Indian J. Pl. Genet. Resources 4(2): 41-49, 1991

ANALYSIS OF GENETIC DIVERSITY IN INDIGENOUS AND EXOTIC *MACROSPERMA* LENTILS

R.K. Chahota and S.K. Sharma

Department of Plant Breeding & Genetics,
Himachal Pradesh Krishi Vishwa Vidyalaya,
Palampur - 176 062 (Himachal Pradesh)

Forty two genotypes of large seeded (macrosperma) lentils, both indigenous and exotic, were evaluated to study the nature and magnitude of genetic diversity by using Mahalanobis's D^2 statistic and canonical analysis. All the genotypes were grouped into 14 clusters. Days to flowering and maturity, seeds per pod and seed yield per plant were important characters in differentiation among the germplasm entries from different geographical regions. Genotypes originating from a particular geographical region grouped into the same or different clusters. Based upon the clustering pattern and performance of genotypes in different clusters, a breeding programme can be initiated for the genetic improvement of macrosperma lentils by crossing L-2961 with L-3991-24 and L-1646 and selecting the recombinants combining the higher seed yield and earliness in the segregating generations.

There is existence of two complexes within the cultivated lentils; the small-seeded (microsperma) and large-seeded (macrosperma). The small-seeded lentils, insensitive to environmental stresses and photoperiod are grown east of Pakistan during winter. The large-seeded lentils, adapted to long days, sensitive to environmental stresses are grown in Afghanistan westward during spring. The latter possesses useful genetic traits such as large-seed size, upright and taller growth habit. So far, *microsperma* attempts have only been made to improve the genetic potential of *microsperma* lentils by introgressing certain desirable characters from *macrosperma* gene pool. However, efforts have not been made to improve the *macrosperma* lentils alone by combining genes scattered in the *macrosperma* gene complex. Hence, there is an urgent need to undertake suitable breeding programme to seek the genetic upgradation of *macrosperma* lentils. Precise information on the nature and degree of genetic diversity present in *macrosperma* lentils

could help in the choice of desirable parents for evolving superior varieties (Moll *et al.*, 1962; Miller and Marani, 1963). Based upon the consideration, multivariate analysis by means of Mahalanobis's D^2-statistic has been used in identifying genotypes to initiate an appropriate breeding strategy to develop suitable varieties in *macrosperma* lentils.

MATERIALS AND METHODS

The materials for the present study comprised 42 *macrosperma* genotypes. Of these, 18 and 24 were of indigenous and exotic origin, respectively. These genotypes were grown in a randomized complete block design with three replications at the Experimental Farm, Himachal Pradesh Krishi Vishwa Vidyalaya, Palampur, located in north-western Himalayas (32°6'N, 76°3'E, 1290m above msl). Each entry was grown in a single 1.5m long row with inter-row distance of 45 cm. The plant to plant distance was 2-3cm. Days to 50 percent flowering and maturity were recorded. Five plants were selected at random in each plot for recording observations on first pod height (cm), Plant height (cm), primary branches per plant, flower clusters per plant, pod clusters per plant, pods per cluster, seeds per pod, pods per plant, seeds per plant, 100-seed weight (g), harvest index (%) and seed yield per plant (g). Protein content (%) was estimated from the pooled sample derived from five plants. The estimation of protein (N% × 6.25) content was done by conventional micro-kjeldhahl method.

Analysis of variance and covariance were done on the basis of mean values of each plot. A simultaneous test of significance of the differences in the mean values of the 15 variables for 42 genotypes was applied using the wilk's criterion as described by Rao (1952). The computerised D^2 values were arranged in an ascending order. Treating D^2 as the square of a generalised distance, all the genotypes were grouped into a number of clusters following the method described by Tocher (Rao, 1952). After finding out the clusters, the square root of the average D^2 between any two clusters was used to represent the relative disposition of the clusters diagramatically. The data were also subjected to canonical analysis (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance revealed that the entries differed among themselves for each of the 15 characters studied (Table 1). Wilk's criterion (λ) also revealed highly significant differences among them for the aggregate of all characters ($\chi 2$ = 1641.84 for df. 615). D^2 values were computed which ranged from 11.47 (LG-171 and L-1633) to 631.31 (L-4163 and L-2297). After computing the individual D^2 values, 42 genotypes were grouped into fourteen clusters such that within individual cluster they had smaller D^2 values among themselves than those belonging to any two different clusters

