

# Gene effects and genetic analysis of indigenous land races and improved cultivars for yield and yield components in rice (*Oryza sativa* L.)

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## Abstract

Rice is one of the crucial staple food crops and its unique grains assist to hold two third of world population. Generation mean analysis is commonly used in studies of inheritance of quantitative traits. Experimental material consisted of ten parents which included six high yielding varieties used as female parents and four traditional landraces used as male parents,  $F_1$ ,  $F_2$  and  $F_3$  generation of six crosses viz., IR 72 x Veeradangan, ADT 39 x Kavuni, ADT 45 x Kavuni, ADT 43 x Navara, ASD 16 x Navara and TPS 4 x Kathanellu. Seven biometrical characters indicated that additive and dominance x dominance gene actions were predominant with duplicate type of gene action for five biometrical characters viz., plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle and single plant yield. The epistatic effects, additive x additive [i] and dominance x dominance [h] were highly significant in most cases. The signs of (h) and (l) were opposite in all studied traits for most crosses. Non-allelic gene interaction was operating in the control of genetic variation in most studied traits. Also, the inheritance of all studied traits was controlled by additive and non-additive genetic effects, but dominance gene effects play the major role in controlling the genetic variation of the most studied traits. Present study indicated that early generation selection is effective and should be practiced for future breeding program.

## Highlights

Genetic systems that control the expression of quantitative traits (Generation mean analysis) to facilitate the choice of the most efficient breeding and selection procedure.

To estimate the gene action for different yield contributing characters.

Dominance and epistatic gene interactions were predominant. Dominance x dominance gene interaction was prevalent.

**Keywords:** Rice, land races, gene action, dominance, additive, generation mean analysis.

Rice (*Oryza sativa* L.) is the most important staple food for about 50% of the world's population that lives in Asia, where 90% of the world's rice is grown and consumed. Rice provides about 29.4% of total calories/capita/day in Asian countries (FAO

2006). However, increase in rice production with population growth. Thus genetic variations for quantitative characters in plant population are of prime concern to the breeders. India is a primary centre of origin of rice and has many land races

(Singh *et al.* 2013). The choice of breeding methods for genetic improvement of a crop depends upon the nature and magnitude of genetic variability present. It is usually not directly measurable. One can measure only the phenotypic expression of genetic values as modified by the environment. This partitioning has provided a better knowledge for genetic analysis of quantitatively varying traits. The further partitioning of epistatic component into additive  $\times$  additive, additive  $\times$  dominance and dominance  $\times$  dominance was shown by Kempthorne (1954). Such partitioning of variability into various components needs variance estimates from a number of specifically related generations. Generation mean analysis as suggested by Hayman (1958) and Jinks and Jones (1958) provides all kinds of non-allelic interaction precisely in addition to the additive and dominance gene effects. The magnitude of additive gene effect is particularly useful in the development of pureline varieties. Generation mean analysis is a relatively simple and statistically reliable tool suitable for preliminary estimation of various gene effects (Mather and Jinks, 1971). Estimation and interpretation of non-allelic interactions are more progressive with generation mean analysis as it utilizes the first order statistics which are less compounded with each other when compared with variance estimates. Intermating of selected segregants and postponement of selection to later generation might be suggested to break undesirable linkages in order to improve yield (Gopikannan and Ganesh, 2013). In present study, generation mean analysis for yield contributing traits in rice was undertaken to find out gene effects controlling in six crosses.

## Materials and Methods

The present investigation was carried out during 2012 to 2014 using the experimental material consisting of five generations including,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$ . The experimental material consisted of four medicinal landraces *viz.*, Veeradangan, Kavuni, Kathanellu and Navara which were collected from Tamil Nadu and Kerala. Navara is a medicinal landrace

of Kerala. These landraces are having superior nutritional, grain qualities and low yielder and six improved semi-dwarf high yielding varieties *viz.*, IR 72, ADT 39, ADT 45, ASD 16 and TPS 4 of medium grain quality along with standard check ADT 43 by adopting a spacing of 30  $\times$  10 cm at Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai during Kharif 2012-13.  $P_1$ ,  $P_2$  and  $F_1$ s of six cross combinations were transplanted in Randomised Block Design with three replication.  $F_2$  and  $F_3$  segregating generations of six crosses were raised in non replicated plots. Single seedling per hill was planted with a spacing of 15  $\times$  10 cm. Recommended agronomic practices were followed throughout the crop growth period. Data were recorded 10 plants for replication in parents and three plants for  $F_1$  hybrids, for 200 and 250 plants in  $F_2$ 's and  $F_3$ 's segregating generation of each six crosses respectively. For days to 50% flowering (days), plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, hundred grain weight (g) and single plant yield (g) in single plant observation for six crosses. Action of the genes controlling quantitative characters can be described by the use of gene models. The four types of gene action *viz.*, additive (d), dominance (h), additive  $\times$  additive (i) and dominance  $\times$  dominance (l) were estimated using five-parameter model. The variances and corresponding standard error of the means were computed from the deviations of the individual values from the pooled mean for each of the generation in each cross. The adequacy of the simple additive-dominance model in a generation was detected utilizing C and D scaling tests according to the method proposed by Mather and Jinks (1971). By using the variances of various generations for the respective mean, tests of significances were made. The t value observed for ratio C/ SE of C and D/ SE of D is compared either to the 't' table at 5 and 1% level of significance. The calculated 't' value is referred to the 't' table to test the significance. In each test, the degrees of freedom are sum of the degrees of freedom of various generations involved. The additive-dominance model was considered inadequate when any one of the two scales was found to deviate



significantly from zero. Mean of five generations *viz.*,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$  could be used to estimate five parameters following a perfect fit solution given by Cavalli (1952).

