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DISEASE RESPONSE OF EXOTIC RICE GENOTYPES AGAINST BACTERIAL LEAF BLIGHT AND ITS EFFECT ON VARIOUS MORPHOLOGICAL TRAITS

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A B S T R A C T

The experiment was conducted for the evaluation of resistance status of near isogenic lines (IRBB lines) obtained from International Rice Research Institute (IRRI) against bacterial blight caused by *Xanthomonasoryzae* pv. *Oryzae* using RCBD design with three replications. For this purpose, 17 near isogenic lines of IR-24(check variety) having resistant genes against bacterial leaf blight of rice were studied for their gene status, resistance behavior and morphological traits. Resistance behavior of these lines was evaluated under natural artificial inoculated conditions. Plant agronomic traits like plant height, number of tillers, panicle length, number of fertile grains/panicle, 1000 grain weight; days to 50% flowering after transplanting (DAT) were also estimated along with the resistant parameters of the lines. The lines IRBB-21(having Xa-21 gene and 4% disease incidence), IRBB-59 (having xa-5, xa-13, Xa-21genes and, 2% disease incidence) and IRBB-66 (having Xa-4, Xa-7, xa-13, Xa-21 genes and, 6% disease incidence), were found to be the best resistant source against bacterial leaf blight of rice (BLB). These lines also have desirable morphological traits. So keeping in view the resistant status of these lines, excellent local breeding programme may be devised.

Keywords: *Oryza sativa* L, Resistance status, IRBB lines, BLB, Morphological traits

INTRODUCTION

Rice (*Oryzae sativa* L.) belongs to family Poaceae and is widely grown worldwide especially in the regions of tropical and subtropical (Ezuka and Kaku, 2000). Most of asian countries like Bangladesh, China, Pakistan, Vietnam, India and Korea use rice as a staple food (FAO, 2004). Rice occupies significant position in the economy of Pakistan and considered as unique crop among cereals globally (Zahid *et al.,*2005). Asian continent plays an important role for rice production and 90% of the world's rice is grown in this continent. More than 3 billion peoples of the world depend upon rice crop (Salim *et al.,* 2003). In Pakistan, rice is cultivated on about 10% area and its share towards cereal grains production of the country is 17% (Ahmad *et al.,* 2005). On the other hand, rice crop is attacked by many types of new emerging diseases that affect the yield of the crop including Bacterial leaf Blight (BLB) caused by *Xanthomonas oryzae* pv. *Oryzae* (Ali *et al.,* 2009). The BLB disease of rice is one of the most devastating and destructive disease causing huge yield losses annually. The yield losses due to BLB at the time of maturity may be 4.5-29.1% (Bedi & Gill, 1960). In Pakistan due to this disease the yield losses up to 20 to 30% (Ou, 1985).It has been reported in all rice growing areas of the world including Pakistan (Ilyas and Javed, 1995; Khan *et al.,*2000) except Europe. In Pakistan, the incidence of BLB has increased in recent years especially in Kallar tract that is famous for producing high quality rice (Akhter, 2003). In view of the severity and significant damage caused by this destructive disease worldwide, the scientists focused

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their attention on its control and management by using resistant varieties. Absence of resistance in basmati varieties against bacterial leaf blight (BLB) is one of the main reasons for the low yield in Pakistan (Tasleem *et al.,* 2005). Host plant resistance is an important component of an integrated management programme for this disease. The genetic basis of the host resistance has been well studied and 22 resistance genes have been identified from cultivated as well as wild rice species (Arif, 2002; Shanti *et al.,* 2001). Although the deployment of resistant genes in host is a very effective approach in controlling the diseases but the occasional and sometime frequent breakdown of resistance in many host plant-pathogen interactions have been reported (Jamil *et al.,* 2000). A total of ten races of *Xanthomonas oryzae* pv. o*ryzae* have been identified in Philippines and verified in many other countries (Vera Cruz *et al.,* 1996). This research describes genetic and morphogenetic traits of rice germplasm against BLB under local condition.

