RESEARCH ARTICLE https://doi.org/10.58297/QYBF5265

Generation Mean Analysis for Blast Resistance and Yield Traits in Rice (*Oryza sativa* L.)

Namrata[1]*, Singh RP[1], Ramlakhan Verma[2], Prashant Bisen[1], Prakash Singh[3], Arsode Pandurang[1], Madhu Choudhry[1], Padma Thakur[1], Bapsila Loitongbam[1] and Ramesh[4]

[1]Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221005, India

[2]Crop Improvement Division, ICAR-NRRI, Cuttack-753006, India

[3]Department of Plant Breeding and Genetics, VKSCA, Bihar Agricultural University, Sabour, Dumraon, Buxar- 802136, India

[4]Department of Genetics and Plant Breeding, College of Agriculture, Barmer Agricultural University, Baytu, Jodhpur- 344034, India

*Corresponding author's email: namratamotasara@gmail.com

Received: 12th July, 2025; Accepted: 9th September, 2025

Abstract

An investigation was performed to study the gene interactions for blast resistance and yield attributes in rice using six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of cross HUR 3022 × Tetep. Results of scaling test, joint scaling test and digenic nonallelic interaction model with six parameters namely *m, d, h, i, j* and *l* indicated that the epistatic interaction model was appropriate to explain the gene action in all the fourteen traits under study. Mean and additive components were found highly significant for number of filled grains per plant, number of unfilled grains per plant, spikelet fertility percentage, grain yield per plant, area under disease progress curve and disease severity per cent. The dominance (*h*) gene effects were found highly significant for all the characters under study. All three types of gene effects (additive, dominance and epistasis) were found highly significant for blast resistance traits studied, except for additive effect in lesion number.

Key words: Blast resistance, gene interaction, duplicate epistasis

Introduction

Rice provides food for nearly half of the world's population which enables it to play a crucial role in the world food security (Billa *et al.,* 2024). Asian countries represent highest production as well as consumption of rice in the world (Khush 2005, Khush 2013, Yin *et al.,* 2021, Kumari *et al.,* 2024, Liu *et al.,* 2022, Boss *et al.,* 2024). Rice is grown globally in an area of 165.25 million hectares with a production of 787.29 million tonnes with an average productivity of 4.76 tonnes per hectare (FAOSTAT, 2021). India being the second largest producer of rice produces 130.29 million tonnes of rice on an area of 46.38 million hectares with productivity of 28.09 q/ha. In Uttar Pradesh it is grown in an area of 5.70 million hectares with production of 15.27 million tonnes and productivity of 26.79 q/ha (DES, 2021-22).

To feed increasing world population with the existing land resources, 26% more rice production is required in next 20 years (Khush, 2013). Rice production has widely increased after the green revolution, but the yield of superior varieties is still not increasing as farmer's expectations due to the influence of several biotic and abiotic factors (Divya *et al.,* 2014). Biotic factors globally cause approximately ~52% annual loss to rice production, among which major portion

is due to the attack of diseases (Yarasi *et al.,* 2008, Ashkani *et al.,* 2015). Rice is reported to be attacked by more than 70 diseases caused by different fungi, bacteria, viruses and nematodes (Zhang *et al.,* 2009). Among these diseases, rice blast caused by fungus *Magnaporthe oryzae* belonging to the class Ascomycetes and the genus *Magnaporthe,* considered to be one of the most significant, potentially damaging and a costly constraint causing major food loss per year at global level. Rice blast has been responsible for up to 30% yield loss in rice globally (Qi *et al.,* 2023), but even if it is causing only 10% loss of the yield it accounts for grain loss equivalent to feed 60 million people for one whole year (Kato, 2001). The dynamic evolution nature of the blast fungus complicates breeding for the blast resistance. To breed for complex traits like yield and resistance to blast disease, a comprehensive idea about the gene interaction and genetics involved in governing these traits are required. Keeping this in view, the present study is formulated to study the gene action involved in governing the yield traits and resistance to blast in a cross of HUR 3022 × Tetep in rice.

