Journal of the Andaman Science Association Vol 29 (2): 160-164 (2024)
ISSN 0970-4183, Printed in India

Genetic Diversity Analysis for Quantitative Traits in Lentil (*Lens culinaris* Medik.) Germplasm

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Abstract

Seventy lentil genotypes, originating from diverse sources, were categorized into 8 clusters through Mahalanobis' D^2 analysis (Mahalanobis, 1936) following the method outlined by Rao (1952). The experiment was conducted using a Randomized Block Design with three replications at the Agricultural Research Farm, Janta Mahavidyalaya, Ajitmal, Auraiya (U.P.) during the *Rabi* season of 2021-22. The largest cluster, Cluster I, comprised 29 genotypes, while the second-largest, Cluster VI, grouped together 20 genotypes. Cluster III was the third largest with 9 genotypes, and Cluster VII included 4 genotypes. Clusters II and IV each consisted of 3 genotypes. The remaining clusters, V and VIII, included only one genotype each (RL-12-180, Tall-7), suggesting a notable divergence compared to the other genotypes in the study. The average maximum intra-cluster D^2 value, recorded in Cluster IV, was 22.970 among the eight intra-cluster distances, indicating the highest genetic diversity within this group. The second-highest average intra-cluster distance was observed in Cluster VI (17.070), followed by Cluster VII (15.698), and Cluster I (13.664). The minimum average intra-cluster D^2 value was recorded in Cluster II (11.165), with Cluster III slightly higher at 11.834. Inter-cluster distances varied from 19.37 (between Clusters I and III) to 591.47 (between Clusters V and VIII). Other clusters with notable inter-cluster distances included IV and VIII (563.11), II and VIII (280.27), II and VIII (279.25), V to VI (244.63), III and VIII (202.74), IV to VI (206.84), V and VII (182.54), IV to VII (165.64), III and V (158.71), VII and VIII (154.91), III and IV (109.38), and VI and VIII (105.49).

Keywords: Lentil, genetic diversity, cluster analysis, D^2, *Lens culinaris* Medik.

Introduction

Lentil (*Lens culinaris* Medik.) is a vital food legume crop in India, primarily cultivated as a rainfed crop during the rabi season. Originating in the East Mediterranean region, such as Asia Minor and Egypt, lentils spread eastward to India. Nutritionists consider lentils an excellent dietary source, with protein concentrations ranging from 22-34.6% and 100g of dried seeds containing 340-346 kcal, 20.2g of protein, 0.6g of fat, 65g of total carbohydrates, approximately 4g of fibre, 0.46mg of thiamine, and 0.33mg of riboflavin (Muehlbauer *et al*., 1985; Adsule et al., 1989). Lentil seeds are crucial for human consumption, especially in dry areas where they are often the sole pulse crop feasible under conditions of low soil fertility and limited moisture. It is a principal crop cultivated in semi-arid regions worldwide, particularly in the Indian subcontinent and dry areas of the Middle East. Lentil exhibits relative drought tolerance and is grown globally, representing only 5-6% of the total pulse area. Asia accounts for 80-95% of the global area and production (Malik, 2005). However, over two-thirds of the cultivated area remains unirrigated, and productivity in these areas can be enhanced only by developing crops well adapted to dry conditions.

In crop improvement programs, germplasm plays a vital role as modern agriculture heavily relies on the selection of desirable parents. These selected parents are utilized in hybridization programs, and the choice of suitable divergent parents is crucial. Crosses involving diverse parents offer a greater possibility of obtaining desirable segregants in subsequent generations. D^2 analysis, developed by Mahalanobis (1936) and based on multivariate analysis, measures the degree of diversification and determines the relative contribution of each component character to the total divergence. This analysis provides insights into the relative contribution

of different components to diversity at both inter-cluster and intra-cluster levels. Genotypes drawn from widely divergent clusters will likely produce heterotic combinations and wide variability in segregating generations. Additionally, D^2 analysis offers information on the parallelism between genetic divergence and the geographical distribution of genotypes, thus quantifying the degree of divergence in germplasm. Utilizing diverse parents in hybridization programs facilitates the combination of desirable genes, ultimately contributing to crop improvement efforts (Gaur *et al*., 2020).

