Research Article

Studies on genetic control of quality traits in rice (*oryza sativa* L.) using six parameter model of generation mean analysis

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Abstract
Analysis of generation means in P_1, P_2, F_1, F_2, B_1 and B_2 generations of the two rice crosses MTU 1075/ MTU 3626 and MTU 1121/ TN 1 was performed to determine the nature of gene action governing 11 quality traits *viz.*, kernel length, kernel breadth, L/B ratio, hulling percentage, milling percentage, head rice recovery, kernel elongation ratio, volume expansion ratio, alkali spreading value, gel consistency and amylose content. All the traits studied showed non allelic gene interaction indicating presence of epistatic gene action. Nature of gene action varied with the character and both additive and non-additive gene action was involved in expression of the characters having the duplicate type of epistasis. The traits were predominantly governed by dominance and dominance x dominance interaction effects and favors heterosis breeding for improvement.

Introduction

Rice is the staple food for over half of the world population and it is ranked as the number one human food crop in world. More than 90% world rice is grown and consumed in Asia (Tyagi *et al.,* 2004), where as 60% calories are consumed by 3 billion Asians. India is the second most populous nation, stands first in areas, second in production followed and preceded by China. Rice occupies a pivotal place in Indian food and livelihood security system. This study is focused on the improvement of quality traits and to elucidate the gene action associated with various quality attributes through generation mean analysis. Besides the yield and yield components quality parameters also gaining importance in development of new high yielding cultivars in rice. Quality characters can be classified as physical, cooking and chemical traits. Physical properties such as grain dimensions (kernel length, kernel breadth and L/B ratio) and milling traits (hulling %, milling % and head rice recovery) are major factors defining market value. Physical properties also include yield of edible and marketable polished grain, uniform shape, whiteness and translucence. These traits are immediately obvious to consumers and so are major factors defining market value. The traits that exert major effects on the eating and cooking qualities are related to the chemical properties of rice grains such as amylose content, alkali spreading value and gel consistency and cooking characteristics volume expansion ratio and kernel elongation ratio. Hence there is an imperative need for a shift in emphasis towards development of high quality rice besides yield. Information concerning the nature of gene action on complex traits would be a valuable tool for breeding high-yielding cultivars with good quality. In addition, an attempt has been made to estimate various kinds of gene effects through standard biometrical and statistical procedures. Quantitative traits of economic importance are governed by complex interaction mechanisms. Genetics of such traits and knowledge on interactions would help to develop a suitable breeding strategy.

Materials and methods

The present research work was conducted during *kharif and rabi* 2012-2013 and *kharif* and *rabi* 2013-2014 at APRRI & RARS, Maruteru, West Godavari District, in Godawari Zone of Andhra Pradesh.

*Crossing programme:*The crossing programme included (i) effecting crosses between divergent parents for all quality traits, to generate F_1 s and (ii) raising F_1 s to develop F_2 and backcross populations (B_1 and B_2) and (iii) evaluation of six generation materials (parents, F_1, F_2, B_1 and B_2) for physical, cooking and chemical quality attributes. During *rabi* 2014, six generations (P_1, P_2, F_1, F_2, B_1 and B_2 of the two promising crosses MTU 1075/ MTU 3626 and MTU 1121/ TN 1 were evaluated and observations were recorded for physical quality (kernel length, kernel breadth, L/B ratio, hulling %, milling % and head rice recovery), cooking traits (volume expansion ratio and kernel elongation ratio) and chemical (alkali spreading value, gel consistency and amylose content). The performance of genotypes was assessed and behaviour of the introgressed genes governing quality traits were quantified and analysed through generation mean analysis. Kernel length and breadth were calculated using dial micrometer, volume expansion ratio was determined as formula suggested by Verghese

(1950), kernel elongation ratio was worked out following standard method of Verghese (1950) as modified by Murthy (1965), Alkali spreading value and gel consistency was estimated as per procedure of Jennings *et al* (1979) and amylose content was determined by using a simple procedure suggested by Juliano (1971).

