99.19	233.21	121.55
Harvest index	0.06	0.33	43.85	45.06	94.68	0.15	87.89
Seed protein content (%)	22.31	26.69	4.12	5.31	59.99	1.58	6.57

**Significance at P<0.01;

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 2), which revealed the less sensibility of characters to environmental factors under field conditions. The high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for biological yield per plant, followed by plant height, harvest index, number of clusters per plant, pod yield per plant, seed yield per plant, number of pods per plant, number of branches per plant, pod weight and days to 50% flowering whereas, the moderate and low estimates of GCV and PCV were observed for traits like seed protein content, pod breadth, number of pods per cluster, pod length, days to maturity, number of seeds per pod and 100 seeds weight. Above findings were supported by earlier observations (Vidya *et al*., 2002; Chauhan *et al*., 2003; Shashidhar *et al*., 2010; Ajayi *et al*., 2014; Chattopadhyay *et al*., 2014; Khanpara *et al*., 2015; Gerrano *et al*., 2015; Aliyu and Makinde, 2016; Srinivas *et al*., 2017).

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 heritability (broad sense) were observed high in biological yield per plant, followed by plant height, number of clusters per plant, days to 50% flowering, days to maturity, pod weight, harvest index, seed yield per plant, number of branches per plant, pod length, pod yield per plant, number of pods per plant, 100 seeds weight, pod breadth and number of seeds per pod but it was moderate in seed protein content and number of pods per cluster. Further, genetic advance as *per cent* of mean observed high for characters like biological yield per plant, followed by plant height, harvest index, number of clusters per plant, seed yield per plant, pod yield per plant, number of pods per plant, number of branches per plant, pod weight, days to 50% flowering, 100 seeds weight, number of seeds per pod, days to maturity and pod length, while the estimates of genetic advance as *per cent* of mean was moderate for pod breadth and number of pods per cluster indicating that the improvement of these through selection as well as their exploitation through combination breeding. The estimates of high heritability coupled with high genetic advance, suggesting that simple selection could be done for the improvement of these traits. Results of the present investigation were also in agreement with earlier workers (Vidya *et al*., 2002; Chauhan *et al*., 2003; Ajeigbe *et al*., 2008; Shashidhar *et al*., 2010; Ajayi *et al*., 2014; Chattopadhyay *et al*., 2014; Khanpara *et al*., 2015; Gerrano *et al*., 2015; Aliyu and Makinde, 2016; Lal *et al*., 2018; Sarath and Reshma, 2017; Srinivas *et al*., 2017).

High heritability coupled with high genetic advance for traits *viz*., biological yield per plant, followed by plant height, harvest index, number of clusters per plant, seed yield per plant, pod yield per plant, number of pods per plant, number of branches per plant, pod weight, days to 50% flowering, 100 seeds weight, number of seeds per pod, days to maturity and pod length indicated additive gene effects. Hence, simple selection can be effective for further improvement in these traits.

High heritability values in yield contributing characters are useful while making selection. It indicated that the variation in these characters was mainly under genetic control and was less influenced by environment but selection based on this factor alone may limit the progress, as the same is also prone to environmental changes. High genetic variations combined with high heritability could provide effective selection of phenotypic trait for further improvement in cowpea through hybridization. The results in genetic analysis of triple test cross by Mittal *et al*. (2010) also indicated the additive genetic variance was presented for most of characters and suggested simple selection to get improvement in cowpea. The evaluation of cowpea genotypes may be reliable based on study of heritability; however, still more solid base may be formed by estimating the performance through genetic advance. Johnson *et al*. (1955) stated that heritability estimated coupled with genetic advance were more helpful than heritability alone in predicting the progress from the selected better genotypes. However, there are limitations of using broad sense heritability as it includes both additive and non-additive gene effects. Therefore, it is necessary to estimate broad sense heritability in conjunction with the genetic advance.

