



Genetic analysis in Indian mustard (*Brassica juncea*) through diallel mating

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Abstract

Genetic analysis in Indian mustard was done by using twelve parents crossed in half diallel mating design excluding reciprocals to obtain sixty six crosses with the objective to estimate the general and specific combining ability of parents and crosses respectively and also to isolate superior crosses for their use in further breeding programme. Sixty six crosses along with twelve parents were raised during *rabi* 2011- 2012, and data were recorded for days to 50% flowering, days to maturity, plant height at maturity (cm), number of primary branches plant⁻¹, number of siliqua plant⁻¹, 1000 seed weight(g), yield plant⁻¹(g), and oil content(%). Considerable variability existed among the genotypes for all characters as observed from the significant mean squares due to genotypes. The four crosses Vardhan x Kranti, Seeta x Ashirwad, Bio-902 x Ashirwad, and Kranti x ACN-9 were identified as best cross combinations on the basis of mean values for yield plant⁻¹ and number of siliqua plants⁻¹; seven crosses Vardhan x Laxmi, Vardhan x Kranti, Seeta x Ashirwad, Bio-902 x Ashirwad, Kranti x ACN-9, Laxmi x Geeta, and Vardhan x Laxmi were identified to exhibit significant sca effect in the desirable direction. The parents Bio-902 and PCR-7 were identified as best general combiners for yield and yield contributing characters on the basis of high mean performance and significant gca effects. Among the crosses Vardhan x Kranti, Seeta x Ashirwad, Bio-902 x Ashirwad, and Kranti x ACN-9 were identified as best F₁ cross combinations on the basis of high mean performance, high significant gca effect of one or both of the parents involved in the crosses and negative sca effects which can be forwarded to the next generation by following a simple selection method, or biparental mating in selected progeny followed by selection in segregating generation.

Key words: Combining ability, diallel, gca,, Genetic analysis, sca

Introduction

Indian mustard [*Brassica juncea* (L) Czern & Coss.] is called as “rai”, “raya” or “laha” is one of the important oilseed crops belonging to Brassicaceae 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*. The oil content in Indian mustard seed varies from 30 to 48 per cent.

The important mustard growing countries of the world are India, China, Canada, France, Poland and Pakistan. India is the second largest rapeseed

mustard growing country in the world and ranks third next to Canada and China in production. Major states producing mustard are Rajasthan, Punjab, Haryana, Uttar Pradesh, Madhya Pradesh, West Bengal and Gujarat. It is a minor crop of Vidarbha region of Maharashtra, often grown as mixed crop and hence, is one of the reason for lower productivity. The various mating designs have been used for assessing the breeding value of the parents through the estimation of variance and combining ability effects and analysis through diallel cross technique as suggested by Griffing (1956). Diallel analysis provides a mating design whereby the selected parents are crossed in all possible combinations.

Materials and Methods

The experimental material comprising of twelve

genotypes of mustard (*Brassica juncea*) were crossed in half diallel mating design excluding reciprocals to obtain 66 crosses during *rabi* 2010-2011. There 66 crosses along with 12 parents were raised in randomized complete block design in three replications with the spacing of 45 cm x 15 cm accommodating 15 plants in each row at the Shankar Nagar Farm of the Botany Section, College of Agriculture, Nagpur during *rabi* 2011-2012. Observations were recorded on five randomly selected plants in each replication for the characters including days to 50% flowering, days to maturity, plant height at maturity, number of primary branches⁻¹, number of siliqua plant⁻¹, 1000 seed weight, and yield plant⁻¹. The data were subjected to analysis of variance (Fisher, 1938), and analysis of combining ability (Griffings, 1956, Method 2 Model I).

