

**MULTIVARIATE ANALYSIS IN RELATION TO BREEDING SYSTEM IN
OPIUM POPPY (*PAPAVER SOMNIFERUM* L.)**

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The opium poppy (*Papaver somniferum* L.) is an important medicinal plant of great pharmacopoeal uses. 101 germplasm lines of different eco-geographical origin maintained at National Botanical Research Institute, Lucknow were evaluated to study the genetic divergence for seed yield/plant, opium yield/plant and its 8 component traits following multivariate and canonical analysis. The genotypes were grouped in 13 clusters and confirmed by canonical analysis. Sixty eight percent genotypes (69/101) were genetically close to each other and grouped in 6 clusters (II, III, IV, V, VIII, XII) while apparent diversity was noticed for 32 percent (32/101) of the genotypes who diversified into rest 7 clusters (I, VI, VII, IX, X, XI, XIII). Inter cluster distance ranged from 47.28 to 234.55. The maximum was between IX and X followed by VII and IX (208.30) and IX and XI (205.53). The genotypes in cluster IX, X, XI, and XII had greater potential as breeding stock by virtue of high mean values of one or more component characters and high statistical distance among them. Based on findings of high cluster mean of component trait and inter-cluster distance among clusters, a breeding plan has been discussed.

Key words: opium, multivariate, canonical, cluster, eco-geographical, germplasm

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INTRODUCTION

Opium poppy (*Papaver somniferum* L.) is an important medicinal plant of pharmacopoeal uses. Opium latex and its derivatives are used in different medicines as analgesic, narcotic, sedative, sudorific, hyponitic, antispasmodic, antidiarrhea and cough etc (SINGH, *et al.* 1995a; 1997; PUSHPANGADAN and SINGH, 2001). The present trend is to breed opium poppy for specific alkaloid on one hand and high seed yield rich in oleic – linoleic acid (SINGH *et al.*, 1995b; 1998) on the other hand. To breed desired plant type, the information about the nature and magnitude of genetic variability among base population and the degree of transmission of traits are prerequisite for successful breeding programme. For creating variability crossing among parental lines is the most potent and assured method. However, selection of divergent parent is most important, as the greater genetic divergence among the parents for the characters; better are the chance of releasing the variability (SINGH, 1991; SINGH *et al.*, 1998). Genetic study based on the multivariate analysis is a powerful tool for determining the degree of divergence between populations, the relative contribution of different components to the total divergence and the nature of forces operating at different levels. To focus on this aspect, the present investigation was undertaken in large germplasm lines of opium poppy representing the relics of Indian landraces, improved varieties as well as selections (pure lines) obtained through different sets of intra and interspecific breeding programme maintained at National Botanical Research Institute, Lucknow, India.

MATERIAL AND METHODS

One hundred one germplasm lines of different eco-geographical origin of opium poppy maintained at National Botanical Research Institute, Lucknow, India were grown in Randomized Block Design with 3 replication in experimental plot of Genetics and Plant Breeding Division during 2002-2003 situated between 26°40' N latitude and 80°45' E longitude and at an altitude of 129 m above sea level. The two rows/treatment per replication were sown. The rows were 3m long. The spacing was 30 cm between rows and 10 cm within rows. Basal dose of NPK@ 45 kg, 50 kg and 40 kg/ha was applied before sowing and rest 45 kg nitrogen was applied in two splits at 40 days and 60 days after sowing. Non-experimental rows were sown to check the border effect. Ten plants of each treatment/replication were selected at random before flowering and observations were recorded on days to flowering, plant height (cm), branches/plant, capsules/plant, capsule size (cm²), leaves/plant, capsule weight/plant (g), seed yield/plant (g), husk yield/plant (g) and opium yield/plant (g).

The statistical analysis was done on the mean basis across the genotypes. The difference among population was tested by analysis of variance for individual traits and by Wilk's lambda Criterion for pooled effect of all the 10 characters. D² analysis was done following RAO (1952) to determine degree of differentiation among n(n-1)/2 pairs of 'n' population. Grouping of genotypes was done according to tochor's method (RAO, 1952).

