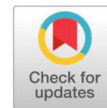# AATCC Review

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Genetic Analysis of Yield and its Components in F1 and F2 Population of Indian Mustard [*Brassica juncea* (L.) *Czern and Coss*]

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Abstract

In present study genetic diversity of seven high-yielding parents of Indian mustard along with four checks viz., Pusa bold, Shatabdi, Bio-902, and Kranti were evaluated using twelve SSR primers. Out of 12 SSR primers, seven primers were found monomorphic and five primers were found polymorphic for the set of selected genotypes. The results of the diversity analysis showed that, almost all the parents are diverse from each other. Again 30 F1 crosses of Indian mustard were obtained in full diallel fashion using six parents. ANOVA for combining ability indicated that mean squares due to GCA were significant for all characters studied except siliquae density on the main branch and 1000 seed weight. Five crosses showed significant negative SCA/RCA effects for seed yield and many of the contributing characters. Considering GCA effects for most of the yield-contributing traits, the parents ACNMM13 and ACNMM14 were recorded as good general combiners for seed yield and it's attributing characters. Selected five crosses along with checks (Kranti, Bio-902 and Shatabdi) for varietal development were sown to study the genetic variability, heritability and genetic advance as per cent of mean for yield and yield attributing traits. High genotypic coefficient of variation, high heritability accompanied with high genetic advance as per-cent of the mean observed for a number of branches plant-1, siliquae density on main branch, number of siliquae plant-1 and seed yield plant-1 which indicated the significant progress by an effective selection of these characters. Selected plants from five good crosses were suggested to carry forward by the plant to-row method for exploiting improvement in selected material.

Keywords: *Full diallel, General combining ability, Genetic diversity, SCA, F1, F2, Brassica, Molecular diversity, GCA*

Introduction

Rapeseed-Mustard are important oilseed crops of the world. It is grown in 53 countries across the six continents. The crop is grown both in sub-tropical and tropical countries. In Asia, it is mainly grown in China, India, Pakistan and Bangladesh. Among different oilseed crops grown in India, the Rapeseed-Mustard (*Brassica* spp.) contributes 29.5% in the total production of oilseeds. In India, it is the second most important edible oilseed crop after soybean sharing 27.8% in the India's oilseeds economy. Out of the total cropped area in India, the share of oilseeds is 14.1% and mustard itself accounts for 3% of it [5]. In the year 2019-20 area under mustard is 6.07 (mha) with production and productivity of 8.70 MT and 1433 Kgha-1 respectively [6].

Combining ability studies provide useful information for selection of good combiners, which are expected to give high performance in their crosses and progenies. Present studies with (6×6) diallel cross was undertaken for isolating superior parental lines and better combining parents for suitable hybrids. To know the presence of genetic diversity in the parents, molecular markers like SSR are more reliable because of their abundance. The markers on A and B genome of *B. juncea* are efficient in identification of polymorphism.

The present study was made with a view to study the combining ability, molecular marker assessment of parents and F_2 generation to test the performance and homozygosity of Indian mustard genotypes for yield and yield attributing traits.

Materials and Methods

Materials required: Six parents of Indian mustard genotype *Brassica juncea* L. were crossed in full diallel fashion. The resultant 30 crosses along with six parents and three checks (Kranti, Bio-902, and Shatabdi) were sown at AICRP on Linseed and Mustard experimental farm, College of Agriculture, Nagpur during *rabi* 2018-19 in randomized block design with three replications. The spacing of 0.45 x 0.10 m^2 was maintained to accommodate 50 plants in each row. The data were recorded on various yield and yield contributing traits. During *rabi* 2019-20, the harvested seed of five F_1 crosses selected on basis of yield and it's contributing characters along with five parents and three checks were sown in a randomized block design with two replications for evaluation. The recommended cultural practices were followed to raise the healthy crop.

The analysis of variance was performed to test the significance of differences between the genotypes (parents, crosses and check) as per [30]. The combining ability analysis was carried out by methodology of Diallel method-1 (model-l) given by [14] and the estimation of genetic parameters in the F_2 population suggested by [4], [9] and [16].

Seven distinct characteristic parental lines were selected along with varieties Bio-902, Pusa Bold, Shatabdi, and Kranti for molecular analysis. 12 SSR markers were used in the present study to know the genetic diversity. For the analysis of molecular data distance-based cluster analysis was performed and a dendrogram based on the unweighted pair group method of the arithmetic mean (UPGMA) was constructed using Jaccard's similarity coefficient with the help of DARwin [35]. The robustness of each dendrogram was evaluated by bootstrap analysis.