Results and Discussion

The analysis of variance for experimental design was performed for seven characters and is presented in table 1. The mean squares due to genotypes was highly significant for all the characters studied i. e. days to 50% flowering, day to maturity, plant height at maturity, number of primary branches⁻¹, number of siliqua plant⁻¹, 1000 seed weight and yield plant⁻¹. The parents exhibited highly significant mean squares for plant height, number of primary branches⁻¹, number of siliqua plant⁻¹, 1000 seed weight and yield plant⁻¹. While the crosses exhibited significant mean squares for days to 50% flowering, days to maturity, number of primary branches⁻¹, number of siliqua plant⁻¹, 1000 seed weight and yield plant⁻¹. However, parents vs. crosses exhibited significant differences for only

Table 1. Analysis of variance for experimental design

Source	d.f.	Mean squares						
		Days to 50 % flowering	Days to maturity	Plant height at maturity (cm)	No. of primary branches plant ⁻¹	No. of siliqua plant ⁻¹	1000 seed weight (g)	Yield plant ⁻¹ (g)
Replication	2	13.67	9.56	345.53	0.51	554.03	0.34	0.24
Genotypes	77	27.91**	22.11**	174.59*	0.59**	1777.52**	0.37**	14.82**
Parents	11	23.96	22.09	362.22**	0.55**	1776.69**	0.47**	6.43**
Crosses	65	28.97**	22.44**	145.38	0.57**	1521.06**	0.35**	14.30**
Parents Vs. crosses	1	2.56	0.95	9.60	2.07**	18456.86**	0.34	140.03**
Error	154	16.28	13.00	115.20	0.17	255.68	0.1161	1.77

Note: * Significant at 5% level, ** Significant at 1% level

three traits namely number of primary branches⁻¹, number of siliqua plant⁻¹ and yield plant⁻¹ while non significant variation was recorded for days to 50% flowering, days to maturity, plant height and 1000 seed weight. Analysis of variance for the experimental design revealed the presence of substantial genetic variability among the genotypes which allows further estimation in the experimental material. The wide variability for per plant yield and yield contributing characters including, plant height (cm), number of primary branches, number of siliqua, and 1000 seed weight (g) in mustard were also observed by Aghao *et al.* (2010), Singh *et al.*

(2010), Ramesh (2010). Nasrin *et al.* (2011), Turi *et al.* (2011), and Vaghela *et al.* (2011).

Analysis of variance for combining ability is presented in table 2. The variation between crosses was partitioned into different components representing mean squares due to general combining ability (GCA) and specific combining ability (SCA). The mean squares due to gca was of higher magnitude than those due to sca indicating the relative importance of parents in the crosses. The mean squares due to gca were highly significant for all characters days to 50% flowering,

Table 2. Analysis of variance for combining ability

Source	d.f.	Mean squares						
		Days to 50 % flowering	Days to maturity	Plant height at maturity (cm)	No. of primary branches plant ⁻¹	No. of siliqua plant ⁻¹	1000 seed weight (g)	Yield plant ⁻¹ (g)
GCA	11	15.76**	11.11**	977.00**	145.43*	0.28**	0.22**	4.69**
SCA	66	8.23*	6.75*	528.43**	43.66	0.18**	0.11**	4.98**
Error	154	5.43	4.34	85.23	38.40	0.06	0.04	0.59
Predictability Ratio		0.79	0.76	0.86	0.75	0.78	0.80	0.65

Note: * Significant at 5% level, ** Significant at 1% level

day to maturity, plant height at maturity, number of primary branches⁻¹, number of siliqua plant⁻¹, 1000 seed weight and yield plant⁻¹ under study. The mean squares due to sca were significant for days to 50% flowering, days to maturity, plant height, number of siliqua plant⁻¹, 1000 seed weight, and yield plant⁻¹ and non significant for only number of primary branches.

The predictability ratio ranged from 0.65 for seed yield plant⁻¹ to 0.86 for plant height (cm). For all the

characters studied, the predictability ratio was observed to be more than 0.50, but not closer to unity. This reveals that both gca effects of parents, well as the sca effect of crosses, should be considered for selecting the parents or crosses for their exploitation to recover transgressive segregation.

