

## Behaviour of Gene Interactions in Rice under Saline Sodic Soil

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### ABSTRACT

*The analysis of variance for test of epistasis detected important role of epistasis or non-allelic interaction of majority of the traits under study. Thus, the epistatic interaction must be examined and considered while formulating the crop breeding strategy. The additive x additive (i) type of epistatic interaction was significant only for panicle bearing tillers per plant, L:B ratio, biological yield and harvest index. The 'j+l' type epistatic component, representing additive x dominance and dominance x dominance interaction, was significant for spikelets per panicle, filled spikelet per panicle, biological yield, days to 50% flowering, plant height, 1000-grain wt., spikelet fertility and panicle length. The estimates of fixable additive genetic variance (D) were highly significant for all the traits except harvest index, indicating thereby considerable scope of improvement in these traits by following conventional breeding procedures leading to development of pure line varieties. The non-fixable dominance variance (H) was highly significant for majority of the traits except panicle length, 1000 grain wt., L:B ratio and grain yield suggested that improvement in these traits may be greater through heterosis breeding or population improvement approach based on maintenance of high heterozygosity. In TTC analysis, the estimate of average degree of dominance suggested over dominance for 1000-grain wt., L:B ratio, biological yield, panicle bearing tillers per plant and days to 50% flowering.*

**Key words:** Triple Test Cross, Epistasis and Non allelic interactions

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## INTRODUCTION

The understanding of gene effects involved in the expression of agronomically important plant characters is usually for successful planning and exclusion of an efficient breeding programme. In any crop the nature and magnitude of gene actions governing the important quantitative characters help not only in the selection of most appropriate breeding method but also in determination of the best cultivar to be developed in a particular situation.

Several biometrical techniques have been developed and used to analyse the inheritance of quantitative characters in various crops. Most of the genetic models, particularly the second degree statistical models like diallel analysis<sup>3,4</sup>, line × tester analysis<sup>5&6</sup> and partial diallel, are based on several other assumptions that there is independent distribution of genes and absence of linkage and epistasis<sup>7</sup>. However, these assumptions are unrealistic. Significant epistasis effect for yield and several yield contributing characters have been reported in rice<sup>2,8</sup>. Therefore, the epistasis interaction effects cannot be ignored and the genetic model employed must account for the estimation of interallelic interaction, otherwise estimates are likely to be biased and misleading. On the other hand, the model of generation mean analysis provides the estimates

of components of epistasis along with additive and dominance gene effects, but the estimates provided by these models are cross wise and cannot be generalized. The models are cross wise and cannot be generalized. The results of generation mean analysis vary with the cross to extent that makes broader understanding impossible. Every year more and more land is becoming non-productive because of salt accumulation in soil in coastal as well as certain inland saline tracts. Salinity is a serious problem affecting 1/3 of all irrigated land in the world out of an estimated 952 × 10<sup>6</sup> ha are estimated to be in India alone. In rice, tissue culture was most successful in japonica types but served little to Indian and African rice due to the salt tolerance of seeds. Nearly 6.73 mha soils in India are salt affected and categorized into two broad groups alkali and saline soils. Recent estimates indicate that more than 1.5 m ha salt affected area has been reclaimed which is contributing about 10 million tones additional food grains to the central pool. At present, in Indo-gangetic plains in India a total 2.348 m ha area is salt affected in which U.P. share 1.37 m ha.<sup>1</sup>

## MATERIALS AND METHODS

The materials for the present investigation comprised of total 12 varieties [7 lines, 3 testers (including F<sub>1</sub>) and 2 checks] of Rice (*Oryza sativa* L.)

**Table 1: Name of the entries and their place of origin**

S.No.	Name of lines/varieties	Source of origin
1.	NDRK 5026	NDAU&T, Faizabad
2.	NDRK 5096	NDAU&T, Faizabad
3.	NDRK 5088	NDAU&T, Faizabad
4.	IR63731-1-1-3-3-2	IRRI, Manila, Philippines

5.	IR21-2-9-B-1-5	IRRI, Manila, Philippines
6.	IR71897-3R-1-1-2	IRRI, Manila, Philippines
7.	CSRC(S)52-1-1	CSSRI, Karnal
8.	JAYA	DRR,Hyderabad
9.	CSR10	CSSRI, Karnal
10.	NARENDRA USAR3	NDUA&T,Faizabad

Geographically the place of research conducted was located in between 240.47' and 260.56'N latitude, 820.12' and 830.98'E longitude and at an altitude of 113 m above from mean sea level. This area falls in sub-tropical climatic zone. The climate of district Faizabad is semi-arid with hot summer and cold winter. The soil of experimental site was saline-sodic with pH 9.6, EC-2.41 ds/m, ESP-54. Twenty one crosses were developed by crossing 7 varieties/ strains used as lines with three testers, namely, Jaya, CSR 10 and F1 (CSR10 x Jaya). A set of twenty one crosses involving 7 lines with Jaya ( $T_1$ ), CSR 10 ( $T_2$ ), and their  $F_1$  (CSR10 x Jaya) (as  $T_3$ ) were used for triple test cross analysis as per method of Ketata *et al.* (1976). The experimental material consisting of 33 genotypes including checks (Narendra Usar 3 and CSR10) constituted by 14 single crosses, 7 three - way crosses, 7 lines, three testers and two checks were evaluated in Randomized Complete Block Design with three replications during Kharif, 2009. Recommended agronomic practices were adopted to raise a good crop.

