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Short Communication

Principal component and genetic diversity analysis for morpho-biochemical traits in cluster bean (*Cyamopsis tetragonoloba* L.)

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Abstract

Precise selection of superior genotypes for yield and its attributing traits is of utmost importance for a successful breeding program, but the complex nature of yield makes this selection difficult. The present study was conducted at dry land research area, CCSHAU, Hisar, Haryana, India, during *Kharif* 2022 to measure the genetic diversity among the cluster bean genotypes and to select the diverse parents for recombination breeding. Data were recorded on 17 quantitative traits using 50 cluster bean genotypes. D^2 analysis distributed all the genotypes into five clusters. Cluster IV had the maximum intra-cluster distance. The crossing among the genotypes of clusters I and III, III and IV, and I and IV would result in novel recombinants, as they showed high inter-cluster distance. In the PCA study, the first five principal components (PCs) had eigenvalues greater than one, and they cumulatively explained 83.29% of the total variation present in the original dataset. The first principal component (PC 1) explained 37.87%, while PC 2, PC 3, PC 4, and PC 5 explained 18.04, 12.90, 8.23, and 6.25% of the total variability, respectively. PC 1 has captured maximum variability for seed yield and its attributing traits, along with gum content. The genotypes, RGr 20-15, X 25, RGr 18-1, HG 884, RGr 20-7, HG 2-20, HG 19-4, HG 563, GD 567, and GG 1806, were the top-ranking genotypes upon PC analysis with high positive PC 1 scores.

Keywords: Cluster bean, Genetic divergence, Principal component analysis

Cluster bean (*Cyamopsis tetragonoloba* L. Taub.) (2n = 14) is an important multipurpose crop of arid and semi-arid regions. It has been utilized as a vegetable, fodder and green manuring crop in India since ancient times. A number of diseases, such as bacterial blight (*Xanthomonas campestris* pv. cyamopsidis), *Alternaria* leaf spot (*Alternaria cyamopsidis*), charcoal rot/damping off (*Macrophomina phaseolina*), dry root rot/leaf blight (*Fusarium solani* & *Rhizoctonia solani*) and wilt (*Fusarium caeruleum*), can drastically reduce its yield (Malik *et al*., 2021). In cluster bean, none of the cultivated germplasm has complete BLB resistance. Therefore, in order to develop disease-resistant varieties, the inheritance of disease resistance must be known, which can be used by breeders for the precise selection of resistant genotypes in segregating generations (Priti *et al*., 2023).

The studies on phenotypic and genetic diversity are essential to determine the genetic distance among genotypes and to identify groups with similar genetic backgrounds for conserving, evaluating and utilizing germplasm for hybridization. Principal component analysis helps researchers to distinguish significant relationships among the traits. Correlation analysis assists the breeder in effectively developing the selection strategy for seed yield, which is related to many component traits and controlled by many genes.

About 50 cluster bean (*Cyamopsis tetragonoloba* L.) genotypes, including checks, HG 2-20, HG 563 and RGC 1033, were evaluated in a randomized block design at the dry land research farm, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, during *Kharif* 2023. The genotypes used for the current study were sourced from CCSHAU, Hisar, Haryana; RARI, Durgapura, Rajasthan; CAZRI, Jodhpur, Rajasthan; and SDAU, Gujarat. Each genotype was sown in three rows of 1.5 m length with a row-to-row distance of 45 cm and plant-to-plant spacing of 15 cm with recommended agronomic practices.

Protein content was determined by multiplying nitrogen content obtained by micro-Kjeldhal method (Stuart,

1936) with a factor of 6.25 (Dubetz and Welis, 1968). The Gum content was estimated by the extraction of galactomannan, followed by its purification, precipitation and the precipitate was finally dissolved to measure spectrophotometrically using methods given by Das *et al.* (1977) and further improved by Joshi (2004).

Observations for disease intensity of bacterial leaf blight were recorded in natural conditions using 0 to 9 disease scale followed by AINP on Arid legumes (2020-21), ICAR-IIPR, Kanpur, India. The disease reaction was categorized as grade 0, which indicated 0% disease intensity and was considered as disease free. Grade 1 represented 0.1 to 5% disease intensity and was categorized as highly resistant. Grades 2–3 corresponded to 5.1 to 10% disease intensity and were classified as resistant. Grades 4–5 showed 10.1 to 20% disease intensity and were adjudged as moderately resistant. Grades 6–7 indicated 20.1 to 50% disease intensity and were categorized as susceptible, while grades 8–9 represented more than 50% disease intensity and were classified as highly susceptible.

