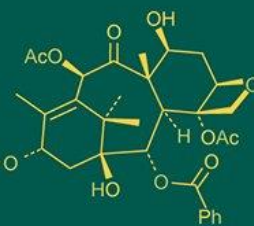
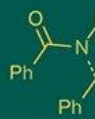


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Genetic variability, character association and principal component analysis for diversity assessment in cowpea [*Vigna unguiculata* (L.) Walp.] Germplasm evaluated through augmented block design

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Abstract

A field experiment was conducted during Kharif 2024 at the Instructional Farm of the Department of Genetics and Plant Breeding, College of Agriculture and Research Station, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, to characterize a set of 98 cowpea [*Vigna unguiculata* (L.) Walp.] germplasm accessions for eleven quantitative traits using an Augmented Block Design comprising four blocks and four common check varieties (UPC-5286, UPC-9202, BL-1 and BL-2) repeated at the end of every block. Analysis of variance (Federer, 1956) revealed that new test genotypes accounted for 72 to 99 percent of the total sum of squares across all eleven traits, confirming the presence of substantial exploitable genetic variability in the evaluated germplasm, while check performance was uniform across blocks. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for plant height (45.5%), number of primary branches per plant (29.9%), leaflet length (31.6%) and hundred-seed weight (31.3%), coupled with high broad-sense heritability and high genetic advance as percent of mean, indicating that these traits are governed predominantly by additive gene action and are amenable to improvement through direct phenotypic selection. Days to 50% flowering and days to maturity were strongly and positively correlated ($r = 0.85$). Principal component analysis extracted six components with eigenvalue greater than unity, together explaining 73.9 percent of the total variation, with the first two components (PC1 and PC2) dominated by phenology-related traits (days to 50% flowering, days to maturity) and branching/foliage-related traits (number of primary branches, leaflet width), respectively. Ward's hierarchical clustering grouped the 102 genotypes into six morphologically distinct clusters. The results demonstrate the utility of augmented design coupled with multivariate analysis for the efficient screening and diversity assessment of large, unreplicated germplasm collections, and identify promising divergent parents for future cowpea hybridization programmes.

Keywords: Cowpea, *Vigna unguiculata*, augmented design, genetic variability, heritability, genetic advance, principal component analysis, genetic diversity

1. Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] ($2n = 2x = 22$) is a self-pollinated, diploid grain legume of the family Fabaceae that constitutes one of the most important and versatile pulse crops of the semi-arid and sub-humid tropics. Owing to its wide adaptability, drought tolerance, short duration and biological nitrogen-fixing ability, the crop is extensively cultivated in India for grain, vegetable and fodder purposes and occupies a central place in cropping systems aimed at improving soil fertility and household nutritional security. The seed is a rich and inexpensive source of dietary protein (approximately 22-25%), essential amino acids, minerals and dietary fibre, making cowpea an important component of nutritional security programmes in resource-poor farming communities.

Genetic improvement of any crop depends fundamentally on the magnitude and nature of variability present in the available germplasm, the extent to which this variability is heritable, and the pattern of association among yield and yield-contributing traits. Phenotypic variation alone is often a poor guide to breeding value because it confounds genotypic and environmental effects; partitioning of total variability into genotypic and environmental

components, and the subsequent estimation of the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2_{bs}) and genetic advance as percent of mean (GAM), therefore constitutes an essential first step in any systematic crop improvement programme (Burton & DeVane, 1953; Johnson, Robinson, & Comstock, 1955) ^[1,3].

When large germplasm collections are to be characterized, conventional replicated designs such as the randomized block design become impractical because of the large number of entries, limited seed availability and constraints of land and labour. The Augmented Block Design, originally proposed by Federer (1956) ^[2], overcomes this limitation by evaluating a large number of unreplicated test entries alongside a small number of common check varieties that are repeated in every block. Block effects are estimated from the replicated checks and used to adjust the means of the unreplicated test entries, thereby permitting the simultaneous and efficient screening of very large collections without the need to replicate every accession.

Beyond univariate variability parameters, a comprehensive understanding of genetic diversity also requires multivariate tools that reduce a large number of correlated traits into a smaller number of independent axes of variation. Principal Component Analysis (PCA) is one such widely used multivariate technique that identifies the traits contributing maximally to the total genetic divergence among genotypes and enables visualization of genotype relationships through biplots, thereby assisting breeders in the identification of diverse and complementary parents for hybridization (Mishra, Gore, & Sahu, 2025a) ^[4]. Complementary multivariate clustering procedures, such as Ward's minimum-variance hierarchical clustering, further partition genotypes into discrete, morphologically homogeneous groups and have been successfully employed alongside variability and correlation studies to characterize indigenous legume germplasm collections (Mishra, Sahu, & Pandey, 2025b) ^[5].

Despite the wide cultivation of cowpea in Chhattisgarh, systematic characterization of locally available and exotic cowpea germplasm using an augmented design coupled with multivariate diversity analysis remains limited. The present investigation was therefore undertaken with the following objectives: (i) to estimate the extent of genetic variability, heritability and genetic advance for eleven quantitative traits in a large cowpea germplasm set evaluated through an augmented block design; (ii) to work out the pattern of association among the component traits; and (iii) to assess the pattern of genetic diversity among the accessions through principal component analysis and hierarchical clustering, so as to identify diverse and agronomically desirable genotypes for future use in cowpea breeding programmes.

