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Genetic diversity studies in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L. Czern & Coss.)

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Abstract

A collection of 33 genotypes of [*Brassica juncea* (L) Czern & Coss.] (12 from Australia, 21 from India) was grown in randomized block design. Seed yield, 1000 seed weight, number of secondary branches, number of seed per siliquae, siliqua length, number of primary branches, plant height and number of silique on main raceme were the maximum contributors for genetic diversity among the genotypes. Cluster I and IX included maximum six genotypes each and cluster IV was having only one genotype (JM-016). Maximum divergence was observed between clusters IV and VIII (8.3) followed by cluster IV and VI (7.1), cluster IV and V (7.1) and cluster V and VIII (6.9). The genotypes JM016, PCR 7 and RH 8812 were observed as most divergent. The genotypes from cluster V had short stature, earliest in days to 50 per cent flowering and in maturity and cluster VIII had highest siliqua length, number of seed per siliqua, 1000 seed weight and seed yield (kg/ha) along with high value of number of primary and secondary branches, main raceme length and oil content. The cluster V and VIII were among the most divergent clusters having high seed yield performance along with its contributing traits and high in oil content. The probability of getting better segregants and promising recombinants is expected to be more, in case the genotypes of these clusters will be used in the hybridization programme.

Key words: *Brassica juncea L. Indian mustard, genetic divergence, D^2 analysis, cluster analysis*

Introduction

India is among the major oilseed producing countries with around 7% contribution in the global production. Oilseeds hold an important position in Indian economy. Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is the second largest oilseed crop in India after soybean. It is cultivated in *rabi* (post-rainy) season mainly in Northwest India and contributes nearly 27 per cent to edible oil pool of the country. Major mustard growing states are Rajasthan, M.P., U.P., Haryana, Gujarat, Bihar, Punjab, West Bengal and Assam in 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. The multivariate analysis is an important tool for the assessment of genetic divergence. Thus, it is utilized to assess genetic divergence along with the relative importance of different traits in the total divergence.

Materials and Methods

Thirty three *Brassica juncea* genotypes (21 from India, 12 from Australia) were grown in Randomized Block Design in three replications during *rabi* 2004-05 and 2005-06 at Oilseed Research Farm, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar. Each genotype was sown in a plot consisting of 5 rows of 5m length in 2 replications with spacing 45 cm x10 cm. All the recommended agronomic practices were followed to raise a good crop (NRCRM, 1999). Data were recorded on 5 randomly selected competitive plants from each entry for 12 quantitative traits. Oil content was estimated by

Sokshlet method (AOAC, 1995). The pooled data of two years were subjected to D^2 analysis (Mahalanobis, 1928) as elaborated by Murty and Arunachalam (1966). The genotypes were grouped into different clusters by following Tocher's method as described by Rao (1952).

Results and Discussion

The analysis of variance and dispersion were highly significant among the different genotypes for all the twelve traits under study, which revealed the presence of considerable variability among the genotypes. All 33 genotypes were grouped into nine clusters, using the Tocher's method, in such a way that the genotypes within the cluster had smaller D^2 values among themselves than those belonging to different clusters (table 1).

Table 1: Grouping of *Brassica juncea* genotypes in different clusters

Cluster	No. of genotypes	Genotypes / Accessions
I	6	JN 004, JO 006, JN 010, JM 018, JO 009, JN 032
II	4	JN 028, JN 031, JR 042, JR 049
III	2	Durgamani, RH 8113
IV	1	JM 016
V	3	Seetha, Pusa Agrani, Sanjucta
VI	4	RL 1359, Vaibhav, GM-1, RH 30
VII	5	RH 781. PBR 97, Kranti, Vardan, JN 033
VIII	2	PCR 7, RH 8812
IX	6	Rohini, RLM 619, PBR 91, Prakash, RH 819, Varuna

