Annals of Arid Zone 40(4): 445-449, 2001

Multivariate Analysis of Lentil (*Lens culinaris* Medik.) under Three Rainfed Environments

I.S. Solanki, D.S. Phogat, B.P.S. Malik and Y.S. Tomer
Department of Plant Breeding, CCS Haryana Agricultural University, Hisar 125 004, India

Abstract: Thirty genotypes of lentil (*Lens culinaris* Medik.), collected from different eco-geographical regions, were used for multivariate analysis under three rainfed environments, viz., 1997-98 (E_1), 1998-99 (E_2) and 1999-2000 (E_3) at CCS HAU, Hisar. The data recorded for different characters (days to 50% flowering, plant height, number of fruiting branches and pods plant^{-1}, 100-seed weight and seed yield plant^{-1}) of each genotype were subjected to multivariate analysis using D^2 statistics. The genotypes were grouped into six clusters each in E_1 and E_2, and seven clusters in E_3 by adopting the Tocher's method. The constitution of different clusters with regard to the genotypes changed significantly in E_1, E_2 and E_3 due to the G x E interaction. The clustering pattern depicted that the genetic diversity was not necessarily parallel to the geographic diversity. Taking into consideration the higher genetic divergence between different clusters, higher difference in cluster means for maximum number of characters and *per se* performance of genotypes in all the environments, the crosses should be attempted between the genotypes from clusters II (LH 96-29, PL4, LH97-17 and LH97-25) and VI (L9-12) in E_1, clusters V (LH82-6 and L4076) and VI (LH97-33) in E_2 and clusters IV (LH 97-15 and LH 97-34) and VI (LH 84-8) in E_3.

Key words: Genetic variability, genotype, *Lens culinaris*, multivariate analysis, yield attributes.

Lentil (*Lens culinaris* Medik.) is one of the important drought-hardy winter food legumes grown on all types of soil (Kant and Singh, 1998). Considerable amount of variability for the economic traits must exist in the germplasm for profitable exploitation following recombination breeding or selection. The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop, such as lentil, to recover transgressive segregants has been repeatedly emphasized (Singh and Tiwari, 1991; Chahota *et al.*, 1994; Kumar, 1998). The more diverse the parents, more are the chances of obtaining the increased spectrum of variability. In the present study, multivariate analysis by means of D^2 statistic (Mahalanobis, 1936), which is a powerful tool in quantifying the degree of divergence at genotypic level, has been used to analyze the data on various traits.

Materials and Methods

The experimental material comprising 30 diverse genotypes of lentil (15 *microsperma* and 15 *macrosperma*) was grown at CCS HAU, Hisar during *rabi* seasons of 1997-98, 1998-99 and 1999-2000, constituting three different environments, i.e., E_1, E_2 and E_3, respectively. In E_2 and E_3, sowing was done after applying pre-sowing irrigation, and after that the crop was raised completely under

rainfed condition following normal cultural practices, whereas in E_1, even pre-sowing irrigation was not applied. In different environments, all the genotypes were planted in the last week of November in a randomized block design with three replications in 4 m long three-row plots with a distance of 22.5 cm between rows and 5 cm between plants within rows. Five competitive plants were taken at random from each plot to record the data on five characters, viz., plant height, fruiting, branches and pods plant^{-1}, 100-seed weight and seed yield plant^{-1}. The data on days to 50% flowering were recorded on plot basis. The data were subjected to the multivariate analysis of D^2 statistic (Mahalanobis, 1936). The genotypes were grouped into different clusters by adopting the Tocher's method described by Rao (1952).

Results and Discussion

The analysis of variance revealed significant variation among the genotypes for different characters under all the environments. Based on D^2 values all the genotypes were grouped into six clusters in E_1 and E_2, and seven clusters in E_3 (Table 1). The genotypes within each cluster were closer to each other than the genotypes grouped in different clusters. Cluster I was the largest comprising 15, 13 and 18 genotypes in E_1, E_2 and E_3, respectively, and clusters possessing single genotype in all the environments were V and VI, except cluster V in E_2 which possessed two genotypes. Cluster VII in E_3 also possessed only one genotype, L4076. Apart from single genotype clusters and also cluster III, all other clusters in atleast one or more than one environment were observed to be

Table 1. Composition of clusters based on D^2 statistic under three environments in lentil