Results and Discussion

SSR marker studies - In the present study, DNA was isolated from seven parents (derived from a mutant of Bio-902 and Pusa bold) and four checks (Bio-902, Pusa bold, Kranti, and Shatabdi). Twelve SSR primers were used for molecular analysis. Distance-based

cluster analysis was performed and a dendrogram based on the unweighted pair group method of arithmetic mean (UPGMA) was constructed using Jaccard's similarity coefficient (Fig. 1). All genotypes were grouped into two major clusters at zero similarity coefficient, cluster 1 having only one parent ACNMM9. The Second clades consist of five parents and checks from so many sub-clades which showed diversity from one another to form different sub-clades (Fig. 1). [48], [38] also found similar results for their study. Sharma *et al* (2022), [40], [29] also studied genetic diversity using SSR markers in F_1 generation and reported similar results. The parent ACNMM9 was observed to be diverse from the checks and other parents as they appeared in the different clade. Some of them were found similar to the checks in clades viz. Bio-902 and ACNMM 27 found in the same sub-clade, ACNM 52 found in sub clade with checks Shatabdi and Kranti. The parents ACNMM 29 and ACNM50 were found in same clade and ACNMM 13, ACNMM 14 and Pusa Bold as they occupied the different sub clade as that of the check, so that almost all the parent were diverse from each other.

The cluster 2 was also divided into two sub clusters having Pusa Bold in one sub cluster and second sub-cluster divided into so many sub cluster which contain ACNMM 27, ACNM 52, ACNMM 13, ACNMM 14, ACNMM 29, ACNM 50 and checks Bio-902, Shatabdi and Kranti (Fig. 1). Similar work was also conducted by [39].

Analysis of variance for combining ability was estimated for days to first flower, days to maturity, plant height (cm), number of branches plant^{-1}, siliqua density on main branch, number of siliquae plant^{-1}, 1000 seed weight and seed yield plant^{-1} (Table 1). The variation among the crosses was partitioned into different components representing due to GCA, SCA, and RCA. The mean squares due to general combining ability were significant for all the eight characters under study except siliqua density on the main branch and 1000 seed weight. The mean squares due to specific and reciprocal combining ability were significant for all eight characters. Similar results and concluded that mean squares due to both GCA and SCA were highly significant for seed yield and its contributing characters in Indian Mustard [8], [11], [12], [18], [45], [42].

The predictability ratio ranged from 0.25 for seed yield plant^{-1} to 0.84 for number of branches plant^{-1}. For all the characters studied except 1000 seed weight and
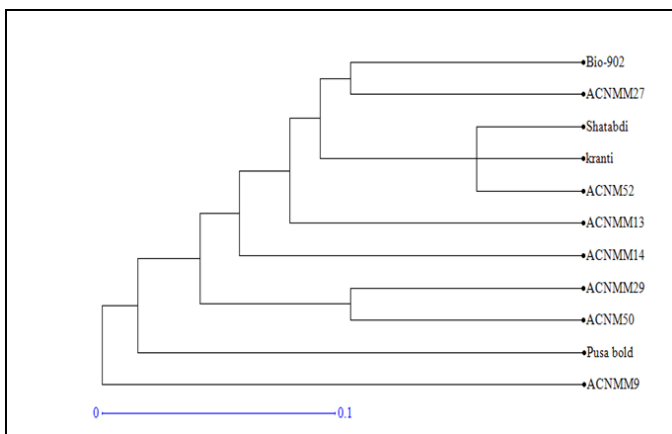
Fig.1 Dendrogram derived from banding pattern of SSR marker analysis of seven parents and four checks

siliquae density on the main branch, the predictability ratio was observed to be more than 0.50, but not closer to unity. This reveals that both GCA effects of parents as well as the SCA effect of crosses should be considered for selecting the parents or crosses for their exploitation to recover transgressive segregates. The ratio of variance due to GCA and SCA was below unity for all the characters under study were reported by [16], [18], [45] which is following present study. From table 3a and table 3b among the six parents, ACNMM 13 was found to be the best general combiner as it recorded a highly significant positive GCA effect for days to first flower and days to maturity and seed yield plant[-1]. The parent ACNMM 14 exhibited highly significant positive GCA effects for number of branches plant[-1] and seed yield plant[-1]. Therefore, two parents ACNMM 13 and ACNMM 14 were identified as best general combiners for yield and other yield-contributing characters. Earlier worker [1] and [36] identified as good general combiners on the basis of significant GCA effects for yield and yield contributing characteristics which supported the present findings. These two parents ACNMM 13 and ACNMM 14 were identified as good general

combiners and can be used in crossing program for seed yield plant[-1].

