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Evaluation of BC₃F₄ and BC₄F₅ progenies of Tellahamsa and MTU1010 for yield and yield related traits

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Abstract

In India, 65% of the population depends on rice as their staple food and the country is a huge contributor to the global rice production. However, biotic and abiotic stresses are causing huge yield losses. Many developed new improved cultivated rice for resistance against Blast and BB through molecular breeding approach involving DNA marker, but the improved cultivars yield was not up to the mark. In order to improve rice production and productivity there is an urgent need to improve popular rice varieties by having resistance genes against biotic stresses along with yield related traits. Agro-morphological evaluation was carried out in 29 advanced backcross lines. Replication wise data was recorded for eight yield and yield contributing characters *viz.*, days of 50% flowering (DFF), plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, grain yield per plant (g), 1000 seed weight (g) and grain type and RBD analysis was carried out. In case of Tellahamsa derived lines, six progenies shown significant superiority over Tellahamsa and four lines were on par with Tellahamsa for yield. Among 10 MTU1010 derived lines, five lines showed significant superiority over MTU1010 for yield.

Keywords: BC₃F₄, BC₄F₅, MTU1010, Tellahamsa and yield traits

Introduction

Rice is the most valuable and primary food crop for more than 50% of the world's population (Khush, 2005 and Latif *et al.*, 2011) [5, 8]. The rice consumer is increasing and demand for rice is also moving up due to better living standards. Various studies have shown that to meet the increase demand for rice, production has to be increased more than 40% by 2030 (Khush, 2005) [5]. This challenge has to be overcome by the development of high yielding rice varieties with tolerance to biotic and abiotic stress (Selvaraj *et al.*, 2011) [14]. This yield difference is due to diseases in rice. Among the biotic stresses blast and BB diseases are the most harmful threat to high productivity of rice (Li *et al.*, 2007 and Kwon *et al.*, 2002) [10, 7]. Due to its wide distribution and ability to survive in wide range of environmental conditions. Due to this disease, yield loss ranged from 1 to 50%, meaning each year destroys abundant rice to feed more than 60 million. This loss in rice yield should be minimized in order to help the marginal and poor farmers of developing countries (Latif *et al.*, 2011) [8]. Even though some of the cultivars has the resistance to the above mentioned diseases, the yield is very low which cannot withstand the upcoming crisis in the country. Farmers also mostly prefer the varieties which give high yields. Many rice researchers and breeders (Narayanan *et al.*, 2002 and Zhao *et al.*, 2010) [11] have developed new improved cultivated rice for resistance against Blast and BB through molecular breeding approach involving DNA marker, but the improved cultivars yield was not up to the mark. In order to improve rice production and productivity there is an urgent need to improve popular rice varieties by incorporating resistance genes of bacterial blight and blast along with high yield traits. In order to address the above said issues, the efforts have been made and developed advanced backcross progenies of MTU1010 and Tellahamsa pyramided with both bacterial blight (*xa13* and *Xa21* from GPP2) and blast (*Pi54* and *Pi1* from NLR145) resistance genes by Institute of Biotechnology, Rajendranagar, Hyderabad where in GPP2 was used as a donor for bacterial blight resistance genes, *xa13* and *Xa21*, while NLR145 was used as donor for blast resistance genes, *Pi54* and *Pi1*. A total of 29 advanced backcross lines of Tellahamsa (BC₃F₄) and MTU1010 (BC₄F₅) were evaluated in our study along with parental lines *viz.*, NLR145, GPP2, MTU1010 and Tellahamsa. Among the developed advanced backcross progenies some lines has shown resistance to both BB and blast disease causing pathogens. Now there is a need to evaluate the yield traits of these developed lines comparing with their recurrent parents. On addressing the above issue the present work has been framed.

Material and Methods

Experimental location

The crop was raised at College Farm, PJTSAU during *Kharif*, 2017. The standard agronomic practices recommended for rice were followed to raise a good crop.