The percent disease index was calculated as:

$$\textit{Percent Disease Severity} = \frac{\textit{Sum of all Individual rating} \times 100}{\textit{Total no. of leaves assessed} \times \textit{Maximum rating}}$$

Five plants from each replication were selected randomly, tagged and 6 to 8 leaves from each plant were selected at random for assessing the infected leaf area, according to the standard method using a 0 to 9 scale. D^2 analysis measuring genetic divergence was done as per Mahalanobis (1936). Grouping the genotypes into distinct clusters was done as suggested by Tocher (Rao, 1952). Principal component analysis was also estimated following Sneath and Sokal (1973).

In the present study, genetic divergence analysis was done for 17 characters using Mahalanobis D^2 statistics. All the 50 genotypes were grouped into 5 clusters (Fig 1). Cluster IV had the maximum, 19 genotypes, followed by cluster III having 16 genotypes, cluster I had 12 genotypes, while clusters II and V possessed one genotype each (Table 1). Intra and inter-cluster distance among different groups revealed that cluster I and III had the maximum inter-cluster distance (Table 1). Cluster mean for 17 characters suggested that cluster V showed the highest mean values for seed yield per plant, gum content, 100 seed weight, pod length, number of seeds per pod, number of clusters on main stem, and plant height (Table 2). Cluster I had a high mean value for number of pods per plant, number of clusters on side branches, number of clusters per plant, number of branches per plant and crude protein. Cluster II observed best for days to 50% flowering and days to maturity; similarly, cluster V exhibited the lowest value for bacterial leaf blight severity. It was evident that Cluster V was found to be the best performing for agronomic and other characters, *viz.*, plant height, number of clusters on main stem, number of pods per cluster in main stem, number of seeds per pod, pod length, gum content, seed yield per plant, followed by Cluster I. The involvement of genotypes belonging to Cluster I and III, III and IV, and I and IV in hybridization would help in achieving novel recombinants, as they were showing maximum

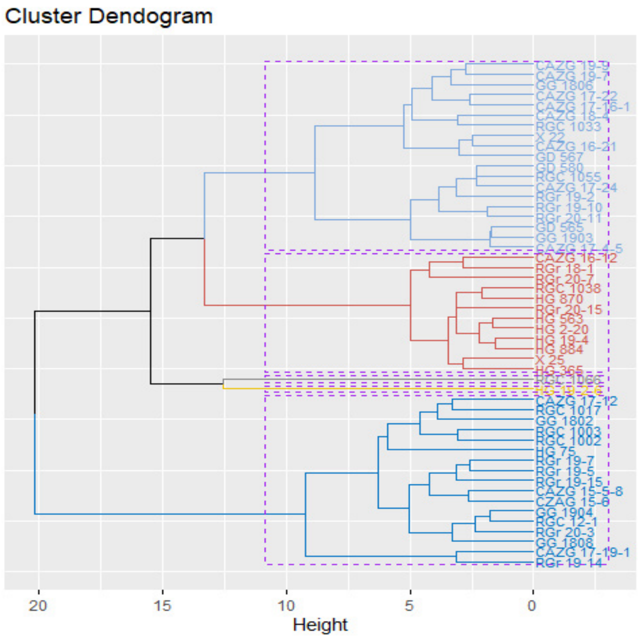

Fig 1. Dendrogram showing the clustering pattern of 50 cluster bean genotypes

Table 1. Distribution pattern of 50 genotypes into 5 clusters

Cluster no.	Number of genotypes	Genotypes	D^2 (D)
1	12	HG 2-20, HG 884, HG 870, HG 563, HG 365, HG 19-4, RGC 1038, RGr 18-1, RGr 20-7, RGr 20-15, CAZG 16-12, X 25	27.828 (5.270)
2	1	HG 19-2-6	0.00
3	16	HG 75, RGC 12-1, RGC 1017, RGC 1002, RGC 1003, RGr 20-3, RGr 19-5, RGr 19-7, RGr 19-14, RGr 19-15, CAZG 15-6, CAZG 15-5, CAZG 17-1, GG 1802, GG 1808, GG 1904	50.644 (7.116)
4	19	RGC 1055, RGC 1033, RGr 20-11, RGr 19-2, RGr 19-10, CAZG 16-2, CAZG 19-7, CAZG 19-9, CAZG 18-4, CAZG 17-4, CAZG 17-1, CAZG 17-2, GG 1806, GG 1903, GD 565, GD 580, GD 567, X 22	60.211 (7.823)
5	1	RGC 1066	0.000

