

GENETIC DIVERGENCE IN INDIAN MUSTARD (*BRASSICA JUNCEA* L. CZERN. & COSS.

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Abstract

Genetic divergence was carried out in 15 Indian mustard varieties/strains, 4 testers and 60 F₁s developed by crossing 15 lines with 4 testers. Based on D² values between the pair of genotypes, 19 parental lines were grouped into five clusters in E1 (timely sown) & E2 (late sown) condition. In E1, cluster II was the largest having 8 genotypes followed by cluster I and IV with four genotypes. Whereas, in E2 cluster I was largest having 9 genotypes followed by cluster V which had four genotypes. In E1 the intra-cluster distance ranged from 0.00 (cluster V) to 581.64 (cluster IV). Cluster IV and V were the most diverse with inter-cluster distance of 7169.70 followed by cluster II and V (4829.11). Whereas, in E2 the intra-cluster distance ranged from 0.00 (cluster IV) to 296.03 (cluster V). Clusters IV and V were the most diverse with inter-cluster distance of 1894.16. The 60 F₁s were grouped into eight clusters in E1 and E2. In E1, the maximum number of genotypes were grouped in clusters I and VI (12) and the intra-cluster distance ranged from 111.59 to 318.07. The maximum inter-cluster distance was observed between cluster IV and VIII (3554.76). Whereas, in E2 maximum number of genotypes grouped in cluster III (15) and intra-cluster distance ranged from 0.00 to 351.31. The maximum inter-cluster distance (D²) was observed between cluster V and VIII (43829.30).

Introduction

India occupies the second position in area after China and third position in production of rapeseed-mustard in the world after China and Canada. Multivariate analysis by means of Mahalanobis's D² statistics is a powerful tool in quantifying the degree of divergence at genotypic level. This investigation was undertaken with a view to analyzing the genetic divergence of genotypes having heterogenous geographical origin. Selection of genetically diverse genotypes is important for exploitation of heterosis and development of desirable recombinants. An assessment of nature and magnitude of diversity will help to choose better parents for hybridization. In the present study, 15 lines and 4 testers and their 60 F₁ cross products were evaluated and D² was prepared to group the parents based on D² values.

Materials and Methods

The material was derived by crossing 15 varieties/strains of Indian mustard (*Brassica juncea* L. Czern. & Coss.) with 4 tester varieties, namely Kranti (T₁), Basanti (T₂), Narendra Ageti Rai-4 (NDRE-4) (T₃), and Narendra Swarna Rai-8 (NDYR-8) (T₄) in a line × tester mating design. A set of 60 crosses involving 15 lines and four testers was evaluated along with their 19 parents in RBD with three replications at Research Farm of Department of Genetics & Plant Breeding, Narendra Deva University of Agriculture and Technology, Narendra Nagar, Faizabad (UP) under timely sown (E1) and late sown (E2) conditions during Rabi, 2009-2010. The observations were recorded for days to 50 per cent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, length of main raceme (cm), siliquae on main raceme, seeds per

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siliqua, 1000-seed weight (g), seed yield per plant (g), biological yield (g), harvest index (%) and oil content (%). The entries were sown in a single row plot of 5 m length with inter and intra-row spacing of 45 and 15 cm, respectively. Based on D^2 values between the pair of genotypes, 19 parental lines were grouped into five clusters in both E1 and E2 (Tables 1 and 2). In E1, cluster II was the largest having 8 genotypes followed by cluster I and IV with four genotypes. There was one solitary clusters V with single genotype NDRE-4. Whereas, in E2 cluster I was the largest having 9 genotypes followed by cluster V which had four genotypes. There was one solitary cluster IV with single genotype NDRE-4. The genetic divergence analysis was done following standard procedure of Mahalanobis's (1936).

Table 1. Grouping of 19 parental genotypes (15 lines + 4 testers) of Indian mustard into different clusters in E1.

Cluster No.	No. of genotypes	Genotypes included
I	4	Pusa Karishma, BPR 1205-5, Sahib-36, LET-14-1
II	8	SKM-0301, RK-08-1, Maya, JMM-08-1, RGN-228, RRN-631, NDRS-2001, PARASMANI-2-10
III	2	Basanti, NDYR-8
IV	4	Kranti, PRKS-28, TERIWRBJ-32-1, TERIHOJ-48
V	1	NDRE-4

Table 2. Grouping of 19 parental genotypes (15 lines + 4 testers) of Indian mustard into different clusters in E2.

