

## Short Communication

# Screening of Some Exotic Rice Germplasm Against Brown Spot (*Bipolaris oryzae*) Disease under Rainfed Conditions

Muhammad Yaqoob

Arid Zone Research Institute, PARC, D.I. Khan, Pakistan

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**Abstract.** Ten different lines including one approved variety and one susceptible check were tested against brown spot disease of rice under low water application conditions. The disease data were recorded on 1-9 rating scale. The results revealed highly significant differences among various rice genotypes against disease reaction ranging from highly resistant to highly susceptible in different genotypes. Three lines remained highly resistant, four resistant and two moderately resistant under rainfed conditions.

**Keywords:** *Oryza sativa* L, *Bipolaris oryzae*, rice genotypes

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Plant diseases are the major yield reducing agents in rice therefore, exploitation of genetic resistant is the most effective and economical way to control the rice disease (Mew, 1991). The farmers had only believed on resistant varieties in Philippine and Indonesia during epidemics of brown spot disease on rice in 1970s and 1980s (Patil *et al.*, 2010). Among various diseases, the brown spot of rice is one of the major problems caused by fungus *Cochliobolus miyabeanus* and it become more harsh under dry conditions, whereas, its effect is not too severe in flood irrigated conditions (Yaqoob *et al.*, 2011). Yield losses (60 to 100%) in rice were caused to widely grown cultivars Punshi and KD-2-6-3 due to sudden spread of *Pyricularia oryzae* disease that have been influenced due to dry spell (Singh, 1987).

The only way to overcome disease is development of resistant lines through screening under high disease pressure. Bacterial blight, blight resistant genes and rice yield losses due to this disease in irrigated and dry conditions have been studied earlier by many researchers. (Ghazanfar *et al.*, 2009; Mohanta *et al.*, 2003; Azzam and Chancellor, 2002; Chen, *et al.*, 2002; Khush and Virk, 2002; Shanti, *et al.*, 2001. Mekwatanakarn, *et al.*, 2000; Bonman *et al.*, 1991; Datnoff *et al.*, 1991; Fomba and Singh 1990).

The experiment was conducted at National Agricultural Research Centre, Islamabad, Pakistan during 2011. Ten diversified varieties/lines of rice were involved to identify the source of resistance against brown spot disease. The

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\*Authour for correspondence;

E-mail: yaqoobawan313@gmail.com

experiment was laid out in randomised complete block design with three replications. The crop was sown directly without raising proper nursery. Each genotype was planted in eight rows plot measuring 5 m in length. Row to row and plant to plant spacing was kept at 20 cm. The crop was maintained under low water (rainfed) conditions. A high yielding well adopted rice variety KSK-133 and a susceptible check (IR-83140-B-28-B) were also included in this experiment. To establish a good crop stand, the crop was however, kept under well watered conditions during early growth for a period of 30 days. After one month the crop was given light irrigation, only to keep the soil wet and the irrigation was suspended during rainy days. The disease data were recorded at panicle completion stage on 1-9 rating scale. The data were analysed through computer's software MSTAT-C for analysis of variance and significant means were further compared through LSD at 0.5% level of probability (Steel and Terrie, 1997).

The results of analysis of variance revealed highly significant variability among rice genotypes in reaction to brown spot disease and days to maturity. The mean values regarding disease reaction data given in Table 1, reveal that various rice lines have shown differential response to brown spot disease. The disease ranged from highly resistant (score 1) to highly susceptible (score 9). Out of the 10, three lines namely, HUA 564, SACG 4 and JH-15-1-1-1 scored 1 and remained highly resistant against brown spot under rainfed conditions. In our studies, the late lines HUA 564 did not show any disease symptoms and therefore, rated highly resistant (Table 1). This behaviour of HUA 564 may or may not

be considered as resistant against brown spot disease, as the data were recorded at panicle completion stage while, the line HUA 564 was still green with no panicle initiation and disease symptoms as well. Since the lines SACG 4 and JH-15-1-1-1 have shown proper resistance against disease with their normal maturity period therefore, these lines may be considered as source of resistant against brown spot disease. Likewise, the lines weed tolerant, HHZ5-Y3-SAL-DT1, HHZ9DT7-SAL2-DT1 and HHZ5-SAL10-DT2-DT1 have also showed resistance against brown spot (*Bipolaris oryzae*) by scoring 3 on the rating scale. All these genotypes were found normal in maturity (Table 1).

**Table 1.** Disease reaction of various rice lines against brown spot disease (*B. oryzae*)

Designation	Disease reaction	Maturity (Days)
HUA 564	1 <sup>d</sup>	140 <sup>d</sup>
SACG 4	1 <sup>d</sup>	120 <sup>bcd</sup>
Weed tolerant	3 <sup>c</sup>	123 <sup>bc</sup>
JH-15-1-1-1	1 <sup>d</sup>	122 <sup>bc</sup>
HHZ-11-Y-11-Y3-DT1	5 <sup>d</sup>	125 <sup>b</sup>
HHZ5-Y3-SAL3-DT1	3 <sup>c</sup>	124 <sup>b</sup>
HHZ9DT7-SAL2-DT1	3 <sup>c</sup>	123 <sup>bc</sup>
HHZ5-SAL10-DT2-DT1	3 <sup>c</sup>	126 <sup>b</sup>
IR-83140-B-28-B	9 <sup>a</sup>	120 <sup>bcd</sup>
KS-133	5 <sup>b</sup>	122 <sup>bc</sup>

Any two means sharing common letter are statistically non-significant at 5% level of probability.

Similarly, the lines HHZ-11-Y-11-Y3-DT1 and cultivar KS-133 were found to be moderately resistant by scoring 5. The susceptible check (IR-83140-B-28-B) remained highly susceptible by scoring 9 (Table 1). Mohanta *et al.* (2003) have also identified three highly resistant, 12 resistant and 16 moderately susceptible among 31 genotypes of rice against blast. Similarly, Ghazanfar *et al.* (2009) have also screened 1 resistant, 9 moderately resistant lines against brown spot disease of rice. The previous reports revealed that more than 40 blast resistance genes (Pi); 20 bacterial blight resistance genes (Xa) (Khush and Virk, 2002; Chen *et al.*, 2002) and rice tungro resistance genes (Azzam and Chancellor, 2002) had been identified. The development of near isogenic lines (NILs) and molecular markers has provided the essential tools for understanding pathogen diversity and population structures that form the basis of developing disease

resistant varieties. The NILs carrying individual resistance genes provide an efficient means to detect changes in pathogen corresponding to specific resistance genes. This approach has been widely used in characterising the bacterial blight (Shanti *et al.*, 2001) and blast pathogen populations (Mekwatanakarn *et al.* 2000). In view of above discussion, it can be concluded that source of resistance against *Bipolaris oryzae* is available in existing rice germ plasm. The level of resistance is however differential and specific to genotypes. The check entry IR-83140-B-28-B appeared to be highly susceptible against brown spot by scoring 9 which clearly indicates that disease infestation and spread was at full potential. The lines SACG 4 and JH-15-1-1-1 showing resistance against brown spot disease may be further utilised in rice breeding programme for development of brown spot resistance varieties.

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