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## Genetic divergence analysis in Indian mustard (*Brassica juncea* (L.) Czern & Coss)

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**Abstract**

All the 25 genotypes were grouped into 6 clusters based on D<sup>2</sup> analysis. The cluster-I with 9 strains had maximum genotypes among all the clusters followed by cluster-III, II, IV, V and VI. The inter cluster distance was recorded highest between cluster-III and cluster-IV (90.88). The minimum inter cluster distance was observed between cluster-I and IV (15.38)

**Keywords:** Genetic divergence and Indian mustard.

**1. Introduction**

Rapeseed and mustard oil is used primarily for edible purposes and is the principle cooking oil in the mustard growing area of the country. Known for its great taste and subtle flavor, this vegetable oil is the world's second leading source of protein meal. Besides seeds, it is used as condiments. The meal cake left after oil extraction forms important cattle feed and may also be used as organic manure. *Brassicac*s are rich source of vitamins, minerals and contains many medicinal properties. They provide high amounts of vitamin C, soluble fiber and contain multiple nutrients with potent anti-cancer properties. Oil is used in Northern India for cooking and frying purposes. It is also used in preparation of hair oil and medicines. It has industrial importance in soap making and in mixtures with mineral oils for lubrication and grease for various machines. Tender leaves of young plants are used as green vegetable and are good source of sulphur and other minerals in diet.

**2. Materials & Methods**

The present field experiment was conducted at the Oilseed Research Farm, Kalyanpur of Chandra Shekhar Azad University of Agriculture & Technology, Nawabganj, Kanpur during *rabi* 2014-15. The experiment comprising 25germplasm accessions was laid out in Randomized Block Design with three replications. These lines were grown in single row plot of 5 meter length. The spacing between row to row and plant to plant was 45 cm and 15 cm, respectively maintained by thinning. Recommended agronomic practices were adopted to raise a good crop. Five competitive plants from each plot were randomly selected for recording observations for all the quantitative characters except days to flowering and days to maturity which were recorded on the plot basis. The Data were recorded for the following characters namely, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, length of main raceme, 1000-seed weight, biological yield per plant, harvest index, oil content and seed yield per plant. The oil content was estimated by using Near Infra-Red Analyzer (NIR) at Directorate of rapeseed-mustard, Bharatpur (Rajasthan).

**3. Results and Discussion**

25 strains/varieties of Indian mustard were grouped into 6 clusters under late sown condition. The genotypes from one source of origin clustered with the genotypes of other source of origin. This indicated that there was no parallelism between geographical distribution and genetic diversity. Verma and Sachan (2000) [2], Chaubey and Katiyar (1979) [3] also found the similar trend. The grouping of genotypes from same geographical origin into different clusters may be due to the different genetic backgrounds and wide divergence in features. Different genetic background is perhaps due to the free exchange of materials among different regions of country for breeding purpose; genetic drift and selection in different environments could be the other important factors contributing to the divergence. Murty and Anand (1966) [4], Singh and Gupta (1968) [5], Singh *et al.* (1977) [6] also reported similar reasons for genetic diversity.

In present investigation, on the basis of magnitude of  $D^2$  values, 25 genotypes of Indian mustard were grouped into 6 clusters. The distribution of genotypes in both the environments was different. Maximum genotypes (8) were present in cluster-I. The perusal of Table-1 revealed that the maximum inter cluster distance was observed between cluster-III and cluster-IV (90.88) indicated wide diversity between these groups. Hybridization among the genotypes separated by high inter cluster distance will result in most heterotic crosses. The estimates of genetic divergence for most of the characters under study are in accordance with earlier reports. Amar Singh *et al.* (2005)<sup>[7]</sup>, Binesh Goyal *et*

*al.* (2012)<sup>[8]</sup>. The maximum intra cluster distance was observed for cluster-III (35.05) followed by cluster-II and cluster-I. The maximum intra cluster value indicated maximum divergence among various genotypes within the cluster. A comparison of cluster mean for thirteen characters under study revealed considerable genetic differences between the clusters regarding one or more characters. The maximum character contribution towards divergence was observed for days to 50% flowering (29.66%). Similar findings were also reported by Singh *et al.* (2005)<sup>[7]</sup>, Goyal *et al.* (2012)<sup>[8]</sup>.

**Table 1:** The average intra and inter cluster value of different clusters in Indian mustard.

Clusters	1 cluster	2 cluster	3 cluster	4 cluster	5 cluster	6 cluster
1 cluster	11.887	26.954	52.704	15.383	31.070	34.592
2 cluster		18.368	48.633	39.952	27.233	30.768
3 cluster			35.054	57.755	58.158	90.883
4 cluster				0.000	29.720	58.423
5 cluster					0.000	66.710
6 cluster						0.000

**Table 2:** Cluster mean for 13 characters in Indian mustard

Clusters	Days 50% flowering	Days to maturity	Plant height (cm)	No. of primary branch / plant	No. of secondary branch / plant	Length of main raceme (cm)	No. of siliquae / plant	No. of seeds / siliqua	1000-seed Weight (g)	Biological Yield / plant (g)	Harvest index (%)	Oil Content (%)	Seed yield / plant (g)
Cluster1	80.444	131.148	174.424	7.963	18.667	56.843	325.556	13.148	3.388	51.630	23.228	39.287	12.000
Cluster2	75.500	128.778	170.838	7.667	18.556	45.871	311.722	12.889	3.600	51.833	22.097	38.678	11.444
Cluster3	67.048	122.190	155.975	7.476	15.429	57.668	313.143	13.048	3.703	51.905	22.785	38.971	11.857
Cluster4	78.000	133.333	166.477	9.333	21.333	60.700	307.667	15.000	2.960	52.333	21.055	40.840	11.000
Cluster5	75.333	127.333	175.143	9.333	20.000	44.973	329.000	13.333	2.327	52.333	22.953	37.950	12.000
Cluster6	84.667	132.667	182.163	8.000	20.000	47.173	300.333	14.333	4.453	52.333	23.510	38.753	12.333

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