Correlation coefficient: The result of correlation analysis indicated that the absolute values of genotypic correlation coefficient were slightly higher than corresponding phenotypic correlation coefficient values for almost inter-relationships among 17 studied traits (Table 3). In the present study, the seed yield per plant exhibited highest and positive significant correlation at both genotypic and phenotypic levels with pod yield per plant (0.941, 0.901), followed by number of pod per plant (0.711, 0.693), number of clusters per plant (0.599, 0.588), number of pods per cluster (0.450, 0.382), harvest index (0.420,

Table 3. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among different traits in cowpea

Traits	1	3	4	6	7	8	9	10	11	12	13	14	15	16	17
Plant height (cm)	1	0.513**	-0.151	0.291**	0.110	0.274**	-0.486**	-0.038	-0.054	0.434**	-0.648**	-0.022	0.683**	-0.679**	0.285**
Days to maturity	0.501**	1	-0.053	-0.062	-0.270*	0.254*	-0.120	0.023	-0.302**	0.114	-0.343**	-0.371**	0.606**	-0.796**	0.220*
Number of branches / plants	-0.147	-0.043	1	-0.071	0.249*	-0.244*	-0.064	0.071	0.300**	0.030	-0.112	0.282**	0.162	0.006	-0.133
Number of pods / clusters	0.211*	-0.042	-0.059	1	0.780**	-0.363**	-0.708**	-0.402**	0.508**	-0.063	-0.479**	0.450**	0.002	0.162	-0.101
Number of pods per plant	0.112	-0.248*	0.227*	0.698**	1	-0.467**	-0.552**	-0.359**	0.794**	-0.114	-0.359**	0.711**	0.045	0.255*	0.013
Pod length (cm)	0.267*	0.229*	-0.226*	-0.232*	-0.419**	1	0.393**	0.813**	-0.037	0.756**	0.280**	0.007	0.457**	-0.273**	0.173
Pod breadth (cm)	-0.438**	-0.112	-0.038	-0.372**	-0.463**	0.350**	1	0.533**	-0.251*	-0.021	0.767**	-0.264*	-0.211*	0.171	0.094
Pod weight (g)	-0.037	0.011	0.049	-0.262*	-0.323**	0.761**	0.457**	1	0.231*	0.661**	0.505**	0.279**	0.343**	0.026	-0.137
Pod yield per plant (g)	-0.046	-0.284**	0.261*	0.490**	0.801**	-0.023	-0.217*	0.232*	1	0.267*	-0.011	0.941**	0.180	0.352**	-0.093
Number of seeds per pod	0.399**	0.085	-0.026	0.072	-0.058	0.692**	0.007	0.610**	0.277**	1	-0.149	0.404**	0.430**	-0.090	0.069
100 seeds weight (g)	-0.615**	-0.302**	-0.104	-0.327**	-0.323**	0.255*	0.657**	0.449**	-0.021	-0.123	1	-0.006	-0.272**	0.384**	-0.346**
Seed yield per plant (g)	-0.015	-0.347**	0.261*	0.382**	0.693**	0.015	-0.207	0.265*	0.901**	0.400**	-0.003	1	0.166	0.420**	-0.116
Biological yield/plant (g)	0.679**	0.594**	0.157	0.021	0.054	0.438**	-0.196	0.337**	0.181	0.398**	-0.263*	0.166	1	-0.783**	0.203
Harvest index	-0.657**	-0.760**	0.01	0.122	0.238*	-0.247*	0.176	0.015	0.327**	-0.073	0.368**	0.429**	-0.767**	1	-0.314**
Seed protein content (%)	0.210*	0.156	-0.102	-0.038	-0.022	0.112	0.093	-0.099	-0.113	0.025	-0.243*	-0.101	0.156	-0.241*	1

*Significance at P<0.05; **Significance at P<0.01;

