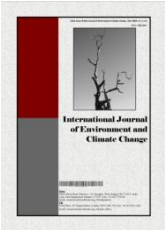

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Phenotypic Evaluation of Advanced Breeding Lines for Resistance against Bacterial Leaf Blight Disease in Rice (*Oryza sativa* L.)

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Bacterial Leaf Blight disease epidemically damaged the rice crop. Absence of resistance against BLB disease in MTU1010 is one of the main reason for these epidemics. Thus, there is urgent need to search for resistant source and subsequently, their phenotypic evaluation to validate the resistant source. In this paper discussing about the highlights of phenotypic evaluation of Bacterial Leaf Blight resistance in MTU1010 NIL variety of rice. In the present study, fifty advanced breeding lines along with parents *i.e.,* MTU1010 NIL X Akshayadhan NIL, were screened for bacterial leaf blight disease, Thirty-four breeding lines were shown resistance against bacterial leaf blight disease.

Keywords: Bacterial leaf blight, MTU1010 NIL and akshayadhan NIL.

1. INTRODUCTION

Rice is the principal staple food crop of the world and rice production has so far kept pace with the growing population, predominantly due to cultivation of high-yielding, high-input demanding, and semi-dwarf varieties [1]. Rice cultivation source of income for millions of

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households around the globe and several countries of Asia and Africa are highly dependent on rice as a source of foreign exchange earnings and government revenue. The rice crop is susceptible to number of diseases among which bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *Oryzae* is one of most devasting disease throughout Asia and they are endemic to several rice growing states in Telangana of India (Production Oriented Survey, DRR, 2008). MTU1010, a short duration rice variety released in 2000 derived from the cross Krishnaveni/IR64, is extremely popular and has been planted for many years in a minimum of one million hectares. This variety possesses resistance against brown plant hopper with long slender grains and is highly susceptible to bacterial blight which limits its spread to areas where the disease is endemic. Bacterial blight (BB) can cause yield loss as high as 50% or more. Sometimes, the disease may occur at different period of growth stages causing severe loss to rice crop (POS, 2008). In the absence of effective chemicals or any other methods of control agents against BB pathogen [2], development of durable, broad-spectrum resistant varieties has been encouraged [3,4,5]. Breeding for host-plant resistance is considered as the most economical and eco-friendly strategy for management of pests and diseases of crop plants and achieving yield stability. The only feasible and economical way of controlling diseases is the use of resistant rice cultivars. In view of the importance of genetic resistance for disease control, studies were undertaken to evaluate the rice genotypes against BLB disease.

2. MATERIALS AND METHODS

2.1 Plant Material

The plant material includes two rice varieties which are used as a parents of single cross MTU1010 NIL /Akshayadhan NIL. The fifty advanced breeding lines were screened for bacterial blight resistance as per SES scale, 2013.

2.2 Isolation and Characterization of the Bacterial Blight Pathogen

Virulent race of *Xanthomonas oryzae pv. oryzae (Xoo)* was isolated from the infected leaf samples on modified Wakimoto's medium which is collected from Hyderabad, Telangana were maintained on Hayward's agar media at 28^0C for 96 hours. After incubation period, the bacterial cells were harvested and diluted with 10ml of sterile distilled water to get a final concentration of approximately 10^{8-9} cfu/µl [6]. The pathogenicity of the bacterial pathogen was confirmed on susceptible rice variety MTU1010.

2.3 Screening of Advanced Breeding Lines

Fifty advanced breeding lines along with parents (with 3 rows of 2 meter length plot size, with 15 x 15 cm spacing and with 2 replications using RBD design) were screened in the field for bacterial blight disease resistance during *Rabi* season using virulent race of *Xanthomonas oryzae pv. oryzae (Xoo)*. The bacterial pathogen was multiplied on modified Wakimoto's medium at 28 ± 1^0C. Advanced breeding lines were inoculated with bacterial suspension at maximum tillering stage (55 days after transplanting) by following leaf clipping method described by Kauffman et al. [7]. Inoculation was carried out by clipping the tip (about 1 to 2 cm) of fully expanded uppermost leaf with scissors dipped into the inoculum. Ten leaves were inoculated per plant and disease reaction was scored after 15 days after inoculation. The Lines were categorized as resistant (lesion length d" 4 cm), moderately resistant (lesion length 4.1-8 cm) or susceptible (lesion length > 8 cm) [8].