Materials and Methods

The present experiment was conducted during two main crop seasons of *Kharif* 2016 and 2018 at Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi and two off season crops were taken at Research Farm of ICAR-National Rice Research Institute (NRRI), Cuttack, Orissa during *Rabi* 2016-17 and 2017-18. Geographically, experimental site of Varanasi is situated at 25°18′ North latitude and 83°03′ East longitude and at altitude of 123.23 m from sea level while experimental site of Cuttack is situated between 85°55' E to 85°56' E longitudes and 20°26' to 20°27' N latitudes with altitude of 24 m from sea level. Parents used in the study includes an early maturing locally popular rice variety, HUR 3022 (Malviya Dhan 3022) as a recurrent parent and as a donor parent, well known rice blast resistant *Indica* rice cultivar Tetep.

Crossing plan

The season wise crossing programme is illustrated in **Figure 1**.

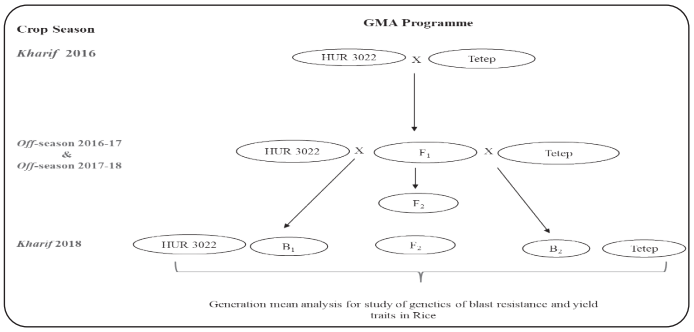

Figure 1: Season wise crossing programme for study of gene interaction.

During *Kharif* 2018, six generations of the cross HUR 3022 × Tetep (P_1, P_2, F_1, F_2, B_1 and B_2) along with the susceptible check Co-39 were planted in randomized block design in the open field condition. They were sprayed with 15 days old culture of *Magnaporthe oryzae* isolate *LB-TN-2,* obtained from Oat Meal Agar media at a concentration of 1 x 10^5 conidia/ml along with 0.2% Tween-20 at 24 days after sowing. Epiphytotic conditions were maintained by spraying water and covering the plants with polythene sheet to create humidity for the better establishment of the disease during night. Phenotypic traits were assessed on each individual entry in the segregating generations and observations were recorded for yield and blast resistance traits like Days to panicle emergence (DPE), Days to 50 per cent flowering (DF), Days to maturity (DM), Plant height (PH), Number of effective tillers per plant (NET), Panicle length (PL), Number of filled grains per panicle (NFG), Number of unfilled grains per panicle (NUG), Test weight (g) (TW), Grain yield per plant (GY), Lesion Number (LN) and calculated as per standard formula for the traits like- Spikelet fertility per cent (SFP), Disease severity (DS %) and Area under disease progressive curve (AUDPC) (Sabin *et al.,* 2016). Disease scoring for blast disease was performed using 0-9 scale as described in standard evaluation system (SES), IRRI (2013) and the host response was decided as described in Singh *et al.,* (2013).

Generation mean analysis

The generation mean analysis was performed to estimate the genetic components of variation, epistasis model and gene effects using two step procedure: (i) To perform scaling tests for determining the absence or presence of interallelic interactions, (ii) Determination of gene effects, variances and type of epistasis involved in yield and blast resistance traits. Six generations *viz.,* parental (P_1 and P_2), F_1, F_2, and two backcross generation (B_1 and B_2) were used to perform the tests. Average values were subjected to scaling test presented in **Table 2**. The significance of these scales (A, B, C and D) depicted the presence of non - allelic interaction. Presence of epistasis was detected by using Hayman and Mather (1955) approach. Further, the joint scaling test given by Cavalli (1952) was used which includes any combination of families at a time and tests the adequacy of additive-dominance model using a χ^2 test. For estimation of gene effects, Hayman's (1958) six parameter model was used to obtain the information about the inheritance of various traits.

Results and discussion

Generation means analyses reveals the relative importance of additive effects, dominance effects and epistatic effects (non-allelic interactions) in determining the genotypic values of the individuals and subsequently mean genotypic values of the generations. Generation means analysis is an effective technique for estimating gene effects for quantitative traits; its greatest merit lying in the ability to estimate all the three types of epistatic gene effects *viz*., additive × additive (*i*), additive × dominance (*j*) and dominance × dominance (*l*) effects.

