

ASSESSMENT OF GENETIC DIVERSITY AND GENETIC POTENTIAL OF RECOMBINANT INBRED LINES OF *Brassica juncea* (L.)

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ABSTRACT

Twenty four recombinant lines along with four checks were evaluated to estimate the extent of variation between recombinant lines and to find the extent of deviation of these recombinant lines from the checks and to select the best recombinant lines for further use in breeding programme. Twenty four recombinant lines along with four checks were raised during *rabi* 2014-15 in three replications at the farm of Agricultural Botany Section, College of Agriculture, Nagpur and data were recorded for days to 50% flowering, days to maturity, plant height at maturity (cm), number of branches plant⁻¹, number of siliquae plant⁻¹, number of seeds siliquae⁻¹, length of siliquae (cm), seed yield plot⁻¹ (Kg ha⁻¹), seed yield plant⁻¹ (g) and 1000 seed weight (g). Considerable variability existed among the genotypes for all characters studied as observed from the significant mean squares due to genotypes. The recombinant lines were grouped into six clusters indicating the presence of wide range of diversity among them. Seed yield plot⁻¹, seed yield plant⁻¹, number of siliquae plant⁻¹, plant height at maturity and days to maturity contributed maximum towards genetic divergence. Twenty four recombinant lines and four checks were grouped into six clusters. The grouping of recombinant lines into different clusters clearly showed that many of recombinant lines were highly deviating from the checks. Only five recombinant lines ACN 205, ACN 198, ACN 196, ACN 195, ACN 194 were found promising which had maximum intercluster distance between the clusters and the cluster involving checks, along with high mean performance for seed yield plot⁻¹, seed yield plant⁻¹, number of siliquae plant⁻¹ and hence, may be promoted for evaluation in trial for further varietal improvement.

(Key words: Recombinant lines, inter cluster distance, genetic diversity)

INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern and Coss.] is called as “rai”, “raya” or “laha” is one of the important oilseed crops belonging to Brassica group. Indian mustard belongs to the family Cruciferae, genus *Brassica* with chromosome number 2n=36. Over 159 species have been reported in genus *Brassica*. The important species of *Brassica* that are extensively cultivated commercially are *B. rapa*, *B. juncea* and *B. napus*. Mustard is an important oilseeds crop contributing more than 13 per cent to the global production of edible oil. Seed is having 33 to 48 per cent oil (Choudary *et al.*, 2015).

Planned hybridization between two or more selected lines is very useful and effective technique to recombine selected variability into desired combination. The number of possible recombinants that can be obtained through hybridization depends on number of loci for which the parent differ, the number of alleles at each locus and linkage relationship of genes at different loci. Higher the number of loci difference between the two parents, more is possible numbers of genotypes in F₂ assuming the absence of linkage. Hence, screening of the potential F₁'s which

would produce superior recombinants is necessary. Such superior F₁'s may be further handled by pedigree, bulk or single seed descent method (S.S.D.). But S.S.D. is preferable as the entire genetic variability is maintained. For further advancement of generation after homozygosity has reached, the genotypes may be evaluated for superiority over checks by testing randomized block design. The present investigation was carried out to evaluate the performance of 24 recombinant lines and test its deviation from the check varieties on basis of multivariate analysis used in D² statistics.

MATERIALS AND METHODS

The experiment was carried out at the farm of Agricultural Botany Section, College of Agriculture, Nagpur during *rabi* 2014-15. The experimental material consisted of twenty eight recombinant lines planted in randomized block design with three replications in plot size of 3 m x 1.5 m. The row to row and plant to plant distance was maintained at 45 cm x 15 cm. All recommended package of practices was applied to maintain good crop. The data was recorded on ten characters, *viz.*, days to 50% flowering, days to maturity,

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plant height at maturity (cm), number of branches plant⁻¹, number of siliquae plant⁻¹, number of seeds siliquae⁻¹, length of siliquae (cm), seed yield plot⁻¹ (kg ha⁻¹), seed yield plant⁻¹ (g) and 1000 seed weight (g). Mahalanobis (1936) D² statistics was used for assessing genetic divergence among all the genotypes. The clustering of D² values was done using Tocher's method as described by Rao (1952), while the intra and intercluster distances were calculated using the formula given by Singh and Choudary (1985).