From the estimate of specific and reciprocal combining ability effect of 30 crosses, highest positive significant SCA/RCA effect was observed in ACNMM 14 x ACNMM 13 (3.11) followed by ACNM 52 x ACNMM 29 (1.87), ACNMM 13 x ACNMM 27 (1.76), ACNMM 29 x ACNM 52 (1.70) and ACNMM 29 x ACNMM 14 (1.39) for seed yield plant[-1]. In addition to yield, ACNM 52 x ACNMM 29, ACNMM 13 x ACNMM 27, ACNMM 29 x ACNM 52 and ACNMM 29 x ACNMM 14 out of five crosses selected for yield showed desirable significant SCA/RCA effect for 1000 seed weight, ACNMM 29 x ACNM 52, ACNMM 14 x ACNMM 13 and ACNM 52 x ACNMM 29 for number of primary branches plant[-1]. [23], [27], [31], [32], [43], [44], [47]

The cross ACNMM 9 x ACNM 52 (-2.32) exhibited highest negative SCA/RCA effect followed by cross ACNMM 27 x ACNMM 13 (-2.16), ACNMM 27 x ACNM 52 (-1.62), ACNMM 27 x ACNMM 14 (-1.52) and ACNMM 27 x ACNMM 9 (-1.40) for seed yield plant[-1]. Similarly, four crosses viz., ACNMM 27 x ACNMM 13 (-2.16), ACNMM 27 x ACNM 52 (-1.62), ACNMM 27 x ACNMM 14 (-1.52) among five selected crosses for seed yield also exhibited negative significant SCA/RCA effect for number of branches plant[-1] and plant height. Similar kind of selection of parents and crosses on basis of significant GCA, SCA and RCA effect for seed yield and its contributing characters also done earlier by [1], [17], [22], [26], [28], [36], [42], [45].

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

Table 1. Analysis of variance for combining ability

Sources of variation	Degrees of Freedom	Means squares							
		Days to first flower	Days to maturity	Plant height (cm)	Number of branches plant[-1]	Siliqua density on main branch	Number of siliquae plant[-1]	1000 seed weight (g)	Seed yield plant[-1] (g)
GCA	5	14.59**	10.30**	977.77**	1.68**	0.02	3053.99**	0.26	18.91**
SCA	15	20.60**	12.04**	533.96**	0.62**	0.07**	3390.39**	1.55**	7.74**
RCA	15	17.12**	9.50**	777.01**	1.02**	0.06**	1998.93**	1.35**	13.80**
Error	70	1.47	0.55	40.01	0.08	0.01	244.78	0.07	0.55
Predict-ability ratio	-	0.59	0.63	0.79	0.84	0.36	0.64	0.25	0.83

*, ** = significance at 5% level and at 1% level.
Note = the degrees of freedom is only 70 as check (Bio-902, Kranti and Shatabdi) is not included in the analysis

TABLE 2. Potential crosses identified on the basis mean performance, GCA effect of parents and SCA/RCA effect of crosses for yield and other traits

Sr. No.	Crosses	Character	Mean	SCA/RCA effect	GCA effects	
					P1	P2
1	ACNMM27 x ACNMM13	Yield	14.32	-2.16**	-0.50*	0.69**
		NOB	2.51	-0.45*	-0.23**	-0.02
		PH	150.06	-22.07**	0.98	2.09
		DTFF	34.97	-2.05*	-0.68*	1.06**
2	ACNMM27 x ACNM52	Yield	12.62	-1.62**	-0.50*	-0.02**
		1000sw	5.45	-0.37*	0.08	0.10
		NOS	218.33	-21.05	-4.04	11.58**
		SD	0.53	-0.09	0.05*	-0.01
		NOB	2.51	-0.52*	-0.23**	0.12
		PH	173.34	-15.08**	0.98	6.80**
		DTM	104.07	-0.30	-0.21	-0.08
3	ACNMM27 x ACNMM14	Yield	12.39	-1.52**	-0.50*	0.90**
		1000sw	4.98	-0.60**	0.08	-0.12
		NOS	191.99	-27.61*	-4.04	-4.18
		SD	0.57	-0.02	0.05*	-0.01
		NOB	3.40	-0.51*	-0.23**	0.36**
		Plant Ht	168.36	-19.34**	0.98	2.14
4	ACNM52 x ACNMM14	Yield	14.94	-1.17**	-0.02**	0.90**
		1000sw	4.85	-0.53**	0.10	-0.12
		NOB	4.28	-0.01	0.12	0.36**
		DTFF	36.59	-2.43**	-0.26	-0.15
5	ACNMM29 x ACNMM27	Yield	12.38	-1.07**	-0.02	-0.50*
		1000sw	5.14	-0.44**	0.03	0.08
		NOS	217.31	-25.04**	10.62*	-4.04
		PH	156.84	-7.76**	-7.93**	0.98

