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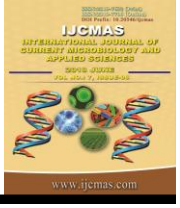

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Genetic Diversity for Seed Yield, Its Components and Oil Content in Indian mustard (*Brassica juncea* L. Czern and Coss.) under Normal and Saline/Alkaline Condition

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ABSTRACT

The twenty genotypes along with four checks in Indian mustard (*Brassica juncea* L. Czern & Coss.) were studied for genetic diversity with respect to seed yield and thirteen related traits under normal condition (NS) and saline/alkaline condition (SS). D^2 analysis classified the twenty genotypes of Indian mustard into five diverse clusters in both the conditions. In normal condition, plant height, secondary branches per plant, siliquae on main raceme, seeds per siliqua, 1000 seed weight, biological yield per plant and seed yield per plant were the major contributors for genetic diversity among the genotypes, whereas, in saline/alkaline condition, days to 50 % flowering, days to maturity, plant height, seeds per siliqua and harvest index were the major contributors for genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster IV and V in NS and in SS, between cluster II and IV. Character *viz.*, harvest index followed by siliquae on main raceme and length of main raceme in NS whereas in SS, plant height followed by siliquae on main raceme contributed maximum towards divergence. In (NS), maximum inter cluster D^2 values were observed between cluster IV and V (2156.013); while in (SS), maximum inter cluster distance was observed between cluster II and IV (1750.460) indicating wider genetic diversity between the genotypes in these clusters. Hybridization among the genotypes separated by high cluster distance will result in most heterotic crosses.

Keywords

Brassica juncea L. Czern and Coss., genetic divergence, D^2 statistics

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Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss], which is cultivated under the genus *Brassica* is cultivated all over India and it is throughout the world belongs to family Cruciferae (Brassicaceae). It has 38 to 42 % oil and 24% protein. Among rapeseed and mustard, rai (*B. juncea*) is very popular among the farmers due to higher yield and greater tolerance against lodging, shattering, drought condition, heat and relative diseases as well as the saline sodic conditions. *Brassica* also performs well on neglected sites where problems like soil acidity, low available nutrient content, poor drainage, drought, and soils with topographical limitations exist. India is endowed with a great diversity of Indian mustard germplasm in its vast territorial land area. A large number of Indian mustard genotypes are known to exist in this country. Amongst them, a variety of special quality Indian mustard are of great significance which deserves better premium in the domestic as well export market. Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is one of the most important oilseed crops of the country occupying considerably larger acreage among the *Brassica* crops. It is cultivated in *rabi* season mainly in Northwest India, and contributes nearly 27 per cent to edible oil pool of the country (Singh *et al.*, 2010). Assemblage and assessment of divergence is essential to know the spectrum of diversity in any crop. Genetic divergence study is essential to develop cultivars with increased yields, wider adaptation, desirable qualities, and pest and disease resistance. Inclusion of more diverse parents in hybridization programme increases the chances of obtaining maximum heterosis and gives a broad spectrum of variability in segregating generations. Keeping this back ground in view, the present study was undertaken to analyse genetic diversity among twenty genotypes of Indian mustard under normal condition (NS) and saline/alkaline (SS) condition.

Materials and Methods

The materials for present study comprised of 20 genotypes along with four checks viz., CS-52, CS-54, Narendra rai (NDR-8501), Maya in Indian mustard (*Brassica juncea* L. Czern & Coss.) under normal condition (NS) and saline/alkaline condition (SS). The experiment was conducted at the Research Farm of Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture & Technology, Narendra Nagar (Kumarganj), Faizabad, during *Rabi* season of 2013-14 in two conditions (Normal and saline/alkaline condition). The material was sown in Randomized Block Design with three replications. Each block consisted of single row of five meter length, following spacing (row to row and plant to plant) of 45 cm and 15 cm, respectively. In each entry, five plants were randomly tagged and utilized to collect data on yield and its component characters *viz*., days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, length of main raceme, siliquae on main raceme, seeds per siliqua, 1000-seed weight (g), biological yield per plant (g), seed yield per plant (g), harvest index (%) and oil content (%). Mahalanobis (1936) D^2 statistics was used for assessing genetic divergence among all the genotypes. The clustering of D^2 values was done using Tocher’s method as described by Rao (1952), while the intra- and inter- cluster distances were calculated using the formula given by Singh and Choudhary (1977).