RESULTS AND DISCUSSION

The analysis of plot means revealed significant differences among 101 genotypes for each of ten characters suggesting appreciable variability among the genotypes. The simultaneous testing of significance based on Wilk's (Lambda) criterion also showed significant differences among cultivars for aggregate of all the character (χ^2 1000 df = 1937.40**). The D² values estimated for 101 germplasm lines in $n(n-1)/2 = 5050$ combinations varied from 18.75 to 320.56 indicating the presence of substantial amount of genetic diversity in the population. The 101 genotypes were grouped in 13 clusters depending upon their morphological similarity. The cluster XII was the largest having 13 genotypes followed by clusters II, III, and VIII with 12 varieties in each. The cluster IV and V contains 10 genotypes each. The minimum single genotype was noticed in cluster IX and X followed by cluster VII and VI having 2 and 6 genotypes respectively. Clustering

Table. 1. Composition of different clusters in opium poppy

Clusters	No. of Varieties	Source/origin of varieties
I	8	NC57934 (21), NC57919 (30), NBPGR-1 (32), Vivek (64), Big Cap (65), IS-7 (83), IS-21 (98), IS-23 (99).
II	12	BK (2), M-11 (8), DCG (1), NC57923 (11), NC57913 (12), NC 57921 (31), UO-1185 (33), UO-1785 (38), UO-1885 (39), IC-140 (41), IC-133 (47), Papline (66).
III	12	KDB (7), NC57958 (13), NC57948 (16), NC57945 (19), Dholia (28), Sanchita (63), NBRI-1 (67), MOP-541 (71), MOP-576 (72), ND1001 (73), IS-9 (85), IS-18 (94).
IV	10	ND-7 (17), UO-590 (43), MOP-4 (55), UO-601 (75), IS-01 (76), IS-2-1 (77), IS-2-12 (78), IS-4 (80), IS-20 (96), IS-21 (97).
V	10	SP (6), UO-290 (45), Shyama (61), IS-3 (79), IS-5 (81), IS-11A (87), IS-13 (90), IS-15 (91), IS-16 (92), Shweta (62).
VI	6	MOP-17 (14), NC 57950 (15), UO-1385 (34), UO-1485 (36), IC-128 (42), UO-1285 B (51).
VII	2	NC 57947 (18), UO-1285A (35).
VIII	12	KD (3), MOP-47 (4), Telia (9), NC 57932 (22), DCG-B (27), UO-1585 (37), UO-1985 (40), UO-190 (46), IC-30 (48), GP-74 (50), NBPGR-3 (54), BR0P-1 (70).
IX	1	BR 113 (100)
X	1	GZ (1)
XI	7	NC 57925 (24), Ranjhatak (26), MOP-1047 (56), NBPGR-5 (59), NBRI-6 (69), IS-6 (82), IS-17 (93).
XII	13	NBRI-2 (5), NC 57936 (20), NC 57924 (25), UO-490 (44), IC-131 (49), MOP-1072 (52), ND-1186 (53), NDHS-201 (58), NBPGR-4 (60), NBRI-5 (68), IS-10 (86), IS-19 (95), NBRI-11 (101).
XIII	7	NC 57928 (23), NC 57916 (29), NDHS-101 (57), ND-1002 (74), IS-8 (84), IS-11B (88), IS-12 (89).

* Values in parentheses denote the serial number of germplasms

pattern (Table 1) indicated that majority of genotypes i.e. 69 (68%) were genetically close to each other and grouped in 6 clusters, while apparent diversity was mainly noticed due to 32 genotypes (32%) distributed over 7 clusters. The genotypes involved in clustering are group of Indian land races, improved varieties and selections obtained through different breeding programme maintained at National Botanical Research Institute, Lucknow for the last one decade (SINGH *et al.*, 1997; 1998; 1999). The clustering pattern was also confirmed by spatial distribution of genotypes under canonical analysis. The Distribution pattern of genotypes of diverse origin in a single cluster indicates that the geographical origin in opium poppy was not related to genetic divergence. The tendency of genotypes occurring in clusters cutting across the geographical boundaries demonstrate that geographical isolation need not necessary be related to genetic diversity and was at random (SINGH, 1991; SINGH *et al.*, 2003a). This means that geographical diversity though important may not be factor in determining genetic divergence. The genotypes originating from one place as in present study were scattered in 13 clusters. Such parallelism between geographical distribution and genetic diversity might be due to some forces other than geographical distance like genetic architecture of population, heterogeneity, history of selection, proximity of development of traits etc. Genetic drift may be another cause for genetic diversity.

