

GENETIC DIVERSITY ANALYSIS IN RELATION TO SEED YIELD AND ITS COMPONENT TRAITS IN INDIAN MUSTARD (*BRASSICA JUNCEA* L. CZERN & COSS)

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ABSTRACT

In any crop improvement programme, the choice of genetically divergent parents for hybridization is dependent upon categorization of breeding materials on the basis of appropriate criteria. A total of 60 genotypes of Indian mustard (*Brassica juncea* L. Czern and Coss) were evaluated in Randomized Block Design with two replications during 2011-2012 *rabi* season to study genetic diversity using Mahalanobis D² statistics for seed yield and its components. The 60 genotypes were grouped into 13 clusters based on D² analysis. The maximum inter-cluster distance (D) was found between cluster VI and VII (824.53), followed by that between VI and XI (798.76). The minimum inter-cluster distance was observed between cluster II and XII (99.24). The intra-cluster distance (D) ranged from 75.43 (cluster-III) to 113.18 (cluster-VI). The attributes, viz., seed yield per plant (27.33%), number of siliqua per plant (24.13%) and length of main branch (21.17%) contributed much to the total genetic divergence. On the basis of cluster means, cluster XII (34.84) was superior for seed yield per plant, whereas cluster XI was good for number of secondary branches per plant (27.67), number of seeds per siliqua (16.45) and protein content (32.22). The cluster VIII had desirable rating in respect of days to 50% flowering (48.00), days to maturity (111.00) and length of main branch (127.20), while the maxima for number of primary branches per plant (8.67) and number of siliqua per plant (564.00) were observed in cluster VII. Cluster IX was the best for test weight (5.07 g) and plant height (189.00 cm). Therefore, intercrossing of such genotypes involved in these clusters would be useful for generating variability for the respective characters, and their rational improvement for increasing the seed yield per plant.

INTRODUCTION

Oilseed crops are next to cereals in production of agricultural commodities in India which occupy a place of prime importance in Indian economy. Indian mustard [*Brassica juncea* (L.) Czern and Coss] is the second most important oilseed crop of the world as well as India after groundnut. Indian mustard (*Brassica juncea* (L.) Czern and Coss) is a natural amphidiploid (2n=36) of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16). It is self-compatible and largely self-pollinated crop (85-90%). However, owing to insects, especially honeybees, the extent of cross-pollination varies from 4 to 16.6 % (Rambhajan *et al.*, 1991). It is a plant of Asiatic origin with its major center of diversity in China (Vaughan, 1977).

The major mustard producing countries are Canada, China, India, Germany and France. Globally, India accounts for 21.7 % and 10.7 % of the total acreage and production (Anonymous 2010). India with an area of 6.51 million hectares, 7.67 million metric tonnes production and 1179 kg/ha productivity ranks second in area and third in production in rapeseed-mustard scenario of the world in 2010-2011 (Anonymous, 2011). Mustard seeds contain about 38-42 % oil, which is golden

yellow, fragrant and considered among the healthiest and most nutritional cooking medium. Mustard meal or cake is also nutritious and contains about 12 % oil and 38 to 42 % protein (Nagraj, 1995). In addition to this, it is also utilized as condiment, for medicinal uses and in preparation of soaps, hair oil, lubricants, paints, plasticizers and as a condiment in pickles (Prakash and Hinata, 1980).

Genetic divergence is essential to select the parents for future breeding program. In general, the genetically divergent parents are utilized to obtain the desirable recombinants in segregating generations. In plant breeding, genetic diversity plays an important role because hybrids between lines of diverse origin, generally, display greater heterosis than those between closely related parents and may generate broad spectrum of genetic variability in segregating population (Arunachalam, 1981). The pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa (Kumar *et al.*, 2013a). Multivariate analysis by means of Mahalanobis D² statistics (Mahalanobis, 1936) is a useful tool in quantifying the degree of divergence at genotypic level. Hence, the present study was planned to estimate the extent and nature of genetic

Table 1: Grouping of 60 genotypes of Indian mustard in various clusters on the basis of D² statistics