Results and Discussion

The analysis of variance and dispersion were highly significant among all the genotypes for all twenty characters studied, which revealed the presence of considerable genetic variability among the genotypes under normal condition (NS) and saline/alkaline condition (SS). All twenty genotypes were grouped into 5 clusters in both the conditions (NS and SS) using the Tocher’s method (table 1 and 2) but their distribution in both the environments was different. In normal condition (NS), out of 5 clusters, cluster II was the largest comprising 8 genotypes followed by cluster I and cluster IV with 5 genotypes, respectively; clusters III, and V consisted of one genotype, which cannot be grouped together and formed separate cluster, while in saline/alkaline condition (SS), out of 5 clusters, cluster I was the largest comprising 8 genotypes followed by cluster II with 7 genotypes, cluster IV and cluster II had 2 genotype. Clusters III consisted of one genotype, which cannot be grouped together and formed separate cluster.

The clustering pattern indicated that there was a considerable diversity among the genotypes, and there was no relationship between the genetic and geographical diversity of the genotypes, but the distribution of the genotypes was random and independent. This could be due to genetic drift, selection pressure and environmental effect, which create morphological diversity rather than actual genetic distances. Similarly, the strains developed at one station were also grouped in different clusters which suggested that there might have been introgression of genes among the genotypes of various origins and operation of similar forces of selection. Similar results have also been reported earlier by Singh *et al.*, (2010) in Indian mustard.

The characters *viz.*, harvest index (30.53), siliquae on main raceme (23.68) and length of main raceme (23.16) in normal condition (NS) whereas, plant height (38.95), siliquae on main raceme (26.32) contributed more than 75 % towards the total divergence (table 7). Parallel to the present results, maximum contribution towards the divergence for harvest index was previously reported by Doddabhimappa *et al.*, (2010), number of siliquae on main raceme by Somu (2001) and plant height by Ratnesh Pandey *et al.*, (2013).

Table.1 Distribution of 20 genotypes of Indian mustard in different clusters under normal condition

Cluster No.	Number of genotypes	Genotypes included
I	5	NUDH YJ-10, NUDH-YJ-6, Kranti, NDRS 2004-3, NDRS 2004-1.
II	8	NDR-2001, NDR-8501, NDRS 2010, CS-54, CS-52, NDRS 2006-1-2, NDRS 2008-1, RGN-73.
III	1	NDRE 08-4.
IV	5	NDRS 2011, PRB 2004-3, NDRE 08-1, Maya,Albeli.
V	1	NDRS 2001-1.

Table.2 Distribution of 20 genotypes of Indian mustard in different clusters under saline/alkaline condition

Cluster No.	Number of genotypes	Genotypes included
I	8	RGN-73, NDRS 2008-1, Kranti, NDR-8501, NDRS 2011, NDRS 2004-3, NDRS 2004-1, NDR-2001.
II	7	NUDH YJ-10, NUDH-YJ-6, NDRS 2010, CS-54, CS-52, NDRS 2006-1-2, Maya.
III	1	PRB 2004-3.
IV	2	NDRE 08-4, NDRE 08-1.
V	2	Albeli, NDRS 2001-1.

Table.3 Intra- cluster and inter-cluster D^2 values among 5 clusters in Indian mustard under normal condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**208.259**	514.683	272.276	539.709	2138.739
Cluster II		**405.052**	647.176	875.248	1183.494
Cluster III			**0.000**	608.470	2122.975
Cluster IV				**500.636**	2156.013
Cluster V					**0.000**

Bold figures indicate intra-cluster D^2 values.

Table.4 Intra- cluster and inter-cluster D^2 values among 5 clusters in Indian mustard under saline/alkaline condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**445.630**	803.530	591.620	805.720	1185.820
Cluster II		**374.080**	1042.310	1750.460	1437.350
Cluster III			**0.000**	325.190	768.260
Cluster IV				**210.420**	1391.590
Cluster V					**351.240**

Bold figures indicate intra-cluster D^2 values.

Table.5 Cluster mean for 13 characters in Indian mustard under normal condition

	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ Plant	Secondary branches/ Plant	Length of main raceme (cm)	Siliquae on main raceme	Seeds/ siliqua	1000 seed weight (g)	Biological yield/ plant (g)	Seed yield/ plant (g)	Harvest index (%)	Oil content (%)
Cluster I	61.600	123.533**	140.114	4.480*	6.561*	53.953	33.025	12.000*	3.413*	20.847*	5.609	26.945**	41.810**
Cluster II	60.708	123.000	160.162	5.346	7.165	49.995*	38.243	13.808	4.288	26.954	6.760	25.435	40.975*
Cluster III	62.000**	118.000*	142.433	5.673**	8.233	62.593**	27.867*	13.600	3.560	22.553	4.670*	20.693	41.083
Cluster IV	61.267	122.733	126.701*	4.708	7.894	54.351	40.555	12.005	3.881	30.832	6.543	21.264	41.079
Cluster V	60.667*	122.000	186.900**	4.667	12.067**	60.740	53.867**	13.880**	6.193**	42.797**	7.927**	18.453*	41.307

