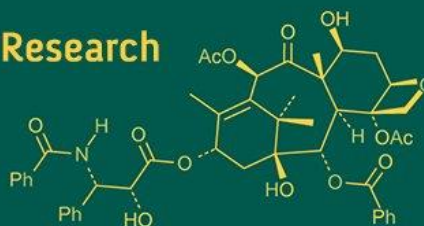


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(6): 662-665
www.biochemjournal.com
Received: 19-03-2026
Accepted: 22-04-2026

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Principal component analysis in chickpea (*Cicer arietinum* L.) genotypes in South-Eastern Rajasthan, India

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i6Sh.8687>

Abstract

Chickpea (*Cicer arietinum* L.) is a nutritionally important grain legume with substantial relevance to global food and protein security. The present investigation aimed to dissect the multivariate structure of agro-morphological traits and identify key determinants of yield using principal component analysis (PCA) in a diverse set of forty chickpea genotypes evaluated under a randomized block design with three replications during Rabi 2019-20 at Kota, Rajasthan, India. Eleven quantitative traits were subjected to PCA based on the correlation matrix. Eigenvalue decomposition revealed that the first four principal components (PCs) with eigenvalues >1 cumulatively accounted for 69.2% of the total phenotypic variance, which increased to 77.8% upon inclusion of the fifth component. PC1 explained the largest proportion of variance (30.2%) and exhibited high positive loadings for seed yield per plant, biological yield, and number of pods per plant, indicating a strong yield component axis. PC2 (18.1%) was primarily associated with phenological traits, particularly days to 50% flowering and days to maturity, reflecting adaptation-related variation. PC3 (11.4%) captured the trade-off between seed size and seed number, while PC4 (9.5%) represented structural and quality attributes. The results underscore the predominance of yield-contributing and phenological traits in governing genetic divergence. Hence, simultaneous selection based on PC1 and PC2 scores would be an efficient strategy for the improvement of yield potential and development of climate-resilient chickpea cultivars.

Keywords: Principal component analysis, Chickpea (*Cicer arietinum* L.)

Introduction

Chickpea (*Cicer arietinum* L.) is a self-pollinated, annual pulse crop, diploid ($2n = 2x = 16$) with a genome size of 738.09 Mbp (Varshney *et al.*, 2013)^[18]. It belongs to kingdom Plantae, genus *Cicer*, family Fabaceae, sub family Papilionaceae. The Middle Eastern region between Southeast Turkey and Iran's northwest region, and parts of Syria, have been proposed as the primary centre of origin. Grown in about 57 countries, chickpea is an important nutritionally rich grain legume with a significant role in global food security (Merga and Haji 2019)^[13]. Nutritionally, chickpea seeds contain about 20-25% protein, 40-60% carbohydrates, substantial dietary fiber, and essential minerals including iron, zinc, calcium, and magnesium, making it an important component of balanced diets, particularly in vegetarian populations (Jukanti *et al.* 2012)^[10].

The area under chickpea cultivation decreased due to lack of high yielding varieties and susceptibility to insects and diseases (Hameed *et al.*, 2009)^[8]. Currently, chickpeas are grown world over in an area of 14.1 million hectares, with an annual production of 16.5 million tonnes and productivity 1170.2 kg/ha (Anonymous, 2024^a)^[2]. India is the largest producer of chickpea with more than 2/3rd share in area and production of chickpea in the world. Chickpea has played a major role in realization of 'Pulse Revolution' in India making the country nearly self-sufficient in pulses. During 2024-25, the area under cultivation was 9.6 million hectares, yielding a production of 11.34 million tonnes with an average yield of 1181.25 kg/ha (Anonymous, 2025^a)^[5]. States like Maharashtra, Madhya Pradesh, Rajasthan, Gujarat and Uttar Pradesh are major chickpea producing states of India (Anonymous, 2024^b)^[3]. Within Rajasthan, the crop spans 1.65 million hectares, producing 1.97 million tonnes with an average yield of 1193 kg/ha (Anonymous, 2025^b)^[6], with contribution by key districts including Tonk followed by S. Madhopur, Kota and Dausa (Anonymous, 2024^c)^[4].

With the increasing trend of the market of products based on plant protein (protein isolates), importance of chickpea to the processing sector has enhanced further.

PCA is a standard tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. It involves a mathematical procedure that transforms a number of correlated variables into a number of uncorrelated variables called principal components (Muniraja *et al.*, 2011) ^[14]. In the present study, we carried out a PCA to identify agronomic attributes whose selection would lead to improvement in seed yield of chickpea.