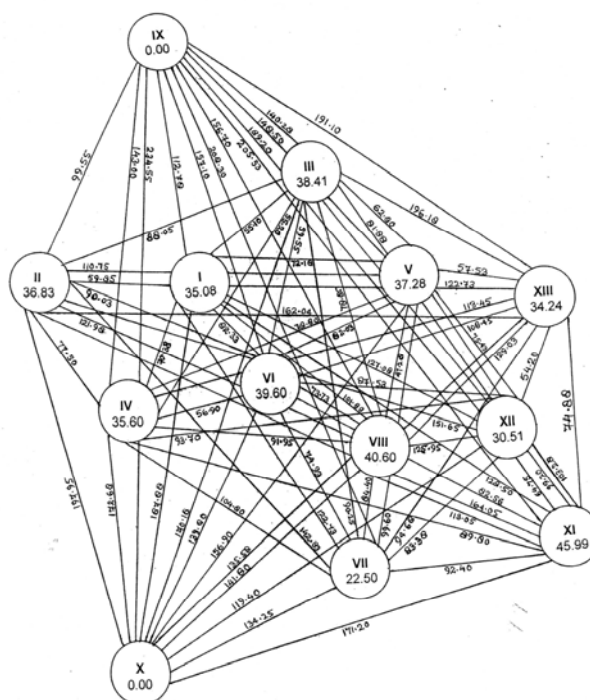


Fig. 1. Statistical distance expressed as linear cluster relationship in opium poppy (*Papaver somniferum* L.)

Table 3. Cluster mean for different characters in opium poppy (*Papaver somniferum L.*)

Clusters	Days to flowering	Plant height (cm)	Branches /plant	Capsules /plant	Capsule size (cm ²)	Leaves/ plant	Capsule weight/ plant (g)	Husk yield/ plant (g)	Seed yield/ plant (g)	Opium yield/plant (g)
I	93.40 ± 0.64	110.6 ± 1.93	1.94 ± 0.19	1.53 ± 0.13	15.49 ± 0.34	15.81 ± 0.55	8.88 ± 0.35	4.09 ± 0.14	4.88 ± 0.25	0.16 ± 0.01
II	98.30 ± 0.45	107.83 ± 1.99	1.69 ± 1.99	1.25 ± 0.07	13.49 ± 3.90	14.96 ± 0.35	8.02 ± 0.39	3.71 ± 0.20	4.29 ± 0.21	0.15 ± 0.01
III	94.88 ± 0.38	115.88 ± 1.17	2.12 ± 0.15	1.67 ± 0.12	16.94 ± 0.50	16.81 ± 0.38	10.83 ± 0.42	4.75 ± 0.27	6.08 ± 0.20	0.23 ± 0.01
IV	97.76 ± 0.43	124.04 ± 1.81	2.13 ± 0.16	1.67 ± 0.11	14.75 ± 0.61	16.71 ± 0.27	10.73 ± 0.36	4.85 ± 0.22	5.85 ± 0.19	0.19 ± 0.01
V	93.09 ± 0.52	112.80 ± 1.96	3.22 ± 0.11	2.40 ± 0.09	15.64 ± 0.37	16.61 ± 0.51	12.12 ± 0.31	4.93 ± 0.19	7.20 ± 0.27	0.17 ± 0.01
VI	97.93 ± 0.58	118.92 ± 1.97	2.33 ± 0.14	1.67 ± 0.10	17.07 ± 0.53	13.83 ± 0.23	12.08 ± 0.76	5.33 ± 0.31	6.79 ± 0.51	0.21 ± 0.02
VII	98.07 ± 0.43	114.62 ± 1.63	2.62 ± 0.31	2.00 ± 0.50	22.12 ± 0.18	15.75 ± 0.25	14.50 ± 1.26	6.75 ± 0.70	7.75 ± 0.50	0.19 ± 0.01
VIII	96.68 ± 0.45	114.10 ± 2.35	3.77 ± 0.08	2.71 ± 0.90	16.02 ± 0.40	16.03 ± 0.31	13.08 ± 0.35	5.77 ± 0.23	7.40 ± 0.21	0.19 ± 0.01
IX	95.10 ± 0.00	94.25 ± 0.00	2.25 ± 0.00	2.25 ± 0.00	8.30 ± 0.00	15.00 ± 0.00	6.00 ± 0.00	2.50 ± 0.00	3.50 ± 0.00	0.15 ± 0.00
X	95.25 ± 0.00	108.25 ± 0.00	2.75 ± 0.00	2.50 ± 0.00	15.70 ± 0.00	11.75 ± 0.00	20.00 ± 0.00	10.50 ± 0.00	9.50 ± 0.00	0.24 ± 0.00
XI	94.06 ± 0.83	125.39 ± 0.30	2.79 ± 0.29	2.18 ± 0.18	19.08 ± 0.65	19.04 ± 0.46	14.07 ± 0.60	6.25 ± 0.38	7.79 ± 0.22	0.28 ± 0.02
XII	95.95 ± 0.46	119.95 ± 1.82	3.12 ± 0.12	2.56 ± 0.08	16.06 ± 0.33	17.01 ± 0.23	15.72 ± 0.27	7.32 ± 0.22	8.40 ± 0.15	0.24 ± 0.01
XIII	92.27 ± 0.24	117.25 ± 0.73	3.64 ± 0.22	2.94 ± 0.10	17.61 ± 0.48	17.27 ± 0.66	14.89 ± 0.49	6.61 ± 0.27	7.29 ± 0.32	0.22 ± 0.01
Mean ± SE	95.66 ± 1.09	115.90 ± 4.66	2.67 ± 8.84	2.06 ± 0.60	16.05 ± 1.38	16.34 ± 1.41	12.07 ± 2.08	5.40 ± 1.09	6.68 ± 1.24	0.20 ± 0.03

