Genetic Effects of Grain Yield and Yield Components in Rice (*Oryza Sativa* L.) Using Generation Mean Analysis

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ABSTRACT: *Information on the inheritance of polygenic traits is worthful for planning and executing a breeding strategy leading to their genetic improvement. Gene action in rice has been determined mostly by using L x T analysis which furnishes information only on additive and dominant gene effects. Hence to study the epistatic gene effects, generation mean analysis has to be carried out and in the present investigation an attempt was made to decipher the gene effects of the panicle and yield traits in rice. Two crosses namely MTU 1075 / MTU 3626 and MTU 1121 / TN 1 were studied at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru, West Godavari, Andhra Pradesh. Six basic generations including P_1, P_2, F_1, F_2, BC_1 and BC_2 of the two crosses were used to study nature of inheritance by deploying six parameter model of generation mean analysis. The additive x dominance model was significant for all the traits in both the crosses, indicating the presence of epistasis. The scaling test indicated that the inheritance of traits related to panicle and yield was genetically controlled by both additive and dominance main effects and among non-allelic interactions mainly additive x additive and dominance x dominance effects played a significant role in the inheritance of these traits.*

Keywords: *Generation Mean analysis, Gene effect, Panicle traits, Yield traits, Six parameter model, Rice.*

INTRODUCTION

Rice is supplying more than 40% human food requirement in the world and provides food for more than half of people living on the Earth. More than 80% daily calorie and 75% required protein is obtained from rice in Asia. At the current rate of population growth in India, estimated rice production should be around 135 to 140 million tonnes by 2020. So it is critical to produce high yield cultivars with high quality by inbreeding methods. Yield is complex character and various morphological and physiological characters contribute to grain yield (Luo *et al.*, 2011). The plateau in yield levels of existing rice varieties and the adverse effects of climate and deteriorating soil health on crop yield are the major cause of concern. Rice varieties with increased yield potential in adverse conditions as well as in normal conditions have to be developed, in order to sustain the rice production across wide range of environments and over the years. In this regard we

need primary information about genetic structure of different traits to attain high yield and quality. Knowing about genetic structure of each trait, such as inheritance method and gene mode of action are necessary because this information make us able to design breeding strategies. Therefore quantitative genetic method such as generation mean analysis is used.

The most commonly used mating designs Diallel and Line x Tester provide estimates of additive and dominance/non-additive components of gene effect in relation to whole population studied. However, partitioning of genetic variance into its all the probable components *i.e,* additive, dominance and all types of epistasis with regard to individual cross is of immense value in formulating an effective and sound breeding programme. Among the common approaches followed to understand the nature of gene effect, generation mean analysis using first degree statistics is an accurate one, and gives detail account

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of gene effects and quality of the genes carried by the parents. Thus, the present study was carried out to estimate different kinds of gene effects in the inheritance of yield and its related traits through generation mean analysis. Shashikant (2015) studied the generation mean analysis for yield components in rice and demonstrated the importance of additive, dominance and epistatic gene effects in the inheritance of grain yield and their attributing traits. Hence, he suggested that, selection in the early segregating generations may not give desirable recombinants. This may 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.

MATERIAL AND METHODS

The mean value was computed for all the six generations over all replications for each cross. The generation mean analysis was carried out following the methodology of Hayman (1958) using six generations and estimated the gene effects *viz.,* m (mean), d (additive main effect), h (dominance main effect), i (additive x additive interaction effect), j (additive x dominance interaction effect) and l (dominance x dominance interaction effect).

The present investigation was carried out at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station (APRRI & RARS), Maruteru, West Godavari, Andhra Pradesh from *kharif* -2012 to *kharif* -2013. The material comprised of four varieties of rice *i.e.,* MTU 1075, MTU 3626, MTU 1121 and TN 1. The crosses have been done between parents MTU 1075 and MTU 3626 and between MTU 1121 and TN 1 to generate F_1s during *kharif*, 2012 and during *rabi*, 2012-13, back crosses (BC_1 and BC_2) were made in both the crosses and simultaneously, F_2 populations were developed by selfing F_1s for both the crosses. During *kharif*- 2013, six basic generations including P_1, P_2, F_1, F_2, BC_1 and BC_2 of two crosses namely MTU 1075 / MTU 3626 and MTU 1121 / TN 1 were planted in a randomized complete block design with two replications to study nature of inheritance for twelve panicle and yield traits *viz.,* days to 50% flowering, plant height (cm), number of ear bearing tillers plant[-1], panicle length (cm), number of grains primary rachis branch[-1], number of grains secondary rachis branch[-1], number of fertile grains panicle[-1], spikelet fertility percentage, high density grain index, 1000-grain weight (g), grain yield panicle[-1](g) and grain yield plant[-1](g). The total

number of population raised in each replication was 10 in parents and F_1, 80 in back cross generations and 200 in F_2.

