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EXPLOITATION OF LOCAL LINES OF MUSTARD FOR RECOMBINATION BREEDING

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ABSTRACT

Twenty local lines of mustard were crossed with three testers during *rabi* 2011 to obtain 60 crosses which were evaluated during *rabi* 2012 by growing in RBD with three replications on the farm of Agricultural Botany section, College of Agriculture, Nagpur. Analysis of variance for experimental design in crosses revealed highly significant mean squares due to genotypes for all the characters except days to maturity, which indicates significant variation among the experimental material. The significant mean squares due to lines for days to first flower, days to maturity, plant height, number of primary branches plant^{-1}, number of siliquae plant^{-1}, seed yield plant^{-1} and due to line x tester for days to first flower, number of primary branches plant^{-1}, number of siliquae plant^{-1}, 1000 seed weight and seed yield plant^{-1} revealed the presence of gca among lines and sca among crosses. Estimation of variances and degree of dominance revealed the predominance of non additive or dominance genetic component for all the characters studied except days to maturity. But mustard being self pollinated crop only additive genetic component could be exploited worth fully, hence preference in this study was given to additive genetic component. Among lines ACNM 20, ACNM 21, ACNM 3 and ACNM5 were identified as good combiners for seed yield plant^{-1} and number of siliquae plant^{-1}. Based on the performance of crosses three crosses ACNM 18 x BioYSR, ACNM 19 x Geeta and ACNM 16 x Geeta were identified as potential crosses for their exploitation in recombination breeding. It is suggested from this study that, six three way crosses viz.,(ACNM 18 x BioYSR) x ACNM 20, (ACNM 19 x Geeta) x ACNM 20, (ACNM16 x Geeta) x ACNM 20, (ACNM 18 x BioYSR) x ACNM 21, (ACNM 19 x Geeta) x ACNM 21, (ACNM16 x Geeta) x ACNM 21 and two double crosses (ACNM 18 x BioYSR) x (ACNM 19 x Geeta) and (ACNM 18 x BioYSR) x (ACNM 16 x Geeta) involving the identified superior crosses and parents should be performed and carried over further by Single seed descent method if the genetic base is to be broadened.

(Keywords : Mustard, local lines, gca and sca effects, variances)

INTRODUCTION

Indian mustard (*Brassica juncea*) called as rai, raya or laha is an important oil seed crop belonging to Brassicae group. Oil content in Indian mustard seeds varies from 30 to 48 per cent. Crop Brassica encompass many diverse type plants, which are grown as vegetables, fodder or sources of oil and condiments. In India, the area, production and productivity were 6.69 million hectares, 6.60 million tonnes and 1145 kg ha^{-1} respectively (Anonymous, 2011). In Maharashtra area, production and productivity were 1200 hectares, 4000 tonnes and 308 kg ha^{-1} (Anonymous, 2011). In recent years though there has been an increase in the area and production of rapeseed mustard, the average productivity in India is quite low in comparison to that in some of the developed countries. In India, however production of edible oil is grossly short of the requirements. Consequently, large quantities have to be imported for making up the shortfall, which in turn is a heavy drain on foreign exchange resources. Vigorous efforts therefore are needed to increase the yield level and to achieve self sufficiency. Yield is one of the most important economic characters and is the product of multiplicative interaction of contributing characters. Hence, the important objective in mustard improvement is oriented to develop varieties which have high yielding potential.

The concept of combining ability analysis is important in designing plant breeding programmes. Information on combining ability provides guidelines to the plant breeders in selecting the elite parents and desirable cross combinations and at the same time reveals the nature of gene action involved in the inheritance of various traits and thereby helps in formulation of breeding methodology to be used. The nature of gene action would help in predicting the effectiveness of selection in population. A distinct type of gene action, its magnitude and constitution of genetic architecture is of fundamental importance to the plant breeder.

Keeping in view the above facts this work was executed to evaluate 20 local lines of mustard and the crosses involving these lines.

MATERIALS AND METHODS

Twenty Local lines viz. ACNM 1, ACNM 2, ACNM 3, ACNM 4, ACNM 5, ACNM 6, ACNM 8,

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ACNM 10, ACNM 11, ACNM 12, ACNM 13, ACNM 14, ACNM 15, ACNM 16, ACNM 17, ACNM 18, ACNM 19, ACNM 20, ACNM 21and ACNM 22 collected from different places of Vidarbha were crossed with three testers Geeta, RH−819 and Bio YSR to obtain 60 crosses during *rabi* 2011.