Note: NOB = Number of branches plant^{-1}, 1000SW= 1000 Seed Weight

DTFF = Days to first flower, PH = Plant height

DTM = Days to maturity, NOS = Number of siliquae plant^{-1}

SD = Siliqua density on main branch, Yield = Seed yield plant^{-1} (g)

involved in the cross and with negative SCA effects. Based on the above criteria, promising crosses and their selected per se performance is given in table 2. Among thirty crosses studied, the cross combination ACNMM 27 × ACNMM 13 showed negative highly significant SCA/RCA effects for seed yield plant^{-1}, number of branches plant^{-1} and plant height and days to first flower. Similarly, the same cross was significantly superior over the best check for seed yield plant^{-1} and plant height and *at par* over the mean of best check for days to first flower. The GCA effects of parents involved in the cross possessed Low × High GCA effects for seed yield plant^{-1}, Low × Medium GCA effects for a number of branches plant^{-1}, Medium x Medium GCA effect for plant height, and Low x high GCA effect for days to first flower.

The cross ACNMM 27 × ACNM 52 showed a highly negative significant SCA/RCA effect for seed yield plant^{-1}, and also a significant negative SCA/RCA effect for 1000 seed weight, number of branches plant^{-1}, and plant height. Same cross also had a negative non-significant SCA/RCA effect for a number of siliquae plant^{-1}, siliquae density on main branch and days to maturity. Likewise, the same cross was significantly superior over best check for seed yield plant^{-1} and *at par* over the mean of best check for 1000 seed weight and plant height. The GCA effects of parents of the cross exhibited Low × Low GCA effects for seed yield plant^{-1}, Medium × Medium for 1000 seed weight, Low × high for a number of siliquae plant^{-1}, High x Low for siliquae density on main branch, Low × Medium for number of branches plant^{-1}, Medium × High for plant height and Medium x Medium for days to maturity.

The cross ACNMM 27 x ACNMM 14 recorded negative significant SCA/ RCA effect for seed yield plant^{-1}, 1000 seed weight, number of siliquae plant^{-1},

TABLE 3a. GCA effects of parents, SCA effects of direct crosses and RCA effect of reciprocal crosses

