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Multivariate Analysis for Genetic Divergence in Lentil (Lens Culinaris Medic)

KEYWORDS: Lentil, Cluster, Diversity, Variability

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ABSTRACT *The objective of this study was to assess the genetic divergence available in lentil germplasm, based on Euclidean distances for the identification of genetically diverse and agronomically superior accessions. Wide physio-morphological divergence was obtained for all the traits under study. Principal component analysis, which transformed for all the metric traits into single index of similarity, yielded twelve eigen vector and roots. Based on first seven principal components (which accounted for 91.57% of the total variation), non-hierarchical Euclidean cluster analysis grouped the 60 lentil accessions into twelve well characterized groups.*

INTRODUCTION

Lentil is one of the most nutritious amongst *cool season legume*. It is grown throughout the northern and central India for grains, which are used as dal (whole or dehulled) and in various other preparations. Lentil contains 25% protein, 0.7% fat, 2.1% mineral, 0.7% fibre and 59% carbohydrate. It is rich in phosphorus and carotene. It is generally grown as rainfed crop during rabi season after rice, maize, pearl millet or *kharif* fallow. It is also grown as intercrop with barley, linseed, mustard and autumn planted sugarcane. In North-eastern parts of the country, lentil is also cultivated as *paira* crop with rice in which seeds of lentil are broadcasted in the standing crop of rice just before its harvest. It is grown on a wide range of soils from light loamy sand to heavy clay soil in northern parts and moderately deep black soils in Madhya Pradesh and Maharashtra.

Magnitude of genetic divergence among different genotypes of a species determines the spectrum of variability expected in segregating generation. The variability offers a working bench for selection intensity and direction which is determined by the crop breeders according to breeding objectives of crop improvement. Genetic diversity is generally considered as an important criterion for choosing diverse for obtaining high yielding line for efficient and hybridization programme greater the diversity in crop species, better is the chance of evolving promising and desired types .In a present study, the classification of 60 genotypes of lentil into different clusters through D^2 analysis are determination of genetic closeness and for assessing diversity among the genotypes.

MATERIALS AND METHODS

The experimental material consisted of 60 genotypes of lentil. These strain was collected from germplasm pool of lentil maintained at legume section of C.S. Azad University of Agriculture and Technology, Kanpur. The experiment was carried out in a complete randomized block design with three replications during currently two years pooled data.. Each plot consisted of six rows of four meter length, and spaced 30 cm apart, maintaining plant to plant distance of 10 cm. Observation were recorded on randomly chosen ten competitive plants in each genotype in each replication. Data were recorded for nine characters viz., days to 50 per cent flowering, plant height (cm), number of branches per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, 100-seed weight (g), days to maturity and grain yield per plant(g). D^2 analysis was carried out as given by Mahalanobis's (1936).

RESULTS AND DISCUSSION

The need of parental diversity in optimum magnitude to obtain superior genotypes for recovery of transgressive segregants has also been repeatedly emphasized **(Griffing and Lindstrom, 1954; Moll and Robinson, 1962 and Arunachalam, 1988).** Hence characterization of genetic divergence for selection of suitable and diverse parents should be based on sound statistical procedures, such as D^2 statistics and non- hierarchical Euclidean cluster analysis. These procedures characterized genetic divergence using the criteria of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters. The analysis of variance was highly significant among the divergent genotypes for all the 9 traits under study, which revealed the presence of considerable variability among the genotypes. This suggested that adequate scope is available for selection of superior genotypes aimed at enhancing genetic yield potential of lentil. The mean, range and heritability estimates for different characters are given in Table 1. A wide range was observed for all the traits. The heritability was high for days to maturity (95.86%), days to 50 per cent flowering (94.76%), number of seeds per pod (94.29%), 100-grain weight (91.61%), plant height (91.11%) and grain yield per plant (69.93%). This suggests that these traits are least affected by the environment and, therefore, can be effectively used as selection criteria. High variability for these traits has been reported by several workers.

The principal component analysis was carried out to transform the interdependent variables into a set of dependent variables. These principal component scores were used to compute Eucildan distances based on non-hierarchical cluster analysis. This method characterizes genetic divergence on the basis of similarity and dis-similarity denoted by aggregate effects of agronomic traits under study.

