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The Nature of Diversity in Yield Influencing Traits of Lentil Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Original Research Article

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ABSTRACT

Lentil (*Lens culinaris*), an annual plant of the Fabaceae family, is extensively cultivated in Europe, Asia, and North Africa. In India, it is cultivated in *rabi* season (winter) and is an important legume due to its highly nutritious nature. Thirty-seven distinct lentil (*Lens culnaris* Medik) genotypes were examined for 10 quantitative traits, including seed yield and its associated characters. Among them, the maximum contribution most towards genetic divergence was observed by 100 seed weight. Seven clusters were created based D^2 values comprising of all the genotypes. The cluster analysis revealed that the number of genotypes in each cluster ranged from 1 to 22. The clustering pattern confirmed the non-correspondence among geospatial and genetic diversity. Due to the fact that clusters IV and VI (670.74) had the greatest inter-cluster distance, their members were very diverse from one another. Days to flower initiation (61.73), days to maturity (112.47), no. of pods per plant (128.51), biological yield per plant (26.46), harvest index (44.41), and seed yield per plant (11.65) were among the traits for which entries from Cluster VI recorded the highest values. As a result, the genotypes from clusters IV and VI might be used in a hybridization scheme to create genotypes with high yields.

Keywords: Cluster analysis; divergence; D^2 analysis; genetic diversity; lentil; lens culinaris.

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1. INTRODUCTION

Lentil (*Lens culinaris* Medik.) is a cool-season pulse crop of autogamous nature (2n = 2X = 14). This crop was domesticated in the fertile crescent of the Mediterranean basin, probably round the seventh century B.C. [1], and subsequently its area extended throughout Middle East, Ethiopia, and the Indian Subcontinent. It is among the leading pulse crops grown in the semi-arid areas, especially in the Indian subcontinent and the dry Middle Eastern countries [2]. In India, Lentil covered an area of 1.56 million hectares in India, producing 1.23 million tonnes and yielding 901 kg per hectare [3]. Lentil seeds are renowned as a nutritional source of high-quality plant proteins. To boost availability per capita and address the issues of a rising population and food security, there must undoubtedly be an exponential leap in total pulse production and in lentil production in particular. However, as a rainfed crop lentil output is still insufficient as it is affected by a range of stressors. Furthermore, a limited genetic foundation of recent cultivars has surfaced as a serious challenge for lentil development. Selecting a suitable parent is crucial for hybridization and selection process and it serves as the foundation for any crop improvement activity [4]. The D^2 statistic, created by Mahalanobis in 1936, is an effective multivariate statistical method for evaluating genetic divergence between genotypes. It has been established that crossing programmes requires level of genetic diversity between the two parental genotypes. In order to enhance the genetic base, it is necessary for breeders to identify yield-related attributes and genetic diversity. By enhancing yield component traits, high yielding varieties can be created by genetically reconstructing plant types. The readily available genotypes will act as the most beneficial resource for supplying the desired plant characteristic for creating high yielding crop variants [5]. Thus, the goal of the current study was to choose diverse parents for use in improving lentils in the future.

2. MATERIALS AND METHODS

The experiment comprised 37 different lentil genotypes obtained from AICRP on MULLaRP, JNKVV, Jabalpur. The genotypes were characterized during the *rabi* season of 2021–2022, using a RCBD with three replications. Each genotype had been sown in six rows of 4 meters. Plants were kept at 8 to 10 cm while rows were spaced at 22.5 cm. From each replication, five plants were selected to collect data on traits including; plant height (cm), no. of primary branches per plant, no. of pods per plant, no. of seeds per plant, 100 seed weight (g), biological yield per plant (g), harvest index (%), and seed yield per plant (g). Data for days to flower initiation and days to maturity was taken on plot basis. Windostat version 9.1 was used to conduct the statistical analysis. For the divergence analysis, the transformed uncorrelated character means were used to calculate the D^2 statistic according to Mahalanobis (1936) [6]. Thereafter, Tocher's method was used to classify the populations into several clusters, as demonstrated by Rao (1952) [7].