The generation mean analysis was performed according to Hayman (1958) and Jinks and Jones (1958) for the estimation of genetic components of variation, epistasis model and gene effects in two steps (i) testing for epistasis to determine the presence or absence of interallelic interaction and (ii) estimation of gene effects and the type of epistasis involved.

Results and discussion
Results of individual scaling tests *i.e.,* A, B and C scaling tests were presented in Table 1. The calculated values of all the three scaling tests were found significant for kernel breadth, L/B ratio, milling percentage, head rice recovery, kernel elongation ratio, volume expansion ratio and amylose content, while remaining characters hulling percentage, alkali spreading value and gel consistency had shown significance of two out of three scaling tests performed except kernel length which had shown significance for one scaling test in the cross MTU 1075/ MTU 3626. In the cross MTU 1121/ TN 1 all the three scaling tests were significant for kernel length, L/B ratio, head rice recovery and kernel elongation ratio, while remaining characters milling percentage, volume expansion ratio, alkali spreading value and gel consistency had shown significance of two out of three scaling tests performed except kernel breadth, hulling percentage and amylose content which had shown significance for one scaling test. Hence, epistasis contributed significantly towards the inheritance of these characters of the respective crosses.

The results of main gene effects *i.e.*, additive [d] and dominance [h] effects and interaction effects *i.e.,* additive x additive [i], dominance x dominance [j] and additive x dominance [l] effects were presented in Table 2. Study of gene effects revealed that both additive [d] and dominance [h] genetic effects had significant contributions for the expression of majority of the characters.

Additive [d] gene effect was more important in L/B ratio, kernel elongation ratio, gel consistency and amylose content in the cross MTU 1075/ MTU 3626 because of the highest magnitude for the additive gene effect. Positive and significant additive x additive [i] interaction effects were found for the characters hulling percentage, milling percentage, head rice recovery and alkali spreading value in both the crosses and for the characters L/B ratio and volume expansion ratio in the cross MTU

1075/ MTU 3626 and for the character amylose content in the cross MTU 1121/ TN 1. These additive and additive x additive gene effects would be fixable in later generations. Hence, these traits in respective crosses offer scope for improvement through phenotypic selection based on pedigree method.

Dominance [h] gene effect was more important than the additive gene effect [d] in the inheritance of kernel length, hulling percentage, milling percentage, head rice recovery and alkali spreading value in both the crosses. Dominance [h] gene effect was significant for L/B ratio, kernel elongation ratio and amylose content in MTU 1121/ TN 1 and for the character volume expansion ratio in MTU 1075/ MTU 3626. Development of hybrids in the above mentioned cases would be a useful proposition provided hybrid seed production is relatively simple and economically viable.

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

Dominane x dominance [l] gene effects were significant and greater in magnitude than both the main effects *i.e* additive [d] and dominance [h] gene effects for the traits, kernel elongation ratio and amylose content in the cross MTU 1075/ MTU 3626 and the type of epistasis was duplicate as the signs of dominanance [h] gene effects and dominance x dominance [l] interaction effects were opposite in sign. Duplicate epistasis was also found for the characters hulling percentage, alkali spreading value and amylose content in the cross MTU 1121/ TN 1. This type of epistasis tends to cancel or weaken the effect of each other in hybrid combination and hinder the progress made under selection and therefore, selection would have to be deferred till later generations of segregation where dominance effects are dissipated. Bi parental mating and recurrent selection especially reciprocal recurrent selection to break undesirable linkages followed by isolation of purelines in advanced generations would be more appropriate strategy as compared to pedigree method alone. Duplicate epistasis was reported by Mahalingamand Nadarajan (2010) for hulling percentage, Nayak (2007) for kernel elongation ratio and amylose content, Tomar and Nanda (1985) for alkali spreading value.