RESULTS AND DISCUSSION

The analysis of variance (Table 1) was highly significant among all the genotypes for all ten characters studied which revealed the presence of considerable genetic variability among the genotypes. Data regarding the

contribution of each character towards genetic divergence are presented in table 2. Contribution of seed yield plot⁻¹ was maximum (52.65%), followed by seed yield plant⁻¹ (18.78%), number of siliquae plant⁻¹ (11.11%), siliquae length (6.35%), number of seeds siliquae⁻¹ (4.76%), number of branches plant⁻¹ (3.17%), days to 50% flowering (1.59%), 1000 seed weight (1.06%), days to maturity (0.53%) and plant height (0.00%). This indicates that character like seed yield plot⁻¹, seed yield plant⁻¹ and number of siliquae plant⁻¹ were important traits contributing towards genetic divergence. Similar to this results Singh *et al.* (2010) and Zaman *et al.* (2010) also reported maximum contribution of seed yield plant⁻¹ towards total divergence in mustard. Pandey *et al.* (2013) and Kumar *et al.* (2013) reported high contribution of number of siliquae plant⁻¹ towards total divergence in mustard.

Table 1. Analysis of variance for ten characters

Source of variation	d.f.	Mean sum of squares									
		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of siliquae plant ⁻¹	No. of seeds siliquae ⁻¹	Length of siliquae (cm)	1000 seed weight (g)	Seed yield plot ⁻¹ (kg ha ⁻¹)	Seed yield plant ⁻¹ (g)
Replication	2	49.08	53.72	354.18	0.23	33.57	1.09	0.08	0.37	1439.79	1.84
Treatment	27	112.77**	115.21**	637.94**	2.31**	3235.25**	31.23**	0.53**	1.55**	62998.43**	32.69**
Error	54	31.51	20.57	230.85	0.21	29.37	0.96	0.04	0.25	2623.77	0.65

All 28 genotypes were grouped into six clusters by using Tocher's method (Table 3). Out of six clusters, cluster I was the largest comprising 10 recombinant inbred lines followed by cluster IV with 9 recombinant inbred lines clusters II, III, V and VI contained 4, 3, 1 and 1 recombinant inbred lines, respectively. The checks Shatabdi, BIO 902, Pusabold and Kranti grouped into cluster I along with six

recombinant lines. Grouping of mustard genotypes into different clusters was also reported by Budhanwar *et al.* (2010), who grouped 270 recombinant inbred lines of mustard into 18 clusters. Recombinant lines grouped in the same cluster as that of the check showed very little diversity between them in respect of the ten characters under study.

Table 2. Contribution of different characters towards genetic divergence in mustard

Sr. No.	Characters	Times ranked 1 st	Per cent Contribution
1	Days to 50% flowering	6	1.59%
2	Days to maturity	2	0.53%
3	Plant height at maturity (cm)	0.01	0.00%
4	Number of branches plant ⁻¹	12	3.17%
5	Number of siliquae plant ⁻¹	42	11.11%
6	Number of seeds siliquae ⁻¹	18	4.76%
7	Length of siliquae (cm)	24	6.35%
8	1000 seed weight (g)	4	1.06%
9	Seed yield plot ⁻¹ (kg ha ⁻¹)	199	52.65%
10	Seed yield plant ⁻¹ (g)	71	18.78%
	Total	378	100%

The clusters having high inter cluster distance between themselves and checks are expected to yield better. Data regarding average intra and inter cluster distance among ten characters were worked out and are presented in table 4. The intra cluster distance ranged from 0.00 to 27.28.

Cluster IV possessed highest intra cluster distance (D²= 27.28) followed by cluster III (D²= 25.48) and cluster II (D²=16.80). The average inter cluster-cluster distance was maximum between cluster III and cluster VI (D²=1112.04) followed by cluster V and VI (D²=775.42) and cluster II and

cluster VI ($D^2=506.66$) suggesting more variability in genetic makeup of genotypes included in these clusters. The inter cluster distance was found to be minimum between cluster

I and cluster VI ($D^2=28.29$) followed by cluster I and II ($D^2=47.18$). (Table 4)

Table 3. Grouping of recombinant lines into different clusters

Cluster	No. of recombinant lines	Name of recombinant line
I	10	Shatabdi, BIO 902, ACN 204, Pusabold, IC 342718, Kranti, ACN 208, IC333199, ACN 202, ACN 199
II	4	ACN 206, ACN 207, ACN 200, ACN 195
III	3	ACN 194, ACN 196, ACN 205
IV	9	IC355314, IC355327, GSL 1, ACN 203, ACN 193, Bhawani, ACN 197, ACN 201, PC 5
V	1	ACN 198
VI	1	Ragini