Cluster No.	No. of genotypes	Genotypes included
I	9	Pusa Karishma, NDYR-8, BPR 1205-5, JMM-08-1, PRKS-28, PARASMANI-2-10, TERIHOJ-48, Kranti, TERIWRBJ-32-1
II	2	NDRS-2001, LET-14-1
III	3	Sahib-36, RGN-228, Maya
IV	1	NDRE-4
V	4	SKM-0301, RRN-631, RK-08-1, Basanti

Results and Discussion

Based on D^2 values between the pair of genotypes, 19 parental lines (15 Indian mustard varieties/strains and 4 testers) were grouped into five clusters in E1 and E2 (Tables 1 and 2). The clustering pattern of different genotypes did not follow their geographical distribution barring a few exceptions, which showed that geographical diversity was not necessarily an index of genetic diversity. This might be due to human selection and/or genetic drift and same is supported by Verma and Sachan (2000) and Solanki *et al.* (2006).

The genotypes within the cluster had smaller D^2 values among themselves than the genotypes belonging to other clusters. The smaller D^2 values within cluster indicated that genotypes were closely related. On the other hand, genotypes belonging to the two different clusters had large D^2 values, which indicated more genetic diversity with each other. In E1, the maximum intra-cluster distance (7169.70) was found in cluster IV and V with diverse genotypes and the minimum inter-

cluster distance was observed in cluster II and III (Table 3). Whereas, in E2 the maximum intra-cluster distance (1894.16) was found in cluster IV and V and the minimum inter-cluster distance was observed in cluster I and III (Table 4). The cluster I exhibited very high means for days to 50% flowering. However, genotypes of cluster II showed minimum mean value for number of primary branches per plant. The genotypes of cluster III had highest mean values for plant height, length of main raceme, number of siliquae on main raceme, days to 50% flowering, harvest index and oil content. While the genotypes of cluster IV had very high mean for biological yield and seed yield per plant (Table 5). In E2, the cluster I was observed with a very high mean for days to 50% flowering, biological yield and seed yield per plant. Genotypes of cluster III had highest mean values for plant height, number of siliquae on main raceme, number of primary branches per plant and 1000-seed weight. Whereas, the genotypes of cluster IV had minimum mean value for days to maturity, plant height, days to 50% flowering, length of main raceme, number of siliquae on main raceme, number of secondary branches per plant, seed yield per plant, number of primary branches per plant and 1000-seed weight. However, genotypes of cluster V showed highest mean values for oil content and number of secondary branches per plant (Table 6).

Table 3. Intra and inter-cluster D^2 and D values (parenthesis) among five clusters for 19 parental lines (15 lines + 4 testers) in Indian mustard in E1.

Clusters	I	II	III	IV	V
I	579.70 (24.077)	837.02 (28.93)	1011.64 (31.80)	2028.80 (45.042)	2933.99 (54.17)
II		338.49 (18.398)	696.12 (26.384)	982.37 (31.34)	4829.11 (69.49)
III			210.32 (14.50)	2178.40 (46.67)	4554.68 (67.49)
IV				581.64 (24.12)	7169.70 (84.67)
V					0.00 (0.00)

Diagonal bold values are intra- and rest intercluster

Table 4. Intra and intercluster D^2 and D values (parenthesis) among five clusters for 19 parental lines (15 lines + 4 testers) in Indian mustard in E2.

Clusters	I	II	III	IV	V
I	188.59 (13.73)	422.57 (20.56)	355.19 (18.85)	1412.77 (37.59)	452.99 (21.28)
II		186.60 (13.66)	383.60 (19.59)	926.42 (30.44)	1021.78 (31.97)
III			199.08 (14.11)	1567.94 (39.60)	973.14 (31.20)
IV				0.00 (0.00)	1894.16 (43.52)
V					296.03 (17.21)

Diagonal bold values are intra- and rest intercluster

The 60 F₁s were grouped into eight clusters in both E1 and E2 (Tables 7 and 8). The maximum number of genotypes were observed under the cluster I and VI followed by V, II, VII, III, VIII and IV in E1. Whereas, in E2 maximum number of genotypes were witnessed in the cluster III and II followed by VI, I, VII, VIII, IV and V. The Intra and inter-cluster D² values of eight clusters for 60 F₁'s revealed that maximum intra-cluster value was observed in cluster II in E1 while cluster VIII in E2. The genotypes of this cluster were the most diverse among themselves. The maximum inter-cluster distance was recorded between cluster IV and VIII followed by cluster III and VIII in E1. In E2, however, the maximum inter-cluster distance between cluster V and VIII was reported, followed by cluster IV and VIII. The mean value for each of the 13 characters of five clusters in E1 showed that the mean for the number of seeds per siliqua was very high in cluster I. However, cluster III had very high

