RESEARCH ARTICLE

ANALYSIS OF GENETIC DIVERSITY IN LENTIL (*LENS CULINARIS* MEDIK.) GENOTYPES UNDER HUMID SOUTH-EASTERN PLAIN ZONE OF RAJASTHAN

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Abstract: Genetic divergence analysis in 155 genotypes of lentil (*Lens culinaris* Medik.) by applying Mahalanobis's D^2 statistics indicated the presence of wider genetic diversity among the material for 13 characters. The genotypes were grouped into twelve clusters by Tocher's method. Cluster V was the largest group of 34 genotypes, whereas cluster II was the second largest group consisting 29 genotypes grouped together. Cluster VI was the third largest cluster based on the genotypes (28 genotypes) followed by cluster IV (18 genotypes), cluster I (13 genotypes), cluster III (11 genotypes). Two clusters X and XII comprised of five genotypes each cluster and cluster VII and IX comprised of three genotypes in each cluster. The remaining cluster XI comprised four genotypes. Cluster VIII have only two genotypes indicating that this genotype is much more divergent than rest of the genotypes in the study. It was concluded that in general there was parallelism between genetic and geographic diversity. Cluster XI had higher mean values for most of the desirable characters like seed yield per plant (3.69) followed by harvest index (48.91), number of pods per plant (108.75), number of peduncles per plant (64.57), number of primary branches per plant (15.77). The genotypes accommodate under cluster XI were found desirable for seed yield per plant (3.69 g).

Keywords: Cluster, Genetic divergence, Lentil, Productivity

INTRODUCTION

Lentil is a self-pollinated diploid (2n = 14 chromosome numbers) annual cool season important 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 and in addition, the remaining plant residues can be used as animal feed and fodder. According to Ladizinsky (1979) lentil has been originated in Southern Turkey. Cubero (1984) in a detailed review concluded that the region between Western Turkey and Kurdis could be its place of origin, 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, Aleppo, Syria) has a global mandate for research on lentil improvement. It is very diverse crop. 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. The total area under lentil in India was 14.94 lakh hectares with a total production of 15.06 lakh tones with productivity of 1008 kg/hectare during 2017-18 (Anonymous, 2019) and contributes about 7.88% in total pulse production and in Rajasthan state covering the total area of 0.31 lakh hectares, producing 0.43 lakh tonnes with productivity of 1408 kg/hectare. The selection of suitable divergent parents for hybridization is required because the cross involving diverse parents offer great possibility of obtaining desirable segregates in the segregating generations. The present study was conducted to study the genetic diversity of lentil genotypes in respect of thirteen quantitative characters, to determine the relationship between yield and yield contributing traits and to select the promising lentil genotypes.

MATERIALS AND METHODS

The research was conducted at the experimental field of Agricultural Research Station, Kota, Rajasthan during *Rabi* season 2019-20. The experimental material of the present work consisted of one hundred fifty-five genotypes obtained from AICRP on MULLaRP, Agricultural Research Station, Ummedganj, Agriculture University, Kota including five check varieties viz., Kota Masoor-1 (KM-1),

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Kota Masoor -2 (KM-2), JL-3, IPL-316 and L-4076. The experiment was laid out in an augmented randomized complete block design (Federer, 1956). The material was sown in 10 blocks. Each block had 4 meter long 20 lines placed 30 cm apart. Thus 15 genotypes and 5 checks were sown in each block. The checks were common in the blocks and they were randomized among themselves. After two weeks of germination, thinning was done to maintain a plant-to-plant distance of 10 cm. Recommended cultural practices were adopted for raising the crop. The recommended packages of practices were followed for raising a healthy crop and all necessary plant protection measures were taken to control the pest and diseases. The data was recorded on thirteen quantitative characters *viz*., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of peduncles per plant, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index, protein content and seed yield per plant.

