Indian J. Genet., 57 (1): 11–13 (1997)

۱

GENETIC DIVERGENCE IN OPIUM POPPY (PAPAVER SOMNIFERUM L.)

M. M. BHANDARI,^{*} G. S. GUPTA AND RAJENDRA GUPTA

Directorate of Research, Rajasthan Agricultural University Beechwal, Bikaner 334002

(Received: May 3, 1993; accepted: June 1, 1993)

ABSTRACT

Eighteen advanced selections and varieties were grouped into five clusters using D^2 statistic. Clusters comprised 9, 4, 2, 2 and 1 genotypes. Latex yield, capsule husk yield, seed yield, capsule volume, capsule number and capsule breadth were the major contributors to D^2 values. On the basis of wide diversity and highest contributing characters, the crosses IC 88 x IC 85, IC 88 x IC 30, IC 88 x IC 42, IC 128 x IC 85, IC 128 x IC 30 and IC 128 x IC 42 are identified for high level of manifestation of heterosis and production of desired recombinants.

Key words: Genetic divergence, D^2 statistic, opium poppy.

For the choice of diverse parents, and their use in hybridization programme, multivariate analysis with Mahalanobis D^2 statistic has been used extensively as a quantitative measure of genetic divergence among parents in numerous crops. It appears that relatively little information is available on opium poppy [1]. The present investigation is based on a different set of genotypes and characters than reported earlier.

MATERIALS AND METHODS

The material comprised eighteen advanced selections (IC 15, IC 19, IC 30, IC 83, IC 85, IC 88 and IC 128), varieties developed at Udaipur (UO 177-1, UO 177-2), Mandsaur (MOP 16, MOP 319, MOP 379), Lucknow (NBRI 3, NBRI 4) and New Delhi (NBPGR 1, NBPGR 2, IC 42) under All-India Coordinated Project on Medicinal and Aromatic Plants, and Ranjhatak Local. The material was grown at Udaipur in RBD with 4 replications. The plot size was 1.8 x 4 m with 30 x 10 cm planting distance. Ten plants were selected randomly from each plot for recording the data on nine characters.

Present address: Agricultural Research Station, Mandor, Jodhpur 342304.

The data were subjected to analysis of variance and then multivariate analysis of D^2 statistic [2]. The genotypes were grouped into different clusters following the Tocher's method [3]. The relative contributions of different characters towards genetic divergence were also worked out.

RESULTS AND DISCUSSION

The significant treatment mean squares indicated adequate variability among the genotypes for all the nine characters. On the basis of D^2 values for all possible 153 pairs of populations, the 18 genotypes were grouped into five clusters (Table 1). The intra and

intercluster D² values are presented in Table 2. Intracluster D^2 values ranged between 0.0 and 30.3. The intracluster distance was maximum (210.5) between clusters III and IV, followed by that between clusters III and V (142.2). The results revealed that different genotypes from different sources and states were included in different clusters, indicating that genetic diversity and geographic diversity are not related. At least one genotype of Madhya Pradesh was present in all the clusters. The results cannot be compared with earlier work on opium poppy [1] carried out using only exotic collections. Saini and Kaicker [1] had grouped seventy five opium poppy genotypes into twelve clusters. Consequently the intra and intercluster

 Table 1. Cluster composition based on D² statistic in opium poppy

Cluster	No. of genotypes	Genotypes				
I	9	IC 15, IC 19, UO 177-1, UO 177-2, NBPGR 1, NBPGR 2, MOP 319, MOP 379, MOP 16				
II	4	IC 83, NBRI 3, NBRI 4, Ranjhatak Local				
ш	2	IC 88, IC 128				
IV	2	IC 85, IC 30				
v	1	IC 42				

IC — Indigenous Collections; UO – Udaipur Opium Poppy; MOP — Madhya Pradesh Opium Poppy; NBPGR — National Bureau of Plant Genetic Resources; and NBRI — National Botanical Research Institute.

distances reported were also very high. The intracluster D^2 values ranged between 43.9 and 141.8 and intercluster D^2 values were as high as 51001.

Clusters							
	I	II	111	IV	v		
I	22.6	48.9	61.8	97.4	69.0		
П		23.9	124.4	36.7	43.8		
III			30.3	210.5	142.2		
IV				20.5	35.9		
v					0.0		

Table 2. Intra- (in bold) and intercluster D^2 values for five clusters in opium poppy

The traits contributing maximum to divergence are given greater emphasis while deciding about the clusters to be used for the purpose of further selection and choice of parents for hybridization [4]. The highest contributors in this regard were latex yield, capsule husk yield, seed yield, capsule volume, number of capsules per plant, and capsule breadth (Table 3). On considering cluster means in respect of

Character		Contribution to				
	I	Π	III	IV	v	D^2 values (%)
Latex yield (kg/ha)	27.0	22.2	21.7	26.8	27.3	27
Morphine (%)	10.5	10.7	11.3	11.2	12.5	3
Seed yield (q/ha)	8.7	7.3	9.7	6.4	7.3	17
Capsule husk yield (q/ha)	8.8	7.5	9.9	6.4	7.1	25
Plant height (cm)	83.7	82.6	91.3	91.6	96.2	2
Capsules per plant	2.6	2.8	2.9	2.8	2.0	8
Capsule length (mm)	42.2	41.2	43.8	41.9	42.4	1
Capsule breadth (mm)	40.5	39.9	37.3	38.8	34.6	7
Capsule volume (ml)	31.2	30.1	23.9	25.6	22.1	10

Table 3. Cluster means and relative contribution of different characters to D^2 values in opium poppy

these six characters, cluster V for latex yield and low capsule number, cluster III for capsule husk yield and seed yield, and cluster I for capsule volume and capsule breadth are most important. The crosses involving parents from the most divergent clusters are expected to manifest maximum heterosis and generate wide variability in genetic architecture. Thus, crosses between the genotypes of cluster III with IV and cluster III with V would exhibit high heterosis and produce new recombinants with desired traits in opium poppy.

REFERENCES

- 1. H. C. Saini and U. S. Kaicker. 1987. Genetic diversity in opium poppy. Indian J. Genet., 47: 291–296.
- 2. P. C. Mahalanobis. 1936. On the generalised distance in statistics. Proc. Nat. Acad. Sci., India, 2: 49–55.
- 3. C. R. Rao. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley & Sons, New York.
- 4. R. N. De, R. Seetharaman, M. K. Sinha and S. P. Banerjee. 1988. Genetic divergence in rice. Indian J. Genet., 48: 189–194.