Plant material

Cottondora Sannalu (MTU1010) is a mega rice variety released from APRRI, Maruteru derived from the cross, Krishnaveni/IR64 possessing short duration, high yielding ability with long slender grain. This variety is tolerant to brown plant hopper, a major insect pest but has been found to be susceptible to Bacterial leaf blight (BB) and Blast diseases. Tellahamsa (RNR 10754), released from Rice Research

Centre, Rajendranagar, Hyderabad derived from the cross, HR12/TN1 occupied maximum area in Telangana State particularly during *rabi* season because of its cold tolerance coupled with fine grain quality. However, it is susceptible to BB and blast diseases which are endemic to many rice growing states in India.

GPP2 was developed from ICAR-IIRR from the cross B95-1 (Improved Samba Mahsuri/Abhaya) and having BB and gall midge resistance genes (*xa13*, *Xa21* and *Gm4*). It was used as a donor parent for BB resistance (*xa13* and *Xa21*) genes. NLR 145 (Swarnamukhi), a popular semi dwarf rice variety released from ARS, Nellore, derived from three way cross, CICA-4/IR-625-23-3-1//Tetep, in which Tetep was the source for blast resistance (*Pi54* and *Pi1*) genes.

Table 1: List of advanced backcross progenies evaluated during *Kharif*, 2017

S. No	Code No. of advanced backcross progenies	Generation	Recurrent parent	Target genes
1	TPL-53	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i> , <i>Pi1</i>
2	TPL-54	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i> , <i>Pi1</i>
3	TPL-55	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i> , <i>Pi1</i>
4	TPL-56	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i> , <i>Pi1</i>
5	TPL-57	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i>
6	TPL-58	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i>
7	TPL-59	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i>
8	TPL-60	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i>
9	TPL-61	BC ₃ F ₄	Tellahamsa	<i>Pi54</i> , <i>Pi1</i>
10	TPL-62	BC ₃ F ₄	Tellahamsa	<i>Pi54</i> , <i>Pi1</i>
11	TPL-63	BC ₃ F ₄	Tellahamsa	<i>Pi54</i> , <i>Pi1</i>
12	TPL-64	BC ₃ F ₄	Tellahamsa	<i>Pi54</i> , <i>Pi1</i>
13	TPL-65	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi1</i>
14	TPL-66	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i> , <i>Pi1</i>
15	TPL-67	BC ₃ F ₄	Tellahamsa	<i>xa13</i> , <i>Pi54</i> , <i>Pi1</i>
16	TPL-68	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>Pi54</i> , <i>Pi1</i>
17	TPL-69	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>Pi54</i> , <i>Pi1</i>
18	TPL-70	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i>
19	TPL-71	BC ₃ F ₄	Tellahamsa	<i>Xa21</i> , <i>xa13</i>
20	MPL-1	BC ₄ F ₅	MTU1010	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i> , <i>Pi1</i>
21	MPL-2	BC ₄ F ₅	MTU1010	<i>xa13</i> , <i>Pi54</i> , <i>Pi1</i>
22	MPL-3	BC ₄ F ₅	MTU1010	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i>
23	MPL-4	BC ₄ F ₅	MTU1010	<i>Xa21</i> , <i>Pi54</i> , <i>Pi1</i>
24	MPL-5	BC ₄ F ₅	MTU1010	<i>Xa21</i> , <i>xa13</i> , <i>Pi1</i>
25	MPL-6	BC ₄ F ₅	MTU1010	<i>Xa21</i> , <i>xa13</i>
26	MPL-7	BC ₄ F ₅	MTU1010	<i>Xa21</i> , <i>Pi54</i>
27	MPL-8	BC ₄ F ₅	MTU1010	<i>Xa21</i> , <i>Pi1</i>
28	MPL-9	BC ₄ F ₅	MTU1010	<i>Xa21</i> , <i>xa13</i> , <i>Pi54</i> , <i>Pi1</i>
29	MPL-10	BC ₄ F ₅	MTU1010	<i>Xa21</i> , <i>xa13</i>

Evaluation of advanced backcross progenies for agro-morphological parameters along with the recurrent parents

Nineteen progenies of Tellahamsa and 10 progenies of MTU1010 along with recurrent parents MTU1010 and Tellahamsa were grown during *Kharif* season 2017 at College Farm, PJTSAU, Rajendranagar.

