



# Genetic Architecture of Grain Quality Traits in Nutrient Rich Rice (*Oryza sativa* L.) Crosses

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## ABSTRACT

The precise knowledge of the nature of gene action for quality traits in rice helps to choose an effective breeding strategy to accelerate the pace of genetic improvement of quality traits in rice. The Generation mean analysis indicated absence of epistasis in case of certain quality characters like hulling percent, milling percent, kernel length, breadth and kernel elongation ratio in first and second crosses. The interaction was of duplicate epistasis for milling percent and kernel length, therefore, in addition to the main genetic effects, ([d], [h] components), for development of a variety / hybrid from the cross (RP-Bio-5478-185 x NH-686), the interaction components also have to be taken into consideration in breeding. Selection was recommended for head rice recovery improvement, for two crosses viz., MTU 1010 x NH-686, WGL-32100 x RP-Bio-5478-166, due to presence of fixable genetic variation. The interaction components are highly variable, therefore, a cross and trait specific breeding strategy is required for quality improvement in three crosses.

**Key words:** Additive gene effects, Epistasis, Generation mean analysis, Quality traits, Rice.

## INTRODUCTION

The precise knowledge of the nature of gene action for quality traits helps to choose an effective breeding strategy to accelerate the pace of genetic improvement of quality traits in rice. Most of the reports for gene action in rice are based on the diallel mating which does not provide information regarding non-allelic gene actions. The non-allelic gene actions could inflate the measures of additive and dominance components. Estimation of gene effects based on generation mean analysis provides requisite information to formulate the breeding strategy. Thus, generation mean analysis is a useful technique in plant breeding for estimating main gene effects (additive and dominance) and their digenic (additive x additive, additive x dominance and dominance x dominance) interactions responsible for inheritance of quantitative traits. It helps us in understanding the performance of the parents used in crosses and potential of crosses to be used either for heterosis exploitation or pedigree selection. Considering the fact that grain yield and quality of rice are the most important complex traits and that their improvement is the most frequent goal of rice breeding programs. Keeping this aspect in view, the present investigation was undertaken to study the gene action for grain quality characters.

## MATERIALS AND METHODS

Five rice genotypes viz. MTU 1010, WGL-32100, RP-Bio-5478-185, NH-686 and RP-Bio-5478-166 were selected based on contrasting characters viz., kernel dimensions (long slender and short bold; medium slender x short bold), flowering duration (early and long; long and early duration) and developed material ( $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) for 3 independent crosses to study the presence of non allelic interactions through generation mean analysis for grain yield (Parents: MTU 1010- 24.00g, NH-686 – 19.20g, WGL-32100 – 20.77g, RP-Bio-5478-166 – 14.63g and RP-Bio-5478 -

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185 – 15.76g. Crosses: MTU 1010 X NH – 686 – 28.96g, WGL-32100 X RP-Bio-5478-166 – 24.23g and RP-Bio-5478 -185 X NH-686 – 28.15g) and its attributing characteristics.

1. MTU 1010 X NH - 686

2. WGL-32100 X RP-Bio-5478-166

3. RP-Bio-5478 - 185 X NH-686

Variation for kernel dimensions (long slender x short bold (cross 1), medium slender x short bold (cross 2) and short bold x short bold (cross 3) and flowering duration was considered as criteria for selection of parents for generation mean analysis. The entire work (crossing and evaluation) taken up at Regional Agricultural Research Station, (RARS), Warangal, PJTSAU.

During *Kharif*, 2014 crossing programme has been taken up to get  $F_1$  seed from these three crosses. During *Rabi* 2014-15, raising  $F_1$ 's to get  $F_2$  seed and simultaneous

crossing of these  $F_1$ 's with their respective parents to get  $BC_1$  and  $BC_2$  seed of three crosses. Parents were also selfed to ensure 100% genetic purity. Thus, seed of six basic generations,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  was in hand for these three crosses at the end of the season *Rabi* 2014-15. During *Kharif*, 2015  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  of 3 crosses were raised to study the generation mean analysis. The material was sown in randomized block design with three replications. Recommended cultural practices were adopted. The total number of population raised in each replication was 30 for parents and  $F_1$ , 60 for back cross generations and 300 for  $F_2$ .