## RESULTS AND DISCUSSION

TTC analysis provides not only prices test of epistasis, but also gives unambiguous estimates of additive (D) and dominance (H) components of genetic variance and average degree and direction of dominance. Moreover, result of this design provide a broader general understanding in respect of gene effects as these are based on larger number of crosses involving several parents.

Analysis of various for 31 entries (7 female line +3 testers +21 crosses) was done for thirteen characters viz. days to 50% flowering, size of flag leaf, plant height panicle bearing tillers plant-1, panicle length spikelet panicle, filled spikelet panicle-1, spikelet fertility, 1000-grain weight, biological yield plant-1, L:B ratio, harvest index and grain yield plant-1. A perusal of Table 2, revealed that variance due to treatments, parent and crosses were highly significant for the characters except L:B ratio. It indicated sufficient variability existed in the treatment, parent and crosses. Mean square due to parent vs crosses were non significant for days to 50% flowering, panicle length, 1000-grain weight and L:B ratio, rest all eight characters showed highly significant indicating the presence of substantial heterosis in the crosses.

**Table 2: Analysis of variance for parental lines and cross for thirteen characters in rice**

Sources of variation	Days to 50% flowering	Size of flag leaf	Plant height	Panicle bearing <sup>-1</sup> tillers plant	Panicle length	Spikelet panicle <sup>-1</sup>	Filled spikelet panicle <sup>-1</sup>	Spikelet fertility	1000-grain weight	Biological yield plant <sup>-1</sup>	L: B ratio	Harvest index	Grain yield plant <sup>-1</sup>
Replication	1.86	4.139*	4.123*	0.14	1.865	5.411**	1.583	0.579	0.865	0.109	0.004	4.183*	26.445**
Treatment	204.834**	30.466**	427.946**	5.575**	12.17**	2037.706**	1761.387**	43.547**	18.424**	132.628**	0.427	20.178**	31.553**
Parents	211.481**	14.255**	764.42**	4.004**	10.407**	1290.204**	973.061**	16.501**	38.998**	85.818**	0.813	16.548**	9.069**
Crosses	212.053**	38.834**	291.304**	5.749**	13.485**	1863.198**	1557.918**	37.94**	10.07**	144.253**	0.265	14.066**	38.803**
Parent vs Crosses	0.62	9.019**	132.503**	16.23**	1.693	12255.15**	12925.76**	398.961**	0.33	321.432**	0.188	175.092**	88.907**
Females	367.177**	78.016**	255.287**	12.534**	18.033**	5838.674**	4827.608**	58.851**	8.428**	290.85**	0.197	27.072**	82.438**
Males	495.436**	139.202**	1979.988**	2.016	56.056**	56.664**	258.585**	169.217**	24.499**	137.831**	0.699	35.363**	61.872**
Females x Males	87.261**	2.515	27.865**	2.979	4.117*	176.549**	139.628**	5.605*	8.487**	72.024**	0.227	4.013	13.141**
Error	1.249	0.726	4.075	1.162	0.847	4.494	3.537	1.661	1.283	1.035	0.006	1.243	8.463

\*,\*\* Significant at 5% and 1% probability level, respectively

The analysis of variance for triple test cross set of crosses and their parents was done for all the thirteen quantitative characters (Table 3). The treatment (genotypes) variance was further partitioned into various elements viz., hybrid, parents, line, testers, P1 + P2, Vs F1, P1 Vs P2 lines vs testers and hybrids vs parents. The mean sum of squares due to genotypes (treatments) and hybrids were significant for all the characters. Significant differences were found among parent and lines for all the characters except harvest index. The difference among tester were significant except panicle bearing tillers plant<sup>-1</sup>, 1000-grain weight and harvest index.

The differences among P<sub>1</sub> + P<sub>1</sub> vs F<sub>1</sub> were found significant in days to 50% flowering, size of flag leaf, spikelet panicle<sup>-1</sup> filled spikelet panicle<sup>-1</sup>, spikelet fertility and L:B ratio and grain yield plant<sup>-1</sup>. The variation due to line versus tester was found to be significant for eight characters, namely days to 50% flowering, size of flag leaf, plant height spikelet panicle<sup>-1</sup>, filled spikelet panicle<sup>-1</sup>, biological yield plant<sup>-1</sup>, L:B ratio and grain yield plant<sup>-1</sup>. While three characters showed non significant, namely panicle length, 1000-grain weight and harvest index for hybrid versus parents.