Cluster	No. of genotypes	Name of genotypes
I	25	IC-342773, B-1281, KHADI-1, BIO-Q-44-279, SKM-0124, DIR-325, RH-0114, PHJ-J-96-418, RAVRD-9201, AA-58, DIR-747, KHELARU-1, GDM-4, BIO-341-92, SBF-2, RS-9302, SKM-214, HUM-9801, CSR-100, NPJ-90, TM-28, ORM-39, IC-491446, CSP-930, UP-1-88
II	13	KRANTI-PB-15, PCR-10, JM-1, RSK-29, BIO-902, ZEM-1, PBR-357, PM-67, RAYAD-9602, GM-1, NRCM-353, DIRA-342, SW-1-9017
III	5	GM-3, KRANTI, IC-241632, GM-2, RH-593
IV	4	LALPURA-7, IC-331819, IC-355650, IC-399797
V	4	IC-560696, JSI-45, LAXMI, VARDAN
VI	2	HNS 0004, HYOLA-401
VII	1	VARUNA
VIII	1	HNT-33
IX	1	JMG-8
X	1	NRCM-120
XI	1	SKM-9033
XII	1	RSK-27
XIII	1	SKM-0123

Table 2: Average inter-cluster and intra-cluster D² values in Indian mustard Clusters Diagonal values indicates intra-cluster D² value

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	85.66	151.30	243.28	134.07	126.62	213.10	391.98	148.21	132.28	198.43	314.26	139.25	155.63
II		82.23	129.58	197.16	178.42	268.77	185.56	272.90	187.38	138.49	181.55	99.24	167.20
III			75.43	269.57	296.52	468.20	116.33	356.52	310.99	216.45	188.55	106.94	175.72
IV				78.22	192.66	177.08	438.36	220.79	237.27	266.68	488.56	147.64	246.88
V					90.69	208.93	400.43	146.33	158.84	155.15	322.65	247.17	254.97
VI						113.18	824.53	521.44	326.56	490.66	798.76	440.31	596.45
VII							0.00	521.55	493.12	252.84	117.75	181.63	375.92
VIII								0.00	216.88	152.87	403.57	273.88	239.22
IX									0.00	268.33	324.30	302.99	219.38
X										0.00	234.17	199.66	236.96
XI											0.00	214.42	296.39
XII												0.00	132.90
XIII													0.00

diversity through Mahalanobis D² technique among 60 Indian mustard genotypes in respect of 13 characters influencing economic yield.

MATERIALS AND METHODS

An experiment was conducted at Agronomy Farm, B. A. College of Agriculture, Anand Agricultural University, Anand (Gujarat) during *rabi* season of the year 2011-12. The material for present study comprised of 60 genotypes of Indian mustard. The seeds of these genotypes were obtained from the the Directorate of Rapeseed-Mustard Research (DRMR), Bharatpur and S.D.A.U., Sardarkrushinagar (Gujarat). Experiment was laid out in randomized block design with two replications. Each plot consisted of a single row of 18 plants. Inter and intra row spacing was kept 40 and 15 cm, respectively. The recommended package of practices was adopted to raise a good crop. The phenological characters *viz.*, days to 50 % flowering and days to maturity were recorded on plot basis. For other traits, the observations were recorded on five randomly selected competitive plants in each genotype in each replication. For quality traits like oil and protein content, the observations were recorded on randomly selected sample of seeds from each genotype. The replication wise mean values were used for statistical analysis. Oil content and protein content were estimated by using Near Infrared Reflectance Spectros-

copy (Kumar *et al.*, 2003). Differences among genotypes were tested by analysis of variance of individual characters and by Wilk's criterion (Rao, 1952) for the pooled effect of all the 13 characters. The D² values for all the possible pairs of varieties were grouped into a number of clusters according to Tocher's method as suggested by Rao (1952). The characters were ranked on the basis of their contribution to D² values, in all the combinations.

RESULTS AND DISCUSSION

The analysis of variance for individual characters revealed significant differences among genotypes. The value of V-statistic (2245.03) which follows χ^2 distribution for 767 degrees of freedom showed highly significant differences among the genotypes for aggregate of 13 characters. The D² values between all 1770 pairs ranged from 10.85 (between IC-342727 and B-1281) to 949.06 (between HYOLA- 401 and GM-2), which indicated the presence of high genetic diversity among the genotypes for all the traits. Thus, one can proceed for further diversity analysis.

Grouping of the genotypes was carried-out by following the Tocher's method (Rao, 1952) with the assumption that the genotypes within cluster have smaller D²-values among themselves than those from groups belonging to different clusters. In all, 13 clusters were formed from 60 genotypes.