D^2 statistic

Classification using D^2 analysis of genetic divergence aims at grouping the genotypes precisely and objectively into various groups. In the present investigation simultaneous variations in all characters of 155 lentil genotypes were tested for assessment of the nature of genetic divergence among them following Mahalanobis D^2 statistics. The D^2 values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables. For each pair of combination, the mean deviation i.e. $d_i = Y_i^1 - Y_i^2$, where Y_i denotes the transformed variables (i = 1, 2, 3, 4, 5……….p) were calculated and the D^2 was then calculated as sum of the squares of those deviations, i.e.

$$D^2 = \sum (Y_i^1 - Y_i^2)^2$$

Where, p = Number of characters.

The significance of D^2 values was tested by treating them as chi-square (χ^2) at p degrees of freedom where p is the number of characters considered.

Grouping of genotypes by Tocher's method

After arranging the D^2 values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952). The criterion used in this method was that any two varieties belonging to the same cluster, at least on an average, show a smaller D^2-value than those belonging to two different clusters. Then inter-cluster and intra-cluster distances were calculated and their relationships were diagrammatically represented.

RESULTS AND DISCUSSION

155 genotypes of lentil, included in the present study were grouped into twelve different clusters on the basis of genetic divergence or genetic closeness by D^2 following Tocher's method of clustering. The clustering pattern of the genotypes has been shown in Table-1. Cluster V was the largest group of 34 genotypes, whereas cluster II was the second largest group consisting 29 genotypes grouped together. Cluster VI was the third largest cluster based on the genotypes (28 genotypes) followed by cluster IV (18 genotypes), cluster I (13 genotypes), cluster III (11 genotypes). Two clusters X and XII comprised of five genotypes each cluster and cluster VII and IX comprised of three genotypes in each cluster. The remaining cluster XI comprised four genotypes. Cluster VIII have only two genotypes indicating that this genotype is much more divergent than rest of the genotypes in the study. It was concluded that in general there was parallelism between genetic and geographic diversity. This view point has been supported by the work of Maurya *et al*. (2018), Alam *et al*. (2011), Azad *et al*. (2011), Tyagi and Khan (2010).

Maximum intra-cluster D^2 value (29.32) was recorded in cluster X among the twelve intra-cluster distances, which revealed maximum genetic diversity among the genotypes of this group. Second highest average intra-cluster distance was observed by cluster VI (22.97) followed in order by cluster I (20.25), cluster XII (18.64), cluster IV (17.36), cluster III (16.87), cluster V (16.62), cluster II (15.56), cluster VIII (15.47), cluster VII (14.32) and cluster XI (12.82). The minimum average intra-cluster D^2 value (11.53) was recorded for cluster IX (Table-2).

The inter-cluster distances ranged from 8.91 (between II and VI) to 94.37 (between IX and XI). The other clusters with high inter-cluster distances were VIII and XI (90.15) followed by cluster V and XI (79.56), VII and XI (78.85), IV and XI (77.30) and I and XI (75.32). The minimum average inter-cluster distance (D^2 value) was observed of between II and VI (8.91) followed by cluster I and II (10.99), cluster IV and V (11.35) and cluster VI and XII (13.25). The lowest inter cluster distances indicate that the genotype of these clusters had close relationship and hence, may not be emphasized upon to be used in hybridization programme. These results are somewhat in accordance with the findings of Chauhan *et al*. (2005), Gohil *et al*. (2006).

luster XI had higher mean values for most of the desirable characters like seed yield per plant (3.69) followed by harvest index (48.91), number of pods per plant (108.75), number of peduncles per plant (64.57), number of primary branches per plant (15.77). The genotypes accommodate under cluster XI were found desirable for seed yield per plant (3.69 g).[Table 3]

Table 1. Distribution of 155 genotypes of Lentil (*Lens culinaris* Medik.)

