



Genetic Diversity using Cluster and Principal Component Analysis in Chickpea (*Cicer arietinum* L.)

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Abstract: A comprehensive assessment of genetic diversity was conducted in 46 chickpea genotypes using Principal Component Analysis (PCA) and hierarchical cluster analysis based on seven quantitative traits. PCA revealed that the first three principal components (PCs) had eigenvalues greater than one and together accounted for 72.87% of the total phenotypic variation. PC1 was primarily associated with days to flowering and maturity, PC2 with seed yield and PC3 with plant height and test weight. These components effectively captured the major dimensions of variability, facilitating trait-based genotype classification. The PCA biplot identified genotypes such as DCR 24-2, RVSSG-137 and NBeG 1149 as promising for seed traits while VCD-23-3 and KCD-120029 exhibited superior yield potential. Cluster analysis further grouped the genotypes into four distinct clusters, with the blue cluster showing maximum genetic divergence. The clustering pattern supported PCA results and highlighted genotypes with unique trait combinations suitable for breeding. This integrated multivariate approach proved effective in identifying genetically diverse and agronomically desirable genotypes, offering valuable insights for parent selection and trait-specific improvement in chickpea breeding programs.

Key words: Chickpea, Principal components, Variability, Cluster analysis, Biplot analysis.

Chickpea (*Cicer arietinum* L.), commonly known as Bengal gram, is an important cool-season, self-pollinated legume crop of the family *Fabaceae* and subfamily *Papilionaceae*. It is among the earliest domesticated legumes, with its centre of origin traced to South-Eastern Turkey and adjoining regions. In India, chickpea is cultivated across diverse agro-ecological zones, ranging from the northern and northeastern hills to the central drylands and southern regions. While states such as Punjab, Haryana, Uttar Pradesh, and Bihar have witnessed a decline in chickpea cultivation due to the expansion of wheat monocropping, significant increases in acreage have been recorded in Madhya Pradesh, Andhra Pradesh, Maharashtra, and Karnataka (Arya *et al.*, 2019).

Nutritionally, chickpea is a vital dietary component, consumed extensively in the form of dal. It contains about 21% protein, enriched with essential amino acids like aspartic acid, leucine, and lysine, thereby serving as one of the most affordable and accessible sources of protein in vegetarian diets (Begum *et al.*, 2023). Its adaptability to drought-prone regions and high nutritional value has earned chickpea the title of the “king of pulses.” However, despite its resilience and nutritional richness, chickpea productivity remains below potential, mainly due to narrow genetic bases and limited genetic progress in breeding programs. Enhancing chickpea productivity requires identification and utilization of genetically diverse and agronomically superior genotypes. Genetic diversity analysis provides a foundation for selecting suitable parental lines for hybridization, thereby enabling the development of high-yielding and stress-resilient varieties. In this context, multivariate statistical approaches such as cluster analysis and Principal Component Analysis (PCA) are widely used to dissect genetic variability. PCA, in particular, reduces data complexity by transforming correlated traits into a smaller set of uncorrelated principal components, while retaining most of the variability in the original dataset (Muniraja *et al.*, 2011). Such analyses not only quantify the contribution of individual traits to overall diversity but also facilitate the identification of superior genotypes for targeted breeding programs. Considering these aspects, the present study was undertaken to assess the genetic diversity in chickpea genotypes using cluster and principal component analyses, with the objective of identifying promising genotypes for future breeding strategies.

Materials and Methods

Present study was undertaken at Rajasthan Agricultural Research Institute (SKNAU), Durgapura, Jaipur (Rajasthan), India during *rabi* season, 2024-25. Forty six high yielding genotypes of chickpea which were collected from different centres of All India Coordinated Improvement Project of Chickpea (Table 1). Randomized block design (RBD) was followed with three replications. The experimental plot was 4m long consisting of four rows and spacing between row to row was kept to 30 cm and plant to plant was 10 cm. Sowing was done in first week of November under timely

sown conditions. Basel dose of fertilizer was applied in the form of NPK 20:40:00. Five plants from each genotype were randomly selected for recording of data *viz*, days to 50% flowering, plant height (cm), days to maturity, pods per plant, 100-seed weight (g), grain yield kg ha⁻¹ and plant stand at harvest (0-9 Scale). To assess the genetic diversity among the genotypes, Wilk’s cluster analysis and Principal Component Analysis (PCA) were performed to identify genetically divergent and promising lines suitable for utilization in future breeding programmes (Murthy and Arunachalam, 1966; Singh and Chaudhary, 1985; Wilks, 2019). R software was used for both PCA and cluster analysis.