RESULTS AND DISCUSSION

Mean performance of the six populations, *i.e.,* P_1, P_2, F_1, F_2, BC_1 and BC_2 for all traits studied in the cross I (C_1) and cross II (C_2) is presented in the Table 1. The estimated mean effect (m) parameter, which reflects the contribution due to the overall mean plus the locus effects and interaction of the fixed loci, were found to be highly significant for all the traits in the two crosses.

The mean performance of the basic generations *viz.,* P_1, P_2, F_1, F_2, BC_1 and BC_2 of both the crosses showed existence of substantial variability in the material for all the 12 traits pertaining to panicle and yield. In general, F_1 performance was better than either of the parents for number of ear bearing tillers plant[-1], number of grains primary rachis branch[-1], number of fertile grains panicle[-1], spikelet fertility, high density grain index, 1000 grain weight and grain yield plant[-1] in the cross MTU 1075 / MTU 3626. Superiority of F_1 performance over the parents in number of ear bearing tillers plant[-1], number of grains primary rachis branch[-1], number of fertile grains panicle[-1], spikelet fertility may be due to contribution of the parent, MTU 1075 for these traits. The parent MTU 3626 seems to be contributing towards high density grain index, 1000 grain weight and grain yield plant[-1]. Intermediate values of F_1 for the remaining characters showed presence of partial dominance.

Decline in the performance of F_2 for number of ear bearing tillers plant[-1], high density grain index, grain yield panicle[-1] and grain yield plant[-1], suggested presence of dominance and epistatic interactions in expression of these traits in the cross MTU 1075 / MTU 3626. Significant increase in plant height in F_2, showed presence of transgressive segregant in F_2 population indicating importance of additive gene action for plant height. The BC_1 generation showed better performance for days to 50% flowering, number of grains primary rachis branch[-1], number of fertile grains panicle[-1] and grain yield plant[-1] in comparision to BC_2 generation in the cross MTU 1075 / MTU 3626.

In the cross, MTU 1121 / TN 1, the hybrid was better in performance for number of ear bearing tillers plant[-1], panicle length, number of grains primary rachis branch[-1], number of grains secondary rachis branch[-1], number of fertile grains panicle[-1], high density grain index, 1000 grain weight, grain yield panicle[-1] and grain yield plant[-1] over the parents. Intermediate performance of F_1 over parents for days

to 50% flowering and spikelet fertility showed partial dominance for these characters.

Significant decline in F_2 mean performance for number of ear bearing tillers plant[-1], spikelet fertility, grain yield panicle[-1] and grain yield plant[-1] indicated the presence of dominance and epistatic interactions in expression of these traits in the cross MTU 1121 / TN 1. The BC_1 generation was better for number of ear bearing tillers plant[-1], panicle length, number of grains primary rachis branch[-1], number of grains secondary rachis branch[-1], number of fertile grains panicle[-1], spikelet fertility and grain yield panicle[-1] over BC_2 generation in the cross MTU 1121 / TN 1.

Results of individual scaling tests *i.e.*, A, B and C scaling tests is presented in Table 2. Findings of A,B and C scaling tests revealed that the calculated values of all the three scaling tests were found significant for ear bearing tillers plant[-1], number of grains primary rachis branch[-1], number of fertile grains panicle[-1], spikelet fertility percentage, high density grain index, 1000 grain weight and grain yield panicle[-1], while remaining characters *viz.*, days to 50% flowering, plant height, panicle length, number of

grains secondary rachis[-1] and grain yield plant[-1] had shown significance of two out of three scaling tests performed in the cross MTU 1075 / MTU 3626. While, in the cross, MTU 1121 / TN 1, the calculated values of all the three scaling tests were found significant for all the 12 panicle and yield traits studied.

