



Characterization, Evaluation and Multivariate Analysis of Cowpea (*Vigna unguiculata* L.) Genotypes for Yield and Yield Contributing Traits

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ABSTRACT

Background: Cowpea (*Vigna unguiculata* L.) is a nutritionally valuable pulse crop with considerable scope for improving dietary protein and mineral intake. Assessing genetic variability in yield and yield related attributes is necessary in finding promising cowpea genotypes for breeding initiatives under semi-arid conditions of Haryana.

Methods: A pot experiment was conducted at Chaudhary Charan Singh Haryana Agricultural University, Hisar during the summer season of 2023-24 to evaluate genotypic variability in seed yield and yield attributes of ten cowpea varieties. The experiment was laid out in a completely randomized design (CRD) using three replications with uniform agronomic and nutrient management practices. Growth and yield parameters including plant height, number of branches, days to 50% flowering, number of pods per plant, number of seeds per pod, seed yield per plant and test weight were recorded at harvest while pod weight, pod length and pod yield per plant were recorded at tender green pod stage.

Result: Correlation analysis revealed that seed yield per plant showed strong and significant positive associations with number of pods per plant ($r = 0.812$), pod length ($r = 0.866$), number of seeds per pod ($r = 0.813$), pod weight ($r = 0.860$) and test weight ($r = 0.840$). Similarly, pod yield per plant was strongly correlated with number of pods per plant ($r = 0.849$), pod length ($r = 0.871$), pod weight ($r = 0.885$) and seed yield per plant ($r = 0.878$). Principal component analysis (PCA) explained 96.17% of total variation among the first three components, with PC1 representing a yield axis dominated by number of pods per plant, pod length, pod weight, test weight, seed yield per plant and pod yield per plant. Genotypes Kashi Kanchan and Cowpea-263 consistently had high value of yield attributes, highlighting their effectiveness of multivariate analysis in identifying promising cowpea genotypes for breeding under semi-arid conditions.

Key words: Correlation, Cowpea, Genotypic variation, Principal component analysis, Yield attributes.

INTRODUCTION

Cowpea (*Vigna unguiculata* L.) is a widely cultivated pulse crop of considerable nutritional and economic significance, especially in tropical and subtropical regions of Asia and Africa. It provides a important source of dietary protein, carbohydrates, essential minerals and micronutrients, not only contributing to food security but also to nutritional security in low-income populations (Nimbal and Ameen, 2024). In addition to its nutritional value, cowpea improves soil fertility through symbiotic nitrogen fixation and is well adapted to semi-arid environments, making it a critical element of sustainable cropping systems (Shukla *et al.*, 2024).

Despite the importance of cowpea as a nutritious legume crop, productivity remains relatively low in several regions due to inadequate utilization of available genetic variability and limited understanding of relationships among yield-determining traits.

Seed yield in cowpea is a complex polygenic trait governed by many constituent traits. Performing indirect selection based on yield attributing traits is more effective than selection based on yield alone (Jogdhande *et al.*, 2017). Although several studies have evaluated cowpea genotypes under field conditions, systematic characterization of yield attributes using multivariate

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statistical tools under controlled environments remains limited for semi-arid regions of Haryana. Controlled experiments allow precise evaluation of inherent genetic variability by minimizing environmental variability. Hence, provide reliable information to breeders regarding development of cultivars with enhanced yield and to agronomists to assess the nutrient management techniques that improve yield and yield attributing traits (Khandait *et al.*, 2016). Therefore, the present study was undertaken to evaluate genetic variability among cowpea genotypes and to identify key yield-contributing traits using correlation analysis and principal component

analysis for selecting promising genotypes for crop improvement.

MATERIALS AND METHODS

The present investigation was conducted as a pot experiment during the summer season of 2023-24 at the Research Farm of the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India. During the crop season, the average temperature ranged from 18-40°C with relative humidity 21-48%. Earthen pots of 30 cm diameter were used for raising the crop and each pot was filled with 17 kg of air-dried soil. The soil used for filling the pots was sandy loam in texture with pH 7.8, organic carbon 0.25%, available nitrogen 132 kg/ha, phosphorus 13.80 kg/ha and potassium 238 kg/ha. The soil was collected from the surface layer (0-15 cm) of the research farm, air-dried, gently crushed and passed through a 2-mm sieve to ensure uniformity. Ten cowpea varieties, namely Kashi Kanchan, Kashi Nidhi, Kashi Shyamal, Kashi Gauri, Cowpea-263, Arka Garima, Konkan Safed, Konkan Sadabhar, Pusa Komal and C-152 were used as experimental material. Five seeds of each cowpea genotype were sown per pot at a depth of 3-4 cm. After germination, seedlings were thinned to two healthy and uniform plants per pot to maintain a consistent plant population throughout the experimental period. All recommended package of practices for cowpea cultivation as prescribed by CCS HAU were followed uniformly across treatments, including irrigation scheduling, nutrient management and plant protection measures.

