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Genetic analysis of yield and quality traits in improved parental lines of the rice hybrid Rajalaxmi

Biswajit Sahoo[1], Sunil Kumar Nair[1], Debarchana Jena[2], Diptibala Rout[2,] Vineeta Singh[2], P. Arsode3, Amrita Giri[1], Sadhna Saha[1], Anushree Pramanik[1], D.K. Rana[2,] JL Katara[2], S. SD Mohapatra[2], Sanghamitra Samantaray[2,] and Ramlakhan Verma[2*]

[1]*Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, C.G. 492012, India*
[2] *ICAR-National Rice Research Institute, Cuttack, 753006, Odisha, India*

*For correspondence, E-mail: ramlakhan.verma@icar.gov.in

Abstract

Nature of genetics of targeted and basic traits is very crucial for selection of appropriate parents and breeding strategies for BPH tolerance and yield enhancement in rice. In this study, six generations (P1, P2, F1, F2, B1 and B2) of CRMS32B/CR 2711-76 and IR42266-29-3R/CR 2711-76 analysed at ICAR-NRRI, Cuttack, Odisha. Gene actions analysis for yield and contributing traits along with BPH resistance was studied. Results revealed that panicle initiation, grain yield per plant, test weight, pollen load (IR42266-29-3R based generations) pest severity, ASV, AC and HRR exhibited duplicate epistasis gene action whereas other traits indicated complimentary gene actions.

KEY WORDS: Gene action, BPH, Duplicate, Complimentary, Epistasis, Enhancement

Introduction

Rice (Oryza sativa L.) is one the crucial food crop feeding more than half of the population of World (Khush, 2013) which meets up to 73% total calorie needs. Day by day population size is increasing with a alarming rate and it will be great challenge in future to feed the entire population of the World. Biotic stresses and abiotic stresses are major constraints which reduces the yield tremendously. Among all biotic stresses play significant role to reduce the yield in rice. Brown plant hopper is one of the devastating biotic factors which reduces significant yield of rice (Kumar et al., 2018 and Brar et al. 2009). Chemical management and other cultural practices are not so effective to control the BPH spread. Another substitute to this problem is the searching of resistance gene against BPH which can manage the BPH spread satisfactorily.

Keeping in vision, experiment started to introgress Bph31 in the parentages of rice hybrid Rajalaxmi which is susceptible to BPH. Marker assisted Back-cross breeding method was used to introgress the *Bph31* gene (Jairin, 2010 and Prahalada et al., 2017). Two BC_2F_2 populations were developed which were subjected to different agro-morphological and quality traits trials. This mainly focused on the gene interactions in the rice hybrid Rajalaxmi parents i.e. CRMS32B and IR42266-29-3R (recurrent parent), CR2711-76 (Donor) and their derivatives. Genetics of such traits interactions will be helpful to develop a suitable breeding strategy.

Materials and methods

The research work was carried out at research farm, ICAR-NRRI, Cuttack, Odisha, division of crop Improvement during 2018-19 to 2021. Materials used for the study included CRMS32B and IR42266-29-3R (recurrent parent), CR2711-76 (Donor). Marker Assisted Back-cross Breeding technique was used to introgress the *Bph31* gene in the hybrid parentage (B and R line).

Work Plan:

1. Crossing between susceptible (CRMS32B and IR42266-29-3R) and donor parent CR2711-76. Further F_1, F_2, B_1 and B_2 populations were developed.
2. Phenotypic observations were recorded for yield and quality traits. These traits involved plant height (PH), number of effective tillers (NET), panicle initiation (PI), Days to fifty percent flowering (DFF), Days to maturity (DM), panicle length (PL), Grain per panicle (GPP), Spikelet Fertility (SF), Grain Yield Per Plant (GYPP), Test Weight (TW), Stigma Exertion (SE), pollen Load (Pl), Kernel Length (KL), Kernel Breadth (KB), Kernel length and breadth (KLBR), Alkali spreading Value (ASV), Gel consistency(GC), Amylose Content (AC), Head Rice Recovery (HRR) and pest incidence (PI).
3. Analysis of these traits will give raise to understand the contribution of introgressed gene and agronomic performances of NILs.
4. Scaling test :

