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Evaluating Genetic Diversity and Analyzing Yield-Related Traits for Selection Criteria in Lentil (*Lens culinaris* Medik)

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ABSTRACT

The study aimed to identify productive selection criteria for genetic enhancement in lentils. An experiment involving 50 lentil genotypes with 4 check variety (IPL-526, IPL-329, IPL-315, IPL-225) was conducted to evaluate 13 quantitative traits in augmented design during the *rabi* season, 2023-24. This study focused on genetic diversity parameters and principal component analysis (PCA). Data were collected for the following traits: days to flowering initiation, days to 50% flowering, days to maturity, primary branches per plant, secondary branches per plant, chlorophyll content (mg/m^2), pods per plant, plant height (cm), seed index (g), number of seeds per plant, biological yield per plant, harvest index (%) and seed yield (g). The collected data was analyzed using K-means clustering and PCA. Analysis of variance indicated significant variation among the genotypes for all measured traits. K-means clustering grouped the 54 genotypes into 10 clusters, with clusters II and VIII showing the highest inter-cluster distance (115.748), indicating substantial genetic diversity between the genotypes. PCA identified 13 principal components (PCs), with the first five components having eigen value greater than 1, collectively accounting for 80% of the genetic variation. PC-I highlighted genotypes with high yield-contributing traits, including EC-542206, ILL-9979, ILL9970, L-556, BR-2, EC542161, EC208355, ILL7928, and BAM-6. These diverse genotypes can be used directly in hybridization programs.

Key words: *Genetic Diversity, K-mean cluster, PCA, Lentil Genotype*

Introduction

Lentil (*Lens culinaris* Medikus) ranks among the earliest domesticated crops, originating in the Neolithic era. As a legume, lentils are highly valued for their rich nutritional content and their ability to improve soil fertility through nitrogen fixation, making them integral to sustainable agriculture. Global production of lentils has significantly increased, expanding beyond traditional regions in South Asia and the Middle East to include North America and Australia. This growth is driven by the rising demand for plant-based proteins and the crop's adaptability to diverse climatic conditions. Lentil is a cold-season diploid species with 2n=2x=14 chromosomes, known for its self-pollinating nature. Lentil seeds are rich in protein (25%), carbohydrates, nitrogen, and fiber. They contain significant amount of vitamin A, vitamin B, potassium and iron, while low in sodium and fat content. They are also an important source of fatty acids, amino acids, and trace minerals. Additionally, their low glycemic index makes them beneficial for managing chronic diseases such as diabetes and cardiovascular conditions. Due to these nu-

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tritional properties, lentils are often called the "poor man's meat". Nutritionally, lentils are crucial for combating protein-energy malnutrition in developing countries. During the process of domestication, lentils expanded from their centre of origin to different regions globally. Throughout their evolution, various climatic pressures such as temperature, day length and precipitation, along with soil-related factors and biotic stresses, have driven the selection of traits crucial for adaptation (Materne and Siddique, 2009). In recent years, the varietal development program has concentrated on boosting yield potential by hybridizing diverse genotypes. This approach aims to gather genes associated with high yield and integrate genes for multiple disease resistance within high- yielding genotypes (Kumar *et al.*, 2004). K-means cluster diversity analysis identified the most divergent clusters as II- VIII, followed by II-VI, VIII-X, and IV-X (Table 1). This indicates that the genotypes in cluster VIII exhibit the highest diversity compared to the other germplasms studied. Principal component analysis (PCA) highlighted the parameters that primarily contribute to this variation. Understanding the genetic diversity in lentil germplasm and investigating the associations among yield components is crucial. To maintain consistent yields, it is crucial to tackle these issues using advanced breeding techniques, genetic research, and enhanced agronomic practices. Utilizing molecular tools enables precision breeding, facilitating targeted genetic improvements in lentils (Kumar *et al.*, 2016). To ensure stable yields, it is essential to address these aspects through advanced breeding, genetic research, and improved breeding practices.