2. Materials and Methods

2.1 Experimental site and plant material

The present investigation was carried out during Kharif (rainy) season 2024 at the Instructional Farm of the Department of Genetics and Plant Breeding, College of Agriculture and Research Station, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, India. The experimental material comprised 98 diverse cowpea [*Vigna unguiculata* (L.) Walp.] accessions, including indigenous collections, exotic (EC) accessions and germplasm (GP)

lines procured from the National Bureau of Plant Genetic Resources and the departmental germplasm bank, together with four released/popular check varieties, namely UPC-5286, UPC-9202, BL-1 and BL-2. The crop was raised following recommended agronomic and plant protection practices for the region to ensure a uniform and healthy crop stand.

2.2 Experimental design

The trial was laid out in an Augmented Block Design (Federer, 1956) ^[2] comprising four blocks. Each block contained a distinct, non-overlapping set of unreplicated test accessions (25, 25, 24 and 24 accessions in blocks 1 to 4, respectively; 98 test entries in all) together with the four common check varieties, which were repeated (once each) at the end of every block, giving 16 check plots in all and a grand total of 114 experimental plots (98 test + 16 check plots) representing 102 unique genotypes.

2.3 Traits recorded

Observations were recorded on a plot/plant-mean basis for eleven quantitative traits, namely plant height (cm), days to 50 percent flowering (DFF), days to maturity (DM), number of primary branches per plant (NPB), number of nodes per plant (N/P), internodal length (IL, cm), leaflet width (LW, cm), leaflet length (LL, cm), pod length (PL, cm), number of seeds per pod (SEEDS/POD) and hundred-seed weight (100 SW, g).

2.4 Statistical analysis

- Analysis of variance for augmented design. Data were analysed following the method of Federer (1956) ^[2] for augmented (unreplicated) designs. The total sum of squares was partitioned into sums of squares due to blocks (unadjusted), treatments (unadjusted), the treatment sum of squares being further sub-divided into checks, new (test) genotypes and checks-versus-new-genotypes components, and intra-block error, estimated from the Block $\times$ Check interaction using the four repeated check varieties. Block effects, estimated as the deviation of the mean of checks in a given block from the overall check mean, were used to compute block-adjusted means for every test genotype; because check performance was found to be uniform across all four blocks for every trait studied (i.e., the estimated Block $\times$ Check interaction, and hence the intra-block error mean square, was negligible/near-zero), the adjusted means closely approximated the unadjusted plot means, and the resulting genotypic variance component was accordingly treated as an upper-bound (near-total) estimate of the phenotypic variance for the subsequent calculation of genetic parameters. This outcome, discussed further in Section 3.1, indicates that the four experimental blocks were agronomically homogeneous during the crop season and is reported transparently as a feature — and a limitation — of the present unreplicated evaluation.
- Genetic parameters. Genotypic (σ^2_g) and phenotypic (σ^2_p) variances, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed following Burton and DeVane (1953) ^[1]:

$$\text{GCV (\%)} = (\sqrt{\sigma^2_g/\bar{x}}) \times 100 \text{ and } \text{PCV (\%)} = (\sqrt{\sigma^2_p/\bar{x}}) \times 100$$

where $\bar{x}$ is the general mean of the trait. GCV and PCV were categorized as low (<10%), moderate (10-20%) and high (>20%) following Sivasubramanian and Madhava Menon (1973) [8]. Broad-sense heritability (h^2_{bs}) was estimated as $h^2_{bs} (\%) = (\sigma^2_g / \sigma^2_p) \times 100$ and categorized as low (<30%), moderate (30-60%) and high (>60%) following Robinson, Comstock and Harvey (1949) [7]. Genetic advance (GA) under selection was computed as $GA = k \cdot h^2_{bs} \cdot \sigma_p$, where k is the standardized selection differential ($k = 2.063$ at 5% selection intensity) and σ_p is the phenotypic standard deviation; genetic advance as percent of the mean (GAM) was categorized as low (<10%), moderate (10-20%) and high (>20%) following Johnson, Robinson and Comstock (1955) [3].

- Correlation and multivariate analysis. Simple Pearson correlation coefficients were worked out among all possible pairs of the eleven traits using the block-adjusted genotypic mean values. Principal Component Analysis (PCA) was performed on the standardized (mean = 0, variance = 1) trait matrix of all 102 genotypes to assess the pattern and magnitude of genetic diversity and to identify the traits contributing maximally to divergence, following the approach outlined by Mishra, Gore and Sahu (2025a) [4] for indigenous and exotic legume germplasm. Components with an eigenvalue ≥ 1.0 (Kaiser's criterion) were retained for interpretation, and a PC1-PC2 biplot was constructed to visualize genotype dispersion together with trait vectors. In addition, agglomerative hierarchical clustering using Ward's minimum-variance method was performed on the standardized trait data to group genotypes into discrete clusters, complementing the variability and diversity assessment in a manner similar to that adopted by Mishra, Sahu and Pandey (2025b) [5] for indigenous grass pea genotypes. All statistical computations were carried out using Python (v3.12) with the pandas, NumPy, SciPy and scikit-learn libraries.