Cluster	**Number of Genotypes**	**Genotypes**
I.	13	RKL-46-E, RKL-24C-290, RKL-67G-77, RKL-14-24, RKL-14-30, RKL-14-201, RKL-3-91, RKL-16-324, RKL-16-312, RKL-16-315, RKL-16B-108, RKL-14B-3, RKL-16-3223
II.	29	RKL-14-270, RKL-16-306, RKL-60F-31, RKL-3-91, RKL-14-35, RKL-16-321, RKL-24C-29, RKL-55F-188, RKL-25C-193, RKL-27C-127, RKL-14-175, RKL-58F-111, RKL-14-101, RKL-23C-274, RKL-61F-215, RKL-24C-290, RKL-16-305, RKL-15-450, RKL-16-337, RKL-16-1384, RKL-16-306, RKL-16-332, RKL-15-450, RKL-16-300, KM-1 (C), KM-2 (C), JL-3 (C), IPL-316 (C), L-4076 (C)
III.	11	RKL-14-130, RKL-14-130, RKL-60F-216, RKL-607-1-1, RKL-60F-31, RKL-16-348, RKL-16-361, RKL-14-1322, RKL-16-302, RKL-16-365, RKL-16-301
IV.	18	RKL-16-301, RKL-29C-139, RKL-14-32, RKL-47E-1170, RKL-60F-1216, IPL-29C-139, IPL-16-313, RKL-16-3022, IPL-14-49, RKL-16-339, RKL-16-368, RKL-16-300, RKL-12F-132, RKL-16-316, RKL-23C-34, RKL-603-44, RKL-16-1383, RKL-16-364
V.	34	RKL-16-333, RKL-16-309, RKL-14-276, RKL-14B-3, RKL-14-21, RKL-16-342, RKL-58F-3206, RKL-60F-1209, RKL-19C-288, RKL-9F-38, RKL-12-3F-91, RKL-19C-288, RKL-14B-3, RKL-12F-136, RKL-35-62E, RKL-16-335, RKL-16-367, RKL-16-367, RKL-16-348, RKL-16-364, RKL-16-3011, RKL-16-346, RKL-16-367, RKL-16-323, RKL-16-303, RKL-16-3372, RKL-16-305, RKL-16-336, RKL-61F-26, RKL-16-361, RKL-603-11-6, RKL-16-313, RKL-16-316, RKL-16-3152
VI.	28	RKL-603-44, RKL-58F-111, RKL-35D-3132, RKL-35D-3132, RKL-64F-3, RKL-14-195, RKL-603-11-1, RKL-14-151, RKL-23C-2741, RKL-603-11-1, RKL-14-2, RKL-605-3, RKL-25C-193, RKL-16-363, RKL-16-314, RKL-27C-12106, RKL-16-311, RKL-16-368, IPL-14-49, RKL-16-322, RKL-19C-291, RKL-16-303, L-4076, RKL-16-1383, RKL-16-308, RKL-16-1382, RKL-16-338, RKL-16-341
VII.	3	RKL-60F-216, RKL-16-313, RKL-14-132
VIII.	2	RKL-16-348, RKL-14B-3
IX.	3	RKL-14-25, RKL-24C-290, RKL-16-348
X.	5	RKL-27C-12107, RKL-73 iii-13, RKL-16-310, RKL-56F-73, RKL-14-31
XI.	4	RKL-14-49, RKL-14-276, RKL-14-276, RKL-14-42
XII.	5	RKL-16-311, RKL-16-3232, RKL-16-3222, RKL-46E, RKL-16-3123

Table 2. Average intra-clusters (diagonal) and inter-cluster distance (D^2 value) in 155 genotypes of Lentil

Cluster	I.	II.	III.	IV.	V.	VI.	VII.	VIII.	IX.	X.	XI.	XII.
I.	20.25	10.99	14.36	16.00	14.49	15.79	27.62	21.95	23.86	23.35	75.32	20.63
II.		15.56	17.10	15.48	15.65	**8.91**	21.77	26.99	26.76	22.31	70.37	17.10
III.			16.87	17.54	16.43	16.09	30.59	24.62	30.76	26.95	72.65	18.77
IV.				17.36	11.35	17.92	26.40	18.27	27.29	23.80	77.30	23.29
V.					16.62	16.23	28.20	15.80	27.09	22.90	79.56	22.45
VI.						22.97	24.39	28.96	32.73	22.55	65.86	13.25
VII.							14.32	35.48	26.51	37.99	78.85	32.70
VIII.								15.47	23.98	35.10	90.15	35.12
IX.									11.53	43.06	**94.37**	41.03
X.										**29.32**	68.58	19.24
XI.											**12.82**	61.89
XII.												18.64

