Genetic analysis of yield and quality traits through generation mean analysis in rice

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ABSTRACT

The present investigation in rice (Oryza sativa L.) was undertaken to study the magnitude of gene action in two cross combinations for eleven yield and twelve quality traits deploying generation mean analysis following six parameter model for parents (P_1 and P_2), F_1 , F_2 , BC_1 and BC_2 generations during three crop seasons. The results of the scaling tests revealed that the additive-dominance model was inadequate for all of the characters evaluated in both the crosses suggested the existence of epistasis in the inheritance of these characters. Mean values of both the crosses revealed significant for most of the traits except effective bearing tillers per plant, SCMR, harvest index, kernel length and kernel L/B ratio in the cross BPT 5204 x IR 64. Major contribution of duplicate epistasis was revealed by the two crosses, for most of the characters. Few traits revealed complementary epistasis in both the crosses. The present study demonstrates the importance of additive, dominance and epistatic gene effects for the inheritance of almost all the yield as well as quality characters studied.

Key words: Gene action, generation mean analysis, rice, yield and quality traits

INTRODUCTION

Rice, a major staple food crop feeds more than half of the world's population and employs millions of people. Globally rice crop is planted in about 160 mha. Area with a production of 493 mt of milled rice. In India rice plays a major role in diet, economy, employment, culture and history. It is the staple food for more than 65% of the Indian population contributing about 40% of the total food grain production, thus playing a pivotal role in the food and livelihood security of the people. At the estimated population in India is 13.8 billion and the estimated rice production should be around 135-140 million tons by 2020. Thus takes a quite challenging and the options available are very limited in view of plateauing trend of yield in high productivity areas and to address various challenges like decreasing and degrading land and scarcity of labour and land. Hence, there is an urgent need to develop rice technologies that will result in higher yield. The choice of an effective rice breeding approach to select for a particular characteristic depends substantially on the knowledge of the gene genetic system contributing the characters. Genetic improvement depends primarily on the effectiveness of selection among the progenies that differ in genetic value. The additive, dominance effects and their interactions are known as gene actions and are closely associated with the breeding value.

Generation mean analysis is used to estimate the gene actions controlling the quantitative traits and determining the components contributes to a better understanding of the action of genes involved in the expression of the characters. Hence, the present study was formulated to study the additive, dominant effects and also its interaction effects for yield and cooking quality traits in rice to study the inheritance of traits

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and the nature of the epistatic gene effects.

MATERIAL AND METHODS

The experiment was conducted at Agricultural Research Station, Nellore, Andhra Pradesh from 2014-2017 rabi season. Geographically, the research farm was located at 14º27' N latitude and 79º59' E longitudes, at an elevation of 20 m above mean sea level. The experimental material comprised of 4 parents viz., RNR 2465, NLR 145, BPT 5204 and IR 64. By using these four parents two different crosses were made viz., RNR 2465 x NLR 145 and BPT 5204 x IR 64. Six generations viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of the above crosses were made and used to study the genetic analysis of quantitative and qualitative traits. The material was planted with a spacing of 20 x 15 cm and all the recommended agronomic practices were followed to raise a good crop. Observations were recorded on five randomly selected plants in each P₁, P_2 and F_1 , 10 plants each in BC_1 and BC_2 , 20 plants in F₂ generation for different yield and qualitative traits viz., days to 50% flowering, days to maturity, plant height, panicle length, effective bearing tillers per plant, number of filled grains per panicle, number of unfilled grain per panicle, test weight, SCMR, harvest index, grain yield per plant, kernal length, kernel breadth, kernel L/B ratio, hulling %, milling %, head rice recovery, water uptake, volume expansion ratio, kernel elongation ratio, alkali spreading value, gel consistency and amylose content. The mean values was computed for all the six generations for each cross. The generation mean analysis was carried out following the methodology of Hayman (1958) using six generations to estimate the gene effects viz., mean (m), Additive effect (d), dominance effect (h), additive x additive (dxd), dominance x dominance (hxh) and additive x dominance (dxh) interaction effect.

RESULTS AND DISCUSSION

Mean performance of the six generations *viz.*, P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 for all the characters studied in two crosses are presented in 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 significant for most of the characters studied in the two crosses. Similar results were reported by Jhansi et

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al. (2015) and Prabhu et al. (2017). The average performance of the six generations of both the crosses shown existence of sustainable variability in the population for all the 23 characters studied.

