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Short Communication

Genetic divergence in novel determinate variants of resynthesized Indian mustard (*Brassica juncea* (L.) Czern & Coss)

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Abstract

A field experiment was conducted to study the genetic diversity in 125 genotypes with determinate plant growth habit in *Brassica juncea* along with 3 indeterminate check varieties PBR 357, Coral 432 and DMH 1 as per alpha lattice design with two replications at PAU, Ludhiana. Mahalanobis' D^2 analysis grouped genotypes into 12 clusters. Clusters 1, 2 and 6 were considered ideal for future breeding efforts based on inter genotypic distance and other agronomic performance. Out of the fifteen traits evaluated, yield (kg/ha) and pods/plant contributed the most towards the divergence (81.06% and 18.58%, respectively).

Key words: Indian mustard, determinate, Mahalanobis' D^2, flowering, genetic diversity

The genus Brassica belongs to the Brassicaceae family which comprises important oilseed, vegetable, condiment, and fodder crops from economic and industrial perspective. In India, rapeseed (6.34 million ha) ranks third after soybean and groundnut for the area occupied for oilseeds and total oil seed production (www.faostat.fao.org).

Indian mustard (*B. juncea*) has a narrow genetic base (Bañuelos et al. 2013) and by resynthesis, novel alleles can be mobilized from extant progenitors to the cultivated varieties. Resynthesized amphiploids form rich reservoirs of genetic diversity inspite of their lower yields (Bansal et al. 2009). A technique of derived amphiploidy was developed that allowed resynthesis of *B. juncea* (AB; n = 18), through hybridizing elite genotypes from related digenomic species, *B. napus* (genome AC; n = 19) and *B. carinata* (genome BC; n = 17). It allowed capitalization of the enormous variation that followed the initial resynthesis through derived amphiploidy. A very important and rather unexpected outcome from these studies was the occurrence of determinate *B. juncea* segregants in the progenies generated following derived amphiploidy (Gupta et al. 2014, Kaur and Banga 2015). *B. juncea* is naturally indeterminate and the indeterminate inflorescence continues to grow, generating flowers from their periphery. On the other hand, determinate inflorescence has its apical meristem converted to floral meristem that terminates into pod. Tip sterility is present in indeterminate inflorescence. The objective of the present study was to develop the concept of determinate growth habit further by demonstrating high genetic diversity of determinate *B. juncea* genotypes.

A set of 125 A_8 determinate derived *B. juncea* allopolyploid genotypes (Kaur et al. 2014) along with three commercial controls, a variety PBR 357 and two hybrids *viz*., DMH 1 and CORAL 432 were sown in an alpha lattice design with two replications. In total, fifteen traits were measured. Days to flowering, maturity etc. was recorded based on the total plants/genotype whereas yield/plant, pods/plant, plant height, etc. data was recorded from five plants in each replication. Five rows were bulked harvested to measure seed yield of the genotype. Oil and protein content were evaluated using Near Infrared Reflectance Spectroscopy (NIRS) technique. For conducting Mahalanobis D^2 statistics, the computer programme, WINDOSTAT 8.0 cluster analysis was used. Tocher's method (Rao, 1952) was used for analyzing the contribution of each trait towards divergence.

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For the evaluation of genetic diversity among the genotypes and selection of parents for the breeding programme, D^2 analysis is an important method. D^2 analysis resulted in the grouping of genotypes to 12 clusters (Table 1). Variable number of genotypes in each cluster indicates the presence of genetic diversity in the material. Cluster 3 and 7 contained maximum number of accessions (29), followed by cluster 5 (28 accessions). Other clusters had 1-11 genotypes.

The important points considered while selecting genotypes were: (1) Choices of the clusters which are separated by maximum inter-cluster distance, (2) Selection of particular accessions that showed superior performance in the selected clusters. The inter cluster distances ranged from 330 (cluster 7 and cluster 8) to 3065.963 (cluster 6 and cluster 12). The genotypes included in clusters 6 and 12 exhibited maximum divergence indicating that the accessions included in these clusters were diverse in morphological features and performance than other clusters, followed by the genotypes of cluster 6 and 11. The genotypes of cluster 7 and 8 were least divergent. The minimum intra cluster distances were found to be zero in cluster 10 and 12 and maximum intra cluster distance in cluster 6.

The cluster mean values for 15 characters in Table 2 indicated considerable differences for all the characters between clusters. The cluster 10 had the lowest mean values for days to 50% flowering while cluster 2 had lowest value for days to 100% flowering and seed filling phase (Table 2). Maximum duration of flowering was in clusters 6 and 10. Determinacy has a great impact on the flowering habits and it shortened the flowering phases and maturity days in Indian mustard. All the mean values indicated a relatively earlier onset of complete flowering in determinate genotypes as compared to indeterminate commercial cultivars. In addition, mutations of the *TFL* locus are also known to impact flowering behaviour in *Arabidopsis* (Conti and Bradley 2007). Due to their earlier flowering and relatively a shorter duration of seed filling phase, a majority of the determinate plants showed lesser heights than that recorded for indeterminate plants. Cluster 11 had the lowest mean plant height. Dwarf stature is a preferred trait in mustard as tall plants tends to lodge easily. Cluster 10 had the maximum

Table 1. Cluster groups representing various genotypes and their number in each cluster