* Figures in bold letters indicate maximum and minimum (intra/inter-cluster) values

Table 3. Cluster means values of 155 genotypes for thirteen characters in Lentil

Character / Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of peduncles per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Protein content (%)	Seed yield per plant (g)
I	64.18	105.54	39.40	8.07	14.07	32.82	42.55	1.49	3.09	3.76	38.21	19.39	1.41
II	62.40	110.00	38.32	10.22	10.72	28.86	50.18	1.39	3.44	5.46	40.06	19.31	2.16
III	57.58	99.34	44.84	13.75	12.95	33.11	43.70	1.44	2.67	4.90	45.38	21.88	2.22
IV	54.38	105.14	32.08	13.87	16.91	25.57	43.50	1.36	2.24	3.97	41.32	18.62	1.68
V	54.38	102.34	34.96	9.59	8.31	26.16	40.62	1.29	2.88	4.25	38.18	19.89	1.62
VI	58.18	106.54	38.60	10.07	6.87	30.67	53.70	1.33	2.99	3.75	42.34	22.54	1.56
VII	54.98	128.14	40.36	14.99	8.27	27.10	45.82	1.52	1.55	1.99	44.14	20.27	0.78
VIII	54.58	101.34	29.36	5.49	13.47	26.20	28.92	1.41	5.31	3.00	43.60	19.80	1.33
IX	67.58	119.14	37.68	8.59	13.51	24.14	26.90	1.49	5.68	3.66	44.61	20.55	1.64
X	54.98	100.14	35.76	11.19	14.87	31.12	55.02	1.44	2.77	8.99	23.53	21.85	2.21
XI	56.98	100.34	39.44	**15.77**	11.67	**64.57**	**108.75**	1.48	2.50	7.39	**48.91**	21.71	**3.69**
XII	54.98	101.14	45.16	7.19	12.87	30.92	59.22	1.52	2.56	3.77	38.20	21.50	1.39

