

## Research Article

# Detection of epistasis, additive and dominance variation in rice (*Oryza sativa* L.) using triple test cross analysis

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### Abstract

An investigation was carried out to detect the epistasis, additive and dominance components of genetic variance for yield and yield attributing traits through triple test cross analysis, involving three testers ( $P_1$ ,  $P_2$  and their  $F_1$ ) and ten lines of rice. The estimate of total epistasis was found non-significant for all the traits while partitioning of total epistasis revealed that,  $i$  type of epistasis (additive x additive) were highly significant for yield per plant, plant height, number of panicle per meter square, panicle length and number of grains per panicle. The additive (D) and dominance (H) effects were highly significant for yield per plant, plant height, panicle length, number of grains per panicle and 1000 grain weight. The degree of dominance  $(H/D)^{1/2}$  was less than the unity indicating, partial dominance for plant height, panicles /  $m^2$  and 1000 grain weight whereas, yield per plant, panicle length and number of grains per panicle indicating over dominance ( $>1$ ). Since, the predominance components of epistasis in autogamous crop is additive x additive ( $i$  type), we suggest that the selection may be delayed to later generation for the improvement of yield through yield components in rice.

### Key words

Rice, triple test cross analysis, gene action, epistasis, yield.

### Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops of the world and about 90 per cent of the people of South East Asia consume rice as staple food. About 20 percent of the total calorie supply worldwide comes from rice and especially in Asia; more than 2 billion people derive 60-70 per cent of their daily energy requirement. According to FAO, the productivity level of rice in India is very low (3.21 t/ha) as compared to the average productivity of the China (6.35 t/ha) and world (4.15 t/ha). Selection of the efficient breeding method depends to large degree on understanding of the genetic scheme controlling the traits to be selected. A good genetic model is that which enable the breeder to have precise and unbiased estimates of all the components of genetic variance. Triple test cross (TTC) design proposed by Kearsy and Jinks(1968), which is a modification of "North Carolina III Design" has been widely used because it allows an accurate detection of the presence of epistasis, regardless of the alleles frequency, inbreeding level and occurrence of linkage disequilibrium in the populations. In the present study, triple test cross analysis has been carried out to investigate the gene action in rice for yield and yield attributing traits and making breeding strategies for the development of high yielding cultivars or valuable genotypes.

### Material and Methods

The plant material used in this experiments consisted of two distinct basmati rice varieties,

Pusa sugandh-4 and Pusa basmati-1 and their  $F_1$  (Pusa sugandh-4 x Pusa basmati-1) designated as  $L_1$ ,  $L_2$  and  $L_3$  respectively, and were crossed with ten true breeding lines of basmati rice viz; Basmati-370, Basmati-385, Mahisugandh, Kasturi, Pusa sugandh-3, P- 2511, P-1460, Taraori, Super basmati and Pakistani basmati to produce 30 triple test cross families. Each male had three crosses and a total of 30 crosses (20 single and 10 three-way crosses) were produced. Nursery seedlings of 43 genotypes (30 crosses + 13 parents) were grown and then transplanted in to the field following randomized complete block design with three replications at Agricultural Research Station, Ummedganj, Kota (Raj.) during *kharif* 2011. The plot size of each family was kept single row of two meters long (20 plants) with the spacing of 20 x10 cm (row to plant). The standard agronomic and plant protection practices were followed to grow healthy crop.

Data were recorded on ten randomly selected plants from each of parents and crosses in each replication on seven quantitative traits like, plant height (cm.), number of panicles per meter square, panicle length (cm.), number of grains per panicle, 1000 grain weight (g) and grain yield per plant (g). The analysis of variance was calculated for traits under the study. The test of epistasis was performed according to the method of Singh and Chaudhary (1985), since the total epistasis was non-significant; the additive-dominance model was fitted to the data as described by Jinks *et al.* (1969). The direction of dominance (rs.d) was analyzed by calculating the

linear correlation coefficient between the sums ( $L_1j + L_2j$ ) and the corresponding differences ( $L_1j - L_2j$ ) for all the genotypes.

### Results and Discussion

**Analysis of variance:** Analysis of variance (Table-1) showed highly significant differences among the treatments, between crosses, parents, lines and between the first parent ( $L_1$ ) and second parent ( $L_2$ ). The highly significant differences among the treatments indicated considerable genetic variations existed in the lines, testers and hybrids included in the study. The significant differences between the two parents clearly disclosed that  $L_1$  and  $L_2$  testers are the extreme high vs. low selections and would provide an estimate of additive and dominance variation with equal precision as reported by Kearsey and Jinks (1968).

**Detection of epistasis:** The total epistasis effects were found non-significant for all the traits (Table-2). Whereas, further partitioning of total epistasis in to, *i* type (additive x additive) and *J + i* type (additive x dominance and dominance x dominance) interactions showed that, *i* type interaction was highly significant for all the traits except, 1000 grain weight. The greater magnitude of *i* type epistasis than the *J + i* type epistasis for these traits has a significance in rice, being a self-fertilized crop where a linear directional and fixable components (*i* type epistasis) of genetic variation can be effectively exploited as compare to non-directional and unfixable components. Similar results were reported by Ram *et al.* (2007) and Wan *et al.* (2005) in rice. The discrepancy relating to our study might have resulted from environment influences. Genotype-environment interactions may have some influences on the epistatic effect. Such influence of epistasis was also reported by Saleem *et al.* (2005), Ram *et al.* (2007) and Verma *et al.* (2006). The non-significant estimates of epistasis may be due to involvement of common alleles or limited number of lines used (Wan *et al.* 2005). The presence or absence of epistasis may depend upon the environment in which the plant material has been evaluated and thus, it may not always be related to the inherent capacity of a genotype.