To elucidate the nature of gene action for yield traits and blast resistance, generation mean analysis was carried out using the data recorded from six generations of the cross HUR 3022 × Tetep. The mean performances for 14 traits studied in the six generation P_1 (HUR 3022), P_2 (Tetep), F_1, F_2, B_1 (F_1 × HUR 3022) and B_2 (F_1 × Tetep) were presented in **Table 1.** F_1 generation showed early panicle emergence, flowering and maturity duration as compared to parents while three segregating populations (F_2, B_1 and B_2) observed taking slightly longer time for above three traits as compared to non-segregating generations. These findings are found in partial agreement with the earlier reports of early flowering of F_1, F_2, B_1 and B_2 generations than recurrent parent in rice (Divya *et al.,* 2014). Plant height in F_1 and F_2 were slightly shorter than recurrent parent HUR 3022, while B_1 and B_2 generations had intermediate plant height in comparison with both the parents. It was observed that F_1 generation having highest number of effective tillers followed by B_2 generation among all six generations studied. In B_1 generation intermediate number of effective tillers per plant recorded while F_2 had lesser number of effective tillers per plant than both the parents. These findings are in good agreement with previous reports for panicles per plant or number of effective tillers per plant in rice (Hassan *et al.,* 2016). B_2 generation in present study showed slightly better panicle length than better parent HUR 3022 while B_1 generation showed intermediate panicle length. F_1 and F_2 generation had lesser panicle length as compared to both the parents. These findings are in partial agreement with earlier reports for panicle length in rice (Divya *et al.,* 2014, Jondhale *et al.,* 2018). Not a single generation showed better number of filled grains per panicle than blast resistant parent Tetep. Highest number of unfilled grains per panicle found in B_2 generation followed by B_1 generation while lowest unfilled grains per panicle observed in blast resistant parent Tetep. Highest spikelet fertility observed in blast resistant parent Tetep followed by HUR 3022 while F_1, F_2, B_1 and B_2 had lesser spikelet fertility compared to both parents. Better test weight observed in F_1, B_1 and B_2 as compared to both parents but F_2 generation showed intermediate test weight. These findings are in good agreement for earlier reports of test weight in rice in similar experiment (Kiani *et al.,* 2013) and in partial agreement with earlier reports for number of filled grains per panicle and spikelet fertility per cent (Divya *et al.,* 2014).

Highest grain yield was observed in blast resistant parent Tetep followed by B_2 and F_1 generations while B_1 and F_2 generations showed intermediate and lower grain yield, respectively. In Comparison with recurrent parent HUR 3022, all three generations *viz.,* F_1, B_1 and B_2 generations showed higher grain yield. These findings showed similarity with the earlier reports of economic yield in blast condition in rice (Divya *et al.,* 2014).

Table 1: Mean performance of six generations of the cross HUR 3022 × Tetep for various yield attributing and blast resistance traits

Traits	P_1±Sem	P_2±Sem	F_1±Sem	F_2±Sem	B_1±SEm	B_2±SEm
#DPE	76.00 ± 0.30	75.47 ± 0.88	71.13 ± 0.41	82.72 ± 0.80	84.45 ± 1.02	85.85 ± 0.88
DOF	78.46 ± 0.50	78.20 ± 0.78	73.33 ± 0.57	84.89 ± 0.78	86.85 ± 1.01	88.06 ± 0.92
DOM	108.73 ± 0.73	106.00 ± 0.93	103.93 ± 0.75	115.26 ± 0.79	117.08 ±0.97	118.60 ± 0.82
PH	93.93 ± 3.73	126.33 ± 2.85	93.40 ± 3.01	89.90 ± 0.96	98.82 ± 0.90	100.27 ± 1.22
NET	13.60 ± 1.28	11.27 ± 0.70	17.73 ± 0.76	9.90 ± 0.53	13.55 ± 0.72	14.52 ± 0.73
PL	26.43 ± 061	25.86 ± 0.53	24.27 ± 0.76	20.99 ± 0.24	26.22 ± 0.42	26.47 ± 0.31
NFG	149.27 ± 16.18	157.80 ± 11.60	94.67 ± 11.30	125.25 ± 4.57	106.43 ± 3.96	130.26 ±4.74
NUG	51.80 ± 6.76	31.07 ± 7.90	62.10 ± 7.90	63.10 ± 3.80	112.75 ±6.78	122.28 ± 6.90
SFP	73.71 ± 9.48	84.29 ± 8.99	59.59 ± 10.32	66.72 ± 1.72	49.23 ± 1.17	51.97 ± 4.90
TW	15.76 ± 0.11	17.23 ± 0.36	19.48 ± 0.05	15.95 ± 0.20	20.89 ± 0.15	21.83 ± 0.39
GY	19.82 ± 3.31	40.69 ± 1.81	24.83 ± 1.30	15.42 ± 1.16	20.50 ± 1.12	26.46 ± 2.04
LN	48.20 ± 4.33	6.60 ± 0.60	4.00 ± 0.63	17.30 ± 1.40	16.00 ± 0.71	15.15 ±0.53
AUDPC	605.62 ± 30.14	127.95 ± 11.95	224.7 ± 26.128	477.51± 21.71	464.75 ± 26.52	318.20 ± 19.38
DSP	43.66 ± 1.62	9.32 ± 0.74	17.54 ± 1.48	34.22 ± 1.28	32.86 ± 1.51	22.84 ± 1.08