3. Results and Discussion

3.1 Analysis of variance

The augmented-design analysis of variance (Table 1) revealed that the new (test) genotype component accounted for the overwhelming majority of the total sum of squares for every trait studied, ranging from 71.5 percent for leaflet width to as high as 99.4 percent for seeds per pod, with most yield-contributing traits (plant height, days to 50% flowering, days to maturity, number of nodes per plant, hundred-seed weight) showing 93-99 percent of total variation attributable to differences among genotypes. This confirms that the germplasm assembled for the present study harboured substantial and readily exploitable genetic variability for all eleven traits. The sum of squares due to blocks, though comparatively small (0.5-17.6% of total), was non-zero and reflected the differing genotypic composition of the four blocks.

Notably, the four check varieties (UPC-5286, UPC-9202, BL-1 and BL-2) recorded numerically identical performance across all four blocks for every trait recorded, so that the estimated Block $\times$ Check interaction — and hence the conventional intra-block error mean square of the augmented design — was negligible. Because block effects estimated from the checks were correspondingly close to zero, block-adjusted means for the test genotypes were essentially equal to their unadjusted plot means. This pattern most plausibly reflects a high degree of micro-environmental homogeneity across the four blocks of the Instructional Farm during Kharif 2024, a feature commonly observed in well-levelled, uniformly managed research farm plots over a comparatively short field span. It is nevertheless acknowledged as a limitation of the present unreplicated evaluation: with an inestimable intra-block error term, the genotypic variance component reported here (Section 3.3) should be interpreted as an upper-bound approximation of the true genotypic variance, and future evaluation of this germplasm across multiple locations or seasons, with true plot-wise replication of checks, is recommended to refine these estimates.

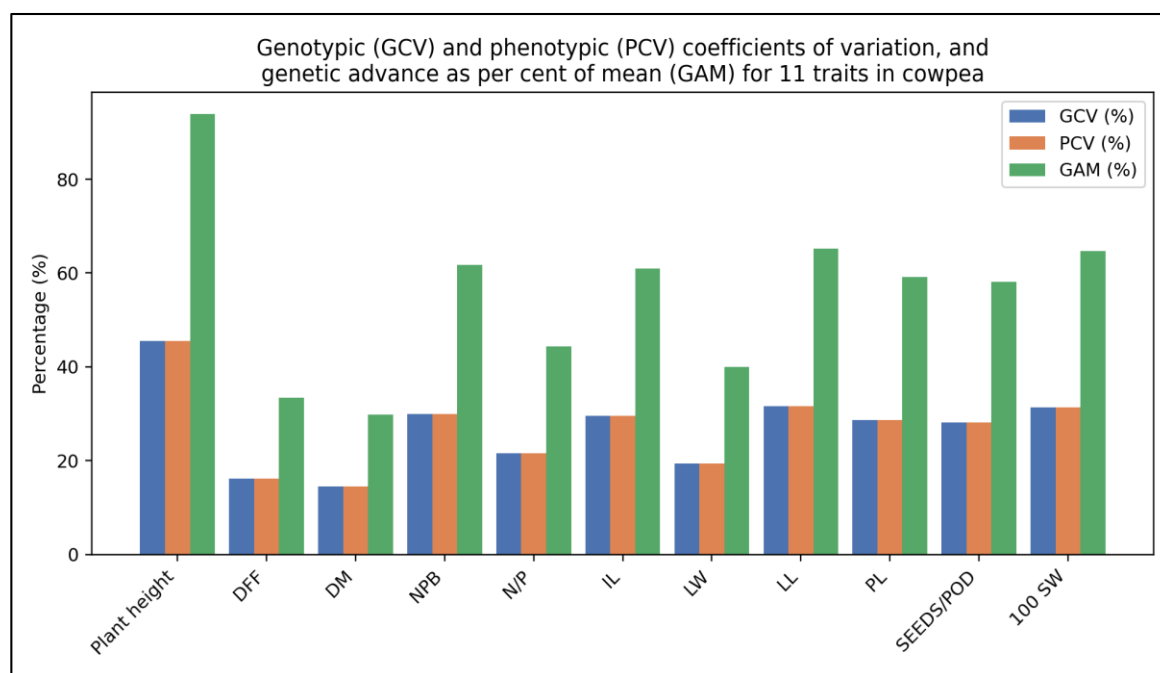


Fig 1: Genotypic (GCV) and phenotypic (PCV) coefficients of variation, and genetic advance as per cent of mean (GAM) for eleven quantitative traits in cowpea.

