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Study of genetic diversity under varied environments in lentil (*Lens culinaris Medik*)¹

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Abstract

Genetic diversity of 30 diverse genotypes of lentil was studied through D^2 statistic. Genotypes from different geographical locations have been observed in same cluster and *vice-versa* indicating that clustering of populations does not follow their geographic or location distribution. The intra cluster distance was observed to be highest for cluster III in all the environments except environment II thereby indicating greater genetic divergence between the genotypes belonging this cluster. The maximum inter-cluster distance was observed between cluster I and III in all environments except environment II where maximum inter-cluster distance was observed in cluster I and II. The diversity among the cultivars measured by inter cluster distance was adequate for improvement of lentil by hybridization and selection. Cluster II had late flowering genotypes with maximum primary and secondary branches per plant, number of pods per plant, plant height, biological yield per plant and seed yield per plant in almost all the environments where as cluster I had genotypes with early maturity type in all the environments. This clearly indicated that the genotypes included in these clusters are having broad spectrum of genetic diversity and could be used in hybridization programme of lentil for obtaining desirable segregates through selection in the advanced breeding programme.

Keywords: Genetic divergence, lentil, seed yield, inter and intra cluster distance

Introduction

Crosses between divergent parents usually produce greater heterosis than those between closely related ones (Moll and Stuber, 1971) [7]. In addition to facilitate the selection of divergent parents for hybridization, D^2 analysis measures the degree of diversification and determines the relative proportion of each component character to the total divergence. Use of diverse parents in hybridization programme can serve the purpose of combining desirable genes or to obtain recombination. The multivariate D^2 analysis (Mahalanobis, 1936) [6] is one of the important biometrical tool in quantifying the genetic divergence in the germplasm. Using this method in the present study, an attempt has been made to classify the 30 elite strains of lentil into different groups at four diverse environments and to quantify the magnitude of genetic divergence for their further use in recombination breeding with expectation of getting potential transgressive segregants.

Materials and methods

The present experiment was conducted during two years (2004-05 and 2005-06) with early and late sowing under rainfed condition. The thirty genotypes procured from Division of Genetics, IARI, New Delhi, were grown in Randomized Block Design with three replications under four environments {normal sown 2004-05 (E_1), late sown 2004-05 (E_2), normal sown 2005-06 (E_3), late sown 2005-06 (E_4)}. Each entry was sown in single row plot of 3 m length with a distance of 25 cm and 10 cm between rows and plants, respectively. In each replication the observations were recorded on five randomly selected plants in each plot on eleven characters *viz.*, days to 50% anthesis, days of maturity, number of primary branches, number of secondary branches, number of pods per plant, plant height (cm), number of seeds per pod, biological yield per plant (g), seed yield per plant (g), 100-seed weight (g) and harvest index (%). Plot means were used to analyse the genetic divergence following Mahalanobis' generalized distance method (1936) [6].

Results and discussion

Genetic diversity arises due to geographical separation or due to genetic barriers to cross ability. One of the potent techniques measuring genetic diversity is the D^2 analysis proposed by Mahalanobis (1936) [6].

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The technique measures the focus of differentiation at two levels *viz*, intra and inter cluster levels and thus helps in the selection of genetically divergent parents for their exploitation in hybridization/breeding programme.

Based on D^2 statistics, the thirty genotypes of lentil were grouped into three clusters in all the environments (Table 1-4). An analysis of divergence showed that cluster II had the minimum intra-cluster distance while maximum distance was shown by cluster III in all the environments except environment II where minimum cluster distance was shown by cluster III and maximum distance in cluster I (Table 5-8). The maximum inter-cluster distance was observed between cluster I and III in all environments except environment II where maximum inter-cluster distance was observed in cluster I and II. Yadav *et al.* (2005) [8], Kumar and Sharma (2010) [5] and Asghar *et al.* (2010) [2] also observed that the genetic diversity is not necessarily parallel to the geographical diversity. The crosses involving the parents from above clusters may exhibit high heterosis for desirable traits.