Materials and Methods

The experimental material consisted of forty chickpea genotypes sown in randomized block design with three replications during Rabi 2019-20 at Agricultural Research Station, Umedganj, Kota, Rajasthan. Each genotype was accommodated in four rows plot of 4.0 m length with a spacing of 30×10 cm. The genotypes were randomly allotted to each plot in each replication. All the recommended agronomic package of practices was followed timely for successful raising of crop. The observations were recorded on five randomly selected plants per replication for eleven traits viz., plant height, number of branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, 100 seed weight, protein content and seed yield per plant except days to 50% flowering and maturity which were recorded on plot basis. According to the Massay (1965) ^[12] and Jolliffe (1986) ^[9] PCA is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set. Therefore, the present investigation was aimed to evaluate the germplasm for identify and rank important traits and genotype on the basis of principal component analysis before taking up hybridization programme for evolving better hybrid.

Results

A multivariate statistical method for exploration and

simplifying complex data sets is principal component analysis. PCA was used in the current work to analyse chickpea quantitative traits.

Principal component analysis was performed using 11 quantitative traits, namely plant height, days to 50% flowering, 100 seed weight, number of branches per plant, number of seeds per pod, days to maturity, number of pods per plant, seed yield per plant, biological yield, harvest index and protein content. The eigen analysis of the correlation matrix revealed that the first four principal components had eigen values greater than unity (3.3186, 1.9893, 1.2561 and 1.0436) collectively explaining 69.2% of the total phenotypic variation. Inclusion of the fifth component increased the cumulative variance explained to 77.8% although its eigenvalue was marginally below 1.0 (Table 1 and Figure 1).

PC1 accounted for 30.2% of the total variance and was predominantly associated with seed yield per plant (0.532), biological yield (0.495), number of pods per plant (0.480), harvest index (0.310), number of seeds per pod (0.269) and number of branches per plant (0.258). The positive and relatively high loadings of yield and its major components indicate that PC1 primarily represents a yield productivity axis. PC2 explained 18.1% of the total variation and mainly influenced by days to 50% flowering (-0.572) and days to maturity (-0.566) with moderate positive contributions from number of branches per plant and protein content. This component can be interpreted as a phenological axis, distinguishing early and late maturing genotypes. PC3 contributed 11.4% of the total variance and was strongly associated with 100 seed weight (-0.742) and the number of seeds per pod (0.459) reflecting a seed versus seed number trade off axis. PC4 accounted for 9.5% of the variation and showed notable loadings for plant height, protein content, number of seeds per pod and harvest index. This component appears to represent structural and quality related variation. The remaining principal components each explained less than 9% of the total variation and were considered less biologically informative (Table 2 and Figure 2).

Table 1: Eigen analysis of the Correlation Matrix

Eigenvalue	3.3186	1.9893	1.2561	1.0436	0.9512	0.7631	0.5997	0.5219	0.3809	0.1727	0.0029
Proportion	0.302	0.181	0.114	0.095	0.086	0.069	0.055	0.047	0.035	0.016	0.000
Cumulative	0.302	0.483	0.597	0.692	0.778	0.847	0.902	0.949	0.984	1.000	1.000

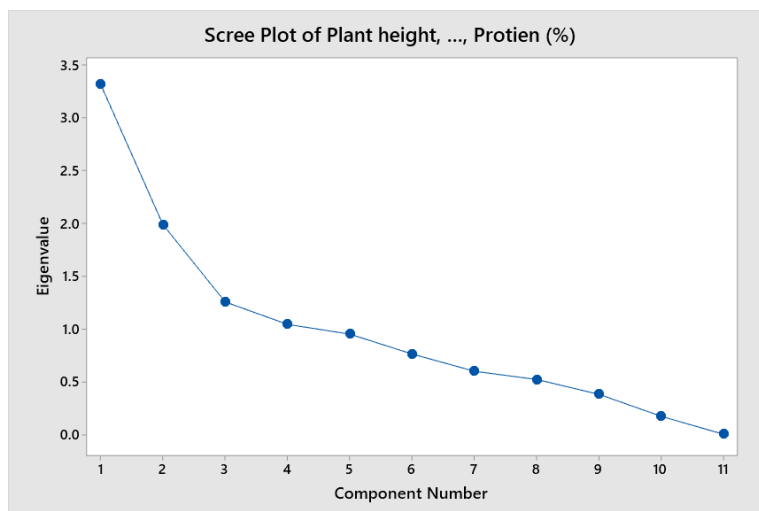
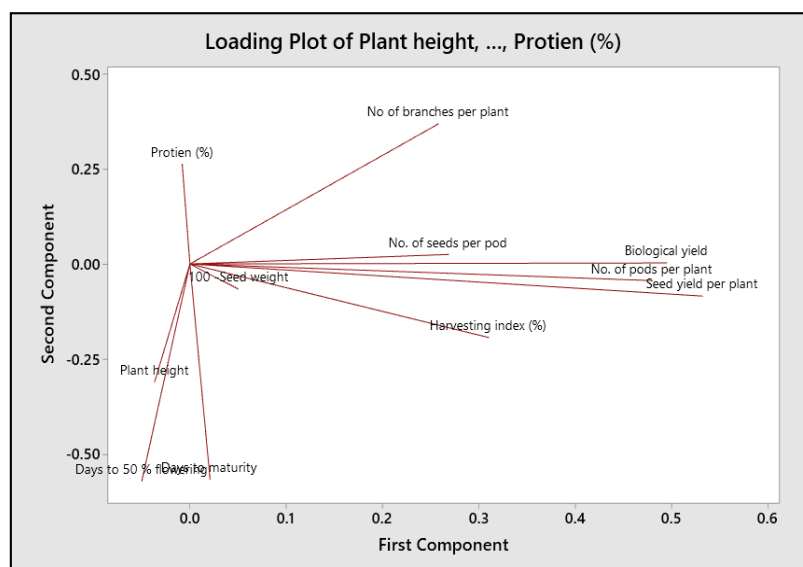


