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Diversity analysis in lentil (*Lens culinaris* Medik.)

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Abstract
In this experiment 74 Lentil genotypes, along with four check varieties (NDL-1, DPL-15, IPL-81, DPL-62) were analyzed for genetic diversity by Mahalanobis D2 statistics. Presence of diversity pave way for exploitation of genotypes in breeding programme intended to improve yield and yield attributing traits. The cluster analysis grouped 74 lentil genotypes into the 9 clusters. In this context, the cluster pairs exhibiting very high inter-cluster distance were between cluster V and cluster IX, followed by cluster III and cluster IX, cluster I and cluster IX and cluster IV and cluster IX consideration for their direct use as parents in hybridization programs to develop high yielding lentil varieties. Thus, hybridization among these cluster pairs is recommended for getting high transgressive segregants in F2 generation.

Keywords: diversity, lentil, *Lens culinaris*

1. Introduction
Lentil is a self-pollinated diploid (2n = 14 chromosomes) annual cool season grain legume, with a relatively large genome of 4,063 Mpb (Arumuganathan and Earle 1991). Lentil seeds are valued as a food source of both high quality plant proteins and fiber, in addition, the remaining plant residues can be used as animal feed and fodder. This ancient pulse crop was domesticated in the Fertile Crescent where it has been cultivated since at least the seventh century B.C. (Ladizinky, 1979), and its cultivation area expanded around the Mediterranean Basin, Middle East, Ethiopia and the Indian Subcontinent. The International Centre for Agriculture in Dry Areas (ICARDA) has a global mandate for research on lentil improvement. As such, ICARDA houses the world collection of Lens, totaling 10,509 accessions. The ICARDA collection includes 8789 accessions of cultivated lentil from 70 different countries, 1146 ICARDA breeding lines, and 574 accessions of 6 wild Lens taxa representing 23 countries. A comprehensive understanding of the genetic variation within any lentil breeding program is important for the efficient selection of parents, for introgresion of genetic material into superior cultivated lines and for the implementation of an effective genetic conservation program for the cultivated species.
The selection of suitable divergent parents for hybridization is required because the cross involving diverse parents offer great possibility of obtaining desirable segregants in the segregating generations.

2. Materials and Methods
The experiment was conducted to evaluate 70 germplasm lines including four checks under irrigated, normal soil condition in Augmented Design. The entire experimental field was divided into 10 blocks of equal size and each block had 11 plots. Out of 11 plots in a block, 7 plots were used for accommodating the test genotypes which were not replicated while remaining 4 were allocated to checks *i.e.* NDL-1, DPL-15, IPL-81, DPL-62. The four checks were randomly allocated along with the test genotypes in a block. Observations on the following characteristics were recorded on the basis of five plants randomly selected. The analysis of variance for different characters in Augmented Block Design was done according to Federer (1956). Genetic divergence was studied through Nonhierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) [4, 29].

3. Results and Discussion
The distribution of 74 Lentil genotypes in nine clusters is given in (Table 1). Jeena, A.S. and Singh, I.S. (2002) [15] observed nine clusters too while analyzing 90 genotypes. The highest number of genotypes appeared in cluster III which contained 13 entries followed by cluster IX having 12 entries. Cluster IV possess 10 entries, while cluster Vand VIII were constituted of 9

lines. Cluster VI having 8 entries. Cluster I having 7 entries. Cluster VII having 4 lines. Cluster II was represented by 2 entries. The estimates of intra and inter cluster distance for 11 characters are presented in Table 2. The highest intra-cluster distance was observed in case of cluster II (14.53), followed by cluster III (10.88). The lowest intra-cluster distance was noted for cluster V (5.74) followed by cluster VIII (6.85). The maximum inter cluster distance was observed between cluster IX and V (51.61) followed by cluster IX and III (46.89). The minimum inter-cluster distance was observed between cluster VI and I (11.03) followed by cluster VIII and VI (12.52). Cluster mean for 11 characters are presented in Table 3. The genotypes of cluster V were responsible for highest cluster mean for days to 50% flowering (88.58 days) followed by entries of cluster VIII (85.78 days) and cluster I (84.89 days). The genotypes, with early flowering were concentrated in cluster VI (62.53 days). The highest cluster mean for plant height was observed in case of cluster VII (29.68 cm) followed by cluster II (25.19 cm). The lowest cluster mean for plant height was found in case of cluster VII (3.37 cm). Considering the variation in number of primary branches per plant cluster VI (1.77) showed highest mean value while, cluster IX (3.51) had lowest value for number of primary branches per plant.