Sr.No.	Parents	Days to first flower	Days to maturity	Plant height (cm)	Number of branches plant⁻¹
1	ACNMM29	-0.41	0.01	-7.93**	-0.13
2	ACNMM13	1.06**	1.00**	2.09	-0.02
3	ACNM52	-0.26	-0.08	6.80**	0.12
4	ACNMM14	-0.15	-0.12	2.14	0.36**
5	ACNMM27	-0.68*	-0.21	0.98	-0.23**
6	ACNMM9	0.43	-0.60**	-4.08*	-0.10
	Direct crosses				
7	ACNMM29 xACNMM13	0.55	2.24**	8.42*	0.21
8	ACNMM29 x ACNM52	1.40	-0.07	-6.50	0.45**
9	ACNMM29 xACNMM14	-1.44	-2.99**	10.70**	-0.04
10	ACNMM29 xACNMM27	1.72*	0.30	-7.76*	0.20
11	ACNMM29 x ACNMM9	-0.07	-0.21	5.20	0.02
12	ACNMM13 x ACNM52	-0.18	0.31	1.99	0.41*
13	ACNMM13 xACNMM14	2.08**	0.04	5.44	-0.13
14	ACNMM13 xACNMM27	-1.17	0.22	-9.23*	-0.23
15	ACNMM13 x ACNMM9	-1.69*	-0.53	0.88	0.25
16	ACNM52 x ACNMM14	-2.43**	0.82	13.94**	-0.01
17	ACNM52 x ACNMM27	-2.27**	1.39**	2.35	-0.03
18	ACNM52 x ACNMM9	1.27	-0.26	-1.89	-0.32
19	ACNMM14x ACNMM27	-1.75*	0.64	6.28	0.32
20	ACNMM14x ACNMM9	0.01	1.79**	-16.64**	0.14
21	ACNMM27x ACNMM9	-0.53	0.10	5.57	0.11
	Reciprocal crosses				
22	ACNMM13 xACNMM29	-0.46	-2.93**	5.55	0.28
23	ACNM52xACNMM29	-2.31**	0.35	-14.20**	0.55**
24	ACNMM14 xACNMM29	4.03**	3.03**	-2.98	-0.42*
25	ACNMM27 xACNMM29	0.37	1.30*	6.74	-0.19
26	ACNMM9x ACNMM29	-1.75*	1.46**	12.93**	-0.01
27	ACNM52 xACNMM13	-1.09	-0.50	-2.16	-0.18
28	ACNMM14 xACNMM13	1.00	0.14	-3.31	0.43*
29	ACNMM27 xACNMM13	-2.05*	0.21	-22.07**	-0.45*
30	ACNMM9 xACNMM13	-0.27	-1.05	-1.75	-0.40*
31	ACNMM14 x ACNM52	-1.62	-0.12	-1.51	-0.33
32	ACNMM27 x ACNM52	2.24*	-0.30	-15.08**	-0.52*
33	ACNMM9 x ACNM52	0.27	0.01	-17.14**	-0.25
34	ACNMM27 xACNMM14	0.08	0.42	-19.34**	-0.51*
35	ACNMM9 x ACNMM14	-0.56	-0.01	9.11*	-0.66**
36	ACNMM9 x ACNMM27	1.82*	-0.57	-1.68	0.50*
	S.E.(gi)	**0.32**	**0.20**	**1.66**	**0.08**
	S.E.(sij)	**0.73**	**0.45**	**3.80**	**0.17**
	S.E.(rij)	**0.86**	**0.53**	**4.47**	**0.20**

number of branches plant⁻¹ and plant height and negative non-significant for siliquae density the on main branch. The same was found to be significantly superior over best check for seed yield plant⁻¹ and *at par* over the mean of the best check for the number of siliquae plant⁻¹, siliquae density on the main branch,

number of branches plant⁻¹ and plant height. The GCA of parents involved in this was Low x high for seed yield plant⁻¹, Medium x Medium for 1000 seed weight, Medium x Medium for a number of siliquae plant⁻¹, Low x high for a number of branches plant⁻¹, Medium x Medium for plant height and high x low

TABLE 3b. GCA effects of parents, SCA effects of direct crosses and RCA effect of reciprocal crosses

Sr.No	Parents	Siliquae density on main branch	Number of siliqua plant[-1]	1000 seed weight	Seed yield plant[-1] (g)
1	ACNMM29	-0.02	10.62*	0.03	-0.02
2	ACNMM13	-0.01	-11.78**	-0.07	0.69**
3	ACNM52	-0.01	11.58**	0.10	-0.02**
4	ACNMM14	-0.01	-4.18	-0.12	0.90**
5	ACNMM27	0.05*	-4.04	0.08	-0.50*
6	ACNMM9	-0.01	-2.19	-0.03	-1.05**
	Direct crosses				
7	ACNMM29 xACNMM13	-0.08*	-7.12	-0.09	-0.65
8	ACNMM29 x ACNM52	0.04	14.12	0.51**	1.70**
9	ACNMM29 xACNMM14	-0.04	3.23	0.85**	1.39**
10	ACNMM29 xACNMM27	0.04	-25.04**	-0.44**	-1.07*
11	ACNMM29 x ACNMM9	-0.03	22.28*	-0.27	-0.47
12	ACNMM13 x ACNM52	0.20**	1.68	-0.53**	-0.97*
13	ACNMM13 xACNMM14	0.06	-2.98	-0.38*	-0.73
14	ACNMM13 xACNMM27	-0.03	34.34**	0.23	1.76**
15	ACNMM13 x ACNMM9	0.06	-0.39	0.57**	-0.16
16	ACNM52 x ACNMM14	0.12**	21.84*	-0.53**	-1.17**
17	ACNM52 x ACNMM27	-0.04	18.61	0.54**	-0.36
18	ACNM52 x ACNMM9	-0.15**	-29.26**	-0.29	0.89*
19	ACNMM14x ACNMM27	-0.07	14.57	0.51**	-0.71
20	ACNMM14x ACNMM9	0.06	21.24*	0.34*	0.10
21	ACNMM27x ACNMM9	0.12**	2.67	-0.27	-1.40**
	Reciprocal crosses				
22	ACNMM13 xACNMM29	0.05	-7.37	-0.04	0.71
23	ACNM52xACNMM29	0.16**	16.36	0.81**	1.87**
24	ACNMM14 xACNMM29	0.13*	15.77	-0.41*	1.31*
25	ACNMM27 xACNMM29	0.02	-22.52*	-0.36*	0.39
26	ACNMM9x ACNMM29	0.13*	-13.25	-0.38*	-0.34
27	ACNM52 xACNMM13	-0.12*	26.32*	-0.16	0.29
28	ACNMM14 xACNMM13	0.02	13.65	-0.24	3.11**
29	ACNMM27 xACNMM13	0.15**	20.02	0.38*	-2.16**
30	ACNMM9 xACNMM13	-0.13*	-0.68	-0.65**	-1.20*
31	ACNMM14 x ACNM52	-0.06	-12.49	-0.29	1.01
32	ACNMM27 x ACNM52	-0.09	-21.05	-0.37*	-1.62**
33	ACNMM9 x ACNM52	0.02	-0.96	0.05	-2.32**
34	ACNMM27 xACNMM14	-0.02	-27.61*	-0.60**	-1.52**
35	ACNMM9 x ACNMM14	-0.12*	-32.45**	-0.99**	-1.02
36	ACNMM9 x ACNMM27	0.03	-6.98	0.32	-0.58
	S.E.(gi)	**0.02**	**4.12**	**0.07**	**0.19**
	S.E.(sij)	**0.04**	**9.40**	**0.15**	**0.44**
	S.E.(rij)	**0.05**	**11.06**	**0.18**	**0.52**