$$\begin{aligned}\hat{m} &= \bar{F}_2 \\ \left[\hat{d}\right] &= \frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2 \\ \left[\hat{h}\right] &= \frac{1}{6}(4\bar{F}_1 + 12\bar{F}_2 - 16\bar{F}_3) / \\ \left[\hat{i}\right] &= \frac{1}{6}(4\bar{F}_1 + 12\bar{F}_2 - 16\bar{F}_3) \\ &\quad \bar{P}_1 - \bar{F}_2 - \frac{1}{2}(\bar{P}_1 - \bar{P}_2 + h) - \frac{1}{4}1 \\ \left[\hat{l}\right] &= \frac{1}{3}(16\bar{F}_3 - 24\bar{F}_2 + 8\bar{F}_1)\end{aligned}$$

Variances of the estimates of these parameters are obtained as follows:

$$\begin{aligned}V_m &= \bar{V}_{F_2} \\ V_d &= \frac{1}{4}(V_{P_1} + V_{P_2}) \\ V_h &= \frac{1}{36}(16V_{F_1} + 144V_{F_2} + 256V_{F_3}) \\ V_i &= \frac{V_{P_1} + V_{F_2} + \frac{1}{4}(V_{P_1} + V_{P_2} + V_h) + 1/16}{V_1} \\ V_l &= \frac{1}{9}(256V_{F_3} + 576V_{F_2} + 64V_{F_1})\end{aligned}$$

Standard errors of these estimates can be had by working out the square root of the respective variances.

$$\begin{aligned}\text{S.E for } m &= \sqrt{V_m} \\ \text{S.E for } d &= \sqrt{V_d} \\ \text{S.E for } h &= \sqrt{V_h} \\ \text{S.E for } i &= \sqrt{V_i} \\ \text{S.E for } l &= \sqrt{V_l}\end{aligned}$$

The 't' value of the various estimates were calculated as follows:

$$\begin{aligned}t(m) &= m / \text{S.E}(m) \\ t(d) &= d / \text{S.E}(d) \\ t(h) &= h / \text{S.E}(h) \\ t(i) &= i / \text{S.E}(i) \\ t(l) &= l / \text{S.E}(l)\end{aligned}$$

The calculated 't' value is referred to the 't' table to test the significance. In each test, the digress of freedom is sum of the degrees of freedom of various generations involved.

## Results and Discussion

High yielding continuous to be the major objective in rice breeding programme. Although considerable success has been achieved by introduction of dwarfing genes, still high yielders of rice varieties can be improved by combining favorable genes from the germplasm or landraces for quality improvement. The magnitude of success in such a programme depends on the genetic information about yield contributing traits. Such information on nature of gene effects is particularly important to provide basis for formulating new approach in rice breeding programme (Table 1, 2 and 3).

The generation mean analysis with first degree statistics was adopted to detect non-allelic interaction component of the means of the phenotypic distribution. For days 50% flowering generation mean studies, the scaling test values were significant in all the crosses indicating the inadequacy of the simple additive-dominance model (Figure 1). Therefore, digenic epistatic model was found to fit for this trait. The mean effect 'm' was significant in all the crosses. The additive effect was positively significant in three crosses *viz.*, cross 1, cross 4 and cross 5 and negatively significant in other three crosses *viz.*, cross 2, cross 3 and cross 6. The dominance (h) effect was negatively significant in all the crosses. The relative magnitude of (d) and (h) showed the predominance of additive effect in three crosses (cross 2, cross 3 and cross 6)

whereas, (h) effect was higher in the remaining three crosses *viz.*, cross 1, cross 4 and cross 5. The interaction effect of (l) was positively significant in four crosses *viz.*, cross 1, cross 2, cross 3 and cross 6 whereas, it was negatively significant in cross 4. The effect (i) was negatively significant in cross 2, cross 3 and cross 6. The relative magnitude of (l) and (i) showed that (l) effect was predominant except in cross 3. The (h) and (l) effects showed opposite signs indicating duplicate gene action. Almost all the crosses except cross 4 (complementary gene action) components of (h) and (l) having opposite sign in the inheritance of the trait indicates duplicate gene action. The present study clearly showed both additive and non-additive type of gene action involved for this trait. Because of duplicate epistasis observed for this trait hinders the rapid improvement of selection. Therefore it was inferred that this trait was governed by additive, dominance, dominance x dominance and duplicate type of gene action for this trait. Hence, selection had to be postponed to later generations for fixing early duration genotypes. Saradana and Borthakur (1987) and Ram *et al.* (1989) reported the role of dominance gene action for this trait. Dominance x dominance gene interaction for this trait was attributed by Padmavathy (1997) and Kumar *et al.* (2004).

Plant height the scaling tests were significant in all the crosses indicating the inadequacy of the simple additive-dominance model (Figure 2). A digenic epistatic model was found to fit for this trait. The mean effect 'm' was significant in all the crosses. The additive effect was negatively significant in all the crosses whereas, (h) effect was positively non-significant for all the crosses. The relative magnitude of (d) and (h) effects showed the predominance of additive effects in cross 1, cross 2, cross 3 cross 4 and cross 6 along with dominance effects in cross 5. The interaction effect (l) was negatively significant in all the crosses. The (i) effect was negatively significant in all other five crosses except cross 5. The relative magnitude of (l) and (i) revealed the equal role of additive x additive and dominance x dominance interaction. The component of (h) and (l) opposite sign implied that the involvement of duplicate gene

action in the inheritance of this trait. Thus, this trait was found to be under the control of additive gene action, further epistatic interaction of dominance x dominance and duplicate gene action also influences this trait. The additive gene action with duplicate interaction indicated that segregants with desirable plant stature either of parents could be selected through direct selection. Another aspect was that higher magnitude of dominance component interfere with the process of improvement of the trait. This could be overcome by random mating among segregants. Since rice being a self pollinated crop, improvement could be undertaken at later generations. Additive, dominance x dominance and duplicate type of gene action was reported by Robin (1997). Anbumalarmathi *et al.* (2005) reported additive, dominance x dominance and duplicate interaction for this trait.