Fig 1: Screenplot for PCA analysis

Table 2: Eigenvectors

Variable	PC1	PC2	PC3	PC4	PC5
Plant height	-0.037	-0.310	-0.329	0.560	0.139
Days to 50% flowering	-0.050	-0.572	0.215	0.131	0.023
100-Seed weight	0.050	-0.066	-0.742	0.050	-0.217
No of branches per plant	0.258	0.369	0.010	0.297	0.047
No. of seeds per pod	0.269	0.025	0.459	0.370	0.239
Days to maturity	0.021	-0.566	0.137	0.110	-0.290
No. of pods per plant	0.480	-0.044	-0.044	-0.228	0.027
Seed yield per plant	0.532	-0.084	-0.075	-0.003	-0.041
Biological yield	0.495	0.003	-0.126	0.197	0.110
Harvesting index (%)	0.310	-0.193	0.104	-0.442	-0.340
Protien (%)	-0.008	0.263	0.176	0.377	-0.812

**Fig 2: PCA biplot for 11 traits**

Discussion

The present investigation revealed that a substantial proportion of total phenotypic variability in chickpea genotypes was captured by the first few principal components, thereby confirming the efficiency of PCA in dimensionality reduction and pattern recognition in complex datasets.

The first principal component (PC1), which explained the highest proportion of variance, was predominantly associated with seed yield per plant and its component traits, including biological yield and number of pods per plant. This indicates that yield-related traits are the primary contributors to genetic variability in chickpea. Such strong associations among yield components have also been reported by Mahendran *et al.*, (2015) ^[11] and Ojo *et al.*, (2012) ^[15] suggesting that these traits can be effectively utilized for indirect selection in breeding programmes. The positive loadings of these traits further imply the presence of synergistic relationships, which are advantageous for simultaneous trait improvement.

The second principal component (PC2) was mainly governed by phenological traits, particularly days to flowering and maturity, which exhibited strong negative loadings. This indicates divergence between early and late maturing genotypes and highlights the importance of phenological adaptation. Early flowering and maturity are key traits for escaping terminal drought stress in chickpea, as also emphasized in recent studies (Varshney *et al.*, 2021) ^[17]. Therefore, PC2 can be interpreted as a phenological axis with significant implications for climate-resilient breeding.

The third principal component (PC3) revealed a negative association between seed size (100 seed weight) and number of seeds per pod, indicating a trade-off relationship. Such antagonistic interactions among yield components are commonly attributed to limited assimilate partitioning and have been widely reported in crop plants (Araus *et al.*, 2018) ^[7]. This suggests that breeding strategies should aim at optimizing rather than maximizing individual traits to achieve balanced improvement.

The fourth principal component (PC4) was associated with plant height and protein content, indicating the contribution of structural and quality-related traits to overall variability. Recent studies have also highlighted the importance of integrating yield and nutritional quality traits in chickpea improvement programmes (Merga and Haji, 2019) ^[13]. Overall, the PCA results demonstrated that variability in chickpea genotypes is primarily structured around four major axes: (i) yield and its components, (ii) phenological traits, (iii) seed size-number relationship and (iv) structural and quality traits. From a breeding perspective, simultaneous selection based on PC1 and PC2 would be highly effective for developing high-yielding and climate-resilient cultivars. These findings are in close agreement with recent advances in chickpea genomics-assisted breeding strategies Amrita *et al.*, (2014) ^[1], Toker and Cagiran (2004) ^[16], Varshney *et al.*, (2021) ^[17].

Conclusion

The study demonstrated that principal component analysis (PCA) effectively explained the variability among chickpea

genotypes, with the first four components accounting for 69.2% of the total variation. PC1 was mainly associated with yield and its contributing traits, indicating their major role in genetic divergence, while PC2 represented phenological variation related to flowering and maturity. PC3 reflected the trade-off between seed size and seed number, and PC4 captured structural and quality traits. Overall, the results suggest that selection based on yield components (PC1) and phenological traits (PC2) would be most effective for developing high-yielding and climate-resilient chickpea cultivars.

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