Table 5. Intra- and intercluster D² and D values (parenthesis) among eight clusters for 60 F₁s in Indian mustard in E1.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	209.641 (14.479)	409.277 (20.231)	529.405 (23.009)	914.925 (30.248)	510.151 (22.587)	377.976 (19.442)	451.972 (21.259)	1230.383 (35.077)
II		318.072 (17.835)	685.545 (26.183)	853.154 (29.209)	554.023 (23.538)	583.997 (24.166)	889.756 (29.829)	1649.881 (40.619)
III			309.139 (17.582)	664.574 (25.779)	1264.632 (35.562)	841.472 (29.008)	1154.742 (33.981)	2421.627 (49.210)
IV				111.593 (10.564)	1694.563 (41.165)	1696.874 (41.193)	1895.979 (43.543)	3554.761 (59.622)
V					314.058 (17.722)	450.577 (21.227)	499.105 (22.341)	794.288 (28.183)
VI						236.256 (15.371)	409.297 (20.231)	771.937 (27.784)
VII							181.938 (13.488)	583.406 (24.154)
VIII								236.837 (15.389)

Diagonal bold values are intra-cluster and rest inter-cluster.

mean for plant height. Whereas, cluster IV possessed maximum mean values for days to maturity, days to 50% flowering, oil content and number of primary branches per plant. The cluster VI had very high mean for length of main raceme and biological yield. While the genotypes of cluster VIII had high cluster means for number of siliquae on main raceme, harvest index, seed yield per plant and number of secondary branches per plant in E1. Whereas in E2, Cluster I had very high mean for 1000-seed weight. However, cluster IV had a very high mean for days to 50% flowering. The genotypes of cluster V had a very high mean for length of main raceme, number of siliquae on main raceme, biological yield, number of seeds per siliqua and number of primary branches per plant. The genotype of cluster VI had a very high mean for days to maturity while, genotype of cluster VII had very high mean for plant height and number of secondary branches per plant. The cluster IV in E1 and cluster I in E2 could be regarded as useful sources of genes for seed yield. The cluster V in E1 and cluster IV in E2 with the minimum number of days to 50% flowering and maturity can be considered as good source for earliness.

Table 6. Intra- and inter-cluster D^2 and D values (parenthesis) among eight clusters for 60 F_1 's in Indian mustard in E2.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	237.413 (15.408)	2305.610 (48.017)	951.461 (30.846)	2958.925 (54.396)	6305.290 (79.406)	9318.612 (96.533)	5954.129 (77.163)	17291.940 (131.499)
II		251.738 (15.866)	599.809 (24.491)	9766.458 (98.825)	15484.920 (124.438)	2760.174 (52.537)	1146.743 (33.864)	7502.263 (86.616)
III			237.276 (15.404)	6500.457 (80.625)	11261.010 (106.118)	4917.787 (70.127)	2622.459 (51.209)	10995.360 (104.859)
IV				278.715 (16.695)	898.447 (29.974)	21970.900 (148.226)	16517.280 (128.519)	33605.220 (183.317)
V					0.000 (0.000)	30337.650 (174.177)	23820.040 (154.327)	43829.300 (209.354)
VI						298.169 (17.268)	710.311 (26.651)	1542.985 (39.281)
VII							288.282 (16.979)	3325.677 (57.669)
VIII								351.313 (18.743)

Diagonal bold values are intra-cluster and rest inter-cluster.