Number of productive tillers per plant for scaling test values was significant in all the crosses indicating the inadequacy of the simple additive-dominance model (Figure 3). The scaling tests showed the presence of digenic epistatic model was found to fit for this trait. The genetic estimates of 'm' was significant in all the crosses. The additive gene effects was positively significant in cross 2, cross 3 and cross 5 and negatively significant in other crosses *viz.*, cross 1 and cross 6. The dominance effect (h) was negatively significant in two crosses *viz.*, cross 1 and cross 2. The (h) effect was predominant over (d) effect in this trait. The (l) effect was positively significant in cross 1, cross 2 and cross 5, whereas negatively significant in cross 4 and cross 6. The non-allelic interaction (i) effects were negatively significant in cross 1 and cross 5. The magnitude of (l) effect is more predominant in all the crosses. The (h) and (l) effects showed opposite signs indicating the presence of duplicate gene action. The negative sign of (i) indicated that the selection should be deferred to later generations. Selection in early segregating generations might not yield desirable results. Hence, delaying selection to later generations when dominance gene effects disappear as well as resorting to intermating of segregants in  $F_2$  generation might be advocated not

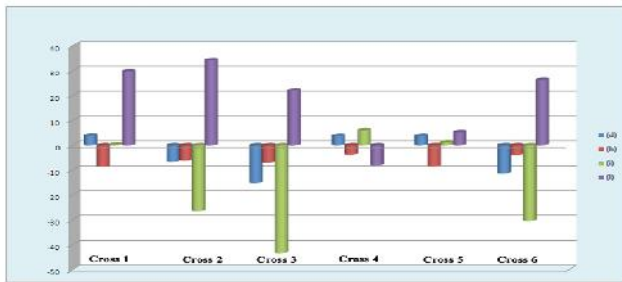


Fig. 1. Genetic effects – days 50% flowering

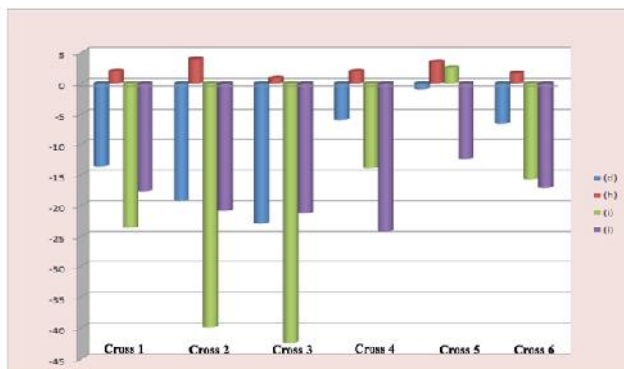


Fig. 2. Genetic effects – Plant height

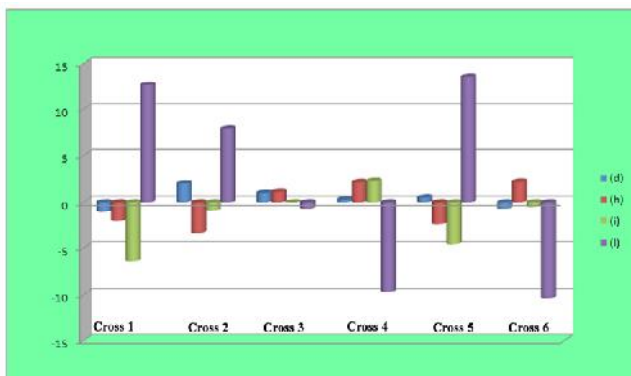


Fig. 3. Genetic effects – Number of productive tillers per plant

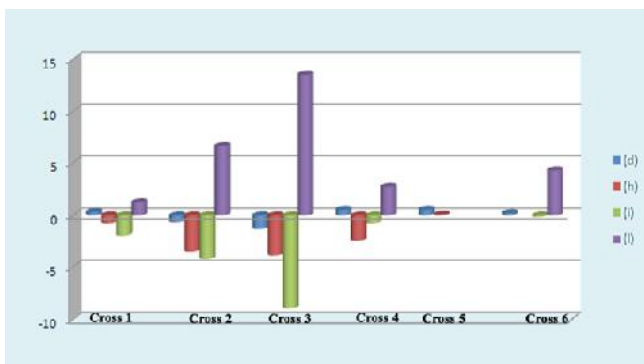


Fig. 4. Genetic effects – Panicle length

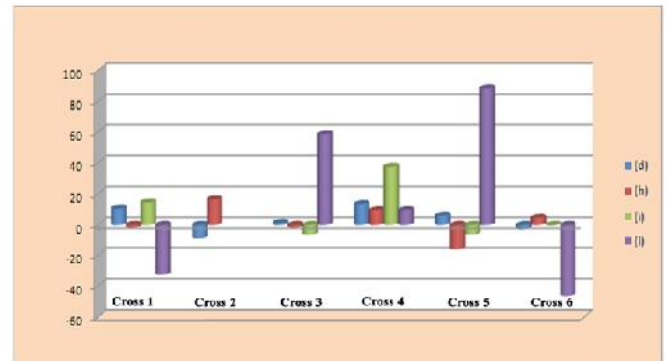


Fig. 5. Genetic effects – Number of filled grains per panicle

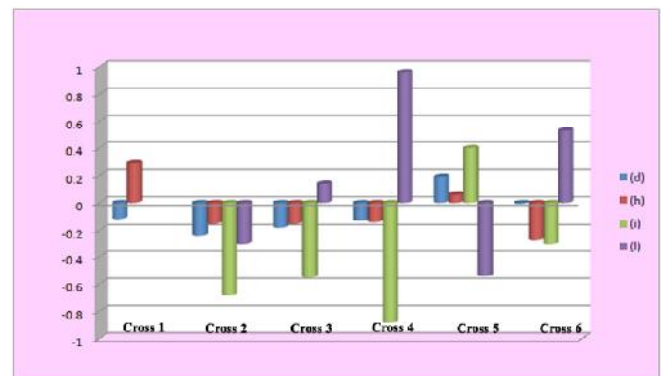


Fig. 6. Genetic effects – Hundred grain weight

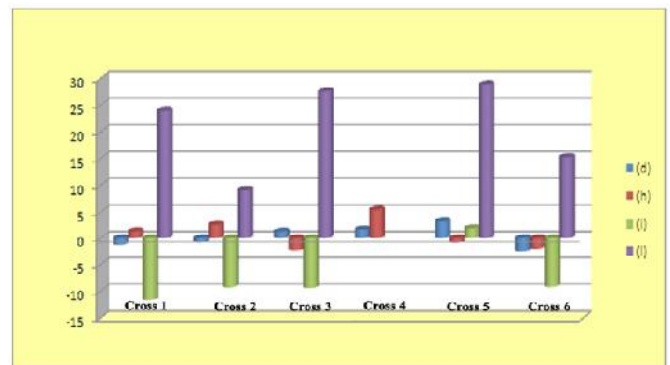


Fig. 7. Genetic effects – Single plant yield





only to harness dominant type of gene action but also to break any undesirable linkage. On a whole, this trait was influenced by additive, dominance x dominance and duplicate gene action. Predominance of additive effect was reported by Patil *et al.* (2003) and Subbulakshmi (2013) reported the presence of additive, dominance x dominance and duplicate gene action for this trait.

For panicle length, simple additive-dominance model was found to be inadequate in all the crosses except for cross 5 and hence for other crosses the scaling tests was extended to digenic epistatic model (Figure 4). The mean effect 'm' was significant in all the crosses. Significant positive additive effects were observed in crosses 4 and 5 whereas, negatively significant in crosses 2 and 3. The (h) effect was negative and significant in three crosses *viz.*, cross 2, cross 3 and cross 4. The magnitude of (h) was higher in five crosses whereas, the (d) effect was higher in cross 5. The (h) effect was predominant over (d) effect. The interaction effect (l) was positively significant in three crosses (cross 2, cross 3 and cross 6) whereas, (i) effect was negatively significant in three crosses (cross 1, cross 2 and cross 3). The negative sign of (i) indicated that the selection should be deferred to later generations of cross 1, cross 2 and cross 3. The components of (h) and (l) having opposite sign implied the involvement of duplicate epistasis in the inheritance of this trait in all the crosses except cross 5. The present study, clearly showed involvement of additive, dominance x dominance, duplicate type of gene action for this trait. Intermating programme among  $F_2$  segregants (or) multiple crossing programme with selected segregants would help in realizing of superior genotypes with improved panicle length. Koodalingam (1994) reported the duplicate epistatic interaction for panicle length in inter-varietal crosses of rice.