In this study F_1 shows better performance than both the parents for the traits *viz.*, effective bearing tillers per plant, number of filled grains per plant, SCMR, grain yield in both the crosses studied. Superiority of F_1 was observed for head rice recovery, volume expansion ratio in the cross RNR 2465 x NLR 145 while, harvest index, kernel L/B ratio, hulling%, water uptake and kernel elongation ratio in the cross BPT 5204 x IR 64 indicating that the presence of dominant gene effects in hybrids of the two crosses. The F_1 s with average performance over the two parents of that particular cross represented the presence of a trial dominance.

The performance of the F_2 declined for the characters *viz.*, ear bearing tillers per plant, number of filled grains per panicle, harvest index, SCMR, Grain yield per plant, head rice recovery, kernel elongation ratio, gel consistency and alkali spreading value in both the crosses studied indicating the presence of dominance and epistatic interactions in both the crosses. BC₁ performed better than the BC₂ in both the crosses for filled grains per panicle, hulling % and alkali spreading value whereas, for harvest index both the crosses showed more or less similar value of BC₁ and BC₂.

The results of scaling tests *i.e.*, A, B, C and D (Table 2) revealed that the calculated values of at least any one of the scaling tests found significant for almost all the characters studied in both the crosses indicating the presence of non-allelic gene interactions. The estimated value of various types of gene effects and interaction effects governing the traits viz., d (additive), h (dominance), i (additive x additive), l (dominance x dominance) and j (additive x dominance) are presented in the Table 2. In both the crosses for most of the traits, the additive x dominance (j) interaction effect was nonsignificant in nature. These results indicated that high degree of inbreeding depression for most of the traits and revealed that predominant role of non additive gene action which includes both dominance as well as epistatic interactions.

A perusal of gene effects in generation mean analysis revealed the presence of significant proportion