3. RESULTS

3.1 Phenotyping for Bacterial Blight Resistance Gene in Advanced Breeding Lines

A total 50 advanced breeding lines along with parents were screened using bacterial cultures of a virulent local isolate of the bacterial blight pathogen, DX-020. The advanced breeding lines were inoculated with bacterial culture at maximum tillering stage by following leaf clip inoculation method of kaufman et al. (1973). Along with the breeding lines, resistant checks, Improved Samba Mahsuri and Akhayadhan (NIL) and susceptible parent MTU1010 NIL were also screened for bacterial blight resistance under field conditions. The lesion length on leaves was measured at 15 days after inoculation. Scoring was done as per SES scale, IRRI, 2013. Out of 50 advanced breeding lines evaluated against BB, 34 breeding lines *viz*., VSR-1, VSR-2, VSR-3, VSR-4, VSR-5, VSR-6, VSR-13, VSR-14, VSR-15, VSR-17, VSR-18, VSR-19, VSR-20, VSR-21, VSR-22, VSR-23, VSR-24, VSR-25,

VSR-26, VSR-27, VSR-28, VSR-29, VSR-30, VSR-31, VSR-33, VSR-34, VSR-35, VSR-36, VSR-42, VSR-44, VSR-45, VSR-47, VSR-48 and VSR-50 were found resistance with disease score of 1. Thirteen breeding lines *viz*., VSR-7, VSR-8, VSR-9, VSR-10, VSR-11, VSR-12, VSR-16, VSR-33, VSR-37, VSR-38, VSR-40, VSR-41 and VSR-46 were found moderately resistant to BB pathogen with disease score 3, remaining four breeding lines *viz*., VSR-32, VSR-39, VSR-43 and VSR-49 were found susceptible to BB pathogen with disease score 7. Susceptible check MTU1010 showed high susceptibility to the disease with a disease score of 9 and resistant checks Improved Samba Mahsuri and Akshayadhan showed highly resistant reaction to the disease respectively with a disease score of 1 in the Table 1.

Table 1. Screening details Advanced breeding lines for BB resistance and scoring details as per IRRI-SES scale (IRRI 2013)

Parents and Checks	Reaction against BB	
	DX020	
	Score	R/MR/S
MTU1010 NIL	9	S
Akshayadhan NIL	3	R
ISM (Resistant Check)	1	R
Improved breeding lines	Score	R/MR/S
VSR 1	1	R
VSR 2	1	R
VSR 3	1	R
VSR 4	1	R
VSR 5	1	R
VSR 6	1	R
VSR 7	3	MR
VSR 8	3	MR
VSR 9	3	MR
VSR 10	3	MR
VSR 11	3	MR
VSR 12	3	MR
VSR 13	1	R
VSR 14	1	R
VSR 15	1	R
VSR 16	3	MR
VSR 17	1	R
VSR 18	1	R
VSR 19	1	R
VSR 20	1	R
VSR 21	1	R
VSR 22	1	R
VSR 23	1	R
VSR 24	1	R
VSR 25	1	R
VSR 26	1	R
VSR 27	1	R
VSR 28	1	R
VSR 29	1	R
VSR 30	1	R

Parents and Checks	Reaction against BB	
	DX020	
	Score	R/MR/S
VSR 31	1	R
VSR 32	7	S
VSR 33	1	R
VSR 34	1	R
VSR 35	1	R
VSR 36	1	R
VSR 37	3	MR
VSR 38	3	MR
VSR 39	7	S
VSR 40	3	MR
VSR 41	3	MR
VSR 42	1	R
VSR 43	7	S
VSR 44	1	R
VSR 45	1	R
VSR 46	3	MR
VSR 47	1	R
VSR 48	1	R
VSR 49	7	S
VSR 50	1	R

4. DISCUSSIONS

Gene pyramiding with two or more genes is successful as per the studies Sundaram et al. [9] and Rekha et al. [14], but a single major BB resistance gene like *Xa21* have shown the desired level of resistance against the known isolates of BB pathogen. Similar results of single gene conferring resistance was observed with Hari et al. [10], Balachiranjeevi et al. [11], Abhilash et al. [12] and Laxmi Prasanna et al. [13] and the known isolates of BB pathogen confers good level of resistance. In the present study, the improved breeding lines for bacterial blight with major dominant gene is expected to show high level of resistance against the disease bacterial leaf blight in Telangana and South Indian States, as the *Xa21* gene are known to be effective in these locations (Aruna kumari et al., 2016 [13].

5. CONCLUSIONS

Results from mean disease score show similar trend for resistant, moderately resistant, moderately susceptible and susceptible genotype as obtained through SES scale visual scoring. In final words, through this study, out of 50 breeding lines, 34 breeding lines are resistant to bacterial leaf blight. These breeding lines can be utilized in various breeding programmes for bacterial blight resistance.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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