



RESEARCH ARTICLE

# Decoding diversity: Integrative assessment of genetic variability, trait associations and nutritional profiling in cowpea genotypes

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## Abstract

Pulses occupy a unique place in India's nutritional food security, as they are a rich source of protein. Cowpea (*Vigna unguiculata* L.) is an important pulse crop contributing significantly to protein and micronutrient security in India. However, there is a need for more research on the potential and actual yields of cowpea in India. Cowpea, being a self-pollinated crop, exhibits limited variability. The present study aimed to assess genetic variability, divergence, character association and nutritional quality among 65 cowpea genotypes to identify superior yield-contributing traits and promising genotypes. A field experiment was carried out at the College of Agriculture, Navile, Shivamogga, using an augmented design. High genotypic and phenotypic coefficients of variation were recorded for pods per cluster, pods per plant, clusters per plant and seeds per pod, indicating substantial variability. High heritability coupled with high genetic advance as a percentage of mean for these traits suggested the predominance of additive gene action and a good response to selection. K-means clustering grouped the genotypes into five clusters, with the maximum inter-cluster distance observed between Clusters IV and V, indicating wide genetic divergence. Crossing these divergent genotypes is expected to generate higher heterosis and wider variability. Correlation and path coefficient analyses revealed that clusters per plant exerted the strongest positive direct effect on seed yield per plant. Based on mean performance, genotypes VCP-17-019, PMCP-1131, 202854(97) and EC-472271 were identified as superior, exhibiting high yield and enhanced nutritional quality. These genotypes recorded crude protein content ranging from 20.00–27.25 %, along with appreciable levels of calcium, magnesium, iron and zinc. The study highlights key yield-associated traits and nutritionally rich genotypes that can be effectively utilised in cowpea breeding programmes aiming at yield improvement and nutritional enhancement.

**Keywords:** correlation; cowpea; diversity; genotypes; heritability; nutritional quality; path analysis; variability; yield

## Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is a highly adaptable grain legume known for its drought tolerance, versatility and rich nutritional value. India and Africa are considered centres of origin of cowpea (1). It is a self-pollinated species of the family Fabaceae with a chromosome number of  $2n=22$  and is cultivated worldwide.

The growth habit ranges from erect, determinate, non-branching, climbing, to bushy and is usually indeterminate under favourable conditions. The most prominent nodules are found in the root system and *Bradyrhizobium* spp. are the specific symbiotic nodular bacteria. The symbiotic relationship of *Bradyrhizobium* with cowpea allows it to fix 40–50 kg of atmospheric nitrogen per hectare.

Cowpea is a tropical grain legume that improves food security while serving a vital nutritional function in underdeveloped nations. It is frequently called the "poor man's meat" due to its high protein content. Cowpea is a drought-tolerant crop that can be used as food for humans and feed for livestock, providing a substantial amount of macro- and micronutrients (2). Cowpea dry seeds are used to prepare several snacks and meal recipes. It contains significant amounts of high-quality protein (23.52 g/100 g), carbohydrates (60.03 g/100 g) and fat (1.26 g/100 g), as well as adequate amounts of calcium (110 mg/100 g), magnesium (184 mg/100 g), iron (8.27 mg/100 g), zinc (3.37 mg/100 g) and vitamins such as thiamine (0.92 mg/100 g), riboflavin (0.18 mg/100 g) and nicotinic acid (1.9 mg/100 g). Cowpea is a rich source of the essential fatty acids linoleic and linolenic acids (3).

Grain yield is a complex quantitative character and an integrated function of several component traits. The creation of genetic variability in a gene pool is a prerequisite for a breeding programme. Any crop improvement programme requires appropriate comprehension and manipulation of key genetic factors. Genetic parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are functional biometrical tools for determining genetic variability in the germplasm.

The degree to which heritable components within a group of plants differ is known as genetic diversity and the assessment of genetic diversity in cultivated crop plants is critical for selecting appropriate genotypes for a hybridisation programme. Correlation measures the mutual relationship between yield and yield-contributing characters. Thus, it helps in selecting superior genotypes from a diverse genetic population. Path analysis measures the direct influence of one trait on another and permits the partitioning of the given correlation coefficients into their direct and indirect effects.

Nutritional analysis of cowpea genotypes based on grain mineral elements and crude protein content is essential for the identification of potential parental genotypes to develop nutritionally enhanced cowpea cultivars. Although several earlier studies have independently reported genetic variability, trait associations, or nutritional composition in cowpea, most of these investigations addressed these aspects in isolation. Comprehensive studies integrating genetic variability, yield component relationships and nutritional profiling within the same set of cowpea genotypes remain limited. Such integrated assessments are essential for identifying genotypes that combine superior yield performance with enhanced nutritional quality. Therefore, the present study was undertaken to evaluate genetic variability, trait associations and nutritional characteristics of selected high-yielding cowpea genotypes, thereby providing valuable information for crop improvement and biofortification programmes.