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Table 1. Estimates of gene	eration means and sta	ndard errors for yield	and quality traits in sele	sted crosses.		
Cross	\mathbf{P}_1	\mathbf{P}_2	${ m F}_{_{ m I}}$	${ m F_2}$	BC_1	BC_2
			Days to 50% flowerin	8		
RNR 2465 x NLR 145 BPT 5204 x IR 64	97.000 ± 0.470 103.000 ± 0.594	102.450 ± 0.578 91.050 ± 0.387	92.550 <u>+</u> 0.659 94.050 <u>+</u> 0.352 Days to maturity	87.967 ± 0.562 108.483 ±0.307	99.025±0.555 92.500±0.611	94.925 ± 0.271 103.600 ±0.779
RNR 2465 x NLR 145 BPT 5204 x IR 64	128.950 ± 0.591 135.400 ± 0.659	134.650 ± 0.595 123.050 ± 0.478	124.550±0.705 124.550±0.515 Plant height (cm)	121.483 ± 0.646 144.017 ± 0.375	131.000 <u>+</u> 0.598 124.525 <u>+</u> 0.607	126.925 ± 0.396 135.925 ± 0.708
RNR 2465 x NLR 145 BPT 5204 x IR 64	77.95 <u>±</u> 0.531 73.110 <u>±</u> 0.321	79.200 ± 0.760 71.750 ± 0.602	68.250±0.655 72.039±0.597 Number of ear beari	98.633±1.409 95.200±0.866 g tillers per plant	80.300 ± 1.227 67.425 ± 1.432	75.300 ± 1.159 75.300 ± 1.240
RNR 2465 x NLR 145 BPT 5204 x IR 64	14.200 ± 0.427 12.200 ±0.468	$\frac{12.162\pm0.333}{11.560\pm0.421}$	20.585±0.534 17.800±0.964 Panicle length (cm)	$\frac{13.167\pm0.560}{13.500\pm0.323}$	10.800 <u>+</u> 0.463 16.515 <u>+</u> 0.513	$\frac{17,800\pm0.556}{16.410\pm0.395}$
RNR 2465 x NLR 145 BPT 5204 x IR 64	22.050±0.387 17.200±0.321	22.515 ± 0.300 19.950 ±0.399	21.400 <u>±</u> 0.387 19.655±0.521 Number of filled grai	25.000 <u>±</u> 0.372 20.500±0.277 ns per panicle	22.325 ± 0.366 20.612 ± 0.235	23.000 ± 0.416 23.830 ± 0.402
RNR 2465 x NLR 145 BPT 5204 x IR 64	165.900 ± 4.053 180.100 ± 3.764	135.900 ± 3.678 118.050 ± 1.512	179.600 <u>+</u> 9.221 191.550 <u>+</u> 7.147 Number of unfilled g	149.183 <u>+</u> 4.367 134.517 <u>+</u> 4.015 rains per panicle	139.400 ± 3.298 130.875 ± 2.475	131.100 ± 2.545 109.625±1.348
RNR 2465 x NLR 145 BPT 5204 x IR 64	$\frac{16.100\pm1.256}{18.500\pm1.374}$	17.500 ± 1.247 13.800 ± 0.702	13.500 <u>±</u> 0.884 16.900 <u>±</u> 1.654 SCMR	30.900 ± 1.740 12.683 ±0.490	$\frac{18.800\pm1.257}{8.100\pm0.320}$	22.000 ± 1.077 21.525 ± 1.301
RNR 2465 x NLR 145 BPT 5204 x IR 64	43.410 ± 0.602 42.375 ± 0.591	44.325 ± 0.441 42.900 ± 0.422	45.025±0.422 46.650±0.958 Test weight (g)	37.465 <u>+</u> 0.479 37.218 <u>+</u> 0.415	47.045 ± 0.814 48.102 ± 0.685	40.535 ± 0.786 48.270 ± 0.896
RNR 2465 x NLR 145 BPT 5204 x IR 64	$\frac{15.765\pm0.079}{13.352\pm0.082}$	23.865 ± 0.180 25.020 ± 0.291	13.977 <u>±</u> 0.086 16.370±0.158 Harvest index (%)	14.649 ± 0.170 16.257 ± 0.191	15.762 ± 0.334 17.848 ± 0.413	17.252 ± 0.460 19.130 ±0.298
RNR 2465 x NLR 145 BPT 5204 x IR 64	53.710 ± 0.712 46.985±1.144	60.010±0.607 54.370±0.731	56.450±1.370 65.265±1.346 Grain yield	55.858 <u>+</u> 0.784 41.608 <u>+</u> 1.021	53.053 ± 1.060 59.625 ± 1.017	53.090 ± 0.986 45.188 ± 0.733
RNR 2465 x NLR 145 BPT 5204 x IR 64	36.650±040 26.925±0.964	39.220 ± 1.824 30.483 ± 1.017	51.090 <u>+</u> 3.288 54.050 <u>+</u> 2.900 Kernal length (mm)	30.915 ± 1.234 28.958 ± 0.951	29.894 ± 1.119 35.430 ± 1.151	40.561 ± 1.768 37.990 ± 1.006
RNR 2465 x NLR 145 BPT 5204 x IR 64	5.985 ± 0.049 5.600 ± 0.054	7.155 ± 0.034 7.090 ± 0.054	5.375 ± 0.029 6.059 ± 0.067	6.478 ± 0.069 5.799 ± 0.100	6.375 ± 0.098 6.400 ± 0.079	6.452 <u>±</u> 0.133 6.802 <u>±0.060</u> <i>Continued</i>

