

HETEROSIS, GENE ACTION AND COMBINING ABILITY STUDY OF YIELD AND SOME OF THE YIELD COMPONENTS OF A FOUR-PARENT DIALLEL CROSS IN RICE

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Heterosis, gene action, and combining ability of yield and some of the yield components in rice were studied using a four-parent diallel cross. The characters studied were the number of primary branches per panicle, number of secondary branches per panicle, panicle weight and yield per plant. Significant heterosis over mid-parent ranged from 15.64% for the number of primary branches/panicle (DM 16-5-1/DM 107-4), to 124.06% for grain yield/plant (Kashmir Basmati/DM 16-5-1). Most of the hybrids showed significant and positive heterosis over mid-parental values indicating dominant type of gene action for the four quantitative characters. Mean values of some hybrids for a number of primary and secondary branches/panicle and several hybrids for panicle weight and grain yield/plant exceeded significantly the better parent showing overdominance due to positive genes. However, some of the cross combinations showed non-significant deviation in either direction from mid-parental values suggesting the presence of additive gene action.

A narrow range of variation for all four characters with respect to general combining ability and specific combining ability was observed. Both dominant and additive genes were involved for number of primary and secondary branches/panicle, while non additive gene action controlled panicle weight and grain yield/plant.

INTRODUCTION

Among the principal objectives in Basmati rice breeding, higher yield is of prime importance. However, yield is a complex character and depends upon a number of direct and indirect components [1]. In order to achieve the desired goal and to develop a variety of Basmati rice with a high yield potential, information on the inheritance of yield and yield components is imperative. Diallel analysis and heterosis studies are generally considered important for such basic information. Diallel analysis is a useful technique for analysing the pattern of genes regulating the quantitative characters, their dominance relationship and selection of parents [2, 3]. This technique has also been utilized to study the general combining ability (GCA) and specific combining ability (SCA) for plants [4] and animals [5]. In rice, Singh *et al* [6] observed that SCA variances were greater than those due to GCA, indicating the predominance of non-additive genes in the control of the characters studied. Heterosis studies may also be useful in identifying the potential cross combinations on the basis of hybrid vigour.

In rice few workers have reported on the extent of heterosis in quantitative characters. Maurya and Singh [7] reported that significant heterosis for yield was found to show heterosis for more than one yield component. Singh and Singh [8] observed heterosis in yields ranging from 33 to 64%.

Hence the present studies in rice deal with combining ability; gene action and heterotic effects for some of the important yield components, viz. (a) the number of primary branches/panicle, (b) the number of secondary branches/panicle (c) panicle weight and (d) grain yield/plant.

MATERIALS AND METHODS

Two rice cultivars, viz., Basmati 370 and Kashmir Basmati and two true breeding mutant lines, i.e. DM16-5-1 and DM107-4, derivatives of Basmati 370, following gamma rays irradiation (25KR), were crossed in all possible combinations excluding reciprocals in 1981. During 1982 seeds of six F₁ hybrids and their parents were grown in the field in a randomized complete block design with three replications. Each entry consisted of a single row 3m long, having plant-to-plant and row-to-row distance of 20 cm. Sixty-

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seven kg. of N + 30 kg P₂O₅/hectare were applied as fertilizer. Nitrogen was applied in two splits, half as basal and half as top dressing at the time of tillering and boot stage respectively.

At maturity, the parents and F₁'s were harvested individually and data were recorded on each of the above mentioned character on 10 guarded plants.

Heterosis was estimated from mid-parent (MP) and better parent (BP) by using the formula $F_1 - MP / MP \times 100$ and $F_1 - BP / BP \times 100$ respectively. GCA and SCA effects were estimated by the Griffing's method 4 model 1 [9]. This method is most commonly used in diallel crossing system as reciprocal genotypic effects are generally non-existent in plant data. It gives an exact genetic interpretation of the GCA and SCA variances. The critical differences (CD₁) were computed for the paired comparison of these effects following by Singh and Chaudhry [10].

RESULTS AND DISCUSSION

The heterosis of F₁ hybrids with respect to MP and BP for the number of primary branches/panicle, the number of secondary branches/panicle, panicle weight and grain yield/plant are given in Table 1. The degree of heterosis varied greatly for different characters and in different cross combinations but heterosis was in the same direction.