The material was raised in Randomized Block Design (RBD) with three replications. A healthy crop was raised by following standard agronomic practices recommended by PJTSAU.

The data on days of 50% flowering (DFF), plant height (cm), Number of productive tillers per plant, Number of filled grains per panicles, panicle length (cm), Grain yield per plant (g), 1000 seed weight (g) and grain type was collected and analysed for determining the potentiality of genotypes. Days to 50% flowering was recorded on entire plot basis, while remaining characters were recorded from five plants randomly selected plants. The average values of five plants per replication was considered for RBD analysis.

1. Days to 50% flowering (DFF)

Number of days taken for 50 percent of plants having at least one panicle emerged. Days to 50% flowering was calculated from the date of sowing.

2. Plant Height (cm)

The plant height is measured from ground level to the tip of the longest panicle/leaf, measured in centimeters.

3. Number of productive tillers per plant

Total number of productive tillers per plant was counted at the time of maturity.

4. Panicle length (cm)

This parameter was measured in centimeters from the basal node of the panicle to the tip of upper most kernels.

5. Number of filled grains per panicles

The data on filled spikelets per panicle was recorded at maturity.

6. Grain yield per plant (g)

Panicles from five plants of each replication were harvested at maturity, threshed, cleaned and dried to 12-14 per cent moisture content and the weight was recorded in grams.

7. 1000 seed weight (g)

One thousand well filled grains were counted from five

individual plants in each replication and weighed with the help of electronic balance.

8. Grain type

Grain type was recorded from 10 randomly selected seeds from each plant based on length and breadth in millimeters.

Table 2: Classification of rice lines based on Length/Breadth ratio (SES, IRRI, 1996)

State	Length/breadth ratio	Kernel length (mm)
Short Slender	> 3.0	< 6.0
Short Bold	< 2.5	< 6.0
Medium Slender	2.5-3.0	< 6.0
Long Slender	> 3.0	> 6.0
Long Bold	< 3.0	> 6.0
Extra Long Slender	> 3.0	> 7.5
Basmati type	> 3.0	> 6.61

Statistical analysis

The mean data collected from three replications of advanced backcross progenies of Tellahamsa and MTU1010 was subjected to analysis of variance (ANOVA) by using OPSTAT version 9.1 software.

Results and Discussion

Evaluations of advanced back cross lines for Agro-Morphological Characters

A total of Twenty nine advanced back cross lines along with recurrent parents (MTU1010 and Tellahamsa) were evaluated in three replications for yield and yield related traits. and The data was recorded as described in material and methods at College Farm, PJTSAU, Rajendranagar, Hyderabad. Eight traits *viz.*, days of 50% flowering (DFF), plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, grain yield per plant (g), 1000 seed weight (g) and Grain type were considered for final selection of lines with yield on par or above recurrent parents along with resistance to BB and blast. The mean values of replicated data were subjected to RBD analysis with OPSTAT version 9.1 software. The mean values of the above listed traits are given in Table 3

The DFF values of the improved lines are ranged from 86 to 101 days with a mean of 93 days. The recurrent parents, MTU1010 and Tellahamsa have displayed an average value of 93 and 85 days, respectively. Among Tellahamsa derivatives, TPL-57 recorded on par for DFF when compared to Tellahamsa (85 days). Seven lines of MTU1010 (MPL-1, MPL-2, MPL-3, MPL-4, MPL-5, MPL-6) flowered significantly late, while MPL-7, MPL-9 flowered early compared to MTU1010. The flowering duration of MPL-8 is similar to MTU1010. As expected from marker assisted back cross breeding, 50% flowering duration of lines majority of lines are on par with their respective recurrent parents.