Significant additive x additive [i] type of interaction was found besides duplicate epistasis in case of hulling percentage and alkali spreading value in both the crosses and for amylose content in the cross MTU 1121/ TN 1. Gnanamalar and Vivekanandan (2013) reported the same results for alkali spreading value. Significance of [i] and [l]

besides duplicate epistasis revealing the scope of recovering plants showing transgressive effect. Complementary epistasis was found for the character head rice recovery in both the crosses.

Thus, both additive and nonadditive gene effects were important for inheritance of almost all the characters studied. The use of population improvement concept may become an amenable solution in highly autogamous crop like rice. Biparental mating, recurrent selection and diallel selective mating system might be profitable in exploiting both additive and nonadditive gene action to obtain desirable recombinants for different quality characters.

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Table 1.Scaling tests for eleven quality traits in two crosses of rice (*oryza sativa* L.)

Character	Cross combination	A	B	C
Kernel length(mm)	MTU 1075/MTU 3626	-0.069±0.090	-0.041±0.100	-0.425[**]±0.151
	MTU 1121/TN 1	-0.199[**]±0.074	-0.163[*]±0.068	-0.718[**]±0.126
Kernel breadth(mm)	MTU 1075/MTU 3626	-0.274[**]±0.050	-0.615[**]±0.070	-0.776[**]±0.080
	MTU 1121/TN 1	-0.015±0.043	0.107[*]±0.050	0.119±0.074
L/B ratio(mm)	MTU 1075/MTU 3626	0.302[**]±0.076	0.725[**]±0.092	0.671[**]±0.108
	MTU 1121/TN 1	-0.409[**]±0.068	-0.258[**]±0.059	-0.575[**]±0.098
Hulling percentage	MTU 1075/MTU 3626	1.507±2.306	-2.820[*]±1.395	-16.840[**]±2.653
	MTU 1121/TN 1	-0.194±1.300	-1.214±1.405	-13.432[**]±2.545
Milling per centage	MTU 1075/MTU 3626	-4.879[*]±1.973	-4.088[*]±1.926	-25.482[**]±2.715
	MTU 1121/TN 1	-4.122±2.233	-14.889[**]±1.322	-26.573[**]±3.109
Head rice recovery	MTU 1075/MTU 3626	-15.318[**]±2.073	-12.237[**]±1.822	-34.985[**]±2.880
	MTU 1121/TN 1	-12.645[**]±2.061	-24.168[**]±1.467	-49.965[**]±2.814
Kernel elongation ratio	MTU 1075/MTU 3626	-0.122[**]±0.036	-0.142[**]±0.036	-0.170[**]±0.045
	MTU 1121/TN 1	0.130[*]±0.057	-0.501[**]±0.042	-0.652[**]±0.077
Volume expansion ratio	MTU 1075/MTU 3626	1.478[**]±0.145	1.784[**]±0.149	2.027[**]±0.232
	MTU 1121/TN 1	-0.200±0.253	0.948[**]±0.143	2.342[**]±0.315
Alkali spreading value	MTU 1075/MTU 3626	1.818[**]±0.158	-0.476[*]±0.226	-0.247±0.428
	MTU 1121/TN 1	0.375±0.323	1.068[**]±0.231	-1.508[**]±0.431
Gel consistency(mm)	MTU 1075/MTU 3626	-22.938[**]±3.518	-4.312±2.298	-23.830[**]±3.490
	MTU 1121/TN 1	-13.075[**]±3.446	-24.500[**]±3.531	-32.500[**]±5.163
Amylose content(%)	MTU 1075/MTU 3626	-2.575[**]±0.474	-3.988[**]±0.408	-4.785[**]±0.703
	MTU 1121/TN 1	0.180±0.589	0.203±0.337	-4.980[**]±0.836

Table 2.Estimates of gene effetcs for eleven quality traits in two crosses of rice (*oryza sativa* L.)