The estimated values of the various types of gene effects *viz.*, m, d, h, i, j and l are presented in Table 3. Results of main effects and interaction effects governing quantitative traits are discussed below each trait wise.

Days to 50 percent flowering: For this trait, additive [d] gene effect was negative and non significant for the cross MTU 1075 / MTU 3626 and it was positive and significant for the other cross. Both the crosses exhibited highly significant and negative dominance [h] gene effects as well as additive x additive [i] interaction effects, which is highly desirable for development of earliness. Dominance x dominance [l] interaction effects were positive and significant and was in opposite direction with dominance [h] effects for both the crosses studied indicated the presence of duplicate epistasis and

Table 1
Estimates of generation means and standard errors of two crosses for panicle and yield traits in rice (*Oryza sativa* L.)

Generation	Days to 50% flowering		Plant height (cm)		Number of ear bearing tillers plant[-1]		Panicle length (cm)	
	C_1	C_2	C_1	C_2	C_1	C_2	C_1	C_2
P_1	121.8±1.405	100.9±1.178	106.45±1.008	106.31±2.726	10.5±0.543	9.8±0.389	27.93±0.535	27.20±0.482
P_2	96.1±0.971	95.1±0.795	93.75±2.424	110.43±1.166	9.6±0.618	8.5±0.401	23.34±0.323	20.92±0.462
F_1	100.1±0.948	100.6±1.024	106.03±1.006	113.45±1.199	12.1±0.379	12.5±0.341	26.98±0.342	28.44±0.190
F_2	104.74±0.446	95.35±0.442	112.41±0.576	107.48±0.495	6.74±0.144	6.66±0.144	25.15±0.193	24.67±0.190
BC_1	99.76±1.101	94.93±0.605	104.90±0.600	99.87±1.278	9.98±0.266	8.06±0.176	26.38±0.248	25.18±0.309
BC_2	100.93±0.930	90.63±0.539	91.45±1.509	107.19±1.563	9.71±0.259	7.23±0.267	25.29±0.276	23.85±0.272

Generation	Number of grains primary rachis branch[-1]		Number of grains secondary rachis[-1]		Number of fertile grains panicle[-1]		Spikelet fertility (%)	
	C_1	C_2	C_1	C_2	C_1	C_2	C_1	C_2
P_1	71.4±1.185	62.9±1.670	217.1±2.834	177±2.060	288.5±3.807	239.9±2.297	83.90±0.863	93.4±0.897
P_2	59±1.892	50.2±1.482	77.3±1.513	117.3±2.825	136.3±2.887	167.5±2.729	86.84±0.738	91.03±0.830
F_1	106.4±1.64	92.33±0.563	187.8±0.712	188.8±1.126	294.2±0.964	281.1±1.384	91.86±0.310	91.46±0.445
F_2	63.87±1.150	52.26±1.123	115.96±2.888	107.69±2.081	179.38±3.182	159.95±2.568	80.46±0.583	86.07±0.555
BC_1	67.94±2.111	65.52±1.466	140.20±5.340	113.56±2.939	208.14±6.909	179.08±3.412	81.57±1.212	86.08±0.839
BC_2	60.07±1.677	50.42±2.163	129.85±4.041	86.85±3.476	189.93±4.664	137.26±5.264	75.24±0.763	83.57±1.125

Generation	High density grain index		1000 grain weight (g)		Grain yield panicle[-1] (g)		Grain yield plant[-1] (g)	
	C_1	C_2	C_1	C_2	C_1	C_2	C_1	C_2
P_1	92.05±0.474	92.2±0.629	21.96±0.276	21.8±0.441	4.90±0.114	4.89±0.116	28.14±0.418	34.02±0.628
P_2	93.6±0.846	88.9±1.169	27.65±0.463	26.1±0.666	4.80±0.072	4.67±0.110	29.99±0.481	22.83±0.438
F_1	94.8±0.489	94.6±0.581	30.99±0.324	29.93±0.283	4.81±0.005	5.10±0.076	34.49±0.106	41.74±0.564
F_2	80.58±0.835	88.60±0.463	20.99±0.185	21.87±0.317	2.71±0.056	2.72±0.061	24.61±0.577	21.35±0.527
BC_1	83.45±1.188	87.93±0.802	20.45±0.371	20.26±0.321	2.96±0.122	3.06±0.097	39.82±2.097	26.96±1.348
BC_2	85.24±0.895	87.38±0.697	20.85±0.364	22.35±0.215	2.45±0.071	2.33±0.054	31.66±0.812	27.33±0.828

C_1 = MTU 1075/ MTU 3626 C_2 = MTU 1121/ TN1

Table 2
Scaling tests for panicle and yield traits in two crosses of rice (*oryza sativa* L.)

