Genetic diversity analysis in Indian mustard (*Brassica juncea*)

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Abstract

Genetic divergence assessed in ninety genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] using D^2 statistics for fifteen characters enabled grouping of all the genotypes into nine clusters. Number of primary branches/ plant, number of secondary branches/ plant, siliqua angle, siliquae on main shoot, primary branch angle, 1000- seed weight, and main shoot length were the major contributors for genetic diversity among the genotypes. Out of 9 clusters, cluster I was the largest comprising 20 genotypes followed by cluster II consisting of 18 genotypes, cluster III with 15 genotypes, whereas, clusters IV, V, VI, VII, VIII and IX contained 10, 8, 7, 7, 3 and 2 genotypes, respectively. The cluster V exhibited maximum intra- cluster distance (5.69), while maximum inter-cluster distance was observed between cluster VIII and IX (9.76).

Key words: Indian mustard, genetic divergence, D^2 analysis, cluster analysis

Introduction

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. These crops are cultivated on an area of 6.51 million ha with a total net production of 7.67 million tonnes, and with an average yield of 1179 kg/ha (Anonymous, 2011). 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 90 elite genotypes of Indian mustard.

Materials and Methods

The present study was carried out at the research farm of the Oilseeds Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *rabi*, 2010-11. Ninety diverse genotypes of Indian mustard (*B. juncea*) were planted in randomized block design with three replications in plot size of 1.5 x 5m. The row to row and plant to plant distance was maintained at 30x15 cm. All recommended package of practices was applied to raise a good crop. The data were recorded on fifteen characters, *viz.* days to 50% flowering, days to maturity, plant height (cm), number of primary branches/plant, number of secondary branches/plant, primary branch angle, main shoot length (cm), number of siliquae on main shoot, siliqua density, arrangement of siliqua based upon angle from main shoot, siliqua length (cm), number of seeds/ siliqua, seed yield/ plant (g), 1000- seed weight (g), 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 (1985).

Results and Discussion

The analysis of variance and dispersion were highly significant among all the genotypes for all fifteen

Table 1: Clustering pattern of 90 genotypes of Indian mustard

Cluster	No. of genotypes	Genotypes
1	20	RH-0555, RH-8812, RH-0506, RH-0935, RH-0703, RH-0956, RH-0813, RH-30, RH-0644, RH-0406, RH-0504, RH-0868, RH-0427, RH-0878, RH-0831, RH-0630, RH-0882, RH-0923, RH-0950, RH-0931
2	18	RH-0572, RH-0717, RH-0664, RH-0708, RH-0675, RH-0673, RH-0725, RH-0843, RH-0640, RH-0959, RH-0731, RH-0707, RH-0948, RH-0902, RH-0903, RH-0915, RH-9304, RH-0784
3	15	RH-0447, RH-0832, RH-0749, RH-0830, RH-0748, RH-0865, RH-0836, RH-0901, RH-0833, RH-0840, RH-0856, RH-0871, RH-0735, RH-0834, RH-0905
4	10	RH-0954, RH(OE)-0903, EC-597328, RH-8814, RH(OE)-0904, Pusa Krishma, RH(OE)-0901, EC-597340, JM-6011, RH(OE)-0204
5	8	RH-0835, RH-0818, RH-0847, RH-0907, RH-0857, RH-0922, RH-0911, RH-0919
6	7	RH-0613, RH(OE)-0801, RH-0904, RH-0910, RH-0913, RH-0908, RH-0920
7	7	RH-0838, RH-0912, RH-0825, RH-0952, RH-0906, RH-0932, RH-0807
8	3	RH-0848, EC-552578, RH(OE)-0902
9	2	RH-0846, RH-0850

characters studied which revealed the presence of considerable genetic variability among the genotypes. All 90 genotypes were grouped into 9 clusters using the Tocher's method (Table 1). Out of 9 clusters, cluster I was the largest comprising 20 genotypes followed by cluster II with 18 genotypes and cluster III with 15 genotypes; clusters IV, V, VI, VII, VIII and IX contained 10, 8, 7, 7, 3 and 2 genotypes, respectively, although these were solitary in regard to multivariate composition. 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.* number of secondary branches/ plant (27.1) followed by number of primary branches/ plant (11.2), siliqua angle (9.7), siliquae on main shoot (9.4), primary branch angle (6.4), 1000- seed weight (5.8), and main shoot length (5.6) contributed more than 75 % towards the total

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

Characters	% contribution
Days to flowering	1.62
Days to maturity	0.52
Plant height	1.89
No. of 1^0 branches/ plant	11.19
No. of 2^0 branches/ plant	27.06
Primary branch angle	6.41
Main shoot length	5.63
Siliquae on main shoot	9.35
Siliqua density	5.1
Siliqua angle	9.74
Siliqua length	3.97
No. of seeds/ siliqua	4.93
1000- seed weight	5.79
Oil content	2.02
Seed yield/plant	4.78