Material and Methods

The present investigation was conducted during the *Rabi* season of 2021-22 at the Agricultural Research Farm, Janta Mahavidyalaya, Ajitmal, Auraiya (U.P.) to evaluate seventy lentil genotypes for their genetic diversity. These genotypes were obtained from the Indian Institute of Pulse Research, Kanpur. The experiment was conducted in a Randomized Block Design with three replications. Each entry was sown in one row of 3.5 m in length with a spacing of 30 cm between the row and 5 cm between the plants. All recommended practices were followed in the conduction of the experiment to grow a good crop. Observations were recorded on randomly selected five plants from each entry in three replications for nine quantitative traits. The characters under study were days to 50 % flowering, days to maturity, plant height (cm), number of primary branches/plant, number of secondary branches/plant, number of pods/plant, number of seeds/pod, 100 seed weight(g), seed yield/plant (g). Genetic diversity was estimated by calculating Mahalanobis (1936) D^2 statistics. The genotypes were further grouped into different clusters as per Tocher's method (Rao, 1952).

Results and Discussion

The analysis of variance was carried out for nine quantitative traits. The analysis of variance showed highly significant differences among the genotypes for all traits (Table 1). The divergence (D^2) analysis revealed that the 70 lentil genotypes were grouped into 8 significant clusters (Table 2). The largest cluster, Cluster I, comprised 29 genotypes, while the second-largest, Cluster VI, grouped together 20 genotypes. Cluster III was the third largest with 9 genotypes, and Cluster VII included 4 genotypes. Clusters II and IV each consisted of 3 genotypes. The remaining clusters, V and VIII, included only one genotype each (RL-12-180, Tall-7), suggesting a notable divergence compared to the other genotypes in the study. The intra-cluster distance values ranged from 0.00 (cluster V and VIII) to 77.8 (cluster IV) (Table 3). The maximum intra-cluster distance was observed in cluster IV (22.970) followed by cluster VI (17.070) and cluster VI (17.070). The maximum intra-cluster distance was mainly due to the wide genetic diversity among the genotypes of these clusters. The maximum inter-cluster distance was observed between Cluster V and Clusters VIII (591.475) followed by Cluster IV and Clusters VIII (563.114). In contrast, minimum inter-cluster distance was observed in clusters I and III (19.370). The lowest inter-cluster distances indicate that the genotype of these clusters had a close relationship hence, may not be emphasized to be used in the hybridization programme. These results are somewhat in accordance with the findings of Kumar *et al.* (2004), Sultan *et al.* (2005), Gautam *et al*. (2014), Rahimi *et al.* (2016) and Pandey and Bhatore (2018).

Table 1: Analysis of variance for nine characters in lentil (*Lens culinaris* Medik.)

Source of variation	D.F.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches / plant	Number of pods/ plant	Number of seed/ pods	100-seed weight	Seed Yield/ plant
Replication	2	68.51	119.05	268.31	1.37	94.24	442.43	0.09	5.01	47.54
Treatment	69	78.57	134.66	52.26	1.53	19.48	9890.62	0.06	0.77	15.86
Error	138	10.02	15.83	22.51	0.55	12.63	3615.73	0.02	0.31	5.22
'F' Calculated		7.83**	8.50**	2.32**	2.78**	1.54*	2.73**	2.71**	2.42**	3.03**

** and * = Significant at 1% and 5% probability level, respectively

Table 2: Distribution of seventy genotypes into different clusters in Lentil (*Lens culinaris* Medik.)

Cluster Number	Number of Genotypes	No. of Genotypes
I	IPL-526, IC-5060291, IC-559613, IPL-315, FLIP-98-31B, PANT L-639, IG-4286, RL-12-171, IC-560117, IG-4200, IC-208336, RL-12-179, IG-5147, IG-4322, IG-4208, IC-559683, EC-348, IPL-406, P-98/155, IPL-321, TALL-5, RL-12-173, L-112-7, SEHORE-74-3, IPL-534, DPL-15, IC-559673, TALL-9, 2002/7/1	29
II	RL-12-175, L-112-17, L-112-16	3
III	IC -559681, HUL-57, 2000-25L, IG-4290, PANT-L-406, WBL-58, IPL-329, IC-560291, EC-141	9
IV	IPL -316, IC-5060341, L-4594	3
V	RL-12-180	1
VI	L-112-15, IG-2580, DPL-62, IPL-225, L-112-19, IC-5060341, IPL-220, L-112-18 2000-13L, KLS-218, IC-5060194, 2000-19LA, L-4596, MONGAI, HUL-56, IG-4290, TALL-3, IC-559771, LL-57, L-112-11	20
VII	IG-3330, T-36, EC-362, RL-12-178	4
VIII	Tall-7	1

