

## COMBINING ABILITY ANALYSIS IN INDIAN MUSTARD: FULL, HALF AND QUARTER DIALLEL ANALYSIS

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### ABSTRACT

Combining ability studies, using Methods 1, 2, 3 and 4, Model I of Griffing were carried out for seed yield using a 14 x 14 diallel set in Indian mustard. The estimates of both the combining ability variances were significant for all the methods except Method 3 where specific combining ability variance was non-significant. Variances due to reciprocal cross effects were also significant. Exclusion of parental generation and the use of Method 3 is, therefore advocated.  $2\sigma^2g / (2\sigma^2g + \sigma^2s)$  ratio revealed preponderance of non-additive gene action for the character studied. Parent T 59 was found to be the best general combiner. The cross RL 18 x T 6342, RLM 240 x RLM 564 and RLM 528 x T 6342 appeared to be the best specific cross combinations. In order to exploit non-additive gene effects, population breeding approach such as recurrent selection, diallel selective mating system has been suggested.

### INTRODUCTION

Combining ability analysis (Griffing, 1956 a, b) has proved to be of considerable use in Indian mustard (Singh, 1973; Labana et al., 1975). Importance of this is even more when it is desired to select the genotypes which, used in a practical breeding programme, could combine well with others in hybrid combinations. Also based on the genetic information obtained from combining ability analysis, the breeder is able to formulate an effective hybridization programme. As evident, less efforts have been made in the past to improve the yield potential among the existing cultivars of Indian mustard in India.

Attempts have, therefore, been made to study the combining ability and a comparison among Methods 1, 2, 3 and 4 Model 1 in order to see the impact of reciprocals and parental generation on the estimates of combining ability variances as well as effects for seed yield using a 14x14 diallel set in Indian mustard [*Brassica juncea* (L.) Czern & Coss].

### MATERIAL AND METHODS

Fourteen genotypes of Indian mustard *Brassica juncea* (L.) Czern & Coss., viz., RL 18, RLM 29, RLM 42, T 59, RLM 188, RLM 196, RLM 222, RLM 240, RLM

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269, RLM 299, RLM 391, RLM 528, RLM 564 and T 6342 to and their maternal were used study their combining ability. During rabi 1977-78, 196 entries (14 parents, 91  $F_1$ s and 91 reciprocal crosses) were sown in a Randomized Block Design with 3 replications. In each replication, each genotype was represented by a single 2.25 m long row with spacing of 30 cm and 15 cm. Recommended cultural practices were followed for raising the crop. Seed yield per plant was recorded on five randomly selected plants in each treatment.

Mean data were analysed for combining ability of the parents,  $F_1$ s and reciprocals by all the four methods of Griffing (1956 b).

### RESULTS AND DISCUSSION

The mean squares due to general combining ability (gca) and specific combining ability (sca) were significant for all the four methods except method 3 where mean square due to sca was non-significant (Table 1). The general assumption usually made in the diallel analysis, that there are no maternal effects, does not appear to hold good in respect of the material, as significant reciprocal cross effects were observed (Table 1), confirming findings of Yadava et al. (1974) and Asthana and Pandey (1977).

The comparison of the variance components revealed that  $\sigma^2_s$  was higher than  $\sigma^2_g$  for all the four methods, whereas for Method 1 and Method 2, it was very high. Several workers compared either the mean squares or the estimated variance components of general and specific combining ability to determine the predominance of additive over non-additive gene action in different crops (Murty, 1975). However, such a procedure may be misleading which can easily be seen by studying the expectations of general and specific combining ability mean squares given by Griffing (1956 a,b). As shown by Griffing (1956 b), the total genetic variance among single cross progenies is equal to twice the general combining ability variance ( $\sigma^2_g$ ) plus the specific combining ability variance ( $\sigma^2_s$ ). Based on this relationship, Baker (1978) postulated that the relative importance of general and specific combining ability should be assessed by estimating the components of variance and expressing them in the ratio,  $2 \sigma^2_g / (2 \sigma^2_g + \sigma^2_s)$ . In the present study, by all the four methods,  $2 \sigma^2_g / (2 \sigma^2_g + \sigma^2_s)$  ratio deviated from unity to show the predominance of non-additive gene action for seed yield.

Out of the 14 cultivars, T59 was the best general combiner by all the methods, followed by RLM 196 with Method 3, and RLM 222 with Method 4 (Table 2). RLM 391 was the poor general combiner with Methods 1, 3 and 4. RLM 528 was the poor general combiner only with Method 1. All other cultivars were average general combiners.

Table 1. Analysis of variance for progeny means and combining ability for seed yield in a diallel cross in Indian mustard

Source	Method 1		Method 2		Method 3		Method 4	
	df	squares	df	squares	df	squares	df	squares
Replication	2	545.85**	2	299.38**	2	544.86**	2	299.55**
Genotype	195	3.33**	104	3.51**	181	3.41**	90	3.23**
Error	390	2.17	208	2.12	362	2.19	180	2.13
General combining ability	13	1.71**	13	1.64**	13	1.62**	13	1.48**
Specific combining ability	91	2.12**	91	1.10**	77	0.89	77	1.01*
Reciprocal cross Effects	91	1.06**	—	—	91	1.06*	—	—
Error	390	0.72	208	0.71	362	0.73	180	0.71
$\sigma^2g = \frac{1}{2}\sigma^2A$		-0.014		0.034		0.030		0.039
$\sigma^2s = \sigma^2D$		0.748		0.398		0.080		0.300
$\sigma^2r$		0.169		—		0.167		—
$2\sigma^2g : (2\sigma^2g + \sigma^2s)$		0.040		0.145		0.431		0.206