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			Kernal L/B ratio			
RNR 2465 x NLR 145	3.055 ± 0.066	3.265 ± 0.062	2.665 ± 0.050	3.023 ± 0.048	3.334 ± 0.091	3.521 ± 0.109
BPT 5204 x IR 64	2.958 ± 0.042	3.150 ± 0.081	3.316±0.084 Unilian 92	2.984 ± 0.091	3.595 ± 0.110	3.696 ± 0.092
RNR 2465 x NLR 145	73.400 ± 0.550	75.600 ± 0.455	75.220 ± 0.603	76.750 ± 0.243	74.975 ± 0.378	66.567 ± 0.441
BPT 5204 x IR 64	74.870 ± 0.795	77.125 ± 0.473	77.900 ± 0.362	77.100 ± 0.235	76.825 ± 0.306	75.300 ± 0.394
			Milling%			
RNR 2465 x NLR 145	67.650 ± 0.525	68.700 ± 0.657	67.650 ± 0.682	69.550 ± 0.304	64.800 ± 0.489	59.520 ± 0.555
BPT 5204 x IR 64	67.150 ± 0.678	70.365 ± 0.660	67.500 ± 0.643	65.113 ± 0.432	68.650 ± 0.400	69.725 <u>+</u> 0.324
			Head rice recovery			
RNR 2465 x NLR 145	43.400 ± 0.617	58.100 ± 1.036	59.495 ± 0.701	54.375 ± 0.497	46.043 ± 0.412	47.920 ± 0.430
BPT 5204 x IR 64	52.335 ± 0.549	58.600 ± 0.622	51.600 ± 0.564	49.850 ± 0.360	53.330 ± 0.701	49.751 ± 0.456
			Wateruptake			
RNR 2465 x NLR 145	233.450 ± 3.471	245.400 ± 4.023	195.250 ± 4.406	223.767 ± 5.599	220.025 ± 7.320	181.575 ± 4.498
BPT 5204 x IR 64	170.350 ± 2.528	179.450 ± 4.722	295.000 ± 7.158	171.700 ± 2.663	164.525 ± 3.445	185.625 ± 3.992
			Volume expansion ratio			
RNR 2465 x NLR 145	3.440 ± 0.035	4.205 ± 0.041	4.810 ± 0.082	5.119 ± 0.073	4.140 ± 0.065	3.755 ± 0.104
BPT 5204 x IR 64	4.140 ± 0.048	4.295 ± 0.055	3.942 ± 0.045	4.170 ± 0.104	2.565 ± 0.039	3.320 ± 0.099
			Kernal elongation ratio			
RNR 2465 x NLR 145	1.485 ± 0.017	1.575 ± 0.020	1.430 ± 0.013	1.273 ± 0.016	1.310 ± 0.014	1.452 ± 0.031
BPT 5204 x IR 64	1.619 ± 0.020	1.570 ± 0.028	1.793 ± 0.043	1.219 ± 0.015	1.284 ± 0.015	1.276 ± 0.015
			Gel consistancy			
RNR 2465 x NLR 145	45.000 ± 1.177	60.800 ± 0.735	45.200 ± 1.426	33.683 ± 1.057	40.250 ± 1.072	38.500 ± 1.181
BPT 5204 x IR 64	49.800 ± 0.427	44.000 ± 0.669	43.100 ± 1.203	38.483 ± 1.268	50.150 ± 1.164	36.600 ± 0.819
			Alkali spreading value			
RNR 2465 x NLR 145	4.700 ± 0.164	5.190 ± 0.076	3.750 ± 0.132	2.550 ± 0.141	2.975 ± 0.136	2.000 ± 0.148
BPT 5204 x IR 64	5.200 ± 0.117	4.145 ± 0.043	3.555 ± 0.150	2.000 ± 0.104	2.525 ± 0.164	2.025 ± 0.121
			Amylose content			
RNR 2465 x NLR 145	24.590 ± 0.213	22.035 ± 0.289	20.600 ± 0.300	22.590 ± 0.310	19.782 ± 0.272	23.927 ± 0.472
BPT 5204 x IR 64	23.090	24.475	19.735	21.000	24.535	23.452

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of epistatic effects besides the major components *viz.*, additive (d) and dominance (h) for important yield and quality attributes. Partitioning of variance indicated that the mean vales (m) for gene effects were highly significant in both the hybrids for all the characters except effective bearing tillers per plant, SCMR, harvest index, kernel length and kernel L/B ratio in the cross BPT 5204 x IR 64.

Additive gene component was significant in both the hybrids for most of the characters except plant height in both the crosses, kernel length and milling % in the cross RNR 2465 x NLR 145, ear bearing tillers per plant, SCMR, water uptake and kernel elongation ratio in the cross BPT 5204 x IR 64 suggesting the importance of additive gene effects in the expression of these traits and simple selection would be useful for improvement of these traits. Similar results were reported by Kumar et al. (2007) for days to maturity, Yadav et al. (2013) for test weight and Nayak et al. (2007) for kernel elongation ratio in rice.

Positive sign of additive gene effects 'd' indicates that the high yielding (P_1) parent showed the highest number of genes for increasing the yield and negative sign for 'h' demonstrated that the dominance was towards the male parent (P_2) of the respective hybrids.

Dominance (h) component was significant in both the hybrids for majority of the traits except ear bearing tillers per plant, kernel length, kernel breadth and kernel elongation ratio in RNR 2465 x NLR 145 and in BPT 5204 x IR 64, number of unfilled grains per panicle, test weight and head rice recovery. It was noticed that in general, higher magnitude of negative dominance gene effects were recorded in both the hybrids as compared to additive gene effects with negative sign in the hybrids for all the traits indicated the dominance of decreaser alleles in the inheritance of the traits and therefore, selection would be effective only at later generations. Among the interaction effects additive × additive (i) type of epistasis was significant and important in both the hybrids for maximum number of characters. But these are mostly with negative sign indicating little scope of improvement through simple pedigree selection except kernel elongation ratio, water uptake, kernel L/B ratio and SCMR which were common in both the crosses having positive significant

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axa effects. The additive x dominance (j) type of interaction was non significant in all the traits in the hybrids studied. The non allelic epistatic interactions were observed by Jhansi and Satyanarayana (2015) for gel consistency and Mahalingam and Nadarajan (2013) for hulling % in rice.

