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STUDIES ON GENETIC DIVERSITY, HETEROSIS AND COMBINING ABILITY IN INDIAN MUSTARD [*BRASSICA JUNCEA* L. (CZERN & COSS)]

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ABSTRACT

Genetic diversity, heterosis and combining ability studies were conducted in Indian mustard. A set of 48 apparently diverse lines was picked up from a germplasm of 118 lines on the basis of multiple regression analysis for seed yield. These 48 lines could be divided into five distinct groups on the basis of D^2 analysis for seed yield and component traits. The clustering pattern suggested that geographical diversity was not necessarily an index of genetic diversity. The study pointed out that relation existed between genetic diversity of parents and specific combining ability effects as well as heterosis exhibited by the crosses. Selection of parents based on diversity estimates, coupled with combining ability analysis, may be useful in the selection of suitable parents for a breeding programme.

Key words: Divergence, combining ability, heterosis, Indian mustard.

It has been a generally accepted view that genetic diversity plays a role in the manifestation of heterosis. The existence of heterosis in a hybrid usually demonstrates the existence of some degree of genetic diversity [1]. The choice of diverse parents with good general combining ability may help in substantial genetic improvement in crop plants with different breeding behaviours [2–5]. In the present study, the parents selected on the basis of diversity were crossed in a line x tester mating design to study the relationship between diversity as exhibited by parents and heterosis and specific combining ability effects of the crosses.

MATERIALS AND METHODS

EXPERIMENT I

As a prelude to the present study, a germplasm of 118 lines, taken from different geographic regions of India, were grown in augmented design. Normal cultural practices were followed to raise the crop. Data were recorded on seed yield, 1000-seed weight, pod number, primary and secondary branches, plant height, days to maturity, and days to 50% flowering. Multiple regression analysis for seed yield was conducted for preliminary screening of lines for diversity. Based on this screening, 48 lines were selected for further studies. Also, a set of 48 crosses was generated on 12 x 4 line x tester crossing pattern to study heterosis and combining ability effects.

EXPERIMENT II

The above mentioned 48 lines were grown during the next season in randomized block design using tier system with three replications for field study of morphological traits. These traits included length of main shoot and number of pods on the main shoot in addition to those for which data were recorded in experiment I. D^2 estimates were made following Mahalanobis' generalised distance as detailed by Rao [6]. Clusters were constructed following Tocher's method (cf. [6]).

EXPERIMENT III

The 48 crosses generated as a result of 12 x 4 line x tester crossing pattern were grown in compact family block design with three replications. In addition to the traits for which data were recorded in experiment II, observations were also made on oil content and oil yield. The data were analysed for combining ability using the method of Kempthorne [7].

RESULTS AND DISCUSSION

Analysis of variance in 118 germplasm lines showed highly significant genotypic differences for all the characters, namely, seed yield, 1000-seed weight, pod number, primary and secondary branch number, plant height, days to maturity, and days to 50% flowering. Multiple regression analysis was conducted using four characters which showed significant correlation with seed yield. However, partial regression of seed yield was significant only on secondary branch number ($b = 0.21^{**} \pm 0.07$) and pod number ($b=0.02 \pm 0.005$), whereas it was nonsignificant on plant height ($b = 0.01 \pm 0.01$) and primary branch number ($b = 0.34 \pm 0.30$). These four characters accounted for 62.60% of the variation for seed yield. However, an index based on only two characters, i.e. secondary branch number (SB) and pod number (PN), accounted for 61.4% of the total variation for seed yield. So, only these two characters were used to construct a regression function. The regression equation was :

$$Ye = 2.08 + 0.24\ SB + 0.02\ PN$$

The expected yields worked out from this function were used as index score for classifying the genotypes into five different groups (Table 1).

Table 1. Grouping of germplasm lines of *Brassica juncea* into clusters and their mean performance

Cluster	No. of genotypes	Observed mean yield	Yield expected on MRF	Genotypes selected for further studies
I	2	25.2	21.9	RLM 29/25, Prakash
II	7	14.2	17.4	RLM 198, RLM 612, RLC 1006
III	32	12.4	11.9	RLM 514, RLM 629, RLC 1000, RLC 1008, RLC 1101, RH 7859, RH 8113, P Rai 1002, P Rai 1118, P Rai 2081, KR 31, KR 5610, RK 14, RIK 80-3, Varuna, RG-I, RAUR I
IV	68	7.5	7.5	RLM 619, RLC 701, RLC 1017, RH 7823, RH 8112, RH 8304, P Rai 2002, KR I, RK 8301, RS 61, RS 64, RAURD 101, Kranti, KRV Tall, KRV Bold, Pusa Bold, UUR 751, DIR 152, RW 8559, YSR-I, TM 4
V	9	3.2	4.1	RLM 185, RH 765, RIK 3, RAURD-82-I, RW 1765

MRF: Ye = 2.08 + 0.24 SB + 0.02 PN; R^2 = 61.4%.

Six characters, namely pod number, pods on main shoot, primary and secondary branch number, plant height and days to 50% flowering, which showed significant correlation with seed yield, were used along with seed yield to perform D^2 analysis in 48 lines selected from germplasm on the basis of multiple regression analysis. Based on D^2 analysis, 48 lines were grouped into five clusters (Table 2). The average intracluster values ranged from a minimum of 13.8 in cluster V to a maximum of 21.9 in cluster III. Intercluster values also ranged from as low as 29.7 between clusters IV and V to as high as 81.3 between clusters I and V.