#(DPE) Days to panicle emergence, (DOF) Days to 50 per cent flowering, (DOM) days to maturity, (PH) plant height, (NET) number of effective tillers per plant, (PL) panicle length, (NFG) number of filled grains per panicle, (NUG) number of unfilled grains per panicle, (SFP) spikelet fertility per cent, (TW) test weight, (GY) grain yield per plant, (LN) lesion number, (AUDPC)area under disease progress curve and (DSP) disease severity per cent

To understand the adequacy of simple additive-dominance model both scaling and joint scaling tests were performed **(Table 2)**. The scaling test showed all A, B, C and D scales were significant for twelve traits *viz.,* days to panicle emergence, days to 50 % flowering, days to maturity, plant height, numbers of filled grains per panicle, numbers of unfilled grains per panicle, spikelet fertility percentage, test weight, grain yield per plant, lesion numbers, area under disease progress curve and disease severity per cent. Only three scales were observed significant for two traits *viz.,* A, C and D scales for number of effective tillers per plant while B, C and D scales for panicle length, respectively. These results showed that for above studied twelve traits simple additive- dominance model was inadequate and epistatic interactions were present. Similar findings were previously reported in rice (Bano *et al.,* 2017). Results of chi square test performed under joint scaling test showed significance for all the traits related to yield as well as blast resistance studied in present investigation. The inadequacy of simple additive-dominance model revealed by results of scaling and joint scaling tests. The role of epistatic interactions was identified by lack of goodness of fit into three parameter models and the data was further subjected to six parameter models.

Table 2: Estimates from scaling and joint scaling tests for fourteen traits

Character	Scaling test				Joint scaling test			
	Scale A	Scale B	Scale C	Scale D	m	D	h	χ^2
#DPE	-21.77**± .21	-25.10** ± 1.16	-37.15** ± 1.96	-4.86** ± 1.20	79.04**	2.44*	-5.42**	974.75**
DOF	-21.90**±1.24	-24.60** ± 1.20	-36.21** ± 1.98	-5.14** ± 1.19	81.22**	1.19	-3.52**	849.07**
DOM	-21.50** ± 1.27	-27.27** ± 1.17	-38.46** ± 2.12	-5.15** ± 1.16	111.67**	0.34	-1.09	840.66**
PH	-10.30** ± 2.98	19.20** ± 2.81	47.50** ± 5.01	-19.30** ± 1.41	108.74**	4.65**	-23.55*	334.72**
NET	4.23** ± 1.20	-0.03 ± 1.04	-20.80** ± 1.74	-8.30** ± 0.85	10.34**	0.21	5.33**	162.04**
PL	-0.73 ± 0.74	-2.81** ± 0.65	16.88** ± 1.14	-10.71** ± 0.41	25.44**	0.54	-3.28**	741.41**
NFG	31.07** ± 12.28	-8.06** ± 10.84	-4.60** ± 20.34	13.80** ± 6.37	147.63**	19.14**	-54.59**	13.87**
NUG	-111.60** ± 9.10	-151.40** ± 9.51	-45.32**± 11.77	108.84** ± 7.10	63.02**	-3.76**	13.83**	392.27**
SFP	34.82** ± 3.35	39.93** ± 3.75	10.29** ± 6.66	32.23** ± 2.39	72.06**	7.70**	-29.59**	276.32**
TW	-6.55** ± 0.19	-6.95** ± 0.50	8.16** ± 0.51	-10.83** ± 0.33	16.63**	0.28	2.30**	1867.48**
GY	3.64** ± 2.43	12.60** ± 2.68	48.48** ± 3.77	-16.12** ± 1.9	25.03**	10.24*	-3.72**	205.76**
LN	20.20** ± 2.65	-19.70** ± 0.80	-6.40** ± 4.17	3.45** ± 1.70	18.96**	-8.38**	-11.05**	720.32**
AUDPC	-79.17**±38.32	-263.74**± 27.86	-687.08** ± 61.45	172.08**± 31.44	390.75**	-242.94**	-30.05**	173.04**
DSP	-4.53** ± 2.16	-18.82**± 1.57	-48.84** ± 3.56	12.75** ± 1.83	28.105**	-17.09**	-2.56**	267.50**