Results and Discussion

The analysis of variance revealed highly significant differences among chickpea genotypes for most of the studied traits, indicating the presence of substantial genetic variability. The results are presented in Table 2. Significant variation was observed for grain yield, days to 50% flowering, plant height, pods per plant, days to maturity, and 100-seed weight, suggesting ample scope for selection and improvement. However, plant stand at harvest showed non-significant variation, indicating uniformity plant population among the genotypes.

Multivariate analysis provided a comprehensive understanding of the variability and genetic diversity among 46 chickpea genotypes evaluated for seven quantitative traits. To reduce the complexity inherent in multivariate data and identify the traits contributing most to diversity, principal Component Analysis (PCA) was applied. The analysis revealed that the first three principal components had eigenvalues greater than 1.0 and together explained 72.87% of the total variation, indicating that a large portion of the variability present in the dataset was adequately summarized by these components (Fig. 1). This substantial cumulative contribution clearly highlights the efficiency of PCA in dimensionality reduction, ensuring that most of the essential information is retained while simplifying the dataset. Similar observations on the utility of PCA in chickpea germplasm evaluation were earlier emphasized by Lakshmi

Table 1. Genotypes with source, pedigree and specific traits

S. N.	Entry	Pedigree	Source	Traits
1.	IPC L 4-14	(DCP 92-3/ICC4958/*3DCP 92-3	Kanpur	High yield, Rain-fed
2.	GNG 2461	(KWR 108/GNG 1861)// (Pant G 186/GNG 1958)	Sriganganagar	High yield, Rain-fed
3.	BG 4005	Pusa 362/3/Pusa 362// (Pusa 362/ICC 4958-6)	New Delhi	High yield, Rain-fed
4.	CSJ 515	FG 712/CSJ 146	Durgapura	High yield, Rain-fed
5.	H 19-20	HC 5/ ICCV 312	Hisar	High yield, Rain-fed
6.	H 20-105	H 10-22/ JG 315	Hisar	High yield, Rain-fed
7.	BG 2244	BGD 98/JG 11	ICAR-IARI	High yield, Rain-fed
8.	BG 4059	ICCV 97126/ICCV03214	ICAR-IARI	High yield, Rain-fed
9.	BG 4069	BG 372/ICC4958	ICAR-IARI	High yield, Rain-fed
10.	GNG 2645	RVSSG 34/GNG1581	Sriganganagar	High yield, Rain-fed
11.	GNG 2655	GNG 3068/GNG 1581	Sriganganagar	High yield, Rain-fed
12.	RSGD-1257	RSG 973/RSG 991	Durgapura	High yield, Rain-fed
13.	RSGD-1332	RSG 973/ Avrodhi	Durgapura	High yield, Rain-fed
14.	GJG 2211	ICCV 08108/ ICCV 96836	Junagarh	High yield, Rain-fed
15.	GJG 2212	ICCV 97105/ICCV 11601	Junagarh	High yield, Rain-fed
16.	Phule G-1623-3-4	[(ILC-166/WR-315)//Vijay]/3/RCBM	Rahuri	High yield, Rain-fed
17.	Phule G-1609-4-18	[(JG 24/ICCV 96854)//WR 315]/3/JG 24	Rahuri	High yield, Rain-fed
18.	RVSSG-137	RVG 202/ JSG 37	Sehore	High yield, Rain-fed
19.	RVSSG-138	HC 5/ICC 4958	Sehore	High yield, Rain-fed
20.	NBeG 1634	JAKI 9218/ICCV11601	Nandyal	High yield, Rain-fed
21.	NBeG 1149	JAKI 9218/ ICCV 07110	Nandyal	High yield, Rain-fed