Cluster	No. of genotypes	Genotypes
1	8	DT-127-34, DT-124-1-34, DT-124-1-57, DT-108-1, DT-124-1-6, DT-124-1-17, DT-127-33, DMH1
2	4	DT-124-1-4, DT-57-8, DT-127-13, DT-127-14
3	29	DT-127-35, DT-124-1-44, DT-124-1-23, DT-124-1-52, DT-1-2- 5, DTA-49-1-2, DTA-72-1, DT-124-1-30, DT-124-1-62, DT-127-12, DT-127-20, DTA-91-19, DT-1-7, DTA-72-5, DT-1-2-3, DT-124-1-66, DT-72-3, DT-1-2-2, DT-38-2, DT-127-32, DTA-101-4, DT-1-6, DT-124-1-75, DT-124-1-64, DT-127-7, DT-124-1-7, DTA-91-12, DTA-49-1-1, DT-124-1-60
4	11	DT-124-1-12, DT-127-15, DT-108-4, DT-124-1-51, DT-127-18, DT-18-2, DT-124-1-35, DT-124-1-54, DT-127-25, DT-49-1-6, DTA-49-1-3
5	28	DT-124-1-19, DT-127- 40, DTA-72-7, DT-108-2, DT-57-20, DT-124-1-8, DT-92-1, DT-1-5, DT-1-2-4, DT-124-1-31, DT-124-1-3, DT-124-1-67, DT-127-11, DT-1-2-1, DT-72-1, DT-124-1-32, DT-57-10, DT-124-1-22, DT-124-1-38, DT-124-1-60, DT-127-39, DT-127-54, DT-124-1-5, DT-113-3, DT-124-1-73, DT-124-1-70, DT-124-1-71, PBR 357
6	2	DT-124-1-69, DT-127-30
7	29	DT-127-37, DTA-92-13, DTA-57-1, DTA-124-1-22, DT-1- 8, DT-124-1-56, DT-108-6, DT-127-16, DT-124-1-1, DT-124-1-36, DTA-27-18, DT-124-1-33, DT-72-4, DT-103-4, DT-127-51, DT-127-I12, DTA-92- 2, DT-124-1-43, DT-124-1-16, DT-49-1-2, DT-127-8, DT-108-5, DTA-57-3, DT-38-3, DT-124-1-76, DTA-72-21, DTA-91-9, DTA-72-27, Coral432
8	7	DT-127-42, DT-108-2, DT-127-36, DT-124-1-2, DT-38-1, DT-103-2, DTA-27- 20
9	2	DT-127- 50, DTA-57-4
10	1	DT-127-4
11	3	DT-127-31, DT-57-13, DT-127-9
12	1	DTA-101-3

Table 2. Character-wise cluster means of determinate genotypes

Cluster	Days to 50% flowering	Days to 100% flowering	Seed filling phase	Flowering phase (days)	Maturity days	Plant height (cm)	Pods/ plant	Pod length (cm)	Harvest index	1000-seed weight (gms)	Seed yield (kg/hec)	Oil (%)	Protein (%)	Glucos-inolates
1	54.6	65.6	125.7	71.0	140.7	158.3	491.7	4.6	.181	4.5	3248.9	37.8	28.8	85.3
2	52.5	62.1	123.6	71.1	145.5	168.5	805.6	4.6	.188	4.7	3170.8	37.0	28.7	83.6
3	60.3	73.6	127.1	66.8	148.2	162.4	536.3	4.7	.140	4.5	2455.5	38.4	28.4	88.3
4	61.5	77.6	130.0	68.4	149.5	168.7	750.1	4.5	.145	4.2	2701.8	37.8	28.9	85.2
5	56.3	67.8	126.0	69.6	147.8	161.4	466.8	4.7	.175	4.7	2824.5	38.1	28.7	90.7
6	53.0	64.0	127.0	74.0	149.0	156.4	484.5	4.6	.175	4.1	4133.7	38.3	28.8	86.1
7	58.3	70.3	126.4	68.1	147.8	157.9	423.0	4.7	.129	4.5	2123.9	38.1	28.4	90.7
8	64.2	77.2	127.7	63.4	150.7	166.8	560.0	4.7	.157	4.2	1875.5	38.0	28.5	93.8
9	59.2	75.7	130.5	71.2	149.2	162.4	778.3	4.3	.150	3.5	2208.8	36.5	27.5	78.3
10	50.5	68.0	124.5	74.0	152.0	143.1	1206.8	5.1	.100	4.7	2005.1	36.2	28.9	80.0
11	54.3	66.1	125.6	71.3	144.3	137.4	463.0	4.5	.117	3.7	1496.7	38.3	28.4	83.6
12	85.0	100.5	136.0	51.0	154.0	172.4	432.0	4.3	.100	3.1	1070.3	38.7	25.9	70.7
Mean	58.5	71.1	126.8	68.3	147.7	161.1	526.1	4.7	.150	4.4	2509.3	38.1	28.5	88.6

value for pods/plant. The variation for seeds/ pod expectedly reflected trend recorded for pod length as the values were higher than the indeterminate genotypes. Cluster 6 had the highest value for seeds/pod. 1000 seed weight value was highest in cluster 5 while cluster 2 had highest mean harvest index (Table 2). Yield was highest for cluster 1. Thus, Clusters 1, 2 and 6 were ideal for superior performance of yield contributing traits. Oil and protein was highest for cluster 12 and cluster 10, respectively. Oil content was generally higher in indeterminate mustard check genotypes. It may be more due to the background genetics rather than the growth habit. The choice of the genotypes should be made considering the mean performance of the genotypes in respect to various characters as well as inter cluster differences. Tocher's method was used to calculate the individual contribution of all the traits to divergence. Out of the 15 traits evaluated, seed yield contributed highest (81.06%) towards the divergence, followed by pods/plant (18.58%) and plant height (0.23%). Remaining traits contributed in significantly towards the genetic divergent in resyntehsized variants. To recapitulate, the present study ensues that genotypes showing greater divergence can be considered for utilization in crossing program. The study revealed the broader genetic base of the resynthesized *B. juncea* genotypes and use of determinate germplasm for breeding programme.

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