**Additive and dominance components:** The estimates of additive (D) and dominance (H) variance, degree of dominance  $(H/D)^{1/2}$  and direction of dominance (rs.d) are presented in Table-3. The additive and dominance effects have significantly equal importance for all the traits except, number of panicles per meter square. The higher magnitude of additive variance for plant height, panicles/m<sup>2</sup> and 1000 grain weight, indicate the presence of common alleles in the testers and their cumulative effect in the expression of these

traits which can be improved by pedigree method of selection. The predominance of additive and non-additive gene action for yield and yield related traits in rice have been reported by Swain *et al.* (2003), Saleem *et al.* (2005) and Ram *et al.* (2007). The estimated degree of dominance  $(H/D)^{1/2}$  showed, over dominance gene effect for yield per plant, panicle length and number of grains per panicle indicating the high influence of dominance components. Whereas, plant height, panicles per meter square and 1000 grain weight showed less than unity value of degree of dominance indicating, partial or incomplete dominance. These results confirm with the finding of Surek and Korkut (1998) and Ram *et al.* (2007). The non-significant correlation between sums and differences for all the traits indicated that, these traits did not supply any evidence for directional dominance in rice. Saleem *et al.* (2005) and Ram *et al.* (2007) reported incomplete dominance and found no evidence of directional dominance for these traits.

In the present study, *i* type of epistasis showed significance for most of the traits except, 1000 grain weight which indicated that additive x additive type of gene interaction is pronounced. The additive and additive x additive effects or any other digenic complementary gene interactions are fixable and thus can be exploited effectively for the improvement of characters through pedigree method of selection. The presences of additive, dominance as well as epistatic components for these traits suggest simple selection procedure in the immediate segregating generation may not be contribute significantly to the improvement and needs postponement of selection to later generations. The random intermating in segregating generations and selection in later generations could be effective in pooling up the useful genes of interest.

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**Table 1. Analysis of variance of yield and yield related traits in rice.**

Source of variation	DF	Mean Squares					
		Yield / plant (g)	Plant height (cm)	No. Panicles/m <sup>2</sup> (No.)	Panicle length(cm)	No. grains / panicle	1000 grain weight (g)
Rep	2	0.053	12.838	728.752	1.183	744.767**	0.538**
<b>Treat</b>	42	2.618**	143.748**	2262.006**	13.229**	883.262**	5.100**
Hybrid	29	3.176**	155.251**	2067.473**	10.639**	1039.862**	4.823**
<b>Parents</b>	12	1.346**	120.474**	1742.009**	17.608**	339.897**	5.085**
lines	9	0.595**	65.316**	1321.763**	19.125**	347.070**	4.057**
<b>Testers</b>	2	1.221**	254.590**	3082.333**	2.458*	30.333	3.441*
P1+P2 Vs F1	1	1.227**	6.845	3960.500**	4.109*	50.000	0.056
<b>P1 Vs P2</b>	1	1.215**	502.335**	2204.167**	0.807	10.667	6.827**
Lines Vs Tester	1	8.350**	348.665**	2843.569**	34.256**	894.469**	17.625**
<b>Hybrid Vs Parents</b>	1	1.690**	89.477**	14143.423**	35.776**	2862.254**	13.316**
Error	84	0.173	21.999	317.125	0.683	122.577	0.869

\*, \*\* = Significant at 0.05 and 0.01 level of probability, respectively.

**Table 2. Analysis of variance for the test of Epistasis, additive (D) and dominance(H) components, degree of dominance (H/D)<sup>1/2</sup> and direction of dominance (rs.d) for yield and its related traits in rice.**

Source of variation	DF	Mean Squares					
		Yield / plant (g)	Plant height (cm)	No. Panicles / m <sup>2</sup> (No.)	Panicle length(cm)	No. grains / panicle	1000 grain weight (g)
Total Epistasis	10	9.884	320.799	8841.570	14.596	1290.570	5.146
i type Epistasis	1	257.547**	7562.053**	268285.63**	326.700**	7394.700*	21.505
j + i type Epistasis	9	17.634	483.78437	19985.548	20.082	612.333	3.329
i type Epistasis x block	2	64.387	1890.5140	67071.408	81.675	1848.675	5.376
j + i type Epistasis x block	18	13.749	566.4382	12919.846	21.744	2300.528	9.068
Total Epistasis x block	20	18.812	698.8458	18335.003	27.737	2255.343	8.699

\*, \*\* = Significant at 0.05 and 0.01 level of probability, respectively.

**Table 3. Estimation of additive (D) and dominance(H) component of variance, degree of dominance (H/D)<sup>1/2</sup> and direction of dominance (rs.d) for yield and its related traits in rice.**

Source of variation	Mean Squares					
	Yield / plant (g)	Plant height (cm)	No. Panicles / m <sup>2</sup>	Panicle length(cm)	No.grain / panicle	1000 grain weight (g)
D	1.859**	357.442**	1254.296	12.904**	128.80**	16.066**
H	3.183**	189.417**	640.403	18.141**	2244.163**	4.698*
(H/D) <sup>1/2</sup>	1.319	0.683	-0.549	1.154	1.355	0.451
rs.d	0.520	-0.029	-0.117	-0.226	-0.364	0.0806

\*, \*\* = Significant at 0.05 and 0.01 level of probability, respectively.