The mean performance of thirteen characters for nine clusters of 79 genotypes (Tables 9 and 10) revealed that the cluster II had a very high mean for length of main raceme. However, cluster III showed high mean for harvest index and 1000-seed weight. Genotypes of cluster IV had a very low mean value for harvest index. The cluster V was observed with high cluster means for oil content and number of seeds per siliqua. Cluster VI showed high mean for plant height, number of siliquae on main raceme, days to 50% flowering and number of secondary branches per plant. Genotypes of cluster VII showed low mean for oil content. However, genotype of cluster IX showed high mean performance for number of primary branches per plant, number of seeds per siliqua (15.16). Whereas in E2, cluster II had a very high mean for oil content. However, cluster III showed very high mean for number of siliquae on main raceme and 1000-seed weight. Genotype of cluster IV showed very high mean for number of primary branches per plant and low mean for seed yield per plant and oil content. The cluster V had a very high cluster mean for biological yield while genotype of cluster VI had a very high cluster mean for days to 50% flowering and harvest index. However, genotype of cluster VII showed low mean performance for 1000-seed weight, number of secondary branches per plant, number of primary branches per plant, biological yield, number of siliquae on main raceme, length of main raceme, days to 50% flowering and days to maturity, number of secondary branches per plant and seed yield per plant. However, genotype of cluster IX showed high mean performance for length of main raceme. The estimates of genetic divergence for most of the characters under study are in accordance with the earlier reports of Monalisa *et al.* 2005, Singh *et al.* 2005, Kumar *et al.* 2007 and Goyal *et al.* 2012.

Table 7. Cluster mean for thirteen characters of 60 genotypes (F₁s) in Indian mustard in E1.

Clusters No.	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/plant	No. of secondary branches/plant	Length of main raceme (cm)	No. of siliquae on main raceme	No. of seeds/siliquae	1000-seed weight (g)	Seed yield/plant (g)	Biological yield (g)	Harvest index (%)	Oil content (%)
I	52.14	128.67	201.93	5.97	12.72	73.43	47.03	14.95+	4.57	11.99	37.38	32.66	39.20
II	49.00	128.81	178.25#	5.90#	13.22	73.31	48.80	14.80	4.74	14.91	43.12	34.78	39.71
III	51.61	128.39	214.41+	6.51	14.12	69.72	50.96	15.20	4.50	15.14	50.56	30.10	40.28
IV	52.67+	128.83+	190.07	6.46+	12.03#	54.81#	50.19	14.82	4.92	8.42#	29.30#	28.92#	40.81+
V	46.13#	127.63	179.30	6.27	12.53	72.89	49.79	14.53	4.46#	13.27	40.32	33.31	38.50
VI	50.58	130.03	201.80	6.28	12.93	79.91+	55.85	14.70	4.72	16.00	50.91+	31.96	38.71
VII	50.57	128.33	212.36	6.14	12.98	66.90	40.97#	14.34#	4.97+	14.29	40.88	35.19	37.99
VIII	52.00	127.58#	199.17	6.01	14.51+	78.46	58.19+	14.63	4.84	16.54+	42.67	39.12+	36.97#

#, + indicate lowest and highest values, respectively.

Table 8. Cluster mean for 13 characters of 60 genotypes (F₁s) in Indian mustard in E2.

Clusters No.	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/plant	No. of secondary branches/plant	Length of main raceme (cm)	No. of siliquae on main raceme	No. of seeds/siliquae	1000-seed weight (g)	Seed yield/plant (g)	Biological yield (g)	Harvest index (%)	Oil content (%)
I	72.86	120.43	167.68	4.70#	13.76	67.64	41.03	14.80	4.82+	10.05	31.52	33.15	36.21
II	70.13	120.44	169.51	5.44	14.75	71.81	44.44	14.83	4.73	9.89	30.62	32.83	37.23
III	73.80	121.16	166.80	5.13	15.01	69.77	40.14	15.10	4.81	9.48	33.87	29.12	36.81
IV	74.33 +	120.67	167.88	5.60	15.90	72.03	41.20	14.93	4.57	7.33	23.50 #	31.88	35.08
V	64.33 #	121.33	162.67 #	5.97+	14.33	75.20+	46.13+	15.37+	4.33 #	10.00	35.33+	28.39 #	34.50 #
VI	74.15	121.44+	163.46	5.40	13.54 #	69.44	41.24	15.29	4.76	9.19	31.15	31.64	38.32
VII	69.33	120.44	175.33+	5.39	16.22+	72.68	39.96 #	14.93	4.59	9.111 #	31.07	29.61	37.90
VIII	73.73	120.27 #	165.57	5.48	15.59	65.85 #	41.87	14.69 #	4.65	10.33+	31.13	33.36+	39.10+

#, + indicate lowest and highest values, respectively.

Table 9. Cluster mean for thirteen characters of 79 genotypes (19 parents + 60 F₁s) in Indian mustard in E1.