## Materials and Methods

The experiment was conducted at the College of Agriculture, Navile, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka, India, which is situated at 13.28° N latitude and 75.34° E longitude, at an altitude of 617 m above mean sea level.

The experimental material consisted of 65 cowpea genotypes, including five checks. The cowpea genotypes were collected from the All India Coordinated Research Project (AICRP) on Pulses at the University of Agricultural Sciences, GKVK Campus, Bengaluru. The experiment was laid out in the research block of the College of Agriculture, Navile, Shivamogga, in an augmented design with four blocks (4). Each block contained 15 genotypes along with five checks. Sowing was done using the dibbling method with a row spacing of 45 cm and plant-to-plant spacing of 15 cm. Each genotype was sown in two rows; the length of each row was 5 m and each row consisted of 30 plants. An augmented design was chosen to accommodate a large number of cowpea genotypes (sixty-five) with limited seed availability, along with five replicated check varieties for error estimation. This design is particularly suitable for preliminary evaluation, variability and diversity studies, as it allows efficient comparison of unreplicated genotypes by adjusting their performance using replicated checks, thereby enabling reliable

assessment of genetic variability and trait diversity.

The experimental field received a basal application of 25:50:25 kg N: P<sub>2</sub>O<sub>5</sub>: K<sub>2</sub>O ha<sup>-1</sup> through urea, single superphosphate and muriate of potash at the time of sowing. Irrigation was provided at critical growth stages, including flowering and pod development, to avoid moisture stress. Weed management was carried out by hand weeding at 20–25 days after sowing, followed by need-based intercultural operations. Plant protection measures were adopted uniformly using recommended insecticides and fungicides to control major pests and diseases, ensuring healthy crop growth across all genotypes.

Protein estimation was done by determining the nitrogen content in the seed sample and multiplying it by the conversion factor (6.25). The seed samples were ground into powder using an electric grinder and stored in clean double polyethene bags. Total nitrogen in 20 cowpea genotypes was determined by Kjeldahl's method of nitrogen determination (5).

Ground samples were digested in a diacid mixture, which was used to determine Ca and Mg. Exchangeable Ca and Mg together as well as exchangeable Ca alone were determined by the versenate titration method. For each genotype, three independent replicates of finely ground seed samples (approximately 0.5 g per replicate) were analysed to ensure reproducibility. The minerals were quantified using an atomic absorption spectrophotometer (AAS). Calibration standards for each element were prepared using certified reference solutions and instrument calibration was verified before each run. Analytical precision was ensured by performing duplicate measurements for each sample and the mean values were used for analysis.

## Statistical analysis

The experimental data from the augmented design were used for the analysis of variability, diversity, correlation and path analysis using R software version 4.1.0 with the augmented design package. Statistical analysis was performed on the mean values of traits recorded from fifteen selected plants in each genotype for twelve yield and yield-attributing traits.

The augmented block design consisted of unreplicated test genotypes and replicated check varieties. The statistical model used for analysis was:

$$Y_{ij} = \mu + B_i + G_j + e_{ij}$$

Where  $Y_{ij}$  represents the observed value of the  $j^{\text{th}}$  genotype in the  $i^{\text{th}}$  block,  $\mu$  is the overall mean,  $B_i$  is the effect of the  $i^{\text{th}}$  block,  $G_j$  is the effect of the  $j^{\text{th}}$  genotype and  $e_{ij}$  is the random experimental error. The experimental error was estimated using the replicated check varieties and adjusted means were obtained for the unreplicated test genotypes.

Analysis of variance (ANOVA) was performed to test the significance of genotypic effects. Genetic parameters, including GCV and PCV, broad-sense heritability and genetic advance as a percentage of the mean, were estimated using standard biometrical procedures. Phenotypic correlation coefficients among traits were computed and path coefficient analysis was conducted to partition the correlations into direct and indirect effects, with grain yield considered as the dependent variable.

Before statistical analysis, the data were examined for normality of residuals and homogeneity of variances using diagnostic plots. All statistical tests were performed at a 5 % level of significance.

K-means clustering was used to classify cowpea genotypes based on multiple quantitative traits. Before clustering, all variables were standardised to a zero mean and unit variance to eliminate the effect of differing measurement scales. Euclidean distance was employed as the distance metric to compute dissimilarities among genotypes.

The optimal number of clusters (k) was determined using a graphical approach by plotting the within-cluster sum of squares against increasing values of k (elbow method). The value of k corresponding to a noticeable inflexion point, indicating a reduced rate of decrease in within-cluster variance, was considered optimal. Based on this criterion and the biological relevance of the resulting groups, five clusters were selected for the final K-means analysis.

