Diversity analysis in Indian mustard (*Brassica juncea* Czern & Coss.)

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Abstract

Genetic divergence was studied for seed yield and 11 other important yield components in 84 entries/ genotypes of Indian mustard (*Brassica juncea* Czern & Coss.). Cluster analysis partitioned the entries into six clusters. The clustering pattern indicated that all the 28 entries having tetralocular siliqua were accommodated in a single cluster VI whereas remaining 56 entries with bilocular siliqua were spread over in five clusters (I to V). Clusters I, II, III and IV had 27, 4, 17 and 7 entries, respectively. Cluster V was a solitary cluster having a single entry. The mean values of the characters in various clusters exhibited that different clusters were superior in respect of different characters. The inter-cluster Euclidean^2 distance was maximum between clusters V and VI (110.8) followed by clusters I and V (88.5), clusters III and V (79.8), clusters II and V (76.9) and clusters IV and V (64.9). The crosses between genotypes of these diverse clusters might be having more chances of getting desirable segregants. Contribution of different characters towards total genetic divergence revealed highest contribution of seeds/ siliqua (10.5%) followed by main raceme length (10.4%), siliquae on main raceme (10.0%), siliqua length (8.5%), primary branches/ plant (8.1%) and seed yield (8.1%).

Key words: *Brassica juncea*, genetic diversity, cluster analysis

Introduction

Amongst oilseed *brassica*s, Indian mustard (*Brassica juncea* Czern and Coss.) is the major crop in India occupying nearly 90% of the area under oilseed *Brassica* (Prakash *et al.* 2004). To increase productivity of any crops, breeders have aimed to develop high yielding and better quality cultivars. This is normally achieved by selecting the desirable genotypes in the segregating generation following hybridization. For the choice of diverse parents, the information on genetic relationships and diversity among the available genotypes are helped in formulation of crop improvement programme. Assessment of genetic diversity in germplasm collection can facilitate classification and identification of genotypes with possible utility for specific breeding purposes. The utility of classifying germplasm to select diverse parents for hybridization had been appreciated (Bhatt, 1970). Therefore, an attempt has been made to study genetic divergence among the genotypes of Indian mustard.

Materials and Methods

A total of 84 entries, including 28 tetralocular siliqua and brown seeded, 27 bilocular siliqua and yellow seeded, and 29 bilocular siliqua and brown seeded, were sown in group block design with three replications at Agricultural Research Station, Mandor- Jodhpur, India. The plots were comprised of five rows of 5 m length, and the spacing between rows and between plants within the row were 30 and 10 cm, respectively. Observations on 12 agronomical important characters were recorded on five randomly selected plants from each plot, except days to flowering, days to maturity, oil content and seed yield which were recorded on whole plot basis. The data were subjected to analysis of variance following standard method (Gomez and Gomez 1976). The clustering was performed by procedure of Ward's minimum variance method (Ward 1963) using INDOSTAT software (Indostat Services, Hyderabad).

Results and discussion

Mean sum of squares (MSS) between three groups were highly significant for all the characters showing greater variability among the groups (Table 1). Similarly MSS for all the characters within groups, except plant height, primary branches/ plant, main raceme length, siliquae/ plant and siliqua length in tetralocular group, were also significant depicting large variability for these attributes.

A hierarchical cluster analysis of Ward's minimum variance method produced a dendrogram showing successive fusion of individuals which clearly partitioned the genotypes into six clusters (Fig. 1). The clustering pattern indicated that all the 28 entries having tetralocular siliqua were accommodated in a single cluster VI whereas remaining 56 entries having bilocular siliqua were spread over in five clusters (I to V). Clusters I comprised 27 entries (24 brown seeded and 3 yellow seeded). Cluster II had four entries having brown seed color while cluster III comprised 17 entries all with yellow seed color. Cluster IV had seven entries (6 yellow seeded and 1 brown seeded). Cluster V was a solitary cluster having a single entry with yellow seed color.

The mean values of the characters in various clusters exhibited that different clusters were superior in respect of different characters (Table 2). Cluster I comprised entries with the earliest maturity and maximum seed yield. Cluster II had entries with the longest main raceme and maximum siliquae on main raceme. Cluster III comprised entries with the maximum oil content.