MATERIALS AND METHODS

Experiment was performed in RCBD design at the field area of Rice Research Institute Kala Shah Kaku. Seventeen Near Isogenic Lines of IR 24 (check variety) having resistant genes for bacterial leaf blight of rice (IRBB Lines) were selected to study resistance status against bacterial leaf blight (Table 1). The Near Isogenic Lines (NILs) include IRBB 3,4,5,7,8,10,11,13,21,54, 57, 58,59,61,64,65 and 66 using IR-24 as check. Nursery was sown on 20-05-2012 in one marla with appropriate number of seeds of each line and transplanted in the field at the age of 30 days with plant to plant spacing 9 inches and row to row distance 18 inches. Two rows of each entry were sown with plot size 2x3 m. Standard agronomic practices were performed and additional nitrogen application was applied at maximum tillering stage.

For inoculum preparation, the diseased leaf samples of rice were cut up to 5-10 mm, sterilized with 70 % ethanol for 10 seconds. Samples were washed twice with distilled water and placed in a Petri plate dipped in distilled water for 15 minutes. Bacteria were streaked out (isolated from diseased leaf sample) on artificial nutrient media (Marella *et al*., 2001) with the help of sterilized wire loop. Yellow colonies appeared on streaked plates after three days incubation at 30°C. Prepared inoculum was prepared by suspending bacterial cells in to flasks wrapped with aluminum foil to protect bacteria from sunlight. Inoculation was carried out using clip method (Kauffman *et al.,* 1973). For this purpose, 1 to 2 cm of the tips of three fully expanded leaves of each plant in each bucket were clipped with scissors dipped in inoculum. Control plants were inoculated similarly with sterilized distilled water.

Disease symptoms were appeared after fourteen days of inoculation and plants were observed every 24 h time of interval. All the data were recorded after 3 weeks of inoculation. The lesion length was recorded for first three leaves of five plants randomly and disease incidence was calculated. The disease scoring was made using standard evaluation system of rice (IRRI, 1996) Philippine (Table 2). Following formula was used for the calculation of percent disease incidence (Gnanamanickam *et al.,* 1999):

$$\%\ \text{Disease incidence} = \frac{\text{Lesion length}}{\text{Total leaf length}} \times 100$$

The data regarding morphological characteristics *viz.* plant height (cm), no. of tillers, panicle length (cm), no. of grains/panicle, 1000 grains weight (g), days to 50% flowering after transplanting (DAT) were recorded at the time of maturity.

RESULTS AND DISCUSSIONS

It has been witnessed during the last century that breeding crop plants is the only area for securing the global food provision. The breeding methods along with some innovation are used for evolving and screening crops (Ahmad *et al.,*2008; Khan *et al.,*2008; Gul *et al.,*2007; Nisar *et al.,*2007; Ahmad, 2001). Bacterial leaf blight is considered as an important disease in various parts of rice growing areas of Pakistan. Among the major diseases of rice, bacterial leaf blight causes substantial loss in quantity and quality of the crop. Bacterial leaf blight attacks on leaves and leaf sheath of rice plant at tillering and booting stage (Chunming*et al,.*2005). Bacterial leaf Blight of rice adversely affect grain filling and emergence of panicles which results about 28-30% yield reduction in susceptible cultivars (Karish *et al.,* 2003; Inamullah *et al.,* 2006). On the other hand, different rice lines were tested on the basis of various morphological traits that linked with resistant gene for identification and classification of resistant, moderately resistant and susceptible genotypes under disease stress condition. Gene status of Near Isogenic lines (NILs) depicted that the lines from

Table 1. Gene status and Origin of IRBB lines.

