

Full Length Research Paper

# Studies on hereditary structural engineering of biparental offspring for critical yield attributes in rice (*Oryza sativa* L.)

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An experiment was conducted to develop and evaluate the biparental progenies (BIPs) for important yield component traits in three rice cross combinations, namely, JGL 384 × Rasi (Cross I), KJTCMS 5B × IR 64 (Cross II), WGL 14 × Rasi (Cross III). Genetic analysis of biparental progenies revealed that, the traits namely, days to 50% flowering, plant height and number of productive tillers per plant in Cross I and number of productive tillers per plant in Cross II were governed by additive gene action and for the improvement of these traits pure line selection, mass selection and or progeny selection and pedigree breeding method may be followed. Preponderance of non – additive type of gene action was observed for all the traits studied in Cross III and remaining traits in Crosses I and II. Hence, improvement of these characters could possible through heterosis breeding or single plant selection at later generation after hybridization or two or more cycles of intermating among the selected segregants and to exploit the hidden genetic variability in heterozygous condition.

**Key words:** Biparental progenies, North Carolina design II (NCD II), mean performance, gene action.

## INTRODUCTION

Rice (*Oryza sativa* L.) is the world's most important food crop and a primary source of food for more than half of the world's population. More than 90% of the world's rice is grown and consumed in Asia, where 60% of the earth's people live. Rice accounts for 35 to 75% of the calories consumed by more than 3 billion Asians. It is planted to about 154 million hectares annually or on about 11% of the world's cultivated land. The modern day cultivars of rice, in spite of all their high yielding potential and other desirable features are handicapped with narrow genetic base for most of the agronomically important traits including the dwarf habit, which is the major yield enhancing trait. Recent study of high yielding Indian rice varieties for their ancestry revealed that hardly 5 to 6 accessions accounted for more than 90% of their genetic constitution, confirming that the cultivar gene pool being depended on now for improvement represent hardly 15% of the total genetic variability available in rice germplasm (E A Siddiq, personal communication). Success in any

breeding programme is depended on the knowledge and understanding of genetic architecture and inheritance of the character of interest. But the main drawback in breeding for high yield is that it is a very complex character.

Biparental mating is one of the simplest random mating design available to effect forced recombination and breaking down undesirable linkages as pointed out by Comstock and Robinson (1952). To develop high yielding genotypes coupled with good grain quality, drought tolerance, and resistance to pest and diseases a population with high variability serves always as prime source for effective selection, particularly the role by  $F_2$  segregants in throwing much variability is highly recognized. The  $F_2$  are the critical generation in rice breeding and they determine the eventual success or failure of hybridization programme (Jennings et al., 1979). The intercrossing or intermating in the  $F_2$  segregants provides chances of finding superior recombinants in  $F_3$  or later generations and a greater amount of concealed genetic variations particularly of the additive type would be released there by improving response to selection (Moll and Robinson, 1967). Frederickson and Kronstad (1985) stressed that in

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**Table 1.** Details of parents used in the crosses.

S/N	Genotypes/variety	Special attributes	Origin
1	JGL 384	Good grain quality	Jagatigael
2	WGL 14	Good grain quality	Warangal
3	KJTCMS 5B	Good grain quality	KKV, RARS, Karjat
4	RASI	High yield and resistance to blast	DRR, Hyderabad
5	IR 64	High yield and resistance to blast	IRRI, Philippines

autogamous crops, intermating among early segregants could open vistas to new levels of genetic variability by breaking up of the genetic recombination within the linkage group. Hence the present study was undertaken to know the genetics behind the yield and yield component traits in rice following North Carolina Design II of biparental mating.