Table 2. Cluster mean for 17 characters in 50 genotypes of cluster bean

Characters	I	II	III	IV	V	Mean
Plant height (cm)	88.83	64.00	89.12	88.68	97.00	85.53
Days to 50% flowering	31.95	27.67	32.94	32.63	31.33	31.30
Days to maturity	94.69	74.67	96.61	96.74	93.33	91.21
No. of pods per plant	96.50	78.00	43.24	75.84	74.00	73.52
No. of clusters on main stem	4.83	6.00	4.82	4.79	14.00	6.88
No. of clusters on side branches	20.67	14.00	6.82	16.47	3.00	12.19
No. of clusters per plant	25.83	21.00	11.59	21.42	17.00	19.37
No. of pods per cluster on main stem	5.17	7.00	4.49	4.39	8.33	5.88
No. of pods per cluster on side branches	4.59	6.00	3.92	3.84	6.00	4.87
No. of seeds per pod	8.72	8.00	8.71	8.74	10.00	8.83
Pod length (cm)	5.65	5.52	5.61	5.65	6.03	5.69
No. of branches per plant	6.58	3.00	5.06	6.47	1.00	4.42
100 seed weight (g)	2.84	2.67	2.47	2.60	2.99	2.71
Gum content (%)	29.58	26.53	26.43	27.66	30.60	28.16
Crude protein (%)	23.96	23.38	23.60	23.93	23.75	23.72
Bacterial leaf blight severity (%)	29.70	30.48	36.09	33.92	28.33	31.70
Seed yield per plant (g)	21.97	16.92	14.46	17.55	22.58	18.70

inter-cluster distance. The similarity /dissimilarity matrix of the genotypes under study indicated that most of the genotypes are highly similar, except the genotypes RGC 1066 and HG 19-2-6, which are more diverse than the rest of the genotypes. This result was in accordance with the previous report of Sushmitha *et al*. (2025), Remzeena *et al*. (2021), Vishnoi *et al*. (2017) and Kumar *et al*. (2014) in cluster bean.

Out of 17 principal components (PCs), five PCs have eigen value more than 1. First PC contributes 37.87% of the total variability, and PC5 contributes to only 6.25%. First five PCs cumulatively contribute 83.29% of the variation (Table 3). Similarly, the first five principal components contributed more than 80% of the variation in the studies conducted by Sushmitha *et al*. (2025), Khalid *et al*. (2017) and Zubair *et al*. (2017). Further, principal component analysis is used to check character association with respective principal components.

PC 1 was showing high positive loading for seed yield and its attributing traits *viz*., seed yield per plant, number of clusters per plant, number of pods per plant, 100 seed weight and gum content, whereas it exhibited negative loading for BLB intensity. Since PC 1 has captured maximum variability for seed yield and its attributing traits, along with gum content. Therefore, the genotypes captured under this component can be utilized in the improvement of cluster bean for the above-mentioned traits. PC 2 has shown positive loading for the number of branches per plant and days to maturity, while negative loadings for the number of pods per cluster on main and side branches. In PC 3, the traits like plant height, pod length, days to maturity, number of clusters on the main stem and days to 50% flowering have shown negative loadings. The traits, *viz*., protein content, number of seeds per pod and number of pods per cluster on side branches, were found to have the highest values of loadings in PC 4. In PC 5, positive loadings were exhibited by the number of clusters on the main stem and days to 50% flowering, while negative loadings were found with the number of seeds per plant and pod length. Similarly, yield and its contributing traits were captured by different PCs in the studies reported by Sushmitha *et al*. (2025), Khalid *et al*. (2017) and Zubair *et al*. (2017). In PC 1, the genotypes RGr 20-15, X 25, RGr 18-1, HG 884, RGr 20-7, HG 2-20, HG 19-4, HG 563, GD 567, and GG 1806 showed the maximum score. The genotypes showing maximum PC score in PC 1 showed the highest overall mean values for the traits positively related to seed yield and its attributing traits. The genotypes RGC 1003, HG 75, RGC 1066, RGr 18-1, GD 580, X 25, RGC 1002, CAZG 18-4, GD 567, and RGr 20-15 scored maximum in PC 2. In PC 3, the genotypes