0.429), number of seeds per pod (0.404, 0.400), number of branches per plant (0.282, 0.261) and pod weight (0.279, 0.265). If the selection is made any of the component traits, simultaneous selection of the all the traits could be achieved. The concurrent results were reported by Aliyu and Makinde (2016), Lal *et al.* (2018), Srinivas *et al.* (2017) for number of clusters per plant; by Vidya and Oommen (2002), Arora *et al.* (2010), Ushakumari *at al.* (2010), Chattopadhyay *et al.* (2014), Meena *et al.* (2015), Lal *et al.* (2018), Srinivas *et al.* (2017) for number of branches per plant; by Vidya and Oommen (2002) and Aliyu and Makinde (2016), for number of pods per cluster; by Vidya and Oommen (2002), Chattopadhyay *et al.* (2014) for pod weight; and by Chauhan *et al.*, 2003, Arora *et al.* (2010), Mohammed *et al.* (2010), Ushakumari *et al.* (2010), Manggoel *et al.* (2012), Udensi *et al.* (2012), Chattopadhyay *et al.* (2014), Meena *et al.* (2015), Aliyu and Makinde (2016), Lal *et al.* (2018), Lazaridi *et al.* (2017) and Srinivas *et al.* (2017) for number of pods per plant or number of seeds per pod. Whereas, seed yield per plant has shown negative and significant correlations with days to 50% flowering (-0.358, -0.346) and days to maturity (-0.371, -0.347) and with pod breadth (-0.264) at genotypic level. Similarly, the negative and significant correlation between the days to 50% flowering and seed yield per plant was reported by Arora *et al.* (2010), Ushakumari *et al.* (2010), Manggoel *et al.* (2012), Udensi *et al.* (2012), Chattopadhyay *et al.* (2014), Sapara and Javia (2014), Aliyu and Makinde (2016), Patel *et al.* (2016), Lal *et al.* (2018). 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 branches per plant, number of pods per cluster, pod weight, number of seeds per pod and harvest index 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.

The days to 50% flowering and days to maturity besides positively associated together, they also showed positive and significant correlation with plant height and biological yield per plant at both genotypic and phenotypic levels and with seed protein content at genotypic level. Conversely, two both traits had negative and significant correlations with number of clusters per plant, number of pods per plant, pod yield per plant, 100 seeds weight, seed yield per plant and harvest index at both genotypic and phenotypic levels. The negative and significant association was also found between days to 50% flowering and pod breadth at genotypic level. The concurrent results for positive correlation among these traits were reported by Arora *et al*. (2010), Umar *et al*. (2010), Manggoel *et al*. (2012), Ajayi *et al*. (2014), Sapara and Javia (2014), Meena *et al*. (2015), Aliyu and Makinde (2016), Lazaridi *et al*. (2017). While reports for negative association with 100 seeds weight were revealed by Chauhan *et al*. (2003).

The estimates of correlation coefficient exposed that biological yield per plant was significantly and positively associated at both genotypic and phenotypic levels with plant height (0.683 and 0.679), days to 50% flowering (0.576, 0.568), days to maturity (0.606, 0.594), pod length (0.457, 0.438), pod weight (0.343, 0.337) and number of seeds per pod (0.430, 0.398). But it was significantly and negatively correlated with harvest index (-0.783, -0.767) and 100 seeds weight (-0.272, -0.263). The phenotypic association between biological yield and pod breadth was also negative and significant. Some workers also reported the positive correlation between biological yield per plant and plant height (Peksen and Artik, 2004; Mittal *et al*., 2006; Bhandari and Verma, 2007; Umar *et al*., 2010; Sahai *et al*., 2013).

The genotypically and phenotypically positive and significant correlations were found between seed protein content and plant height (0.285, 0.210). As well seed protein content correlated positively and significantly with days to 50% flowering and days to maturity at genotypic level (0.252 and 0.220, respectively). Moreover, it showed significantly negative correlation with 100 seeds weight (-0.346, -0.243) and harvest index (-0.314, -0.241). No or less correlation between protein content with the other traits was also found in previous studies (Kumari *et al*., 2005; Sapara and Javia, 2014).

