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GENETIC DIVERGENCE FOR YIELD AND ITS COMPONENTS IN LENTIL (*Lens culinaris* Medik.)

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ABSTRACT

Genetic divergence using Mahalanobis D^2 analysis was carried out in 50 diverse genotypes of lentil. All the 50 genotypes were grouped into seven clusters. The genotypes L-532-02, P-7, P-56, P-109, L-7481, L-63, L-62, P-11-106, P-96 had distinct identity with respect to yield attributes. Hybridization between genotypes of cluster V and VI should result in desirable combinations leading to development of valuable genetic stock and varieties. Among the yield contributing characters, plant height, number of seeds per pod, biological yield and harvest index were the important traits responsible for the divergence recorded.

INTRODUCTION

Lentil (Lens culinaris Medik.) with 2n=14, is one of the most important food legume crop in India, generally grown as rainfed crop during rabi season. Lentil has been originated in East

Mediterranean region, such as Asia Minor and Egypt, from where it diffused eastward to India. Lentil seed is an important source of protein for human consumption, especially in dry areas where it is often the only pulse crop that can be produced under prevailing conditions of low soil fertility and limited moisture. It is one of the principle crop cultivated in semi-arid regions of the world, particularly in the Indian subcontinent, and the dry areas of Middle East. It is relatively tolerant to drought and is grown throughout the world. Globally, lentil represents only 5-6% of the total area under pulse. It is predominantly grown in Asia which accounts for 80-95% global area and production, respectively (Malik, 200 5). However, even now over 2/3rd of the cultivated area is un-irrigated and productivity in these areas can only be increased by the development of crops that are well adapted to dry conditions. In India, lentil occupied 1.59 million hectare area with 0.94 million 60 tons production and productivity of 591 kg per hectare in 2011 (Anonymous, 2012). About a third of the worldwide production of lentil is from India, most of which is consumed in the domestic market. India has the largest cultivated area of pulse in the world, but average productivity is very low, and the production is not sufficient to meet the per capita requirement. Pulses shortfall may increase to 6.8 million tons by 2020-21 and the anticipated increase in per capita consumption of pulses from 9 kg per year in 2007-08 to 10.9 kg by 2020- 21 (Joshi, 2009). The genetic reconstruction of plant is required for developing high yielding varieties by incorporating and improving the characters. Yield improvement through genetic means usually comes from exploitation of new germplasm or traits. Germplasm serves as the most valuable natural source in providing needed attributes for developing desirable improved varieties (Hawkes, 1981).Genetic diversity has been considered as an important factor in discriminating the genotypes for selecting genetically diverse parents for obtaining high yielding lines for efficient and successful hybridization programme. The utility of techniques like Mahalonobis D^2 analysis to detect divergence in a group of genotypes and to identify genotypes which can effectively be used in crossing programme has been stressed repeatedly. Potential source of genes for different characters can be identified by taking into consideration the clusters of genotypes which excel in each traits and diversity

between the genotypes. In the present investigation, genetic diversity in a set of 50 genotypes of lentil has been assessed by Mahalanobis D^2 statistic for yield and yield related components.

MATERIAL AND METHODS

The experimental material comprising of 50 genotypes of lentil (*Lens culinaris* Medik.) collected from Indian Agricultural Research Institute, New Delhi. Each genotypes were raised in 4 rows of 3 meter length in Randomized Block Design (R.B.D.) with three replications during *rabi* 2015-16 and 2016-17 at Research farm, Department of Genetics and Plant Breeding, Post Graduate College Ghazipur, (U.P.), India. A spacing of 45 and 10 cm. was followed between rows and plant respectively. Observations were recorded on 11 quantitative characters *viz*. days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height, number of pods per plant, number of seeds per pod, 100-seed weeight, biological yield, seed yield per plant and harvest index. D^2 analysis was carried out as per Mahalanobis (1936).

RESULTS AND DISCUSSION

The analysis of variance exihibited significance differences among the varieties for all the characters studied based on D^2 values, 50 genotypes were grouped into 7 clusters (Table 1) according to the method described by Rao (1952). The cluster strength varied from 7 clusters 13 to 1 in cluster II and V. The cluster II have the maximum number of genotypes (13) and cluster V (1). The pattern of distribution of these germplasm lines into 7 clusters clearly showed the existence of diversity among the material studied. The distribution of genotypes from different eco-geographical regions into these clusters was apparently random (Jeena and Singh, 2002). Genotypes of similar origin were grouped into different clusters and vice versa, thereby indicating non-relationship between geographical and genetic diversity. The tendency of