Pattern of distribution of genotypes among various clusters reflected the considerable genetic variability present in the genotypes under study. Cluster I and IX each comprised of maximum number of genotypes, followed by cluster VII with five genotypes. Cluster II and VI each included four genotypes. Cluster V consisted of three genotypes and cluster III and VIII of two genotypes, each. Cluster IV was monophyletic (JM-016). Most of the Australian accessions fell in cluster I, II & IV, whereas, Indian genotypes were in cluster III, V, VI, VIII and IX. Cluster VII had genotypes from both the Indian as well as Australian collections. The grouping of genotypes indicated that geographical distribution need not necessarily be the indicator of genetic divergence as reported by Verma and Sachan (2000), Jeena and Sheikh (2003). The possible reason could be common ancestor of these genotypes, due to free exchange of germplasm among the breeders of different regions and/or due to unidirectional selection practiced by the breeders in tailoring the promising cultivars for different regions. On the other hand, the presence of genetic diversity within the genotypes of same region could be distributed into different clusters. It was also observed that genotypes of quite different pedigree may fall into the same cluster, due to unidirectional selection pressure that could yield the genotypes, which were genetically closer than their parents. Likewise, it is also true that selection produce genetically diverse genotypes of same pedigree. This indicates that the pedigree record may not necessarily be an indicator of genetic divergence. Seed yield (20.3%) followed by 1000 seed weight (11.9%), number of secondary branches (10.0%) and number of seed per siliqua (9.2%) contributed maximum towards the total divergence (table 2).

Table 2: Contribution of different characters towards genetic divergence in *Brassica juncea*

Characters	% contribution
Plant height (cm)	7.5
Days to 50% flowering	5.2
Days to maturity	3.6
No. of primary branches	7.7
No. of secondary branches	10.0
Main raceme length (cm)	6.7
No. of siliquae on main raceme	7.1
Siliqua length (cm)	7.9
No. of seeds per siliqua	9.2
Oil content (%)	3.1
1000-seed weight (g)	11.9
Seed yield (kg/ha)	20.3

The variance for the cluster means were calculated for 12 quantitative characters. Maximum variance for cluster mean was observed for seed yield, plant height, days to maturity, main raceme length, number of

siliquae on main raceme, days to 50% flowering and number of secondary branches, which suggested that these characters were highly responsible for genetic divergence in the present material. This indicated that the parents selected for hybridization on the basis of these characters are represented to be genetically diverse. The above results were supported by Verma and Sachan, 2000, Goswami and Behl, 2006, Kumar *et al.*, 2007 and Yu-cheng *et al.*, 2007. The D^2 analysis showed intra and inter-cluster distance (table 3).

Table 3: Average intra and inter-cluster distance D^2 values in *Brassica juncea*

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	3.29	4.25	4.28	5.46	6.07	5.94	4.88	5.64	4.63
II		3.58	4.22	4.92	6.09	5.54	4.64	6.36	4.46
III			2.43	5.60	6.76	5.87	5.27	5.40	3.87
IV				0.00	7.09	7.13	5.66	8.30	6.21
V					3.44	5.92	6.27	6.95	5.80
VI						3.26	3.66	5.10	3.59
VII							2.71	5.04	3.54
VIII								2.43	3.67
IX									2.35

The maximum inter-cluster distance of 8.3 existed between cluster IV and VIII followed by 7.1 between cluster IV and VI and between cluster IV and V. The lowest inter-cluster distance (3.5) was found between cluster VII and IX, indicating a close relationship between them. The highest intra-cluster distance was 3.58 observed in cluster II and lowest (0.0) in cluster IV (fig. 1).