Cluster IV comprised entries with the longest siliqua. Cluster V had a single entry with the tallest height, maximum primary branches/ plant and maximum siliquae/ plant. While entries comprised in cluster VI were earliest in flowering and had the maximum seeds/ siliqua and highest 1000-seed weight.

The intra-cluster Euclidean^2 distances ranged from 8.8 (cluster VI) to 15.8 (cluster II) and did not transgress the limit of any of the inter-cluster distances (Table 3). The inter-cluster distances ranged from 18.8 to 110.8. The wide range of distances revealed that enormous diversity among the genotypes under study. The inter-cluster distance was maximum between clusters V and VI (110.8) followed by clusters I and V (88.5), clusters III and V (79.8), clusters II and V (76.9), and clusters IV and V (64.9). The crosses between genotypes of these diverse clusters might be having more chances of getting desirable segregants (Arunachalam *et al.* 1984). The inter-cluster proximity was maximum between clusters I and III, indicating that these were closely related.

Contribution of different characters towards total genetic divergence revealed highest contribution of seeds/ siliqua (10.5%) followed by main raceme length (10.4%), siliquae on main raceme (10.0%), siliqua length (8.5%), primary branches/ plant (8.1%) and seed yield (8.1%). These attributes could be offered ample scope for selection of desired genotypes. Dhillon *et al.* (1999) reported that seed yield/ plant and main raceme length were contributed maximum to divergence while Arunachalam *et al.* (2005) found that flowering time and single plant yield were contributed nearly 50% to divergence in *Brassica*.

Table 1. Analysis of variance showing mean sum of squares for different characters in *B. juncea*

Characters	Source of variation						
	Replication	Group	Error (a)	Within groups			
	(2)	(2)	(4)	Tetralocular siliqua and brown seeded (28)	Bilocular siliqua and yellow seeded (27)	Bilocular siliqua and brown seeded (29)	Error (b) (162)
Days to flowering	15.43	391.43**	8.21	48.25**	12.45**	63.17**	1.93
Days to maturity	9.69	1340.03**	2.69	4.65**	3.69**	6.55**	1.45
Plant height (cm)	14.55	10246.87**	23.18	536.55**	163.31	353.16**	123.31
Primary branches/ plant	0.18	16.92*	1.94	0.95**	0.42	0.57**	0.30
Main raceme length (cm)	23.72	987.69**	72.91	252.48**	66.73	230.02**	66.67
Siliquae on main raceme	55.86	4920.97**	64.16	69.91**	66.46**	43.29*	26.38
Siliquae/ plant	3060.60	557735.86**	6335.09	14679.99**	2080.28	12467.31**	2302.37
Siliqua length (cm)	0.33	43.96**	0.08	1.37**	0.09	1.21**	0.13
Seeds/ siliqua	0.05	265.97**	1.02	3.75**	7.57**	4.64**	1.36
1000-seed weight (g)	0.03	200.51**	0.10	1.96**	0.74**	0.67**	0.24
Oil content (%)	8.49	387.95**	2.19	21.96**	7.37**	23.30**	0.92
Seed yield (t/ha)	0.08	4.49**	0.03	0.43**	0.22**	0.50**	0.04

*, ** Significant at 5 and 1 per cent, respectively; figures in parentheses showed *df*

Table 2. Character means in six-clusters of *B. juncea* entries

Characters	I	II	III	IV	V	VI
Days to flowering	46.15	45.25	44.28	50.24	62.00	43.37
Days to maturity	129.83	130.83	130.47	133.24	137.00	130.68
Plant height (cm)	186.57	212.00	187.69	185.57	219.67	173.02
Primary branches/ plant	4.48	4.03	5.48	5.55	6.87	4.92
Main raceme length (cm)	84.67	90.92	87.77	76.24	75.0	88.00
Siliquae on main raceme	43.75	47.83	32.92	29.91	46.33	35.49
Siliquae/ plant	328.33	317.42	327.16	276.57	411.33	183.45
Siliqua length (cm)	5.27	5.00	6.18	7.07	4.17	4.62
Seeds/ siliqua	13.47	11.93	13.30	13.26	11.00	16.16
1000-seed weight (g)	5.29	5.97	5.70	5.95	3.55	8.17
Oil content (%)	37.0	36.28	37.54	33.29	36.47	33.98
Seed yield (t/ha)	2.71	2.30	2.39	2.11	1.36	2.47

