GENETIC DIVERGENCE IN LENTIL

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ABSTRACT

Fifty genotypes of lentil (*Lens culnaris* Medik) were evaluated under eight environments for seed yield and its associated traits. All the genotypes were grouped into seven clusters. The composition of various clusters varied from 2 to 12. Clustering pattern revealed the distribution of the genotypes belonging to the same origin in more than one cluster indicating non-parallism between geographic and genetic diversity. Members of cluster II and VII were highly diverse from each other as these clusters showed maximum inter-cluster distance. The entries of cluster VII showed the highest mean values for number of primary branches[-1], biological yield plant[-1], seed yield plant[-1] and 100-seed weight. The promising genotypes for seed yield, 100-seed weight, pods plant[-1], seeds pod[-1] and early maturity were identified from cluster II and VII on the basis of mean values which could be utilized for hybridization programme for the development of high yielding genotypes.

Key Words: Clusters, genotypes, *Lens culnaris*

RÉSUMÉ

Cinquante génotypes de lentille (*Lens culnaris* Medik) étaient évalués dans huit environnements pour le rendement en grains et les caractères associés. Sept groupes de genotypes de compositions 2 à 12 étaient considérés. Le modèle de regroupement a révélé une distribution des genotypes appartenant à la même origine dans plus d'un groupe, indiquant qu'il n'y a pas de parallelism entre les diversités géographique et génétique. Les membres du groupe II et VII ont été très diverses les uns des autres avec une distance maximale entre les groupes. Les entrées du groupe VII ont montré des valeurs moyennes plus élevées du nombre de branches primaires par plante, le rendement biologique par plante, le rendement en grains par plante et le poids de 100 grains. Les génotypes prometteurs pour le rendement grains, le poids de 100 grains, le nombre de gousses par plant, le nombre de grains par gousse et la maturité précauce éaient identifiés à partir du groupe II et VII sur base des valeurs moyennes qui pourraient être utilisées dans le programme d'hybridation pour le développement de génotypes à haut rendement.

Mots Clés: Groupes, génotypes, *Lens culnaris*

INTRODUCTION

Among pulses, lentil (*Lens culnaris* Medik) with 2n=14 is one of the most important grain legume crop in India. It is one of the principal pulse crops cultivated in semi-arid regions of the world, particularly in the Indian sub-continent, and the dry areas of Middle East (Malik, 2005). It is estimated that India's population will touch nearly 1.35 billion by 2020 and will require 30 million tonnes of pulses as against the present production of 16.5 million tones (Anonymous, 2007). Clearly, a quantum jump is required in the total production of pulses to increase the per *capita* availability and to meet the challenges of increasing population. Conventional strategies for increasing the production of pulses include development and utilisation of improved plant

varieties, production technologies and plant protection measures which are expected to reduce the existing gap in production and requirement of pulses.

The genetic reconstruction of plant type is required for developing high yielding varieties by improving yield component characters. The available genotypes will serve as the most valuable material reservoir for providing the desirable plant attribute for obtaining the high yielding crop varieties (Hawkis, 1981). The present study was conducted with an objective of selecting divergent parents for future use in improvement of lentil.

MATERIALS AND METHODS

Fifty genotypes of lentil obtained from National Bureau of Plant Genetic Resource, New Delhi, India were evaluated in Randomised Block Design with three replications during *rabi* season of two consecutive years 2006-07 and 2007-08 at Crop Research Farm, Kisan (PG) College, Simbhaoli (28^0N, 51^0E), Ghaziabad (UP) India. The soil type of the experimental field was sandy loam with low available nitrogen (Subiah and Asija, 1956), medium available phosphorus (Olsen *et al*., 1954) and high potassium with neutral pH (Jackson, 1967). In each of the eight environments (2 sowing dates x 2 fertiliser doses x 2 years), each genotype was sown in field of three meter length spaced 20 cm apart with intra row spacing of 10 cm. Eight environments were created by manipulating the dates of sowing and fertiliser doses with N: P: S kg ha^{-1} 20:40:20 and 10:20:10, dates of sowing as 1st November and 1st December. All recommended cultural practices and plant protection measures were followed to raise a healthy crop.