Inferences based on the magnitude of additive effects are not advisable, because the distribution of positive and negative gene effects in the parents may result in different degrees of cancellation of effects in the expression of the generation means. Hence, the magnitudes of additive gene effects do not necessarily reflect the magnitude of additive variance (Mather and Jinks, 1971). However, dominance (h) and dominance \times dominance (1) are independent of the degree of gene distribution due to which the combined estimates of these components could be considered to be the best representative of sign and magnitude of individual gene effects. So, practically these are the only components which can safely be used to determine the type of epistasis that may have influence on the observed performance of generations (Mather and Jinks, 1971). For the same reason, emphasis has been given to the characters which were governed by such gene effects.

Dominance x dominance (1) gene effects were significant in both the hybrids for most of the traits except kernel length and gel consistency in both the crosses, days to maturity, ear bearing tillers per plant, head rice recovery, kernel elongation ratio and amylase content with respect to the cross RNR 2465x NLR 145 and for test weight in the cross BPT 5204 x IR 64 indicating that in addition to additive and dominance gene effects, the epistatic interaction effects were also important in the expression of above studied characters in rice. However, the magnitude of epistasis could be biased by the presence of linkage especially (i) and (l) (Kempthorne, 1957). Even though, the effect of epistasis is basic genetic mechanism perhaps cannot be considered as negligible. Hence, biparental mating and recurrent selection especially reciprocal recurrent selection in early segregating generations to break the repulsion phase linkages.

In the present investigation, the results of dominance (h) and dominance \times dominance (l) type interactions revealed prevalence of duplicate type of epistasis for most of the traits in both the hybrids except

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in RNR 2465 x NLR 145 for effective bearing tillers per plant, grain yield, kernel length, kernel breadth and gel consistency whereas in the cross BPT 5204 x IR 64 head rice recovery, water uptake and kernel elongation ratio, where complementary gene action played a vital role in the inheritance of the traits. Divya et al. (2014) observed complementary type gene action governing the trait grain yield in rice. It was evident from the results that the duplicate type of epistasis was common, except in for some characters limiting the pace of progress through selection. Therefore, few cycles of recurrent selection followed by pedigree method would be effective and useful to utilize all types of gene effects by maintaining considerable heterozygosity through mating of selected plants in early segregating generations. Similar results were already reported by Chamundeswari et al. (2010) for days to 50% flowering, kernel L/B ratio, milling %, alkali spreading value; Kumar et al., for days to maturity, test weight, Jhansi and Satyanarayana (2015) for kernel length and volume expansion ratio, Roy and Senapathi (2011) for harvest index, Gnanamalar and Vivekanandan (2013) for hulling %, Nayak et al. (2007) for head rice recovery.

Significance of additive components besides duplicate epistasis indicated the scope for recovering the transgressive plants effect for the characters governed by non additive gene actions and epistasis recurrent selection methods can be recommended. But these methods have certain limitations in self pollinated crops like rice, due to difficulty in crossing and seed sterility. According to Bains et al. (1969), repeated back crossing is more rewarding to pool up the desired genes into single line. Hence biparental mating in early generation followed by selection besides repeated back crossing will give fruitful results.

From the foregoing discussion the following conclusions were drawn. Significance of scaling tests for all the characters under study suggested inadequacy of simple additive and dominance model and presence of non allelic gene interactions. For majority of the yield and quality traits, additive, dominant and epistatic interactions were found significant indicating their complex nature of inheritance. Gamble (1962) suggested that the inheritance of quantitative characters become more complex. In such cases the contribution of dominance gene action to their inheritance becomes greater, while the contribution of additive gene action would be greater for the characters with apparently less complex. In both the hybrids most of the characters showed preponderance of duplicate epistasis suggesting that the inheritance of these traits might pose problems in its genetic improvement. Emphasis should be given to multiple hybrids rather than single ones to make better use of duplicate epistasis.

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