The plant height values of the improved lines are ranged from 84 to 105 cm with a mean of 96 cm height while, MTU 1010 and Tellahamsa have displayed 97 and 102 cm, respectively. Two lines of Tellahamsa (TPL-55 and TPL-56) showed numerical superiority over Tellahamsa where as two lines (TPL-53 and TPL-69) were on par with Tellahamsa for plant height.

The number of productive tillers per plant were ranged from 8 to 13 with a mean value of 10, while MTU1010 and Tellahamsa displayed an average of 10 productive tillers per plant. Except TPL-63, remaining all back cross progenies produced productive tillers like their respective recurrent parents. This result was expected because of recovery of > 96% recurrent parent genome (RPG) after 3 to 4 backcrosses.

The panicle length of the improved lines is ranged from 19 cm to 29 cm panicles with a mean of 22 cm for panicles, while MTU1010 and Tellahamsa displayed panicle lengths of 22 and 22 cm, respectively. Three lines *viz.*, TPL-55 and TPL-56 showed significant superiority over Tellahamsa for panicle length. None of the MTU1010 derived lines significantly differed from MTU1010.

The number of filled grains per panicle of the improved lines ranged from 86 to 145 with a mean of 122. MTU1010 and Tellahamsa displayed mean of 140 and 118 grains, respectively. Ten Tellahamsa derived lines (TPL-53, TPL-55, TPL-56, TPL-57, TPL-58, TPL-59, TPL-60, TPL-62, TPL-64 and TPL-69) exhibited numerical superiority over Tellahamsa. (Table-3). MPL-1 and MPL-2 were found inferior to MTU1010, while remaining entries did not differ significantly from MTU1010 for this trait.

The grain yield of improved lines was ranged from 14 g to 31g with a mean value of 23 g, while MTU1010 and Tellahamsa recorded mean of 25 g and 26 g, respectively. In case of Tellahamsa derived lines, six progenies (TPL-53, TPL-56, TPL-59, TPL-62 TPL-68 and TPL-69) exhibited significant superiority yields over Tellahamsa and four lines (TPL-54, TPL-55, TPL-60 and TPL-71) were on par with Tellahamsa for yield. In case of MTU1010 derived lines, five lines (MPL-1, MPL-4, MPL-7, MPL-8, and MPL-9) were significantly superior over MTU1010 (Table 3). Significant superiority over recurrent parent yield was due to increase in number of filled grains per panicle in TPL-53, TPL-56, TPL-59 and TPL-62 when compared to parent. In case of TPL-68, MPL-1 and MPL-9 yield superiority over parents is due to more number of productive tillers when compared to recurrent parents, whereas in case of MPL-4, MPL-7 and MPL-8 lines was due to increased grain weight of these lines compared to parents.

Table 3: Agro-morphological data of advanced backcross progenies of rice for *kharif* season 2017