22.	KCD-120175	JG-11/ICCV-171111	Gulberga	High yield, Rain-fed
23.	KCD-120029	JG-11/NBeG-3	Gulberga	High yield, Rain-fed
24.	RKG 24-5	[(ICC 4958/ICCV 10)//(Pusa 372/ Pusa)]//[(ICCV 92994/RSG 888)//(GNG 1581/PBG)]	Kota	High yield, Rain-fed
25.	RKG 24-6	RKG 13-515/RSG 931	Kota	High yield, Rain-fed
26.	PG 362	RSG 963/KPG 59	Pantnagar	High yield, Rain-fed
27.	PG 353	GNG 1581/RSG 963	Pantnagar	High yield, Rain-fed
28.	GLD 18152	PBG 5/ HIC94-737	Ludhiana	High yield, Rain-fed
29.	GLD 19079	PBG1//4/(PBG1/3/(ICCV96030/C.pinn.ILWC 188))/ ICCV96030)	Ludhiana	High yield, Rain-fed
30.	IPC 2020-94	JG 14/ICC 4958	ICAR-IIPR	High yield, Rain-fed
31.	IPC 2019-202	KWR 108/ILWC179	ICAR-IIPR	High yield, Rain-fed
32.	BDNG 2020-71	Digvijay/ICC 4958	Badnapur	High yield, Rain-fed
33.	BDNG 2021-53	Vijay/BCP 60	Badnapur	High yield, Rain-fed
34.	VCD-23-3	ICCV 93954/3/ICCV 93954//Haringtars/ICCV 93954	Vijayapura	High yield, Rain-fed
35.	HBGV 1	JG 11/ WR 315	Vijayapura	High yield, Rain-fed
36.	JG 2024-89	ICCV 96970/ ICCV 08108	Jabalpur	High yield, Rain-fed
37.	JG 2024-90	ICCV 05107/ ICCV 10	Jabalpur	High yield, Rain-fed
38.	AKG-2241	JAKI-9218/GJG-0814	Akola	High yield, Rain-fed
39.	DCR 24-1	DC 171115/RSG 888	Dholi	High yield, Rain-fed
40.	DCR 24-2	DC 18-1107/ JG 14	Dholi	High yield, Rain-fed
41.	CSG-20-11	BG 1103/ ICCV10	ICAR-CSSRI	High yield, Rain-fed
42.	CSG-21-6	HC 5/S7	ICAR-CSSRI	High yield, Rain-fed
43.	KSG-4203	ICCX171007-B-B-B-B	Basant Agro. Tech. Ltd.	High yield, Rain-fed
44.	IPCD 2020-143	IPC 2008-57/ICC-14778	ICAR-IIPR	High yield, Rain-fed
45.	IG 2025-1	IG 21-53/ JG-33	Indore	High yield, Rain-fed
46.	IG 2025-2	IG 21-54/ JG-33	Indore	High yield, Rain-fed

Table 2. Analysis of variance for yield and yield related traits in chickpea

Traits	Mean sum of square		
	Replication	Entries	Error
Grain yield kg ha ⁻¹	43071.73	124591.83**	7373.96
Days to 50% flowering	8.86	195.03**	3.59
Plant Height (cm)	113.58	275.15**	10.75
Pods per plant	53.35	758.61*	12.26
Days to maturity	4.00	175.24*	1.95
100-seed weight (g)	7.00	46.39*	1.86
Plant Stand at Harvest (0–9 scale)	0.20	0.28	0.15

**Significant at 1% ($p \leq 0.01$); Significant at 5% ($p \leq 0.05$)

Table 3. Eigenvalues, Variability Explained by Principal Components, and Rotated Component Matrix of Chickpea Genotypes

PCs	EV	PV	CPV	Variables						
				Yield	F	PH	PP	M	TW	PSH
PC 1	2.17	31.07	31.07	0.36	0.89	0.01	-0.09	0.91	-0.55	-0.35
PC 2	1.63	23.29	54.36	-0.80	0.38	-0.02	-0.37	0.33	0.24	0.73
PC 3	1.30	18.50	72.86	0.02	0.21	0.83	0.47	0.14	0.56	-0.06
PC 4	0.86	12.33	85.19	-	-	-	-	-	-	-
PC 5	0.59	8.39	93.58	-	-	-	-	-	-	-
PC 6	0.43	6.09	99.67	-	-	-	-	-	-	-
PC 7	0.02	0.33	100.00	-	-	-	-	-	-	-

PCs: Principal components; EV: Eigen value; PV: Percentage of variance; CPV: Cumulative percentage of variance; Yield: Grain yield kg ha⁻¹; F: Days to 50% flowering; PH: Plant height (cm); PP: Pods per plant; M: Days to maturity; TW: 100-Seed weight (g); PSH: Plant stand at harvest (0-9 Scale).