Table 3. Total variance explained by different principal components in 50 cluster bean genotypes

Particulars	PC1	PC2	PC3	PC4	PC5
Eigen value	6.438	3.067	2.192	1.398	1.063
Variability (%)	37.87	18.04	12.90	8.23	6.25
Cumulative (%)	37.87	55.91	68.81	77.04	83.29

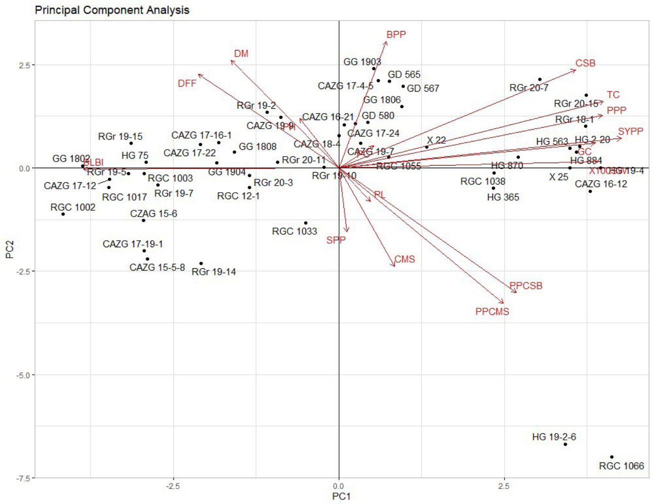

Fig 2. Distribution of cluster bean genotypes based on principle factor 1 and 2

CAZG 17-22, GG 1903, HG 870, RGC 1033, CAZG 19-9, GG 1808, GD 580, RGr 19-10, CAZG 17-4-5, and CAZG 17-12 showed maximum PC score. In PC 4, the genotypes, RGr 20-11, RGr 19-7, RGr 19-2, RGr 19-14, RGr 19-5, GG 1904, RGr 19-15, GG 1806, CAZG 19-9, and CAZG 17-19-1 scored the maximum PC score. In PC 5, the genotypes, CAZG 17-22, GG 1808, RGC 1066, HG 75, CAZG 17-19-1, RGr 19-14, CAZG 17-12, CAZG 19-9, HG 870, and HG 19-4 scored the maximum PC score. A similar kind of grouping of genotypes was also obtained by Sushmitha *et al*. (2025), Khalid *et al*. (2017), Zubair *et al*. (2017) and Manivannan *et al*. (2016).

The PCA bi-plot (Fig 2) accounted for 55.91% of total variability and revealed that seed yield per plant, number of clusters per plant, number of pods per plant, 100 seed weight, gum content, number of branches per plant and days to maturity were the most discriminatory variables. The genotypes, *viz*., RGC 1002, GG 1802, HG 19-4, and CAZG 16-12, were found to be scattered farthest from the bi-plot origin and other genotypes. Therefore, these genotypes accounted for more variability for the traits of the respective principal components than other genotypes. The vectors of gum content, 100 seed weight, number of pods per plant, number of clusters per plant, number of clusters on side branches, number of branches per plant, number of pods per cluster on main stem and side branches are the main contributors to seed yield per plot in cluster bean (acute angle). Similar positive association of seed yield per plot with all the above characters is reported by Makwana *et al*. (2021), for number of branches per plant, number of pods per plant, by Kumar *et al*. (2019) and for number of pods per cluster by Sushmitha *et al*. (2025). The obtuse angle was obtained between seed yield per plot and BLB intensity, days to 50% flowering and days to maturity; these traits are negatively correlated with seed yield per plot. Seed yield per plot has no relation to the number of clusters on the main stem (almost right angle). The vector of days to pod length, plant height and number of seeds per pod is shorter than the rest of the traits, indicating that the variation of this trait across genotypes is either small or not well presented in the bi-plot.

Principal component analysis reduced the original 17 variables into five major principal components, explaining 83.29% of total variation. The first principal component contributed 37.87% of the variation. The second, third, fourth and five principal components contributed 18.04, 12.90, 8.23 and 6.25% of total variation in the data, respectively. According to factor loading after varimax rotation, it can be concluded that PC-1 and PC-2 can be designated as yield factors as they showed high loadings for seed yield per plant, number of clusters per plant, number of pods per plant, 100 seed weight, gum content, number of branches per plant and days to maturity. These findings can be used in breeding strategies for future hybridization programs for yield improvement and are appropriate for the classification of diversity among cluster bean germplasm.

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