Sixty F_1 crosses obtained were grown during *rabi* 2012 in randomized complete block design with three replications. Single row was allotted for each cross which consisted of twenty plants with a spacing 45 x 15 cm. Recommended package of practices were followed as per schedule to raise healthy crop during both *rabi* 2011 and 2012. Five plants from each F_1 cross were randomly selected from each replication for recording observations like days to first flower, days to maturity, plant height (cm), number of primary branches plant^{-1},1000 seed weight (g), number of siliquae plant^{-1} and seed yield plant^{-1}(g). The data were subjected to statistical and biometrical analysis as the methodology given by Panse and Sukhatme (1954) and Kempthrone (1957).

RESULTS AND DISCUSSION

Analysis of variance for the experimental design as observed from table 1 revealed the presence of substantial genetic variability among the genotypes i.e. crosses. The results on mean performance of 60 crosses reported in table 2 revealed that the cross ACNM 18 x BioYSR produced maximum seed yield plant^{-1} of 15.27 g, maximum number of siliquae plant^{-1}(225) and high number of primary branches (5.07) and 1000 seed weight (4.73 g) and attained maturity within 95.87 days. This was followed by cross ACNM 21 x BioYSR producing high seed yield plant^{-1} of 11.73 g, 224.60 siliquae plant^{-1}, 5.27 primary branches plant^{-1} and attained maturity within 99.13 days. The crosses ACNM 20 x BioYSR and ACNM 19 x Geeta also exhibited high seed yield plant^{-1} (10.81g and 10.31g), high siliquae plant^{-1} (216 and 218 respectively), number of primary branches plant^{-1} (5.03 and 5.07) and 1000 seed weight (4.63 g and 4.45 g respectively) and attained maturity within 97.73 and 94.27 days respectively. Hence, these four crosses ACNM 18 x BioYSR, ACNM 21 x BioYSR, ACNM 20 x BioYSR and ACNM 19 x Geeta were identified as superior crosses based on mean performance.

Analysis of variance for combining ability is presented in table 3. Mean squares due to lines were significant for all characters except number of primary branches and 1000 seed weight. Mean squares due to testers were non significant for all the characters studied. Mean squares due to line x tester were highly significant for days to first flower, number of primary branches plant^{-1},1000 seed weight and seed yield plant^{-1} at both the levels of significance and number of siliquae plant^{-1} was significant only at 5 % level of significance. Mean squares due to line x tester were non significant for days to maturity and plant height. The significant mean squares for lines and for line x tester for yield and most of the yield component indicates the presene of gca among lines and sca among crosses. Such significant variation for gca and sca were also reported by Nair *et al*. (2005), Singh (2007), Patel *et al.* (2005) in mustard. Mean squares due to lines were higher than that of testers for all characters studied which indicated greater contribution of lines towards gca for these traits.

Random effect model adopted in the present study allows the estimation of variance components which helps to know precisely the relative importance of additive and dominance component in the control of different characters. σ^2 H (Dominance genotypic variance) was found to be maximum for number of siliquae plant^{-1}(486.62) followed by plant height (152.25), days to first flower (8.93) and seed yield plant^{-1}(3.35), σ^2 D (Additive genetic variance) was found to be high for number of siliquae plant^{-1}(17.51), followed by plant height (7.13), days to first flower (0.25). Dominant or non additive genetic variance was found to be more than additive genetic variance for days to first flower, plant height, number of primary branches plant^{-1}, number of siliquae plant^{-1}, 1000 seed weight and seed yield plant^{-1} except days to maturity indicating predominance of non additive genetic component in the inheritance of these characters. This can also be confirmed from the average degree of dominance for these characters which ranged from 20.38 for 1000 seed weight to 6.53 for plant height. These results were in accordance with the findings of Goswami and Behl (2005), Aher *et al*. (2009) and Parmar *et al*. (2011) who also reported the predominance of non additive genetic component for the inheritance of seed yield plant^{-1} and important yield component like number of siliquae plant^{-1} and 1000 seed weight etc.