Table 1. Analysis of variance for 15 characters

Characters	Mean sum of squares (MSS)	
	Genotypes	Error
Days to flowering	1197.27*	10.18
Days to maturity	11.13*	0.58
First pod height	18.57*	6.78
Plant height	26.76*	9.34
Primary branches/plant	2.47*	1.06
Flower clusters/plant	641.16*	299.77
Pod clusters/plant	258.63*	147.81
Pods/cluster	0.22*	0.14
Pods/plant	526.49*	238.93
Seeds/pod	0.16*	1.74
Seeds/plant	1020.67*	315.34
100-seed weight	1.14*	0.72
Harvest index (%)	119.22*	52.76
Protein (%)	7.49*	0.41
Seed yield/plant	0.76*	0.34

*Significant at P = 0.05
Degrees of freedom: Genotypes = 41; Error = 82
Note: MSS for replications was non-significant for all traits

(Table 2). The cluster II included the highest number of genotypes (7), followed by V(5), II and III (4), VI and XIII (3) and VII to XII (2). Cluster XIV had one genotype. The group constellation obtained by D^2 analysis could also be confirmed by canonical analysis. The small discrepancy in the relative disposition of entries in the chart could possibly be due to the fact that the first two canonical roots accounted for only 78 per cent of the total variation. To obtain an explicit two dimensional representation, contribution of the first two canonical roots should be more than 95 per cent.

The composition of each cluster in *macrosperma* lentils revealed that genotypes originating from a particular geographical region were not only grouped into the same cluster, but also into different clusters (Table 2). Of 42 genotypes, 16 of near Mediterranean countries were distributed in 10 clusters, 20 of south east Asia in 11, 3 of Asia Minor in 3 and 3 of New World in 3. The results could not establish a paralelism between geographical and genetic diversity. The explanation for grouping genotypes with the same geographical origin into different cluster may be due to different genetic background and wide divergence in features, which might have resulted on account of free exchange of materials among different regions of the world

Table 2. Distribution of *macrosperma* genotypes in relation to their origin

Cluster	Total genotypes in the cluster	Genotypes	Origin
I	4	L-2979	Asia Minor
		LG-171, L-1633 and L-1644	South-east Asia
II	7	L-2114	Asia minor
		L-178 and L-3991-11	South-east Asia
		L-24123, L-24118, L-4026 and L-2117	Near Mediterranean
III	4	L-3991-25 and L-4076	South-east Asia
		L-4047	New World
		L-4224	Near Mediterranean
IV	3	L-3038	New World
		L-4228	Near Mediterranean
		LH-82	South-east Asia
V	5	L-4152 and L-416	South-east Asia
		L-3355, L-3284 and L-3293	Near Mediterranean
VI	3	HPL-4 and L-4163	South-east Asia
		L-4266	Near Mediterranean
VII	2	L-1646 and L-3991-24	South-east Asia
VIII	2	L-2297	Asia minor
		L-3034	Near Mediterranean
IX	2	L-4048 and LL-4163	South-east Asia
X	2	L-3991-29 and PL-81-3	South-east Asia
XI	2	L-3046 and L-165446	Near Mediterranean
XII	2	K-303	South-east Asia
		L-3286	Near Mediterranean
XIII	3	Precoz	New World
		L-3991-30	South-east Asia
		L-3304	Near Mediterranean
XIV	1	L-2961	Near Mediterranean

either for direct introduction or for breeding puposes. Genetic drift and selection in different environments could be other important factors contributing to the divergence. Therefore, the selection of genotypes for hybridization with a view to get the maximum chance of identifying transgressive segregants of practical utility should be baed on genetic rather than geographic diversity. Suryawanshi *et al.* (1985) and Sharma and Luthra (1987) reported similar results for hybridization in *microsperma* lentils.

The inter and intra-cluster distances (D) are given in Table 4 and Fig. 1. The intra-cluster distances ranged from 4.89 (cluster V) to 10.70 (cluster XIII). The inter-cluster distance ranged from 6.35 (cluster VI and XIII) to 23.17 (cluster VI and VIII). The dispersion matrix used for D^2 analysis was also utilized for canonical analysis. The first canonical root (λ_1) accounted for 63.5 percent of the variation, while the second root (λ_2) for 15.0% (Table 3). The coefficients of the first two canonical vector, Z_1 and Z_2 indicated that days to flowering and maturity, seeds/pod and seed yield/plant constituted the major axis of differentiation. Besides days to flowering, plant height and protein (%) constituted the second axis of differentiation. Characters such as days to flowering and maturity are related to the photoperiodic response, seem to have contributed to the genetic divergence under natural selection. Similarly, first pod height, plant height and protein (%) appear to have contributed towards genetic divergence through both natural and human selection.