   Scaling test for A, B, C and D scales as suggested by Hayman and Mather (1955) and Mather and Jinks (1971) was applied to test the adequacy of simple additive–dominance model. Utilizing the means of different generations, the values of A, B, C and D scales were constructed using the following formulae. A = 2B1 − P1 − F1; B = 2B2 − P2 − F1; C = 4F2 − 2F1 − P1 − P2; D = 2F2 − B1 − B2; where, P1, P2, F1, F2, B1 and B2 are the means of parent 1, parent 2, F1, F2 and backcross generations B1 and B2, respectively. Utilizing the variance of different generations, the variances of A, B, C and D scales were computed as follows: VA = 4VB1 + VP1 + VF1; VB = 4VB2 + VP2 + VF1; VC = 16VF2 + 4VF1 + VP1 + VP2; VD = 4VF2 + VB1 + VB2; where, VP1, VP2, VF1, VF2, VB1 and VB2 are the variances of means of the P1, P2, F1, F2, B1 and B2 generations, respectively e.g.,VP1 = V(P1)/nP1, where V(P1) and nP1 are variances and number of observation of the P1 generation. The standard errors of A, B, C and D were obtained as square root of the variances VA, VB, VC and VD, respectively and were utilized for testing the significance of the deviations of the respective scales from zero. To test the significance of the scales, the 'Student's t' values for each of these quantities were calculated as follows: t(A) = A/SE(A); t(B) = B/SE(B); t(C) = C/SE(C); t(D) = D/SE(D); where standard error (SE) is the square root of respective variance e.g., SE(A) = (VA) 1/2 . The significance of the scales was evaluated using calculated P values for respective calculated 't' values.

5. Generation Mean Analysis:

The generation means were analyzed by the method suggested by Hayman (1958) to provide information on the inheritance of various traits. The generation means were used to estimate the six genetic parameters viz., m, (d), (h), (i), (j) and (l) of digenic interaction model representing mean, additive genetic effect, dominance genetic effect, additive × additive gene interaction effect, additive × dominance interaction effect and dominance × dominance gene effects, respectively assuming that no linkage and no higher order gene interaction exists. Considering the generation means as reference values, the above six genetic parameters were calculated following relationship between respective generation mean and genetic effects. P1 = m+(d)+(i); P2 = m−(d)+ (i); F1 = m+(h)+(1); F2 = m+1/2 (h)+1/4 (1); B1 = m + 1/2 (d) + 1/2 (h) + 1/4 (i) + 1/4 (j) + 1/4 (1); B2 = m − 1/2 (d) + 1/2 (h) + 1/4 (i) − 1/4 (j) + 1/4 (1). Accordingly, by least squares computation method, the following formulae were used for arriving at different gene effects. Mean = m = F2; additive effect = (d) = B1− B2; dominance effect = (h) = 2B1 + 2B2 + F1 − 4F2 − 1/2P1 − 1/2P2; additive × additive epistatic effect = (i) = 2B1 + 2B2 − 4F2; additive × dominance epistatic effect = (j) = B1 − 1/2P1 − B2 + 1/2P2; dominance × dominance interaction effect = (l) = P1 + P2 + 2F1 + 4F2 − 4B1 − 4B2. The variance of these gene effects involving the variance of means of the generations were calculated as follows: Vm = VF2; Vd = VB1 + VB2; Vh = VF1 + 16VF2 + 1/4VP1 + 1/4VP2 + 4VB1 + 4VB2; Vi = 4VB1 + 4VB2 + 16VF2; Vj = VB1 + VB2 + 1/4VP1 + 1/4VP2; Vl = VP1 + VP2 + 4VF1 + 16VF2 + 16VB1 + 16VB1. Square roots of the variance provided respective standard errors. The standard errors were used to calculate the‘t’ values for testing significance of the corresponding gene effects, t(d) = d/SE (d), where SE (d) = [Vd] 1/2 .

Results and discussion

Genetic improvement depends primarily on the parental selection and effectiveness of selection among progenies that differ in genetic value. The additive and dominant effects and their interactions are reported to be associated with breeding value. Genetic analysis using generation mean analysis (GMA) has been used to estimate the gene actions controlling the quantitative traits, and knowledge of additive, dominance and epistatic effects which are prerequisite in designing the most appropriate breeding strategies for substantial genetic gain enhancement in rice. It is a simple and very effective technique for estimating gene effects for polygenic traits, able to partitioned/estimate total epistatic/interaction gene effects into additive × additive (*i*), additive × dominance (*j*) and dominance × dominance (*l*) effects.