## MATERIALS AND METHODS

The F<sub>2</sub> seeds of three cross combinations, namely, JGL 384 × Rasi (Cross 1 or C<sub>1</sub>), KJTCMS 5B × IR 64 (Cross 2 or C<sub>2</sub>), WGL 14 × Rasi (Cross 3 or C<sub>3</sub>) and five parents obtained from Paddy Breeding Station, Tamil Nadu Agricultural University, Coimbatore formed the materials for the present study. The details of the parents involved in these selected crosses are given in the Table 1. The experiment was conducted at the Paddy Breeding Station, Centre for Plant Breeding and Genetics, Tamil Nadu Agriculture University, Coimbatore. The F<sub>2</sub> generation which comprised the biparental mating block was raised during Kharif 2007 to 2008 and it was raised in non – replicated rows of 800 single plants. In each cross combination within F<sub>2</sub> population, eight plants were selected at random. Among them four were treated as male parents and the remaining four were treated as female parents. Each male parent was crossed with each female parent. Simultaneously, the respective male and female parents were also selfed to generate F<sub>3</sub> families. Thus sixteen biparental progenies (BIPs) were made per cross which would constitute one set. Like wise two sets were made per cross. A total of thirty two BIPs and sixteen F<sub>3</sub> families were produced per cross. For crossing wet cloth method suggested by Chaisang et al. (1967) was followed. The F<sub>3</sub> families and biparental progenies were raised during Rabi 2007 to 2008 in a Randomized Block design with two replications adopting a spacing of 20 cm between rows and 10 cm between plants. In each replication, two sets of BIPs were randomized and in each set, individual BIPs were randomized and in each BIPs, 11 plants were raised per replication and for F<sub>3</sub> families 20 plants were raised per replication. Observations were recorded on days to 50% flowering (DTF), plant height (PH), panicle length (PL), number of productive tillers per plant (NPT), 1000 grain weight (TGW) and single plant yield (SPY). The mean data collected from 98 BIPs and 48 F<sub>3</sub> families were subjected for analysis. After ascertaining the significant difference among the BIPs using RBD, the mean data were subjected to analysis of variance appropriate to North Carolina design II (NCD II) (Comstock and Robinson, 1948).

## RESULTS AND DISCUSSION

The success of any plant breeding programme depends to greater extent on the knowledge of genetic architecture

of the population handled by the breeder (Tai, 1979). An overall understanding of the gene action for different characters is possible by making comparison of variance due to additive and or dominance. The breeding method might be decided based on the relative importance of additive and dominance variances (Barker, 1978). Higher magnitude of additive variance indicated the predominance of additive gene action and that of dominance variance indicated the non – additive type of gene action. The choice of the breeding method primarily depends upon the nature and magnitude of gene action. If additive variance is greater and additive gene action forms the principal component of genetic variance, use of pedigree method would be desirable as the gene effects are fixable, then the choice of fixing superior genotypes in early segregating generation will be high and rewarding. If dominance variance is predominant, the selection has to be postponed to later generations and appropriate breeding techniques should be adopted to obtain useful and superior genotypes. The non – additive effects is non -fixable, yet it can be exploited through heterosis breeding.

Mean performance is a basic and an important criterion in selecting superior segregants. According to Finkner et al. (1973), progenies with highest mean were relatively effective in selecting the superior segregants. Joshi (1979) experienced that intermating of F<sub>2</sub> population found to increase the population mean in BIPs. This is of immense value to the breeder, because usually populations mean go on decreasing progressively from F<sub>2</sub> generation onwards as homozygosity increases from F<sub>3</sub> generation onwards. In the present investigation, the BIPs of all the cross combinations exhibited numerically higher mean performance for almost all the traits studied namely, days to 50% flowering, plant height, panicle length, number of productive tillers per plant, 1000 grain weight and single plant yield. In general, the mean performance of BIPs exceeded their parental mean for the traits such as number of productive tillers per plant, 1000 grain weight and single plant yield in all the cross combinations, except 1000 grain weight in cross 1. Mean performance and range values of Parents, F<sub>1</sub>, F<sub>2</sub>, F<sub>3</sub> and Biparental progenies (BIPs) for different yield attributing characters are presented in Tables 2, 3 and 4. The mean values of BIPs were numerically higher than their respective parents, F<sub>1</sub>, F<sub>2</sub>, and F<sub>3</sub> generation. The mean performance of BIPs was in general, slightly better than

**Table 2.** Mean performance of parents, F<sub>1</sub>s, F<sub>2</sub>s, F<sub>3</sub>s and BIPs for cross 1 (JGL 384 □ Rasi).