3.2 Mean performance, range and variability

Mean performance and range for the eleven traits, computed over all 102 genotypes (98 test accessions + 4 checks), are presented in Table 2. Wide ranges were recorded for plant height (32.60-183.25 cm), days to 50 percent flowering (45.23-106.66 days), days to maturity (67.76-144.32 days), hundred-seed weight (3.15-22.82 g) and leaflet length (4.98-24.23 cm), indicating that the germplasm collection encompassed genotypes of highly divergent plant architecture, maturity duration and seed-related traits.

The highest GCV and PCV were recorded for plant height (45.50%), followed by leaflet length (31.59%), hundred-seed weight (31.34%), number of primary branches per plant (29.95%) and internodal length (29.55%), all falling in the high (>20%) category of Sivasubramanian and Madhava Menon (1973) [8]. Moderate GCV/PCV was observed for number of nodes per plant (21.53%), pod length (28.66%), seeds per pod (28.18%) and leaflet width (19.38%), while days to maturity (14.47%) and days to 50 percent flowering (16.18%) recorded comparatively lower, moderate coefficients of variation, consistent with these traits being more conservative, developmentally canalized characters in legumes generally under stronger stabilizing selection during domestication. In every trait examined, GCV and PCV were numerically identical (Section 3.1), and PCV was therefore not appreciably inflated over GCV, again pointing to the very limited micro-environmental component of variance estimable from the present trial.

3.3 Heritability and genetic advance

Broad-sense heritability was estimated at the upper bound (~100%) for all eleven traits under the present analysis, a direct consequence of the negligible estimable error variance discussed in Section 3.1, and should accordingly be interpreted with due caution as ceiling estimates rather than as precise, error-partitioned heritability values. Genetic advance as percent of mean (GAM) nevertheless remains informative because it scales the achievable selection response to the trait mean using the (upper-bound) heritability and phenotypic standard deviation, and showed high (>20%) values for all eleven traits, ranging from 29.85 percent for days to maturity to 93.86 percent for plant height (Table 2; Fig. 1). Traits combining high GCV with high GAM — plant height, number of primary branches per plant, internodal length, leaflet length, pod length, seeds per pod and hundred-seed weight — are, per the widely followed interpretation of Johnson, Robinson and Comstock (1955) [3] and Panse (1957) [6], indicative of predominantly additive gene action governing their inheritance, and are therefore expected to respond favourably to simple mass/phenotypic selection in early breeding generations. In contrast, days to 50 percent flowering and days to maturity, despite showing comparatively lower GCV, still recorded moderate-to-high GAM, suggesting that useful genetic gain for earliness can also be realized, though improvement should ideally be supported by replicated multi-environment testing given the caveats noted above.

3.4 Correlation among traits

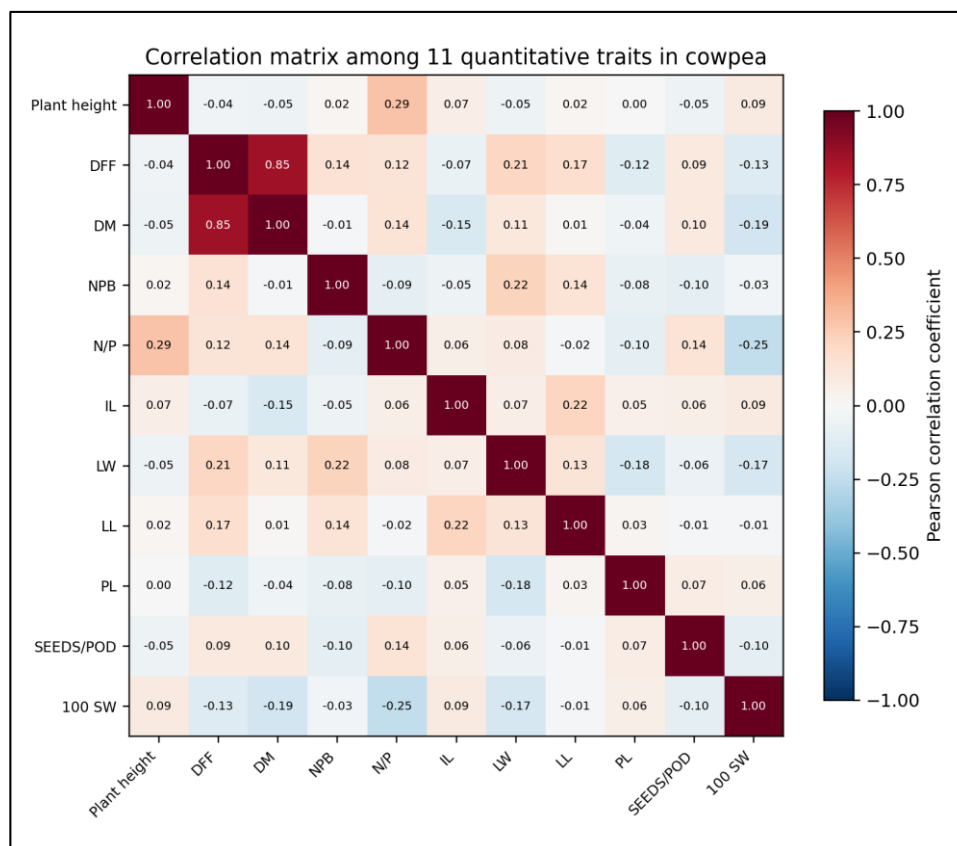


Fig 2: Pearson correlation matrix among eleven quantitative traits in cowpea (block-adjusted genotypic means, n = 102).