Cross combination	m	d	h	i	j	l
			kernel length (mm)			
MTU 1075/ MTU 3626	5.678**±0.022	0.038±0.043	0.352*±0.137	0.315*±0.122	-0.014±0.058	-0.206±0.228
MTU 1121/TN 1	5.471**±0.023	0.340**±0.034	0.659**±0.122	0.355**±0.114	-0.018±0.045	0.008±0.186
			Kernel breadth (mm)			
MTU 1075/ MTU 3626	2.105**±0.012	-0.126**±0.035	0.076±0.090	-0.113±0.084	0.170±0.039	1.002**±0.160
MTU 1121/TN 1	2.233**±0.011	-0.299**±0.022	-0.339**±0.069	-0.027±0.061	-0.061±0.027	-0.066±0.116
			L/B ratio (mm)			
MTU 1075/ MTU 3626	2.715**±0.019	0.170**±0.051	0.113±0.134	0.356*±0.128	-0.211±0.056	-1.384**±0.232
MTU 1121/TN 1	2.461**±0.016	0.315**±0.035	0.375**±0.102	-0.091±0.095	-0.076±0.038	0.758**±0.172
			Hulling percentage			
MTU 1075/ MTU 3626	76.874**±0.478	2.911**±1.072	17.268**±3.017	15.527**±2.873	2.163±1.280	-14.215**±5.041
MTU 1121/TN 1	78.430**±0.583	2.558**±0.706	12.494**±2.773	12.025*±2.725	0.510±0.795	-10.617**±3.802
			Milling per centage			
MTU 1075/ MTU 3626	65.137**±0.511	1.160*±1.146	19.740**±3.199	16.515**±3.072	-0.396±1.300	-7.548±5.329
MTU 1121/TN 1	66.102**±0.580	5.851**±0.807	11.828**±3.011	7.562**±2.828	5.383±1.283	11.450*±4.483
			Head rice recovery			
MTU 1075/ MTU 3626	54.866**±0.544	0.662±1.107	8.224*±3.244	7.430*±3.104	-1.541±1.302	20.126**±5.281
MTU 1121/TN 1	54.312**±0.557	6.637**±0.936	17.890**±3.033	13.152**±2.909	5.762±1.258	23.661**±4.683
			Kernel elongation ratio			
MTU 1075/ MTU 3626	1.667**±0.003	0.084**±0.016	-0.227**±0.041	-0.094**±0.034	0.010±0.023	0.358**±0.079
MTU 1121/TN 1	1.589**±0.007	0.163**±0.018	0.426**±0.057	0.280**±0.045	0.315±0.030	0.092±0.104
			Volume expansion ratio			
MTU 1075/ MTU 3626	4.578**±0.026	-0.122±0.066	1.315**±0.197	1.236**±0.167	-0.153±0.080	-4.499**±0.351
MTU 1121/TN 1	5.228**±0.043	-0.044±0.073	-0.569*±0.262	-1.594**±0.226	-0.574±0.140	0.846±0.430
			Alkali spreading value			
MTU 1075/ MTU 3626	4.209**±0.101	0.672**±0.125	1.321**±0.480	1.589**±0.475	1.147±0.133	-2.931**±0.658
MTU 1121/TN 1	3.858**±0.077	-0.946**±0.152	3.041**±0.459	2.951**±0.434	-0.346±0.182	-4.394**±0.746
			Gel consistency(mm)			
MTU 1075/ MTU 3626	53.393**±0.558	5.487**±1.736	4.480±4.340	-3.420±4.127	-9.313±2.004	30.670**±7.772
MTU 1121/TN 1	54.313**±0.772	3.237±1.864	-1.950±5.266	-5.075±4.842	5.712±2.102	42.650*±9.070
			Amylose content(%)			
MTU 1075/ MTU 3626	22.834**±0.123	0.661**±0.213	-1.727*±0.697	-1.778**±0.651	0.706±0.295	8.341**±1.103
MTU 1121/TN 1	22.531**±0.124	-0.867**±0.163	5.701**±0.681	5.363**±0.592	-0.012±0.300	-5.746**±1.060

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