The data regarding general combining ability effects are presented in table 4. Estimates of gca effects in this study revealed that among the lines ACNM 21 was found to be best general combiner for seed yield plant^{-1}, number of siliquae plant^{-1}, plant height, days to maturity and days to first flower. This was followed by ACNM 20 for seed yield plant^{-1}, number of siliquae plant^{-1}, plant height and days to first flower. ACNM 3 and ACNM 5 were also found to be good general combiners for seed yield plant^{-1} and number of siliquae plant^{-1}. Hence, these four lines ACNM 20, ACNM 21, ACNM 3 and ACNM 5 were identified as good combiners and would therefore, be useful as desirable parents for enhancing the yield potential through assembling favourable genes for desirable yield components.

Study of sca effects (Table 5) revealed that none of the crosses showed significant sca effects in the desirable direction for all the characters studied. Wide variability for sca effects was observed among the crosses for different characters. It is worth to note here that among the crosses showing significant sca in desirable direction in most of the characters involved one parent as good general combiner. Out of the 60 crosses studied, the cross ACNM 21 x BioYSR showed positive significant sca for seed yield plant^{-1}, number of siliquae plant^{-1} and number of primary branches plant^{-1}. Four other crosses ACNM 20 x BioYSR, ACNM 12 x Geeta, ACNM 15 x RH−819, ACNM 22 x RH−819 recorded positive significant sca effect for seed yield plant^{-1} and 1000 seed weight. Predominance of non additive genetic control for seed yield plant^{-1} and its component characters except days to maturity and positive significant sca effect observed in above four crosses indicated potential of heterosis breeding for improving the productivity in this crop by the use of above four crosses. The cross ACNM 21 x Geeta exhibited negative significant sca effect for seed yield plant^{-1}, number of siliquae plant^{-1} and number of primary branches plant^{-1}. Another cross ACNM 6 x Geeta exhibited negative significant sca effect for seed yield plant^{-1}, 1000 seed weight and days to first flower. Simillarly, crosses ACNM 20 x Geeta and ACNM 20 x RH−819 recorded negative significant sca effect for seed yield plant^{-1} and 1000 seed weight. These four crosses ACNM 21 x Geeta, ACNM 6 x Geeta, ACNM 20 x Geeta and ACNM 20 x RH−819 having negative significant sca effects can be exploited for recombination breeding, if they exhibit high mean performance for the seed yield plant^{-1} and number of siliquae plant^{-1}.

In predominantly self pollinated crop like mustard the breeder is restricted to produce true breeding varieties only, as the non additive portion of phenotypic variation is non fixable in later generation. A breeder would therefore prefer to identify the crosses which have low sca effects but have high mean performance and involves good general combiner as parents. The crosses ACNM 18 x BioYSR, ACNM 19 x Geeta and ACNM 16 x Geeta exhibited high mean (15.27, 10.31 and 9.19 g) for seed yield plant^{-1} with low negative sca effect (−0.29, 0.37 and −0.39) for the same character as observed from table 8. These crosses also possessed high mean (225, 218 and 180.87) for number of siliquae plant^{-1} with low sca effects (−9.60, −3.76 and −11.23). The above three crosses were also found to posses low sca effect for days to first flower. Hence, these three crosses ACNM 18 x BioYSR, ACNM 19 x Geeta and ACNM 16 x Geeta appeared to be the most potential crosses and showed the involvement of additive gene action which is the general situation observed in self pollinated crop. The genotype of inherent superiority can be produced from this population by blending and fixing maximum favourable genes.

To broaden the genetic base it is necessary to produce three way cross or double cross involving the selected crosses and good general combining parents viz.,(ACNM18 x BioYSR) x ACNM 20, (ACNM 19 x Geeta) x ACNM 20, (ACNM 16 x Geeta) x ACNM 20, (ACNM 18 x BioYSR) x ACNM 21, (ACNM 19 x Geeta) x ACNM 21, (ACNM 16 x Geeta) x ACNM 21,(ACNM 18 x BioYSR) x (ACNM 19 x Geeta) and (ACNM18 x BioYSR) x (ACNM16 x Geeta) which may be utilized for deriving superior transgrates for seed yield plant^{-1}, number of siliquae plant^{-1} and early flowering. Hence, it is suggested from this study that the above mentioned three way and double crosses should be effected in the next season and should be forwarded through single seed descent method to identify desirable recombinant lines.