The intra cluster value was variable between 0.0 to 45.99 (Table 2, Fig. 1), the maximum being in cluster XI (45.99) followed by VIII (40.26), VI (39.60) and III (38.41). The maximum inter-cluster distance was noticed between IX and X (234.55), followed by VII and IX (208.30), IX and XI (205.53), and II and X (197.45) respectively. This indicates that the genotype of these clusters diverse much to each other. The magnitude of heterosis largely depends on degree of diversity in the parental lines, the higher distance between two clusters, the greater genetic diversity between genotypes. Crosses between genetically diverse parents would manifest more heterosis than the crosses between closely related parents (SINGH, 1991). Hence genetic divergence seems to be more important tool to select perspective parents for crop improvement program.

Considering the cluster means (Table 3) the maximum capsule weight / plant (20.0g), seed yield/plant (9.50 g), husk yield/plant (10.50g) and next to highest opium yield/plant (0.24 g) was noticed in cluster X. This cluster had moderate flowering (95.25 days) and medium plant height (108.25 cm). Contrary to this the cluster IX having single variety (BR113) was separated by other clusters due to lowest mean values of capsule weight/plant (6.0 g), husk yield/plant (2.5 g), seed yield (3.50 g), opium yield/plant (0.15 g), smallest capsule size (8.30 cm²) and plant height (95.10 cm). The low seed yield and opium yield/plant in this cluster is mainly due to smallest capsule size (8.30 cm²). A positive association of capsule size and opium yield was reported by SINGH and KHANNA (1993) and SINGH *et al.* (2003b). Thus selection of medium to large capsule may enhance the opium and seed yield/plant. The cluster IX and X had highest statistical distance with each other and both also exhibited high inter-cluster distance with cluster XI, XII and XIII. The cluster XI is unique and is separated by cluster X due to highest opium yield/plant (0.28 g), leaves/plant (19.04) and tall genotypes (125.39 cm) with medium days to flowering (94.06) and next to highest capsule size (19.08 cm²) and next to third seed yield/plant (7.79 g) and capsule weight/plant (14.79 g).