Character	Cross combination	A	B	C
Days to 50% flowering	MTU 1075/MTU 3626	-22.375**±2.779	5.650*±2.302	0.860±3.113
	MTU 1121/TN 1	-11.650**±1.975	-14.450**±1.687	-15.800**±3.057
Plant height	MTU 1075/MTU 3626	-2.667±1.863	-16.884**±4.000	37.391**±4.031
	MTU 1121/TN 1	-20.017**±3.925	-9.509**±3.546	-13.724**±4.297
Number of ear bearing tillers plant[-1]	MTU 1075/MTU 3626	-2.650**±0.849	-2.275*±0.793	-17.360**±1.258
	MTU 1121/TN 1	-6.175**±0.625	-6.525**±0.750	-16.660**±1.054
Panicle length	MTU 1075/MTU 3626	-2.149**±0.805	0.266±0.726	-4.633**±1.207
	MTU 1121/TN 1	-5.280**±0.806	-1.658*±0.739	-6.327**±1.081
Number of grains primary rachis branch[-1]	MTU 1075/MTU 3626	-41.91**±4.410	-45.25**±3.879	-87.72**±5.199
	MTU 1121/TN 1	-24.19**±3.421	-41.7**±4.607	-88.7**±5.141
Number of grains secondary rachis branch[-1]	MTU 1075/MTU 3626	-124.51**±11.073	-5.391±8.253	-206.15**±12.076
	MTU 1121/TN 1	-132.681**±6.329	-132.405**±7.588	-241.136**±9.304
Number of fertile grains panicle[-1]	MTU 1075/MTU 3626	-166.42**±14.705	-50.65**±10.302	-295.68**±15.1
	MTU 1121/TN 1	-162.87**±7.961	-174.1**±11.395	-288.577**±11.221
Spikelet fertility	MTU 1075/MTU 3626	-12.614**±2.591	-28.218**±1.723	-32.624**±2.669
	MTU 1121/TN 1	-12.692**±1.954	-15.343**±2.439	-23.068**±2.686
High density grain index	MTU 1075/MTU 3626	-19.950**±2.472	-17.925**±2.040	-52.950**±3.614
	MTU 1121/TN 1	-10.950**±1.818	-8.750**±1.910	-15.880**±2.558
1000 grain weight	MTU 1075/MTU 3626	-12.056**±0.857	-16.953**±0.921	-27.620**±1.121
	MTU 1121/TN 1	-11.211**±0.829	-11.330**±0.842	-20.259**±1.604
Grain yield panicle[-1]	MTU 1075/MTU 3626	-3.8**±0.261	-4.715**±0.166	-8.483**±0.258
	MTU 1121/TN 1	-3.877**±0.239	-5.107**±0.172	-8.874**±0.329
Grain yield plant[-1]	MTU 1075/MTU 3626	17.009**±4.217	1.847±1.697	-25.678**±2.404
	MTU 1121/TN 1	-21.867**±2.825	-9.915**±1.803	-54.914**±2.510

clearly underlines the scope for recovering the plants showing transgressive effect due to the presence of significant additive x additive components besides duplicate epistasis. Murugan and Ganesan (2006), Nayak *et al*. (2007) and Divya *et al*. (2014) were also in agreement with the above results.

Plant height (cm): The additive [d] gene effects were significant and positive for this trait in the cross MTU 1075 / MTU 3626, whereas the other cross had negative and significant [d] effects. Highly significant and negative dominance [h] effects recorded in both the crosses studied. The additive x additive [i] interaction effects were highly significant and negative for both the crosses, which is desirable for development of semi dwarf varieties. Both the crosses recorded highly significant and positive dominance x dominance [l] effects and exhibited duplicate type of epistasis. Preponderance of duplicate epistasis suggests that inheritance of this trait might pose problems in its genetic improvement, but one can expect some progress in selection programmes due to presence of substantial amount of non allelic interaction and transgressive segregants could also be recovered due to the presence of significant [i] effects besides the duplicate epistasis. Divya *et al*. (2014) reported duplicate epistasis for this trait