Sr. No.	Line No.	Gene Status	Origin	Taxon
1	IRBB 3	*Xa-3*	IRRI	*Oryza sativa*
2	IRBB 4	*Xa-4*	IRRI	*Oryza sativa*
3	IRBB 5	*xa-5*	IRRI	*Oryza sativa*
4	IRBB 7	*Xa-7*	IRRI	*Oryza sativa*
5	IRBB 8	*Xa-8*	IRRI	*Oryza sativa*
6	IRBB 11	*Xa-11*	IRRI	*Oryza sativa*
7	IRBB 13	*xa-13*	IRRI	*Oryza sativa*
8	IRBB 10	*Xa-10*	IRRI	*Oryza sativa*
9	IRBB 21	*Xa-21*	IRRI	*Oryza sativa*
10	IRBB 54	*Xa-4, Xa-21*	IRRI	*Oryza sativa*
11	IRBB 57	*Xa-4, xa-5, Xa-21*	IRRI	*Oryza sativa*
12	IRBB 58	*Xa-4, xa-13, Xa-21*	IRRI	*Oryza sativa*
13	IRBB 59	*xa-5, xa-13, Xa-21*	IRRI	*Oryza sativa*
14	IRBB 61	*Xa-4, xa-5, Xa-7*	IRRI	*Oryza sativa*
15	IRBB 64	*Xa-4, xa-5, Xa-7, Xa-21*	IRRI	*Oryza sativa*
16	IRBB 65	*Xa-4, Xa-7, xa-13, Xa-21*	IRRI	*Oryza sativa*
17	IRBB 66	*Xa-4, Xa-7, xa-13, Xa-21*	IRRI	*Oryza sativa*
18	IR 24 (Check)		IRRI	*Oryza sativa*

Le *et al.,* 2006

Table 2. Scale used for bacterial leaf Blight disease incidence.

Infection%	Score	Response
0	0	Highly Resistant (HR)
1-10	1	Resistant (R)
10-30	3	Moderately Resistant (MR)
30-50	5	Moderately Susceptible (MS)
50-75	7	Susceptible (S)
75-100	9	Highly Susceptible (HS)

Sanchez *et al.,* 2000

IRBB-3 to IRBB-21 are having single resistant gene (Xa-3, Xa-4, xa-5, Xa-7, Xa-8, Xa-11, xa-13, Xa-10 and Xa-21 respectively) for BLB resistance while lines from IRBB-54 to IRBB-66 having resistant gene in different combination (Table 1).

Resistant/ susceptibility response of IRBB lines under inoculated field conditions is discussed in Table 3. Among the screened lines, IRBB-3 and IRBB-7 having Xa-3, Xa-7 genes with 55% and 59% disease incidence respectively were found susceptible to bacterial leaf blight. Whereas IRBB-4, 5, 54, 57, 58, 61, and 64 were moderately resistant to disease attack. IRBB-8 (Xa-8 and 5% DI), IRBB-11 (Xa-11, 3% DI), IRBB-13 (xa-13, 4% DI), IRBB-10 (Xa-10, 7%), IRBB-21 (Xa-21,4% DI), IRBB-59 (xa-5, xa-13,Xa-21 , 2% DI), IRBB-65 (Xa-4, Xa-7, xa-13, Xa-21, 4% DI) and IRBB-66 (Xa-4, Xa-7, xa-13, Xa-21, 6% DI) were showing the resistant behavior against bacterial leaf blight. These results are in accordance with Le *et al.* (2006) and Jeung *et al.,* (2006). In several crop breeding programs gene pyramiding has been successfully applied to evolve high level of resistance using multiple resistance genes (Huang *et al.,* 1997; Samis *et al.,* 2002). The high level of resistance may be due to the result of gene interaction or quantitative complementation between resistant genes (Yoshimura *et al.,* 1995; Huang *et al.,* 1997; Sanchez *et al* ,2000 ; Salgotra *et al.,*2012).