Adequacy of additive – dominance model was tested by using A, B, C, D scales of Mather (1949) and also further confirmed by the Joint scaling test of Cavalli (1952). Genetic components of quality traits estimated through Joint scale test presented in Table 1 as the Joint scaling test is a comprehensive test of simple additive - dominance model replacing A, B, C, D scaling test and involves weighted regression analysis. A sequential method was followed to identify the best fit model in which the all the possible components would be significant and at the same time the  $\chi^2$  test value becomes non significant. Major advantage of this test is that we can delete a non significant component in the sequential process and estimate the remaining significant components with maximum likelihood precisions. Initially we tried a model with just 'm' first, if this adequately explained the variations in the trait, there was no need to proceed further to estimate any other genetical parameters, otherwise next higher parameters like d, h etc., were introduced until  $\chi^2$  test value become non significant (Kearsey and Ponni, 1996). In the present study, fortunately at least one component out of six was non significant, having at least one degrees of freedom to facilitate the  $\chi^2$  test. This procedure was adopted for three crosses uniformly and estimated the possible parameters by weighted least square method and discussed thoroughly.

## RESULTS AND DISCUSSION

In expression of hulling percentage, no non allelic interactions were noticed which is evident from fitting of simple additive – dominance model in all the crosses uniformly. Besides the 'm' values, only the additive [d] genetic component was found to be highly significant. However, Subbalaxmi *et al.* (2016) reported the importance of both additive and non additive gene actions for improvement of this trait. Because, in the present study, the expression of this trait is solely under the influence additive gene effects, a simple pedigree method would be highly effective for further improvement of this character. For milling trait, among the components estimated, the 'm' was found to be highly significant in the crosses evaluated. The analysis of gene effects in two crosses indicated the presence of interaction effects in two crosses whereas, a simple additive – dominance model was fitted for the first cross, (MTU 1010 x NH-686). The additive gene effects [d] was noticed to be significant in the cross MTU 1010 x NH-686, whereas the dominant gene [h] component effect was prevalent with

respect to the cross contribution, RP-Bio-5478-185 x NH-686. In view of presence of fixable variation ([d] and [i] components) in two crosses (MTU-1010 x NH-686, WGL-320100 x RP-Bio-5478-166), substantial improvement for milling recovery is expected by following conventional breeding procedures (Subbalaxmi *et al.*, 2016). With respect to interaction effect, this trait was influenced by duplicate type of epistasis in the cross RP-Bio-5478-185 x NH-686. Existence of negative dominance gene effects coupled with duplicate epistasis may offer little scope for development of superior hybrid combinations and the only choice is postponing the selection to recover the superior homozygous lines until the population attains the much of the homozygosity. Subbalaxmi *et al.* (2016) also revealed the presence of duplicate epistasis as in the case of present study.

Among the milling characters, a trait head rice recovery is considered as most important one, because, the acceptance of any variety by the traders and millers highly depends on this quantitative trait. The present study revealed that the inheritance of head rice recovery is under the governance of both additive and dominance effects, which are evident from fitting of the simple 2 parameter additive – dominance model in two out of three crosses. It appears that further improvement of this character would be quite easy and straight forward in view of prevalence of fixable additive genetic effects in two crosses viz., MTU 1010 x NH-686 and WGL-320100 x RP-Bio-5478-166. However, Gnanamalar and Vivekanandhan (2013) emphasized the importance of both additive and non additive genetic variations, as pointed in the present study. Only in one cross (MTU 1010 x NH-686) interaction effect was noticed which was of duplicate type. Gnanamalar and Vivekanandhan (2013) noticed that the presence of both duplicate and complementary digenic interactions in contrary to the present findings.