Number of ear bearing tillers plant[-1]: The dominance [h] effects were predominantly significant and positive in both the crosses under study. The additive [d] gene effects were significant and positive in case of MTU 1121 / TN 1, whereas the other cross exhibited positive and non significant additive [d] effects. Among the interaction effects positive and highly significant effects were noticed for additive x additive [i] type in both the crosses. The dominance x dominance [l] effects were positive and significant in MTU 1121 / TN 1 and MTU 1075 / MTU 3626 had negative and significant effect. In the cross MTU 1121 / TN 1 the dominance [h] and dominance x dominance [l] effects were operating in same direction and the results are in conformity with Divya *et al*.(2014). The cross MTU 1075 / MTU 3626 had a possibility of obtaining transgressive segregants as the additive x additive component was significant besides the duplicate epistasis. Kiani *et al*. (2013) also reported duplicate epistasis for this trait.

Panicle length (cm): For panicle length both the crosses recorded significant positive additive [d] gene effects and dominance [h] effects. Among the

Table 3
Estimates of gene effetcs for panicle and yield traits in two crosses of rice (*oryza sativa* L.)

Cross combination	m	d	h	i	j	l	Type of epistasis
			Days to 50% flowering				
MTU 1075/ MTU 3626	104.740**±0.446	-1.163±1.441	-26.435**±3.621	-17.585**±3.389	-14.013±1.675	34.310**±6.551	Duplicate
MTU 1121/TN 1	95.350**±0.442	4.300**±0.811	-7.700**±2.704	-10.300**±2.399	1.400±1.078	36.400**±4.456	Duplicate
			Plant height				
MTU 1075/ MTU 3626	112.412**±0.576	13.457**±1.625	-51.017**±4.313	-56.943**±3.983	7.109±2.088	76.494**±7.647	Duplicate
MTU 1121/TN 1	107.478**±0.495	-7.315**±2.019	-10.720*±4.885	-15.802**±4.497	-5.254±2.505	45.328**±9.148	Duplicate
			Number of ear bearing tillers plant[-1]				
MTU 1075/ MTU 3626	6.735**±0.144	0.263±0.371	14.485**±1.093	12.435**±0.939	-0.187±0.554	-7.510±1.944	Complementary
MTU 1121/TN 1	6.660**±0.144	0.825*±0.320	7.310**±0.967	3.960**±0.860	0.175±0.424	8.740**±1.656	Complementary
			Panicle length				
MTU 1075/ MTU 3626	25.150**±0.193	1.091**±0.371	4.094**±1.167	2.749*±1.071	-1.207±0.485	-0.866±1.913	Duplicate
MTU 1121/TN 1	24.669**±0.190	1.329**±0.411	3.762**±1.184	-0.611±1.120	-1.811±0.530	7.550**±1.969	Complementary
			Number of grains primary rachis branch[-1]				
MTU 1075/ MTU 3626	63.869**±1.150	7.873**±2.696	41.76**±7.190	0.560±7.087	1.673±2.918	86.6**±11.971	Complementary
MTU 1121/TN 1	52.265**±1.123	15.105**±2.613	58.6**±7.004	22.815**±6.891	8.755±2.841	43.07±11.648	Complementary
			Number of grains secondary rachis branch[-1]				
MTU 1075/ MTU 3626	115.963**±2.888	10.342±6.697	116.85**±17.776	76.252**±17.689	-59.558±6.887	53.64±29.384	Complementary
MTU 1121/TN 1	107.691**±2.081	26.712**±4.552	11.7±12.509	-29.950*±12.335	-3.138±4.876	301.036**±20.447	Complementary
			Number of fertile grains panicle[-1]				
MTU 1075/ MTU 3626	179.380**±3.182	18.215*±8.336	160.416**±21.365	78.616**±20.975	-57.885±8.672	138.45*±36.60	Complementary
MTU 1121/TN 1	159.956**±2.568	41.817**±6.273	70.29**±16.66	-7.136±16.215	5.617±6.522	344.109**±28.18	Complementary
			Spikelet fertility				
MTU 1075/ MTU 3626	80.457**±0.583	6.335**±1.432	-1.717±3.750	-8.208*±3.694	7.802±1.540	49.040**±6.318	Duplicate
MTU 1121/TN 1	86.068**±0.555	2.511±1.403	-5.726±3.657	-4.968±3.578	1.325±1.530	33.003**6.222	Duplicate
			High density grain index				
MTU 1075/ MTU 3626	80.575**±0.835	-1.788±1.488	17.050**±4.526	15.075**±4.473	-1.013±1.565	22.800**±6.962	Complementary
MTU 1121/TN 1	88.605**±0.463	0.550±1.062	0.230±2.953	-3.820±2.818	-1.100±1.253	23.520**4.960	Complementary
			1000 grain weight				
MTU 1075/ MTU 3626	20.994**±0.185	-0.398±0.520	4.793**±1.344	-1.389±1.276	2.449±0.586	30.398**±2.364	Complementary
MTU 1121/TN 1	21.875**±0.317	-2.091**±0.386	3.697**±1.565	-2.282±1.487	0.059±0.556	24.823**±2.227	Complementary
			Grain yield panicle[-1]				
MTU 1075/ MTU 3626	2.712**±0.056	0.508**±0.141	-0.074±0.366	-0.032±0.360	0.458±0.156	8.547**±0.621	Duplicate
MTU 1121/TN 1	2.721**±0.061	0.728**±0.111	0.208±0.348	-0.110±0.330	0.615±0.137	9.09**±0.553	Complementary
			Grain yield plant[-1]				
MTU 1075/ MTU 3626	24.609**±0.577	8.157**±2.249	51.458**±5.067	44.534**±5.056	7.581±2.272	-63.389**±9.312	Duplicate
MTU 1121/TN 1	21.353**±0.527	-0.382±1.582	36.443**±3.862	23.131**±3.802	-5.976±1.628	8.651±6.807	Complementary

