



Plant Archives

Journal homepage: <http://www.plantarchives.org>DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.1.279>

PRINCIPAL COMPONENT ANALYSIS FOR GENETIC DIVERSITY ASSESSMENT AND TRAIT SELECTION IN LENTIL(*LENS CULINARIS* MEDIK.)

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(Date of Receiving-28-12-2024; Date of Acceptance-15-03-2025)

ABSTRACT

Principal Component Analysis (PCA) is a multivariate statistical tool used to assess genetic diversity and identify key traits contributing to variability in lentil (*Lens culinaris* Medik.). The study was conducted at ITM University, Gwalior, Madhya Pradesh, during the Rabi season of 2023–2024, using an Augmented Design. A total of 50 genotypes were evaluated for 13 agro-morphological traits. PCA was performed to determine the contribution of each trait to genetic variation. Four principal components (PCs) were identified based on eigenvalues, collectively explaining the majority of the total variation. PC1 accounted for the highest proportion of variability and included traits such as Harvest Index, Biological Yield per Plant, and Pods per Plant. PC2 encompassed Days to Maturity, Days to 50% Flowering, and Days to First Flowering. PC3 was associated with Plant Height, Chlorophyll Content, and Number of Primary Branches, while PC4 included Seeds per Pod, 1000-Seed Weight, and Number of Secondary Branches. The highest variation was observed in PC1, indicating its potential for genotype selection in breeding programs. The study provides a comprehensive understanding of trait contribution to genetic diversity in lentil, facilitating targeted selection for yield improvement.

Key words : Lentil, Principal Component Analysis, Genetic Diversity, Agro-morphological Traits, Breeding Selection.

Introduction

Lentil (*Lens culinaris* Medik.) is a vital cool-season legume widely cultivated across South Asia, North Africa, the Middle East, Europe, and North America (Erskine *et al.*, 2011; Singh *et al.*, 2019). It is highly valued for its nutritional composition, nitrogen-fixing ability, and adaptability to diverse agro-climatic conditions (Tulluet *et al.*, 2011; Kumar *et al.*, 2020). Lentils are traditionally consumed whole, split, or decorticated and serve as a staple food in India, Canada, and Turkey (FAO, 2021). Nutritionally, they are rich in proteins (25–27%), carbohydrates (59%), dietary fiber, essential minerals, and vitamins, contributing significantly to food security and balanced diets (USDA, 2020; Thavarajah *et al.*, 2011). The seeds contain 356 mg of phosphorus, 198 mg

of iron, 2.5 mg of zinc, 71.3 mg of magnesium, 37.6 mg of calcium, 731 mg of potassium, 358 µg of folate, 3 mg of vitamin C, and 2.1 mg of niacin (Bhatty, 1988; FAO, 2019). India remains one of the largest producers, with a cultivation area of 14.94 lakh hectares and a productivity of 1008 kg/ha in 2017–18 (Ministry of Agriculture & Farmers Welfare, Government of India, 2019).

Despite its economic and nutritional significance, lentil productivity is often limited by genetic variability, biotic and abiotic stresses, and yield-attributing traits (Kumar *et al.*, 2018; Khazaei *et al.*, 2021). Breeding programs aim to improve these traits through genetic selection, hybridization, and molecular approaches. Principal Component Analysis (PCA) is a widely used multivariate

statistical tool that helps assess genetic diversity, identify key yield-attributing traits, and classify genotypes (Jolliffe & Cadima, 2016; Khalili & Rameeh, 2021). It aids in detecting patterns, reducing dimensionality in large datasets, and selecting high-yielding genotypes based on trait contributions (Yan & Rajcan, 2002; Pour-Aboughadarehet *al.*, 2019).

This study aims to apply PCA to analyze lentil genotypes for yield and its attributing traits, offering insights into genetic relationships, trait contributions, and selection strategies for breeding and crop improvement programs.

Materials and Methods

The present investigation was conducted during Rabi 2023-24 on 50 genotypes of lentil (*Lens culinaris* Medik.) obtained from the Indian Institute of Pulses Research (IIPR), Kanpur, along with three check varieties. The experiment was laid out in an Augmented Design at the Crop Research Center-1, School of Agriculture, ITM University, Gwalior, Madhya Pradesh (India).

A total of 13 agronomic and physiological traits related to yield and its components were recorded, including days to first flowering, days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height, number of pods per plant, number of seeds per pod, 1000-seed weight, chlorophyll content, harvest index, biological yield, and seed yield per plant. Data were collected from 10 randomly selected plants per genotype, and Principal Component Analysis (PCA) was performed using appropriate statistical tools to assess the genetic variation and relationships among the genotypes.

Results and Discussion

PC1 accounted for the highest variation (28.909%)

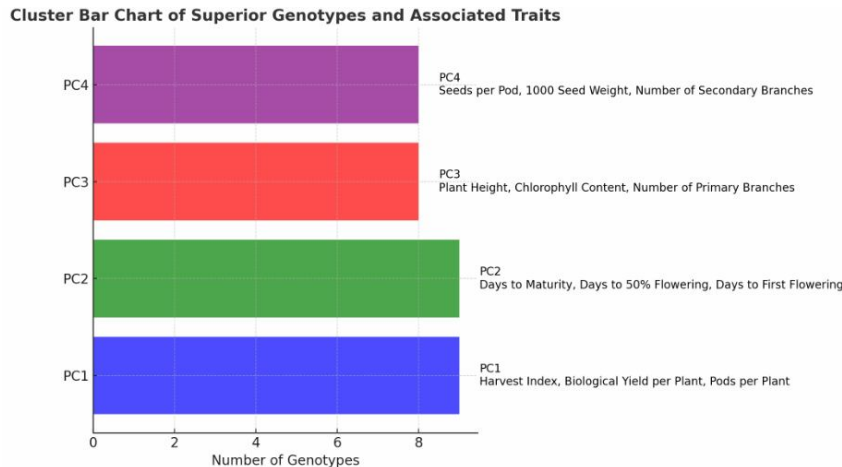


Fig. 1: Clustered Bar Chart of Superior Genotypes and Associated Traits

Table 1: Eigenvalues from the Correlation Matrix.