** and *: Significant at 1 and 5 per cent level, respectively

#(DPE) Days to panicle emergence, (DOF) Days to 50 per cent flowering, (DOM) days to maturity, (PH) plant height, (NET) number of effective tillers per plant, (PL) panicle length, (NFG) number of filled grains per panicle, (NUG) number of unfilled grains per panicle, (SFP) spikelet fertility per cent, (TW) test weight, (GY) grain yield per plant, (LN) lesion number, (AUDPC)area under disease progress curve and (DSP) disease severity per cent

Results of digenic nonallelic interaction model with six parameters namely *m, d, h, i, j* and *l* indicated that the epistatic interaction model was appropriate to explain the gene action in all the fourteen traits under study **(Table 3).** These results showed significant similarity with the earlier reports in rice (Bano *et al.,* 2017, Divya *et al.,* 2014, Makwana *et al.,* 2018). Mean and additive components were found highly significant for number of filled grains per plant, number of unfilled grains per plant, spikelet fertility percentage, grain yield per plant, area under disease progress curve and disease severity per cent. Similar results were reported previously for the number of filled spikelets (Bano *et al.,* 2017), grain yield per plant (Bano *et al.,* 2017, Kumar *et al.,* 2017, Makwana *et al.,* 2018, Kour *et al.,* 2019). The dominance (*h*) gene effects were found highly significant for all the characters under study. All three types of gene effects (additive, dominance and epistasis) were found highly significant for blast resistance traits studied, except for additive effect in lesion number. These results are in contradiction with the previous report of dominance and dominance × dominance (l) mainly governing the blast resistance related traits (Divya *et al.,* 2014). The dominance (*h*) and dominance × dominance (*l*) gene effects displayed opposite signs for all the traits studied indicating presence of duplicate epistasis **(Table 3)**. Presence of duplicate epistasis was previously reported for days to 50 % flowering, days to maturity, plant height, panicle length (Bano *et al.,* 2017), numbers of filled grains per panicle, number of effective tillers per plant (Bano *et al.,* 2017), spikelet fertility percentage (Divya *et al.,* 2014), test weight (Divya *et al.,* 2014, Bano *et al.,* 2017), grain yield per plant (Bano *et al.,* 2017, Kumar *et al.,* 2017, Makwana *et al.,* 2018, Kour *et al.,* 2019) and for blast related traits *viz.,* lesion numbers and disease severity per cent only complementary epistasis was reported earlier (Divya *et al.,* 2014).

Table 3: Estimation of gene effects based on six parameter model for fourteen traits