Table 3: Cluster means for different characters in Indian mustard

Clusters	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 branch (cm)	Number of siliqua per plant	Siliqua length (cm)	Number of seeds per siliqua	Test weight (g)	Seed yield per plant(g)	Oil content (%)	Protein content (%)
I	56.08	122.24	209.77	6.84	19.48	93.87	382.21	5.04	14.57	4.59	25.13	22.79	31.44
II	55.38	120.77	211.35	6.85	20.63	96.21	382.92	5.22	13.25	4.53	23.39	22.74	31.09
III	56.40	125.60	214.20	6.11	22.80	81.69	407.36	4.99	14.00	4.58	26.84	22.67	30.92
IV	59.00	126.75	213.62	6.46	19.71	103.86	353.96	4.47	13.23	4.49	21.41	22.68	30.93
V	58.75	128.50	211.52	6.34	22.92	99.82	337.17	4.82	13.94	4.34	22.24	24.50	31.50
VI	53.50	115.00	222.44	7.75	21.95	118.66	524.00	4.89	16.30	4.49	34.20	22.65	31.42
VII	56.00	113.00	225.30	8.67	24.33	117.47	564.60	5.00	15.60	4.50	33.70	24.26	32.11
VIII	48.00	111.00	205.00	7.80	20.67	127.20	452.00	4.40	14.60	4.89	26.94	22.11	30.55
IX	49.00	115.00	189.00	7.40	21.67	124.40	410.40	4.65	13.80	5.07	28.71	22.76	29.33
X	48.00	118.00	227.50	7.54	25.00	109.30	388.63	3.70	15.70	4.15	26.94	27.80	31.80
XI	49.00	115.00	223.30	8.00	27.67	103.88	412.68	4.68	16.45	4.56	28.76	27.30	32.22
XII	53.00	113.00	230.00	8.20	22.40	106.50	471.67	4.77	16.10	5.00	34.84	22.40	30.50
XIII	51.00	117.00	226.00	7.80	17.44	111.20	492.67	5.06	15.40	4.54	33.78	21.62	29.70
Mean	55.6	121.78	212.24	6.91	20.72	97.64	392.92	4.97	14.25	4.56	25.39	23.01	31.22
S.E.m	2.48	4.41	12.43	0.76	3.52	7.43	51.72	0.29	0.87	0.27	3.67	0.99	0.85
C.V.%	5.57	4.52	7.32	13.78	21.27	9.52	16.45	7.50	7.66	7.49	18.10	5.43	3.40
C.D.(P=0.05)	7.06	12.55	NS	NS	NS	21.17	147.26	0.84	2.48	NS	10.46	2.84	NS
R ² *	0.55	0.46	0.72	0.14	0.42	0.72	0.42	0.48	0.56	0.45	0.45	0.58	0.45
C.V. _b %	9.50	6.95	6.12	15.51	18.68	21.17	24.13	11.87	13.19	6.14	27.33	9.56	3.13

* R²: Ratio of the inter cluster variance to the total variance, NS: Non significant, -: Not estimated due to -ve variance, C.V._b: Inter cluster coefficient of variation

The composition of clusters is given in Table 1. The cluster I was the largest cluster having 25 genotypes. Cluster II was the second largest which contained 13 genotypes. The cluster III was the third largest which contained five genotypes. The cluster IV and V contained four genotypes each. The cluster VI contained two genotypes. The clusters VII, VIII, IX, X, XI, XII and XIII were solitary clusters with single genotypes. Similarly 19 diverse genotypes of Indian mustard were grouped into five clusters by Sinha and Singh (2004). Thirty-three diverse genotypes of Indian mustard were grouped into eight different clusters by Thul *et al.* (2004). Monalisa *et al.* (2005) carried out similar type of genetic divergence study in nine genotypes of Indian mustard and grouped them into six clusters using Tocher's method. Malik *et al.* (2006) studied 30 lines and cultivars of Indian mustard for 12 quantitative characters and grouped them into six clusters using Mahalanobis D²-statistics. Forty six genotypes of Indian mustard, on the basis of Mahalanobis D² following Tocher method for clustering, were grouped into eight clusters by Kumar *et al.* (2013b). Forty cultivars of Indian mustard were grouped into 4 clusters by Patel and Patel (2006). The clustering pattern of genotypes showed that the genotypes of different origins were clubbed in one cluster, whereas the genotypes belonging to same state or origin were grouped in different clusters indicating that the geographic distribution did not considered to be the sole criterion of genetic diversity. Singh *et al.* (2007) was also reported that there was no parallelism between geographic distribution and genetic diversity. Pattern of distribution of genotypes among various clusters reflected the considerable genetic diversity present in the genotypes under study.