The experimental data were analyzed under completely randomized design with three replications to test the significance of treatment effects and analysis of variance including correlation and principal component analysis where each replication consisted of ten genotypes grown in separate earthen pot. Plant height, number of branches, days to 50% flowering, number of pods per plant, number of seeds per pod, seed yield per plant and test weight were calculated at harvest while pod weight, pod length and pod yield per plant were recorded at tender green pod stage. Plant height was measured in centimeters from the soil surface to the apical meristem at maturity. Number of branches and pods per plant were counted manually. Pod length was measured in centimeters using a measuring scale, while pod weight (g), pod yield per plant (g), seed yield per plant (g) and test weight (g) were recorded using a digital electronic balance.

RESULTS AND DISCUSSION

The success of selection in any crop improvement program depends not only on the variability present in yield but also on the interrelationships among these traits within the population.

Mean performance of cowpea genotypes

Legume breeders globally have been utilizing the accessible genetic resources to develop varieties. In cowpea breeding

programs, certain yield attributing traits should be prioritized. Therefore, cowpea germplasm must be thoroughly evaluated for these traits to identify suitable accessions for breeding programs. Thus, in the present investigation, different promising varieties were evaluated under Haryana weather conditions and significant variation was noticed among the cowpea genotypes for yield attributes indicating considerable genetic diversity for improvement (Kandel *et al.*, 2019). The mean performance of these varieties is depicted in Table 1 and further discussed below:

Variability in vegetative characters including plant height and number of branches among cowpea genotypes has been frequently reported and is largely attributed to genetic makeup and growth habit differences (Singh *et al.*, 2018). Plant height varied significantly among the studied genotypes and ranged from 43.18 to 95.24 cm. Arka Garima (95.24 cm) recorded the maximum plant height and was significantly superior to all other genotypes. Number of branches per plant ranged from 4.88 to 8.02. Arka Garima recorded the highest number of branches (8.02), followed by C-152 (7.52) and Kashi Gauri (7.21), while Kashi Nidhi (4.88) recorded the lowest number of branches. More branching contributes to better canopy architecture and may indirectly improve pod-bearing sites. Similar genotypic variations for branching in cowpea have been reported by Pawar *et al.* (2016).

Days to 50% flowering showed significant variation and ranged from 48.10 to 62.11 days. Kashi Kanchan was the earliest to flower (48.10 days), followed by Cowpea-263 (49.70 days). Early flowering accessions are often given preference as they escape terminal drought and certify improved yield stability. Negative associations between delayed flowering and yield have also been noticed in cowpea earlier (Nalawade, 2021).

Variability in seed yield and yield attributing characters including number of pod, number of seeds, pod length and pod weight among cowpea genotypes has been frequently reported. Number of pods per plant varied significantly among the genotypes and ranged from 8.35 to 14.96. Kashi Kanchan recorded the highest number of pods per plant (14.96), which was statistically at par with Cowpea-263 (14.73) followed by Arka Garima (14.10). Number of pods per plant is a chief yield-determining trait in cowpea and similar results have been noticed earlier in legume (Massey *et al.*, 2020). Number of seeds per pod ranged from 6.15 to 10.57. Kashi Nidhi (10.57) recorded the maximum number of seeds per pod, which was statistically at par with Kashi Kanchan (10.25) and Kashi Shyamal (10.32). Genotypic variations in number of seeds per pod highlight differences in reproductive abilities and assimilate translocation and partitioning, as also observed by Vaggar *et al.* (2022). Seed yield per plant exhibited wide variation, ranging from 6.78 to 16.32 g. Cowpea-263 (16.32 g) recorded the highest seed yield per plant and was statistically at par with Kashi Kanchan (16.14 g). High seed

yield in Cowpea-263 and Kashi Kanchan can be attributed to their higher pod number, pod weight and test weight. Singh *et al.* (2018) and Reddy *et al.* (2016) also observed similar trends in high-yielding cowpea genotypes.