Materials and Methods

The present investigation was conducted during the *rabi* season of 2023 on 50 lentil genotypes grown in an augmented design with four checks. The experimental material comprised of 54 genotypes procured from IIPR, Kanpur and KVK, Gwalior, Madhya Pradesh. The research was carried out at the CRC-I farm in the School of Agriculture, ITM University, Gwalior (Madhya Pradesh). Data was recorded for 13 quantitative traits related to yield and its contributing factors: days to flowering initiation, days to 50% flowering, days to maturity, primary branches per plant, secondary branches per plant, chlorophyll content (mg/m^2), pods per plant, plant height (cm), seed index (g), number of seeds per plant, biological yield per plant, harvest index (%) and seed yield (g). Data was collected from 10 randomly selected plants and analyzed using OPSTAT and R-Studio appropriate statistical tools, including analysis of variance by Panse and Sukhatme (1961), K-mean clustering by Afifi, Clark, and Marg (2004), and principal component analysis.

Results and Discussion

The analysis of variance for 13 quantitative traits was found significantly high (Table 1), indicating substantial genetic diversity in the evaluated germplasm, showing significant potential for selecting promising lines for yield and its components from the existing gene pool.

Genetic diversity was analyzed using K-means clustering, in which 54 germplasms were divided into ten clusters (Table 1). In cluster analysis it was found that Cluster V comprised of highest number of genotypes (12), along with two checks IPL-329 and IPL-225, suggesting they share a similar genetic base. Similar results have also been reported by (Sharma *et al*. 2022). Clusters IV and VII consist of only two genotypes: EC- 542206, BR-25-1 and EC-

Table 1. Descriptive statistics of 54 genotypes for studied quantitative traits**.**

Genotype	FFI	50F	DM	PBPP	SBPP	CC	PPP	PH	SW	NSP	BY	HI	SY
Grand Mean	74.9	85.8	127.97	3.1	7.85	10.85	70.36	40.14	2.43	111.47	11.16	26.28	2.8
Minimum	69	77.7	120.6	2.3	3.9	3.34	49.5	27.9	1.64	65.04	4.49	11.81	1.44
Maximum	79	96.37	137.93	4.6	16.6	36.04	121	52	3.34	176.8	30.2	46.25	5.52
CV	1.8	1.87	1.74	5.18	18.64	16.69	3.81	5.78	6.91	6.57	8.69	7.27	10.56
CD(5%)	2.2	1.26	2.62	3.09	1.84	2.61	9.66	0.22	3.2	3.51	1.93	0.23	0.38
SE	1.01	0.58	1.2	1.42	0.85	1.2	4.43	0.1	1.47	1.61	0.89	0.1	0.17

FFI: days to flowering initiation, 50%F: days to 50% flowering, DM: days to maturity, PBPP: primary branches per plant, SBPP: secondary branches per plant, CC: chlorophyll content (mg/m^2), PPP: pods per plant, PH: plant height (cm), SI: seed index (g), NSP: number of seeds per plant, BY: biological yield per plant, HI: harvest index (%), and SY: seed yield (g).

542166, P-1027 respectively (Table 2). Clusters II and VIII exhibited the highest inter-cluster distance (115.748), indicating a high level of genetic diversity between the genotypes while cluster VI and X showed the lowest inter-cluster distance (k = 13.726). Cluster VIII had the highest mean values for secondary branches per plant, number of seeds per plant, and seed yield, followed by Cluster IV, which excelled in pods per plant, seed Index (g), and biological yield. Similar results have also been reported by (Hussain *et al.* (2022). K-means cluster diversity analysis identified the most divergent clusters as II-VIII (115.748), followed by II-VI (113.747), VIII-X (104.189), and IV-X (103.977) (Table 2). This depicted that the genotypes L-556, ILL-9970 and ILL-9979 in cluster VIII exhibits the highest degree of diversity compared to the other germplasms studied.

Principal component analysis (PCA) (Table 3) showed that the first five components accounted for 80% of the total genetic variation. Similar results have also been reported by Sabaghnia *et al.* (2012) and Kumar *et al.* (2020). The eigen values for PC1, PC2, PC3, PC4, and PC5 were 4.925, 1.907, 1.353, 1.247 and 1.091, respectively. A scree plot (Fig. 1) was constructed to illustrate the results. PC1's factor loadings for pods per plant, number of seeds per plant, seed index, and biological yield significantly contributed to seed yield. Similar results have also been reported by Bhattacharya *et al.*(2023). PC1 (Table 4) highlighted genotypes with high yield traits, including EC-542206, ILL-9979, ILL9970, L-556, BR-2, EC542161, EC208355, ILL7928, and BAM-