The highest inter-cluster value (23.17) indicated that cluster VI comprising three genotypes, viz., L-4266, L-4163 and HPL-4, were the most divergent

Table 3. Coefficients of first two canoical vectors

Vector	Characters							
	Dys to flower-ing	Days to maturity	First pod height	Plant height	Primary branches/ plant	Flower clusters/ plant	Pod cluster plant	
Z_1	0.901	0.236	0.042	–0.052	–0.062	–0.068	–0.121	
Z_2	0.072	–0.322	0.029	0.106	0.045	0.069	0.016	
	Pods/ cluster	Pods/ plant	Seeds/ pod	Seeds/ plant	100-seed weight	Harvest index (%)	Protein (%)	Seed yield plant
Z_1	0.001	–0.082	0.144	–0.197	0.009	0.065	0.044	0.176
Z_2	0.011	–0.022	–0.029	0.013	0.005	0.061	0.926	–0.088

$\lambda_1 = 63.369$; $\lambda_2 = 15.027$

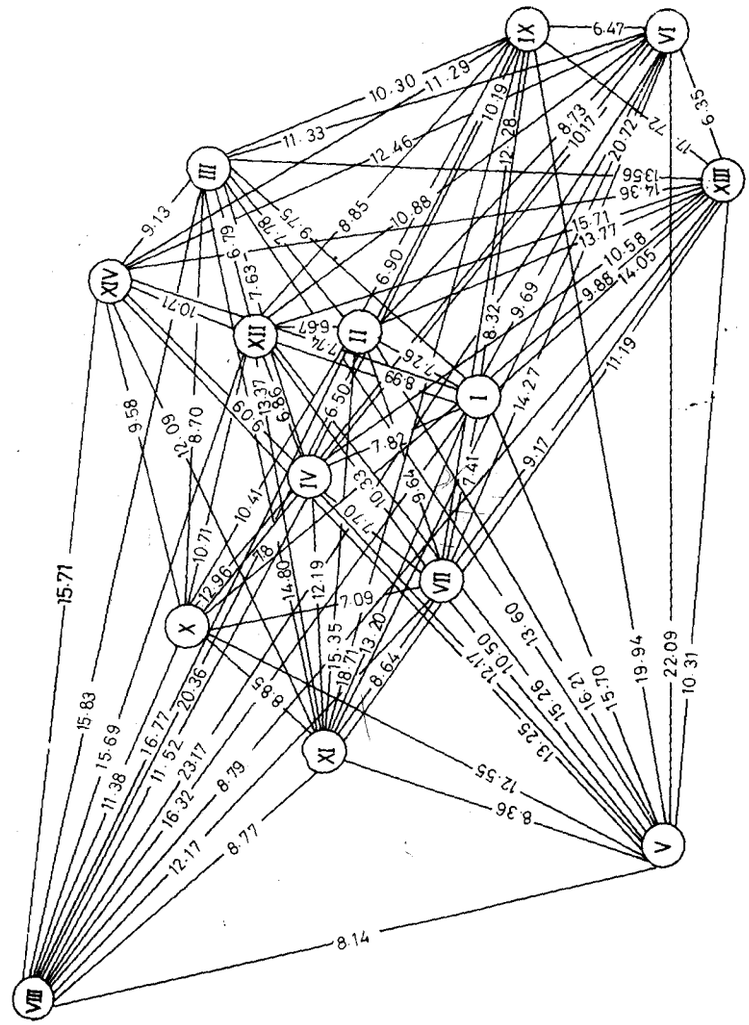

Fig. 1 Spatial distribution of different clusters and their inter-relationships based on D values

Table 5. Cluster means for 15 traits in macrosperma lentil

Cluster	Trait														
	Days to flowering	Days to maturity	First pod height (cm)	Plant height (cm)	Primary branches/plant	Flower clusters/plant	Pod clusters plant	Pods/cluster	Pods/plant	Seeds/pod	Seeds/plant	100-seed weight (g)	Protein (%)	Harvest index (%)	Seed/yield/plant (g)
I	128.30	183.58	11.96	25.46	3.37	50.68	21.70	1.87	28.43	1.21	34.97	2.89	33.44	23.51*	1.41
II	132.69	181.33	12.37	26.54	4.40	46.03	19.49	2.01	26.78	1.03	28.67	3.10	42.08**	26.02	1.38
III	124.33	181.67	13.19	26.84	3.82	40.73	24.12	2.18	31.25	1.36	44.54	2.24	40.84	28.47**	1.42
IV	121.33	180.99	10.72	26.61	5.32**	52.43	25.91	1.65**	34.41	1.00*	38.33	2.78	30.08	25.83	1.30
V	88.21*	181.73	12.01	24.19	3.29	38.39	19.99	1.97	27.36	1.33	37.99	2.72	30.35	26.41	1.27
VI	148.71**	183.67	12.34	25.39	4.30	42.48	13.87	1.95	20.32*	1.22	23.77	3.00	28.20	26.56	1.18
VII	111.48	148.50*	9.23*	23.06	3.11*	26.12*	15.80	2.31	24.15	1.25	29.45	2.69	28.67	24.61	1.13*
VIII	89.26	178.33	10.2	21.55*	4.17	28.51	11.71*	1.78	20.50	1.26	16.73*	3.00	36.20	24.78	1.18
IX	143.11	181.83	15.15	28.60	3.71	48.85	15.51	2.41**	22.67	1.36	27.61	2.10	27.03*	25.42	1.17
X	116.97	182.67	11.81	31.67**	3.41	42.10	22.51	2.11	29.23	1.05	38.13	3.08	31.50	26.56	1.56
XI	91.20	184.00	11.76	28.31	3.46	33.12	28.47	1.78	25.50	1.28	29.31	4.06**	33.80	23.53	1.90
XII	131.26	180.00	11.16	27.15	3.92	40.11	26.78	2.00	33.83	1.33	49.08	1.95	40.89	26.73	1.21
XIII	102.48	178.78	10.24	29.38	3.33	45.84	30.26**	1.97	38.13	1.19	30.90	2.74	33.90	25.37	1.60
XIV	118.37	185.33**	16.10**	26.03	4.57	73.77**	25.43	2.10	64.43**	1.83**	75.40**	1.93*	35.43	25.60	2.13**