## Results and Discussion

Analysis of variance was performed for yield and related traits across 65 cowpea genotypes. The results revealed significant differences among the genotypes for all the traits studied, indicating the presence of sufficient genetic variability and confirming that the choice of material for the investigation was appropriate (Table 1). These findings are in line with those reported by previous studies (6–8).

### Genetic variability

Cowpea genotypes exhibited a considerable amount of variability for all twelve characters studied (Table 2). The range for days to 50 % flowering was 47–49 days, while days to maturity ranged from 72–95 days. Plant height ranged from 35.20–97.80 cm. The number of

primary branches per plant ranged from 5.40–14.60 and the number of secondary branches per plant ranged from 3.80–14.00. The number of clusters per plant ranged from 3.40–13.90 and the number of pods per cluster ranged from 1.60–3.00. The number of pods per plant ranged from 7.20–36.70. Pod length ranged from 10.40–20.60 cm. The number of seeds per pod ranged from 9.20–17.00. The 100-seed weight ranged from 5.50–21.53 g and total seed yield per plant ranged from 9.72–27.58 g.

High PCV and GCV were exhibited by the number of secondary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod. These yield-related traits are polygenically controlled and showed minimal environmental influence, as evidenced by the close association between GCV and PCV. Hence, the observed variability is largely genetic and can be effectively exploited through selection. The high PCV and GCV values suggest good scope for direct selection for these traits. Similar findings were reported for the number of secondary branches per plant and number of clusters per plant; number of pods per plant and number of seeds per pod; and number of pods per cluster (9–11).

Moderate PCV and GCV were recorded for plant height, number of primary branches per plant and test weight. This indicates the presence of variations; therefore, such traits can be improved, as the external environment effect is considerably low. Earlier studies reported similar results for plant height, number of primary branches per plant and test weight (7, 12, 13).

**Table 1.** Analysis of variance for yield and its attributing characters in cowpea genotypes

Source of variation	Degrees of freedom	Mean sum of square											
		DFF	DM	PH (cm)	NPB	NSB	NCP	NPC	NPP	PL (cm)	NSP	TW (g)	SYP (g)
Block (eliminating treatments)	3	3.65	0.73	3.10	2.55	3.70	2.96	1.33	22.32	1.37	4.30	0.42	5.01
Genotypes + checks (eliminating blocks)	64	16.38**	40.52**	180.45**	3.76*	18.72**	6.08**	9.38**	38.80**	6.14*	19.45**	4.61**	77.82**
Genotypes	59	14.68**	23.03**	88.95**	3.34*	17.58*	6.44**	9.23**	38.61**	4.37	20.11**	5.46**	16.79*
Checks	4	58.37**	284.93**	514.33**	4.91*	16.87	5.47*	2.42	37.54*	35.28**	10.50	4.32*	402.49**
Checks vs. genotypes	1	0.94	96.27**	4641.12**	24.51**	86.64**	0.49	42.76**	4.48	2.68	8.29	3.46	2477.29**
Error	12	2.11	3.02	9.81	1.14	5.24	1.63	0.88	9.44	1.56	4.82	1.30	6.14

\* - significant @ 5 %, \*\* - significant @ 1 %

DFF- days to 50 % flowering, DM- days to maturity, PH- plant height (cm), NPB- number of primary branches per plant, NSB- number of secondary branches per plant, NCP- number of clusters per plant, NPC- number of pods per cluster, NPP- number of pods per plant, PL- pod length (cm), NSP- number seeds per pod, TW- test weight (g), SYP- seed yield per plant (g)

**Table 2.** Mean, range and genetic variability parameters for 12 yield and yield related characters in cowpea genotypes

Sl. No.	Characters	Mean	Range		PCV (%)	GCV (%)	h <sup>2</sup> (bs) (%)	GAM (%)
			Min.	Max.				
1	Days to 50 % flowering	55.92	49.00	65.00	6.84	6.33	85.64	12.09
2	Days to maturity	81.49	72.00	95.00	5.93	5.52	86.86	10.62
3	Plant height (cm)	54.83	35.20	97.80	18.53	17.48	88.97	34.02
4	Number of primary branches per plant	9.89	5.40	14.60	18.80	15.26	65.92	25.57
5	Number of secondary branches per plant	9.81	3.80	14.00	33.68	28.21	70.16	48.75
6	Number of clusters per plant	7.80	3.40	13.90	35.62	30.78	74.70	54.89
7	Number of pods per cluster	2.17	1.60	3.00	60.97	58.01	90.52	31.86
8	Number of pods per plant	17.06	7.20	36.70	36.53	31.75	75.56	56.94
9	Pod length (cm)	17.06	10.40	20.60	12.31	9.88	64.40	16.36
10	Number of seeds per pod	13.77	9.20	17.00	30.74	26.81	76.03	48.22
11	Test weight (g)	14.43	5.50	21.53	18.50	16.14	76.12	29.05
12	Seed yield per plant (g)	18.65	9.72	27.55	23.14	18.42	63.44	30.27