Principal Component	Eigenvalue	Proportion of Variability Explained	Cumulative Proportion
PC1	3.758	0.289	0.289
PC2	2.731	0.210	0.499
PC3	2.237	0.172	0.671
PC4	1.073	0.083	0.754

with an eigenvalue of 3.758, indicating its substantial contribution to total trait divergence (Table 1). This component primarily included traits related to yield, such as Harvest Index, Biological Yield per Plant, and Pods per Plant, which are critical in lentil breeding for enhancing productivity. The nine genotypes falling under PC1 (IPL 329, DPL 15, IPL 81, IG TALL 9, IPL 341, IPL 321, IPL 406, IC 560128, IPL 526) exhibit high suitability for these yield-related traits.

PC2 accounted for 21.0% of the total variance and was strongly associated with phenological traits, including

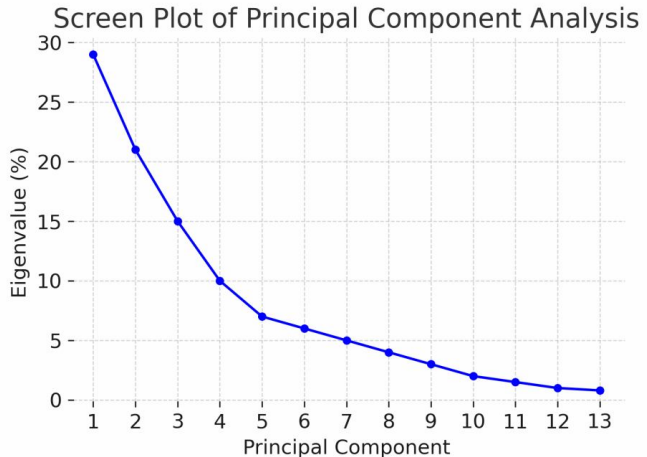


Fig. 2: Graphical representation of Eigenvalues % with 13 characters

Days to Maturity, Days to 50% Flowering, and Days to First Flowering. Thenine genotypesgrouped under this component (DPL 62, JL 3, KLS 218, LL 931, LL 4717, JL1, L 4727, LH-7-26, LCC 9941) showed a strong affinity for these traits, making them crucial for selecting early or late-maturing varieties based on breeding objectives (Gogoi *et al.*, 2021).

PC3 contributed 17.2% to the total variance and was predominantly associated with Plant Height, Chlorophyll Content, and Number of Primary Branches, which are important for biomass accumulation and vigor. The eight

Table 2: Superior Genotypes and Their Associated Traits.

Principal Component	Genotypes	Associated Traits
PC1	IPL 329, DPL 15, IPL 81, IG TALL 9, IPL 341, IPL 321, IPL 406, IC 560128, IPL 526	Harvest Index, Biological Yield per Plant, Pods per Plant
PC2	DPL 62, JL 3, KLS 218, LL 931, LL 4717, JL1, L 4727, LH-7-26, LCC 9941	Days to Maturity, Days to 50% Flowering, Days to First Flowering
PC3	IPL 232, IPL 315, RKL 60503, PL 117, EC 208337, PL-77-2, H*D-3083, IPL 315	Plant Height, Chlorophyll Content, Number of Primary Branches
PC4	LL 1698, IPL 534, EC 520204, LL 1373, L-9-12, EC 348, LL 1641, IPL 220	Seeds per Pod, 1000 Seed Weight, Number of Secondary Branches

genotypes (IPL 232, IPL 315, RKL 60503, PL 117, EC 208337, PL-77-2, HD-3083, IPL 315) exhibited high suitability for these traits, suggesting their potential role in improving plant architecture and photosynthetic efficiency.

PC4 accounted for 8.3% of the variance and was associated with Seeds per Pod, 1000 Seed Weight, and Number of Secondary Branches. The eight genotypes (LL 1698, IPL 534, EC 520204, LL 1373, L-9-12, EC 348, LL 1641, IPL 220) demonstrated strong potential for seed-related traits, which are essential for enhancing grain quality and market value.

Significance of PC1 in Breeding Programs

The screen plot (Fig. 2) demonstrates that PC1 contributes the highest variation (28.909%), which gradually decreases in subsequent components. This finding underscores the importance of traits grouped under PC1 in selection strategies. Previous studies have also highlighted that traits associated with the first principal component tend to have higher heritability and selection efficiency (Yadav *et al.*, 2019). Therefore, selecting genotypes with high PC1 scores can lead to significant genetic gains in lentil breeding.

Conclusion

PCA effectively categorized the genotypes based on their trait associations, aiding in strategic selection for breeding programs. Future studies should validate these findings across different environments to enhance selection efficiency and ensure genotype stability.

Acknowledgments

The authors sincerely express their gratitude to ITM University, Gwalior, M.P., India, for providing the necessary support to conduct this research. Special thanks are also extended to the Indian Institute of Pulses Research (IIPR), Kanpur, for supplying the seed material essential for this study.

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