Table 2. Distribution of 54 Lentil Genotypes into Clusters

Cluster No	Number of Genotype	Members
I	6	BAM-6, ILL-7928, EC-522180, EC-542161, EC-208355, LL-147
II	6	EC542186, IG-3546, L-4076, K-75, EC-208363, IPL-526
III	7	EC-542197, L-555, PANT-L406, EL-208362, EC-208362, VL-4, PANTL-04
IV	2	EC-542206, BR-25-1
V	12	ILL-9976, EC-362, P-4991, EC208345, EC-141, L-4075, WBL-77, PANT L-639, PANT L-05, T-36, IPL-329, IPL-225
VI	7	EC-542198, ILL9948, ILL9977, ILL-9913, WBL-58, BAM-5, ILL-4594
VII	2	EC-542166, P-1027
VIII	3	L-556, ILL-9970, ILL-9979
IX	4	L-4596, ILL-9967, ILL-5957, ILL-7983
X	5	EC208330, RANJAN, LL-564, L-4147, IPL-315

Table 3. Inter Cluster Distances

Cluster No	I	II	III	IV	V	VI	VII	VIII	IX	X
I	0	95.797	44.67	29.971	64.398	82.061	81.078	21.106	20.165	84.334
II		0	52.107	113.747	35.98	17.612	25.76	115.748	77.044	19.351
III			0	64.116	24.452	39.837	41.378	64.24	27.005	41.556
IV				0	85.662	101.819	96.654	22.889	43.684	103.977
V					0	21.882	31.238	84.479	45.467	21.191
VI						0	25.781	101.996	63.455	13.726
VII							0	100.748	62.251	27.52
VIII								0	40.194	104.189
IX									0	65.277
X										0

Table 4. Principal Component Analysis of 13 Contrasting Characters

	PC1	PC2	PC3	PC4	PC5
Eigen value	4.925	1.907	1.353	1.247	1.091
Proportion of Variability	0.372	0.144	0.102	0.094	0.082
Explained Cumulative Proportion	0.372	0.516	0.618	0.712	0.795

Table 5. The superior genotype of Principle Component analysis

PC1	EC-542206, ILL-9979, ILL9970, L-556, BR-2, EC542161, EC208355, ILL7928, BAM-6
PC2	L-4147, PANTL-04, PANTL-639, BR-25-1, ILL-9979
PC3	WBL-77, L-4075, IPL-329, L-4596, ILL-4594
PC4	ILL5957, P-1027, WBL-77, BR-25-1, ILL-9976
PC5	P-4991, EC542166, EC542161, IG-3546, EC208355

6. PC2 identified genotypes L-4147, PANTL-04, PANTL-639, BR-25-1, and ILL-9979 as having significant contributions. The divergence among genotypes and the contribution of traits to this divergence were effectively explained by PCA.

Conclusion

Diverse germplasm lines with desirable traits can be utilized in future breeding programs to maximize variability across a wide range of characteristics. This approach broadens the genetic base of cultivars, enhancing more than one economic trait simultaneously. The top performing genotypes are EC-542206, ILL- 9970, L-556, BR-25-1, EC-542161, EC-522180, EC-208355, L-4596, ILL-9967, are identified based on trait performance concerning check variety. All the genotypes are divided into ten clusters, with significant cluster distance which shows high genetic diversity in the genotype. The highly genetically diverse line for yield and yield attributing traits can be directly selected as a parent for hybridization program. The genotype depicted in PC-1 has more yield-attributing traits. So, these genotypes can be used for the transfer of such traits.

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Conflict of Interest- None

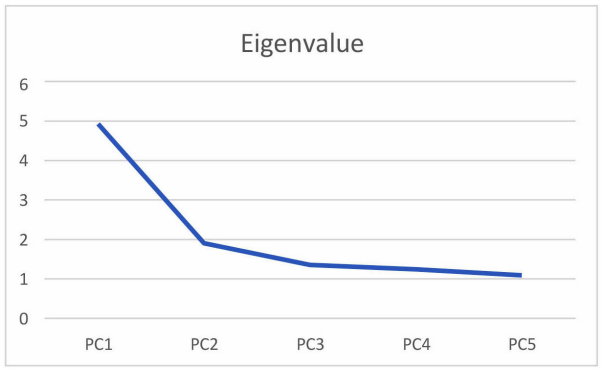

Fig. 1. Scree Plot showing Eigen values

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