Table 1. Analysis of variance for the experimental design in crosses

Sources	d.f.	Mean squares						
		Days to first flower	Days to maturity	Plant height (cm)	No.of primary branches plant^{-1}	No. of siliquae plant^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
Replication	2	14.51	73.88	1780.21	1.35	853.93	0.034	0.99
Crosses	59	26.28**	7.12	600.19**	0.82**	2064.22**	1.36**	10.41**
Error	118	2.42	11.46	228.50	0.12	769.09	0.011	1.33

***, ** = Significant at 5 % and 1% level respectively**

Table 2. Mean performance of crosses for different characters in mustard

Sr. No.	Crosses	Days to first flower	Days to maturity	Plant height (cm)	No.of Primary branches plant^{-1}	No.of siliquae plant^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
1	ACNM 1x Geeta	42.27	96.87	178.33	3.87	128.00	4.81	7.35
2	ACNM 2 x Geeta	42.13	96.27	190.47	5.53	186.40	3.73	8.01
3	ACNM 3 x Geeta	40.20	96.13	176.47	4.73	155.00	4.43	8.49
4	ACNM 4 x Geeta	44.67	96.27	190.53	5.20	184.00	3.72	8.77
5	ACNM 5 x Geeta	39.87	95.07	181.13	4.07	129.87	5.07	8.56
6	ACNM6 x Geeta	37.80	94.93	170.60	4.07	152.67	3.71	7.63
7	ACNM 8 x Geeta	39.87	94.60	180.40	4.60	187.20	3.27	9.85
8	ACNM22 x Geeta	38.00	94.47	180.20	4.73	193.33	3.40	8.27
9	ACNM 10 x Geeta	38.33	95.20	181.13	4.07	172.47	3.51	7.37
10	ACNM11 x Geeta	42.73	94.93	177.83	5.27	153.67	3.67	8.33
11	ACNM12 x Geeta	38.60	93.27	180.33	4.70	175.53	3.76	8.13
12	ACNM13 x Geeta	37.87	93.87	162.00	4.00	158.80	3.45	6.69
13	ACNM14 x Geeta	41.93	93.07	183.07	4.80	194.80	4.07	8.61
14	ACNM15 x Geeta	40.87	93.13	170.00	4.87	170.47	3.55	7.62
15	ACNM16 x Geeta	40.53	96.27	182.40	4.80	180.87	3.64	9.19
16	ACNM17 x Geeta	38.60	93.93	158.93	4.20	126.67	3.84	5.78
17	ACNM18 x Geeta	42.47	96.47	181.07	3.73	136.07	5.17	8.96
18	ACNM19 x Geeta	43.80	94.27	195.33	5.07	218.00	4.45	10.31
19	ACNM20 x Geeta	42.33	93.80	180.67	3.67	128.53	4.79	6.71
20	ACNM21 x Geeta	38.60	93.67	168.33	3.47	126.07	3.83	4.73
21	ACNM 1x RH-819	35.40	93.13	157.67	3.40	114.27	4.43	6.58
22	ACNM 2x RH-819	36.47	93.07	160.40	4.20	127.67	3.53	4.41
23	ACNM 3 x RH-819	35.27	94.20	152.07	4.07	134.47	4.49	7.08
24	ACNM 4 x RH-819	38.67	93.60	154.27	4.43	153.87	3.49	6.58
25	ACNM 5 x RH-819	35.80	93.53	153.60	3.93	125.33	4.69	7.39
26	ACNM 6 x RH-819	35.47	94.60	149.00	4.00	123.00	4.35	6.31
27	ACNM 8 x RH-819	41.67	94.33	168.13	4.40	159.07	4.01	8.01
28	ACNM 22 x RH-819	35.27	92.87	162.53	4.60	145.07	3.71	6.45
29	ACNM10 x RH-819	35.13	91.93	149.73	4.13	157.87	2.99	6.53
30	ACNM11 x RH-819	41.20	94.53	171.00	4.53	154.87	3.47	5.61
31	ACNM12 x RH-819	35.07	93.93	161.87	4.13	170.27	4.46	9.39
32	ACNM13 x RH-819	36.67	93.47	163.73	4.27	169.00	3.75	6.76
33	ACNM14 x RH-819	37.33	92.47	166.67	4.40	141.47	3.28	5.73
34	ACNM15 x RH-819	37.47	92.07	159.33	4.20	129.87	3.43	4.08
35	ACNM16 x RH-819	36.13	93.40	151.87	4.27	133.87	3.19	4.03
36	ACNM17 x RH-819	37.53	93.07	149.47	3.73	122.20	4.49	5.57
37	ACNM18 x RH-819	37.47	93.80	164.73	3.67	135.27	4.75	7.32
38	ACNM19 x RH-819	37.47	91.47	163.87	4.73	170.47	3.86	6.75
39	ACNM20 x RH-819	39.00	94.53	166.40	3.80	122.00	4.73	6.71
40	ACNM21 x RH-819	37.93	92.20	164.40	3.67	148.07	3.23	6.09
41	ACNM 1x BioYSR	41.73	94.80	190.60	3.87	139.40	4.64	7.82
42	ACNM 2 x BioYSR	43.47	93.53	184.27	4.40	149.27	2.98	5.55
43	ACNM 3 x BioYSR	39.07	93.47	168.87	3.80	139.60	4.43	6.81
44	ACNM 4 x BioYSR	41.93	93.47	176.60	4.87	175.93	3.31	7.51
45	ACNM 5 x BioYSR	40.33	95.53	192.53	3.60	151.87	5.45	7.87
46	ACNM 6 x BioYSR	41.53	95.47	190.53	4.40	140.47	4.59	6.70
47	ACNM 8 x BioYSR	43.20	93.73	184.80	4.90	133.27	2.97	4.99
48	ACNM22 x BioYSR	42.40	94.73	190.07	4.60	170.13	3.10	6.44
49	ACNM10 x BioYSR	43.13	94.33	190.40	4.67	170.53	3.33	9.37
50	ACNM11 x BioYSR	41.73	93.60	184.93	4.93	164.07	2.84	6.33