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Table 3. Euclidean^2 distances between the six clusters of *B. juncea* entries

Cluster	I	II	III	IV	V	VI
I	12.5	20.5	18.8	36.0	88.5	25.9
II		15.8	27.0	44.3	76.9	35.6
III			11.9	25.4	79.8	25.4
IV				13.5	64.9	35.8
V					0.0	110.8
VI						8.8

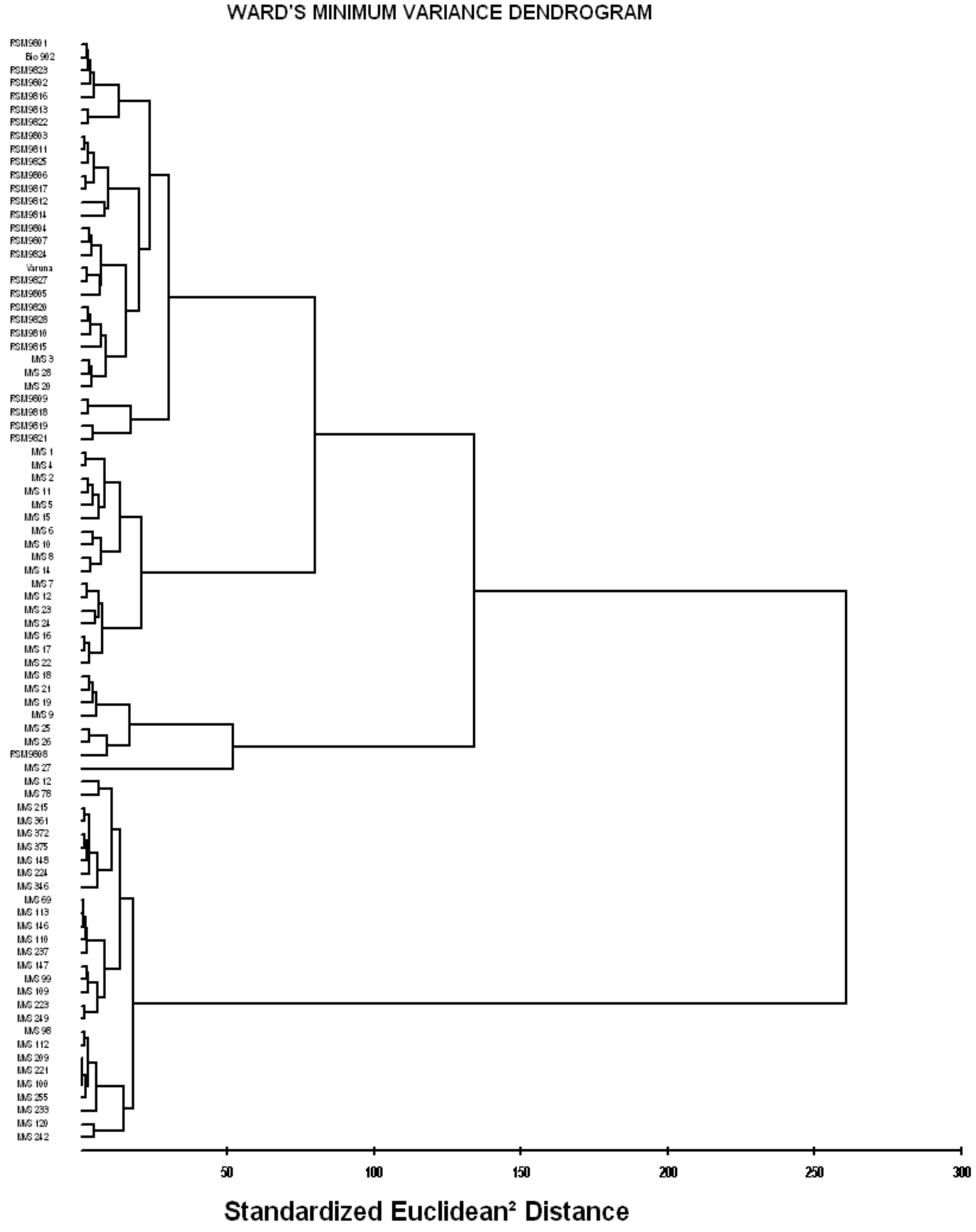

Figure 1. Dendrogram showing different clusters of *Brassica juncea* entries