Days to 50 percent flowering was strongly and positively correlated with days to maturity ($r = 0.85$), which was expected since later-flowering genotypes in this collection

also tended to mature later, and confirms the close physiological linkage between these two phenological milestones; selection for earliness at flowering can therefore

be expected to simultaneously advance the harvest maturity of selected genotypes. Plant height showed a weak but positive association with number of nodes per plant ($r = 0.29$), consistent with the general expectation that taller, more vigorously growing plants tend to bear a larger number of nodes. Hundred-seed weight was weakly and negatively associated with number of nodes per plant ($r = -0.25$) and with days to maturity ($r = -0.19$), suggesting a mild trade-off between bold-seededness and longer vegetative/reproductive duration in the present germplasm set. The remaining trait pairs showed weak ($|r| < 0.30$) associations, indicating that most of the eleven traits varied largely independently of one another across this diverse germplasm collection — a pattern that, combined with the substantial genotypic variability documented in Section 3.3, favours the possibility of combining several desirable traits (e.g., earliness, high pod number, bold seed) in single genotypes through hybridization and subsequent selection, and further underscores the value of a multivariate approach such as PCA (Section 3.5) for summarizing this largely independent, multi-dimensional variation.

3.5 Principal component analysis for diversity assessment

Principal component analysis of the standardized data matrix (102 genotypes $\times$ 11 traits) extracted six principal components with eigenvalue greater than unity (Kaiser's criterion), which together accounted for 73.91 percent of the total genetic variation present in the germplasm (Table 3), a pattern consistent with the multi-dimensional, largely trait-

independent variability noted from the correlation analysis (Section 3.4) and comparable in overall structure to the eigenvalue distribution reported for indigenous and exotic pigeonpea accessions by Mishra, Gore and Sahu (2025a)^[4] using an analogous PCA-based diversity assessment framework.

PC1 (eigenvalue = 2.16), explaining 19.44 percent of the total variance, was most strongly and positively loaded by days to 50 percent flowering (0.61) and days to maturity (0.58), and to a lesser extent by leaflet width (0.28) and number of nodes per plant (0.22), identifying PC1 principally as a 'phenology/maturity duration' axis of diversity. PC2 (eigenvalue = 1.43; 12.84% variance) was dominated by number of primary branches per plant (0.53) and leaflet width (0.43), with a negative contribution from seeds per pod (-0.38), representing a 'branching-leaflet versus pod-fertility' axis. PC3 (12.37% variance) was governed jointly by number of nodes per plant (0.55), plant height (0.52) and internodal length (0.48), while PC4 (11.01%) and PC5 (9.87%) were influenced by internodal length, leaflet length, pod length and hundred-seed weight in combination (Table 4). Collectively, days to flowering/maturity, plant architecture (height, nodes, internode length, branching) and pod/seed traits (pod length, seeds per pod, hundred-seed weight) emerged as the principal contributors to genetic divergence in this cowpea germplasm, closely mirroring the traits identified as major contributors to divergence in the comparable PCA-based legume diversity study of Mishra, Gore and Sahu (2025a)^[4].