GCV- genotypic coefficient of variation, PCV- phenotypic coefficient of variation, h<sup>2</sup>(bs)- broad-sense heritability, GAM- genetic advance as percent of mean

Moderate PCV and low GCV were noticed for pod length, which indicates a greater influence of the environment on this trait. Similar results were reported by an earlier study (7).

Low magnitudes of PCV and GCV were noticed for days to 50 % flowering and days to maturity. Low estimates of GCV and PCV imply that selection based on these traits would not be appropriate in a crop improvement programme. Similar results were reported earlier (13). The PCV values were greater than the equivalent GCV values for all component qualities examined in the present study. These findings are in agreement with those reported by earlier studies (14–16).

A minimal difference was found between the PCV and GCV estimates for almost all the traits, showing that the environment had little impact on how these traits were expressed and suggesting that phenotypic variations among genotypes can be appropriately considered during selection. If the difference is substantially more pronounced, it indicates a significant environmental influence on these traits. Therefore, for such traits, other variability parameters such as heritability may also be considered for selection.

Estimates of heritability indicate that genes act in both additive and non-additive ways. As a result, significant genetic increase does not always entail high heritability. Therefore, heritability and genetic advance can be used together as effective selection criteria rather than relying on heritability alone. High heritability accompanied by high or moderate GAM specifies the predominance of additive gene action in controlling traits and such traits are least influenced by environmental effects. High heritability with low GAM indicates that the trait is controlled by non-additive gene action and selection for such a trait may not be rewarding.

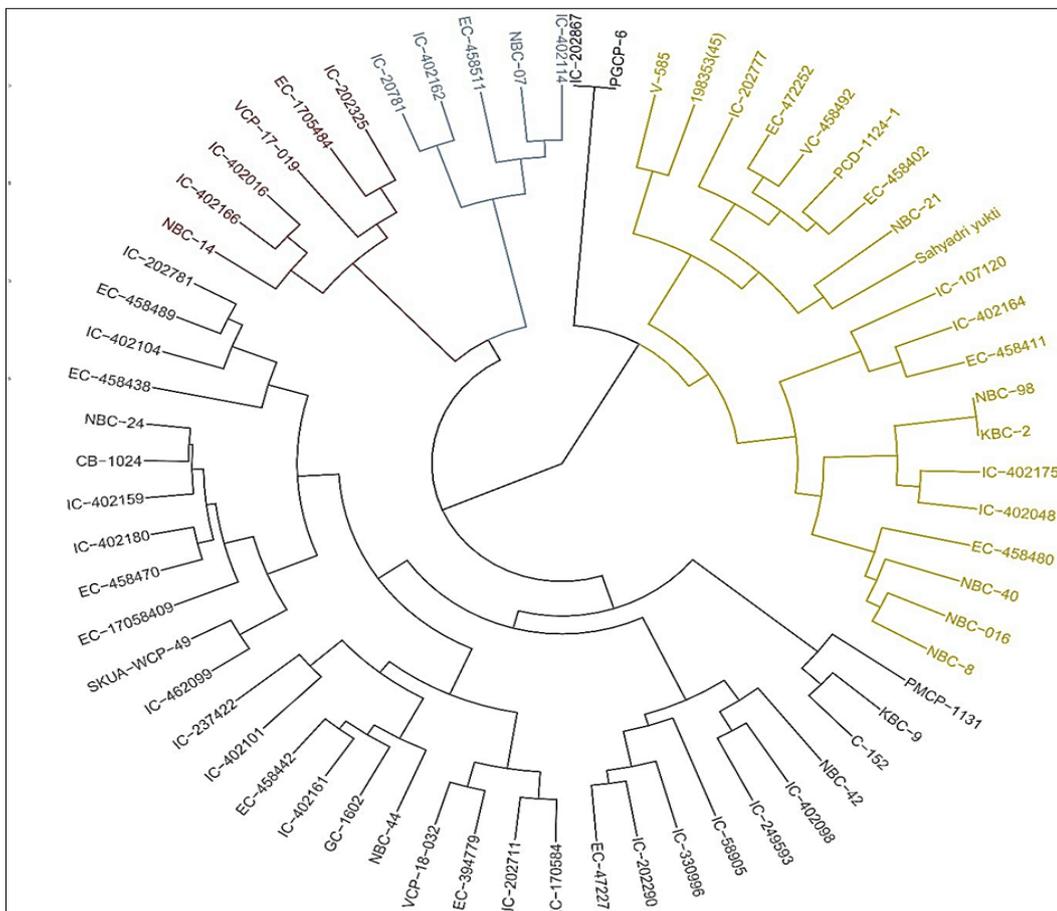
The results of the present field experiment clearly indicate

that the number of secondary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod exhibited higher values of PCV, GCV, heritability and genetic advance. Therefore, selection based on these traits is strongly recommended for yield improvement.