Table 1: Clustering pattern of 74 lentil genotypes (including checks) on the basis of non-hierarchical Euclidean cluster analysis of eleven characters

Cluster No.	Number of genotypes	Genotypes
I	7	GM-223199A, DPL-15, PL-7, NDL-96-12, NDL-96-15, NDL-96-4, NDL-96-10
II	2	L-4594, LL-699
III	13	EC-78389, GM-223199A, GM-78532, EC-267604, EC-223199A, 78536, L-4603, GM-223233, GM-267687, EC-262572, 78471, 255401, NDL-1
IV	10	EC-267672, EC-223397, EC-1, GM-223209, EC-78409, GM-78474, 78417, EC-223229, LL-1122, LL-631
V	9	LL-1161, PL-117, IPL-321, EC-78405, EC-223789, GM-27190, GM-78521, EC-75483, NDL-98
VI	8	GM-2675630, GM-78505, PL-02, ILWL-118, EC-78536, LL-1203, GM-267638, ILL-766
VII	4	78474, NDL-21, NDL-96-3, NDL-96-1
VIII	9	LL-1114, GM-223150, EC-223188, NDL-96-21, NDL-96-11, NDL-96-31, NDL-96-36, NDL-96-21, DPL-15
IX	12	DPL-62, NDL-97-1, EC-78425, IPL-81, NDL-36, L-4147, DPL-58, NDL-24, L-4076, L-639, DPL-62, IPL-81

Table 2: Estimates of average intra and inter- cluster distances for the 9 clusters in lentil

	I	II	III	IV	V	VI	VII	VIII	IX
I	4.892	12.550	12.584	17.672	25.168	11.034	14.745	26.277	37.986
II		10.013	18.917	25.407	38.004	14.265	20.391	18.467	33.575
III			10.967	20.921	31.669	17.937	24.967	39.459	46.898
IV				13.213	24.171	24.676	20.295	31.508	34.614
V					5.913	46.297	33.316	36.776	51.617
VI						4.695	12.525	28.098	28.793
VII							10.339	22.054	24.546
VIII								8.667	24.109
IX									17.600

Bold figure represent intra-cluster distance

Table 3: Cluster mean for different characters for 9 cluster in lentil germplasm

Cluster number	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/ plant	Seeds/ pod	100 Seed weight (g)	Biological yield/ plant (g)	Harvest index (%)	Seed yield/ plant (g)
I	84.89	114.89	21.00	2.26	10.20	26.92	1.96	4.25	8.41	20.31	42.20
II	79.20	108.65	25.19	2.66	10.50	30.43	2.01	4.25	16.19	33.36	48.70
III	71.32	101.02	18.51	2.44	10.79	23.33*	2.06	4.98	6.29*	15.71	41.92
IV	73.23	98.97	23.37	3.10	9.09*	26.93	1.90	4.99**	21.13	36.41	59.65
V	88.58**	116.50**	24.11	2.32	9.22	26.60	1.95*	3.72	11.53	27.57	40.24*
VI	62.53*	95.63*	29.68**	1.77*	9.24	28.96	1.78	3.57*	12.00	25.66	45.66
VII	72.78	100.38	23.09	3.37**	12.74**	35.06	2.33**	4.93	32.70**	56.26	56.41
VIII	85.78	110.38	20.75	2.17	9.54	36.86**	2.13	7.69	30.50	61.66**	47.36
IX	65.78	98.13	16.90*	1.92	10.29	34.66	2.03	4.59	6.80	10.11*	70.58**

Lca8Rse1xKK8fsMmZp78rrN4HxbggMP7cf

The highest cluster mean for number of secondary branches per plant was observed in case of cluster VII (12.74) followed by cluster III (10.79) while genotypes with very low number of secondary branches per plant were found to be grouped in cluster VI (9.9). The highest cluster mean for number of capsules per plant was exhibited by cluster VIII (36.86) followed by cluster VII (35.06), while the lowest cluster mean of capsules per plant was produced by entries of cluster III (23.33).The genotypes occurring in cluster VII (2.33) and cluster VIII (1.13) showed highest mean for number of seed per capsule while the genotypes of cluster VI (1.78) were responsible for lowest means for number of seed per capsule. Cluster IV (4.99g) followed by cluster VI (3.57g) were comprised of entries which produced highest mean for biological yield per plant. The lowest cluster mean for biological yield per plant was observed for cluster V (3.72g). The highest cluster mean for seed yield per plant was observed in case of cluster VIII (61.66g) followed by cluster

VII (56.26g). The lowest cluster mean for seed yield per plant was exhibited by cluster IX (10.11g).

The nine clusters in the aforesaid divergence analysis contained genotypes of heterogeneous origin frequently. The highest inter-cluster distance was observed between cluster VI and I, followed by cluster VI and III. The lowest inter-cluster distance was observed between cluster VIII and VII followed by cluster VIII and IV, which indicated that genotypes present in these cluster pairs were genetically close to each other. The crosses between genotypes belonging to the clusters separated by low inter cluster distances are unlikely to generate promising recombinants in segregating generations. Also proposed hybridization between lines belonging to clusters separated by large inter cluster distance in lentil. The intra-cluster group mean for 11 characters revealed considerable differences between clusters in respect of cluster means (Table 3). An examination of the estimates of within and between cluster diversity presented by intra and inter cluster D2 values revealed that the genotypes of same cluster had little divergence from each other with respect to aggregate effect of 9 characters under study (Table 2). Therefore, the chances of obtaining good recombinants in segregating generations by crossing the members of same cluster are very low. It is, therefore, suggested that crosses should be attempted between the genotypes belonging to clusters separated by large inter-cluster distance. This finding is in agreement with the report advocating lack of definite relationship between genetic and geographic diversity in lentil (Chauhan, *et al*. (2005, Singh, and Gupta, (2004); Sharma, *et al*. (2002) [6, 7, 27].

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