Annapurna *et al.* (2008) and Shivwanshi and Babbar (2017).

Among the principal components, PC1 contributed 31.07% of the total variance and was strongly associated with days to flowering (0.89) and days to maturity (0.91). This component primarily reflected the influence of phenological traits, thus distinguishing the genotypes into early and late maturing groups. The identification of early- and late-flowering lines through PCA is of practical importance in breeding programs where adaptability to specific agro-climatic zones or cropping systems depends largely on crop duration. The second principal component (PC2) accounted for 23.29% of the variability and exhibited a negative loading for yield per plot (-0.80) while showing a positive correlation with plant stand at harvest (0.74). This indicated that genotypes with stable plant populations at harvest may not necessarily be the highest yielding ones, reflecting an inverse association between yield and survival in certain environments. Such relationships often arise under stress-prone

conditions where genotypes may differ in their ability to partition resources between survival and productivity. The third principal component (PC3) explained 18.50% of the variance and had strong positive loadings for plant height (0.83) and test weight (0.56). This component represented variation in plant architecture and seed quality traits, which are of significance in both breeding and commercialization, as seed weight has direct market value and plant height influences harvesting ease. Collectively, the three components accounted for the majority of variation, capturing the essential differences among genotypes based on phenological, yield, and morphological characters (Table 3).

The biplot constructed from PC1 and PC2 further facilitated visualization of trait associations and genotype distribution. Genotypes such as DCR 24-2, RVSSG-137, NBeG 1149, RSGD-1257, GJG 2212, HBGV 1, RKG 24-5, and KCD-120175 were positioned close to the trait vectors for test weight, plant stand at harvest, and pods per plant (Fig. 2). Their proximity to these vectors indicated their

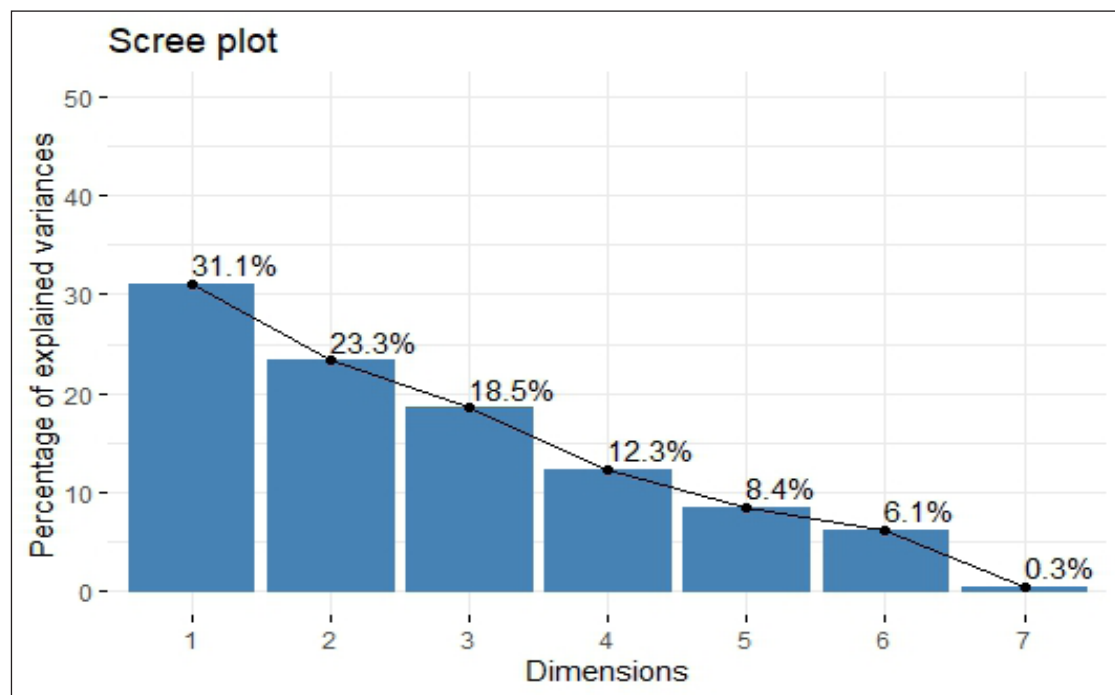


Fig. 1. Scree Plot between Eigen Value and Principal Component.