It was observed that the number of branches per plant was positively and significantly associated with number of clusters per plant (0.297, 0.283); number of pods per plant (0.249, 0.227) and pod yield per plant (0.300, 0.261). However, it exhibited significant negative correlation with pod length (-0.244, -0.226) only. The positive and significant correlations were found between number of clusters per plant with number of pod per plant (0.923, 0.890); pod yield per plant (0.670, 0.652), number of pods per cluster (0.635, 0.483) and harvest index (0.410, 0.402). Moreover, number of clusters per plant exhibited significantly negative correlation at both genotypic and phenotypic levels with pod length, pod breadth, pod weight, number of seeds per pod and 100 seeds weight. The number of pods per cluster had positive and significant correlations with number of pod per plant (0.780, 0.698); pod yield per plant (0.508, 0.490) and plant height (0.291, 0.211). However, it showed negative and significant correlation with pod length, pod breadth, pod weight and 100 seeds weight at both genotypic and phenotypic levels. The number of pods per plant exhibited positive and significant correlation with pod yield per plant (0.794, 0.801) and harvest index (0.255, 0.238). On the other hand, this trait had shown negative and significant associations with pod length, pod breadth, pod weight and 100 seeds weight at both genotypic and phenotypic levels. Pod length and pod breath were not only positively and significantly associated together but also with pod weight and 100 seeds weight at both levels. This implied that if pod size is large resulting in high seed weight. However, both these traits exhibited genotypically, phenotypically significant and negative correlation with number of clusters per plant, number of pods per cluster and number of pods per plant.

***Path analysis*:** Correlation coefficients reveal the extent and nature of association between yield and its contributing characters but does not exhibit the direct and indirect effects of different contributing characters on yield *per se* performance. When more variables are considered in correlation, their indirect associations become more complicated, less obvious and somewhat perplexing. In this situation, path coefficient analysis provides an effective means of splitting direct and indirect cause of association and also provides an opportunity of critical evaluation of that specific cause acting to produce a given correlation and also measures the relative importance of each causal factor. In present study, path coefficients were calculated based on phenotypic correlation coefficient. The residual effect value was 0.049 (Table 4), indicating that characters studied, contributed 95.1% towards total variance in cowpea and only 4.9% variation in remained unaccounted. The estimates of residual effect reflect the adequacy and appropriateness of the characters chosen for path analysis.

Table 4. Path coefficients (direct: on diagonal and indirect: off diagonal) on seed yield per plant (SY) in cowpea

Traits	1	3	4	6	7	8	9	10	11	12	13	14	15	16	SY
Plant height (cm)	**0.018**	0.007	0.002	-0.020	0.013	-0.055	0.018	0.003	-0.020	0.110	-0.049	0.458	-0.508	0.011	-0.015
Days to maturity	0.009	**0.014**	0.001	0.004	-0.028	-0.048	0.005	-0.001	-0.124	0.024	-0.024	0.400	-0.588	0.008	-0.347
Number of branches/ plants	-0.003	-0.001	**-0.013**	0.006	0.025	0.047	0.002	-0.005	0.114	-0.007	-0.008	0.106	0.007	-0.005	0.261
Number of pods per cluster	0.004	-0.001	0.001	**-0.095**	0.078	0.048	0.016	0.024	0.214	0.020	-0.026	0.014	0.094	-0.002	0.382
Number of pods per plant	0.002	-0.003	-0.003	-0.066	**0.112**	0.087	0.019	0.029	0.349	-0.016	-0.026	0.037	0.184	-0.001	0.693
Pod length (cm)	0.005	0.003	0.003	0.022	-0.047	**-0.207**	-0.015	-0.069	-0.010	0.192	0.021	0.295	-0.191	0.006	0.015
Pod breadth (cm)	-0.008	-0.002	0.0005	0.035	-0.052	-0.073	**-0.042**	-0.042	-0.095	0.002	0.053	-0.132	0.136	0.005	-0.207
Pod weight (g)	-0.001	0.0002	-0.001	0.025	-0.036	-0.158	-0.019	**-0.091**	0.101	0.169	0.036	0.227	0.012	-0.005	0.265
Pod yield per plant (g)	-0.001	-0.004	-0.003	-0.046	0.090	0.005	0.009	-0.021	**0.436**	0.077	-0.002	0.122	0.253	-0.006	0.901
Number of seeds per pod	0.007	0.001	0.0003	-0.007	-0.006	-0.143	-0.0003	-0.056	0.121	**0.277**	-0.010	0.268	-0.056	0.001	0.400
100 seeds weight (g)	-0.011	-0.004	0.001	0.031	-0.036	-0.053	-0.028	-0.041	-0.009	-0.034	**0.081**	-0.178	0.285	-0.013	-0.003
Biological yield/ plant (g)	0.012	0.008	-0.002	-0.002	0.006	-0.091	0.008	-0.031	0.079	0.110	-0.021	**0.674**	-0.593	0.008	0.166
Harvest index	-0.012	-0.011	0.0001	-0.012	0.027	0.051	-0.007	-0.001	0.143	-0.020	0.030	-0.517	**0.773**	-0.012	0.429
Seed protein content (%)	0.004	0.002	0.001	0.004	-0.002	-0.023	-0.004	0.009	-0.049	0.007	-0.020	0.105	-0.186	**0.052**	-0.101