for siliquae density on main branch.

A highly negative significant SCA/ RCA effect for seed yield plant[-1] was observed in the cross ACNM 52 x ACNMM 14 and also had a negative significant SCA/RCA effect for 1000 seed weight and days to first flower and negative non-significantly effect for number of branches plant[-1]. Same cross also showed significantly superiority over best check for seed yield plant[-1] and number of branches plant[-1]. The parents of this cross had Low x High GCA effect for seed yield plant[-1], Medium x Medium for 1000 seed weight and

TABLE 4. Analysis of variance for yield and yield contributing characters in F_2 generations of Mustard

Source of Variation	Degree of freedom	Mean sum of square							
		Days to first flower	Days to maturity	Plant height (cm)	No. of branches plant^{-1}	Siliqua density on main branch	No. of silique plant^{-1}	1000 seed weight (g)	Seed yield plant^{-1}(g)
Replications	1	0.16	2.74	197.82	0.02	0.001	102.67	0.02	0.11
Genotypes	12	2.66**	12.59**	1050.08**	0.79**	0.01**	836.77**	0.32**	3.40**
Error	12	0.64	3.03	249.42	0.16	0.001	200.85	0.07	0.81

** Significant at 1 % and 5 % level.

TABLE 5a. Performance of selected crosses of F_2 population

Parameters	Characters	ACNMM27 X ACNMM13	ACNMM27 X ACNM52	ACNMM27 X ACNMM14	ACNM52 X ACNMM14	ACNMM29 X ACNMM27
Mean	Days to first flower	37.79	37.69	36.82	36.81	35.95
	Days to maturity	109.82	110.30	110.30	110.30	108.00
	Plant height	183.94	180.53	178.27	176.29	190.15
	1000 seed weight	5.38	5.38	5.34	5.41	5.36
GCV (%)	Days to first flower	5.99	6.16	5.83	5.78	4.11
	Days to maturity	1.40	2.07	2.09	2.03	0.88
	Plant height	12.63	12.94	12.55	11.56	9.53
	1000 seed weight	10.03	10.57	10.49	10.82	9.77
h² (%)	Days to first flower	82.82	86.91	87.23	86.68	76.45
	Days to maturity	87.25	93.06	94.05	89.50	59.97
	Plant height	90.18	86.62	90.54	91.37	80.83
	1000 seed weight	80.77	85.73	91.57	87.95	90.13
GAM	Days to first flower	11.23	11.83	11.21	11.08	7.40
	Days to maturity	2.70	4.12	4.16	3.96	1.41
	Plant height	24.70	24.81	24.60	22.76	17.65
	1000 seed weight	18.57	20.15	20.67	20.91	19.10

day to first flower and Medium x High for a number of branches plant^{-1}.