Entry No	Gene combination	Days to 50% flowering	Plant height (cm)	Number of productive tillers per plant	Panicle length (cm)	Number of filled grains per panicle	Grain yield per plant (g)	1000 seed weight (g)	Grain type
TPL-53	<i>xa13, Xa21, PI54, PII</i>	90	102	9	22.0	136	31.0	22.67	LS
TPL-54	<i>xa13, Xa21, PI54, PII</i>	91	99	12	21.6	86	30.2	23.67	LS
TPL-55	<i>xa13, Xa21, PI54, PII</i>	90	103	9	27.6	145	30.4	19.00	LS
TPL-56	<i>xa13, Xa21, PI54, PII</i>	97	105	9	28.6	145	31.2	23.33	LS
TPL-57	<i>xa13, Xa21, PI54</i>	86	84	12	22.3	141	26.4	22.67	LS
TPL-58	<i>xa13, Xa21, PI54</i>	88	94	9	22.0	138	21.0	22.67	LS
TPL-59	<i>xa13, Xa21, PI54</i>	90	87	9	22.3	126	31.2	21.00	LS
TPL-60	<i>xa13, Xa21, PI54</i>	89	86	11	20.3	126	30.5	22.33	LS
TPL-61	<i>PI54, PII</i>	96	94	10	22.6	117	24.4	23.33	LS
TPL-62	<i>PI54, PII</i>	96	93	11	23.6	135	30.6	25.67	LB
TPL-63	<i>PI54, PII</i>	96	84	13	20.6	104	15.0	24.00	LS
TPL-64	<i>PI54, PII</i>	96	88	12	21.0	131	18.0	24.67	LS
TPL-65	<i>xa13, Xa21, PII</i>	89	100	10	21.0	108	18.4	22.00	LS
TPL-66	<i>xa13, Xa21, PII</i>	92	97	8	22.0	98	14.4	22.67	LS
TPL-67	<i>xa13, PI54, PII</i>	93	101	10	20.0	108	20.2	21.00	LS
TPL-68	<i>Xa21, PI54, PII</i>	91	99	12	22.0	110	30.7	21.67	LS
TPL-69	<i>Xa21, PI54, PII</i>	93	102	10	18.6	133	30.6	20.00	LS
TPL-70	<i>xa13, Xa21</i>	94	97	10	20.6	105	17.1	21.67	LS
TPL-71	<i>xa13, Xa21</i>	94	98	10	20.3	103	30.2	20.00	MS
TH		85	102	10	22.3	118	26.0	23.33	LS
MPL-1	<i>xa13, Xa21, PI54, PII</i>	98	90	12	20.6	104	30.3	18.67	LS
MPL-2	<i>xa13, PI54, PII</i>	97	101	8	21.0	106	15.2	17.00	LS
MPL-3	<i>xa13, Xa21, PI54</i>	99	93	9	21.6	132	14.2	19.33	LS
MPL-4	<i>Xa21, PI54, PII</i>	98	90	9	22.6	118	29.8	25.67	LB
MPL-5	<i>xa13, Xa21, PII</i>	101	90	11	21.6	120	22.0	22.00	LS
MPL-6	<i>xa13, Xa21</i>	98	100	9	21.6	133	22.0	23.00	LB
MPL-7	<i>Xa21, PI54</i>	90	99	9	20.6	113	30.1	24.00	LB
MPL-8	<i>Xa21, PII</i>	92	99	9	219.6	117	29.6	23.67	LS
MPL-9	<i>xa13, Xa21, PI54, PII</i>	90	100	12	21.6	125	29.6	17.67	LS
MPL-10	<i>xa13, Xa21</i>	96	98	11	21.6	135	19.2	21.33	LS
MTU1010		93	97	10	22.6	140	25.0	22.33	LS
MEAN		93	96	10	21.86	122	23.0	22	
SE(M)		0.4	2.80	0.81	0.99	10.15	1.61	0.815	
SE(D)		0.66	3.96	1.14	1.413	14.36	2.27	1.15	
CV		0.87	5.05	13.87	7.920	14.44	12.13	6.42	
CD 95%		1.32	7.91	2.29	2.828	28.72	4.55	2.30	

The 1000 seed weight values of the improved lines are ranged between 17 g and 26 g with a mean of 22 g. MTU1010 and Tellahamsa displayed test weights of 22 g and 23 g, respectively. In case of Tellahamsa derived lines, two lines (TPL-62 and TPL-64) were significantly superior over Tellahamsa and three lines (TPL-55, TPL-69 and TPL-71) were significantly inferior to Tellahamsa. Among MTU 1010 derived lines MPL-4 recorded significantly superior test weight over MTU1010. MPL-1, MPL-2, MPL-3 MPL-9 were significantly inferior to MTU1010 for test weight.

The recurrent parents, Tellahamsa and MTU1010 are having long slender grain type. Like recurrent parents long slender grain was observed in all lines except TPL-62, MPL-4, MPL-6 and MPL-7.