The mean values of morphological traits distinctly characterized each group with differential values for different traits. Cluster I was characterized by low mean values for all traits. Cluster II was also characterized by low estimates for all characters, except number of primary branches, plant height and days to flowering. The estimates for cluster III varied from high for most traits to average for plant height and days to flowering. Although high estimates for all traits characterized clusters IV and V, yet the sufficient numerical differences for mean values of different traits between these two clusters justifies their separate identity.

The grouping pattern of the lines indicates that the clusters were heterogeneous with regard to the geographical origin of genotypes included in them. Lines from different geographic regions were pooled in the same cluster. That the genetic diversity is not related to geographical distribution has also been previously reported [8, 9] in Indian mustard.

Table 2. Inter- and intracluster (in bold) values in different clusters of *Brassica juncea* and group characteristics

Clusters	I	II	III	IV	V	Genotypes	Total genotypes	Origin of genotypes
I	**20.8**	31.4	49.3	65.8	81.3	Varuna, RLM 514, RLM 619, RH 7823, RH 7859, RH 8113, P Rai 1002, P Rai 2002, KRV Tall, KRV Bold, RAUR D 82-I, RAUR D 101, DIR 152, Pusa Bold	14	1–Kanpur, 2,3–Ludhiana, 4–6–Hissar, 7,8–Pantnagar, 9,10–Kanpur, 11,12–Dholi, 13,14–Delhi
II		**19.1**	30.1	42.6	59.1	Kranti, RLC 1101, RK 3301, RH 765, RH 8112, RIK-80-3, RW 1765, KR 31, YSR I	9	1–Pantnagar, 2–Ludhiana, 3–Kanpur, 4,5–Hissar, 6–Kalyanpur, 7–Berhanpore, 8–Kanpur, 9–Ludhiana
III			**21.9**	29.7	42.5	RLM 198, RLM 612, RLM 629, RLC 1000, RLC 1006, RLC 1018, RK 14, RS-64, RIK 3, RW 8559, P Rai 1118, KRI, KR 5610 RAUR I	14	1–6–Ludhiana, 7,8–Kanpur, 9–Kalyanpur, 10–Berhanpore, 11–Pantnagar, 12,13–Kanpur, 14–Dholi
IV				**15.6**	29.7	Prakash, RLM 29/25, RLM 185, RLC 701, RLC 1017, RH 8304, RS 61, P Rai 2081, UUR 751	9	1–Hissar, 2–5–Ludhiana, 6–Hissar, 7–Kanpur, 8–Pantnagar, 9–Udaipur
V					**13.8**	RG-I, TM-4	2	1–Gurgaon, 2–Trombay

The genetic diversity between parents in the crosses along with heterosis and combining ability effects for certain selected crosses is presented in Table 3. Six crosses each for seed and oil yield, and four crosses for oil content exhibited high sca effects. Most of these crosses had at least one parent with high general combining ability (gca). All these crosses, except RH 8304 x Prakash, were the result of intercluster matings. The results suggested that heterosis and specific combining ability (sca) effects were related to the genetic divergence between parents. All the high sca crosses also exhibited high heterosis over midparent (MP) and better parent (BP). The cross PRai 1118 x Prakash, which exhibited highest sca for seed and oil yield, was a combination of high x high combining parents. It also exhibited the highest MP and BP heterosis. The cross RLM 185 x RLM 514 was another desirable cross. It exhibited the second highest sca for seed yield, oil yield, and also oil content. The parent genotypes RLM 185 and RLM 514 exhibited the highest divergence amongst all the parents. Their cross also exhibited highest BP heterosis for oil content and second highest BP and MP heterosis for seed and oil yield, and MP heterosis for oil content.

Table 3. Combining ability effects, diversity estimates (between parents) and heterosis for oil and seed yield, and oil content in selected crosses between high sca parents of *Brassica juncea*

Character	Cross (gca of parent)	Average cluster distances		Sca effect	Heterosis, %	
		cluster	$\sqrt{D^2}$		BP	MP
Oil and seed yield	RLM 185 (A) x RLM 514 (A)	IV x I	65.9	1.75 (3.62)	101.0 (92.5)	134.1 (118.6)
	RLM 612 (A) Prakash (H)	III x IV	29.7	1.24 (3.02)	76.0 (67.1)	98.5 (94.1)
	RH 8304 (A) x Prakash (H)	IV x IV	15.6	1.32 (2.87)	94.4 (81.1)	107.5 (8.4)
	RS 61 (A) x RLM 198 (L)	IC x III	29.7	1.46 (3.88)	37.3 (51.8)	46.8 (61.8)
	P Rai 1118 (H) x Prakash (H)	III x IV	29.7	2.34 (6.72)	161.0 (156.5)	172.6 (180.9)
	RAURI (A) x Kranti (A)	III x II	30.1	1.52 (3.36)	52.5 (51.8)	52.9 (52.8)
Oil content	KRV Tall (H) x Kranti (A)	I x II	31.4	1.71	3.8	9.0
	RLM 185 (H) x RLM 514 (H)	IV x I	65.8	2.00	4.7	7.1
	P Rai 1118 (L) xKranti (A)	III x II	30.1	1.57	0.9	6.6
	RLC 701 (A) x RLM 514 (H)	IV x I	65.8	2.10	2.3	6.1

Sca effects and heterosis for seed yield given in parentheses along with those for oil yield.
H, A, L—lines with high, average and low gca, respectively.

It can be concluded from the above findings that the breeder should not consider a particular geographic area as a uniform entity for genetic divergence but must evaluate the breeding lines on the basis of their individual merit and genetic diversity. It would be rewarding to select the parents based on the diversity estimates of the parents, heterotic effects of the crosses, and combining ability analysis. Anand and Rawat [4] also advocated the use of diversity coupled with combining ability to select suitable parents for a breeding programme in the Indian mustard.

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