Parameter	DTF	PH	PL	NPT	TGW	SPY
P <sub>1</sub>	104.40	80.80	21.40	11.43	18.80	25.29
P <sub>2</sub>	84.60	79.20	22.200	10.80	20.71	20.84
F <sub>1</sub>	94.20	80.00	23.20	17.40	20.25	28.98
F <sub>2</sub>	86.54	79.12	20.76	13.29	19.10	23.88
Range	78.00 – 100.00	67.00 – 90.00	19.00 – 23.00	7.00 – 20.00	17.56 - 21.44	17.78 - 31.11
SD	4.82	3.32	0.97	3.31	1.01	3.18
F <sub>3</sub>	88.29	76.56	20.92	11.46	19.04	19.51
Range	81.95 - 97.21	73.60 - 80.18	19.82 - 21.91	10.34 - 13.02	18.30 - 20.08	18.12 - 21.61
SD	4.12	2.78	0.72	0.91	0.63	0.97
SE (d)	0.74	2.04	0.49	0.37	0.45	0.46
BIPs	85.53	78.69	22.14	16.39	20.45	27.90
Range	73.91 -100.09	70.78 – 85.74	18.51 – 23.87	11.46 – 22.61	16.84 – 23.05	21.44 – 33.83
SD	6.22	4.15	1.23	3.46	1.89	3.09
SE (d)	0.62	0.68	0.32	0.36	0.33	0.46

**Table 3.** Mean performance of parents, F<sub>1</sub>s, F<sub>2</sub>s, F<sub>3</sub>s and BIPs for cross 2 (KJTCMS 5B □ IR 64).

Parameter	Days to 50% lowering (days)	Plant height (cm)	Panicle length (cm)	Number of productive tillers per plant	1000 grain weight (gm)	Single plant yield (gm)
P <sub>1</sub>	85.40	79.60	22.00	10.40	17.21	20.86
P <sub>2</sub>	90.60	72.80	23.80	11.60	20.98	23.49
F <sub>1</sub>	86.80	75.20	25.40	15.40	21.93	26.93
F <sub>2</sub>	85.27	77.10	22.89	12.42	20.83	23.38
Range	83.00 – 95.00	75.00 – 84.00	22.00 – 27.00	10.00 – 16.00	20.38 - 23.55	20.05 - 28.99
SD	2.74	2.95	0.99	1.93	0.80	2.09
F <sub>3</sub>	87.18	77.34	21.98	11.73	20.09	23.06
Range	82.13 - 94.16	73.23 -85.88	21.01 - 25.77	10.23 - 13.42	19.11 - 22.22	21.59 - 25.34
SD	2.04	1.87	0.87	0.49	0.98	0.91
SE (d)	0.88	1.08	0.52	0.25	0.45	0.55
BIPs	84.24	78.76	23.16	16.78	21.70	27.90
Range	72.82 – 94.56	72.19 – 89.48	19.37 – 25.55	11.43 – 22.73	17.73 – 24.58	21.21 – 32.62
SD	5.07	4.28	1.38	2.97	1.68	3.04
SE (d)	0.79	0.83	0.56	0.19	0.50	0.44

their F<sub>2</sub> and F<sub>3</sub> progenies for almost all the characters in all the three cross combinations, except days to 50 per cent flowering and plant height. Enhancement in the trait mean value might be due to pooling of favorable alleles through recombination which was possible because of intermating. In cross 1 the days to 50% flowering was considerably reduced in BIPs than parent 1, F<sub>1</sub>, F<sub>2</sub>, and F<sub>3</sub> generation. Biparental mating thus has thrown additional variability for duration which would enable to select early genotypes. It was interesting to find that the mean performance of intermated population was improved considerably for single plant yield when compared to parents, F<sub>1</sub>, F<sub>2</sub>, and F<sub>3</sub> generation except in cross 1. The BIPs even surpassed the mean of F<sub>1</sub> generation in respect to characters like number of productive tillers per plant and single plant yield in cross

2. In rice, Palaniswamy (1980), Shanthi (1989), Yuvaraja (2000) and Amudha et al. (2006) have also reported that mean values of BIPs had exceeded the F<sub>3</sub>s as well as their parents. Biparental mating thus proves as an efficient breeding strategy for yield enhancement.

Increase in mean values for many of the characters in biparental progenies as compared to F<sub>3</sub> progenies could be the result of considerable heterozygosity (heterotic effect) in BIPs as it is derived by crossing selected parents in F<sub>2</sub>s and reduction in F<sub>3</sub>s due to inbreeding depression as it is obtained by selecting the F<sub>2</sub>s (Gardner et al. 1953). The higher mean and wider range in biparental progenies for most of the characters might be due to creation of additional variability than in the F<sub>3</sub> progenies by nullifying the effect of selfing (Nemathullah and Jha, 1993) in wheat. The superior mean performance

**Table 4.** Mean performance of parents, F<sub>1</sub>s, F<sub>2</sub>s, F<sub>3</sub>s and BIPs for cross 3 (WGL 14 × Rasi).