The over all picture indicated that the clusters I and III were quite divergent from rest of the clusters and also from one another. Selecting genotypes from such divergent group for hybridization is likely to yield heterotic response and release better segregants in subsequent generations. However, caution may be exercised in selecting very divergent genotypes because such crosses may not yield proportionate heterotic response since a cross between extremely divergent parents creates a situation where the harmonious functioning of alleles is rather distributed and consequently the physiological functions are not so efficient (Dobhal and Ram 1985) [3]. This is further substantiated by the fact that if 'm' is the mean and 's' is the standard deviation of divergence value (D^2) among parents whose genetic divergence falls between (m-s) and (m+s) then crosses will have better chances of producing higher frequency and magnitude of heterosis as compared to a cross whose parental divergence falls outside the limits, (m-s and m+s) (Arunachalam and Bandhopadhyay, 1984) [1]. They

imply that the selection of parents should also be based on their *per se* performance.

The cluster means for the eleven traits revealed considerable differences among all the clusters (Tables 1-4). The cluster I having 4-6 genotypes in all the environments possesses either higher or lower value for most of the traits justifying its inclusion as a separate cluster. Cluster I and cluster II among them had the maximum values for the yield related traits. Cluster II had late flowering genotypes with maximum primary and secondary branches per plant, number of pods per plant, plant height, biological yield per plant and seed yield per plant in almost all the environments where as cluster I had genotypes with early maturity type in all the environments. Hence, the genotypes with these two clusters could be used as parents to obtain better recombinants and widen the genetic base of the germplasm pool (Edang *et al.*, 1971) [4].

Breeding for earliness coupled with high yielding development varietal programme genotype L-4677 exhibiting minimum days to flowering (46 days) and minimum days to maturity (128 days) could be used as one of the parental line for future hybridization programme. Additionally it also possesses maximum number of secondary branches per plant, number of pods per plant and highest seed yield per plant. On the other hand, cluster II representing genotypes with maximum number of primary branches, secondary branches, pods per plant, highest seed yield per plant and long plant type could be used as one of the parents if the aim of the breeding programme is to improve any of these traits. Edang *et al.* (1971) [4] stated that the clustering pattern could be utilized for choosing parental combinations for generating maximum possible variability for various economic traits. The genotypes in cluster II exhibiting maximum seed yield might be tested for their stability for few years in multi-location trials and if found suitable, may be directly adopted as high yielding varieties.

Table 1: Clusters mean and grouping pattern for eleven characters of thirty genotypes of lentil (normal sown) 2004-05 (E₁)

Cluster no.	No. of genotypes	Name of genotypes	Days of anthesis	Days of maturity	Primary branches	Secondary branches	No. of pods per plant	Plant height (cm)	No. of Seeds per pod	Biological yield (g)	Seed yield (g)	100-seed weight (g)	Harvest index (%)
I	4	P-32225, L-412, L-4661, L-4677	55.42	128.00	4.49	8.30	96.62	34.94	1.59	24.29	8.00	5.09	32.98
II	16	L-415, L-396, L-4676, L-4618, L-386, L-381, L-4594, L-4148, L-4598, L-2147, L-4596, L-414, L-4597, L-416, L-417, L-310	90.71	146.67	4.41	7.85	90.46	34.44	1.69	23.96	7.93	5.22	33.15
III	10	L-307, L-4595, L-4674, L-308, L-306, L-309, L-4671, L-395, L-4672, L-4620	94.10	146.87	3.83	7.08	66.46	30.17	1.60	16.05	5.31	5.18	33.07

Table 2: Clusters mean and grouping pattern for eleven characters of thirty genotypes of lentil (late sown) 2004-05 (E₂)

