

## Comparative efficacy of diallel, partial diallel and line x tester analyses in the study of gene action in rice (*Oryza sativa* L.)

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### ABSTRACT

*Comparative efficacy of diallel (Method 2 and 4 Model 1), partial diallel (sample size more and less than  $n/2$ ) and line x tester analyses were studied to understand the nature of gene action of 14 traits (both quantitative and qualitative) affecting grain yield in rice. Both the methods of diallel analysis and partial diallel analysis with "s" equal to 6 (i.e. more than  $n/2$ ) gave similar and comparable results. The nature of tester parents played a significant role in the estimates of gene effects. Line x tester analysis using tester parents with broad genetic base gave results fairly close to the diallel and partial diallel analysis. Hence, it was concluded that the line x tester analysis with profusely selected testers or partial diallel analysis with sample size equal to more than  $n/2$  may be preferred to screen a large number of genotypes.*

**Key words:** Diallel, partial diallel, line x tester mating designs, gene action, rice, comparison of mating designs

The choice of appropriate breeding strategy depends on the nature of gene action of economically important characters. Diallel (DL) and line x tester (LT) mating designs have been widely used to understand the gene effects in nonaromatic rice. However, diallel set becomes unmanageable with large number of parents while with the smaller it gives poor estimate due to large sampling errors. In case of LT analysis the choice and number of tester parents continued to be unsolved. The partial diallel (PD) cross analysis has also been proposed to evaluate large number of parental lines but has rarely been used in rice. Sharma and Mani (1996) had compared the efficacy of these mating designs in estimating the combining ability of parental lines / hybrids and the gene effects of various traits in rice. The present study was undertaken to study the efficacy of DL, PD and LT mating designs on the basis of gene action involving early, medium and late maturing varieties of rice.

### MATERIALS AND METHODS

Nine diverse genotypes of rice viz., HPR1164, HPR2047, China 988, VL91-1754, VL93-3613, VL93-6052, IR57893-08, VLDhan221 and JD8 were crossed

in all the possible combinations in a diallel mating design excluding reciprocals in both polyhouse and glasshouse at the Experimental Farm of Department of Plant Breeding and Genetics of Choudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur during wet season 2001 and 2002. In wet season 2003, all the 36 hybrids ( $F_1$ 's) along with parents including (standard check) were raised in randomized block design with three replications with single row of each parent and hybrid having 3m length with 20 and 15 cm, row to row and plant to plant spacing, respectively. The fertilizers were applied at the rate of 90N:45P:30K per hectare as recommended. The nitrogen was applied in three splits 50% as basal, 25% at tillering and 25% at panicle initiation stage. The recommended cultural practices were followed. Observations were recorded on 10 randomly selected plants of parents and 25 plants of hybrids for the following traits viz., grain yield per plant (g), leaf area index, dry matter (g), biological yield (g), plant height (cm) panicle length (cm), days to 50% flowering, grain length (mm), grain breadth (mm), L/B ratio, 100 grain weight (g), harvest index (%)  $g/cm^2/day$  and net assimilation rate. The data were subjected to diallel (Griffing, 1956 Method 2 and 4, Model 1), partial diallel with sample sizes six and four

(Kempthorne and Curnow, 1961) and line x tester (Kempthorne, 1957) analyses. The nine parental genotypes were divided into three groups for LT analyses having three parents each. Early maturing varieties namely HPR1164, HPR2047 and China 988 were grouped together in set A, while medium maturing and highly blast resistant varieties like VL91-1754, VL93-3613 and VL93-6052 were included in group B. The group consisted of IR57893-08, JD8 and

VLDhan221. Each set of three parents worked as testers, while remaining two groups were used as lines.

## RESULTS AND DISCUSSION

The analysis of data using diallel and partial diallel mating designs (Table 1 and 2) indicated the predominance of non additive gene effects on plant height, grain yield, biological yield, harvest index, days to maturity, leaf area index, dry matter, panicle length, grain breadth, 100-

**Table 1. Estimates of  $\sigma^2_g$ ,  $\sigma^2_s$  their ratio and mean degree of dominance for different characters in diallel analyses**