Estimates from scaling tests

The gene action of the traits undertaken in the study were analyzed based on simple additive × dominance model to understand the pattern of the gene action of the target (*Bph31*, *Xa21*, *xa13*, *xa5*) as well as product profile traits (basic trait of recurrent parent like duration, height, grain dimension and cooking quality and productivity) undertaken in this study (Table-1 and 2). The scaling test analysis (Hayman and Mather, 1955) showed all scale, A, B, C and D were significant for the traits like days to panicle initiation, days to 50% flowering, days to maturity, plant height, number of ear bearing tillers, panicle length, number of grain per panicle, spikelet fertility, grain yield per plant indicates presence of epistasis/non-alleliec interaction in expression of these traits. Whereas, A scale was not-significant for spikelets fertility and kernel L/B ratio; scale B was also non-significant for pest severity, kernel length, kernel breadth and kernel L/B ratio; scale C was non-significant for test weight, pest severity, stigma exsertion and ASV; and scale D was also non-significant for stigma exsertion and amylose content based on the CRMS32B/CR 2711-76 population

(Table1). Likewise, same pattern of gene action recorded in IR42266-29-3R/CR 2711-76 based populations (Table 2). All the basic (yield and related) and value added traits (BPH and bacterial leaf blight resistance) in the present study were reported significant in either one of the scales or in combination representing the existence of epistatic interactions between the genes involved.

Further, goodness of fit of this model was tested by following chi-square test analysis. The adequacy of simple additive-dominance model suggests the absent of non-allelic interaction effect (epistasis) and means value of different generations depends only on additive × dominance gene interaction or effect of the gene. The chi-squire test analysis revealed that all the traits studied in the cross of CRMS32B/CR 2711-76 and IR42266-29-3R/CR 2711-76 were found significant value which indicates presence of epistatic effect between these traits. The results showed the data does not fit into simple additive × dominance model; role of epistatic is prevalent which is not fit into three parameter model hence data were further subjected to be analyzed under six-parameter model (Hayman, 1958). `

Table 1. Scaling test and generation mean analysis for yield and quality traits with pest severity in the parents P_1, P_2 and combinations F_1, F_2, B_1 and B_2 of CRMS32B/CR 2711-76

Traits/ Parameters	Scaling test				Generation mean analysis						X^2 test
	A	B	C	D	m (Hayman)	d (Hayman)	h (Hayman)	i (Add × Add)	j (Add × Dom)	l (Dom × Dom)	
Panicle initiation	12.48**	1.22**	3.71**	2.32**	5.45**	22.65**	-15.55**	-1.82	18.65**	17.25**	142.13**
Days to 50% flowering	16.45**	10.09**	-25.50**	-22.52**	49.21**	-16.01**	12.34**	57.74**	-2.9	2.17**	1604.87**
Days to maturity	13.6**	8.08**	-4.30**	22.36**	52.78**	2.92**	2.95**	3.18**	4.91**	23.42**	872.33**
Plant Height	37.89**	27.34**	24.32**	10.6**	31.07**	52.59**	1.78**	2.81**	-5.03**	1.69**	1034.27**
No. of effective tillers/plant	13.55**	-12.7**	15.08**	8.12**	1.44**	54.72**	37.89**	24.65**	13.88**	24.01**	1436.02**
Panicle length	8.25**	6.88**	7.29**	-22.54**	11.44**	27.67**	-0.42	0.16**	-11.64**	4.88**	659.25**
Grain per plant	28.25**	48.17**	12.00**	8.66**	52.61**	4.13**	3.79**	-1.72	2.5**	85.33**	1120.45**
Spikelet fertility	-4.11	23.65**	15.6**	0.48**	4.08**	12.08**	12.47**	5.18**	-0.18	1.55**	183.9**
Grain yield per plant	4.56**	23.4**	4.18**	10.75**	1.55**	1.88**	12.9**	5.19**	0.98**	1.09**	427.25**
Test Weight	6.1**	-11.5**	-2.34	33.68**	49.93 **	3.9**	3.75*	7.6**	-7.39**	17.71**	1955.85**
Stigma exsertion	4.58**	0.6**	-0.48	-0.85	-14.87**	18.28**	-25.1**	23.42**	-1.98	-2.44	642.14**
KL	0.82**	-0.22	1.25**	1.57**	1.22**	2.85**	-3.65	-1.65	-0.31	1.86**	120.82**
KB	0.36**	0.08	0.10**	0.09**	0.25**	1.62**	0.68**	-0.28	-0.14	0.87**	634.21**
KL BR	0.018	2.48**	2.03**	12.6**	12.56**	9.63**	4.55**	0.65**	22.9**	3.84**	244.085**
ASV	6.24**	54.36**	-2.80	7.55**	61.25**	-4.87	3.21**	-1.62	2.038**	35.43**	953.57**
GC	1.15**	-0.11	0.42**	0.17**	2.58**	1.47**	2.35**	1.98**	0.87**	1.68**	56.47**
AC	8.45**	33.08**	7.25**	-2.44	22.78**	-2.55	40.9**	-2.44	-8.56**	1.76**	139.6**
HRR	10.08**	10.95**	1.86**	3.95**	8.06**	7.22**	47.56**	4.36**	14.7**	0.92**	1208.52**
Pest incidence	1.12**	-3.44	-0.95	3.42**	14.99**	1.74**	3.27**	1.87**	11.74**	22.51**	715.04**