** Highest
*Lowest

Table.6 cluster mean for 13 characters in Indian mustard under saline/alkaline condition

	Days to 50% flowering	**Days to maturity**	**Plant height (cm)**	**Primary branches/ plant**	**Secondary branches/ plant**	**Length of main raceme (cm)**	**Siliquae on main raceme**	**Seeds/ siliqua**	**1000 seed weight (g)**	**Biological yield/ plant (g)**	**Seed yield/ plant (g)**	**Harvest index (%)**	**Oil content (%)**
Cluster I	56.830**	119.040**	132.740**	4.620	7.940	53.930	33.500	13.050**	3.370	22.780*	5.560	25.050**	39.970*
Cluster II	56.480	117.520	129.380	4.380	5.210*	41.170*	37.840	11.760	3.980	24.420	6.000**	24.710	40.400
Cluster III	55.000	115.330*	121.330	4.360	7.850	54.920	33.810	10.730*	4.530	29.260**	5.220	17.840*	40.120
Cluster IV	53.000*	115.830	114.060*	5.300**	6.920	63.060**	31.930*	12.400	2.880*	28.900	5.810	19.860	39.480
Cluster V	55.500	118.670	127.150	3.960*	10.960**	54.990	52.820**	12.250	4.540**	26.790	5.050*	18.930	40.390**

**Highest
*Lowest

Table.7 Percent (%) character contribution towards divergence in Indian mustard under normal and saline/alkaline condition

Character	**Normal condition (%)**	**Saline/alkaline condition (%)**
1 Days to 50% flowering	0.00	0.00
2 Days to maturity	0.00	0.53
3 Plant height (cm)	0.00	38.95
4 Primary branches/ plant	0.00	0.00
5 Secondary branches/ plant	12.11	4.21
6 Length of main raceme (cm)	23.16	16.32
7 Siliquae on main raceme	23.68	26.32
8 Seeds/ siliqua	0.53	1.05
9 1000 seed weight (g)	4.74	8.95
10 Biological yield/ plant (g)	0.00	0.00
11 Seed yield/ plant (g)	0.00	1.58
12 Harvest index (%)	30.53	1.05
13 Oil content (%)	5.26	1.05

The cluster means for different characters are presented in (table 5 and 6). In normal condition (NS), Cluster I possessed high mean values for days to maturity (123.533), harvest index (26.945) and oil content (41.810), cluster III for days to 50% flowering (62.00), primary branches per plant (5.673) and length of main raceme (62.593), cluster V for plant height (186.900), secondary branches per plant (12.067), siliquae on main raceme (53.867), seeds per siliqua (13.880), 1000 seed weight (6.193), biological yield per plant (42.797) and seed yield per plant (7.927) whereas, in saline/alkaline condition (SS), cluster I possessed high mean values for days to 50 % flowering (56.830), days to maturity (119.040), plant height (132.740), seeds per siliqua (13.050) and harvest index (25.050), cluster II for seed yield per plant (6.000) and oil content (40.000), cluster III for biological yield per plant (29.260), cluster IV for primary branches per plant (5.300) and length of main raceme (63.060), cluster V for siliquae on main raceme (52.820) and 1000 seed weight (4.540). This further indicated that good parents could be selected for hybridization on mean basis. These results are supported by Goswami and Behl (2006) and Kumar *et al.*, (2007).

The magnitude of inter- cluster distances was greater than intra-cluster distances suggesting the presence of considerable diversity among the clusters (table 3 and 4). In normal condition (NS), the intra-cluster D^2 values varied from 208.259 to 500.636 within cluster, and 272.276 to 2156.013 between clusters; while in saline/alkaline condition (SS), the intra-cluster D^2 values varied from 210.420 to 445.630 within cluster, and 325.190 to 1750.460 between clusters, this indicated that clusters were homogenous within themselves and heterogeneous between themselves.

In normal condition (NS), the cluster IV exhibited maximum intra-cluster distance (500.636) while in saline/alkaline condition (SS), cluster I exhibited maximum intra-cluster distance (445.630) which indicates that genotypes in this cluster are more diverse than the other clusters. In normal condition (NS), maximum inter cluster D^2 values were observed between cluster IV and V (2156.013) followed by cluster I and V (2138.739); while in saline/alkaline condition (SS), maximum inter cluster distance was observed between cluster II and IV (1750.460) followed by cluster II and V (1437.350) indicating wider genetic diversity between the genotypes in these clusters.

Large inter-cluster distance signifies that genotypes grouped in these clusters were different from the genotype of other clusters for one or more characters, which made them so divergent from other. Selection of diverse parents having most of the desirable characters from such clusters and using them in breeding programs is likely to produce more trangressive segregants and heterotic F1's when crossed.

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