



## Genetic divergence in Indian mustard (*Brassica juncea* L.)

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Forty genotypes of Indian mustard (*Brassica juncea* L.) collected from the germplasm maintained at Main Castor and Mustard Research Station, Gujarat Agricultural University, Sardar Krushinagar were evaluated in a randomized complete block design with three replications during *rabi* season of 2001-2002. Each plot consisted of single row of 5 meter length with inter and intra row spacing of 45 cm and 15 cm, respectively. Ten plants were selected at random from each plot for recording observations on plant height, length of main branch, primary and secondary branches per plant, siliquae per plant, seeds per siliqua, length of siliqua, seed yield per plant, 1000-seed weight, oil content and harvest index. Whereas, days to 50% flowering and maturity were recorded on plot basis.

The data were subjected to multivariate analysis of D<sup>2</sup> statistic [1]. The clustering of genotypes was done by Tochers method [2]. The relative contributions of different characters towards genetic divergence were also worked out.

The analysis of variance showed highly significant differences among the genotypes for all the characters under study. Forty strains were grouped into 4 different clusters (Table 1). Cluster I was the largest which comprises 28 strains and group IV comprised only one strain, suggesting that the genotype Zem 2 diverged most from others.

The intra-cluster distance was maximum in cluster II (102.7) and minimum in cluster IV (0.00), therefore, eight strains in cluster II indicated to be the most heterogeneous. As regards inter-cluster distance, the maximum statistical distance appeared between the cluster III and cluster IV (594.1) followed by cluster I and cluster IV (415.5), suggesting wide diversity between them [3, 4 and 5].

An examination of cluster mean value (Table 2) showed that the importance of cluster IV for number of primary and secondary branches per plant, number of siliquae per plant, seeds per siliqua and seed yield and that of cluster III for early flowering, dwarf plant

**Table 1.** Cluster constellation based on D<sup>2</sup> statistic in Indian mustard

Cluster	No. of genotypes	Genotypes included
Cluster I	28	SKM 223, Varuna, RH 30, BIO 902, PCR 7, BIO 941, RSK 28, Aravali, JMG 425, MJ 94-199, SKM 9927, SKM 9585, PYM 7, Kranti, Pamaru, SKM 9033, Krishna, RL 1359, EC 287711, ORM 21-1, Urvashi, SAL 2, Lalpur 8, RH 781, TM 40, Vaibhav, GM 2, BIO 541
Cluster II	8	TM 1, TM 20, SAL 1, PM 67, Sanjuncta Asech, GM 1, RC 939, B 318
Cluster III	3	SKM 233, TM 24, TM 9
Cluster IV	1	Zem 2

**Table 2.** Cluster means and relative contribution to D values of different characters in Indian mustard

Character	Character means in different clusters				Contribution to D <sup>2</sup> values (%)
	I	II	III	IV	
Length of main branch (cm)	97.57	80.62	94.40	53.60	5.13
Seeds/siliqua	13.20	13.69	13.73	18.07	38.72
Seed yield/plant (g)	20.58	22.19	18.66	25.43	31.92
Length of siliqua (cm)	5.26	5.08	5.11	4.98	22.82

type, high oil content and high harvest index became obvious. The crosses involving parents belonging to most divergent clusters are expected to manifest maximum heterosis. The clusters comprising only one genotype with specific traits could also be used in hybridization programme. Thus, crosses between the genotype of cluster III (SKM 233, TM 24 and TM 9) with that of cluster IV (Zem 2) would produce high heterosis and is also likely to exhibit new recombination with desired traits in Indian mustard [6].

#### Referances

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