superiority for physical plant attributes and seed development, suggesting their suitability as donor parents in breeding programs targeting improvement in plant establishment and seed traits. Similar applications of PCA for the identification of promising donor lines were reported by Jain *et al.* (2023) and Rao *et al.* (2023). On the other hand, genotypes such as VCD-23-

3, AKG-2241, and KCD-120029 were associated with the yield per plot vector, highlighting their potential as high-yielding genotypes either for direct cultivation or as parental material in yield enhancement programs. Another group comprising GLD-18152, DCR 24-1, GNG 2655, and CSG-20-11 showed strong association with late flowering and late maturity traits, thereby

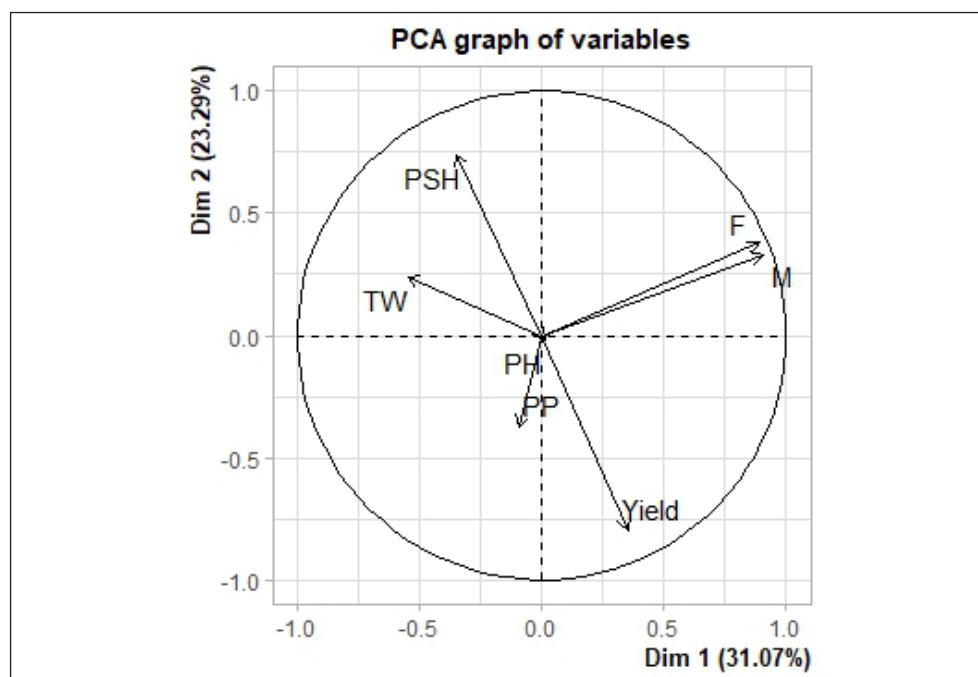


Fig. 2. Principal component graph of variables.