The genotypes in cluster XII had next highest capsule weight/plant (15.72 g), husk yield/plant (7.32 g), seed yield/plant (8.40 g), opium yield/plant (0.24 g), plant height (119.95 cm) and capsules/plant (2.56), which separated this cluster from cluster X. From cluster mean, it is evident that yield in opium poppy (seed/opium) is greatly influenced by different component traits mainly capsule size, leaves/plant, capsule weight/plant, plant height, husk yield/plant (SINGH *et al.*, 2003a). In present investigation capsule size, plant height, capsule weight/plant and leaves/plant and opium yield/plant exhibited maximum towards genetic divergence. Considering vector analysis capsule size (0.673), plant height (0.386), opium yield/plant (0.329), capsule weight/plant (0.314) and leaves/plant (0.241) in first vector and days to flowering (0.726), plant height (0.395), capsule weight/plant (0.045) and opium yield/plant (0.296) in second vector were noticed important contributor respectively to the total divergence. Out of total diversity 95 percent was accounted by first 3 canonical roots and of these more than 86 percent

was contributed by first two vectors ($Z_1 + Z_2$) suggesting that the differentiation for characters was nearly completed in three phases (Table 4).

Table 4. Canonical vectors showing best linear functions of variates in opium poppy

Sl. No.	Characters	Canonical Vector		
		Vector I	Vector II	Vector III
1	Days to flowering	-0.627	0.726	-0.036
2	Plant height	0.386	0.395	-0.605
3	Branches/plant	0.085	0.076	0.182
4	Capsules/plant	0.101	0.045	-0.118
5	Capsule size	0.673	0.227	0.309
6	Leaves/plant	0.241	-0.102	-0.293
7	Capsule weight/plant	0.314	0.368	0.121
8	Husk yield/plant	0.271	0.149	0.089
9	Seed yield/plant	-0.175	-0.051	0.047
10	Opium yield/plant	0.329	0.296	0.151
Canonical percentage		54.38%	32.32%	8.30%

In genetic improvement (for high yield) the choice of parent is important and desirable component characters of yield (opium/seed) should be taken into consideration for component breeding to obtain appropriate plant type (SINGH *et al.*, 1998). Over all cluster IX, X, XI and XII showed greater potential as a breeding stock by virtue of high mean values of one or more component characters as well as high statistical distance. The crossing among genotypes of these clusters selected for specific component traits may be helpful in bringing new gene pool and expanding the range of adaptation. Continuous selection in advance generation may lead to develop strains with high opium and seed yield combining desirable component traits. Intermating at F_2 level among desirable segregants would lead to greater opportunity of variability and selection of desired plant types.

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**MULTIVARIACIONA ANALIZA U ODNOSU NA SISTEM
OPLEMENJIVANJA OPIJUMSKOG MAKA (*PAPAVER
SOMNIFERUM* L.)**

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Izvod

Opijumski mak (*Papaver somniferum* L.) je značajna medicinska biljka široke upotrebe u farmaciji. Vršena je evaluacija germplazme (101 linija različitog eko-geografskog porekla koje se čuvaju u nacionalnom botaničkom istraživačkom Institutu u Lucknow-u) ispitivanjem genetičke divergentnosti za prinos/biljka, prinos opijuma/biljka i 8 osobina primenom multivariacione i kanonične analize. Genotipovi su se grupisali u 13 klastera što je potvrđeno kanoničnom analizom. 69% genotipova (69/101) su genetički bliski i grupisani u 6 klastera (II, III, IV, V; VIII, i XII) dok su jasne razlike utvrđene kod 32 procenta (32/101) između genotipova koji su se grupisali u ostalih sedam klastera (I, VI, VII, IX, X, XI i XIII). Inter-klaster distanca je u rangu između 47.28 – 234.55. Maksimalna je utvrđena između IX i X, zatim između VII i IX (208.30) i između IX i XI (205.53). Za genotipove u klasterima IX, X, XI i XII je utvrđen veći potencijal kao polazni materijal u oplemenjivanju zasnovan na visokim srednjih vrednosti jedne ili više komponenata osobina i visoke statističke distance među njima. Na osnovu utvrđene visoke srednje vrednosti komponenata osobina i inter-klaster distance među klasterima diskutovan je plan oplemenjivanja.

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