Number of filled grains per panicle the inadequacy of the additive-dominance model as shown by the significant scaling test (Figure 5). C and D indicated the existence of non-allelic interaction in the inheritance of number of filled grains per panicle in all the crosses except cross 2 and hence for other

crosses the scaling tests was extended to digenic epistatic model. The genetic estimates of 'm' were significant in all the crosses. Significant positive additive (d) effects were observed in cross 1, cross 4 and cross 5 whereas negatively significant additive effects observed in cross 2. The dominance (h) effect was negative significant in cross 5, whereas, cross 2 positively significant effect was observed. The magnitude of (h) was higher in cross 2, cross 3, cross 5 and cross 6, whereas, the (d) effect was higher in crosses 1 and 4. The (h) effect was predominant over (d) effect. The interaction effect of (l) was positively significant in crosses 3 and 5 whereas, negatively significant in cross 6. The effect of (i) was positively significant in crosses 1 and 4. The components (h) and (l) having opposite sign showed that the cross 3, 5 and 6 involvement of duplicate epistasis in the inheritance of this trait except cross 1 and cross 4 (complementary gene action). The present study, clearly showed involvement of additive, dominance x dominance and duplicate type of gene action for this trait. Gomez *et al.* (2003) revealed the presence of additive gene action for this trait. The predominance of additive and non additive interaction was reported by Ram (1994) and Anbumalarmathi *et al.* (2005).

Hundred grain weight, scaling test values were significant in all the crosses except cross 1, indicating the inadequacy of the additive-dominance model and hence digenic interaction model was extended (Figure 6). The genetic estimates of 'm' were significant in all the crosses. The additive (d) effect was positively significant in cross 5 and negatively significant in crosses 1, 2, 3, 4 and 6. The dominance gene action was positively significant in cross 1 and negatively significant in crosses 2, 3, 4 and 6. The relative magnitude of (d) and (h) revealed the predominance of additive effects in crosses 2, 3 and 5 whereas, (h) effect was higher in remaining three crosses. Hence this shows equal magnitude of both additive and dominance gene action. The interaction effects of (l) is positively significant in cross 4. The (i) effect was negatively significant all four crosses (cross 2, cross 3, cross 4 and cross 6). The (l) effect was predominant over (i) effect in this trait. The (h)



and (l) effects had opposite signs in crosses 3, 4, 5 and 6 indicating duplicate gene action whereas, the (h) and (l) showed the same sign in cross 2 indicating complementary gene action. Thus, hundred grain weight was governed by additive, dominant, dominance x dominance along with duplicate gene action. Duplicate epistasis observed for this trait hinders the rapid improvement by selection. This may possibly be overcome by delaying the selection to later generation when dominance effects disappear as well as by resorting to intermating of segregants in  $F_2$  followed by recurrent selection. The selection in later generations and maintenance of large populations prior to selection providing the maximum opportunity for advantageous combinations of genes to occur. This was in accordance with the finding of Ganapathy (2006) and Subbulakshmi (2013).