3. RESULTS AND DISCUSSION

Regarding each of the traits evaluated, the ANOVA indicated substantial differences between the genotypes (Table 1) and therefore showing that there is a large degree of genetic variability. Each genotype was distinct from the others in terms of days to flower initiation, days to maturity, plant height (cm), no. of primary branches per plant, no. of pods per plant, number of seeds per plant, 100 seed weight (g), biological yield per plant (g), harvest index (%), and seed yield per plant (g). The percentage contribution of these traits towards genetic divergence is presented in Fig. 1.

The maximum part of divergence was observed by 100 seed weight (28.38%) preceded by seed yield per plant (24.17%), days to maturity (15.92%), biological yield per plant (9.31%), no. of seeds per pod (5.86%), days to flower initiation (4.95%), no. of pods per plant (4.65%), harvest index (4.2%) and no. of primary branches per plant (1.8%) while plant height (0.75%) contributed less than 1 percent towards divergence. The fifty genotypes were divided into seven clusters using D^2 values (Table 2).

The genotypes within a cluster ranged from one to twenty-two. Cluster I included twenty-two genotypes, cluster VI had 5 genotypes, cluster IV had 4 and 3 genotypes were placed in cluster III. Whereas, cluster II, V and VII had single genotype each. These clusters contained genotypes with different origins were clustered together, and vice versa, demonstrating the absence of an association between geographic location and genetic diversity. Genetic diversity is caused by a variety of factors, including

geographical isolation, as shown by the likelihood for genotypes to exist in clusters that transcend geographical barriers. This implies that the genotypes inside the cluster could be related to one another, and [8-11] all reported similar findings. The partners for interbreeding should be chosen based on genomic diversity rather than geographical diversity. As a result, a hybridization programme including genotypes from several clusters with high means for nearly all component characteristics may be started. Additionally, these diverse parents must combine more effectively to produce outcomes according to heterotic response.

Table 1. ANOVA for ten quantitative traits of 37 lentil genotypes

S. No.	Traits	Sources of Variation		
		Replication (df=2)	Genotype (df=36)	Error (df=72)
1	Days to flower initiation	12.87	50.47***	1.08
2	Days to maturity	11.36	124.12***	1.18
3	Plant height (cm)	0.06	1.92***	0.10
4	No. of primary branches per plant	23.54	52.46***	2.35
5	No. of pods per plant	4.48	1304.92***	15.77
6	No. of seeds per plant	0.002	0.075***	0.001
7	100 seed weight (g)	0.01	1.78***	0.01
8	Biological yield per plant (g)	0.31	83.17***	0.83
9	Harvest index (%)	1.70	245.79***	2.83
10	Seed yield per plant (g)	0.07	20.47***	0.05