Cluster	Genotype(s) in environment		
	E_1	E_2	E3
I	LH89-48, LH95-12, LH97-10, LH97-17, LH97-19, LH97-29, LH97-32, LH97-33, LH97-34, LH97-35, LH97-36, LH97-38, LH97-39, LH97-53, PL406	LH89-48,LH95-12, LH97-17, LH97-19, LH97-29,LH97-32,LH97-34, LH97-36, LH97-38, LH97-39, LH97-53, L9-12, PL406	LH89-48, LH95-12,LH96-11, LH96-29, LH97-10,LH97-17, LH97-19, LH97-21, LH97-29, LH97-32,LH97-33,LH97-35, LH97-36, LH97-38, LH97-39, LH97-47, LH97-53, PL406
II	LH96-29, LH97-3, LH97-16, LH97-17, LH97-25, LH97-27, PL4	LH84-8, PL4, LH97-1, LH97-3, LH97-16, LH97-25, LH97-27	PL4, LH82-6, LH97-3, LH97-16
III	LH96-11, LH97-15, LH97-21	LH96-11, LH97-15, LH97-21, LH96-29	LH97-1, LH97-25, LH97-27
IV	LH84-8, LH97-1, L4076	LH97-10, LH97-35, LH97-47	LH97-15, LH97-34
V	LH97-47	LH82-6, L4076	L9-12
VI	L9-12	LH97-33	LH84-8
VII	–	–	L4076

Table 2. Average intra-(bold) and intercluster D^2 values under three environments in lentil

Cluster	Environment	Cluster						
		I	II	III	IV	V	VI	VII
I	E_1	**21.0**	120.0	44.1	112.2	57.7	34.3	–
	E_2	**20.4**	155.1	57.0	31.3	195.0	46.4	–
	E_3	**99.0**	278.9	384.8	162.4	338.4	612.4	377.6
II	E_1		**16.3**	45.7	35.0	131.7	186.3	–
	E_2		**17.2**	69.7	162.7	53.5	173.2	–
	E_3		**97.5**	228.4	191.5	471.0	486.8	223.1
III	E_1			**19.0**	34.6	62.7	74.3	–
	E_2			**18.3**	97.8	122.2	44.7	–
	E_3			**90.2**	440.6	260.2	45.4	264.3
IV	E_1				**5.7**	97.2	133.6	–
	E_2				**19.8**	175.4	103.3	–
	E_3				**90.8**	402.1	744.8	403.6
V	E_1					**0.0**	46.0	–
	E_2					**21.9**	258.1	–
	E_3					**0.0**	240.8	662.4
VI	E_1						**0.0**	–
	E_2						**0.0**	–
	E_3						**0.0**	451.8
VII	E_1							**0.0**
	E_2							**0.0**
	E_3							**0.0**

heterogeneous, which included genotypes from different eco-geographic regions. This situation indicated no parallelism between genetic diversity and geographical distribution. Similarly, the genotypes having a common geographic origin were grouped into different clusters, which suggested that the genetic drift and consequently the selection could cause greater genetic diversity as compared to the geographic distance. These observations are in agreement with the results obtained earlier in lentil (Chahota *et al.*, 1974; Singh and Tiwari, 1991; Kumar, 1998). The geographic diversity, though important, may not be the only factor in determining the genetic divergence. The genetic diversity is the outcome of several factors, including the geographic diversity. Therefore, the selection of varieties for hybridization should be based on genetic diversity rather than the geographic diversity.

The intracluster D^2 values varied from 0.0 (clusters V and VI) to 21.0 (cluster I) in E_1, from 0.0 (cluster VI) to 21.9 (cluster V) in E_2 and from 0.0 (clusters V, VI and VII) to 99.0 (cluster I) in E_3, indicating considerable diversity between different clusters (Table 2). Similarly, the intercluster divergence values varied from 34.3 (between clusters I and IV) to 186.3 (clusters II and VI) in E_1, from 31.3 (clusters

Table 3. Mean performance of different clusters for various characters under three environments in lentil