genotypes to occur in clusters cutting across geographical boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity (Sihag et al., 2004). This also suggested that the genotypes within cluster may have some degree of ancestral relationship. Similar findings were also reported by Sirohi et al. (2007), Solanki et al. (2007) and Kumar et al. (2004). The genetic divergence is an outcome of several factors such as changing of breeding material, genetic drift, natural variation and artificial selection other than ecological and geographical diversification (Sirohi and Dar, 2009). Therefore, selection of parents for hybridization should be based on genetic diversity rather than geographic diversity to get more heterotic recombinants and desired transgressive segregants. However, caution should be taken in selecting divergent genotypes because such crosses may not yield proportionate heterotic response (Subhashchandra et al., 2009). Therefore, a hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high means for almost all component traits. Furthermore, these divergent parents should have better combining ability to give results for proportionate to heterotic response. In 1981 Anunachalum also observed that the more diverse parents are within their overall limits of fitness, the greater chances of heterotic expression of F1s and a broad spectrum of variability in segregating generations.

The average intra and inter cluster distances are presented in Table 2. The intra cluster distance ranged from 0.00 to 2.157 for cluster V and VII respectively and did not transgress the limits of any of the cluster distances. Cluster V and VII were the most diverse, the inter cluster distance between them(7.191) being maximum. Hybridization between genotypes falling in the most distant cluster V and VII showed result in maximum hybrid vigour and eventually desirable segregates,(Narsinghania *et al*., 1992). Hybridization between genotypes from highly divergent groups could even produce new to and neither unknown gene combinations. Hybridization between genetically distant genotypes to generate promising breeding material has been suggested frequently (Gupta and Singh 1970).

The average cluster for different characters (Table 3) showed that the genotypes included in cluster V had maximum days to maturity, number of secondary branches per plant, number of pods per plant, number of seeds per pod and biological yield. Cluster VI had number of primary branches per plant, 100-seed weight and harvest index , plant height. The genotypes falling into cluster V and VI should result in desirable combinations leading to development of usual genetic stocks and varieties.

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Table 1 : Distribution of 50 genotypes of lentil in different clusters

Number of Clusters	Number of genotypes	Name of genotypes
I	**8**	P-5243, 543-02, 545-02, 537-02, L-68-17-4-2, P-32210, L-620, P-52232
II	**13**	P-125, L-564, P-121, P-28, L-5256, L-40, P-57, P-78, L-4625, P-5, P-16, P-98, P-12.
III	**2**	L-5214, L-6178.
IV	**7**	L-5125, P-10, L-4614, L-7357, L-55, L-7465, P-95
V	**1**	L-532-02
VI	**8**	P-56, P-7, P-109, L-7481, L-63, L-62, P-11106, P-96
VII	**11**	L-7483, 3-22-97, 541-02, 531-02, L-6169, L-7479, P-22, L-5227, L-58, P-106, P-32212

Table 2. : Estimates of average intra and inter cluster distances D^2 for 7 clusters constructed from 50 genotypes of lentil.

Cluster	I	II	III	IV	V	VI	VII
I	**1.565**	4.713	6.235	5.444	4.852	5.866	3.658
II		**1.981**	6.240	3.031	6.643	2.707	3.392
III			**1.580**	4.435	7.115	6.034	4.466
IV				**1.930**	7.031	2.060	2.461
V					**0.00**	7.191	6.009
VI						**1.837**	3.255
VII							**2.157**

Table 3 : Cluster mean values for eleven characters involving 50 genotypes in lentil.

Cluster	Days to 50% flowering	Days to maturity	No. of primary branches/plant	No. of Secondary branches/plant	Plant height(cm).	No. of pods per plant	No. of seeds per pod	100-seeds weight(g)	Seed yield per plant(g)	Biological yield/plant	Harvest index (%)
I	62.19	118.79	2.36	4.00	39.98	59.80	1.66	2.74	2.50	6.87	36.79
II	90.65	124.24	2.67	4.92	47.39	102.36	1.65	1.71	3.06	12.28	26.14
III	80.22	123.94	2.51	3.98	51.21	88.56	1.40	5.26	6.01	16.70	45.92
IV	86.20	123.41	2.70	4.71	48.08	110.30	1.60	2.71	5.99	13.90	35.97
V	56.67	118.89	3.36	3.05	42.72	46.53	1.57	2.82	2.21	5.68	42.31
VI	90.87	124.43	2.94	5.18	46.77	113.31	1.71	2.58	4.89	15.13	33.33
VII	78.16	119.46	2.53	4.39	46.23	110.36	1.67	3.12	4.88	12.33	40.70