Characters	Variance		$\sigma^2_{gca} / \sigma^2_{sca}$	Degree of dominance
	$\sigma^2_{gca}$	$\sigma^2_{sca}$		
Days to 50% flowering	3.9255.52	51.3044.06	0.081.26	3.620.89
Plant height	51.459.58	84.7870.40	0.600.14	1.282.71
Grain yield	0.080.94	18.7212.13	4.270.08	15.2912.90
Biological yield	1.575.01	120.9372.17	0.020.07	8.773.79
Harvest index	2.721.23	38.0638.61	0.070.07	3.793.74
Days to maturity	3.202.71	43.5837.56	0.070.07	3.693.72
L/B ratio	0.855.28	11.920.08	0.0766	3.740.12
LAI	0.020.10	0.250.24	0.080.42	3.531.54
Dry matter	4.984.96	42.2532.99	0.120.15	2.912.98
Panicle length	0.040.05	0.420.44	0.100.11	2.961.34
Grain breadth	0.010.05	0.090.09	0.110.60	3.001.34
Grain length	0.020.02	0.220.21	0.090.09	3.243.31
100GW	0.020.01	0.090.09	0.220.11	3.002.93
NAR	0.701.23	6.014.81	0.120.26	2.931.98

LAI-leaf area index, 100GW- 100-grain weight, L/B ratio- length breadth ratio and NAR-net assimilation rate

**Table 2. Estimates of  $\sigma^2_g$ ,  $\sigma^2_s$  their ratio and mean degree of dominance for different characters in partial diallel analyses**

Character	Sample size	Variance		$\sigma^2_g / \sigma^2_s$	Degree of dominance
		$\sigma^2_{gca}$	$\sigma^2_{sca}$		
Days to 50% flowering	64	1.741.40	43.7658.47	0.040.02	5.016.46
Plant height	64	1.556.94	89.63130.27	0.020.05	7.604.33
Grain yield	64	1.104.64	14.0410.96	0.080.42	3.571.54
Biological yield	64	7.2320.41	90.68122.50	0.080.20	3.542.44
Harvest index	64	1.493.18	38.3439.04	0.040.08	5.073.51
Days to maturity	64	0.711.03	37.2442.44	0.020.02	7.246.41
L/B ratio	64	0.0060.006	0.100.06	6.000.10	4.083.16
LAI	64	0.070.08	0.510.34	0.140.24	2.702.06
Dry matter	64	1.115.09	27.9733.27	0.040.15	5.022.60
Panicle length	64	0.100.54	3.163.42	0.030.16	5.622.52
Grain breadth	64	0.00040.0011	0.010.01	0.040.10	5.003.16
Grain length	64	0.020.07	0.230.06	0.091.16	3.390.92
100GW	64	0.0010.001	0.080.08	0.010.01	8.948.94
NAR	64	1.060.81	2.906.30	0.360.13	1.652.79

grain weight and net assimilation rate irrespective of methods and sample sizes. However, the estimates of gene action for days to 50% flowering and L/B ratio in partial diallel varied with a change in the sample size. On the basis of all or two out of three sets of line x tester analyses (Table 3), preponderance of non additive

gene effects were found for days to 50% flowering , plant height, grain yield, biological yield, harvest index, days to maturity, L/B ratio, leaf area index, panicle length and net assimilation rate. Both additive and non –additive gene effects were found equally important for grain breadth(for two sets) and 100-grain weight (for one

**Table 3. Estimates of  $\sigma^2_g$ ,  $\sigma^2_s$  their ratio and mean degree of dominance for different characters in Line x tester analyses**

Characters	Tester set	Variance		$\sigma^2_{gca} / \sigma^2_{sca}$	Degree of dominance
		$\sigma^2_{gca}$	$\sigma^2_{sca}$		
Days to 50% flowering	A	1.10	31.01	0.04	5.31
	B	2.03	39.51	0.05	4.41
	C	2.03	32.70	0.06	4.01
Plant height	A	17.86	11.26	1.60	3.50
	B	6.13	75.27	0.08	3.25
	C	7.54	79.66	0.09	2.94
Grain yield	A	4.90	26.04	0.20	2.94
	B	2.22	19.14	0.12	2.30
	C	1.77	23.83	0.07	3.70
Biological yield	A	23.23	143.53	0.16	2.49
	B	8.04	168.98	0.05	1.45
	C	18.60	101.28	0.18	23.72
Harvest index	A	0.63	44.72	0.01	8.43
	B	7.52	78.15	0.096	3.22
	C	8.77	88.27	0.099	5.22
Days to maturity	A	1.13	30.90	0.04	5.22
	B	2.03	39.51	0.05	4.41
	C	2.09	32.52	0.06	3.94
L/B ratio	A	0.01	0.09	0.11	3.00
	B	0.02	0.07	0.29	1.87
	C	0.04	0.08	0.50	1.41
LAI	A	3.76	39.34	0.10	3.23
	B	0.04	44.89	-	-
	C	5.46	29.99	0.18	1.23
Dry matter	A	0.03	0.34	0.09	3.36
	B	0.4	0.26	1.54	0.81
	C	0.50	0.26	1.92	0.72
Panicle length	A	0.50	1.94	0.26	1.97
	B	0.19	0.26	0.73	1.17
	C	0.46	1.84	0.25	2.00
Grain breadth	A	0.01	0.01	1.00	1.00
	B	-	-	-	-
	C	0.01	0.01	1.00	1.00
Grain length	A	0.02	0.22	0.09	1.56
	B	0.01	0.25	0.04	5.00
	C	0.02	0.30	0.07	3.87
100GW	A	0.03	0.03	1.00	2.63
	B	0.01	0.09	0.11	1.00
	C	0.01	0.09	0.11	3.00
NAR	A	0.88	6.08	0.14	2.63
	B	0.06	5.61	0.01	9.66
	C	0.08	6.55	0.01	9.05