Single plant yield, scaling test values were significant in all the crosses except cross 4, indicating the inadequacy of the additive-dominance model and hence digenic epistatic model was extended (Figure 7). The genetic estimates of 'm' were significant in all the crosses. The additive effect (d) was positively significant, noticed in crosses 3, 4 and 5 and negatively significant in crosses 1, 2 and 6. The dominance effect (h) was positively significant in cross 4. The (d) effect was predominant in cross 5 and cross 6, whereas (h) effect was predominant in remaining four crosses. The (l) effect was positively significant in crosses 1, 3, 5 and 6. The (i) effect was negatively significant in four crosses (cross 1, cross 2, cross 3 and cross 6). The relative magnitude of (l) effect was predominant over (i) effect in four crosses. The sign of (h) and (l) effects was same in the cross 1 and 2 indicating complementary gene action whereas, it was opposite sign in the remaining three crosses (cross 3, cross 5 and cross 6) with duplicate gene action. Hence this trait was under the control by additive, dominance x dominance and duplicate gene action. Both additive and non additive gene actions were reported by Babu and Reddy (2002) and Kumar *et al.* (2004) for this trait.

Hence, selection in the early segregating generations may not give desirable recombinants. This may be

possibly be overcome by delaying the selection to later segregating generations when the dominance and epistasis disappear and resorting to intermating of segregants followed by recurrent selection. Simple selection procedures or pedigree breeding method is sufficient to harness additive gene action. But the presence of dominance gene action in most of the characters warrants postponement of selection to later generations after effecting crosses.

Both additive and dominance gene actions played major role in several characters. In such circumstances biparental mating design or reciprocal recurrent selection could be followed which allows further recombination of alleles to produce desirable segregants. These methods can also be well adopted in order to harness the epistatic interactions by way of breaking the undesirable linkages. Genetic analysis of five generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$ ) in six crosses for seven economic characters indicated that significant differences were observed among generation mean for all the characters revealing considerable variability for the characters studied. The fitting of five parameter model to the data indicated involvement of all three kind of gene effects *viz.*, additive, dominance and epistasis in the inheritance of the characters, since the estimates of all the gene effect were mostly significant for single plant yield as well as its component traits. The gene action, additive and dominance x dominance gene actions were predominant with duplicate type of gene action for 5 characters *viz.*, plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle and single plant yield. Additive, dominance, dominance x dominance and duplicate type of interaction were recorded in days to 50% flowering and hundred grain weight. To exploit both additive and non-additive gene effects, one or two cycles of recurrent selection followed by pedigree breeding will be effective and useful for the improvement of yield and yield components. These traits can also be improved by adopting biparental mating in  $F_2$  among selected segregants or following selection procedures such as diallel selective mating. As a whole, additive, dominance and digenic non-allelic interaction effects of different kinds governed the biometrical characters studied.

**Table 1. Estimates of generation means for seven biometrical characters of crosses viz., IR 72 x Veeradangan, ADT 39 x Kavuni, ADT 45 x Kavuni, ADT 43 x Navara, ASD 16 x Navara and TPS 4 x Katha nellu in rice**