Cluster means for days to 50% flowering, days to maturity, plant height at maturity, number of branches plant⁻¹, number of siliquae plant⁻¹, seed yield plant⁻¹ and seed yield plot⁻¹ are highest in cluster II, cluster III and cluster IV (Table 5). The variance for cluster means was maximum for seed yield plot⁻¹, number of siliquae plant⁻¹, days to maturity and plant height. The selection of recombinant inbred lines and subsequent genetic improvement may be made on the basis of the characters exhibiting maximum variation and expected to be genetically

diverse. Thus, from this study it is stated that recombinant inbred lines may be selected for hybridization on the basis of number of branches plant⁻¹, number of siliquae plant⁻¹, seed yield plot⁻¹ and seed yield plant⁻¹. Kumar *et al.* (2013), Lodhi *et al.* (2013) Shathi *et al.* (2012) also reported the importance of 50% flowering, days to maturity, plant height at maturity, number of branches plant⁻¹, number of siliquae plant⁻¹, seed yield plant⁻¹ and seed yield plot⁻¹ for genetic divergence in mustard.

Table 4. Average intra and inter cluster distance

Cluster	I	II	III	IV	V	VI
I	(10.91)	47.18	332.12	28.88	165.79	322.07
II		(16.79)	159.19	96.93	83.76	506.66
III			(25.47)	448.38	102.48	1112.03
IV				(27.27)	253.82	255.17
V					(0.00)	775.41
VI						(0.00)

Note : $\bar{D} = 111.66$

Bold figures are average intra cluster distance.

Table 5. Cluster means for ten characters

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of siliquae plant ⁻¹	No. of Seeds siliquae ⁻¹	Length of siliquae (cm)	1000 seed weight (g)	Seed yield plot ⁻¹ (kg ha ⁻¹)	Seed yield plant ⁻¹ (g)
I	48.40	107.93	123.96	4.13	83.92	14.09	4.61	3.88	476.80	10.54
II	52.23	110.15	139.97	4.51	84.46	12.58	4.74	4.32	604.82	14.11
III	38.66	96.00	99.96	2.50	41.40	29.37	6.12	3.43	237.00	10.43
IV	49.88	110.11	129.95	4.70	174.75	13.61	4.78	3.82	1495.55	20.76
V	50.73	109.73	150.13	4.98	115.72	13.45	4.57	4.67	846.20	16.36
VI	52.33	109.00	132.73	5.93	92.47	13.93	4.39	2.93	1420.00	18.90
S.D.	5.13	18.10	17.02	1.13	44.30	6.48	0.62	0.61	513.17	4.28
Variance	26.40	327.72	289.82	1.28	1963.29	42.08	0.39	0.38	263349.09	18.32

Selection of recombinant lines was done based on yield plant⁻¹ showing significant superiority over best check BIO 902 and for number of siliquae plant⁻¹, superiority over best check Pusabold. Recombinant lines ACN 205, ACN 198, ACN 196, ACN 195, ACN 194 were significantly superior over the best checks Pusabold and BIO 902 for

number of siliquae plant⁻¹ and seed yield plant⁻¹ (Table 6).

On the basis of the present study it will be advisable to evaluate all these five recombinant lines in preliminary yield trial along with standard checks as they have the maximum intercluster distance with those clusters involving checks and also significantly superior mean

performance for seed yield plant⁻¹ and number of siliquae plant⁻¹. These inferences are drawn from the fact that clusters containing the recombinant lines are highly divergent from

clusters containing the check varieties. These recombinant lines on hybridization with existing check varieties may also be used for improvement of the check varieties.

Table 6. Average inter cluster distance of recombinant lines

Clusters	Distance between clusters	Recombinant lines (Selection based on)	
		Seed yield plant ⁻¹	Number of siliquae plant ⁻¹
I & III	332.13	ACN 205*, ACN 196 *, ACN 194*	ACN 205+ , ACN 196 +, ACN 194+
IV & V	253.87	ACN 198*	ACN 198+
I & V	165.79	ACN 198*	ACN 198+
II & III	159.20	ACN 194*, ACN 196*, ACN 194*	ACN 205+ , ACN 196 +, ACN 194+

$$\bar{D} = 111.66$$

Note : * Selection based on best check BIO 902

+ Selection based on best check Pusabold

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