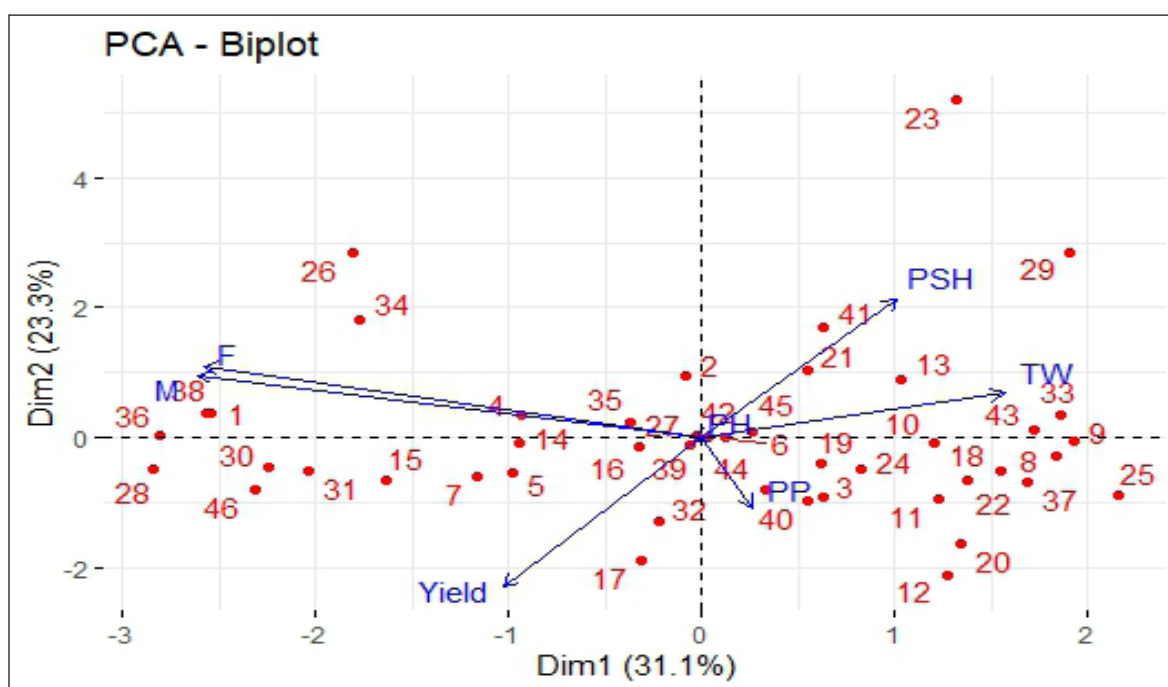


Fig. 3. Scattered Biplot Analysis of chickpea genotypes.

indicating their adaptability to environments with longer growing seasons or to conditions requiring delayed sowing. Such trait-specific associations, identified through PCA, have also been reported in chickpea germplasm studies by Kumari *et al.* (2020) and Kumar *et al.* (2019).

To confirm and further validate the genetic relationships among genotypes, hierarchical cluster analysis was performed using the same set of traits. The dendrogram clearly grouped the 46 genotypes into four distinct clusters – blue, red, grey, and yellow – based on Euclidean distances. At the basal level, individual genotypes with high similarity merged at low dissimilarity coefficients, while distinct groups merged at higher values, reflecting greater genetic distance. The blue cluster included genotypes DCR 24-2, RVSSG-137, and NBeG 1149, which had also emerged as closely associated in PCA, confirming the consistency of multivariate approaches in capturing genetic relationships. This cluster was particularly interesting as it merged with other groups at the highest dissimilarity level of approximately 7.8, making it the most genetically distinct set of genotypes in the study. Such genotypes are valuable in breeding programs since crossing between divergent parents often generates greater variability and higher chances of heterotic combinations. The red cluster formed

the largest group and included genotypes with moderate similarity for phenological and yield-related traits, whereas the grey and yellow clusters showed intermediate merging with the red cluster at dissimilarity coefficients of 5.8 and 6.8, respectively, reflecting moderate relatedness. These results corroborated earlier findings of Aleem *et al.* (2021) who also reported distinct cluster formation in chickpea germplasm based on yield and morphological parameters. Furthermore, Rao *et al.* (2023) and Jain *et al.* (2023) emphasized that genotypes from different clusters are likely to show higher divergence and, when crossed, may lead to superior hybrids with improved performance.