Table 2 continued.....

Sr. No.	Crosses	Days to first flower	Days to maturity	Plant height (cm)	No.of Primary branches plant^{-1}	No.of siliquae plant^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
51	ACNM12 x BioYSR	42.53	94.60	196.80	4.20	159.13	4.21	7.96
52	ACNM13 x BioYSR	41.60	94.80	185.40	4.33	169.27	3.33	6.75
53	ACNM14 x BioYSR	44.47	94.20	191.53	5.00	179.93	3.07	7.57
54	ACNM15 x BioYSR	44.53	96.13	185.53	5.40	184.80	2.95	7.61
55	ACNM16 x BioYSR	43.33	95.53	185.73	5.27	208.93	3.09	8.15
56	ACNM17 x BioYSR	41.40	93.07	182.80	4.73	202.60	3.00	9.17
57	ACNM18 x BioYSR	44.87	95.87	197.40	5.07	225.00	4.73	15.27
58	ACNM19 x BioYSR	43.20	98.87	188.53	3.80	138.53	4.91	7.39
59	ACNM20 x BioYSR	44.47	97.73	195.40	5.03	216.00	4.63	10.81
60	ACNM21 x BioYSR	44.93	99.13	198.07	5.27	224.60	3.41	11.73
	General mean	40.12	94.42	175.34	4.38	157.56	3.88	7.47
	SE (m)	1.27	2.76	12.34	0.28	22.64	0.08	0.94
	SE (d)	0.89	1.95	8.72	0.20	16.01	0.061	0.66
	CD (5%)	2.51	5.45	24.37	0.56	44.72	0.171	1.86
	CD (1%)	3.31	7.20	32.17	0.74	59.03	0.225	2.45

Table 3. Analysis of variance for combining ability

Sources	d.f.	Mean squares						
		Days to first flower	Days to maturity	Plant height (cm)	No.of primary branches plant^{-1}	No. of siliquae plant^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
Lines	19	53.42**	15.49**	1383.66**	1.19	4072.75**	1.65	18.75**
Testers	2	11.49	7.33	173.77	0.28	749.30	0.62	6.15
Lines x Testers	38	13.49**	2.91	230.92	0.66**	1208.04*	1.27**	6.46**
Error	118	2.43	11.45	228.50	0.12	769.09	0.011	1.33
	σ^2 gca	0.12	0.04	3.57	0.002	8.76	0.0009	0.04
	σ^2sca	8.93	-0.61	152.25	0.21	486.62	0.39	3.35
	σ^2 gca vs σ^2sca	0.81	1.49	0.99	0.65	0.88	0.60	0.81
	σ^2D	0.25	0.08	7.13	0.003	17.51	0.002	0.08
	σ^2H	8.93	-0.62	152.25	0.21	486.62	0.39	3.36
Average degree of dominance		8.50	4.40	6.53	11.68	7.45	20.38	9.39