Several researchers evaluated advanced back cross progenies for yield and yield related traits. Aruna kumari, 2013 [1] and Sravanthi, 2017 [16] evaluated ICF₃ and BC₃F₃ generations derived from MTU1010 for yield and yield contributing traits. Similarly, Sundaram *et al.*, 2008 [17] evaluated yield and agro-morphological traits of four of the three-gene pyramid lines at BC₄F₆ generation along with the donor and recipient. The recipient parent Samba Mahsuri recorded an overall mean grain yield of 4,739 kg/ha while, the donor parent recorded 4,486 kg/ha. Three of the pyramided lines showed grain yields on par with Samba Mahsuri. However, the test entries did not show any significant variation as compared to Samba Mahsuri in terms of flowering duration, panicles m⁻², plant stature as well as other characters that are considered under distinctness, uniformity and stability tests. Pandey *et al.*

(2012) [12] also evaluated agronomic and Basmati-type grain quality of 96 and 16 pyramid lines in the BC₁F₄ generation from the crosses RP4693 and RP4694, respectively. They also observed significant variation among the pyramided lines for most of the agronomic traits.

Swathi *et al.* (2015) [19] carried out the study with the objective to improve BB resistance of JGL1798 through marker-assisted backcross breeding coupled with phenotypic selection for agro-morphological traits. Earlier, Sundaram *et al.* (2008) [17], Sundaram *et al.* (2009) [18], Gopalakrishnan *et al.* (2008) [3] and Hari *et al.* (2011) [4] Balachiranjeevi *et al.* (2015) [2] developed improved BB resistant versions of elite varieties Samba Mahsuri, Triguna, Pusa Basmati 1, PusaRH10 and the maintainer line, KMR-3R, respectively, for BB resistance. By comparing the above results, the yield levels of the two gene pyramided lines were not significantly different from that of the parent JGL1798 indicating that there is no yield penalty associated with the presence of the resistance genes. Similar observation was noticed by Shanti *et al.* (2010) [15], when worked with parental lines of hybrid rice for BB resistance.

Conclusion

The lines which are identified to be resistant to BB and blast with significant superiority for yield over parents can be advanced to multilocal yield trials and screening with wide number of BB and blast isolates. The promising lines are to be documented for important DUS descriptors. The superior lines can be further evaluated for their cooking

quality, amino acid and fatty acid profiling in comparison with MTU1010 and Tellahamsa before release them as improved versions of MTU1010 and Tellahamsa.