The gca effects of twelve parents for days to 50% flowering, days to maturity, plant height at maturity, number of primary branches⁻¹, number of siliqua plant⁻¹, 1000 seed weight and yield plant⁻¹ are

Table 3. General combining ability (GCA) effects of parents

Parents	Mean squares						
	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of primary branches plant ⁻¹	No. of siliqua plant ⁻¹	1000 seed weight (g)	Yield plant ⁻¹ (g)
Pusabold	-1.13	-0.52	3.30*	-0.14*	-16.87**	0.23**	-0.69**
Varuna	-0.90	-0.68	-0.86	-0.21**	-1.66	0.00	-0.39*
Vardhan	0.03	0.01	-3.12*	0.01	7.37**	-0.02	-0.15
Seeta	0.53	0.72	1.59	0.02	3.03	-0.11*	-1.03**
Bio-902	1.20*	0.58	4.00*	0.24**	10.72**	0.11*	0.45*
Laxmi	-0.25	0.03	-1.36	-0.22**	-12.35**	-0.12*	-0.57**
PCR-7	1.94**	1.51**	4.81*	0.17**	6.74**	0.02	0.68**
Ashirwad	-0.16	0.06	-2.26	-0.03	3.99	-0.11*	0.42*
Kranti	0.58	0.60	-0.88	-0.02	4.01	-0.06	0.64**
ACN-9	-2.09**	-2.11**	-3.72*	0.00	3.06	-0.17**	0.05
Geeta	0.17	-0.21	3.03	0.04	-7.91**	0.10*	-0.03
RH-819	0.08	0.01	-4.52**	0.14**	-0.12	0.14**	0.62**
SE (gi)±	0.596	0.532	1.535	0.062	2.362	0.050	0.197

Note: * Significant at 5% level, ** Significant at 1% level

Table 4. Specific combining ability (SCA) effects of crosses for different characters

Name of crosses	Days to 50 % flowering	Days to maturity	No. of primary branches	No. of siliqua plant ⁻¹ plant ⁻¹	1000 seed weight	Yield plant ⁻¹ (g) (g)
Pusabold x Varuna	1.42	1.51	0.12	6.45	-0.61*	-0.21
Pusabold x Vardhan	0.16	1.16	0.24	3.89	-0.35	1.33
Pusabold x Seeta	-1.67	-0.22	0.16	10.50	0.09	1.81*
Pusabold x BIO-902	-2.67	-1.08	-0.32	-21.87*	0.42*	-0.44
Pusabold x laxmi	-1.22	-1.20	0.21	13.87	-0.17	-0.22
Pusabold x PCR-7	0.92	0.99	-0.59**	9.99	0.38*	0.69
Pusabold x Ashirwad	1.35	0.44	0.88**	0.80	-0.41*	-0.15
Pusabold x Kranti	-2.72	-2.77	-0.39	-2.89	-0.47*	0.59
Pusabold x ACN-9	-1.72	-2.06	0.12	11.33	-0.09	-0.60
Pusabold x Geeta	2.35	2.04	0.21	-2.57	-0.29	-0.70
Pusabold x RH-819	3.12	2.49	-0.35	-8.43	1.10**	0.56
Varuna x Vardhan	1.59	0.66	-0.23	-21.86*	-0.01	-1.03
Varuna x Seeta	-4.58 *	-3.39	-0.57*	-16.99*	-0.24	-0.40
Varuna x BIO-902	-3.24	-2.91	-0.06	-11.01	0.27	1.56*
Varuna x laxmi	-0.12	-1.03	0.01	-1.68	-0.04	-0.77
Varuna x PCR-7	-0.65	-1.51	0.01	-14.69	0.29	-0.64
Varuna x Ashirwad	0.12	-0.06	-0.18	25.85**	0.32	1.58*
Varuna x Kranti	-0.29	-0.60	0.27	6.10	-0.04	1.43*
Varuna x ACN-9	0.71	0.44	-0.22	-8.22	-0.45*	-0.66
Varuna x Geeta	2.78	1.87	0.68**	19.42*	0.52**	1.14
Varuna x RH-819	2.54	3.66	0.32	38.16**	-0.09	2.32**
Vardhan x Seeta	1.83	0.92	0.28	36.92**	0.45*	2.91**
Vardhan x BIO-902	1.83	3.73	0.52**	38.50**	-0.04	3.32**
Vardhan x laxmi	-1.38	-1.06	-0.28	-25.43**	0.41*	-1.54*
Vardhan x PCR-7	0.42	-0.20	-0.01	8.68	-0.19	0.16
Vardhan x Ashirwad	-0.81	-1.41	-0.14	14.56	-0.07	-1.29
Vardhan x Kranti	3.12	2.04	-0.15	-19.52*	0.06	-3.92**
Vardhan x ACN-9	0.45	1.42	-0.04	-2.58	-0.04	-0.02
Vardhan x Geeta	-1.15	-2.15	-0.14	-7.27	-0.13	-0.97
Vardhan x RH-819	1.95	1.63	0.36	5.07	-0.19	0.00
Seeta x BIO-902	0.33	-0.65	0.18	28.83**	-0.14	0.53
Seeta x laxmi	1.78	1.23	0.24	4.37	0.04	-1.28
Seeta x PCR-7	-2.08	-1.58	-0.22	-6.18	-0.24	-1.89**
Seeta x Ashirwad	1.35	2.87	-0.35	-35.63**	-0.14	-2.45**
Seeta x Kranti	-0.38	0.32	0.11	-6.32	0.03	-0.49
Seeta x ACN-9	3.62	3.71	-0.11	18.63*	0.05	2.66**
Seeta x Geeta	4.35*	3.13	-0.22	-19.27*	-0.02	-0.54
Seeta x RH-819	0.78	-0.08	0.22	6.61	0.20	-2.21**
BIO-902 x laxmi	3.12	1.04	0.82**	31.34**	-0.28	3.01**
BIO-902 x PCR-7	-1.74	-1.77	0.43	7.46	0.09	0.46
BIO-902 x Ashirwad	5.35*	1.01	-0.57*	-31.99**	0.08	-2.61**
BIO-902 x Kranti	0.95	0.80	-0.18	-20.28*	0.10	-0.85