***, ** = Significant at 5% and 1% level respectively**

Table 4. General combining ability effects of parents

Sr. No.	Genotypes Lines	Days to first flower	Days to maturity	Plant height (cm)	No.of siliquae plant^{-1}	Seed yield plant^{-1}(g)
1	ACNM 1	1.40*	2.001	6.41	–1.09	0.47
2	ACNM 2	0.65	1.001	5.41	–2.05	0.84*
3	ACNM 3	–1.39*	0.33	5.23	26.77**	1.02**
4	ACNM 4	–0.39	–0.39	–1.95	5.11	0.24
5	ACNM 5	0.98	–0.26	3.14	24.48*	0.99**
6	ACNM 6	1.49**	0.46	3.09	–9.32	0.87*
7	ACNM 8	–1.35*	–0.88	–6.46	–34.61**	–1.47**
8	ACNM 22	–3.33**	–0.79	–19.77**	–18.89**	–1.45**
9	ACNM 10	–2.48**	–0.27	–18.44**	–21.76*	–0.24
10	ACNM11	–2.93**	–1.31	–14.24**	–4.96	–1.28**
11	ACNM12	–3.77**	–1.13	–11.24**	2.68	–0.18
12	ACNM13	3.08**	1.58	21.79**	28.92**	2.92**
13	ACNM14	–2.15**	–1.15	–10.35*	–14.98	–0.55
14	ACNM15	0.92	–0.91	4.41	–11.98	–0.98**
15	ACNM16	0.32	–0.26	3.98	–1.76	–0.08
16	ACNM17	2.25**	0.22	13.12*	–9.61	–1.43**
17	ACNM18	2.34**	0.24	15.37**	7.02	0.41
18	ACNM19	3.40**	0.62	12.14*	20.44*	–0.17
19	ACNM20	3.07**	0.40	13.29*	54.62**	3.39**
20	ACNM21	4.07**	4.16**	18.65**	18.82*	2.50**
	SE(i)±	**0.57**	**1.15**	**5.27**	**9.53**	**0.36**