Data were recorded on 11 agronomical characters, namely days to 50% flowering, days to maturity, primary branches plant^{-1}, secondary branches plant^{-1}, number of pods plant^{-1}, plant height, seeds pod^{-1}, biological yield plant^{-1}, seed yield plant^{-1}, 100-seed weight, and harvest index from 10 randomly selected plants in each genotype at various phenophasis of the crop. Days to 50% flowering and days to maturity were recorded on plot basis.

The pooled data were subjected to multivariate analysis as suggested by Mahalanobis (1936) and genotypes were grouped into different clusters based on Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The pooled analysis of variance revealed significant differences among genotypes for all the characters studied during both the years (Table 1) and thereby, indicating existence of a good amount of genetic variability. All the genotypes differed from each other with respect to these characters. Through multivariate analysis, the fifty genotypes were grouped into seven clusters based on D^2 values (Table 2). The composition of different clusters varied from two to twelve genotypes. Cluster III comprised of twelve genotypes followed by cluster IV and V consisting of nine genotypes each. There were seven genotypes in clusters I and II, and four genotypes in cluster VI, while cluster VII had only two genotypes. 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. This 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 suggests 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.* (2000) 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 hybridisation should be based on genetic diversity rather than geographic diversity to get more heterotic recombinants and desired

TABLE 1. Analysis of Variance for 11 traits of 50 genotypes of lentil on the basis of two year pooled data

Clusters	df	Days to 50% flowering	Days to maturity	Primary branches plant⁻¹	Secondary branches plant⁻¹	Number of pods plant⁻¹	Plant height (cm)	Seeds pod⁻¹ plant⁻¹ (g)	Biological yield	Seed yield plant⁻¹	100-seed weight (g)	Harvest index (%)
Replication	2	226.63	31.00	1.71	0.56	3.63	8.97	1.71	3.91	0.219	0.033	14.63
Genotypes	49	2529.24**	3325.84**	2.09**	21.56**	2601.01**	125.05**	0.176**	316.41	29.50**	36.09**	49.67**
Error	392	9.76	2.04	2.04	0.44	28.53	2.24	0.120	2.44	0.308	0.028	5.99

** = Significant at P<0.01

transgressive segregants. However, caution should be taken in selecting divergent genotypes because such crosses may not yield proportionate heterotic response (Subhash Chandra $et\ al.$, 2009). Therefore, a hybridisation 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 proportionate to heterotic response. Anunachalum (1981) also observed that the more diverse the parents are within their overall limits of fitness, the greater are the chances of heterotic expression of F_1s and a broad spectrum of variability in segregating generations.

The statistical distances among the different clusters are presented in Table 3. Maximum intra-cluster distance was observed in Cluster VI (2.042), followed by Cluster IV (2.004) indicating wide genetic variability within the genotypes of these two clusters. For inter-cluster distance, the maximum value was observed between Clusters II and VII (6.684) followed by cluster V and VII (6.290), which indicated maximum diversity between the genotypes of these clusters. Therefore, it is suggested that if the diverse genotypes from these groups along with the other desirable attributes are used in breeding programmes, it is expected to through better segregants for high seed yield and yield contributing traits due to non allelic interaction. The minimum inter-cluster distance between Clusters II and V (2.264) indicate that the genotypes of these clusters were genetically least diverse and almost of the same genetic architecture (Jeena and Singh, 2002) Such genotypes can also be used in breeding programmes for developing biparental crosses between the most diverse and closest groups to break the undesirable linkages between yield and its associated traits (Haddad, 2004).