Deviation from MP. Out of six crosses, five crosses, viz. Nos. 1, 3, 4, 5 and 6 for number of primary branches/

panicle, four crosses, i.e., 1, 3, 4 and 5 for number of secondary branches/panicle, cross Nos. viz. 1, 2, 4, 5 and 6 for panicle weight and five crosses viz Nos. 1, 2, 4, 5 and 6 for grain yield/plant showed significant positive heterosis suggesting dominance due to positive genes. In the remaining crosses, the F₁ value did not deviate significantly from the MP values confirming additive gene action. This suggests that the genetic control of the characters studied depends upon the particular cross combination involved.

Deviation from BP. Two crosses, 1 and 5 for the number of primary branches, three crosses i.e. 1, 4 and 5 for the number of secondary branches/panicle, five crosses viz Nos. 1, 2, 4, 5 and 6 for panicle weight and five crosses i.e. 1, 2, 4, 5 and 6 for grain yield/plant exhibited significant positive heterosis over BP (Table 1) indicating over-dominance due to positive dominant genes. On the other hand, only one cross (No. 6) for the number of secondary branches/panicle showed negative but non-significant heterosis, indicating dominance due to negative dominant genes.

GCA and SCA. From the analysis of variance it was observed that there was variation among treatments for all characters as evidenced from the high significance of mean squares (Table 2). The mean squares for GCA and SCA were calculated from the analysis of variance of four characters (Table 3). Only the variance of SCA for panicle weight and grain yield/plant was significant, indicating non-additive genetic variance to be the major component of the

Table 1. Estimation of heterosis of F₁ hybrids expressed as percentages of mid-parent (MP) and better parent (BP)

No. Crosses	No. of primary branches/panicle		No. of secondary branches/panicle		Panicle weight		Grain yield/plant	
	% heterosis over MP	% heterosis over BP	% heterosis over MP	% heterosis over BP	% heterosis over MP	% heterosis over BP	% heterosis over MP	% heterosis over BP
1. Basmati 370/ Kashmir Basmati	+20.26 ^{**}	+9.20 [*]	+48.43 ^{**}	+44.36 ^{**}	+73.93 ^{**}	+71.40 ^{**}	+74.83 ^{**}	+71.60 ^{**}
2. Basmati 370/ DM16-5-1	+ 8.35	+5.88	+14.26	+11.66	+62.29 [*]	+59.65 ^{**}	+70.44 [*]	+58.06 ^{**}
3. Basmati 370/ DM107-4	+17.89 ^{**}	+9.82	+23.68 [*]	+ 7.44	+35.70	+30.07	+58.34	+28.93
4. Kashmir Basmati/ DM16-5-1	+17.65 ^{**}	+4.65	+33.25 ^{**}	+32.59 ^{**}	+103.79 ^{**}	+97.61 ^{**}	+124.06 ^{**}	+111.60 ^{**}
5. Kashmir Basmati/ DM107-4	+31.79 ^{**}	+31.34 ^{**}	+61.41 ^{**}	+36.95 ^{**}	+98.15 ^{**}	+87.27 ^{**}	+93.93 ^{**}	+84.08 ^{**}
6. DM16-5-1/ DM107-4	+15.64 ^{**}	+2.46	+13.82	-3.04	+81.96 ^{**}	+76.82 ^{**}	+91.24 ^{**}	+90.21 ^{**}

*, ** Significant at 5% and 1% levels respectively.

Table 2. Mean squares for various traits in a set of diallel crosses among four rice varieties/mutant lines

Sources of variation	Mean squares				
	Degrees of freedom	No. of primary branches/panicle	No. of secondary branches/panicle	Panicle weight (gms)	Grain yield/plant (gms)
Replications	2	0.56	11.20	23.36	11.67
Crosses	9	4.68**	132.60**	106.53**	95.31**
Error	18	0.32	5.70	9.16	6.00

** = Significant at 1% level.

Table 3. Combining ability analysis for yield and some of the yield components

S.O.V	D.F.	No. of primary branches/panicle	No. of secondary branches/panicle	Panicle weight	Grain yield/plant
GCA	3	1.26**	4.15**	1.92	1.92
SCA	6	1.71**	45.55**	52.30**	46.70**
Error	18	0.11	1.90	3.05	2.00

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

variation. Both GCA and SCA variances were significant for the remaining two characters indicating both additive and non-additive gene actions controlling the number of primary and secondary branches/panicle.