Table 2. Scaling test and generation mean analysis for yield and quality traits with pest severity in the parents P_1, P_2 and combinations F_1, F_2, B_1 and B2 of IR42266-29-3R/CR 2711-76

Traits/ Parameters	Scaling test				Generation mean analysis						
	A	B	C	D	m (Hayman)	d (Hayman)	h (Hayman)	i (Add × Add)	j (Add × Dom)	l (Dom × Dom)	X^2 test
Panicle initiation	8.4**	11.97**	1.171**	1.76**	6.21**	8.59**	45.2**	2.28**	17.27**	-3.36**	1109.79**
Days to 50% flowering	-1.32**	1.108**	-0.589**	-2.1**	-1.6**	2.99**	-1.68**	-2.36**	2.43**	-3.41**	535.48**
Days to maturity	11.92**	9.108**	-4.989**	20.17**	50.93**	4.29**	0.59**	1.1**	7.48**	19.14**	773.6**
Plant Height	36.21**	28.368**	23.631**	8.41**	29.22**	53.96**	-0.58	0.73**	-2.46**	-2.59**	935.54**
No. of effective tillers/plant	11.87**	-11.672**	14.391**	5.93**	-0.41	56.09**	35.53**	22.57**	16.45**	19.73**	1337.29**
Panicle length	2.9**	1.62**	-1.169**	-3.04**	-16.72**	19.65**	-27.46**	21.34**	0.59**	-6.72**	543.41**
Grain per plant	14.77**	11.118**	-26.18**	-24.71**	47.36**	-14.64**	9.98**	55.66**	-0.3	-2.11**	1506.14**
Spikelet fertility	4.56**	55.388**	-3.489**	5.36**	59.4**	-3.5**	0.85**	-3.7**	4.608**	31.15**	854.84**
Grain yield per plant	-0.56	-2.412**	-1.639**	1.23**	13.14**	3.11**	0.91**	-0.21**	14.31**	18.23**	616.31**
Test Weight	10.8**	2.248**	3.021**	0.13**	3.6**	24.02**	-17.91**	-3.9**	21.22**	12.97**	43.4**
Pollen load	6.57**	7.908**	6.601**	-24.73**	9.59**	29.04**	-2.78**	-1.92**	-9.07**	0.6**	560.52**
KL	-0.86	0.808**	0.561**	-0.62	-0.63**	4.22**	-6.01**	-3.73**	2.26**	-2.42**	22.09**
KB	26.57**	49.198**	11.311**	6.47**	50.76**	5.5**	1.43**	-3.8**	5.07**	81.05**	1021.72**
KL BR	-0.53	0.918**	-0.269	-2.02**	0.73**	2.84**	-0.01	-0.1	3.44**	-2.6**	-42.26**
ASV	-5.79**	24.678**	14.911**	-1.71**	2.23**	13.45**	10.11**	3.1**	2.39**	-2.73**	85.17**
GC	4.42**	-10.472**	-3.029**	31.49**	35.89**	5.27**	1.39**	5.52**	-4.82**	13.43**	1857.12**
AC	6.77**	34.108**	6.561**	-4.63**	20.93**	-1.18**	406.64**	-4.52**	-5.99**	-2.52**	40.87**
HRR	-0.5	3.508**	1.341**	10.41**	10.71**	11.08**	2.19**	-1.43**	25.47**	-0.44	145.35**
Pest incidence	2.88**	24.428**	3.491**	8.56**	-0.3	3.25**	10.54**	3.11**	3.55**	-3.19**	328.52**

Estimation of gene effects based on six generation means

Digenic non-allelic/intergenic/epistatic interaction model with six parameters namely m, d, h, i, j and l revealed that the epistatic interaction model was found adequate to explain the gene action in the traits days to panicle initiation, days to panicle emergence, days to fifty percent flowering, days to maturity, plant height, number of ear bearing tillers, panicle length, number of grain per panicle, spikelets fertility, test weight, grain yield per plant, pest severity, head rice recovery, kernel length, kernel breadth, and kernel L/B ratio. The estimates of gene effect clearly illustrate high variation in the observed traits (Table 1 and 2). Mean and additive components for days to panicle initiation, days to panicle emergence, days to fifty percent flowering, days to maturity, plant height, number of ear bearing tillers, panicle length, number of grain per panicle, spikelets fertility, test weight, grain yield per plant, disease severity, head rice recovery, kernel length, kernel breadth, and kernel L/B ratio were highly significant. Additive gene actions were more significant for the

traits no. of productive tillers per plant (Robin (1997), Kalita and Upadhaya (2000b) and Kumar et al. (2007) in this favour days to first flowering exhibited additive gene action found by Anbumalarmathi (2005).