set), while predominance additive gene effects were found for plant height (only in one set) and dry matter (for two sets).

Considering overall analyses of data (Table 4), the non additive gene effects emerged to play an important role in the inheritance of all the characters under study except days to 50% flowering, plant height, dry matter, grain length, grain breadth and 100 grain weight. The additive gene effects played a major role in the inheritance of dry matter, while both types of gene action were found to be important for grain breadth and grain length.

These results are in perfect agreement for majority of traits with the findings of Kalamani and Sundaram (1987), Lokeshprakash *et al.*, (1991), Ramalingam *et al.*, (1993) and Sharma and Mani (1996). Perusal of table 4 further revealed that all the analyse is gave consistent results for grain yield, biological yield, harvest index, days to maturity, L/B ratio, leaf area index, panicle length and net assimilation rate. On the other hand, three characters viz., days to 50% flowering, plant height, and 100 grain weight gave identical results for six out of seven analysis. The findings of PD analyses with sample size 6 and 4 were generally in agreement with those of diallel cross analyses (either of the two methods) for 12 out of 14 characters. However, the results of PD with sample

size 4 showed deviation with the results of DL analyses in few cases. The loss of precision in the estimate of gene action is mainly due to the fact that average standard error also increased with decrease in sample size. These results supported the findings of earlier workers like Dhillon and Singh (1981) in maize.

In LT analyses, 4 out of 14 characters gave inconsistent results over the sets. The estimate of gene action for set B of LT analyses were fairly close to DL and PD analyses. This set consisted the parents VL91-1754, VL93-3613 and VL93-6052 which were recently evolved by genetic dissortative mating. The other sets which consisted of either early (set A) or late duration varieties (set C) did not show much correspondence with the results of DL and PD analysis. This indicated the genetic background of the tester parents had a major impact on the gene effects. That tester parents can not be chosen at random, instead of careful consideration with regards to genetic background, adaptability etc are essential. The findings of several workers Russel and Eberhart (1975), Sharma and Mani (1996) in the past regarding the natures of tester parents were on similar lines.

It can be concluded that PD analysis with sample size more than  $n/2$  or LT analysis using genetically broad based testers gave almost similar or

**Table 4. Gene effects for different characters as revealed by partial diallel, diallel and line x tester analyses.**

Characters	Diallel		Partiall diallel		Line x Tester		
	M2	M4	S=6	S=4	A	B	C
Days to 50% flowering	NA	A	NA	NA	NA	NA	NA
Plant height	NA	NA	NA	NA	A	NA	NA
Grain yield	NA	NA	NA	NA	NA	NA	NA
Biological yield	NA	NA	NA	NA	NA	NA	NA
Harvest index	NA	NA	NA	NA	NA	NA	NA
Days to maturity	NA	NA	NA	NA	NA	NA	NA
L/B ratio	NA	NA	NA	NA	NA	NA	NA
LAI	NA	NA	NA	NA	NA	NA	NA
Dry matter	NA	NA	NA	NA	NA	A	A
Panicle length	NA	NA	NA	NA	NA	NA	NA
Grain breadth	NA	NA	NA	NA	A/NA	-	A/NA
Grain length	A/NA	A/NA	NA	A	NA	NA	NA
100GW	NA	NA	NA	NA	A/NA	NA	NA
NAR	NA	NA	NA	NA	NA	NA	NA

M2=Method 2, M4= Method 4, S=6-S ample size 6 and S=4- Sample size 4

comparable results with DL analysis. The PD and LT analyses also have additional advantage of involving relatively less number of crosses and should be preferred when large numbers of parents are involved for genetic analyses of both quantitative and qualitative traits.

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