*, ** = Significant at 5% and 1 % level respectively

Table 5. Specific combining ability effects of crosses

S.N.	Crosses	Days to first flower	No.of primary branches plant^{-1}	No.of siliquae plant^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
1	ACNM 1x Geeta	0.88	-0.78**	-23.49	0.39**	-0.41
2	ACNM 2 x Geeta	4.03**	0.82**	33.46*	-0.54**	0.64
3	ACNM 3 x Geeta	1.28	0.20	7.84	-0.22*	1.55*
4	ACNM 4 x Geeta	3.14**	0.68**	-4.03	-0.05	0.80
5	ACNM 5 x Geeta	0.96	0.05	17.73	0.22*	0.33
6	ACNM6 x Geeta	-2.88**	0.05	-16.60	-0.75**	-2.38**
7	ACNM 8 x Geeta	3.69**	0.22	10.55	0.34**	0.89
8	ACNM22 x Geeta	-0.19	0.04	-6.03	-0.40**	-1.42*
9	ACNM 10 x Geeta	-1.70	-0.11	-5.49	0.25**	0.35
10	ACNM11 x Geeta	-1.79	0.25	-2.56	0.22*	0.44
11	ACNM12 x Geeta	-1.15	-0.07	14.99	0.54*	2.29**
12	ACNM13 x Geeta	0.57	0.20	6.19	-0.37**	-0.29
13	ACNM14 x Geeta	-0.35	-0.33	-2.34	0.21*	0.58
14	ACNM15 x Geeta	-2.97**	-0.24	7.46	-0.49**	-0.21
15	ACNM16 x Geeta	-1.24	-0.22	-11.23	-0.06	-0.39
16	ACNM17 x Geeta	-0.70	-0.17	-2.51	0.94**	0.85
17	ACNM18 x Geeta	0.80	0.14	10.93	-0.23*	1.67**
18	ACNM19 x Geeta	-1.79	-0.51**	-3.76	0.12	-0.37
19	ACNM20 x Geeta	0.28	0.31	1.73	-0.61**	-2.52**
20	ACNM21 x Geeta	-0.86	-0.53**	-32.87*	0.49**	-2.39**
21	ACNM 1x RH-819	0.95	0.75**	29.11	-0.48**	0.24
22	ACNM 2x RH-819	-0.56	-0.45**	-26.46	1.01**	0.42
23	ACNM 3 x RH-819	-0.38	0.19	8.18	0.12	-0.05
24	ACNM 4 x RH-819	-0.78	-0.02	12.05	0.24	0.59
25	ACNM 5 x RH-819	0.10	-0.02	-12.39	-0.09	-0.68
26	ACNM 6 x RH-819	1.19	-0.56**	-12.99	0.79**	0.79
27	ACNM 8 x RH-819	0.17	-0.11	2.29	-0.41**	-1.09
28	ACNM 22 x RH-819	-1.18	-0.24	-5.02	0.76**	1.24*
29	ACNM10 x RH-819	-1.82	-0.18	-13.62	0.10	-0.75
30	ACNM11 x RH-819	-1.72	-0.34	4.45	-0.29**	0.51
31	ACNM12 x RH-819	0.66	-0.07	7.94	0.02	-0.36
32	ACNM13 x RH-819	-0.56	0.13	4.40	-0.41**	-0.35
33	ACNM14 x RH-819	-0.16	0.59**	27.07	-0.48**	0.01
34	ACNM15 x RH-819	1.04	-0.18	-6.99	1.13**	1.51*
35	ACNM16 x RH-819	1.84	0.71	19.31	-0.98**	0.29
36	ACNM17 x RH-819	1.17	0.19	-15.51	-0.47**	-0.88
37	ACNM18 x RH-819	-0.38	0.27	-1.33	-0.51**	-1.38*
38	ACNM19 x RH-819	1.28	0.02	1.11	0.06	0.44
39	ACNM20 x RH-819	-1.45	-0.36	-10.39	-0.50**	-1.51*
40	ACNM21 x RH-819	0.62	-0.34	-11.19	0.42**	1.01
41	ACNM 1x BioYSR	-1.82	0.02	-5.62	0.09	0.17
42	ACNM 2 x BioYSR	-3.47**	-0.38*	-7.00	-0.47**	-1.06
43	ACNM 3 x BioYSR	-0.89	-0.40*	-16.02	0.10	-1.49*
44	ACNM 4 x BioYSR	-2.36**	-0.66**	-8.02	-0.19	-1.39*
45	ACNM 5 x BioYSR	-1.07	-0.02	-5.33	-0.12	0.35
46	ACNM 6 x BioYSR	1.69	0.51**	29.60	-0.05	1.59*
47	ACNM 8 x BioYSR	-3.87**	-0.11	-12.84	0.07	0.21
48	ACNM 22 x BioYSR	1.38	0.20	11.04	-0.36**	0.19
49	ACNM 10 x BioYSR	3.53**	0.29	19.11	-0.35**	0.40
50	ACNM11 x BioYSR	3.51**	0.11	-1.89	0.07	-0.96
51	ACNM12 x BioYSR	0.49	0.13	-22.93	-0.56**	-1.93**
52	ACNM13 x BioYSR	-0.002	-0.33	-10.60	0.78**	0.64
53	ACNM14 x BioYSR	0.53	-0.27	-24.73	0.27**	-0.59
54	ACNM15 x BioYSR	1.93	0.42*	-0.47	-0.65**	-1.31*
55	ACNM16 x BioYSR	-0.60	-0.49**	-8.09	1.05**	0.10
56	ACNM17 x BioYSR	-0.47	-0.03	18.02	-0.46**	0.023
57	ACNM18 x BioYSR	-0.42	-0.40	-9.60	0.74**	-0.29
58	ACNM19 x BioYSR	0.51	0.49**	2.64	-0.18	-0.07
59	ACNM20 x BioYSR	1.18	0.04	8.67	1.12**	4.04**
60	ACNM21 x BioYSR	0.24	0.87**	44.07**	-0.92**	1.39*
	SE(ij) ±	**0.19**	**0.19**	**16.49**	**0.94**	**0.62**

*, ** = Significant at 5% and 1% level respectively

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