

Original Research Article

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Genetic Divergence Analysis in Indian Mustard [*Brassica juncea* (L.) Czern & Coss.]

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ABSTRACT

Genetic divergence analysis in 60 genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] by applying Mahalanobis's D^2 statistics indicated the presence of wider genetic diversity among the material for 14 characters. The genotypes were grouped into eight clusters by Tocher's method. Cluster IV was the largest group with 18 genotypes, whereas cluster I was the second largest group consisting 16 genotypes followed in order by cluster VI (8 genotypes), cluster II (7 genotypes) and cluster III (6 genotypes). Two clusters, V and VIII comprised of two genotypes each cluster, while cluster VII comprised only one genotype (RH 406). The highest intra-cluster distance was observed for cluster VI (47.94). The highest inter-cluster distance was observed between cluster VIII and V (52.40). The maximum contribution to divergence was from seed yield per plant (11.76 %) in present investigation.

Keywords

Genetic divergence analysis, *Brassica juncea*, Mahalanobis's D^2 statistics

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Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss] is an important *Rabi* season oilseed crop, belongs to family Cruciferae and genus *Brassica*. Indian mustard is a natural amphidiploid ($2n=36$) a cross between *Brassica rapa* ($2n=20$) and *Brassica nigra* ($2n=16$). Mustard is largely self-pollinated but certain amount (2-14%) of cross pollination

may take place and is mainly grown in northern part of India. Rajasthan contributes 44.60 % in area & 52.05 % in production of total rapeseed-mustard of India. Mustard crop required lower water requirement (240–400 mm) for completing life cycle, therefore it is fits well for rain fed cropping systems. Four *oleiferous* brassica species viz. *Brassica juncea*, *Brassica napus*, *Brassica rapa* and *Brassica carinata* are cultivated in about 6.2

million hectares area producing 9.3 million tons with a productivity of 1499 kg/ hectare. Rajasthan has 2.38 million hectares cultivated area with the production of 3.95 million tons and productivity is 1656 kg/ hectares. (Anonymous, 2018-2019). Rapeseed mustard are the third most important oilseed crops of the world and also the first most important oilseed crop of India.

The availability of genetic variability engraved in the breeding material plays major role in planning breeding programme to develop superior cultivars or hybrids. In general, the genetically divergent parents are utilized to obtain the desirable recombinants in segregating generations. Therefore, the present study was undertaken to estimate the genetic divergence Mahalanobis D^2 technique in 60 genotypes of Indian mustard of diverse geographic origin and explore potential to evaluate the relationship of these genotypes based on quantitative trait data. Genetic divergence will further help in identifying genetically potential genotypes, which then can be utilized in creating valuable selectable variation.

Materials and Methods

The present study was administered at the Agricultural Research Station Ummedganj, Kota, Agriculture University Kota, Rajasthan, during Rabi 2019. Sixty genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] were planted in randomized block design with three replications. Each genotype was sown in 2 rows of 5.0-meter length with row to row and plant to plant spacing of 30 cm and 10 cm, respectively. All the recommended agronomic practices for Indian mustard were followed to raise a healthy crop. The data was recorded on 14 quantitative characters viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per

plant, length of main axis (cm), number of siliqua per plant, number of siliquae on main axis, length of siliqua (cm), number of seeds per siliqua, 1000- seed weight (g), oil content (%), Harvest index (%) and seed yield per plant (g).

D^2 statistic

Classification using D^2 analysis of genetic divergence aims at grouping the genotypes precisely and objectively into various groups. In the present investigation simultaneous variations in all characters of 60 Indian mustard genotypes were tested for assessment of the nature of genetic divergence among them following Mahalanobis D^2 statistics. The D^2 values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables. For each pair of combination, the mean deviation

i.e. $d_i = Y_i^1 - Y_i^2$, where Y_i denotes the transformed variables ($i = 1, 2, 3, 4, 5, \dots, p$) were calculated and the D^2 was then calculated as sum of the squares of those deviations, i.e.

$$D^2 = \sum (Y_i^1 - Y_i^2)^2$$

Where, p = Number of characters.

The significance of D^2 values was tested by treating them as chi-square (χ^2) at p degrees of freedom where p is the number of characters considered.

Grouping of genotypes by Tocher's method

After arranging the D^2 values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952). The criterion used in this method was

that any two varieties belonging to the same cluster, at least on an average, show a smaller D^2 -value than those belonging to two different clusters. Then inter-cluster and intra-cluster distances were calculated and their relationships were diagrammatically represented.

Results and Discussion

Sixty genotypes of Indian mustard, included in the present study were grouped into eight different clusters on the basis of genetic divergence or genetic closeness by D^2 following Tocher's method of clustering. The clustering pattern of the genotypes has been shown in Table 1. Cluster IV was the largest group of 18 genotypes, whereas cluster I was the second largest group consisting 16 genotypes grouped together. Cluster VI was the third largest cluster based on the genotypes (8 genotypes) followed by cluster II (7 genotypes) and cluster III (6 genotypes). Two clusters, V and VIII comprised of two genotypes each cluster. The remaining cluster VII comprised only one genotype (RH 406) indicating that this genotype is much more divergent than rest of the genotypes in the study. It was concluded that in general there was parallelism between genetic and geographic diversity. This view point has been supported by the work of Shathi *et al.*, (2012), Khan *et al.*, (2013) Kumar and Pandey (2013), Singh *et al.*, (2014) Yong *et al.*, (2014) and Tripathi *et al.*, (2019).