Parameter	Days to 50% lowering (days)	Plant height (cm)	Panicle length (cm)	Number of productive tillers per plant	1000 grain weight (gm)	Single plant yield (gm)
P <sub>1</sub>	99.00	84.60	22.60	12.40	19.02	22.27
P <sub>2</sub>	84.60	79.20	22.20	10.80	20.71	20.84
F <sub>1</sub>	88.60	82.00	22.40	17.40	20.60	27.18
F <sub>2</sub>	88.60	83.86	21.98	12.98	19.71	24.01
Range	82.00 – 99.00	81.00 – 91.00	20.00 – 25.00	9.00 – 20.00	17.44 - 21.88	19.39 - 31.37
SD	3.64	2.55	1.07	2.23	0.94	2.36
F <sub>3</sub>	89.85	77.80	20.97	11.86	18.16	21.88
Range	84.50 – 97.00	74.14 – 83.59	19.51 – 21.79	10.54 – 12.46	16.08 – 20.10	20.59 – 23.19
SD	3.84	2.75	0.70	0.58	0.88	1.18
SE (d)	1.12	0.88	0.26	0.24	0.71	0.99
BIPs	83.64	79.52	21.48	16.81	21.12	27.82
Range	74.61 – 94.33	71.64 – 87.95	18.16 – 24.32	11.62 – 22.28	17.91 – 23.84	23.24 – 33.56
SD	5.69	4.89	1.87	2.82	1.66	2.93
SE (d)	0.75	0.60	0.24	0.18	0.29	0.27

**Table 5.** Analysis of variance for NCD II in cross 1 (JGL 384 × RASI).

Source of variation	df	Mean sum of square					
		DTF	PH	PL	PT	TGW	SPY
Between male half sib family groups (M)	6	116.35**	62.89**	9.09**	80.08**	7.18**	71.69**
Between female half sib family groups (F)	6	171.94**	105.86**	7.91**	9.86**	10.23**	9.78**
Male × female	18	28.41**	12.79**	5.76**	8.31**	6.31**	8.87**
Within full sib families	30	0.39	0.47	0.19	0.13	0.11	0.13

**Table 6.** Analysis of variance for NCD II in cross 2 (KJTCMS 5B × IR 64).

Source of variation	df	Mean sum of square					
		DTF	PH	PL	PT	TGW	SPY
Between male half sib family groups (M)	6	53.68**	48.30**	4.62**	27.82**	11.16**	29.45**
Between female half sib family groups (F)	6	66.41**	62.03**	14.74**	31.55**	5.70**	27.02**
Male × female	18	46.03**	32.14**	2.79**	5.94**	3.78**	10.82**
Within full sib families	30	0.63	0.70	0.33	0.04	0.26	0.20

of biparental progenies could be attributed to the accumulation of favorable genes of low frequency present over the population, dominance deviations and epistatic interaction in biparental progenies (Srivastava et al., 1989). The release of concealed genetic variability by breaking undesirable linkage might be another reason for increased mean and variability of biparental progenies (Sethi et al., 1995).

In the present study, the genetic architecture of biparental progenies (BIPs) from three rice cross combinations, namely, JGL 384 × Rasi, KJTCMS 5B × IR 64 and WGL 14 × Rasi was studied by employing the North Carolina Design II (NCD II). The combining ability analysis of BIPs for different traits exhibited highly

significant mean square values for all the characters studied namely, days to 50% flowering, plant height, panicle length, number of productive tillers per plant, 1000 grain weight and single plant yield in all three cross combinations. This significance was observed in between male half sib family groups (M), between female half sib family groups (F) and male × female full sib family families. It was evident from the result that adequate genetic variability was present among the intermated progenies (Tables 5, 6 and 7).

A combining ability variance estimates revealed that additive genetic variance was higher than dominance genetic variance and also additive / dominance ratio was more than one for days to 50% flowering, plant height

**Table 7.** Analysis of Variance for NCD II in cross 3 (WGL 14  $\times$  RASI).

Source of variation	df	Mean sum of square					
		DTF	PH	PL	PT	TGW	SPY
Between male half sib family groups (M)	6	72.74**	93.88**	8.53**	51.76**	7.75**	43.99**
Between female half sib family groups (F)	6	98.61**	42.37**	6.96**	7.13**	7.79**	6.95**
Male $\times$ Female	18	55.26**	33.06**	6.61**	6.28**	4.21**	6.88**
Within Full sib families	30	0.57	0.30	0.06	0.04	0.08	0.07

\*\* - significant at 1 % level

**Table 8.** Estimation of variance components of BIPs for different yield attributing traits in three cross combination.