Generations	Days to 50% flowering (days)	Plant height (cm)	Number of productive tillers per plant	Panicle length (cm)	Number of filled grains per panicle	Hundred grain weight (g)	Single plant yield (g)
1. IR 72 x Veeradangan							
$\bar{P}_1$	83.20 $\pm$ 0.48	85.65 $\pm$ 0.30	13.00 $\pm$ 0.31	23.39 $\pm$ 0.19	118.10 $\pm$ 1.36	2.31 $\pm$ 0.01	32.99 $\pm$ 0.29
$\bar{P}_2$	75.40 $\pm$ 0.40	112.79 $\pm$ 0.63	15.20 $\pm$ 0.20	22.75 $\pm$ 0.30	97.02 $\pm$ 1.26	2.55 $\pm$ 0.01	35.46 $\pm$ 0.44
$\bar{F}_1$	78.04 $\pm$ 0.84	97.63 $\pm$ 1.11	16.20 $\pm$ 0.32	24.90 $\pm$ 0.17	112.22 $\pm$ 2.09	2.69 $\pm$ 0.07	44.80 $\pm$ 1.38
$\bar{F}_2$	74.97 $\pm$ 0.44	101.07 $\pm$ 0.71	14.08 $\pm$ 0.25	24.96 $\pm$ 0.15	121.22 $\pm$ 2.50	2.56 $\pm$ 0.03	38.09 $\pm$ 0.76
$\bar{F}_3$	79.02 $\pm$ 0.43	99.46 $\pm$ 0.70	15.40 $\pm$ 0.24	25.22 $\pm$ 0.14	119.66 $\pm$ 1.67	2.49 $\pm$ 0.03	39.24 $\pm$ 0.72
2. ADT 39 x Kavuni							
$\bar{P}_1$	96.00 $\pm$ 0.63	98.32 $\pm$ 0.31	14.60 $\pm$ 0.24	24.67 $\pm$ 0.31	107.37 $\pm$ 1.51	1.84 $\pm$ 0.00	27.47 $\pm$ 0.38
$\bar{P}_2$	109.20 $\pm$ 2.20	136.85 $\pm$ 0.60	10.60 $\pm$ 0.24	25.94 $\pm$ 0.28	125.78 $\pm$ 1.42	2.34 $\pm$ 0.00	29.17 $\pm$ 0.53
$\bar{F}_1$	109.68 $\pm$ 0.72	122.95 $\pm$ 0.94	14.12 $\pm$ 0.40	24.75 $\pm$ 0.20	127.00 $\pm$ 1.88	2.13 $\pm$ 0.02	38.54 $\pm$ 1.22
$\bar{F}_2$	104.18 $\pm$ 0.51	126.19 $\pm$ 0.84	13.85 $\pm$ 0.23	24.82 $\pm$ 0.21	117.72 $\pm$ 2.20	2.28 $\pm$ 0.02	34.88 $\pm$ 0.67
$\bar{F}_3$	107.85 $\pm$ 0.49	123.90 $\pm$ 0.78	15.19 $\pm$ 0.23	26.10 $\pm$ 0.21	113.85 $\pm$ 1.76	2.30 $\pm$ 0.02	34.78 $\pm$ 0.58
3. ADT 45 x Kavuni							
$\bar{P}_1$	81.80 $\pm$ 0.37	92.28 $\pm$ 0.38	12.20 $\pm$ 0.20	23.76 $\pm$ 0.29	124.70 $\pm$ 1.39	1.99 $\pm$ 0.00	30.70 $\pm$ 0.33
$\bar{P}_2$	112.40 $\pm$ 0.50	138.13 $\pm$ 0.44	10.20 $\pm$ 0.37	26.35 $\pm$ 0.19	121.98 $\pm$ 2.38	2.33 $\pm$ 0.00	27.94 $\pm$ 0.52
$\bar{F}_1$	103.00 $\pm$ 0.61	112.62 $\pm$ 0.86	14.36 $\pm$ 0.31	27.59 $\pm$ 0.20	130.67 $\pm$ 2.26	2.18 $\pm$ 0.02	39.09 $\pm$ 1.20
$\bar{F}_2$	100.94 $\pm$ 0.43	117.52 $\pm$ 0.64	13.96 $\pm$ 0.26	26.12 $\pm$ 0.17	116.94 $\pm$ 1.45	2.22 $\pm$ 0.01	33.34 $\pm$ 0.53
$\bar{F}_3$	104.05 $\pm$ 0.38	115.97 $\pm$ 0.59	13.63 $\pm$ 0.25	27.92 $\pm$ 0.16	121.02 $\pm$ 1.44	2.27 $\pm$ 0.01	35.65 $\pm$ 0.51
4. ADT 43 x Navara							
$\bar{P}_1$	75.80 $\pm$ 0.58	85.18 $\pm$ 0.08	12.00 $\pm$ 0.31	23.65 $\pm$ 0.14	128.40 $\pm$ 1.50	1.96 $\pm$ 0.01	29.22 $\pm$ 1.05
$\bar{P}_2$	68.20 $\pm$ 0.58	97.01 $\pm$ 0.68	11.40 $\pm$ 0.40	22.53 $\pm$ 0.25	101.52 $\pm$ 1.02	2.23 $\pm$ 0.01	25.80 $\pm$ 1.04
$\bar{F}_1$	69.72 $\pm$ 0.64	95.16 $\pm$ 0.63	12.20 $\pm$ 0.38	22.54 $\pm$ 0.25	113.65 $\pm$ 1.69	2.29 $\pm$ 0.05	34.09 $\pm$ 1.19
$\bar{F}_2$	73.65 $\pm$ 0.36	100.23 $\pm$ 0.47	13.53 $\pm$ 0.38	23.06 $\pm$ 0.15	106.64 $\pm$ 1.65	2.26 $\pm$ 0.02	31.28 $\pm$ 0.62
$\bar{F}_3$	74.11 $\pm$ 0.37	98.22 $\pm$ 0.41	12.38 $\pm$ 0.31	23.83 $\pm$ 0.12	104.90 $\pm$ 1.53	2.42 $\pm$ 0.02	29.91 $\pm$ 0.56





Generations	Days to 50% flowering (days)	Plant height (cm)	Number of productive tillers per plant	Panicle length (cm)	Number of filled grains per panicle	Hundred grain weight (g)	Single plant yield (g)
5. ASD 16 x Navara							
$\bar{P}_1$	76.40 ± 0.50	94.80 ± 0.23	12.40 ± 0.24	23.88 ± 0.39	114.32 ± 1.65	2.64 ± 0.01	33.29 ± 1.04
$\bar{P}_2$	68.80 ± 0.37	96.73 ± 0.53	11.40 ± 0.24	22.75 ± 0.17	102.28 ± 2.10	2.24 ± 0.01	26.60 ± 0.69
$\bar{F}_1$	70.72 ± 0.53	94.81 ± 0.64	15.04 ± 0.53	23.61 ± 0.22	110.21 ± 2.24	2.49 ± 0.05	33.71 ± 0.74
$\bar{F}_2$	73.60 ± 0.54	96.17 ± 0.67	12.88 ± 0.44	23.33 ± 0.21	96.31 ± 2.36	2.59 ± 0.06	26.93 ± 0.88
$\bar{F}_3$	76.03 ± 0.41	94.52 ± 0.47	14.35 ± 0.33	23.37 ± 0.14	105.95 ± 1.72	2.54 ± 0.03	28.96 ± 0.63
6. TPS 4 x Katha nellu							
$\bar{P}_1$	66.00 ± 0.31	74.96 ± 0.63	12.20 ± 0.37	23.94 ± 0.27	107.64 ± 1.94	2.33 ± 0.00	30.16 ± 0.71
$\bar{P}_2$	88.80 ± 0.37	87.97 ± 0.67	13.60 ± 0.24	23.48 ± 0.36	113.24 ± 2.41	2.34 ± 0.00	35.15 ± 1.03
$\bar{F}_1$	81.08 ± 0.55	85.82 ± 0.52	14.24 ± 0.37	23.58 ± 0.26	109.65 ± 1.28	2.35 ± 0.05	34.81 ± 0.86
$\bar{F}_2$	76.50 ± 0.42	89.25 ± 0.46	15.72 ± 0.41	22.88 ± 0.15	119.01 ± 0.99	2.36 ± 0.03	31.96 ± 0.51
$\bar{F}_3$	79.14 ± 0.38	87.76 ± 0.37	14.52 ± 0.31	23.33 ± 0.13	114.97 ± 1.02	2.46 ± 0.03	33.41 ± 0.48

**Table 2. Estimates of Scaling tests for seven biometrical characters of crosses viz., IR 72 x Veeradangan, ADT 39 x Kavuni, ADT 45 x Kavuni, ADT 43 x Navara, ASD 16 x Navara and TPS 4 x Katha nellu in rice**