Traits	M	D	H	I	J	l
DPE	82.72** ± 0.46	-1.40 ± 0.78	5.12** ± 2.43	9.72** ± 2.40	-3.33** ± 1.65	-56.59** ± 3.68
DOF	84.88** ± 0.45	-1.22 ± 0.79	5.29** ± 2.42	10.28** ± 2.39	-2.70** ± 1.67	-56.78** ± 3.73
DOM	115.27** ± 0.45	-1.52 ± 0.74	6.87** ± 2.39	10.30** ± 2.33	-5.77** ± 1.62	-59.06** ± 3.62
PH	89.90** ± 0.56	-1.45 ± 0.87	21.86** ± 3.60	38.59** ± 2.82	29.50** ± 3.22	-29.70** ± 6.10
NET	9.90** ± 0.31	-0.97 ± 0.60	21.90** ± 1.82	16.56** ± 1.71	-4.27** ± 1.15	-12.36** ± 2.94
PL	20.99** ± 0.14	-0.25 ± 0.30	19.54** ± 0.96	21.42** ± 0.82	-1.07 ± 0.76	-25.96** ± 1.66
NFG	125.25** ± 2.64	-23.83** ± 3.57	-86.48** ± 15.43	-27.61** ± 12.74	-39.13** ± 13.53	50.63** ± 24.85
NUG	63.10** ± 2.20	-9.53** ± 5.58	238.34** ± 14.74	217.67** ± 14.21	-39.80** ± 12.67	-480.67** ± 25.24
SFP	66.72** ± 0.99	-2.73** ± 1.32	-83.88** ± 5.48	-64.47** ± 4.78	5.10** ± 3.98	139.22** ± 8.50
TW	15.95** ± 0.11	-0.94 ± 0.24	24.65** ± 0.67	21.66** ± 0.66	-0.40 ± 0.53	-35.17** ± 1.09
GY	15.42** ± 0.67	-5.96** ± 1.34	26.82** ± 4.02	32.24** ± 3.80	8.96** ± 3.45	-16.00** ± 6.5
LN	17.30** ± 0.81	0.85 ± 0.51	-30.30** ± 3.64	-6.90** ± -39.90	-39.90** ± 2.72	7.40** ± 4.65
AUDPC	477.51** ± 12.53	146.55** ± 18.97	-466.25** ± 65.34	-344.16** ± 62.89	-184.57** ± 42.30	1.23 ± 97.63
DSP	34.22** ± 0.73	10.02**± 1.07	-34.45** ± 3.79	-25.49** ± 3.66	-14.29** ± 2.38	2.15* ± 5.59

** and *: Significant at 1 and 5 per cent level, respectively

#(DPE) Days to panicle emergence, (DOF) Days to 50 per cent flowering, (DOM) days to maturity, (PH) plant height, (NET) number of effective tillers per plant, (PL) panicle length, (NFG) number of filled grains per panicle, (NUG) number of unfilled grains per panicle, (SFP) spikelet fertility per cent, (TW) test weight, (GY) grain yield per plant, (LN) lesion number, (AUDPC)area under disease progress curve and (DSP) disease severity per cent

Results of present experiment revealed that yield attributes and blast resistance traits in the cross HUR 3022 × Tetep of rice are governed by more than one gene showing duplicate epistatic interactions. Although, the additive gene effect was highly significant for all the blast resistance related traits in three parameter model and six parameter model, lesion number revealed that this was due to additive × additive type of epistasis. The grain yield depicted predominance of dominance gene action with higher additive × additive gene action and duplicate epistasis. The results show that for improvement of all the traits under study, biparental mating design and transgressive segregant selection in later generations will be helpful. The individual traits need to be improved simultaneously, to get all the positive alleles in one improved progeny.

Acknowledgments

The financial support in the form of a DST-INSPIRE Fellowship (INSPIRE Code: IF160896) to first author for full-time doctoral (Ph. D.) degree programme at Banaras Hindu University, Varanasi, Uttar Pradesh, India provided by Ministry of Science and Technology, Department of Science and Technology, New Delhi, Government of India as for this study is sincerely acknowledged.

References

Anonymous (2021) Food and Agricultural Organization statistic.www.faostat.org.

Anonymous (2021-22) Directorate of Economics and Statistics, Department of agriculture and farmers welfare, Ministry of agriculture and farmers welfare, GOI. https://eands.dacnet.nic.in/APY_96_To_06.htm.

Ashkani S, Rafii MY, Shabanimofrad M, Miah G, Sahebi M, Azizi P, Tanweer FA, Akhtar M S and Nasehi A. 2015. Molecular breeding strategy and challenges towards improvement of blast disease resistance in rice crop. *Frontiers in Plant Science*, 6(886): 1-14.

Bano DA, Singh SP and Waza SA. 2017. Generation mean analysis for yield and quality traits in aromatic genotypes of rice (*Oryza sativa* L.). *International Journal of Pure and Applied Bioscience*, 5(6): 870-878.

Billa SC, Haritha T, Krishnaveni B, Swapna M and Tushara M. 2024. Character association studies for yield, nutritional and cooking quality characters in coloured rice (*Oryza sativa* L.). *Journal of Rice Research*, 17(1): 65-71.

Boss CGS, Veni K, Rani Ch, Tushara M and Ramesh D 2024. Genetic parameters and association studies for yield and grain quality traits in rice genotypes derived from distant crosses. *Journal of Rice Research*, 17(1): 57-64.