Pod weight ranged from 5.24 to 8.73 g. Kashi Kanchan recorded significantly higher pod weight (8.73 g) and was statistically at par with Cowpea-263 (8.55 g), followed by Kashi Nidhi (8.15). Higher pod weight directly contributes to increased pod and seed yield and is an important yield component trait. Pod length varied from 11.56 to 19.07 cm. Kashi Kanchan recorded the longest pods (19.07 cm), followed by Cowpea-263 (18.05 cm) and Kashi Gauri (17.76 cm). Kavyashree *et al.* (2023) and Jonah *et al.* (2021) also observed that longer pods usually accommodate more seeds, thus increasing yield potential of genotypes. Pod yield per plant ranged from 41.25 to 127.84 g. Kashi Kanchan (127.84 g) recorded the highest pod yield per plant and was significantly superior to all other genotypes except Cowpea-263 (122.87 g). Higher pod number, pod length and pod weight in Kashi Kanchan and Cowpea-263 can be attributed to their higher pod yield.

Test weight ranged from 7.02 to 9.95 g. Cowpea-263 (9.95 g) recorded the highest test weight was statistically at par with Kashi Kanchan (9.58 g) followed by Kashi Gauri (9.38 g). Higher test weight is positively correlated with seed yield and confirms the presence of bold seeds as observed earlier in cowpea and other legumes (Mali *et al.*, 2021).

In general, the results reflected that Kashi Kanchan and Cowpea-263 constantly performed better for majority of the studied growth and yield characters. In agreement with earlier findings of Aliyu *et al.* (2019), the reported variability among accessions provides a strong genetic base for selection and development of high-yielding cowpea cultivars.

Correlation analysis among yield and yield attributing traits

Correlation analysis was carried out to elucidate the nature and magnitude of associations among yield and its contributing traits in cowpea. The correlation coefficients mentioned in Table 2 and depicted in shaded phenotypic correlogram (Fig 1) revealed a complex interrelationship among growth, phenological and yield attributes.

Number of pods per plant exhibited strong and significant positive correlations with pod length ($r = 0.791$), number of seeds per pod ($r = 0.762$), pod weight ($r = 0.861$), test weight ($r = 0.815$), seed yield per plant ($r = 0.812$) and pod yield per plant ($r = 0.849$). This noticeably reflect that number of pods per plant is a key yield-governing trait in cowpea, as increased pod bearing ability directly improve both seed and pod yield. An increase in pod number directly enhances sink strength, leading to higher seed and pod yield (Nagalakshmi *et al.*, 2020).

Pod length showed highly significant positive correlations with number of seeds per pod ($r = 0.787$), pod weight ($r = 0.827$), test weight ($r = 0.846$), seed yield per plant ($r = 0.866$) and pod yield per plant ($r = 0.871$). These associations propose that longer pods be inclined to

Table 1: Mean performance of cowpea genotypes for growth, phenological and yield related traits.

Varieties	Plant height (cm)	No. of branches	Days to 50% flowering	No. of pods per plant	No. of seeds per pod	Seed yield per plant (g)	Pod weight (g)	Pod length (cm)	Pod yield per plant (g)	Test weight (g)
Kashi kanchan	51.60	6.03	48.10	14.96	10.25	16.14	8.73	19.07	127.84	9.58
Cowpea-263	45.21	5.81	49.70	14.73	9.98	16.32	8.55	18.05	122.87	9.95
Kashi nidhi	43.18	4.88	56.15	13.84	10.57	15.15	8.15	17.92	113.21	9.09
Kashi shyamal	73.82	6.97	54.31	12.34	10.32	14.60	7.94	16.64	98.12	9.02
Kashi gauri	79.57	7.21	58.10	12.10	9.20	13.09	7.60	17.76	88.7	9.38
Arka garima	95.24	8.02	57.67	14.10	9.05	12.42	7.35	15.72	99.28	8.37
C-152	89.93	7.52	62.11	11.90	9.45	11.85	6.75	14.92	77.05	8.95
Pusa komal	52.84	5.18	51.26	11.75	8.76	9.44	6.96	13.45	78.03	7.81
Konkan sadabhar	49.38	5.63	54.67	8.80	6.85	6.78	5.45	12.75	46.55	7.02
Konkan safed	60.05	5.42	55.10	8.35	6.15	7.05	5.24	11.56	41.25	7.87
C.D at 5%	3.82	0.22	1.45	0.58	0.35	0.90	0.31	0.70	5.46	0.39
S.E.m ±	1.29	0.07	0.49	0.20	0.12	0.30	0.10	0.24	1.84	0.13

accommodate more seeds, thus increasing pod mass and ultimately contributing to higher seed and pod yield. The strong positive association between pod length and yield components emphasizing its function as an integrative trait governing both seed size and seed number (Lokesh and Murthy, 2017).