Table 3: Cluster mean values for seed yield and its component characters in Indian mustard

Cluster	Days to flowering	Days to maturity	Plant height	No. of 1^0 branches/ plant	No. of 2^0 branches/ plant	Primary branch angle	Main shoot length	Siliquae on main shoot	Siliqua density	Siliqua angle	Siliqua length	No. of seeds/ siliqua	1000- seed weight	% Oil content	Seed yield/pla nt
I	54.0	145.9	2.1	4.1	13.8	35.1	80.4	52.8	1.6	25.4	4.1	17.7	5.8	40.1	27.0
II	50.8	146.4	2.2	4.1	12.3	32.5	79.2	43.8	1.8	26.1	4.3	12.8	5.7	41.3	24.0
III	56.6	147.8	2.2	4.2	12.8	32.7	79.8	45.4	1.8	25.5	4.9	14.8	6.0	39.5	25.6
IV	53.8	145.1	2.2	4.3	12.7	21.5	77.3	52.0	1.5	24.5	3.7	13.5	4.4	39.5	24.0
V	51.4	147.0	2.4	5.0	20.1	34.3	91.7	53.6	1.7	26.7	5.0	15.8	4.9	38.6	32.5
VI	51.8	142.7	2.2	5.2	19.1	33.0	88.4	58.0	1.5	26.0	4.2	13.8	4.9	38.5	27.4
VII	52.1	145.4	2.1	4.2	16.5	31.4	91.6	44.8	2.1	26.3	4.5	15.3	4.9	38.7	26.6
VIII	56.2	147.4	2.4	4.7	14.1	26.3	82.0	47.8	1.7	40.3	4.2	12.8	4.2	36.0	23.8
IX	52.3	147.2	2.2	7.4	39.5	29.3	108.7	75.2	1.5	23.2	4.5	14.7	5.5	38.7	31.1
Mean	53.3	146.1	2.2	4.5	15.0	31.7	82.9	49.9	1.7	26.1	4.4	14.9	5.2	39.0	26.9

divergence (Table 2). Parallel to the present results, maximum contribution towards the divergence for number of secondary branches/ plant was previously reported by Doddabhimappa *et al.* (2010), and number of siliquae on main shoot by Somu (2001).

The cluster means for different characters are presented in Table 3. Cluster IX possessed high mean values for number of primary branches/ plant (7.43), number of secondary branches/ plant (39.50) , main shoot length (108.67), and number of siliquae on main shoot (75.17); cluster V for siliqua length (4.95) and seed yield/ plant (32.45); cluster I for primary branch angle (35.14) and number of seeds/ siliqua (17.68); cluster VIII for plant height (2.36) and siliqua angle (40.33); cluster VII for siliqua density (2.06); cluster II for oil content (41.25); cluster III for days to flowering (56.62), days to maturity (147.80), and 1000- seed weight (5.99). However, genotypes of clusters V were early in flowering and higher in seed yield. Cluster VI had minimum value for days to maturity (142.66). This further indicated that good parents could be selected for hybridization on mean basis. These results are supported by Goswami and Behl (2006), Kumar *et al.* (2007), and Yu-cheng *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 4). The intra-cluster D^2 values varied from 3.81 to 5.69 within cluster, and 4.70 to 9.76 between clusters**.** This indicated that clusters were homogenous within themselves and heterogeneous between themselves. The cluster V exhibited maximum intra-cluster distance (5.69) which indicates that genotypes in this cluster are more diverse than the other clusters. Maximum inter-cluster distance was observed between cluster VIII and IX (9.76) followed by cluster II and IX (9.62); cluster IV and IX (9.12); cluster III and IX (9.09); cluster I and IX (8.76); cluster VII and IX (8.57); cluster V and IX (7.68), and cluster VI and IX (7.20) 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

Table 4: Average intra (diagonal) and inter-cluster distances distance D^2 values in Indian mustard

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	3.81	4.94	4.70	5.29	6.09	5.13	5.04	6.62	8.76
II		3.99	4.82	5.29	6.44	5.58	4.89	6.13	9.62
III			3.99	5.76	6.00	5.83	5.03	6.23	9.09
IV				3.90	6.86	5.14	5.57	5.94	9.12
V					5.69	5.76	5.85	7.06	7.68
VI						3.88	5.17	6.47	7.20
VII							3.83	6.30	8.57
VIII								4.81	9.76
IX									4.80

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 F_1's when crossed.

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