BIO-902 x ACN-9	-2.05	-1.49	-0.13	-7.20	-0.04	-1.37
BIO-902 x Geeta	6.35**	6.28**	-0.10	11.91	0.06	0.04
BIO-902 x RH-819	-6.88**	-6.60**	-0.13	1.64	-0.44**	-0.92
laxmi x PCR-7	6.38**	5.44**	0.56**	18.86*	0.03	2.79**
laxmi x Ashirwad	-2.86	-2.10	0.30	18.34*	0.52**	0.96
laxmi x Kranti	2.40	3.01	-1.05**	-9.41	0.37*	-0.19
laxmi x ACN-9	-2.27	-1.27	0.06	3.07	-0.06	1.40
laxmi x Geeta	-6.53**	-5.18**	-0.18	-25.49**	-0.37*	-1.90*
laxmi x RH-819	-4.43*	-4.06*	0.33	23.31**	0.39*	3.25**
PCR-7 x Ashirwad	3.28	4.09*	-0.30	-9.48	-0.42*	-0.09
PCR-7 x Kranti	-1.46	0.87	0.56*	24.64**	-0.22	2.70**
PCR-7 x ACN-9	-0.46	-3.75	-0.07	12.25	0.29	1.85*
PCR-7 x Geeta	-6.38**	-5.65**	-0.30	4.89	0.27	1.36
PCR-7 x RH-819	0.71	-0.87	-0.27	-6.50	-0.44*	-2.08**
Ashirwad x Kranti	-1.36	-1.34	-0.04	-7.95	0.22	-0.29
Ashirwad x ACN-9	1.31	1.04	-0.26	0.27	-0.20	-1.74*
Ashirwad x Geeta	-3.29	-2.87	0.23	41.44	-0.24	5.53**
Ashirwad x RH-819	-1.19	-0.08	1.01**	24.18	0.00	4.48**
Kranti x ACN-9	0.90	0.49	-0.34	-32.49**	0.22	-3.38**
Kranti x Geeta	2.31	0.59	0.62**	34.15**	-0.51**	4.57**
Kranti x RH-819	-1.27	-1.63	0.93**	62.56**	-0.15	2.99**
ACN-9 x Geeta	0.31	0.97	0.47**	24.77	0.26	3.44**
ACN-9 x RH-819	-0.60	0.09	0.04	-9.29	-0.14	1.17
Geeta x RH-819	-1.86	-1.15	-0.40	-11.19	-0.61**	-2.95**
SE (sij) ±	1.984	1.940	0.226	8.601	0.183	0.717