The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 4). Cluster VII having two genotypes L-417 and L-4677 possesses either higher or lower value for most of the traits, justifying its inclusion as a separate cluster. Cluster VII exhibited the maximum mean value for primary branches plant⁻¹, biological yield

TABLE 2.   Distribution of 50 genotypes of lentil in different clusters

Cluster	Number of genotypes	Genotypes included
I	7	L-415, L-393, L-32225, L-412, L-4597, L-416, L-4661
II	7	L-830, K-75, DPL-59, PL-81-18, PL-81-1, MC-6, Pusa-4
III	12	L-308, L-309, L-4676, L-386, L-381, L-4594, L-4148, L-4598, L-4147, L-4596, L-414, L-310
IV	9	L-307, L-4595, L-4674, L-306, L-4618, L-4671, L-395, L-4672, L-4620
V	9	PL-81-41, L-1304, PL-81-71, PL-81-59, PL-81-10, PL-81-53, PL-81-61, PL-234, LC-163-4-1
VI	4	JLS-1, LC-362, PKVL-1, P-22201
VII	2	L-417, L-4677

TABLE 3.   Average inter- and intra (bold values) distances involving 50 genotypes of lentil

Clusters	I	II	III	IV	V	VI	VII
I	**1.630**						
II	4.840	**1.991**					
III	2.816	5.603	**1.746**				
IV	2.686	4.368	3.226	**2.004**			
V	4.181	2.264	5.352	3.354	**1.916**		
VI	4.501	3.534	4.988	4.589	3.034	**2.042**	
VII	2.841	6.684	3.797	4.967	6.290	6.156	**0.030**

plant^{-1}, seed yield plant^{-1} and 100-seed weight. Cluster VI had early maturing genotypes with secondary branches plant^{-1}, pods plant^{-1} and more number of seeds pod^{-1}; whereas cluster II had genotypes with maximum harvest index and early maturity. These results showed that different clusters were superior for different characters.

The parents for hybridisation could be selected on the basis of their large inter- cluster distance for isolating useful recombinants in the segregating generations. The better performing genotypes from Clusters II and VII were identified for all the traits. The genotypes viz., DPL-59, L-830, K-75, PL-81-1 and PL-81-18 were identified as donors for seed pod^{-1} and early maturity. The hybridisation programme involving genotypes L-417, L-4677 from Cluster VII and P-81-18, DPL-59, L830, K-75 and P-81-18 from Cluster II could be under-taken to isolate high yielding segregants, since these genotypes have high yielding potential, more number of primary branches, more biological yield, high harvest index, high 100-seed weight and early maturity with more genetic

distances (Table 5). Therefore, progenies derived from such diverse crosses are expected to show wide spectrum of genetic variability and a greater scope for isolating transgressive segregants in the advanced generations. Hence, these genotypes might be used in a multiple crossing programme to recover transgressive segregants.

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TABLE 4. Cluster mean values for 11 agro-morphological traits

Clusters	Days to 50% flowering	Days to maturity	Primary branches plant⁻¹	Secondary branches plant⁻¹	Number of pods plant⁻¹	Plant height (cm)	Seeds pod⁻¹	Biological yield plant⁻¹ (g)	Seed yield plant⁻¹	100-seed weight (g)	Harvest index (%)
I	63.24	136.19	3.67	6.62	84.62	29.62	1.05	18.59	6.04	4.55	32.54
II	82.38	110.71	3.24	9.19	66.48	27.90	1.52	10.08	3.97	1.91	39.80
III	96.94	145.86	3.94	7.22	86.67	33.31	1.03	20.83	6.83	4.95	32.88
IV	88.48	143.85	3.26	6.48	64.96	28.26	1.07	14.72	4.67	4.83	31.74
V	79.04	111.19	3.19	8.26	60.70	26.33	1.37	10.89	3.54	1.96	32.62
VI	83.25	110.67	3.50	10.08	91.33	30.42	1.58	13.06	3.78	1.89	29.40
VII	53.33	138.00	4.17	7.83	86.50	28.50	1.00	26.82	8.70	5.57	32.47
GM	83.60	129.85	3.52	7.72	75.34	29.45	1.21	15.74	5.17	3.69	33.25
CD at 5%	5.91	3.05	0.90	1.50	8.76	3.54	0.58	2.90	1.02	0.45	6.23

TABLE 5. Potent genetic donors in lentil identified from cluster II and VII for different characters

Characters	Promising genotypes
High seed yield	>8.60: L-417, L-4677
100-seed weight	>5.13: L-417, L-4677
Pods plant-1	>82.33: L-417, L-4677, PL-81-18
Seeds pod-1	>1.67: DPL-59, L-830, K-75, PL-81-1
Early maturity	<110: PL-81-18, PL-81-1, K-75

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