\* Significant at P = 0.05

\*\* Significant at P = 0.01

Table 2 : Estimates of general combining ability effects of different parents for seed yield in Indian mustard

Parent	Method 1	Method 2	Method 3	Method 4
1. RL 18	-0.029	-0.076	0.032	0.030
2. RLM 29	-0.260	-0.374	-0.222	-0.335
3. RLM 42	-0.201	-0.253	-0.194	-0.256
4. T 59	0.520**	0.668**	0.487**	0.652**
5. RLM 188	-0.125	-0.024	-0.108	0.045
6. RLM 196	0.259	0.133	0.338*	0.249
7. RLM 222	0.147	0.374	0.213	0.583*
8. RLM 240	-0.049	0.238	-0.234	-0.037
9. RLM 269	0.175	-0.070	0.165	-0.170
10. RLM 299	0.063	-0.065	0.050	-0.134
11. RLM 391	-0.349*	-0.350	-0.406*	-0.466*
12. RLM 528	-0.329*	-0.325	-0.311	-0.288
13. RLM 564	-0.029	-0.270	-0.006	-0.281
14. T 6342	-0.208	-0.394	-0.184	-0.408
SE $\hat{g}_i$	0.1550	0.2024	0.1681	0.2343
SE $(\hat{g}_i - \hat{g}_j)$	0.2275	0.2970	0.2467	0.3438

\* Significant at  $P = 0.05$ \*\* Significant at  $P = 0.01$ 

Specific combining ability effects for ten top ranking crosses are given in Table 3. For Method 1, five crosses showed significant sca effects in desirable directions whereas other two hybrids had a significantly negative effect. The frequency of positively significant sca effects for Method 2, 3 and 4 was 12, 3, and 7, respectively. RL 18 x T 6342 showed significant and the highest sca effect with Methods 1 and 3 followed by RLM 240 x RLM 564 and RLM 528 x T 6342. With methods 2 and 4 six cross combinations viz, RLM 29 x RLM 42, RLM 29 x RLM 222, RLM 29 x RLM 299, RLM 29 x T 6342, T 59 x RLM 222 and RLM 196 x RLM 240 showed significant high sca effects. Most of these cross combinations involved average x average general combiners.

For Methods 1, 3 significant reciprocal cross effects were present in 10 common crosses except cross RL 18 x RLM 222 which showed significant reciprocal cross effect for only Method 1. Crosses T 59 x RLM 222 and RLM 196 x RLM 240 exhibited significantly high reciprocal cross effects. Both these methods have indicated an extra nuclear control, thus suggesting that for its improvement due consideration need to be given to the way parents are involved in the cross or specific cytoplasm which has desirable effect. In this combining ability analysis a chosen set of lines is used and our interest centres on the performance of F<sub>1</sub>s. Therefore, to obtain unbiased estimates the parental lines need not be included in the combining ability analysis. As there are reciprocal genotypic effects, then both sets

Table 3. The specific combining ability effects and reciprocal cross effects of ten top ranking crosses for seed yield in Indian mustard

Cross	Specific combining ability effects				Reciprocal cross effects, methods 1,3
	Method 1	Method 2	Method 3	Method 4	
RL 18 X RLM 222	0.368**	1.451*	0.162	0.992	1.180a
RL 18 X T 6342	1.862**	1.631*	1.747**	1.367	-0.175
RLM 29 X RLM 222	1.089	1.948**	0.906	1.557*	0.890
RLM 29 X T 6342	0.948	1.878*	0.856	1.682*	0.920
RLM 42 X T 59	0.917	1.444*	0.865	1.320	0.540
T 59 X RLM 222	0.544	1.887**	0.432	1.551*	1.635**
T 59 X RLM 240	-0.281	0.703	-0.141	0.851	1.335*
RLM 188 X T 6342	1.138*	1.568*	1.066	1.342	0.635
RLM 196 X RLM 222	0.760	1.242	0.536	0.773	0.500
RLM 196 X RLM 240	-0.190	1.708*	-0.163	1.723*	1.975**
$\hat{A}$ (s <sub>ig</sub> )	0.5607	0.7316	0.5559	0.7747	SE t <sub>ij</sub> (Method 1) = 0.6021
$\hat{A}$ (s <sub>ij</sub> - s <sub>ik</sub> )	0.8205	3.3607	0.8183	1.1404	SE t <sub>ij</sub> (Method 3) = 0.6043
$\hat{A}$ (r <sub>ij</sub> - r <sub>ke</sub> )	0.7883	1.1114	0.7802	1.0873	

\* Significant at P=0.05,

\*\* Significant at P=0.01

a Significant at P=0.05 for method 1 only

of F<sub>1</sub>s should be included and dialled crossing Method 3 should be used. The reciprocal effects can be usefully employed employd to detect variation due to sex linked genes and maternal effects. Thus Method 3 would be most useful.

From our studies, as seed yield is influenced by non-additive gene action, the utility of simple progeny selection may not yield the desired dividends. For exploitation of non-additive gene effects, we had to maintain heterozygosity. Commercial maintenance of heterozygosity can only be either through commercial F<sub>1</sub> hybrid or production of composites/synthetics, which do not seem feasible at present. So the population breeding approach, such as recurrent selection, diallel selective mating system can be followed for recombining the desirable genes and for maximising the exploitation of genetic variability present in the material.

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