For kernel length, a simple additive – dominance model was sufficient to explain the genetic variation with respect to the cross, MTU-1010 x NH-686 as only 'm', [d] and [h] components were significant with insignificant  $\chi^2$  test value. Whereas, in the remaining two crosses digenic interaction 4 and 5 parameter models were fitted. In all the three crosses both additive and dominance genetic effects were observed to be important in view of the significance on positive side, which is in agreement with the earlier findings of Sateesh kumar *et al.* (2017). Besides the presence of duplicate type of epistasis in two crosses, the [j] type (additive x dominance) was also observed to be significant in one cross. Though the dominance effects are significant, owing to the prevalence of duplicate epistasis, it may become a limitation for development of promising heterotic hybrids due to mutual cancellations of positive and negative effects. Sateesh Kumar *et al.* (2017) and Anil kumar and Mani (2010), Mahalingam and Nadarajan (2010) reported preponderance of both duplicate and complementary epistasis suggesting postponement selections to later generations in case of complementary type in certain crosses. In this study, it was known that in addition to main additive and dominance effects, the digenic interaction

**Table 1:** Genetic components of grain yield and grain quality traits estimated through Joint scale test.

Cross	Genetic components	Character	Hulling (%)	Milling per cent (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)
MTU 1010 x NH-686	$\chi^2$ value/probability Model fitted Type of epistasis WGL-32100 x RP-Bio-5478-166	m	76.69** $\pm$ 0.48	68.52** $\pm$ 0.62	54.13** $\pm$ 0.35	5.47** $\pm$ 0.02	2.10 ** $\pm$ 0.047
		[d]	1.68** $\pm$ 0.64	1.82** $\pm$ 0.68	1.19** $\pm$ 0.33	0.75** $\pm$ 0.02	-0.18** $\pm$ 0.045
		[h]	-	-	-9.34** $\pm$ 2.14	0.97** $\pm$ 0.11	-0.22 ** $\pm$ 0.085
		[i]	-	-	-	-	-
		[j]	-	-	-	-	-
		[l]	-	-	9.85** $\pm$ 2.63	-	-
			2.217/ (0.697) NS 2 parameter	1.470/ (0.832) NS 2 parameter	0.05/ (0.97) NS 4 parameter duplicate	3.88/ (0.274) NS 3 parameter	4.93/ (0.176) NS 3 parameter
$\chi^2$ value/probability Model fitted Type of epistasis RP-Bio-5478 -185 x NH-686	$\chi^2$ value/probability Model fitted Type of epistasis RP-Bio-5478 -185 x NH-686	m	76.40** $\pm$ 0.34	64.08** $\pm$ 1.29	52.54** $\pm$ 0.32	5.099** $\pm$ 0.046	2.03** $\pm$ 0.01
		[d]	2.05** $\pm$ 0.61	-	1.48** $\pm$ 0.47	0.36** $\pm$ 0.045	0.04* $\pm$ 0.02
		[h]	-	-	-	1.11** $\pm$ 0.20	-
		[i]	-	6.45** $\pm$ 1.66	-	-	-
		[j]	-	10.33** $\pm$ 2.34	-	-	-
		[l]	-	5.35** $\pm$ 2.26	-	-0.96** $\pm$ 0.20	-
			4.784/ (0.310) NS 2 parameter	3.568/ (0.168) NS 4 parameter	4.890/ (0.299) NS 2 parameter	2.136/ (0.344) NS 4 parameter duplicate	0.825/ (0.935) 2 parameter
$\chi^2$ value/probability Model fitted Type of epistasis	$\chi^2$ value/probability Model fitted Type of epistasis	m	74.64** $\pm$ 0.26	70.29** $\pm$ 0.55	51.07** $\pm$ 0.44	3.28** $\pm$ 0.27	1.99** $\pm$ 0.036
		[d]	1.65** $\pm$ 0.45	-	-	-	-
		[h]	-	-11.63** $\pm$ 2.37	1.68** $\pm$ 0.62	2.69** $\pm$ 0.70	-
		[i]	-	-	-	1.00** $\pm$ 0.26	-
		[j]	-	-	-	0.46* $\pm$ 0.18	-
		[l]	-	11.15** $\pm$ 2.45	-	-1.82** $\pm$ 0.47	-
			6.665 (0.155) NS 2 parameter	1.531 (0.675) NS 3 parameter duplicate	3.371/ (0.498) 2 parameter	4.544/ (0.033) NS 5 parameter duplicate	4.595/ (0.467) NS 1 parameter