Inter and intra-cluster distances are shown in Table 2. The maximum inter-cluster distance (D = 824.53) was found between cluster VI and VII, followed by that between VI and XI (D = 798.76) (Table 2). The minimum inter-cluster distance was observed between cluster II and XII (D = 99.24). The intra-cluster distance (D) ranged from 75.43 (cluster-III) to 113.18 (cluster-VI). The seven clusters (VII, VIII, IX, X, XI, XII and XIII) contained single genotype each and therefore, their intra-cluster distances were zero. The genotypes grouped into same cluster displayed the lowest degree of divergence from one another and in case crosses are made between genotypes belonging to the same cluster, no transgressive segregant is expected from such combinations. Therefore, hybridization programmes should always be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized to get desirable transgressive segregants. The genotypes with high values of any cluster can be used either for direct adoption or for hybridization, followed by selection. Tripathi *et al.*, 2013 studied genetic divergence in 100 Sesame germplasm lines and found that the inter cluster distance in most cases was larger than intra cluster distance suggesting wider diversity among the germplasm of different groups.

Analysis of variance for each of the 13 characters was carried out using mean of sixty genotypes (Table 3). Estimates of inter and intra cluster variances, along with ratio (R²) of inter cluster variance to the total variance and inter cluster coefficient of variation (C.V._b) for 13 characters were worked out. Maximum value of R² (0.72) was observed for length of main branch,

followed by oil content and number of seeds per siliqua and minimum value for R^2 (0.14) was observed for number of primary branches per plant. From inter cluster coefficient of variation (CV_b) it was revealed that the seed yield per plant contributed maximum (27.33%) towards the total divergence in yield (Table 3). The next major contribution came from the number of siliqua per plant (24.13%) towards divergence in yield, followed by length of main branch with 21.17 % contribution. Apart from above mentioned traits, other characters viz., days to 50% flowering (9.50%), days to maturity (6.95), plant height (6.12%), number of primary branches per plant (15.51%), number of secondary branches per plant (18.68%), siliqua length (11.87), number of seeds per siliqua (13.19%), test weight (6.14%) and oil content (9.56%) had low to moderate contribution towards the total divergence, while protein content (3.13%) contributed negligible towards the total divergence in yield. Sinha and Singh (2004) studied genetic divergence among nineteen Indian mustard genotypes and found that the characters viz., number of seeds per siliqua, number of siliquae per main shoot, plant height and number of secondary branches per plant contributed to more than 60 per cent of the total divergence in the genotypes.

Wide ranges of mean values among the clusters were recorded for different traits (Table 3). The cluster XI (SKM-90-33) had the highest mean values for number of secondary branches per plant (27.67), number of seeds per siliqua (16.45) and protein content (32.22 %). The cluster VIII (HNT-33) was desirable in respect of phenological characters like days to 50% flowering (48.00) and days to maturity (111.00) and also had highest value for length of main branch (127.20 cm). The cluster IX (JMG-8) exhibited highest value for test weight (5.07 g) and also showed short plant height (189.00 cm). The cluster VII (Varuna) had highest mean values for number of primary branches per plant (8.67) and number of siliqua per plant (564.60). The maximum mean value for seed yield per plant (34.84), oil content (27.80 %) and siliqua length (5.22 cm) was observed in cluster XII (RSK-27), cluster X (NRCM-120) and II, respectively. The results obtained in the present study are in accordance to the findings of Acharya and Swain (2003), Arha *et al.* (2006), Malik *et al.* (2006), Patel and Patel (2006), Vaishnav *et al.* (2006), Singh *et al.* (2007), Singh *et al.* (2009), Gangapur *et al.* (2010), Singh *et al.* (2010) and Singh *et al.* (2011).

Therefore, from the D^2 analysis of genetic diversity, based upon high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from cluster VI (HNS 0004, HYOLA-401) and VII (Varuna) as parents in hybridization programme. The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. Further research should be done with DNA markers which can be used to determine genetic distance easily and successfully.

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Cont. P. 722