*Note: ***Significant at 0.001% ** Significant at 0.005%*

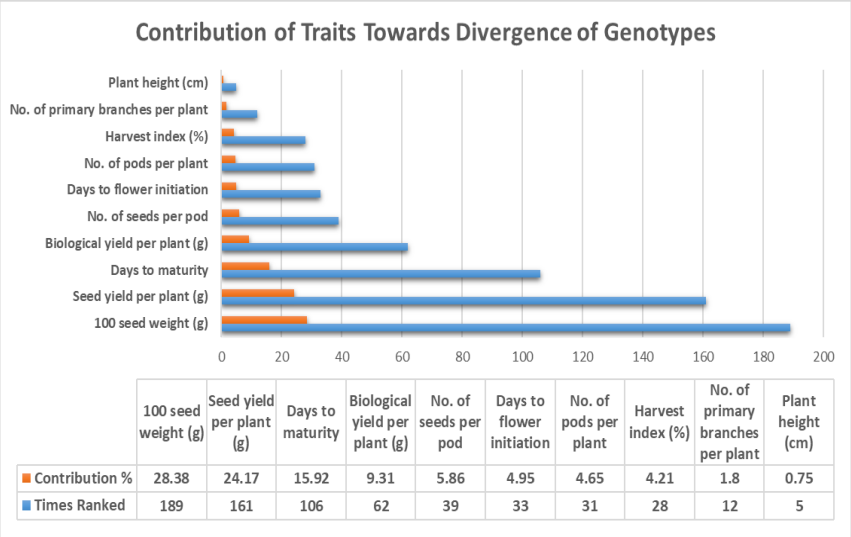

Fig. 1. Percentage contribution of individual traits towards total divergence

Table 2. Different clusters of lentil genotype

Cluster	Number of genotypes	Genotypes
I	22	PL 406, VL 103, LLS 21-194, LLS 21-197, LLS 21-200, LLS 21-204, LLS 21-205, LLS 21-206, LLS 21-207, LLS 21-209, LLS 21-211, LLS 21-215, LLS 21-218 A, LLS 21-124, LLS 21-125, LLS 21-126, LLS 21-127, LLS 21-128, LLS 21-129, LLS 21-130, LLS 21-131, LLS 21-132
II	1	LLS 21-216
III	3	NDL 1, LLS 21-198, LLS 21-202
IV	4	SUBRATA, LLS 21-193, LLS 21-195, LLS 21-133
V	1	ASHA
VI	5	DPL 15, JL 1, JL 3, PL 5, VL 4
VII	1	LLS 21-199

Table 3 displays the typical D^2 values among clusters. Cluster VI showed maximum intra cluster D^2 value (203.73) followed by cluster IV (155.52), cluster I (91.83) and cluster III (38.19). The remaining three clusters, however, did not exhibit intra-cluster variation since they were mono-genotypic. The lines that showed the biggest inter-cluster divergence were of cluster IV and VI (670.74), followed by cluster VI and VII (616.08). Which showed the greatest diversity among those clusters' genotypes. As a result, if the various genotypes from these groups are exploited in hybridization and it is anticipated that improved segregants could be obtained as a result of nonallelic interaction. While, Cluster I and VII (168.70) displayed minimum inter cluster distance. This imply that these genotypes were almost identical in terms of genomic composition. Cluster I (91.83) was largest poly-genotypic cluster with 22 genotypes and was nearest to cluster VII (168.70) followed by cluster V (182.69), cluster II (185.28), cluster IV (230.05), cluster III (233.56) and Cluster VI (436.07) was more distant to Cluster I. Cluster II (0.00) was mono-genotypic, and was closest to cluster VI (170.74), however it was placed at a maximum distance to cluster IV (423.79). Cluster III (38.19) was poly-genotypic with 5 genotypes, and was nearest to cluster V (190.36) however it was placed at a maximum distance to cluster VI (505.56). Cluster IV (155.52) was poly-genotypic and was at a maximum distance to cluster VI (670.74). Cluster V (0.00) was mono-genotypic and was at a maximum distance to cluster VI (593.76). Cluster VI (203.73) was poly-genotypic. Cluster VII (0.00) was mono-genotypic (Fig. 2).

Table 3. The average intra and inter-cluster D^2 values

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	91.83	185.28	233.56	230.05	182.69	436.07	168.70
Cluster II		0.00	280.60	423.79	390.02	170.74	316.95
Cluster III			38.19	285.90	190.36	505.56	504.13
Cluster IV				155.52	247.06	670.74	249.15
Cluster V					0.00	593.76	436.04
Cluster VI						203.73	616.08
Cluster VII							0.00