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Number of seeds per pod was also positively and significantly correlated with pod weight ($r = 0.791$), test

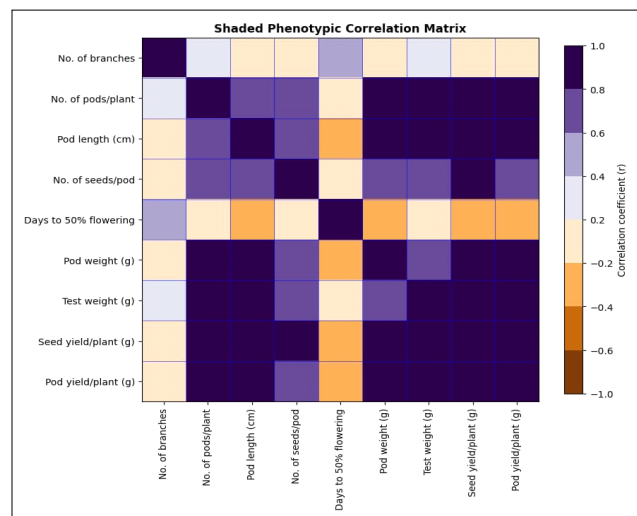


Fig 1: Phenotypic shaded correlogram.

Table 2: Phenotypic correlation matrix among yield and yield attributing traits.

	No. of branches	No. of pods per plant	Pod length (cm)	No. of seeds per pod	Days to 50% flowering	Pod weight (g)	Test weight (g)	Seed yield per plant (g)	Pod yield per plant (g)
No. of branches	1	0.345	0.186	0.059	0.561	0.178	0.364	0.152	0.171
No. of pods per plant	0.345	1	0.791*	0.762*	-0.157	0.861**	0.815*	0.812*	0.849**
Pod length (cm)	0.186	0.791*	1	0.787*	-0.25	0.827**	0.846**	0.866**	0.871**
No. of seeds per pod	0.059	0.762*	0.787*	1	-0.14	0.791*	0.779*	0.813*	0.793*
Days to 50% flowering	0.561	-0.157	-0.25	-0.14	1	-0.358	-0.035	-0.302	-0.327
Pod weight (g)	0.178	0.861**	0.827**	0.791*	-0.358	1	0.788*	0.86**	0.885**
Test weight (g)	0.364	0.815*	0.846**	0.779*	-0.035	0.788*	1	0.84**	0.82**
Seed yield per plant (g)	0.152	0.812*	0.866**	0.813*	-0.302	0.84**	0.84**	1	0.878**
Pod yield per plant (g)	0.171	0.849**	0.871**	0.793*	-0.327	0.82**	0.82**	0.878**	1

**Correlation is significant at 0.01 level (two tailed).

*Correlation is significant at 0.05 level (two tailed).

weight ($r = 0.779$), seed yield per plant ($r = 0.813$) and pod yield per plant ($r = 0.793$). This depicts that genotypes with more seeds per pod tend to show superior yield performance, probable due to better assimilate translocation and partitioning towards reproductive sinks (Nimbal *et al.*, 2024).

Pod weight showed one of the strongest associations with seed yield per plant ($r = 0.860$) and pod yield per plant ($r = 0.885$), reflecting its direct involvement to yield improvement. The strong positive correlation between pod weight and test weight ($r = 0.788$) further recommends that heavier pods are mostly coupled with bolder seeds, which positively affect final yield.

Test weight also confirmed strong positive correlations with seed yield per plant ($r = 0.840$) and pod yield per plant ($r = 0.820$), demonstrating that seed size and density play a significant role in determine seed yield. This result supports the idea that selection for higher test weight can efficiently improve overall productivity (Nkoana *et al.*, 2019).

Days to 50% flowering showed negative correlations with most yield-related traits, including pod weight ($r = -0.358$), seed yield per plant ($r = -0.302$) and pod yield per plant ($r = -0.327$). These negative associations demonstrate that early-flowering genotypes tend to produce higher yields, probably due to a longer effective reproductive period and better exploitation of accessible resources (Sharma *et al.*, 2016).

Number of branches per plant exhibited weak to moderate positive correlations with number of pods per plant ($r = 0.345$) and days to 50% flowering ($r = 0.561$), but its interaction with seed yield ($r = 0.152$) and pod yield ($r = 0.171$) was relatively weak. This suggests that although branching contributes to plant architecture but its direct effect on seed and pod yield is low compared to reproductive traits.