Based on this, 60 lentil accessions were grouped into twelve well-characterized groups (I-XII) based on the similarity in traits (Table2). The maximum number of genotypes (9) fell in cluster VI, namely, IPL 93, KL218, PL117, KL320,

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KL231, KL91, JL71, KL315 and IPL93while, minimum number (2) was observed in cluster XI, i.e., IPL97 and HUL92. This grouping indicated considerable diversity in the germplasm. Clusters III, V and X exhibited 5 entries each followed by 3 accessions each in clusters II, VII and VIII. This finding is in agreement with the report advocating lack of definite relationship between genetic and geographic diversity in lentil. **(Bargale and Billore, 1992).**

The D^2 analysis showed intra and inter-cluster distance (Table 2). The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity existed among the genotypes belonging to distantly spaced groups. The maximum inter-cluster distance (33.12) existed between cluster x and XII followed between cluster II and VII (32.70) and between cluster VII and XII (31.56), suggesting wide diversity between them and the genotypes in these cluster could be used as parents in hybridization programme for isolating transgressive segregates. The highest intra-cluster distance was observed in cluster VI (12.76) and the lowest in cluster VII (9.23). The crosses between genotypes belonging to the cluster separated by low inter cluster distances are unlikely to generate promising recombinants in segregating generations **(Gumber et al. 2006; Jeena et al. 2005; Durga et al.2005).** The genotypes grouped into same cluster displayed the lowest degree of divergence from one another, and when crosses are made among the genotypes of the same cluster, no transgressive segregant is expected from such combinations. Therefore, hybridization programmes should always be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized to get desirable transgressive segregants. The genotypes for hybridization may be chosen from widely separated clusters.

The study depicted the relative divergence in pysio-morphological and yield traits. The screening of genotypes helped in identifying the promising genotypes for different traits, which may serve as good genetic donors for exploitation in further breeding programme. The genotypes occupying the top position in superior clusters may further be assessed for their combining ability and gene effects

following suitable mating designs.

Chauhan, M.

S. N.	Characters	Range	Grand mean	S.E. difference	Heritability (%)
1.	Days to 50 per cent flowering	63.00-70.67	65.10	0.56	94.76
2.	Days to maturity	110.00-128.66	119.36	0.93	95.86
3.	Plant height	30.00-49.65	39.83	0.85	91.11
4.	No .of branches per plant	3.45-7.80	5.62	0.71	54.40
5.	No. of pods per cluster	2.00-3.00	2.53	0.28	71.97
6.	No. of pods per plant	111.67-153.33	132.50	7.65	62.04
7.	No. of grains per pod	1.00-2.00	1.62	0.31	94.29
8.	100- grain weight	1.10-2.85	2.83	0.18	91.61
9.	Grain yield per plant	4.58-6.35	5.45	0.43	69.93

Table 2: Distribution of genotypes in different clusters

Cluster Number	Number of Genotypes	Genotypes
I	7	JL36, KL332, KL156, IPL84, LL147, KL327, IPL91
II	3	LL147, HUL92, DPL 15
III	5	KL116, DPL-62, KL136, KL75, KL129
IV	8	IPL84,KL221, KL223, JL1,JL59, JL61, IPL87, HUL57
V	5	IPL89, KL235, DPL15, IPL97, KL239, HUL97
VI	9	IPL 93, KL218, PL117, KL320, KL231, KL91, JL71, KL315, IPL93
VII	3	KL322, KL339, DPL54
VIII	3	KL156, IPL97, HUL92
IX	4	PL121, KL239, DPL-62, KL136
X	5	KL93, IPL91, LL147, KL136, KL75
XI	2	IPL97, HUL92
XII	6	KL156, KL239, LL147, DPL-62, KL136, IPL89

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Table- 3: Estimates of average intra and inter-cluster distances for the seven clusters in lentil

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	10.37	13.21	18.95	16.93	17.14	27.21	32.16	29.12	28.15	19.35	23.31	26.55
II		11.35	20.42	19.24	22.32	31.25	32.70	30.25	27.15	20.32	26.80	23.40
III			11.87	17.05	16.51	20.41	23.12	27.15	23.15	18.40	20.15	27.45
IV				12.71	13.20	22.72	24.35	22.32	26.35	22.45	23.40	28.35
V					9.80	19.65	22.10	21.45	23.25	27.35	29.55	26.80
VI						12.76	18.29	17.20	21.25	20.24	24.65	27.95
VII							9.23	12.21	18.24	19.75	27.35	29.35
VIII								10.15	17.35	24.56	28.60	31.56
IX									9.80	18.65	24.50	29.32
X										11.76	22.30	33.12
XI											12.34	30.76
XII												10.85

Bold figures represent intra-cluster distances

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