(residual effect: 0.049)

Among all the traits under study, harvest index, biological yield per plant, pod yield per plant, number of seeds per pod and number of pods per plant reflected high direct and positive effect of on seed yield per plant (0.773, 0.674, 0.436, 0.277, 0.112, respectively). This suggested that direct selection based on these traits would result in higher breeding efficiency for improving seed yield per plant. Thus, these traits might be estimated as the most important component traits for seed yield per plant. These results were in agreement with earlier findings (Udensi *et al.*, 2012; Chattopadhyay *et al.*, 2014; Sapara and Javia, 2014; Meena *et al.*, 2015; Srinivas *et al.*, 2017). They reported positive direct effects for number of pods per plant and number of seeds per pod. Likewise, high positive direct of number of pods per plant on seed yield per plant was also reported by Vidya and Oommen (2002), Peksen and Artik (2004), Ushakumari *et al.* (2010) , Nwofia, (2012), Patel *et al.* (2016). In addition to this, Manggoel *et al.* (2012) also observed positive direct effects of number of seeds per pod on seed yield per plant.

The harvest index, which showed highest direct effect, was also contributing to seed yield per plant indirectly through pod yield per plant, pod length, number of pods per plant and 100 seeds weight. While, biological yield per plant, pod yield per plant, number of seeds per pod and number of pods per plant contributed to seed yield per plant indirectly through number of pods per plant, pod yield per plant, number of seeds per pod, biological yield per plant and harvest index.

Plant height had high negative indirect effect (-0.508) *via* harvest index on seed yield per plant. Days to 50% flowering (-0.578) and days to maturity (-0.588) also contributing to seed yield per plant indirectly through biological yield per plant. The traits namely number of branches per plant, number of clusters per plant and number of pods per cluster were also contributing to seed yield per plant indirectly *via* pod yield per plant (0.284, 0.214) and harvest index (0.311, 0.094). Likewise, pod length and pod weight also had positive indirect effects on seed yield per plant through number of seeds per pod (0.192, 0.169) and biological yield per plant (0.295, 0.227). Number of seeds per pod had shown positive indirect effect *via* biological yield per plant (0.268) but negative indirect effect through pod length (-0.143).

Conclusion

The present investigation indicated the wide variation, coupled with high heritability and genetic advance as *per* *cent* 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, harvest index, number of seeds per pod, number of branches per plant and pod weight which were positively correlated with seed yield per plant. In addition, path analysis's results revealed high positively direct and indirect effects on seed yield related characters *viz*., harvest index, biological yield per plant, pod yield 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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