Genetic components		DTF	PH	PL	PT	TGW	SPY
Variance due to males	C <sub>1</sub>	10.99	6.26	0.42	8.97	0.11	7.85
	C <sub>2</sub>	0.96	2.02	0.23	2.74	0.92	2.33
	C <sub>3</sub>	2.19	7.60	0.24	5.68	0.44	4.63
Variance due to females	C <sub>1</sub>	17.94	11.63	0.27	0.19	0.49	0.11
	C <sub>2</sub>	2.55	3.74	1.49	3.20	0.24	2.03
	C <sub>3</sub>	5.42	1.16	0.04	0.11	0.45	0.01
Variance due to male $\times$ females	C <sub>1</sub>	14.01	6.16	2.78	4.09	3.10	4.37
	C <sub>2</sub>	22.70	15.72	1.23	2.95	1.76	5.31
	C <sub>3</sub>	27.34	16.38	3.28	3.12	2.06	3.44
Additive genetic variance	C <sub>1</sub>	57.87	35.79	1.37	18.33	1.20	15.93
	C <sub>2</sub>	7.01	11.51	3.44	11.87	2.32	8.71
	C <sub>3</sub>	15.21	17.53	0.57	11.28	1.78	9.24
Dominance variance	C <sub>1</sub>	56.04	24.65	11.13	16.36	12.40	17.47
	C <sub>2</sub>	90.81	62.88	4.94	11.80	7.04	21.25
	C <sub>3</sub>	109.37	65.52	13.11	12.49	8.25	13.76
Additive/dominance ratio	C <sub>1</sub>	1.03	1.45	0.12	1.12	0.10	0.91
	C <sub>2</sub>	0.08	0.18	0.70	1.01	0.33	0.41
	C <sub>3</sub>	0.14	0.27	0.04	0.93	0.22	0.55

and number of productive tillers per plant in JGL 384  $\times$  Rasi cross combination and number of productive tillers per plant in KJTCMS 5B  $\times$  IR 64 cross combination (Table 8). This indicates the predominance of additive gene in the governance of these traits. Additive genetic variance is associated with homozygosity and also fixable in nature. Therefore, selection for these three traits governed by additive genetic variance will be very effective. Existence of additive genetic variance is prerequisite for improvement through selection because this is the only variance that responds to selection. Additive genetic variance is a measure of additive gene action and this gene action is the chief cause of resemblance between relatives and progress by selection is directly proportional to the degree of resemblance

between parents and progeny. Thus additive gene action is a measure of breeding value of a genotype. Hence, for the traits like days to 50% flowering, plant height and number of productive tillers per plant in Cross I and number of productive tillers per plant in Cross II which showed preponderance of additive gene action, reliance should be placed on pure line selection, mass selection and or progeny selection. This is in agreement with the findings of Shanthi et al. (2004), Manickavelu et al. (2006) and Thirugnana et al. (2007). Further this trait could be improved by pedigree breeding method while going for hybridization and selection.

In WGL 14  $\times$  Rasi (Cross III) cross combination all the traits studied, namely, days to 50% flowering, plant height, panicle length, number of productive tillers per plant,

1000 grain weight and single plant yield exhibited high degree of dominance variance than additive genetic variance (Table 7). Hence, it was concluded that these characters were governed by non – additive type of gene action. It is in accordance with the findings of Raju et al. (2006), Sharma et al. (2006) and Thirugnana et al. (2007). Normally dominance genetic variance is associated with heterozygosity and it is not fixable, therefore, selection for these traits is not effective. Dominance variance is the chief cause of heterosis or hybrid vigor. The preponderance of non – additive gene action for these traits under study indicated that improvement of these characters could be possible through heterosis breeding. But, rice being a self pollinated crop, heterosis breeding is not widely adopted, unlike recombination breeding. Therefore, to get better genotypes by the way of recombination breeding hybridization followed by selection at later generations is suggested for exploiting dominance gene action. Alternatively, two or more cycles of intermating among the selected segregants might not only break the undesirable linkages if any, but also allow accumulation of favorable alleles for the improvement of traits of interest.

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