Although high heritability and genetic advance as a per cent of the mean (GAM) suggest scope for selection, these estimates are based on broad-sense heritability, which includes additive, dominance and epistatic effects. Dominance (allelic interaction at the same locus) and epistasis (interaction among loci) may therefore influence trait expression and selection response (17, 18). Thus, these parameters should be complemented with further genetic evaluation, such as progeny testing and multi-generation selection response, before effective selection.

**Cluster analysis**

Greater heterosis was obtained from crosses between genetically diverse parents than from those between closely related ones (19, 20). Researchers have reported that genetic divergence is one of the key factors influencing the choice of parents for hybridisation, which may result in transgressive segregants in subsequent generations (21). One method for categorising genotypes based on similarity and dissimilarity is K-means clustering (22). K-means clustering is a genetic diversity assessment tool that generates genetically diverse clusters based on the genetic distances among germplasm accessions. This makes it simple for plant breeders to locate genetically varied germplasm accessions that can be used as parental lines in the crossing programmes. Sixty-five genotypes were grouped into five clusters; among them, Cluster I had the maximum number of genotypes (thirty-two) followed by Cluster III (twenty), while Cluster IV had the minimum number of genotypes (two) (Fig. 1).



**Fig. 1.** Dendrogram showing clustering pattern in cowpea genotypes.

### Contribution of individual character towards total divergence

The genetic diversity among the sixty-five cowpea genotypes was assessed using K-means clustering, which resulted in five clusters. The number of pods per cluster (26.15%) contributed the maximum to the total genetic divergence, highlighting its importance for selection in breeding programmes, followed by number of pods per plant (12.99%), number of secondary branches per plant (12.17%), seed yield per plant (9.61%), number of clusters per plant (8.43%), number of seeds per pod (8.28%), pod length (5.48%), test weight (4.85%), plant height (4.51%), days to 50% flowering (2.97%), days to maturity (2.53%) and number of primary branches per plant (2.02%) (Fig. 2). This analysis suggests that yield-related traits are the primary determinants of genetic diversity in these cowpea genotypes and selecting genotypes based on these traits could be effective for crop improvement programmes.

### Intra and inter distance of clusters

The highest inter-cluster distance was observed between Cluster IV and Cluster V (6.82), followed by Cluster II and Cluster IV (6.15), indicating that these clusters were diverse with respect to each other. The minimum inter-cluster distance was observed between Cluster I and Cluster III (4.84), followed by Cluster I and Cluster V (4.85). As a rule of thumb in hybridisation, distant parents are preferred; similarly, genotypes from Cluster IV and Cluster V can be used for hybridisation. The highest intra-cluster distance was observed in Cluster III (4.39), followed by Cluster I (4.27) and Cluster II (4.27). The lowest intra-cluster distance was observed in Cluster IV (1.12) (Table 3). A high inter-cluster distance indicates the presence of wide genetic divergence among the cowpea genotypes, suggesting that genotypes from distant clusters are genetically distinct. Crossing such divergent parents can generate greater heterosis and wider variability, thereby increasing the chances of obtaining superior transgressive segregants for yield and quality traits in breeding programmes.

### Correlation studies

Relationships among several agronomic traits are of relevance to plant breeders, both from a theoretical perspective on the quantitative inheritance of characters and from a practical standpoint. Selection is typically concerned with changing two or more characters simultaneously so that the data can be used to predict their response to directional selection, build selection indices

**Table 3.** Average intra- (diagonal and bold) and inter-cluster distances in cowpea genotypes for seed yield and yield attributing traits based on K-means clustering