Table 3: ANOVA for 13 characters in parents and hybrids of a triple test cross set in rice (MSS)

Source	DF	Days to 50% flowering	Size of flag leaf	Plant height	Panicle bearing tillers plant <sup>-1</sup>	Panicle length	Spikelet panicle <sup>-1</sup>	Field spikelet panicle <sup>-1</sup>	Spikelet fertility	1000-grain weight	Biological yield plant <sup>-1</sup>	L: B ratio	Harvest index	Grain yield plant <sup>-1</sup>
Replication	2	2.049	3.942	3.382	.6883	2.932*	7.346	0.274	0.600	0.535	0.280	1.341	13.844	1.761
Treatment	30	127.264**	47.464**	405.752**	5.266**	14.146**	2151.328**	1960.369**	48.465**	60.85**	156.068**	.168**	28.081**	25.206**
Hybrid	20	92.964**	57.053**	263.106**	4.796**	17.131**	2205.979**	2023.495**	44.145**	9.407**	174.997**	.097**	32.938**	23.015**
Parent	9	198.182**	18.058**	762.866**	4.003**	8.918**	1140.813**	849.555**	17.784**	35.174**	95.292**	.258**	9.065	17.845**
Lines	6	110.936**	8.455**	815.706**	5.714**	10.740**	1121.167**	834.276**	9.45**	51.125**	44.526**	.221**	8.693	5.444*
Tester	2	417.00**	50.845**	479.887**	0.777	7.110**	336.446**	27.971**	50.950**	3.128	125.323**	.343**	9.060	23.693**
P <sub>1</sub> + P <sub>2</sub> vs F <sub>1</sub>	1	337.500**	19.929**	2.006	4.166	1.421	445.481**	38.380**	75.331**	4.292	6.669	.390**	13.216	1.344
P <sub>1</sub> vs P <sub>2</sub>	1	384.00*	75.118**	957.101**	1.517	12.326**	78.915**	4.770	4.460	0.534	250.648**	.166**	.498	45.595**
Line vs tester	1	284.014**	10.108**	1011.813**	0.0192	1.606	2867.415**	2584.446**	1.272	3.563	339.827**	.311**	11.309	80.557**
Hybrid vs parent	1	175.053**	120.347**	41.860**	26.030**	1.472	10152.1**	10695.01**	416.153**	0.660	324.412**	.773**	102.096	135.285**
Error	60	1.231	0.769	39.094	0.988	0.829	4.720	2.833	1.172	1.276	1.084	1.417	7.863	1.338

\*, \*\* significant at 5% and 1% probability level respectively.

The analysis of variance for detection of epistasis for thirteen characters is given Table 4. The interaction between (i) type epistasis × blocks and (l) type epistasis × blocks, was non significant for plant height, panicle bearing tillers plant<sup>-1</sup>, L:B ratio and harvest index, which indicated heterogeneity of interaction variances. Therefore, ‘i’, ‘i×l’, and total epistasis were tested against total epistasis × blocks interaction for these characters.

On the other side days to 50 per cent flowering, size of flag leaf, panicle length, spikelets panicle<sup>-1</sup>, filled spikelets panicle<sup>-1</sup>, spikelet fertility, 1000-grain weight, biological yield plant<sup>-1</sup> and grain yield plant<sup>-1</sup> were significant, which indicated homogeneity of interaction variance. Therefore, ‘i’, ‘i × l’ and total epistasis were tested against total epistasis × block interactions.

**Table 4: Analysis of variance for the test of epistasis of triple test cross for thirteen characters in rice**

Source of variation	d.f	Days to 50% flowering	Size of flag leaf	Plant height	Panicle bearing tillers plant <sup>-1</sup>	Panicle length	Spikelet panicle <sup>-1</sup>	Field spikelet panicle <sup>-1</sup>	Spikelet fertility	1000-grain weight	Biological yield plant <sup>-1</sup>	L: B ratio	Harvest index	Grain yield plant <sup>-1</sup>
'i' type epistasis	1	220.190	3180.289	19369.07	58.330**	782.386	4432.956	10571.930	1700.46	138.441	31.573*	4.489**	488.740*	387.774
'j+1' type epistasis	6	344.857**	4.034	232.979**	8.888	11.653*	1097.512**	606.350**	58.63**	56.861**	664.972**	00.103	93.472	11.910
Total epistasis	7	327.047**	457.785*	2966.707*	15.951	121.758*	1574.000**	2030.000**	293.18**	68.512**	574.482**	0.730*	149.94	65.601*
'i' type epistasis × blocks	2	55.047**	795.072**	4842.268	14.580	195.596**	1108.245**	2642.980**	425.11**	34.611**	7.892	1.123	122.180	96.945**
'j+1' type epistasis × blocks	12	6.404	2.988	15.658	4.860	3.539	11.100	11.030	4.010	2.590	6.523	7.354	58.521	6.730
Total epistasis × blocs	14	13.353	116.143	705.174**	6.250	30.971	167.840	387.033	64.165	7.160	6.723	0.223	67.61	19.623

\*, \*\* significant at 5% and 1% probability level respectively.