Overall, the correlation matrix clearly indicates that number of pods per plant, pod length, number of seeds per pod, pod weight and test weight are the most significant characters contributing towards seed and pod yield in cowpea. The strong positive association among these traits suggests that synchronized yield improvement is feasible through indirect selection (Pushkar *et al.*, 2018).

Principal component analysis (PCA)

PCA was used to analyze the size and structure of variability across cowpea genotypes for seed yield and yield attributing parameters, as well as to elucidate interrelationships between them. The PCA results form a strong multivariate framework for analyzing yield variation and identifying essential traits and superior genotypes (Suganthi *et al.*, 2007). The analysis of Eigen value demonstrated that the first three principal components collectively explained 96.17% of the total variation (Table 3). Such presence of variability within the first few components has been widely reported in multivariate studies on yield traits of legumes (Abdi and Williams, 2010).

The first principal component (PC1) accounted for 61.01% of the total variance and was predominantly associated with major yield-contributing traits such as number of pods per plant, pod length, pod weight, test weight, seed yield per plant and pod yield per plant. The strong positive loadings of these reproductive traits along PC1 indicate that they collectively constitute the principal yield axis in cowpea and play a decisive role in determining productivity. The second principal component (PC2) contributed 25.18% of the total variation and was mainly associated with phenological and architectural traits including days to 50% flowering and number of branches per plant. The near-perpendicular orientation of these traits relative to the yield components in the biplot suggests a comparatively weaker association between vegetative growth traits and direct yield expression (Reddy *et al.*, 2025).

Genotypic distribution in the PCA biplot (Fig 2) further highlighted clear differentiation among accessions. High-yielding genotypes such as Kashi Kanchan and Cowpea-263 were positioned on the positive side of PC1 and clustered close to key yield attributes, reflecting their superior expression of reproductive traits. In contrast, genotypes Konkan Safed and Konkan Sadabhar located on the negative side of PC1 exhibited weaker association with yield components and comparatively lower productivity. However, Pusa Komal, Kashi Nidhi and Kashi Shyamal were located at an intermediate position but remained distant from the primary yield cluster, indicating average performance (Reddy *et al.*, 2021).

Table 3: Table depicting eigen values and variance.

Principal component	Eigen value	Percentage of variance	Cumulative percentage of variance
PC1	5.491	61.014	61.014
PC2	2.276	25.182	86.196
PC3	0.898	9.973	96.169
PC4	0.182	2.026	98.195
PC5	0.082	0.909	99.104
PC6	0.054	0.596	99.70
PC7	0.022	0.241	99.941
PC8	0.004	0.047	99.988
PC9	0.001	0.012	100

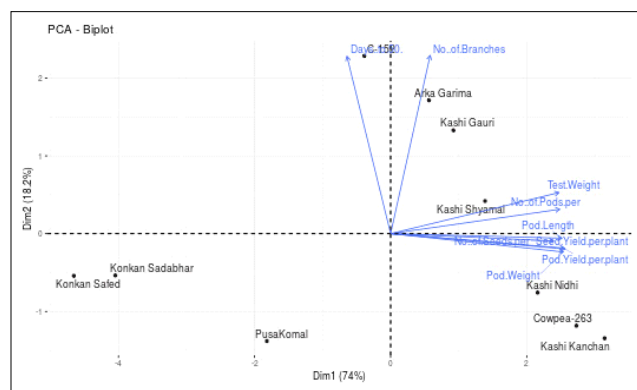


Fig 2: PCA biplot illustrating the relationships between genotype and trait.

Overall, the PCA results demonstrate that yield variability in cowpea is primarily governed by reproductive traits related to pod development and seed size. From a breeding perspective, genotypes positioned near the positive PC1 axis represent promising genetic resources, while traits with high positive loadings on this component may serve as reliable selection criteria for developing high-yielding cowpea cultivars (Girgel, 2021).

CONCLUSION

The present study revealed significant genetic variability among cowpea genotypes for growth and yield-related traits under semi-arid conditions of Haryana. Correlation analysis demonstrated that number of pods per plant, pod length, number of seeds per pod, pod weight and test weight were strongly and positively associated with seed yield per plant and pod yield per plant, indicating their importance as reliable selection criteria for yield improvement. Principal component analysis further confirmed that reproductive traits constituted the major source of variability, with the first two principal components explaining most of the total variation among genotypes. Among the evaluated genotypes, Kashi Kanchan and Cowpea-263 consistently exhibited superior performance for key yield attributes and may serve as promising genetic resources for cowpea improvement programmes. However, further evaluation under multi-location field conditions is required to confirm their stability and wider adaptability.

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Disclaimers

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Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

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