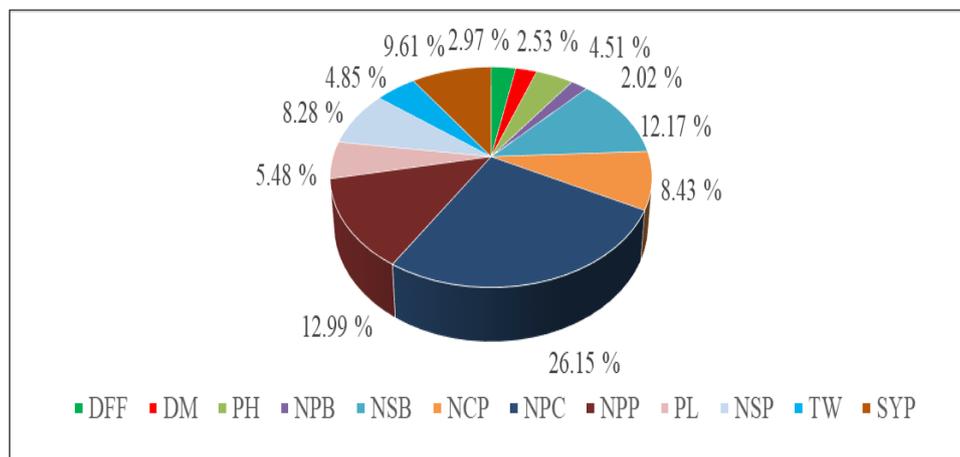
Clusters	I	II	III	IV	V
I	<b>4.27</b>	4.94	4.84	6.10	4.85
II		<b>4.27</b>	5.18	6.15	5.12
III			<b>4.39</b>	5.46	5.22
IV				<b>1.12</b>	6.82
V					<b>3.60</b>

and determine the importance of characters that have no intrinsic value but serve as indicators of more important traits under consideration (23, 24).

The results provide information on the nature and extent of association between pairs of metric characters. Based on this, it may be possible to bring about genetic improvement in one character through the selection of another correlated character. In this context, seed yield per plant exhibited a significant positive association with number of clusters per plant (0.82), number of pods per plant (0.79), number of pods per cluster (0.75), number of primary branches per plant (0.66), number of seeds per pod (0.59), pod length (0.57) and number of secondary branches per plant (0.50) and a non-significant positive association with test weight (0.23) and plant height (0.16). In contrast, a significant negative correlation was observed with days to 50% flowering (-0.28) and a non-significant negative correlation with days to maturity (-0.25) (Table 4).

The results obtained in this investigation for correlation studies are in agreement with previous reports for number of primary branches per plant; number of secondary branches per plant, number of pods per plant and number of seeds per pod; number of clusters per plant and number of pods per cluster; pod length; plant height; and test weight (25–30).

As the number of productive branches increases, the number of clusters per plant, number of pods per plant and number of seeds per pod also increase, which greatly contributes to the maximisation of seed yield per plant. The number of clusters per plant, pods per plant and seeds per pod all rise as the number of productive branches rises, considerably assisting in the maximising of seed yield per plant. These characters may be kept in mind while making individual plant selection. Although these traits showed strong correlations with seed yield, it is important to emphasise that correlation reflects association and does not necessarily imply a



**Fig. 2.** Contribution of individual characters towards total divergence.

DFF - days to 50% flowering, NPC - number of pods per cluster, DM - days to maturity, NPP - number of pods per plant, PH - plant height (cm), PL - pod length (cm), NPB - number of primary branches per plant, NSP - number seeds per pod, NSB - number of secondary branches per plant, TW - test weight (g), NCP - number of clusters per plant, SYP - Seed yield per plant (g)

**Table 4.** Phenotypic correlation coefficient for seed yield and yield-contributing traits in 65 cowpea genotypes

Traits	DFF	DM	PH	NPB	NSB	NCP	NPC	NPP	PL	NSP	TW	SYP
DFF	1.00	0.82**	-0.34**	-0.35**	-0.14	-0.34**	-0.34**	-0.23	-0.26*	-0.21	-0.31*	-0.28*
DM		1.00	-0.30*	-0.36**	-0.09	-0.28*	-0.34*	-0.28*	-0.22	-0.12	-0.26*	-0.25
PH			1.00	0.23	0.13	0.27*	0.18	0.35**	0.25	0.18	0.26*	0.16
NPB				1.00	0.52**	0.69**	0.47**	0.63**	0.63**	0.43**	0.14	0.66**
NSB					1.00	0.59**	0.38**	0.42**	0.56**	0.47**	0.21	0.50**
NCP						1.00	0.78**	0.70**	0.90**	0.79**	0.25	0.82**
NPC							1.00	0.72**	0.63**	0.61**	0.27*	0.75**
NPP								1.00	0.56**	0.53**	0.14	0.79**
PL									1.00	0.73**	0.13	0.57**
NSP										1.00	0.19	0.59**
TW											1.00	0.23
SYP												1.00

\* - significant @ 5 %, \*\* - significant @ 1 %

DFF- days to 50 % flowering, NSB- number of secondary branches per plant, PL- pod length (cm), DM- days to maturity, NCP- number of clusters per plant, NSP- number seeds per pod, PH- plant height (cm), NPC- number of pods per cluster, TW- test weight (g), NPB- number of primary branches per plant, NPP- number of pods per plant, SYP- seed yield per plant (g)

direct cause-effect relationship. The observed positive associations may arise due to the direct effects of these traits on yield or indirect effects mediated through other interrelated characters. Biologically, an increase in productive branches enhances the number of clusters and pods per plant, which in turn increases the number of seeds per plant, ultimately contributing to higher seed yield. Therefore, these traits possess clear physiological relevance to yield formation.