* Significant at 5% level   ** Significant at 1% level

interaction effects significant and positive additive x additive [i] effects were expressed in MTU 1075 / MTU 3626 and negative and nonsignificant effects were observed in MTU 1121 / TN 1. The dominance x dominance [l] effects were positive and significant in MTU 1121 / TN 1 and negative and nonsignificant in MTU 1075 / MTU 3626. Duplicate epistasis was found in the cross MTU 1075 / MTU 3626. Kiani *et al.* (2013) reported duplicate epistasis for this trait. In MTU 1121 / TN 1 all the gene effects were significant and positive suggesting either composite or population improvement programme should be taken

up for the development of superior lines with several desirable genes. Verma *et al.* (2006) and Narendra Pratap *et al.* (2013) reported the importance of both additive and dominance effects.

Number of grains primary rachis branch[-1]: The additive [d] gene effects and dominance [h] gene effects were positive and highly significant in both the crosses. Among the interaction effects additive x additive [i] gene effects were positive and significant for MTU 1121 / TN 1, while in the other cross it was positive and nonsignificant. Dominance x dominance [l] effects were positive and significant for MTU 1075

/ MTU 3626, while in the other cross it was positive and nonsignificant. Dominance [h] gene effects and dominance x dominance [l] effects were in same direction in both the crosses, indicating complementary epistasis. Dominant gene action was more predominant than additive type indicating that selection in early segregating generations is ineffective and the character could be better exploited through the heterosis breeding.

Number of grains secondary rachis branch^{-1}: The additive [d] gene effects were highly significant in MTU 1121 / TN 1 and positive and nonsignificant in the other cross. Dominance [h] gene effects were positive and highly significant in MTU 1075 / MTU 3626 while it was positive and nonsignificant in the other cross. Additive x additive [i] interaction effects were positive and highly significant for MTU 1075 / MTU 3626, while in the other cross it was negative and significant. Dominance x dominance [l] effects were positive and significant for MTU 1121 / TN 1, while in the other cross it was positive and nonsignificant. All the gene effects were positive, the magnitude of additive gene effects were predominant in MTU 1121 / TN 1 in which pedigree breeding will be rewarding for improvement of this trait and the magnitude of dominant gene effects were positive in the other cross in which heterosis breeding could be useful for better exploitation of this trait.