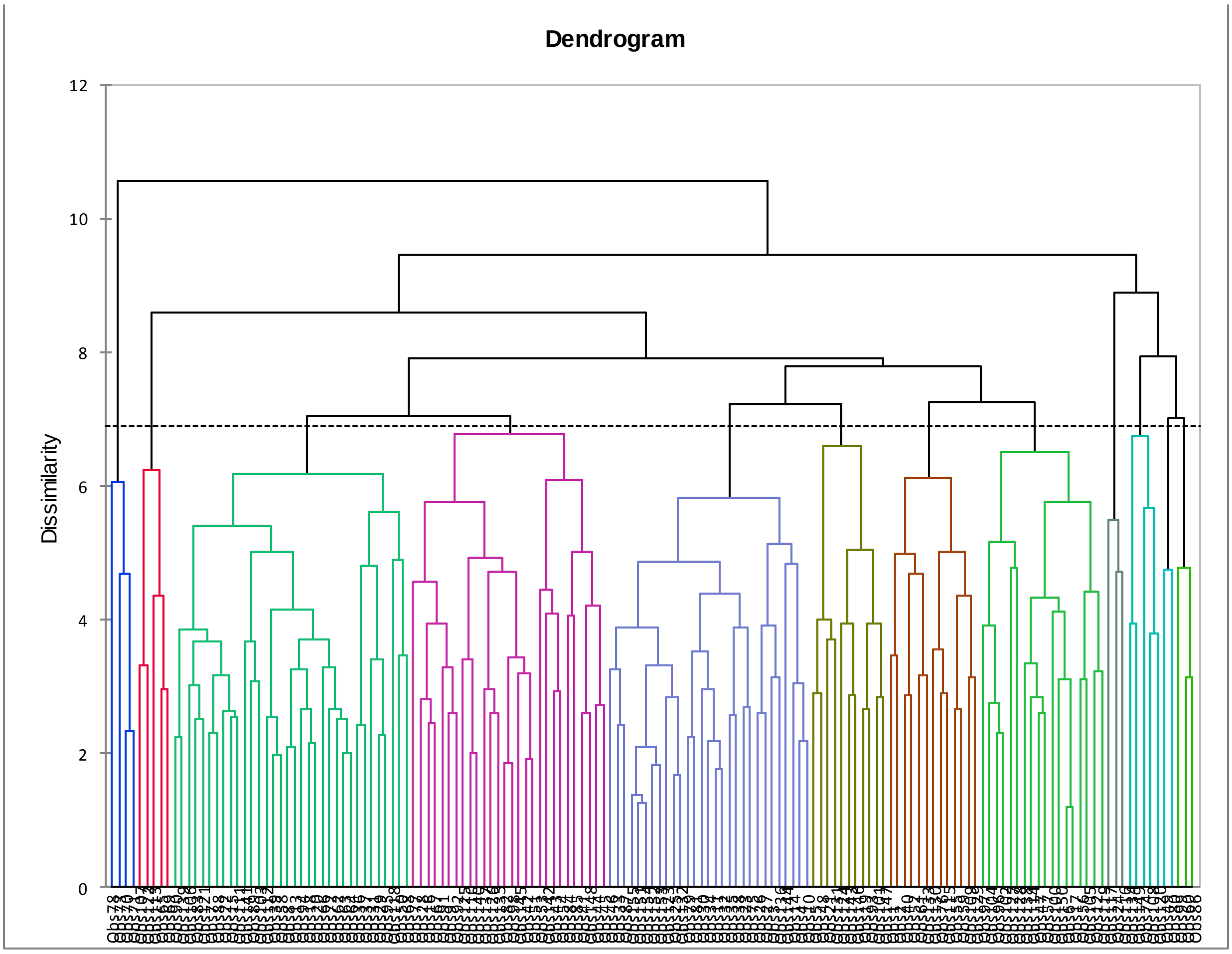
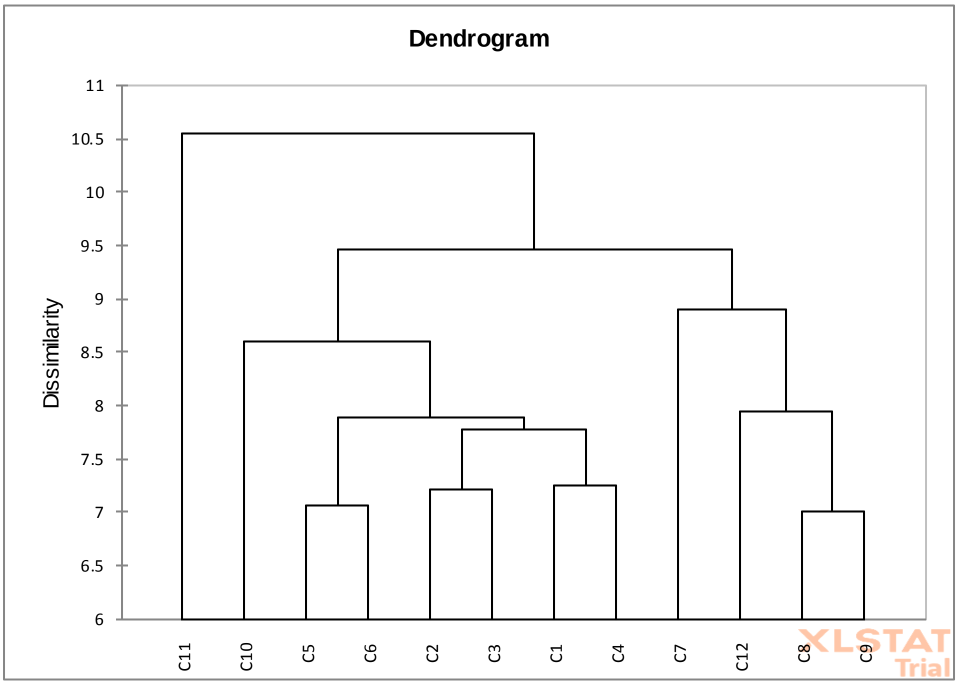


Fig. 1. Agglomerative hierarchical clustering (AHC) of 155 lentil genotypes



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