Seed yield is generally under polygenic control; therefore, direct selection for economic yield enhancement may not be fruitful, as it affects other associated traits and vice versa. To understand the influence of different agro-morphological traits on seed yield, the association of these traits with seed yield were divided into direct and indirect effects; this gives more clarity while selecting essential traits that may contribute to increased seed yield per plant. The path coefficients between yield and yield-related traits were estimated and the results are presented in Table 5.

**Path analysis**

The number of clusters per plant exerted the highest positive direct effect on seed yield per plant (1.2885); similar results were reported earlier (28, 29, 31, 32). Pod length showed the highest positive indirect effect on seed yield per plant through the number of clusters per plant (1.1619); comparable results were previously reported (33). In this context, the indirect effects should also be considered simultaneously during selection. Therefore, this trait plays a major role in seed yield improvement.

The number of clusters per plant, days to maturity and number of pods per plant have greater positive direct effects on seed yield per plant. Pod length exerted the highest positive indirect effect on seed yield per plant through the number of clusters per plant, number of pods per plant and number of primary branches per plant. Therefore, taking these traits into account when selecting genotypes for a breeding programme would be beneficial.

**Quality traits**

In the present study, twenty cowpea genotypes were selected based on yield and subjected to quality analysis for nitrogen, protein, calcium, magnesium, zinc and iron. VCP-17-019, PMCP-1131, 202854 (97) and EC-472271 were identified as high-yielding genotypes. Cowpea is an inexpensive source of protein, micronutrients and mineral components that can help resource-constrained subsistence farmers improve their nutritional status. Quality analysis revealed that nitrogen content of seed varied from 3.2–4.36 % and crude protein ranged from 20–27.25 %. Calcium content varied from 120–184 mg/100 g and magnesium content ranged from 180–250 mg/100 g. The micronutrient zinc content ranged from 2.94–4.13 mg/100 g and iron content ranged from 6.57–13.10 mg/100 g. The twenty top-performing genotypes along with their quality traits are presented in Table 6. Genotype NBC- 21 recorded the highest nitrogen and protein content, IC-402180 recorded the highest calcium content, IC-402104 recorded the

**Table 5.** Direct (diagonal) and indirect effects of different traits on seed yield per plant in 65 cowpea genotypes at phenotypic level

Effect of trait	Via character											
	DFF	DM	PH	NPB	NSB	NCP	NPC	NPP	PL	NSP	TW	
DFF	-0.0320	-0.0261	0.0110	0.0112	0.0045	0.0110	0.0109	0.0072	0.0084	0.0067	0.0100	
DM	0.0493	0.0605	-0.0183	-0.0215	-0.0055	-0.0172	-0.0205	-0.0169	-0.0130	-0.0071	-0.0158	
PH	0.0404	0.0356	-0.1174	-0.0270	-0.0151	-0.0322	-0.0213	-0.0409	-0.0294	-0.0210	-0.0302	
NPB	-0.0418	-0.0423	0.0274	0.1191	0.0619	0.0823	0.0558	0.0751	0.0748	0.0507	0.0164	
NSB	-0.003	-0.0019	0.0027	0.0109	0.0211	0.0124	0.0079	0.0089	0.0117	0.0099	0.0044	
NCP	-0.4425	-0.366	0.3537	0.8908	0.7582	1.2885	1.0099	0.9083	1.1619	1.0134	0.3188	
NPC	-0.0048	-0.0048	0.0026	0.0067	0.0054	0.0112	0.0142	0.0102	0.0090	0.0086	0.0039	
NPP	-0.0701	-0.0868	0.1081	0.1957	0.1315	0.2188	0.2226	0.3104	0.1743	0.1641	0.0423	
PL	0.2095	0.1722	-0.2002	-0.5017	-0.4450	-0.7206	-0.5041	-0.4488	-0.7991	-0.5871	0.1068	
NSP	0.0092	0.0052	-0.0079	-0.0189	-0.0209	-0.0349	-0.0269	-0.0234	-0.0326	-0.0444	0.0086	
TW	0.0011	0.0009	-0.0009	-0.0005	-0.0007	-0.0009	-0.0009	-0.0005	-0.0005	-0.0007	0.0035	
r values	-0.2847	-0.2535	0.1607	0.6648	0.4953	0.8185	0.7476	0.7897	0.5655	0.5932	0.2309	

r = correlation coefficient of component traits with grain yield

Residual effect: 0.3226

DFF- Days to 50 % flowering, NSB- number of secondary branches per plant, PL- pod length (cm), DM- days to maturity, NCP- number of clusters per plant, NSP- number of seeds per pod, PH- plant height (cm), NPC- number of pods per cluster, TW- test weight (g), NPB- number of primary branches per plant, NPP- number of pods per plant, SYP- seed yield per plant (g)