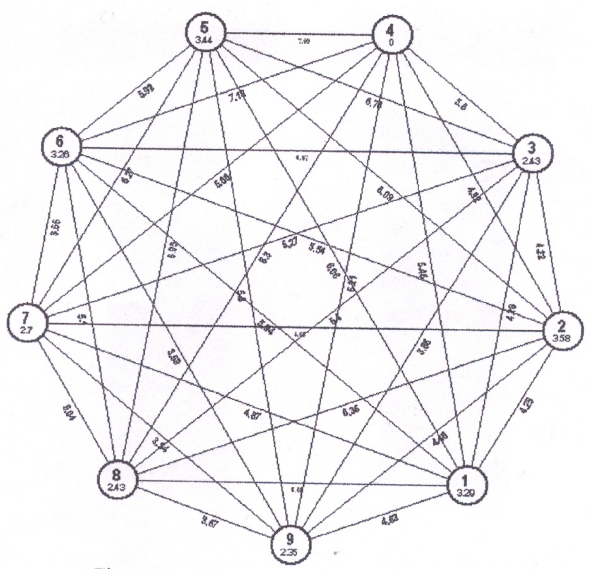
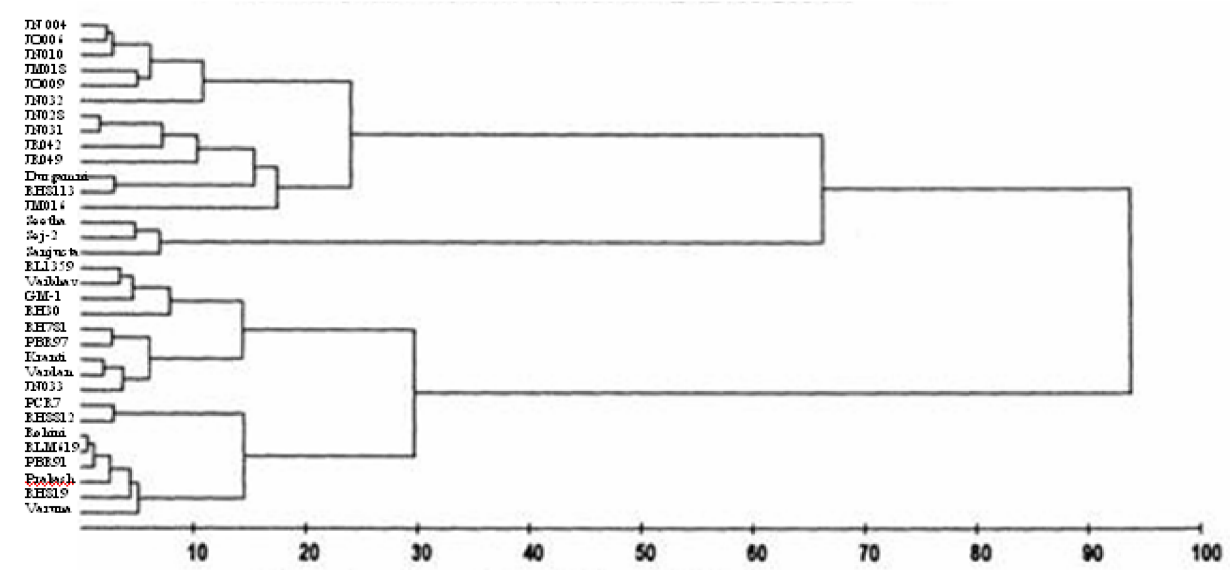


Fig. 1 Eucledean cluster distance diagram

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 for hybridization may be chosen from widely separated



Standardized Euclidean^2 Distance

Figure 2: Wards minimum variance dendrogram

clusters (fig. 2), as it is observed that there are several genotypes included in the crossing programme from widely separated clusters. (e.g. JM-016 with PCR 7 and RH8812). Although, for final selection of the parents for breeding programme, the genotypes to be used may be selected almost without exception or its proven performance in the areas of intended use including quantitative characters and include in crossing with the existing varieties for their further improvement (Allard, 1960). The genotypes from cluster V having shortest plant height, along with earliest in days to 50% flowering and maturity and cluster VIII, having highest mean values for siliquae length, number of seed per siliqua and seed yield along with high mean value for number of primary and secondary branches, main raceme length and for % oil content (table 4) could be utilized in the hybridization programme for getting desirable transgressive segregants and high heterotic response.

Table 4: Cluster mean of different characters of *Brassica juncea* genotypes

Cluster	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of primary branches	No. of secondary branches	Main raceme length (cm)	No. of siliqua on main raceme	Siliqua length (cm)	No. of seed per siliqua	Oil content (%)	1000 seed weight (g)	Seed yield (kg/ha)
I	199.6	54.6	148.4	8.1	18.4	62.2	51.0	3.5	11.6	36.1	3.2	1361.8
II	198.0	56.2	149.9	6.1	13.7	55.9	50.8	3.0	11.3	36.5	3.3	1491.8
III	233.3	58.1	150.2	7.0	16.7	52.9	38.0	3.6	11.7	36.7	3.9	1566.0
IV	219.1	58.3	155.5	6.0	11.0	59.6	52.4	3.9	9.9	33.0	2.8	459.7
V	156.8	44.4	129.7	6.0	13.8	62.6	45.8	3.9	11.6	34.1	3.7	1360.9
VI	199.0	53.8	138.0	5.6	12.3	69.0	52.2	4.3	10.9	38.8	5.0	2029.5
VII	211.9	55.1	147.0	5.7	13.4	74.2	55.4	4.0	11.5	38.1	4.0	1623.5
VIII	208.8	54.3	144.0	7.3	16.8	66.0	48.1	4.4	15.3	38.4	5.1	2100.4
IX	211.9	56.2	143.8	6.5	13.5	64.2	46.4	4.0	12.4	37.7	4.9	1826.7

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