Traits	Crosses	C	D
1. Days to 50% flowering (days)	C1	-14.80** ± 2.55	7.54** ± 2.06
	C2	-7.84 ± 3.40	17.84** ± 3.20
	C3	3.56 ± 2.23	20.12** ± 1.88
	C4	11.16** ± 2.10	5.14** ± 1.84
	C5	7.76** ± 2.51	11.72** ± 2.07
	C6	-10.96** ± 2.07	8.76** ± 1.83
2. Plant height (cm)	C1	10.57** ± 3.71	-2.71 ± 3.24
	C2	23.69** ± 3.94	8.06* ± 3.63
	C3	14.41** ± 3.17	-1.54 ± 2.76
	C4	28.41** ± 2.38	10.24** ± 2.03
	C5	3.50 ± 3.04	-5.79* ± 2.38
	C6	22.46** ± 2.33	9.62** ± 1.99
3. Number of productive tillers per plant	C1	-4.28** ± 1.28	5.24** ± 1.17
	C2	1.96 ± 1.28	7.86** ± 1.10
	C3	4.72** ± 1.30	4.20** ± 1.22
	C4	6.32** ± 1.78	-0.94 ± 1.54
	C5	-2.34 ± 2.09	7.83** ± 1.65
	C6	8.60** ± 1.86	0.84 ± 1.57

4. Panicle length (cm)	C1	3.89** ± 0.78	4.82** ± 0.75
	C2	-0.80 ± 1.03	4.13** ± 1.03
	C3	-0.83 ± 0.89	9.33** ± 0.83
	C4	0.97 ± 0.85	3.02** ± 0.67
	C5	-0.50 ± 1.05	0.18 ± 0.85
	C6	-3.08** ± 0.93	0.14 ± 0.78
5. Number of filled grains per panicle	C1	45.50** ± 11.01	21.01* ± 8.56
	C2	-16.24 ± 9.80	-13.18 ± 8.58
	C3	-40.26** ± 7.87	3.53 ± 7.04
	C4	-30.66** ± 7.66	-23.60** ± 7.20
	C5	-51.78** ± 10.79	14.58 ± 8.76
	C6	35.87** ± 5.65	0.99 ± 5.50
6. Hundred grain weight (g)	C1	0.01 ± 0.19	-0.03 ± 0.15
	C2	0.69** ± 0.10	0.46** ± 0.09
	C3	0.24** ± 0.08	0.34** ± 0.07
	C4	0.25 ± 0.16	0.97** ± 0.11
	C5	0.51* ± 0.26	0.10 ± 0.18
	C6	0.05 ± 0.17	0.45** ± 0.15
7. Single plant yield (g)	C1	-5.70 ± 4.14	12.32** ± 3.32
	C2	5.80 ± 3.70	12.70** ± 2.76
	C3	-3.45 ± 3.27	17.27** ± 2.39
	C4	1.93 ± 3.76	2.07 ± 2.97
	C5	-19.55** ± 4.04	2.09 ± 3.35
	C6	-7.08* ± 2.98	4.42 ± 2.54

**Table 3. Estimates of genetic parameters for seven biometrical characters of crosses viz., IR 72 x Veeradangan, ADT 39 x Kavuni, ADT 45 x Kavuni, ADT 43 x Navara, ASD 16 x Navara and TPS 4 x Katha nellu in rice**