Table 1 Continue...

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Cross		Genetic components		Character		
MTU 1010 x NH-686	$\chi^2$ value/probability Model fitted Type of epistasis WGL-32100 x RP-Bio-5478-166	Kernel L/B Ratio (mm)		Volume expansion ratio	Kernel elongation ratio	Gelatinization temperature
		m	2.70** ± 0.06	3.96** ± 0.07	1.65** ± 0.02	79.29** ± 0.40
		[d]	0.52* ± 0.004	0.91** ± 0.07	0.08** ± 0.02	2.22** ± 0.39
		[h]	-	-2.52** ± 0.34	0.16** ± 0.03	2.45** ± 0.71
		[i]	-	-	-	-
		[j]	1.52* ± 0.40	-	-	-
		[l]	0.82* ± 0.15	3.84** ± 0.34	-	-
		0.169/ (0.919) NS	0.304/ (0.859) NS	0.919/ (0.821) NS	4.652/ (0.199) NS	
		4 parameter	3 parameter	3 parameter	3 parameter	
		-	duplicate	-	-	
RP-Bio-5478 -185 x NH-686	$\chi^2$ value/probability Model fitted Type of epistasis RP-Bio-5478 -185 x NH-686	m	1.90** ± 0.24	3.66** ± 0.054	1.68** ± 0.01	71.60** ± 0.18
		[d]	0.14** ± 0.04	0.82** ± 0.054	0.17** ± 0.016	-1.10** ± 0.22
		[h]	1.77** ± 0.62	0.72** ± 0.12	-	-
		[i]	0.57* ± 0.23	-	-	-
		[j]	-	-	-	-
		[l]	-1.04** ± 0.40	-	-	-
		0.637/ (0.425) NS	3.620/ (0.306) NS	7.730/ (0.102) NS	4.315/ (0.365) NS	
		5 parameter	3 parameter	2 parameter	2 parameter	
		duplicate	-	-	-	
		2.15** <sup>iii</sup> 0.033	2.94** ± 0.06	1.37** ± 0.02	71.24** ± 0.15	
RP-Bio-5478 -185 x NH-686	$\chi^2$ value/probability Model fitted Type of epistasis RP-Bio-5478 -185 x NH-686	[d]	-	-	0.12** ± 0.04	-
		[h]	-	-	-	-
		[i]	-	-	-	-
		[j]	-	-0.54* ± 0.25	-	-
		[l]	-	0.97** ± 0.11	-	-
		6.601/ (0.252) NS	1.007/ (0.799) NS	5.198/ (0.268) NS	5.157/ (0.397) NS	
		1 parameter	3 parameter	2 parameter	1 parameter	
		-	-	-	-	
		-	-	-	-	
		-	-	-	-	

\*\*Significant at 1% level, \*Significant at 5% level.

effects have to be taken in to consideration while handling the segregating generations and doing selections. As both [d] and [h] components are equally important in these crosses, adopting recurrent selection and biparental matings in early segregating generations and selections in later generations would be the appropriate approach. In the process of sequential method, insignificant value of  $\chi^2$  test indicated fitting of simple additive - dominance model in all three crosses for kernel breadth. In none of the crosses, the interaction effects were significant. As slenderness is desirable, the accumulation of dominant genes acting towards negative side would be more useful. In this line, one superior cross (MTU 1010 x NH-686) was identified for further exploitation.