**Table 6.** Quality traits of cowpea genotypes

Sl. No.	Genotypes	Seed yield per plant (g)	Nitrogen (%)	Protein (%)	Ca (mg/100 g)	Mg (mg/100 g)	Fe (mg/100 g)	Zn (mg/100 g)
1	VCP-17-019	25.57	3.94	24.62	160	190	8.90	3.76
2	PMCP-1131	25.52	3.83	23.90	134	245	7.82	3.30
3	202854(97)	25.29	3.41	21.31	150	224	10.10	3.75
4	EC-472271	24.92	4.00	25.00	135	195	4.05	3.70
5	EC-458470	24.75	3.70	23.12	130	184	13.10	3.47
6	NBC-98	24.68	3.90	24.37	127	216	16.50	3.06
7	EC-170584	23.53	3.27	20.50	124	225	10.74	3.73
8	IC-402164	23.50	4.03	25.20	129	210	11.30	4.13
9	IC-402098	22.37	3.20	20.00	145	234	6.57	3.22
10	EC-458442	22.24	4.00	25.00	134	220	8.06	3.55
11	EC-458511	22.16	4.30	26.87	120	242	7.03	2.94
12	CB-1024	22.10	4.30	26.87	120	190	10.70	3.65
13	IC-402104	22.01	3.83	23.94	128	250	10.36	3.43
14	IC-402180	21.94	3.32	20.75	184	195	9.71	3.43
15	IC-462099	21.88	3.72	23.25	170	184	11.96	3.25
16	NBC-21	21.65	4.36	27.25	136	226	8.92	3.30
17	IC-58905	21.59	3.81	23.81	134	189	5.80	3.59
18	SKUA-WCP-49	21.43	4.02	25.37	160	190	11.10	3.63
19	NBC-14	21.40	3.46	21.62	126	248	11.29	3.70
20	PCD-1124-1	21.09	4.03	25.20	133	234	8.03	3.48
<b>Checks</b>								
1	PGCP-6	25.27	4.25	26.56	175	245	13.22	3.50
2	KBC-2	24.85	3.54	22.13	164	238	15.24	3.48
3	KBC-9	25.05	4.22	26.38	179	229	15.62	4.05
4	C-152	27.55	4.05	25.31	159	247	14.96	4.11
5	Sahyadri Yukthi	25.50	3.90	24.37	169	241	15.98	4.08

highest magnesium content, EC-458470 recorded the highest iron content and IC-402164 recorded the highest zinc content.

Superior-performing lines for quality traits should be prioritised during selection, as enhancement of the nutritive value in a crop variety is a primary objective along with yield improvement to combat malnutrition and ensure food security in our country. Therefore, these traits should be considered an essential selection index for crop improvement.

## Conclusion

The present study provides valuable insights into the genetic variability, heritability, genetic advance and diversity of cowpea genotypes, as well as the direct and indirect contributions of key traits to seed yield and quality. Traits such as number of clusters per plant, number of pods per plant and number of seeds per pod, which exhibited high heritability and genetic advance, represent promising targets for selection in breeding programmes.

The identified divergent genotypes, particularly those from Clusters IV and V, can serve as potential parents for hybridisation to maximise heterosis and yield improvement. Additionally, genotypes with superior nutritional quality, such as NBC-21 (high protein), IC-402180 (high calcium), IC-402104 (high magnesium), EC-458470 (high iron) and IC-402164 (high zinc), can be prioritised in breeding programmes for biofortification.

Correlation and path coefficient analyses together help identify key yield-contributing traits, enabling breeders to prioritise components with strong direct effects for selection and yield improvement.

Future work should focus on molecular characterisation and validation of these traits, multi-location trials to assess yield stability and screening for tolerance to biotic and abiotic stresses. Incorporating these approaches will strengthen the development of

high-yielding, nutrient-rich and resilient cowpea cultivars suitable for diverse agro-climatic conditions.

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## Authors' contributions

ITJ carried out the research work. DL performed the corrections. RCJ participated in the sequence alignment. HBM assisted with the arrangement of the tables. SD and CNN helped in reorganising the subheadings and finalising the manuscript. HMA and ITJ contributed to the revision and modification of the manuscript. All authors read and approved the final manuscript.

## Compliance with ethical standards

**Conflict of interest:** Authors do not have any conflict of interests to declare.

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