Cluster	Environment	Days to 50% flowering	Plant height (cm)	Fruiting branches plant^{-1}	Fruiting pods plant^{-1}	100-seed weight (g)	Seed yield plant^{-1} (g)
I	E_1	79.12	37.19	8.00*	79.19	1.63	2.00*
	E_2	79.57	34.88^{X}	7.31	63.71	1.57^{X}	1.71
	E_3	90.19	41.86	7.51	55.00	1.75^{+}	1.55
II	E_1	78.72*	39.89	9.47	82.22**	2.68**	2.58
	E_2	78.94	37.17	7.41	61.61	2.62	2.25
	E_3	92.22	48.67	7.95	69.00	2.71++	2.14
III	E_1	79.33	40.00**	8.48	69.78	2.13	2.20
	E_2	77.25	38.00	7.41	59.42	2.06	1.71
	E_3	83.89	40.00^{+}	7.29^{+}	59.89	2.70	2.09
IV	E_1	80.44	39.11	9.62	67.78*	2.58	2.82**
	E_2	81.56^{XX}	35.00	7.88	73.22	1.59	2.10
	E_3	92.50^{++}	55.34^{++}	7.70	50.00^{+}	2.07	1.54
V	E_1	79.00	37.00	14.77**	78.67	1.77	2.30
	E_2	79.83	42.67^{XX}	8.20^{XX}	87.00^{XX}	2.67^{XX}	3.29^{XX}
	E_3	79.00	50.00	9.13^{++}	56.00	1.77	1.53^{+}
VI	E_1	81.00**	32.33*	8.50	71.00	1.43*	2.10
	E_2	76.67^{X}	35.67	5.43^{X}	34.67^{X}	1.60	1.10^{X}
	E_3	78.00^{+}	40.00^{+}	8.97	66.00	2.57	2.60
VII	E_1	–	–	–	–	–	–
	E_2	–	–	–	–	–	–
	E_3	92.00	42.67	8.57	70.67^{++}	2.63	3.10^{++}
General mean	E_1	79.60	37.59	9.81	74.77	2.04	2.33
	E_2	78.97	37.23	7.27	63.27	2.01	2.03
	E_3	86.82	45.51	8.16	60.94	2.31	2.08

*, **; X, XX and +, ++: Lowest and highest values of characters in E_1, E_2 and E_3, respectively.

I and IV) to 258.1 (clusters V and VI) in E_2 and 145.4 (between clusters III and VI) to 744.8 (clusters IV and VI) in E_3. It is obvious that varieties with narrow genetic base are affected more by seasonal variation than those with broad genetic base, particularly under rainfed conditions. Under such circumstances, availability of genetically diverse genotypes for hybridization program becomes more important. In E_1, the highest genetic distance (186.3) among genotypes existed between cluster II and VI, followed by IV and VI (133.6). Similarly, in E_2, clusters V and VI (258.1), followed by I and V (195.0), and in E_3, clusters IV and VI (744.8), followed by V and VII (662.4) depicted the higher intercluster divergence, suggesting that the hybridization among genotypes from these distantly related

clusters would produce heterotic hybrids and desirable transgressive segregants in further generations.

This diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 3). A comparison of the mean values in the most diverse clusters in all the environments showed marked variation with respect to seed yield and other traits. Overall, clusters II, V and VI were observed to possess higher mean for different characters in E_1, E_2 and E_3, respectively, whereas cluster VI in E_1 and E_2, and cluster IV in E_3 possessed lower mean for majority of the traits. On the basis of cluster means, most of the characters studied, except days to 50% flowering, could be considered responsible for creating divergence and differentiation among genotypes in lentil (Singh and Tiwari, 1991; Kumar, 1998).

Therefore, hybridization involving the genotypes from clusters with the highest genetic distance, higher difference in cluster mean for maximum number of yield contributing characters and *per se* performance in all the environments, as discussed above, is advocated in the breeding program in order to achieve high degree of heterosis as well as higher number of transgressive segregants in further generations. On the basis of above criteria and results of the present study, the crosses should be attempted between genotypes mainly from clusters II (LH96-29, LH97-17, PL4 and LH97-25) and VI (L9-12) in E_1, cluster V (LH82-6 and L4076) and VI (LH 97-33) in E_2 and clusters IV (LH 97-15 and LH 97-34) and VI (LH 84-8) in E_3.

References

Chahota, R.K., Sharma, S.K. and Lal, C. 1994. Genetic divergence in *microsperma* lentil. *Legume Research* 17: 132-134.

Kant, L. and Singh, D.P. 1998. Transgressive segregation of yield and yield components in lentil. *Indian Journal of Genetics and Plant Breeding* 58: 343-347.

Kumar, R. 1998. Genetic architecture of plant type in lentil (*Lens culinaris* Medik.). *Ph.D. Thesis*, Chaudhary Charan Singh University, Meerut, U.P., India.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Journal of Genetics* 41: 159-193.

Rao, C.R. 1952. *Advanced Statistical Methods in Biometrical Research.* John Wiley & Sons Inc., New York: 390.

Singh, B.R. and Tiwari, A.S. 1991. Analysis of biological diversity and disease resistance in lentil (*Lens culinaris* Medik.). *Abstracts: Golden Jubilee Symposium on Genetic Research and Education: Current Trends and the Next Fifty Years.* Indian Society of Genetics and Plant Breeding, New Delhi: 171.