Table 3: Percent contribution of various characters to diversity in Lentil (*Lens culinaris* Medik.).

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of pods/ plant	Number of seeds /pod	100-seed weight (g)	Seed yield/ plant (g)
Contribution (%)	15.57	60.79	1.74	5.34	0.25	2.53	5.13	5.13	3.52

Table 3: Intra (diagonal) and inter (off-diagonal) cluster distance (D^2) values of seventy genotypes of Lentil (*Lens culinaris* Medik.).

	Cluster Distances							
	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**
Cluster I	**13.664**	26.582	19.370	66.098	111.586	60.710	52.490	280.270
Cluster II		**11.165**	34.876	74.820	77.766	66.231	37.434	279.253
Cluster III			**11.834**	109.384	158.719	33.618	40.062	202.749
Cluster IV				**22.970**	52.963	206.843	165.649	563.114
Cluster V					**0.00**	244.639	182.547	591.475
Cluster VI						**17.070**	28.771	105.492
Cluster VII							**15.69**8	154.915
Cluster VIII								**0.00**

The percentage contribution of various characters to genetic divergence is presented in Table 3. Out of nine characters studied, the character days to maturity (60.79%) had the highest contribution to genetic diversity followed by Days to 50% flowering (15.57%), number of primary branches/plant (5.34), number of seeds/pod and 100-seed weight (5.13), number of pods/plant (2.53), seed yield/ plant (3.52) and number of secondary branches/ plant (0.25). Similar findings were also reported by Tyagi and Khan (2010), Sharma *et al*. (2014) and Pandey *et al*. (2017).

The cluster means analyzed for nine characters under study are presented in Table 4 revealing that cluster II exhibited the highest mean value for the number of seeds/ pod (1.80) and 100-seed weight (4.00). Cluster III showed the highest mean value for days to 50% flowering (105.68) and days to maturity (132.33). Cluster IV showed the highest mean value for the number of primary branches/ plant (5.91), and the number of secondary branches/plant (285.10). Cluster VII showed the highest mean value for plant height (48.25) and seed yield/plant (8.12).

Table 4: Cluster mean of eight Clusters for nine characters in Lentil (*Lens culinaris* Medik.)

Cluster Number	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of pods/ plant	Number of seeds /pod	100-seed weight (g)	Seed yield/ plant(g)
I	103.4	130.56	46.51	5.41	31.00	267.79	1.65	3.65	7.54
II	92.8	117.09	40.76	4.89	27.55	228.59	**1.80**	**4.00**	5.16
III	**105.68**	**132.33**	46.03	5.34	30.99	273.09	1.66	3.77	6.39
IV	99.83	128.95	45.07	**5.91**	**33.05**	**285.10**	1.63	3.77	7.65
V	85.56	110.73	24.58	5.73	22.93	221.95	1.61	2.66	3.25
VI	101.18	124.99	45.63	5.21	31.53	280.93	1.68	3.61	7.85
VII	91.29	113.44	**48.25**	5.08	31.89	273.17	1.77	3.58	**8.12**
VIII	100.63	120.28	44.05	5.22	30.6	215.73	1.60*	3.33	4.16
Mean	101.47	127.144	45.644	5.329	31.024	270.2	1.676	3.657	7.31

The results from the present study suggest that crossing among genotypes from different clusters exhibiting good mean performance may help in achieving a high yield. The incorporation of more divergent parents in hybridization can enhance the chances of attaining potential varieties and provide a broad spectrum of genetic variability in segregating generations. Similar results were reported by. Based on divergence and cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of cluster V, IV and VIII in varietal improvement.

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