Maximum intra-cluster D^2 value (47.94) was recorded in cluster VI among the eight intra-cluster distances, which revealed maximum genetic diversity among the genotypes of this group. Second highest average intra-cluster distance was observed by cluster II (40.21) followed in order by cluster III (40.11),

cluster I (28.65), cluster VI (22.61), cluster V (19.12) and cluster VIII (14.01). The minimum average intra-cluster D^2 value (0.00) was recorded for cluster VII (Table 2).

The inter-cluster distances ranged from 12.06 (between III and IV) to 52.40 (between V and VIII). The other clusters with high inter-cluster distances were V and VII (52.01) followed by cluster VI and VIII (46.81), III and V (46.37), VI and VII (42.20), IV and V (41.26) and I and V (41.05). The minimum average inter-cluster distance (D^2 value) was observed of between III and IV (12.06) followed by cluster I and VII (15.15), cluster I and IV (15.58) and cluster II and IV (15.69). The lowest inter cluster distances indicate that the genotype of these clusters had close relationship and hence, may not be emphasized upon to be used in hybridization programme. These results are somewhat in accordance with the findings of Singh *et al.*, (2010), Singh *et al.*, (2011), Kumar and Pandey (2013), Tudu *et al.*, (2018) and Tripathi *et al.*, (2019).

Cluster III had higher mean values for most of the desirable characters like seed yield per plant (13.27) followed by number of primary branches per plant (8.23) number of secondary branches per plant (22.53), number of siliquae per plant (387.82), number of siliquae on main axis (46.82), number of seeds per siliqua (15.05) seed harvest index (23.70). The genotypes accommodate under cluster V were found desirable for seed yield per plant (15.52 g). Similarly, other traits like number of primary branches per plant (7.40), number of secondary branches per plant (20.95), number of siliquae per plant (397.57), number of siliquae on main axis (45.50) and number of seeds per siliqua (16.15) were also found desirable.

Table.1 Distribution of 60 Indian mustard genotypes into different clusters

Cluster	Number of Genotypes	Name of genotypes
I	16	Pusa Jai Kishan, NPJ-208, YSRL-9, Pusa Mahak, PM-26, PM-28, Shivalik, Urvashi, JM-1, Basanti, Vardaan, JM-1, Jaggnath, Giriraj, GM-1, RGN-236.
II	7	RH-725, PBR-91, Pusa Tarak, RH-30, Maya, Krishna, Vaibhav.
III	6	RGN-229, Pusa Bahar, RH-51, Pusa Bold, Varuna, DRMR-601.
IV	18	Rohini, PM-27, RGN-73, NRCDR-2, EJ-20, RGN-48, RVM-2, RH-749, RH-781, Vasundhara, JA-96, NPJ-206, RGN-34, RH-10, RH-419, RH-904, RM-51, GM-3.
V	2	RGN-303, Kranti.
VI	8	PDZ-1, GM-1, Ashirwad, Shivani, CS-54, Swarn Jyoti, Kanti, GM-3.
VII	1	RH-406.
VIII	2	NRCHB-101, RH-819.

Table.2 Average intra-clusters (diagonal) and inter-cluster distance (D^2 value) in 60 genotypes of Indian mustard

Cluster	I.	II.	III.	IV.	V.	VI.	VII.	VIII.
I.	28.65	18.64	22.15	15.58	41.05	36.03	15.15	18.10
II.		40.21	19.15	15.69	29.37	19.09	27.55	30.44
III.			40.11	12.06	46.37	32.16	22.18	25.54
IV.				22.61	41.26	32.75	22.49	22.49
V.					19.12	26.54	52.01	52.40
VI.						47.94	42.20	46.81
VII.							0.00	16.78
VIII.								14.01

* Figures in bold letters indicate maximum and minimum (intra/inter-cluster) values

Table.3 Cluster means values of 60 genotypes for fourteen characters in Indian mustard