The six parameter analysis of the crosses, CRMS32B/CR 2711-76 and IR42266-29-3R/CR2711-76 revealed the dominance (h) and dominance × dominance (l) gene interaction or effects opposite signs (opposite direction) for the traits viz., panicle initiation, grain yield per plant, test weight, pollen load (IR42266-29-3R based generations) pest severity, ASV, AC and HRR indicates duplicate epistasis. These results were supported by Subbulakshmi et al., 2016 found a duplicate dominance gene action in the cross1 for the traits viz., no. of productive tillers, no. of grains per panicle, 1000 grain weight, hulling %, milling % and single plant yield where the dominance (h) and dominance × dominance (l) were opposite in sign. The values of most of the traits shows same sign for dominance (h) and dominance × dominance (l) interaction were fit into complementary epistasis model in both populations. Subbulakshmi et al., 2016 also found a complementary epistasis gene action in the cross1 for the traits viz., plant height, panicle length, days to fifty percent flowering, L/B ratio and amylose content where dominance (h) and dominance × dominance (l) interaction were in same sign and this result favored by Chauhan et al., 1993. Traits like number of tillers, productive tillers, leaf length, leaf width, economic yield, lesion number, infested leaf area and potential disease incidence per cent had a sign in the same direction exhibiting complementary gene action (Thirugnanakumar et al. 2007).

The classification of gene interactions depends on the magnitudes and signs of the estimates of dominance (h) and dominance × dominance (l) gene interaction or effects, when there are many pairs of interacting genes. The sign associated with the estimates of (d) and (h) indicates the parent that concentrates the highest number of genes for increasing the trait. Additive (d) effect and dominant × dominant (l) gene interaction were the only significant portion of gene controlling grain yield per plant of the rice and spikelet fertility of plants. Finally, additive and dominance gene effects were found important in controlling BPH and bacterial leaf blight disease reaction. The sign indicates the concentration of gene towards the parents (Falconer, 1989). The plus sign in the additive gene effect implies that CRMS32B and IR 42266-29-3R contributes positively to the trait as compared to CR 2711-76 and vice versa. The positive sign for the additive (d) effects was observed in the all studied traits except spikelet fertility, grain per plant and AC content. while the negative sign for (h) was observed in the traits days to 50% flowering, plant height, Panicle length, test weight, pollen load and grain dimension in IR 42266-29-3R based generation (Table 2); and panicle initiation, panicle length, stigma exsertion and kernel length in cased of CRMS 32B based generation (Table 1). A positive sign for (d) observed for the traits no. of tillers, productive tillers, panicle length, days to first flowering and filled grains per panicles pointing towards high yielding susceptible parent, ADT43 (P1) exhibited more no. of for increasing the yield whereas the negative (*h*) produced dominance effect to the Resistant parent CT13432-3R as per the previous findings (Paul et al. 2003; Cruz et al. 2006; Thirugnanakumar et al. 2007; Li et al. 2010) explaining the dominance effect on yield and biotic and abiotic stress linked traits in rice. This study also supported by Ray and Islam (2008) and Sharifi et al. (2011) explaining the priority of additive gene effect in rice.

Epistatic nonallelic interaction model was able to explain the gene action satisfactorily through generation mean analysis in the derivatives of CRMS32B/CR 2711-76 and IR42266-29-3R/CR 2711-76. It was also identified that there was presence of duplicate gene action for panicle initiation, grain yield per plant, test weight, pollen load (IR42266-29-3R based generations) pest severity, ASV, AC and HRR and complementary gene action for days to fifty percent flowering, days to maturity, plant height, panicle length, stigma exertion, Spikelet fertility, Kernel L/B ratio, no. of effective Tillers and GC content.

Mean and additive gene action was more significant for days to panicle initiation, days to panicle emergence, days to fifty percent flowering, days to maturity, plant height, number of ear bearing tillers,

panicle length, number of grain per panicle, spikelets fertility, test weight, grain yield per plant, disease severity, head rice recovery, kernel length, kernel breadth, and kernel L/B ratio. It is noteworthy that duplicate and complimentary gene actions were significant for grain yield and most of the contributing traits. So it will not be possible to make selection in this generation and selection will be delayed for few generations to reduce the epistatic interaction. The information's regarding BPH and yield related traits will further studied for future selection.

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