Number of fertile grains panicle^{-1}: The additive [d] and dominance [h] gene effects were positive and highly significant in both the crosses. Additive x additive [i] interaction effects were positive and highly significant for MTU 1075 / MTU 3626, while in the other cross it was negative and nonsignificant. Dominance x dominance [l] effects were positive and highly significant for both the crosses. Dominance [h] and dominance x dominance [l] gene action were predominant and were operating in same direction indicating complementary epistasis for which only biparental mating in early segregating generations followed by selection in advanced generations would be more effective rather than direct selection in early segregating generations. Murugan and Ganesan (2006) and Verma *et al.* (2006) were also in conformity with the above results.

Spikelet fertility (%): The additive [d] gene effects were positive and significant in MTU 1075 / MTU 3626 and positive and nonsignificant in the other cross. Dominance [h] gene effects were negative and nonsignificant for both the crosses studied. Among the interaction effects additive x additive [i] effects were negative and significant for the cross, MTU 1075

/ MTU 3626, while in the other cross it was negative and nonsignificant. Dominance x dominance [l] effects were predominant and were positive and highly significant for both the crosses, [h] and [l] components were in opposite direction indicating duplicate epistasis, hence simple recurrent selection can be resorted for improvement of this character. Asante *et al.* (2006) and Divya *et al.* (2014) reported similar results.

High density grain index: The additive [d] gene effects were negative and nonsignificant in MTU 1075 / MTU 3626 and positive and nonsignificant in the other cross. Dominance [h] gene effects were positive and significant for the cross, MTU 1075 / MTU 3626, while it was positive and nonsignificant for the other cross. The additive x additive [i] interaction effects were positive and significant for MTU 1075 / MTU 3626, while in the other cross it was negative and nonsignificant. Dominance x dominance [l] effects were positive and highly significant for both the crosses. Magnitude of dominant gene action was high and complementary epistasis was observed hence crosses can be better utilized by exploiting hybrid vigour through heterosis breeding.

1000 grain weight (g): The additive [d] gene effects were negative and nonsignificant for this trait in MTU 1075 / MTU 3626, while it was negative and significant in the other cross. Significant and positive dominance [h] effects were recorded in both the crosses studied. Among the epistatic interaction effects, additive x additive [i] gene effects were negative and nonsignificant and dominance x dominance [l] effects were positive and highly significant in both the crosses studied. Dominant gene action was predominant and complementary epistasis was observed, hence this character could be better exploited through hybridization. Patil *et al.* (2006) and Verma *et al.* (2006) were also reported the similar results.

Grain yield panicle^{-1} (g): The additive [d] gene effects were positive and significant for both the crosses, while it was negative and significant in both the crosses for dominant [h] effects. Among the interaction effects, additive x additive [i] gene effects were negative and nonsignificant, while, dominance x dominance [l] effects were positive and significant in both the crosses studied. The dominance x dominance [l] effects were higher than additive [d] gene effects suggesting the importance of dominant gene action, hence bi parental mating and recurrent selection especially reciprocal recurrent selection to break undesirable linkages followed by isolation of

pure lines in advanced generations would be more appropriate strategy as compared to pedigree method alone.

Grain yield plant⁻¹ (g): The additive [d] gene effects were positive and significant in MTU 1075 / MTU 3626 and negative and nonsignificant for the other cross. The dominance [h] effects were highly significant and positive in both the crosses. Additive x additive [i] interaction effects were positive and highly significant in both the crosses. Dominance x dominance [l] effects were negative and significant in MTU 1075 / MTU 3626, while it was positive and nonsignificant in the other cross. Both [h] and [l] effects were positive and significant but the magnitude of dominant gene action was higher indicating predominance of dominant gene action. Duplicate epistasis was observed in case of MTU 1075 / MTU 3626, while complementary epistasis was found in MTU 1121 / TN 1. Presence of duplicate epistasis in one cross and complementary epistasis in the other cross for the same trait indicates that improvement of yield mainly depends upon the cross selected for improvement, for which only bi parental mating in early generations followed by selection in advance generation would be more effective than direct selection in early segregating generations. Predominance of non additive gene action was also earlier reported by Verma *et al.* (2006). Complementary epistasis was reported by Mahalingam and Nadarajan (2010) and Divya *et al.* (2014) for this trait. Thakare *et al.* (2013) reported that this trait was governed by mainly dominance and interaction effects.

The additive x dominance [j] type of interaction was found nonsignificant for all the characters in both the crosses, indicating less importance of this type of interaction.

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