Character Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Length of main axis (cm)	Number of siliquae per plant	Number of siliquae on main axis	Length of siliqua (cm)	Number of seeds per siliqua	1000-seed weight (g)	Oil content (%)	Harvest index (%)	Seed yield per plant (g)
I	49.51	135.72	213.06	7.96	22.29	73.56	388.06	41.51	5.36	15.13	4.21	40.19	23.00	12.00
II	50.01	133.79	224.86	8.59	19.91	74.50	374.19	42.36	5.72	14.24	5.23	39.83	22.35	13.31
III	51.47	135.62	231.33	8.23	22.53	84.60	387.82	46.82	5.27	15.05	4.17	40.77	23.70	13.27
IV	49.08	135.76	228.00	8.20	22.16	73.83	388.71	45.32	5.67	14.72	4.56	40.91	21.18	11.63
V	53.50	139.35	221.50	7.40	20.95	57.20	397.57	45.50	4.53	16.15	3.05	38.83	20.69	15.52
VI	48.69	129.56	229.13	7.43	19.61	78.78	357.28	45.49	5.49	15.81	4.50	39.40	24.25	11.19
VII	52.70	136.00	211.00	11.30	22.70	85.10	393.50	45.00	6.46	16.80	4.64	41.62	26.89	9.28
VIII	60.65	132.00	213.50	6.95	19.15	75.25	399.35	48.10	4.60	15.30	4.14	41.45	24.47	12.70

Table.4 Relative contribution of different characters to genetic divergence among 60 genotypes of Indian mustard (*Brassica juncea* L.)

S. No.	Character	% contribution
1.	Days to 50% flowering	5.53
2.	Days to maturity	2.76
3.	Plant height (cm)	4.41
4.	Number of primary branches per plant	8.04
5.	Number of secondary branches per plant	9.75
6.	Length of main axis (cm)	6.99
7.	Number of siliquae per plant	6.47
8.	Number of siliquae on main axis	7.27
9.	Length of siliqua (cm)	8.07
10.	Number of seeds per siliqua	6.32
11.	1000-seed weight (g)	11.09
12.	Oil content (%)	1.93
13.	Harvest index (%)	9.61
14.	Seed yield per plant (g)	11.76

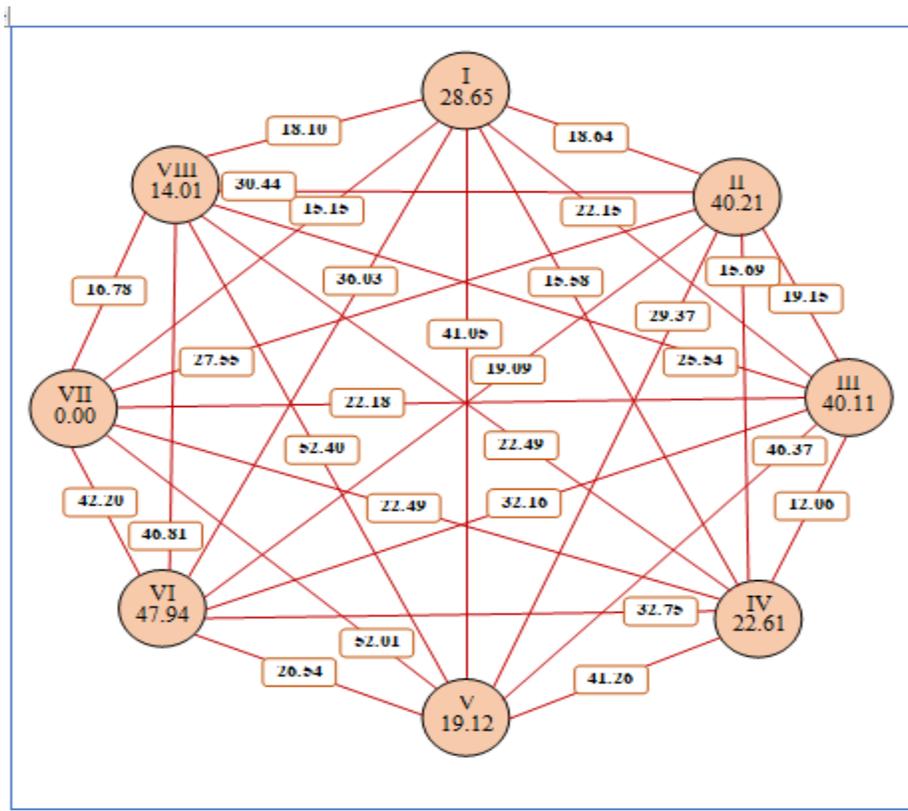


Figure 01: Cluster diagram showing average intra-cluster & inter-cluster genetic distances by Tocher's methods in Indian mustard (not to scale)

The contribution of various characters under study towards the expression of genetic divergence is presented in Table 4. It is clear from the table that on the basis of average D^2 the highest contribution to divergence was from seed yield per plant (11.76 %) followed by 1000-seed weight (11.09 %). The relative contribution of different character to the total divergence in order was number of secondary branches per plant (9.75%), harvest index (9.61 %), length of siliqua (8.07 %), number of primary branches per plant (8.04 %), number of siliquae on main axis (7.27 %), length of main axis (6.99 %), number of siliquae per plant (6.47 %) and number of seeds per siliqua (6.32 %). Oil content contributed least towards the total divergence (1.93 %) followed by days to maturity (2.76 %), plant height (4.41 %) and days to 50% flowering (5.53 %). These results are in conformity with the findings of Khan *et al.*, (2013), Kumar *et al.*, (2013), Shekhawat *et al.*, (2014), Kumari and Kumari (2018) and Rout *et al.*, (2019).

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