Analysis of variance for sum and differences in triple test cross progenies for different characters under study has been presented in table5. The variation due to sums (L1 + L2) were found to be highly significant for majority of the traits except grain yield plant<sup>-1</sup>. The variation due to differences (L1 - L2) were highly significantly for days to 50 per cent flowering, plant height, spikelet panicle<sup>-1</sup>, field spikelet panicle<sup>-1</sup>, spikelet fertility, biological yield and grain yield plant<sup>-1</sup> and significant for size of flag leaf, rest of all non significant characters.

The mean square due to sums and differences were used to estimate additive (D) and dominance (H) variances, respectively. The additive and dominance components of genetic variance and degree and direction of

dominance are given in Table 6. The estimates of additive (D) genetic variance were highly significant for all characters except grain yield plant<sup>-1</sup>. The H component representing dominance variance was highly significant for days to 50 per cent flowering, size of flag leaf, plant height, panicle bearing tillers plant<sup>-1</sup>, spikelet panicle<sup>-1</sup>, field spikelet panicle<sup>-1</sup>, spikelet fertility, biological yield plant<sup>-1</sup> as harvest index, rest were non significant, like panicle length, 1000-grain weight, L:B and grain yield plant<sup>-1</sup>. The estimates of 'r' were the estimates of heterosis were calculated in per cent as increase or decrease over better parent and standard variety for all thirteen characters and are presented in Tables below.

**Table 5: Analysis of variance for sums and differences in TTC progenies for different characters in rice**

Source	DF	Days to 50% flowering	Size of flag leaf	Plant height	Panicle bearing tillers plant <sup>-1</sup>	Panicle length	Spikelet panicle <sup>-1</sup>	Field spikelet panicle <sup>-1</sup>	Spikelet fertility	1000-grain weight	Biological yield plant <sup>-1</sup>	L: B ratio	Harvest index	Grain yield plant <sup>-1</sup>
Sum ( $L_{1i} + L_{2i}$ ) Replication	2	16.05*	0.60	2.76	3.19	4.98	6.5	5.58	0.46	1.86	2.01	0.09	31.14	3.54
Lines (sum)	6	234.54**	113.70**	277.89**	11.94**	35.40**	7637.69**	7189.61**	100.54**	43.24**	673.17**	0.15**	23.53	89.80**
Error	12	2.32	1.38	7.98	1.24	1.43	3.90	3.38	0.43	0.70	1.39	0.30	18.80	3.38
Difference ( $L_{1i} - L_{2i}$ ) replication	2	0.99	2.11	1.12	1.28	0.03	7.20	9.70	13.47*	0.40	2.54	0.40	5.14	0.70
Line (difference)	6	219.30**	3.93*	37.35**	8.19	3.08	189.32**	325.70**	27.32**	0.53	12.15**	0.40	78.73**	2.95
Error	12	0.61	0.86	5.96	1.12	1.87	3.17	4.70	3.11	0.48	1.67	0.06	9.33	3.11

**Table 6: Estimates of additive (D) and dominance (H) variance components, average degree of dominance (H/D)<sup>1/2</sup> and direction of dominance (r)**

Source	Days to 50% flowering	Size of flag leaf	Plant height	Panicle bearing tillers plant <sup>-1</sup>	Panicle length	Spikelet panicle <sup>-1</sup>	Field spikelet panicle <sup>-1</sup>	Spikelet fertility	1000-grain weight	Biological yield plant <sup>-1</sup>	L: B ratio	Harvest index	Grain yield plant <sup>-1</sup>
D	309.62**	149.77**	359.90**	14.25**	45.30**	10178.25**	9581.71**	133.48**	56.72**	895.71**	0.16**	6.30	115.22**
H	291.58**	4.09**	41.85**	9.43**	1.61	248.20**	428.00**	32.29**	0.06	13.97**	@ negative estimates	92.53**	@ negative estimates
(H/D) <sup>1/2</sup>	17.60	12.23	18.97	3.77	6.73	100.88	97.89	11.55	7.53	29.92	@ negative estimates	2.50	10.73
R	0.77*	-0.37	0.26	0.26	0.96**	-0.73	-0.82*	-0.61	0.76*	-0.35	-0.55	0.21	-0.42

\*, \*\* Significant at 5% and 1% probability level respectively

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