*Minimum and **maximum value

Table 4. Intra-and inter-cluster average divergence ($\sqrt{D^2}$) values of 14 clusters

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	6.21	7.26	9.75	7.82	15.70	9.69	7.41	16.32	8.25	10.25	13.20	8.99	14.05	7.74
II		5.44	7.78	6.50	16.21	8.73	9.64	16.77	6.90	10.41	15.35	6.67	13.77	9.80
III			5.38	7.63	13.60	11.35	9.39	15.83	10.30	18.70	14.80	6.79	13.56	9.13
IV				4.92	12.17	12.96	7.70	11.52	10.19	7.84	12.19	6.86	10.58	9.09
V					4.89*	22.09	10.50	8.14	19.94	12.55	8.36	15.26	10.31	13.25
VI						5.69	14.27	23.17**	6.47	15.05	20.72	10.88	6.35*	12.46
VII							5.17	12.17	12.28	7.09	8.64	10.33	9.17	7.13
VIII								5.53	20.36	11.38	8.77	15.69	8.79	15.71
IX									5.33	13.89	18.71	8.85	17.24	11.29
X										6.18	8.85	10.17	9.88	9.58
XI											6.89	13.37	11.19	12.09
XII												7.42	15.71	10.17
XIII													10.70**	14.36
XIV														—

* Minimum and ** maximum value.

from cluster VIII having L-2297 and L-3034 genotypes. Although the genotypes of cluster VI and VIII had the maximum diversity, yet their performance for seed yield and its various components was poor (Table 5). Hence, these genotypes may not be direct choice for the hybridization programme. In autogamous species, while considering genetic diversity for the selection of the parents to be included in hybridization programme, yielding potential of clusters should also be considered. The only genotype L-2961 of cluster XIV had the highest flower clusters/plant, pods/plant, seeds/plant, seeds/pod and seed yield. However, it had the maximum first pod height and late maturity, which are not desirable traits for the improvement of *macrosperma* lentils. So, these traits should be complemented with the desirable traits of other clusters. Genotypes L-3991-24 and L-1646 of cluster VII were desirable for the early maturity and the lower first pod height. The genetic diversity between these two clusters was substantial ($\sqrt{D^2} = 12.46$). The genetic upgradation of *macrosperma* lentils seeks to require high yield with early-medium maturity. Based upon this consideration, a breeding programme for the genetic amelioration of *macrosperma* lentils could be envisaged by crossing genotypes of cluster XIV (L-2961) with the genotypes of cluster VII (L-3991-24 and L-1646), and selecting the transgressive segregants of practical utility. Useful heterobelteosis may also be obtained by intercrossing genotypes of clusters VI and VIII, which have otherwise shown poor expression. It is also worthwhile to attempt crosses between clusters having better *per se* performance and average genetic diversity i.e. genotypes of cluster XIV with cluster XI, or cluster XI with cluster III.

REFERENCES

Miller, P.A. and A. Marani. 1963. Heterosis and combining ability in diallel crosses of upland cotton (*Gossypium hirsutum* L.). *Crop Sci.* 3: 441-444.

Moll, R.H., W.S. Salhuana and H.F. Robinson. 1962. Heterosis and genetic diversity in variety of crosses of maize. *Crop Sci.* 2: 197-198.

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

Sharma, P.C. and S.K. Luthra 1987. Genetic diversity in lentil (*Lens culinaris* Med.). *Genet. Agr.* 41: 349-356.

Suryawanshi, R.K., S.K. Rao and C.B. Singh. 1985. Genetic diversity in lentil. *Lens Newsletter* 12: 28-31.