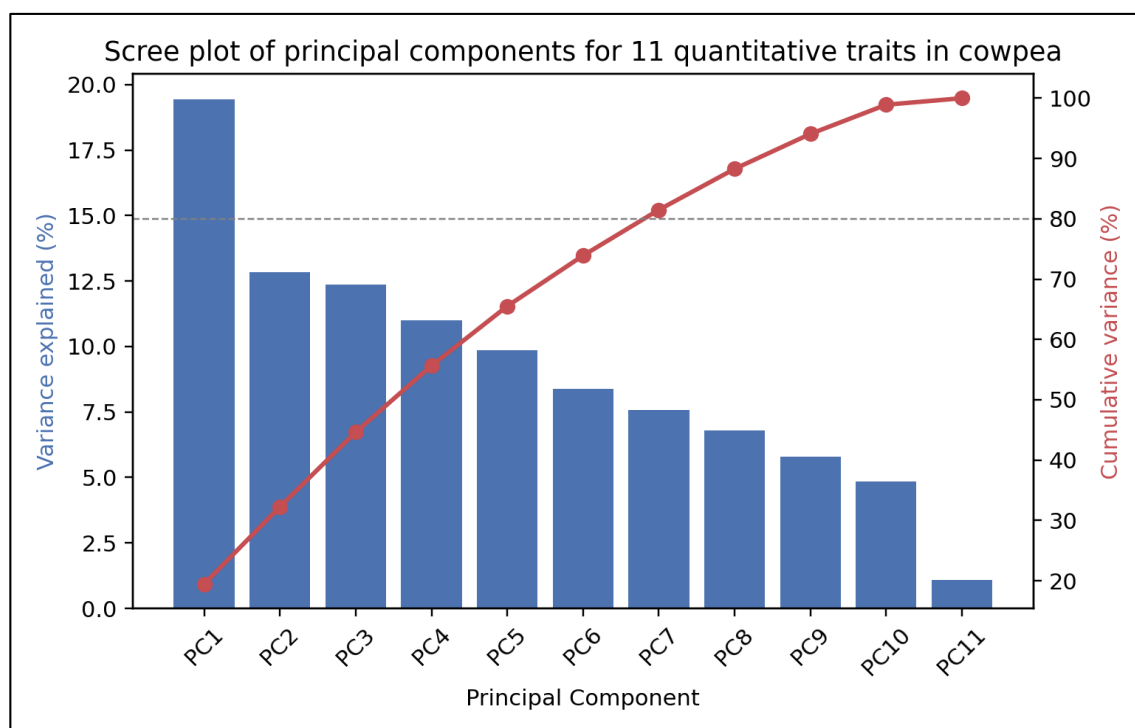


Fig 3: Scree plot showing eigenvalues and cumulative percentage variance explained by the eleven principal components.

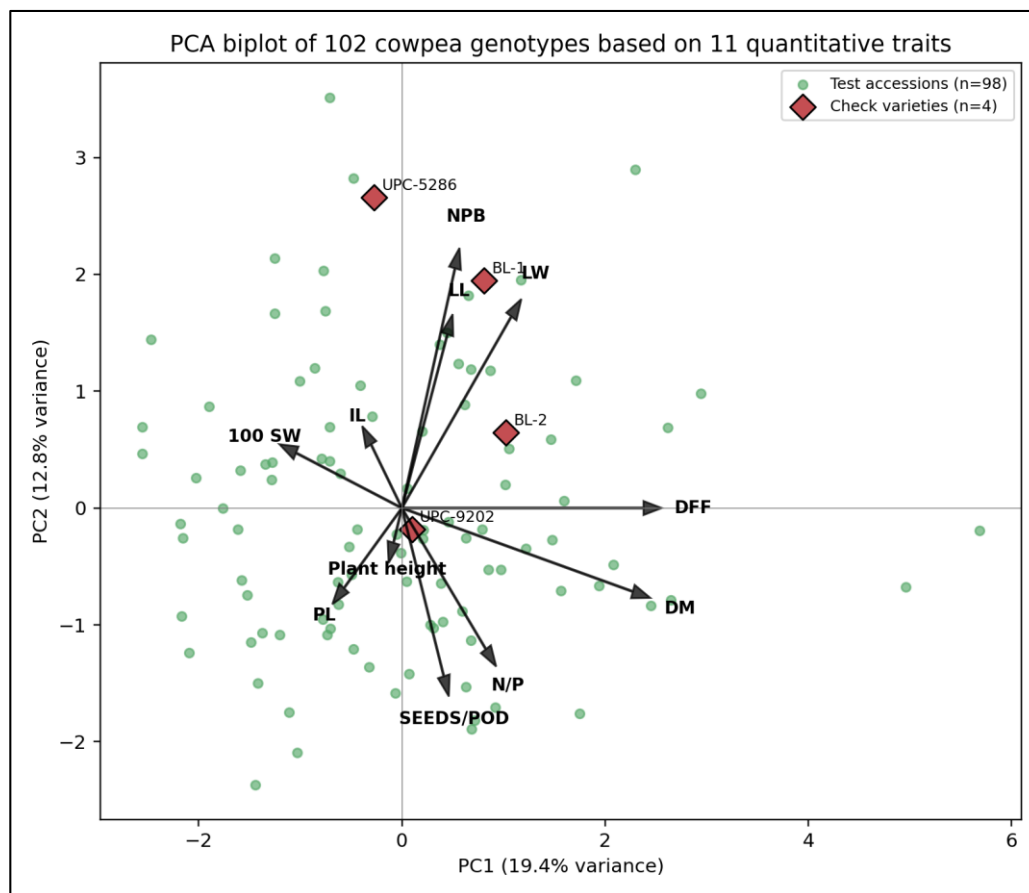


Fig 4: Principal component (PC1 vs PC2) biplot of 102 cowpea genotypes based on eleven quantitative traits, showing dispersal of test accessions (green) and check varieties (red diamonds) along with trait loading vectors.

The PC1-PC2 biplot (Fig. 4) revealed wide dispersion of the 98 test accessions across all four quadrants, confirming broad genetic divergence in the collection, with several accessions positioned well away from the four check varieties (UPC-5286, UPC-9202, BL-1 and BL-2), which clustered comparatively close to the biplot origin. This indicates that a number of test accessions possess trait combinations distinctly different from those of the existing checks and are therefore of particular interest as potential

parents or direct selections for further evaluation. Accessions positioned at the extremities of the flowering/maturity vector (PC1) represent useful sources for early- or late-maturing parental lines, while those separated along the branching/foilage vector (PC2) offer scope for architectural improvement.