Traits	Crosses	m	d	h	i	l
1. Days to 50% flowering (days)	C1	74.97** $\pm$ 0.44	3.90** $\pm$ 0.31	-8.75* $\pm$ 1.57	0.30 $\pm$ 1.62	29.78 ** $\pm$ 4.84
	C2	104.18** $\pm$ 0.51	-6.60** $\pm$ 1.14	-6.12** $\pm$ 1.74	-26.40** $\pm$ 2.11	34.24** $\pm$ 5.27
	C3	100.94** $\pm$ 0.43	-15.30** $\pm$ 0.31	6.92** $\pm$ 1.41	43.42** $\pm$ 1.45	22.08** $\pm$ 4.37
	C4	73.65** $\pm$ 0.36	3.80** $\pm$ 0.41	-3.84** $\pm$ 1.29	6.03** $\pm$ 1.41	-8.02* $\pm$ 3.90
	C5	73.60** $\pm$ 0.54	3.80** $\pm$ 0.31	8.40** $\pm$ 1.58	1.08 $\pm$ 1.70	5.28 $\pm$ 5.08
	C6	76.50** $\pm$ 0.42	-11.40** $\pm$ 0.24	-3.98** $\pm$ 1.38	-30.46** $\pm$ 1.39	26.29** $\pm$ 4.22
2. Plant height (cm)	C1	101.07** $\pm$ 0.71	-13.57** $\pm$ 0.35	1.98 $\pm$ 2.48	-23.57** $\pm$ 2.40	-17.70* $\pm$ 7.49
	C2	126.19** $\pm$ 0.84	-19.26** $\pm$ 0.33	3.94 $\pm$ 2.76	-39.94** $\pm$ 2.68	-20.84* $\pm$ 8.36
	C3	117.52** $\pm$ 0.64	-22.92** $\pm$ 0.29	0.85 $\pm$ 2.12	-42.41** $\pm$ 2.10	-21.27** $\pm$ 6.50
	C4	100.23** $\pm$ 0.47	-5.91** $\pm$ 0.34	1.96 $\pm$ 1.52	-13.92** $\pm$ 1.52	-24.21** $\pm$ 4.71
	C5	96.17** $\pm$ 0.67	-0.96** $\pm$ 0.29	3.49 $\pm$ 1.89	2.52 $\pm$ 1.97	-12.40* $\pm$ 6.19
	C6	89.25** $\pm$ 0.46	-6.50** $\pm$ 0.46	1.68 $\pm$ 1.40	-15.68** $\pm$ 1.60	-17.12** $\pm$ 4.45
3. Number of productive tillers per plant	C1	14.08** $\pm$ 0.25	-1.10** $\pm$ 0.18	-2.10* $\pm$ 0.86	-6.40** $\pm$ 0.90	12.69** $\pm$ 2.60
	C2	13.85** $\pm$ 0.23	2.00** $\pm$ 0.17	-3.39** $\pm$ 0.82	-0.91 $\pm$ 0.84	7.86** $\pm$ 2.50
	C3	13.96** $\pm$ 0.26	1.00** $\pm$ 0.21	1.14 $\pm$ 0.88	-0.01 $\pm$ 0.88	-0.69 $\pm$ 2.64
	C4	13.53** $\pm$ 0.38	0.30 $\pm$ 0.25	2.18 $\pm$ 1.15	2.28 $\pm$ 1.20	-9.68** $\pm$ 3.61
	C5	12.88** $\pm$ 0.44	0.50** $\pm$ 0.17	-2.47 $\pm$ 1.31	-4.61** $\pm$ 1.35	13.57** $\pm$ 4.21
	C6	15.72** $\pm$ 0.41	-0.70** $\pm$ 0.22	2.21 $\pm$ 1.20	-0.52 $\pm$ 1.28	-10.34** $\pm$ 3.83
4. Panicle length (cm)	C1	24.96** $\pm$ 0.15	0.32 $\pm$ 0.18	-0.73 $\pm$ 0.51	-1.92** $\pm$ 0.55	1.23 $\pm$ 1.52
	C2	24.82** $\pm$ 0.21	-0.63** $\pm$ 0.21	-3.44** $\pm$ 0.71	-4.16** $\pm$ 0.77	6.59** $\pm$ 2.11
	C3	26.12 ** $\pm$ 0.17	-1.29 ** $\pm$ 0.17	-3.82** $\pm$ 0.58	-8.94 ** $\pm$ 0.65	13.55** $\pm$ 1.76
	C4	23.06** $\pm$ 0.15	0.55** $\pm$ 0.14	-2.39** $\pm$ 0.49	-0.73 $\pm$ 0.53	2.73 $\pm$ 1.57
	C5	23.33** $\pm$ 0.21	0.56* $\pm$ 0.21	0.08 $\pm$ 0.60	-	-
	C6	22.88** $\pm$ 0.15	0.22 $\pm$ 0.22	-0.73 $\pm$ 0.51	-0.15 $\pm$ 0.61	4.30 ** $\pm$ 1.59
5. Number of filled grains per panicle	C1	121.27** $\pm$ 2.50	10.54** $\pm$ 0.93	-1.75 $\pm$ 6.85	14.65 * $\pm$ 7.26	-32.65 $\pm$ 22.63
	C2	117.72** $\pm$ 2.20	-9.20** $\pm$ 1.04	16.50* $\pm$ 6.57	-	-
	C3	116.94** $\pm$ 1.45	1.35 $\pm$ 1.38	-1.72 $\pm$ 5.06	-6.34 $\pm$ 5.18	58.39** $\pm$ 15.22
	C4	106.64** $\pm$ 1.65	13.44** $\pm$ 0.90	9.31 $\pm$ 5.38	37.50** $\pm$ 5.43	9.41 $\pm$ 16.21
	C5	96.31** $\pm$ 2.36	6.02** $\pm$ 1.33	-16.44* $\pm$ 6.75	-6.31 $\pm$ 7.16	88.49** $\pm$ 21.83
	C6	119.01** $\pm$ 0.99	-2.79 $\pm$ 1.54	4.52 $\pm$ 3.48	-0.28 $\pm$ 4.09	-46.50** $\pm$ 10.23
6. Hundred grain weight (g)	C1	2.56** $\pm$ 0.03	-0.12 ** $\pm$ 0.01	0.29 * $\pm$ 0.12	-	-
	C2	2.28** $\pm$ 0.02	-0.24** $\pm$ 0.00	-0.15* $\pm$ 0.07	-0.68** $\pm$ 0.06	-0.30 $\pm$ 0.21
	C3	2.22** $\pm$ 0.01	-0.18** $\pm$ 0.00	-0.15* $\pm$ 0.05	-0.55** $\pm$ 0.05	0.14 $\pm$ 0.17
	C4	2.26** $\pm$ 0.02	-0.13** $\pm$ 0.00	-0.14 ** $\pm$ 0.09	-0.88** $\pm$ 0.09	0.96** $\pm$ 0.30
	C5	2.59** $\pm$ 0.06	0.19** $\pm$ 0.00	0.06 $\pm$ 0.15	0.40* $\pm$ 0.16	-0.54 $\pm$ 0.53
	C6	2.36** $\pm$ 0.03	-0.006 $\pm$ 0.006	-0.27* $\pm$ 0.11	-0.30** $\pm$ 0.11	0.53 $\pm$ 0.36



7. Single plant yield (g)	C1	38.09** $\pm$ 0.76	-1.23** $\pm$ 0.26	1.41 $\pm$ 2.62	-11.63** $\pm$ 2.56	24.03** $\pm$ 8.09
	C2	34.88** $\pm$ 0.67	-0.85** $\pm$ 0.33	2.72 $\pm$ 2.20	-9.20** $\pm$ 2.23	9.19 $\pm$ 7.02
	C3	33.34** $\pm$ 0.53	1.38 ** $\pm$ 0.31	-2.32 $\pm$ 1.90	-9.32** $\pm$ 1.91	27.63** $\pm$ 5.99
	C4	31.28** $\pm$ 0.62	1.71 * $\pm$ 0.74	5.51** $\pm$ 2.11	-	-
	C5	26.93** $\pm$ 0.88	3.34** $\pm$ 0.62	-0.89 $\pm$ 2.50	2.03 $\pm$ 2.81	-9.12** $\pm$ 1.94
	C6	31.96** $\pm$ 0.51	-2.49** $\pm$ 0.62	-1.97 $\pm$ 1.76	-9.12** $\pm$ 1.94	15.35** $\pm$ 5.42

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