As presented in Table-4, plant height ranged from 70.8cm for IRBB-11 to 139 cm for IRBB-59 followed by IRBB-58 with 91.2 cm. Panicle length is an important yield contributing trait, increased panicle length adds towards more number of grains and hence increased panicle length is desirable (Sharma *et al.,*2004). In this experiment, panicle length ranged from 20.6 in IRBB-3 to 28.2 in IRBB-59. Tillering ability is also major yield contributing factor. In present study, IRBB-10 with 23.2 and IRBB-64 with 17 tillers per plant respectively showed excellent tillering ability. However, IRBB-5 and IRBB-8 showed minimum number of tillers per plant (11.2). The numbers of grains per panicle and 1000 grain weight also contributes positively towards grain yield (Giri and Laxmi, 2000). Maximum number of grains/panicle was observed in IRBB-4 (169.2) followed by IRBB-57 (165) and IRBB-11 (161.2) while minimum number of grains/panicle were recorded in IRBB-10 (77). Highest 1000 grain weight was recorded in IRBB-8 with 24.2g, IRBB-21 with 23.95g and 23.06g in IRBB-6. However it was minimum for IRBB-54 (19.49g) followed by IRBB-65 (19.86) and IRBB-64 (19.89). Days to 50% flowering ranged from 44 in (IRBB-66, IRBB-65, IRBB-61, IRBB-58, IRBB-54, IRBB-3, IRBB-4, IRBB-10, IRBB-21 and IRBB-5) to 68 in IRBB 64.

This study reveals that the lines IRBB-21, IRBB-59 and IRBB-66, having best resistant source against BLB and desirable morphological traits, can be used in new breeding experiments for the development of BLB resistant rice variety. The information generated from this experiment would allow us to select resistant gene source for the screening of rice lines against BLB disease of rice. Overall this study will help the breeders, scientists and the farmer's community for the improvement and development of new rice varieties having resistance against bacterial leaf blight of rice and identification of new QTL on different chromosomal locations.

Table 3. Disease screening reaction of IRBB Lines.

Sr. No.	IRBB Line	Lesion length	Reaction Type	% Disease Incidence
1	IRBB 3	11	S	55
2	IRBB 4	3.65	MR	22
3	IRBB 5	4.26	MR	26
4	IRBB 7	10.6	S	59
5	IRBB 8	2.1	R	5
6	IRBB 11	2.72	R	3
7	IRBB 13	2.91	R	4
8	IRBB 10	2.87	R	7
9	IRBB 21	2.57	R	4
10	IRBB 54	2.84	MR	15
11	IRBB 57	3.1	MR	18
12	IRBB 58	3.05	MR	25
13	IRBB 59	3.56	R	2
14	IRBB 61	3.55	MR	20
15	IRBB 64	4.21	MR	13
16	IRBB 65	1.26	R	4
17	IRBB 66	4.25	R	6
18	IR 24 (Check)	12.25	S	63

Table 4. Morphological characters of IRBB lines.

Sr. No	IRBB Lines	Plant Height(cm)	No. of Tillers	50% flowering	Panicle Length(cm)	No. of Fertile Grains/Panicle	1000 Grains weight (g)
1	IRBB 3	75.8	15.2	44	20.6	140.6	22.56
2	IRBB 4	83.2	11.8	44	22	169.2	23.06
3	IRBB 5	82	11.2	44	24.2	119.2	22.09
4	IRBB 7	85.6	12.8	64	24	116.2	21.81
5	IRBB 8	87.8	11.2	53	23.8	120	24.20
6	IRBB 11	70.8	13.2	44	20.8	161.2	22.57
7	IRBB 13	77.6	12.2	58	22	144.4	22.51
8	IRBB 10	78.8	23.2	44	21.2	77.2	22.96
9	IRBB 21	79	14	44	21.6	129.4	23.95
10	IRBB 54	81.2	14	44	20.8	130	19.49
11	IRBB 57	85	13.6	45	23.6	165	21.95
12	IRBB 58	91.2	15.6	44	23.2	111.2	20.17
13	IRBB 59	139	14.4	55	28.2	140.6	22.12
14	IRBB 61	84.8	15.2	44	23.2	116	23.06
15	IRBB 64	85.6	17	64	22.4	98.8	19.89
16	IRBB 65	83	14.8	44	22.4	84.6	19.86
17	IRBB 66	90	16	44	21.6	102.2	22.49
18	IR24(Check)	93.67	31.33	53	24.00	130.00	22.56

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