For kernel length/breadth ratio, in all the crosses, the estimated of 'm' was highly significant and there observed to be lot of variation in the number of significant components. Four and five components were significant in crosses MTU 1010 x NH-686 and WGL-32100 x RP-Bio-5478-166 respectively. Whereas, in the cross (RP-Bio-5478-185 x NH-686), the model was terminated with significance of only 'm'. The additive effects were predominant in first cross (MTU 1010 x NH-686), whereas, in the second cross (WGL-32100 x RP-Bio-5478-166), both [d] and [h] were highly significant. In addition, [j] type of interaction effect was also observed in the first cross. In the second cross (WGL-32100 x RP-Bio-5478-166) although, the [h] component was highly significant, the overall non additive effects were reduced in view of [l] component on negative side. For improvement of L/B ratio, simple pedigree method in first cross and intermating in early segregations followed by selections in second cross would be most the prospective method. Governance of duplicate epistasis in expression of this quantitative trait was also noticed by Sateesh Kumar *et al.* (2017), Gnanamalar and Vivekanandhan (2013).

This important cooking quality *i.e* volume expansion ratio was governed by only additive and dominance effects in two crosses, where as significance of additive x dominance [j], dominance x dominance [l] type of interactions were noticed in the third cross *viz.*, RP-Bio-5478 -185 x NH-686. The estimates of [d] and [h] components are highly significant in two crosses *viz.*, MTU 1010 x NH-686 and WGL-32100 x RP-Bio-5478 -166. However, the [h] type was found to be towards negative side in the first cross. It is interesting to note that only interaction components [j] and [l] type were found to be highly significant in third cross besides 'm'. The results indicated that both additive and non additive type of gene actions governed the inheritance of volume expansion ratio. Gnanamalar and Vivekanandhan (2013), however, noticed a predominant role of non additive gene action in expression of this cooking quality trait.

The analysis of genetic variation clearly pointed out that the important property of kernel elongation after cooking in rice was just influenced by additive and dominance [h] gene effects without any non allelic interactions. A simple additive-dominance model was observed to be sufficient to explain the genetic variation. Only in one cross (MTU 1010 x NH-686), the value of [h] was found to be significant. Prevalence of strong additive gene effects as indicated by highly significant estimates [d] component in all the crosses

expanded a wider scope for development of superior homozygous lines having excellent kernel elongation ratio through simple selection in segregating generations. Mohan and Ganeshan (2003) reported additive and dominant gene effects, but in negative side, besides influence of [i], [j] and [l] type of interactions for kernel elongation. Anil kumar and Mani (2010) revealed the importance of non allelic interactions for this quantitative trait and reported prevalence of both duplicate and complementary epistasis.

Gelatinization temperature in rice is an indicative of cooking temperature at which the starch granules swell irreversibly. Normally rice grains which are hard in nature require higher cooking temperature and energy, thus an optimum temperature in the range of 70-75°C is highly desirable. The joint scaling test confirmed that only the additive and dominance gene effects controlled this cooking property as evidenced from fitting of 3, 2 and 1 parameter models in first, second and third crosses respectively. Whereas, the research results of Gnanamalar and Vivekanandhan (2013) revealed the existence of all the three types of interactions in expression of this trait. Keeping in view the [d] type of genetic effects in negative side in second cross (WGL-32100 x RP-Bio-5478-166) and also the significance of only 'm' in third cross (RP-Bio-5478 -185 x NH-686), among the three, only one cross *viz.*, MTU 1010 x NH-686 was identified as better one. The methods which effectively utilize both additive and non additive genetic variation like recurrent selection would be advocated to obtain better homozygous lines in later generations.

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