Cluster no.	No. of genotypes	Name of genotypes	Days of Anthesis	Days of Maturity	Primary Branches	Secondary Branches	No. of Pods Per Plant	Plant Height (cm)	No. of Seeds per pod	Biological yield (g)	Seed yield (g)	100-Seed Weight (g)	Harvest Index (%)
I	6	L-307, L-309, P-32225, L-412, L-4661, L-4620	73.72	131.61	4.02	7.14	73.88	28.57	1.39	17.54	5.74	5.85	32.72
II	12	L-308, L-4676, L-386, L-381, L-4594, L-4148, L-4598, L-2147, L-4596, L-414, L-417, L-4677	90.08	145.45	4.40	7.82	88.88	33.07	1.68	22.35	7.32	4.97	32.85
III	12	L-415, L-4595, L-4674, L-396, L-306, L-4618, L-4671, L-395, L-4672, L-4597, L-416, L-310	82.14	144.95	3.89	6.82	74.24	30.16	1.61	16.05	5.12	4.32	31.86

Table 3: Clusters mean and grouping pattern for eleven characters of thirty genotypes of lentil (normal sown) 2005-06 (E₃)

Cluster no.	No. of genotypes	Name of genotypes	Days of anthesis	Days of maturity	Primary branches	Secondary branches	No. of pods per plant	Plant height (cm)	No. of Seeds per pod	Biological yield (g)	Seed yield (g)	100-seed weight (g)	Harvest index (%)
I	6	L-396, P-32225, L-412, L-4661, L-4677, L-4620	61.17	132.00	4.53	7.91	93.45	35.57	1.69	24.61	7.86	5.05	31.87
II	15	L-415, L-4676, L-4618, L-386, L-381, L-4594, L-4148, L-4598, L-2147, L-4596, L-414, L-4597, L-416, L-417, L-310	93.29	147.80	4.56	8.29	91.68	34.58	1.73	25.40	8.29	5.28	32.66
III	9	L-307, L-4595, L-4674, L-308, L-306, L-309, L-4671, L-395, L-4672	97.22	150.11	3.92	7.15	68.52	30.96	1.66	17.27	5.45	5.03	31.53

Table 4: Clusters mean and grouping pattern for eleven characters of thirty genotypes of lentil (late sown) 2005-06 (E₄)

Cluster no.	No. of genotypes	Name of genotypes	Days of anthesis	Days of maturity	Primary branches	Secondary branches	No. of pods per plant	Plant height (cm)	No. of Seeds per pod	Biological yield (g)	Seed yield (g)	100-seed Weight (g)	Harvest Index (%)
I	5	P-32225, L-412, L-4661, L-4677, L-4620	56.40	121.80	4.08	7.81	83.34	31.21	1.63	21.33	6.83	5.12	32.09
II	15	L-396, L-4676, L-4618, L-386, L-381, L-4594, L-4148, L-4598, L-2147, L-4596, L-414, L-4597, L-416, L-417, L-310	88.02	142.40	4.35	7.88	89.80	33.23	1.70	23.10	7.40	4.88	32.01
III	10	L-415, L-307, L-4595, L-4674, L-308, L-306, L-309, L-4671, L-395, L-4672	89.63	144.30	3.75	6.84	68.18	28.47	1.62	16.04	5.01	4.73	31.40

Table 5: Inter-and intra-cluster (D²) divergence (normal sown) among three clusters 2004-05 (E₁)

Cluster no.	I	II	III
I	2.643		
II	3.233	2.309	
III	5.155	3.467	2.896

Table 6: Inter-and intra-cluster (D²) divergence (late sown) among three clusters 2004-05 (E₂)

Cluster no.	I	II	III
I	2.859		
II	3.870	2.679	
III	2.801	3.484	2.429

Table 7: Inter-and intra-cluster (D²) divergence (normal sown) among three clusters 2005-06 (E₃)

Cluster no.	I	II	III
I	2.674		
II	2.862	2.200	
III	4.600	3.836	2.880

Table 8: Inter-and intra-cluster (D²) divergence (late sown) among three clusters 2005-06 (E₄)

Cluster no.	I	II	III
I	2.384		
II	3.261	2.231	
III	4.257	3.839	2.922

Bold figure denotes Intra cluster divergence values

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