The hybrid ACNMM 29 x ACNMM 27 exhibited a negative significant SCA/RCA effect for seed yield plant^{-1}, 1000 seed weight, number of siliquae plant^{-1} and plant height. Same hybrid was significantly superior over a superior check for seed yield plant^{-1} and plant height and *at par* over the mean of superior check for several siliquae plant^{-1}. The parents involved in this hybrid possessed Medium x Low GCA effect for seed yield plant^{-1}, Medium x Medium for 1000 seed weight, High x Medium for several branches plant^{-1} and Low x Medium for plant height.

Among thirty crosses studied, the cross combinations ACNMM 27 × ACNMM 13, ACNMM 27 x ACNM 52, ACNMM 27 x ACNMM 14, ACNM 52 x ACNMM 14 and ACNMM 29 x ACNMM 27 involved one parent with highly significant or non-significant positive GCA effect for yield plant^{-1} and some yield contributing characters. These crosses

also recorded significant performance for yield plant^{-1} and some yield contributing characters. The presence of negative SCA/RCA 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 the self-pollinated crop. These five crosses were found to be best crosses that can be forwarded to the next generation. Biparental mating may be used in selected progeny and a further selection of segregant generation or recurrent selection or diallel mating may also be used for the improvement of yield and yield components. Earlier workers [2], [3], and [45] 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.

Analysis of variance for various characters in F_2 generation - The analysis of variance for eight characters has been presented in table 4. The mean squares due to genotypes (crosses, parents and

TABLE 5b. Performance of selected crosses of F_2 population

Parameters	Characters	ACNMM27 X ACNMM13	ACNMM27 X ACNM52	ACNMM27 X ACNMM14	ACNM52 X ACNMM14	ACNMM29 X ACNMM27
Mean	Number of branches plant[-1]	5.01	5.18	3.30	3.45	4.24
	Number of siliquae plant[-1]	162.23	168.48	169.42	165.95	164.29
	Siliqua density	0.50	0.53	0.50	0.52	0.52
	Seed yield plant[-1]	8.70	9.11	9.18	8.68	8.91
GCV (%)	Number of branches plant[-1]	23.99	27.97	31.61	33.78	32.98
	Number of siliquae plant[-1]	31.03	28.72	29.97	30.14	27.50
	Siliqua density	32.59	25.45	23.08	21.93	19.82
	Seed yield plant[-1]	27.02	22.66	25.35	27.20	24.96
h² (%)	Number of branches plant[-1]	88.13	91.98	81.13	87.06	92.39
	Number of siliquae plant[-1]	98.09	98.18	98.19	98.01	98.38
	Siliqua density	92.56	93.60	85.92	89.18	87.93
	Seed yield plant[-1]	93.01	91.63	94.31	94.14	94.64
GAM	Number of branches plant[-1]	46.40	55.26	58.71	64.93	65.30
	Number of siliquae plant[-1]	63.32	58.63	61.19	61.46	56.20
	Siliqua density	64.58	50.73	44.07	42.66	38.28
	Seed yield plant[-1]	53.68	44.68	50.71	54.37	50.02
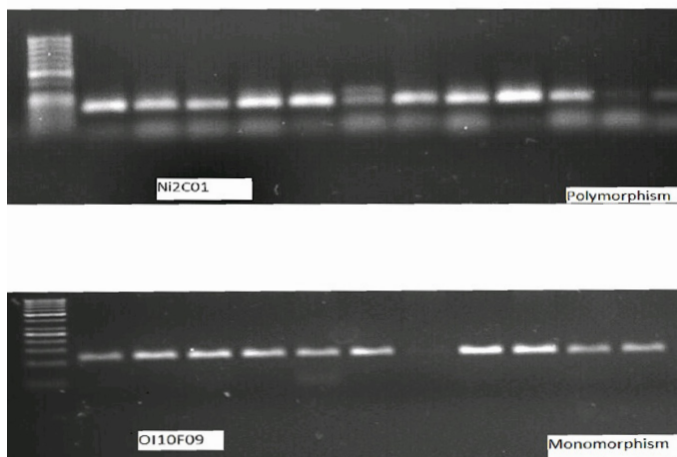
Plate 1. SSR banding profile of 7 selected parents along with 4 checks amplified with primers Ni2Co1 and OI10F0

checks) were highly significant for all eight characters *viz.* days to first flower, days to maturity, plant height, number of branches plant[-1], number of siliquae plant[-1], siliquae density on the main branch, 1000 seed weight and seed yield plant[-1] indicating the substantial genetic variability among the genotype for these characters. Hence, the genetic parameters were worked out for all the significant characters. [10], [19], [25], [41] have reported similar results in their study.