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References

1. Aruna Kumari K. Improvement of MTU1010 for bacterial leaf blight and blast resistance through marker assisted breeding. Ph. D Thesis. Acharya N.G. Ranga Agricultural University, Hyderabad, India, 2013.
2. Balachiranjevi CH, Naik SB, Abhilash V, Akanksha S, Viraktamath BC, Madhav MS *et al.* Marker assisted introgression of bacterial blight and blast resistance into DRR17B, an elite, fine-grain type maintainer line of rice. *Molecular Breeding*. 2015; 35:151.
3. Gopalakrishnan S, Sharma RK, Anand Rajkumar K, Joseph M, Singh VP, Singh AK *et al.* Integrating marker assisted background analysis with foreground selection for identification of superior bacterial blight resistant recombinants in Basmati rice. *Plant Breeding*. 2008; 127:131-139.
4. Hari Y, Srinivasarao K, Viraktamath BC, Hari Prasad AS, Laha GS, Ilyas M *et al.* Marker-assisted improvement of a stable restorer line, KMR-3R and its derived hybrid KRH2 for bacterial blight resistance and grain quality. *Plant Breeding*. 2011; 130:608-616.
5. Khush GS. What it will take to feed 5.0 billion rice consumers in 2030. *Plant Mol Biol*. 2005; 59:1-6. doi:10.1007/s11103-005-2159-5
6. Khush GS, Jena KK. Current status and future prospects for research on blast resistance in rice (*Oryza sativa* L.). In: Wang GL, Valent B (eds.) *Advances in genetics, genomics and control of rice blast disease*. Springer, Dordrecht, 2009, 1-10. doi: 10.1007/978-1-4020-9500-9
7. Kwon JO, Lee SG. Real-time micro-weather factors of growing field to the epidemics of rice blast. *Res Plant Dis*. 2002; 8:199-206.
8. Latif MA, Badsha MA, Tajul MI, Kabir MS, Rafii MY, Mia MAT. Identification of genotypes resistant to blast, bacterial leaf blight, sheath blight and tungro and efficacy of seed treating fungicides against blast disease of rice. *Sci. Res Essays*. 2011; 6(13):2804-2811. doi: 10.5897/SRE11.315
9. Latif MA, Rahman MM, Kabir MS, Ali MA, Islam MT, Rafii MY. Genetic diversity analyzed by quantitative traits among rice (*Oryza sativa* L.) genotypes resistant to blast disease. *Afr J Microbiol Res*. 2011; 5(25):4383-4391. doi:10.5897/AJMR11.492
10. Li YB, Wu CJ, Jiang GH, Wang LQ, He YQ. Dynamic analyses of rice blast resistance for the assessment of genetic and environmental effects. *Plant Breeding*. 2007; 126:541-547. doi: 10.1111/j.1439-0523.2007.01409.x
11. Narayanan NN, Baisakh N, Vera Cruz CM, Gnanamanickam SS, Datta K, Datta SK. Molecular breeding for the development of blast and bacterial blight resistance in rice cv. IR50. *Crop Sci*. 2002; 42(6):2072-2079. doi:10.2135/cropsci2002.2072
12. Pandey S, Bhandari H, Ding S, Prapertchob P, Sharan R, Naik D *et al.* Coping with drought in rice farming in Asia: insights from a cross country comparative study. *Agriculture Economics*. 2012; 37:213-224.
13. Scheuermann KK, Raimondi JV, Marschalek R, de Andrade A, Wickert E. Magnaporthe oryzae genetic diversity and its outcomes on the search for durable resistance. *Mol Basis Plant Genet Divers*, 2012, 331-356. doi: 10.5772/33479.
14. Selvaraj CI, Nagarajan P, Thiagarajan K, Bharathi M, Rabindran R. Studies on heterosis and combining ability of well-known blast resistant rice genotypes with high yielding varieties of rice (*Oryza sativa* L.). *Int J Plant Breed Genet*. 2011; 5(2):111-129. Doi: 10.3923/ijpb.2011.111.129
15. Shanti LM, Lalithadevi G, Naveen Kumar G, Shashidhar HE. Molecular marker assisted selection. A tool for insulating parental lines of hybrid rice against Bacterial Leaf Blight. *International Journal of Plant Pathology*. 2010; 1(3):114-123.
16. Sravanthi P. Marker assisted selection in Advanced backcross Population of rice variety, MTU1010 for bacterial blight and blast resistance. Ph.d. Thesis, 2017.
17. Sundaram RM, Priya MRV, Biradar SK, Laha GS, Reddy GA, Rani NS *et al.* Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety. *Euphytica*. 2008; 160:411-422.
18. Sundaram RM, Priya MRV, Laha GS, Shobha Rani N, Srinivasa Rao P, Balachandran SM *et al.* Introduction of bacterial blight resistance into Triguna, a high yielding, mid-early duration rice variety by molecular marker assisted breeding. *Biotechnology Journal*. 2009; 4:400-407.
19. Swathi G, Durga Rani CHV, Jamal-Oddin Arun Prem Kumar N, Vanisri S, Sheshu Madhav M. Marker-assisted breeding for resistance to bacterial leaf blight in popular fine grain variety Jagitial Sannalu. *International Journal of Current Research*. 2015; 7(12):23520-23525.
20. Zhao F, Cai Z, Hu T, Yao H, Wang L, Dong N *et al.* Genetic analysis and molecular mapping of a novel gene conferring resistance to rice stripe virus. *Plant Mol Biol Rep*. 2010; 28(3):512-518. doi:10.1007/s11105-009-0178-0