The integration of PCA and cluster analysis thus provided a comprehensive understanding of both trait associations and genetic diversity. While PCA identified the major components explaining variability and revealed trait-specific differentiation among genotypes, cluster analysis validated these findings by grouping genotypes into clusters based on similarity and divergence. Together, the two approaches enabled a robust assessment of diversity and identification of superior genotypes. In particular, PC1 highlighted phenological differentiation, PC2 emphasized the trade-off between yield and plant survival, and PC3 captured morphological and seed-size

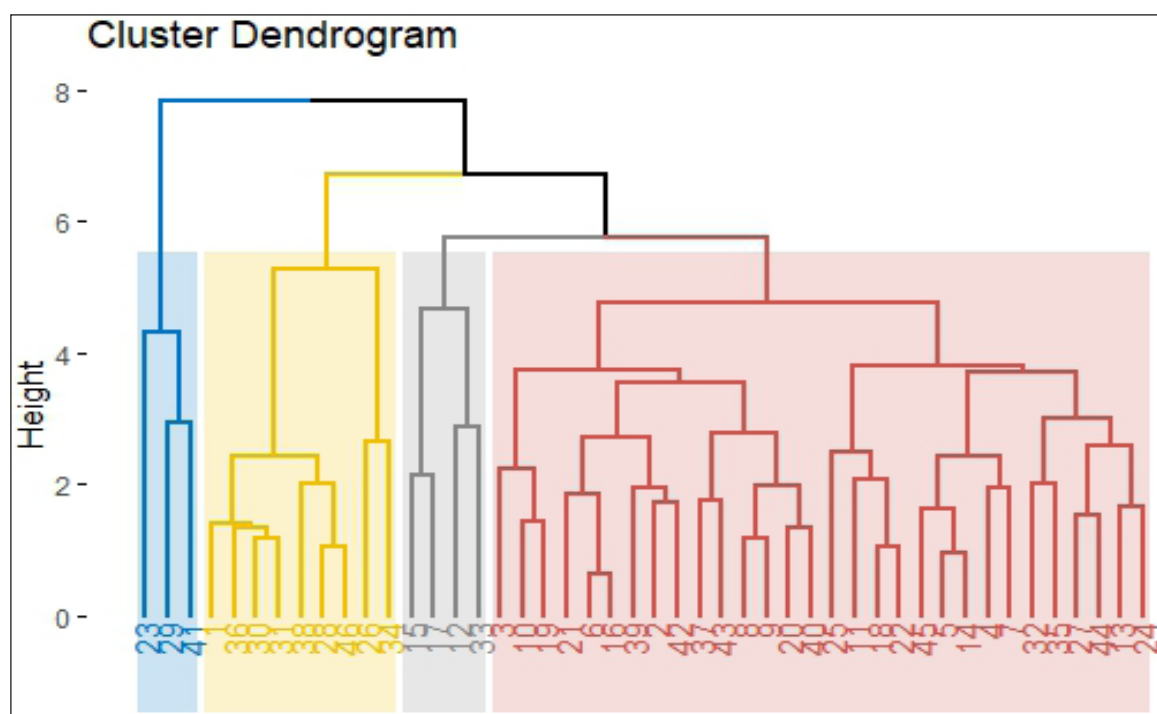


Fig. 4. Dendrogram showing clustering pattern of genotypes.

variation (Fig. 3). Genotypes from the blue cluster such as DCR 24-2, RVSSG-137, and NBeG 1149 emerged as unique and promising for seed and plant stand traits, while VCD-23-3, AKG-2241, and KCD-120029 were identified as high yielders. Late-maturing lines like GLD-18152 and CSG-20-11 may be valuable under specific environments where longer growth duration is desirable (Fig. 4). These results corroborated earlier findings of Arora *et al.* (2018) and Jain *et al.* (2023). These findings highlight the importance of exploiting both phenological diversity and yield stability traits in chickpea breeding.

Conclusions

Overall, the study clearly demonstrates that the combined use of PCA and cluster analysis provides a powerful and reliable approach to dissect the genetic diversity of chickpea genotypes. The identification of divergent groups and trait-specific superior lines offers valuable opportunities for breeders to select suitable parental combinations. As Arya *et al.* (2019) pointed out, the success of chickpea breeding programs is largely dependent on the effective utilization of genetic diversity, and the present results reaffirm that multivariate statistical techniques can greatly enhance the precision of such efforts. Therefore, the

present investigation not only identified high-yielding and trait-specific genotypes but also underscored the significance of adopting PCA and clustering as indispensable tools in chickpea improvement programs under varied agro-climatic conditions.

Declarations

The authors have no competing interests.

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