Clusters No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	Length of main raceme (cm)	No. of silique on main raceme	No. of seeds/silique	1000-seed weight (g)	Seed yield/plant (g)	Biological yield (g)	Harvest index (%)	Oil content (%)
I	50.93	128.33	189.17	6.12	12.89	74.62	50.19	14.60	4.50	13.04	39.19	33.23	39.24
II	51.09	129.30	203.83	6.13	14.05	83.19 +	56.37	14.84	4.66	14.41	46.49	31.37	38.89
III	50.58	127.96	212.94	6.06#	12.67	66.70	40.68#	14.61	5.18 +	14.08	39.36	36.32 +	38.10
IV	49.40	129.80 +	205.16	6.54	12.76	68.94	45.95	14.61	4.85	17.62 +	62.73 +	28.04#	38.55
V	51.94	128.11	205.58	6.46	12.63#	59.71	46.16	15.14 +	4.61	12.17	41.32	29.51	40.41 +
VI	53.67 +	128.40	216.64 +	6.33	15.28 +	82.45	59.57 +	14.86	4.62	16.03	48.33	35.30	40.18
VII	52.63	127.89	198.16	6.25	14.97	78.91	54.13	14.59	4.81	15.28	45.26	34.68	36.94#
VIII	46.05	128.86	171.82	6.24	12.79	63.23	41.93	14.44	4.52	13.75	39.76	35.46	38.44
IX	40.67#	109.67#	118.90#	6.67 +	13.95	62.33#	42.07	13.47#	3.57#	9.000 #	31.92#	28.17	38.14

#, + indicate lowest and highest values, respectively.

Table 10. Cluster mean for thirteen characters of 79 genotypes (19 parents + 60 F₁s) in Indian mustard in E2.

Clusters No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	Length of main raceme (cm)	No. of silique on main raceme	No. of seeds/silique	1000-seed weight (g)	Seed yield/plant (g)	Biological yield (g)	Harvest index (%)	Oil content (%)
I	73.28	120.74	164.54	5.39	14.08	71.64	41.03	15.16+	4.77	9.08	29.87	32.32	38.33
II	74.29	120.00	163.50	5.50	15.19	68.19	41.10	14.86	4.63	10.12	30.38	33.60	39.19+
III	73.48	121.07	172.79	4.88	14.14	72.82	44.53+	15.00	5.06 +	9.52	27.52	35.01	36.06
IV	72.13	120.33	157.85	5.647+	14.94	68.47	40.45	15.16	4.37	8.33#	25.47	33.33	34.93#
V	73.47	120.49	164.64	5.17	14.29	67.11	39.66	14.99	4.77	9.02	37.47+	23.92#	36.76
VI	74.47+	121.06	157.47	5.50	13.80	70.54	38.60	14.89	4.45	9.83	27.00	36.74+	37.04
VII	53.33#	112.67#	93.93#	4.67#	9.73#	46.53#	32.47#	14.83	3.64#	7.17	24.00#	29.95	37.24
VIII	74.17	122.42+	191.23+	5.59	16.400+	72.08	41.45	14.82#	4.75	10.46+	36.85	28.89	37.65
IX	67.54	120.15	173.40	5.07	15.02	73.11+	44.42	14.92	4.79	9.18	29.51	31.24	37.23

#, + indicate lowest and highest values, respectively.

References

- Goyal B, Singh D, Ram A and Singh A 2012. Genetic divergence in elite gene pool of Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]. *Research on Crops* **13**: 1102-1104.
- Kumar M, Singh KP and Singh Dharendra 2007. Genetic divergence analysis for seed yield, its parameters and oil content in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]. *Crop Res.* **8**(1): 183-185.
- Mahalanobis PC 1936. On the generalized distance in statistics. *Proc. Nat. Acad. Sci., India.* **2**: 49-55.
- Monalisa P, Singh NB, Singh NG and Laishram JM 2005. Genetic divergence and combining ability in relation to heterosis in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]. *Indian J. Genet.* **65**(4): 302-304.
- Singh A, Kumar K, Chauhan YS and Singh OP 2005. D² analysis in Indian mustard (*Brassica juncea*) under normal and salt affected soils. *Farm Science J.* **14**(1): 7-9.
- Solanki R.K, Tomar RS and Arha MD 2006. Genetic divergence analysis in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]. *J. Oilseeds Res.* **23**(2): 156-158.
- Verma SK and Sachan JN 2000. Genetic divergence in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]. *Crop Res. (Hisar).* **19**(2): 271-276.

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