Note: * Significant at 5% level, ** Significant at 1% level

Note: SCA effect for plant height at maturity was not calculated because mean square due to crosses were non significant

presented in table 3. The sca effects of 66 crosses for days to 50% flowering, day to maturity, number of primary branches⁻¹, number of siliqua plant⁻¹, 1000 seed weight and yield plant⁻¹ are presented in table 4. Results showed that the parent PCR-7 recorded significant positive gca effect for yield plant⁻¹, plant height, number of siliqua plant⁻¹, number of primary branches⁻¹, days to maturity, and days to 50% flowering (Table 3). Similarly another parents Bio-902 exhibited higher significant gca effect for yield plant⁻¹, 1000 seed weight, plant height, number of siliqua plant⁻¹, number of primary branches⁻¹, and days to 50% flowering (Table 3). These two parents PCR-7 and Bio-902 were identified as good general combiners and can be used in crossing programme. Out of 66 crosses, twenty nine exhibited significant sca effects of which eighteen

showed positive and eleven had negative significant sca effects (Table 4). Ashirwad x Geeta (5.53) recorded highest significant positive sca effects followed by Kranti x Geeta (4.57), Ashirwad x RH-819 (4.48), and ACN-9 x Geeta (3.44) (Table 4). The cross Vardhan x Kranti (-3.92) exhibited highest significant negative effects followed by Kranti x ACN-9 (-3.38), and Geeta x RH-819 s(-2.95) (Table 4). The crosses Vardhan x Laxmi, Vardhan x Kranti, Seeta x Ashirwad, Bio-902 x Ashirwad and Kranti x ACN-9 were observed to record negative significant sca effects for yield plant⁻¹ and number of siliqua plant⁻¹ (Table 4).

The potentiality of a variety may be judged by comparing performance *per se*, while the combining ability of the parents can be judged by

Table 5. Selected crosses and its performance for important characters

Crosses	Mean	GCA effects		SCA effects
		P1	P2	
Number of siliqua plant ⁻¹				
Vardhan x Kranti	137.9	7.4**	4.0	-19.5*
Seeta x Ashirwad	117.4	3.0	4.0	-35.6**
Bio-902 x Ashirwad	128.7	10.7**	4.0	-32.0**
Kranti x ACN-9	120.6	4.0	3.1	-32.5**
Vardhan x Kranti	8.46	-0.2	0.6**	-3.9**
Seeta x Ashirwad	8.82	-1.0**	0.4*	-2.5
Bio-902 x Ashirwad	10.15	0.5*	0.4*	-2.6**
Kranti x ACN-9	9.20	0.6**	0.1	-3.4**

the F_1 values. The potentiality of the cross to be forwarded to next generation is decided on the basis of high mean performance, high gca of one or both the parents involved in the cross, and with the negative sca effects. The selection of crosses in this manner was also done by Khumbalkar *et al.* (1999) and Aghao *et al.* (2010) in mustard. Based on this criteria promising crosses and their selected *per se* performances are given in table 5. Out of the crosses which recorded desirable sca effects, only four crosses Vardhan x Kranti, Seeta x Ashirwad, Bio-902 x Ashirwad, and Kranti x ACN-9 were found to be the best crosses which can be forwarded to the next generation. These crosses involved one parent with highly significant or non-significant positive gca effect for yield plant⁻¹ and number of siliqua plant⁻¹. These crosses also recorded appreciable performance for yield plant⁻¹ and number of siliqua plant⁻¹. The presence of negative sca effects for several yield components in the above crosses indicates the predominant role of additive gene action for yield components, which is a general situation observed in self pollinated crop. Singh *et al.* (2003) and Aghao *et al.* (2010), also identified superior crosses based on sca and *per se* performance and suggested the suitability of biparental matings in selected progeny and further selection in segregating generation in mustard.

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