Any appraisal of the breeding material permitting early elimination of material of low potential is clearly advantageous because all improvement programs have limitations and elimination of poor material enhances the probability of finding superior segregates in the remaining material by [4]. One of the criteria as suggested by [15] for the identification of potential F_2 population was with high mean yield, high genotypic coefficient of variation and high expected genetic advance. Since only the genetic portion of the total variability contributes to gain under selection, the importance of information about the parameter of genotype-environment complex should be clear to the breeder. As better estimates of these parameters are obtained for a variety of plant materials, the breeder will be able to anticipate the gain, as he can expect from different intensities of selection [4]. Therefore, in an actual breeding program with limited facilities, the highest advance may result from such crosses.

In the present study, five F_2 populations were evaluated for important genetic parameters such as genotypic coefficient of variation, heritability, and expected genetic advance for eight quantitative traits (table 5a and 5b). Characters viz., days to first flower and days to maturity exhibited low genetic variation. Similarly, plant height and 1000 seed weight showed low to moderate genetic variation, so it can be inferred to exhibit low variation [7], [13], [20]. But variation is the prerequisite for the selection. Hence this above character can't be considered for the selection. Characters namely number of branches, number of siliquae plant[-1], siliquae density on main branch and seed yield plant[-1] exhibited high genotypic coefficient of variation which indicates the presence

of substantial variability for these characters. High heritability is associated with high estimated genetic advance in these characters indicating the significance of additive gene action. Hence, these characters can be considered for the selection of potential F_2 plants for further improvement.

From table 5, five crosses studied were reported to exhibit high mean, genotypic coefficient of variation, heritability and genetic advance as per-cent of mean for number of branches, number of siliquae plant^{-1}, siliquae density on main branch and seed yield plant^{-1} and hence would be useful for obtaining potential segregants with high number of branches plant^{-1}, siliquae density on the main branch, number of siliquae plant^{-1} and seed yield plant^{-1}. [21], [24], [33], [34]. So, single plants were selected on basis of these four traits at 5% selection intensity from each cross and are listed in table 6. Selected 50 plants were superior having better performance than mean performance of respective crosses. These single plants selected are suggested to carry forward to F_3 generation by plant-to-row method for exploiting improvement in the selected material.

Conclusion

From the estimates of GCA effect, parent ACNMM 13 was found to be best general combiner as it recorded highly significant positive GCA effect for days to first flower and days to maturity and seed yield plant^{-1}. Among thirty crosses studied, the cross combinations ACNMM 27 × ACNMM 13, ACNMM 27 x ACNM 52, ACNMM 27 x ACNMM 14, ACNM 52 x ACNMM 14 and ACNMM 29 x ACNMM 27 involved one parent with highly significant or non-significant positive GCA effect for yield plant^{-1} and some yield contributing characters. These crosses also recorded significant performance for yield plant^{-1} and some yield contributing characters. The presence of negative SCA/RCA effects for several yield components in the above crosses indicated the predominant role of additive gene action for yield components. Therefore, these five crosses were identified as potential crosses and recommended for their use in varietal breeding programme in mustard. Five crosses viz. ACNMM 27 × ACNMM 13, ACNMM 27 x ACNM 52, ACNMM 27 x ACNMM 14, ACNM 52 x ACNMM 14 and ACNMM 29 x ACNMM 27 recommended for varietal development and hence would be useful for obtaining potential the segregants with maximum number of branches plant^{-1}, plant height, number of siliqua plant^{-1} and seed yield plant^{-1}. In the molecular

analysis, Among 12 SSR primers, seven primers were found to be monomorphic and five primers were found polymorphic patterns which may be used for further analysis. The parent ACNMM 9 was observed to be diverse from the checks and other parents as they appeared in different clade. Some of them were found similar to the checks in clades *viz.* Bio-902 and ACNMM 27 found in same sub clade, ACNM 52 found sub clade with checks Shatabdi and Kranti. The parents ACNMM 29 and ACNM50 were found in same clade and ACNMM 13, ACNMM 14 and Pusa bold as they occupied the different sub clade as that of the check, so that almost all the parent diverse from each other.

Future scope of the study: Five crosses studied were reported to exhibit high mean, genotypic coefficient of variation, heritability and genetic advance as per-cent of mean for several traits. Single plants were selected on basis of these four traits at 5% selection intensity from each cross. These single plants selected are suggested to carry forward to F_3 generation by plant-to-row method for exploiting improvement in the selected material.

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