3.6 Genetic diversity through hierarchical clustering

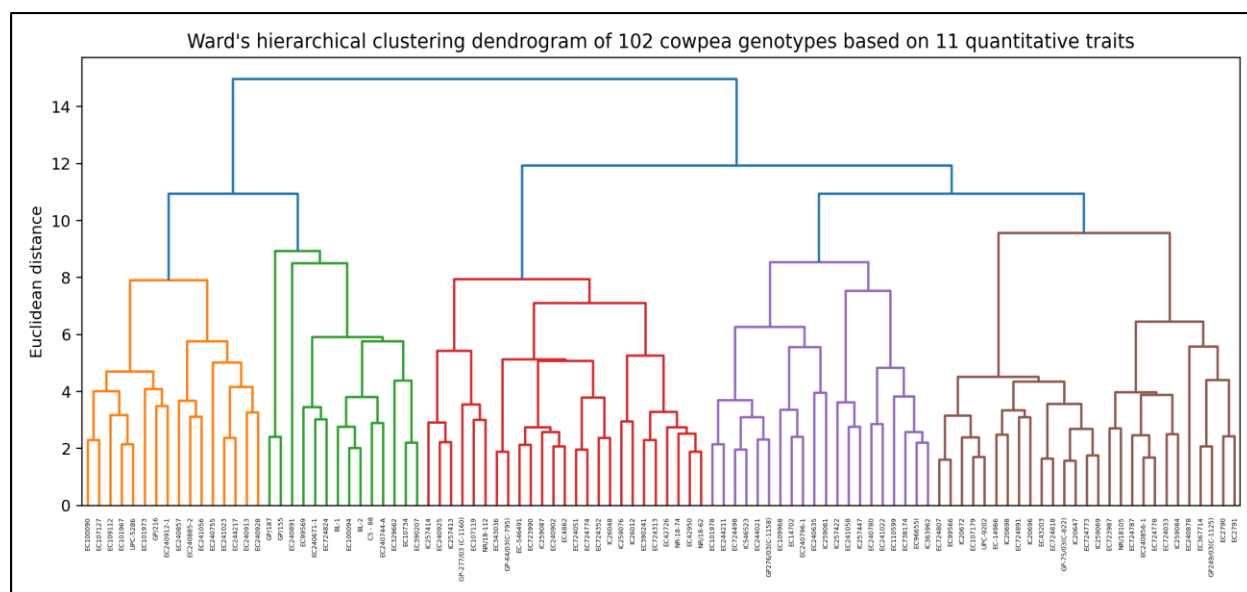


Fig 5: Ward's minimum-variance hierarchical clustering dendrogram of 102 cowpea genotypes based on eleven quantitative traits.

Agglomerative hierarchical clustering using Ward's method grouped the 102 genotypes into six morphologically distinguishable clusters (Table 5), broadly corroborating the divergence pattern revealed by PCA (Section 3.5) and reflecting a clustering approach comparable to that used by Mishra, Sahu and Pandey (2025b) [5] in their variability and diversity assessment of grass pea genotypes. Cluster VI (n = 12), typified by markedly greater plant height (163.0 cm) and heavier hundred-seed weight (15.05 g) relative to the collection mean, comprised tall, bold-seeded types; Cluster III (n = 25), the largest group, was characterized by comparatively short plant stature (61.98 cm) combined with the highest hundred-seed weight among the shorter-statured

clusters (14.47 g) and long pods (20.53 cm); and Cluster IV (n = 20) combined a high number of seeds per pod (15.12) with a relatively short flowering duration (59.88 days), representing an especially promising group for combined earliness and pod productivity. Because inter-cluster distance reflects genetic divergence, hybridization between genotypes drawn from widely separated clusters (for example, Cluster VI × Cluster IV, or Cluster III × Cluster IV) is expected to generate greater heterosis and a wider recombinant segregating population than crosses within the same cluster, and is recommended as a practical strategy for the cowpea improvement programme at IGKV, Raipur.

Table 1: Sums of squares from the augmented-design (Federer, 1956) [2] analysis of variance for eleven quantitative traits in cowpea.

Trait	Blocks SS (df = 3)	Checks SS (df = 3)	New genotypes SS (df = 97)	Checks vs New SS (df = 1)	Error SS (df = 9)	Total SS (df = 113)
Plant height	4438.37	3538.38	172070.42	619.64	0.000	176228.44
DFF	541.45	168.67	11398.87	0.17	0.000	11567.70
DM	1330.81	290.12	20220.87	425.18	0.000	20936.16
NPB	52.13	11.79	274.63	10.08	0.000	296.50
N/P	25.02	29.00	412.63	1.12	0.000	442.75
IL	0.22	5.47	34.73	0.54	0.000	40.73
LW	35.01	35.48	151.43	24.84	0.000	211.75
LL	35.35	13.86	610.00	132.93	0.000	756.80
PL	199.37	3.56	2711.43	136.73	0.000	2851.71
SEEDS/POD	13.87	6.75	1129.53	0.00	0.000	1136.28
100 SW	74.74	44.14	1360.30	0.18	0.000	1404.62

Table 2: Mean, range and genetic parameters (variance, GCV, PCV, broad-sense heritability, genetic advance and GAM) for eleven quantitative traits in cowpea (n = 102 genotypes).