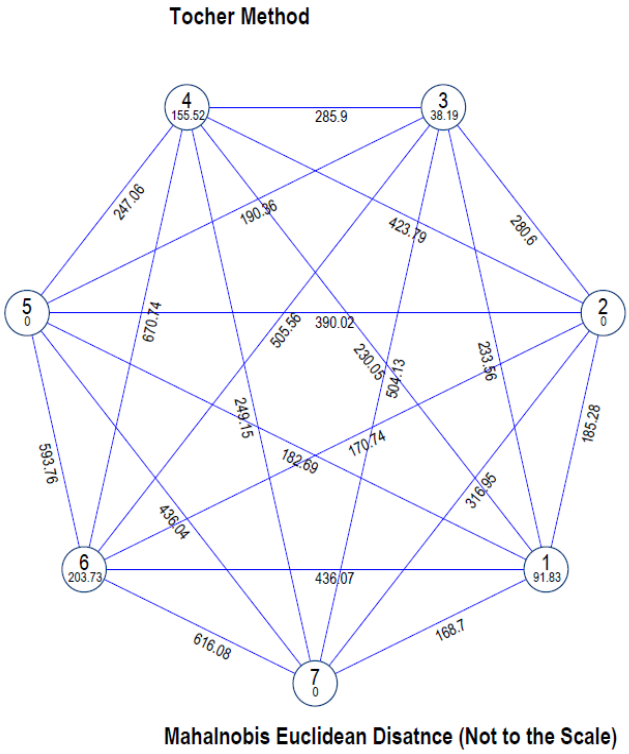

Fig. 2. Cluster diagram based on tocher method

Table 4. Cluster means values showing importance of grouped traits

Clusters	Days to flower initiation	Days to maturity	No. of primary branches per plant	Plant height	No of pods per plant	No. of seeds per pod	100 seed weight	Biological yield per plant	Harvest index	Seed yield per plant
Cluster I	56.36	105.15	3.03	39.61	81.52	1.67	4.10	18.21	31.23	5.61
Cluster II	55.33	104.00	3.44	**44.64**	118.33	1.69	**5.08**	24.83	38.14	9.47
Cluster III	56.44	89.22	3.18	38.56	90.74	1.70	3.49	20.85	31.02	6.30
Cluster IV	59.50	102.83	2.25	37.88	87.24	1.43	2.85	25.33	15.24	3.68
Cluster V	52.67	101.67	2.44	35.57	72.33	**1.82**	2.71	12.49	37.44	4.67
Cluster VI	**61.73**	**112.47**	4.37	39.44	**128.51**	1.70	4.46	**26.46**	**44.41**	**11.65**
Cluster VII	57.67	110.33	**4.44**	41.42	90.15	1.33	4.40	22.87	21.13	4.83

The significant level of variability among the cluster means for several traits further supported the diversity among the genotypes (Table 4). Cluster VI recorded for highest values for most of the traits viz. days to flower initiation (61.73), days to maturity (112.47), no of pods per plant (128.51), biological yield per plant (26.46), harvest index (44.41) and seed yield per plant (11.65). Cluster V recorded highest values for number of seed per pod (1.82) and least value for maximum traits viz. days to flower initiation (52.67), plant height (35.57), no. of pods per plant (72.33), 100 seed weight (2.71) and biological yield per plant (12.49). Cluster II recorded highest for plant height (44.64) and 100 seed weight (5.08). Cluster III has least value for days to maturity (89.22). Cluster IV recorded least value for no. of primary branches (2.25), harvest index (15.24) and seed yield per plant (3.68). Cluster VII recorded highest value for no. of primary branches (4.44) and recorded least value for no. of seed per pod (1.33). These findings demonstrated that certain clusters performed better for different types of characters. Similar results were reported by [12], [13] and [14].

It is possible to choose the parents for hybridization based on the significant distance between their clusters. The better performers from Clusters IV and VI could be identified for all the desirable traits, considering that these genotypes have high mean values for traits such as days to flower initiation, days to maturity, no. of pods per plant, biological yield per plant, harvest index and seed yield per plant along with high genetic distance. As a result, progenies from such divergent crosses are envisaged to demonstrate a larger opportunity for detecting transgressives in subsequent generations. In order to retrieve transgressive segregants, these genotypes may be employed in a repeated crossing scheme.

4. CONCLUSIONS

The conclusions drawn from the data above indicate that there is substantial diversity among the genotypes examined for the traits that are agronomically desirable. 100 seed weight was shown to contribute the most toward genetic divergence. Cluster IV and cluster VI genotypes had the greatest inter cluster distance. The genotypes of cluster VI recorded highest mean values for most of the traits viz. days to flower initiation, days to maturity, no. of pods per plant, biological yield per plant, harvest index and seed yield per plant. These genotypes might result in transgressive segregants if they are crossed. Further breeding efforts for lentils can make use of the genotypic diversity, resulting in a highly heterotic response in the segregating generation.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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