The GCA effects of each parent, for each of the four characters, are shown in Table 4. For the number of primary branches/panicle, DM16-5-1 and Basmati 370 showed

positive GCA and proved good general combiners. Kashmir Basmati was the best combiner for the number of secondary branches/panicle. None of the parents was found a good combiner for panicle weight and grain yield/plant.

Estimates of SCA effects for four characters are shown in Table 5. SCA effects represent the deviations of a parti-

Table 4. Estimation of general combining ability effects of yield and some of the yield components

Vari/mutant	No. of primary branches/panicle	No. of secondary branches/panicle	Panicle weight	Grain yield/plant
Basmati 370	0.29*	-0.19	-0.29	-0.05
Kashmir Basmati	-0.33**	3.48**	0.85	0.75
DM16-5-1	0.49*	-0.38	-0.28	-0.60
DM1074	-0.44**	-2.91**	-0.27	-0.20
SE (gi-gj)	0.19	0.80	1.01	0.82
CD ₁ (gi-gj)	0.39	1.67	N.S.	N.S.

Table 5. Estimates of specific combining ability effects of yield and some of the yield components

No.	Crosses	No. of primary branches/panicle	No. of secondary branches/panicle	Panicle weight	Grain yield/plant
1.	Basmati 370/ Kashmir Basmati	0.81**	5.87**	6.29**	5.30**
2.	Basmati 370/ DM16-5-1	0.18	0.73	4.61**	4.60**
3.	Basmati 370/ DM107-4	0.65**	0.86	-0.32	-0.23
4.	Kashmir Basmati/ DM16-5-1	0.67**	3.99**	0.61	1.06
5.	Kashmir Basmati/ DM107-4	1.67**	9.33**	7.26**	7.24**
6.	DM16-5-1/ DM107-4	0.53**	-0.42	6.49**	5.80**
	CD ₁ (S _{ij} -S _{ik})	0.88	3.74	4.74	3.84
	CD ₁ (S _{ij} -S _{kl})	0.79	3.34	4.24	3.43

cular cross from the average GCA effects of the two parents.

Cross numbers (1, 3, 4, 5, 6), (1, 4, 5), (1, 2, 5, 6) and (1, 2, 5, 6) are good specific combiners for number of primary branches/panicle, numbers of secondary branches/panicle, panicle weight and grain yield/plant respectively.

The combining ability analysis indicates that non-additive gene action is predominant for panicle weight and grain yield/plant. Both dominance and additive type of gene action were found in the other two characters.

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REFERENCES

- M.A. Khaleque and A.M. Eunos, *Curr. Agri.* 1, 41 (1977).
- B. Povilaitis, *Can. J. Gene. Cytol.* 8, 336 (1966).
- A.B. Joshi, S. Ramanujam and P.N.C. Pilly, *Indian J. Gen. Plant Breed.* 21, 12 (1968)
- M.M. Haque, M.N.I. Faridi, C.A. Razzaque and M. A. Newaz, *Ind. J. Agri. Sci.* 51, 711 (1981)
- S.C. Quah and P.K. Mohan Rao, *SABRAO J.*, 7, 1 (1975).
- R.P. Singh, R.R. Singh, S.P. Singh and R.V. Singh, *Oryza*, 16, 115 (1979).
- D.M. Maurya and D.P. Singh, *Indian J. Gen. Pl. Breed.* 38, 71 (1980).
- S.P. Singh and H.G. Singh, *Oryza*, 15, 73 (1978).
- B. Griffing, *Aust. J. Biol. Sci.* 9, 463 (1956).
- R.K. Singh and B.D. Chaudhry, *Biometrical Methods in Quantitative Genetic Analysis* (Kalyani Publishers, Ludhiana-New Delhi (1979), rev. edition.