Divya B, Robin S, *Rabi*ndran R, Senthil S, Raveendran M and Joel AJ. 2014. Marker assisted backcross breeding approach to improve blast resistance in indian rice (*Oryza sativa* L) variety ADT-43. *Euphytica*, 200(1): 61-77.

Hayman BI and Mather K. 1955. The description of genetic interaction in continuous variation. *Biometrics* 11**(**1**)**: 69-82.

IRRI (2013). Standardization evaluation system for rice. International Rice Research Institute, P.O. Box 933, 1099 Manila, Philippines, 5:18.

Jondhale AS, Bhave SG and Jogi SR. 2018. Genetic evaluation of quantitative traits of rice (*Oryza sativa* L.) by generation mean analysis. *Journal of Pharmacognosy and Phytochemistry*, 1: 2477-2480.

Kato H. 2001. Rice blast disease. Pesticide Outlook 12(1): 23-25.

Khush GS. 2005. What it will take to feed 5.0 billion rice consumers in 2030. *Plant Molecular Biology*, 59: 1-6.

Khush GS. 2013. Strategies for increasing the yield potential of cereals: case of rice as an example. *Plant Breeding,* 132(5): 433-436.

Kiani SH, Kazemitabar SK, Jelodar NAB and Ranjbar GA. 2013. Genetic evaluation of quantitative traits of rice (*Oryza sativa* L.) using generation mean analysis. *International Journal of Agriculture and Crop Sciences*, 5(19): 2329-2336.

Kour A, Kumar B, Singh B, Attri H and Bangarwa SK. 2019. Generation mean analysis for yield and grain quality traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 10(1): 289-292.

Kumar PS, Saravanan K and Sabesan T. 2017. Generation mean analysis for yield and grain quality characters in rice (*Oryza sativa* L.). *Plant Archives*, 17(1): 557-560.

Kumari K, Dass A, Dhar S, Sudhishri, Singh RK, Das TK and Rani A. 2024. Performance of basmati rice (*Oryza sativa* L.) under variable irrigation and nitrogen management. *Indian Journal of Agricultural Sciences*, 94(5): 467–471.

Liu CT, Mao BG, Yuan DY, Chu CC and Duan MJ. 2022. Salt tolerance in rice: physiological responses and molecular mechanisms. *Crop Journal*, 10(1):13–25.

Makwana RR, Patel VP, Pandya MM and Chaudhari BA. 2018. Inferences on magnitude and nature of gene effects for morpho-physiological traits in rice (*Oryza sativa* L.). *International Journal of Pure and Applied Bioscience*, 6(2): 1488-1493.

Mather K. 1949. Biometrical Genetics, Dover Publication, Inc., New York.

Qi Z, Du Y, Yu J, Zhang R, Yu M, Cao H, Song T, Pan X, Liang D and Liu Y. 2023. Molecular detection and analysis of blast resistance genes in rice main varieties in jiangsu province, china. *Agronomy*, 13(1): 157.

Sabin K, Bijay S, Amrit B, Raman GD, Bhuwan S, Priyanka N, Man SS and Prasad GS. 2016. Screening of different rice genotypes against *Pyricularia grisea* Sacc. in natural epidemic condition at seedling stage in chitwan, nepal.

Advances in Crop Science and Technology, 4(4): 1-6.

Singh VK, Singh A, Singh SP, Ellur RK, Singh D, Krishnan SG, Bhowmick PK, Nagarajan M, Vinod KK, Singh UD, Mohapatra T, Prabhu KV and Singh AK. 2013. Marker assisted simultaneous but stepwise backcross breeding for pyramiding blast resistance genes *Piz5* and *Pi54* into an elite basmati rice restorer line 'PRR 78'. *Plant Breeding*, 132(5):486-495.

Yarasi B, Sadumpati V, Immanni CP, Vudem DR and Khareedu VR. 2008. Transgenic rice expressing allium sativum leaf agglutinin (ASAL) exhibits high level resistance against major sap-sucking pests. *BMC Plant Biology*, 8(102): 1-13.

Yin JJ, Zou LJ, Zhu XB, Cao YY, He M and Chen XW. 2021. Fighting the enemy: How rice survives the blast pathogen's attack. *Crop Journal,* 9(3):543–552.

Zhang H, Li G, Li W and Song F. 2009. Transgenic strategies for improving rice disease resistance. *African Journal of Biotechnology,* 8(9):1750-1757.