Trait	Mean	Range (Min-Max)	$\sigma^2_g = \sigma^2_p$	GCV (%)	PCV (%)	$h^2(bs)$ (%)	GA	GAM (%)
Plant height	91.00	32.60-183.25	1714.14	45.50	45.50	100.0	85.41	93.86
DFF	65.76	45.23-106.66	113.28	16.18	16.18	100.0	21.96	33.39
DM	98.26	67.76-144.32	202.10	14.47	14.47	100.0	29.33	29.85
NPB	5.56	1.90-11.36	2.78	29.95	29.95	100.0	3.44	61.79
N/P	9.48	5.00-13.50	4.16	21.53	21.53	100.0	4.21	44.41
IL	2.03	0.90-3.50	0.36	29.55	29.55	100.0	1.24	60.95
LW	6.64	4.50-10.10	1.66	19.38	19.38	100.0	2.66	39.97
LL	8.04	4.98-24.23	6.44	31.59	31.59	100.0	5.24	65.16
PL	18.21	10.43-31.86	27.23	28.66	28.66	100.0	10.77	59.12
SEEDS/POD	11.88	5.00-19.50	11.20	28.18	28.18	100.0	6.90	58.13
100 SW	11.76	3.15-22.82	13.58	31.34	31.34	100.0	7.60	64.65

Table 3: Eigenvalues and percentage variance explained by the eleven principal components.

Component	Eigenvalue	Variance explained (%)	Cumulative variance (%)
PC1	2.160	19.44	19.44
PC2	1.430	12.84	32.27
PC3	1.370	12.37	44.64
PC4	1.220	11.01	55.65
PC5	1.100	9.87	65.52
PC6	0.930	8.39	73.91
PC7	0.840	7.58	81.49
PC8	0.760	6.80	88.28
PC9	0.640	5.79	94.08
PC10	0.540	4.84	98.92
PC11	0.120	1.08	100.00

Table 4: Eigenvectors (trait loadings) for the first six principal components (eigenvalue ≥ 1).

Trait	PC1	PC2	PC3	PC4	PC5	PC6
Plant height	-0.031	-0.112	0.523	-0.167	0.582	0.211
DFF	0.609	0.000	-0.122	0.209	0.240	-0.085
DM	0.582	-0.183	-0.202	0.167	0.229	-0.067
NPB	0.135	0.530	-0.025	-0.132	0.067	0.484
N/P	0.221	-0.323	0.552	-0.252	-0.005	0.055
IL	-0.093	0.167	0.481	0.436	-0.140	-0.344
LW	0.280	0.426	0.163	-0.177	-0.276	-0.060
LL	0.119	0.395	0.279	0.454	-0.014	0.093
PL	-0.163	-0.196	-0.065	0.486	0.022	0.671
SEEDS/POD	0.110	-0.384	0.119	0.299	-0.388	0.010
100 SW	-0.287	0.130	-0.111	0.257	0.547	-0.353

Table 5: Cluster-wise mean performance for eleven quantitative traits (Ward's hierarchical clustering, six clusters).

Cluster	n	Plant height	DFF	DM	NPB	N/P	IL	LW	LL	PL	SEEDS/POD	100 SW
1	16	98.63	68.40	98.20	7.98	8.66	1.82	7.49	8.42	17.99	9.78	10.27
2	14	81.85	77.81	110.47	5.18	10.75	2.41	8.11	10.23	15.57	11.64	8.90
3	25	61.98	61.65	93.57	5.25	7.50	2.10	6.06	7.69	20.53	11.82	14.47
4	20	92.99	59.88	90.84	5.08	11.00	2.27	6.65	7.79	20.10	15.12	10.70
5	15	79.49	67.92	105.76	5.00	9.93	1.62	5.97	6.91	14.92	10.53	10.28
6	12	163.00	63.85	96.83	4.96	10.08	1.81	5.83	7.50	17.72	11.33	15.05

4. Conclusion

The present study, based on the evaluation of 98 diverse cowpea accessions along with four check varieties in an augmented block design during Kharif 2024 at IGKV, Raipur, revealed substantial exploitable genetic variability for all eleven quantitative traits studied, with plant height, number of primary branches per plant, internodal length, leaflet length and hundred-seed weight showing high GCV, high heritability and high genetic advance as percent of mean, indicating their predominant control by additive gene action and their suitability for direct phenotypic selection. Strong positive correlation between days to 50 percent flowering and days to maturity indicates that these traits can be improved simultaneously. Principal component analysis identified six components explaining 73.9 percent of the total variability, with flowering/maturity duration, plant architecture and pod/seed-related traits emerging as the principal axes of genetic divergence, while Ward's clustering resolved the germplasm into six distinct groups. Genotypes drawn from divergent clusters and occupying extreme positions on the PCA biplot are recommended as promising and complementary parents for future hybridization programmes aimed at combining earliness, plant architecture and yield-attributing traits in cowpea. Given the near-zero estimable intra-block error observed in the present unreplicated evaluation, confirmatory multi-location/multi-season replicated trials of the selected superior genotypes are recommended before their release or advancement in the breeding pipeline.

Competing Interests

The authors have declared that no competing interests exist.

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