Introduction

Rice blast caused by *Pyricularia oryzae* Cavara is one of the most serious diseases of rice (*Oryza sativa* L.) in Bangladesh and also worldwide (Khan et al. 2014, Ouy 1985). Breeding for resistance is considered one of the most promising methods to control blast, but no disease-resistant cultivars to combat this problem have yet been released in Bangladesh. The relationships between blast races and rice cultivars have been explained by the gene-for-gene theory (Flor 1956, Silué et al. 1992). In other words, the differentiation of blast races is assumed to correspond with resistance gene(s) in rice cultivars. Khan et al. (2016) clarified the diversity of blast races in various rice cultivation ecosystems and their geographical distributions in Bangladesh. However, the genetic variation in blast resistance in rice cultivars has not yet been clarified in detail in each ecosystem in Bangladesh.

Genetic variation in resistence to blast (*Pyricularia oryzae* Cavara) in rice (*Oryza sativa* L.) germplasms of Bangladesh

Mohammad Ashik Iqbal Khan, Mohammad Abdul Latif, Mohammad Khalequzzaman, Asami Tomita, Mohammad Ansar Ali and Yoshimichi Fukuta

1) Bangladesh Rice Research Institute (BRRI), Gazipur-1701, Bangladesh
2) Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki 305-8572, Japan
3) Tropical Agriculture Research Front (TARF), Japan International Research Center for Agricultural Sciences (JIRCAS), 1091-1 Kawarabaru, Ishigaki, Okinawa 907-0002, Japan

Genetic variation in blast resistance was clarified in 334 Bangladesh rice accessions from 4 major ecotypes (Aus, Aman, Boro and Jhum). Cluster analysis of polymorphism data of 74 SSR markers separated these accessions into cluster I (corresponding to the Japonica Group) and cluster II (corresponding to the Indica Group). Cluster II accessions were represented with high frequency in all ecotypes. Cluster II was further subdivided into subclusters IIa and IIb. Subcluster IIa accessions were represented with high frequency in only Aus and Jhum ecotypes. Cluster I accessions were more frequent in the Aman ecotype than in other ecotypes. Distinct variations in resistance were found, and accessions were classified into 4 groups (A1, A2, B1 and B2) based on their reactions to standard differential blast isolates. The most susceptible group was A2 (which included susceptible variety Lijiangxintuanheigu, most of the differential varieties, and a few Bangladesh accessions), followed in order by A1, B2 and B1 (the most resistant). Accessions from 4 ecotypes fell with different frequencies into each of these resistance groups. These results demonstrated that Japonica Group accessions were found mainly in Aman, and Indica Group accessions were distributed across all ecotypes. Susceptible accessions were limited in Aus and Aman.

Key Words: blast (*Pyricularia oryzae* Cavara), ecotype, genetic variation, resistance, rice (*Oryza sativa* L.).

In Bangladesh, the seasonal moisture regime and cultivation seasons have played an important role in the differentiation of rice into 3 principal ecotypes: Aus, Aman and Boro (Parsons et al. 1999). Aus cultivars are photoperiod-insensitive and are usually used in upland areas in the pre-monsoon season from March–April to July–August. Aman cultivars are mostly photoperiod-sensitive and are traditionally sown as lowland rainfed rice in June, transplanted following the Aus harvest, and harvested from November to December. Boro cultivars are sown in November or December, transplanted around January or February, and then harvested from April to May the following year. Traditionally, they have only been grown as dry-winter-irrigated rice on land which retains sufficient water. In addition to those 3 ecotypes, Jhum cultivation (slash-and-burn agriculture) is the predominant land-use system in the hill regions of Bangladesh (Chakma and Ando 2008). Thus, a complex system of rice cultivation is practiced by farmers in Bangladesh.

Telebanco-Yanoria et al. (2008) assessed the genetic diversity of blast resistance in a worldwide collection of 922 accessions, including 304 cultivars from Bangladesh, and indicated that, with the exception of susceptible types, accessions...
from South Asia including those from Bangladesh maintained a high diversity of resistance; however, they did not clarify in detail the genetic variations among Indica and Japonica Group rice cultivars or ecotypes in Bangladesh.

Glaszmann (1987) identified 6 isozyme groups among Asian rice cultivars, including cultivars from Bangladesh, and recognized the high diversity of Bangladesh rice germplasms. However, no Japonica Group accessions were included in that report. On the basis of KClO₃ resistance and the phenol reaction, Ueno et al. (1990) classified Bangladesh rice accessions into Japonica and Indica Groups, and Aman accessions included a high proportion classified into the Indica and Japonica Groups. Wang et al. (2013) used SSR markers to investigate DNA polymorphisms in 151 landraces from Bangladesh, and classified them into Aus, Indica Group and Japonica Group. However, their study mostly emphasized deep-water rice and did not include improved cultivars. Rahman et al. (2016) also found genetic differentiation of rice into Japonica and Indica Groups and aromatic rice accessions were categorized into the Japonica Group in Bangladesh.

SSR markers have demonstrated the potential to detect genetic diversity in rice germplasms and have been used for the differentiation of rice genome chromosomes among accessions to determine the relationship between Japonica and Indica Groups. Thus, we considered that polymorphism data obtained by using SSR markers would be useful for differentiating between the 4 major rice ecotypes, between the Japonica and Indica Groups and between landraces and improved cultivars in Bangladesh, in order to understand the genetic variation in rice germplasm.

In this study, we used SSR markers to assess genetic variation in 334 rice accessions collected throughout Bangladesh from the 4 major rice ecotypes. We then evaluated the genetic variation in the rice accessions with respect to blast resistance by comparing their patterns of reaction to 20 SDBIs from Bangladesh, Kenya and Japan with the patterns of reaction of 25 differential varieties (DVs).

This is the first systematic genetic study to clarify genomic differences by polymorphism data of SSR markers and to discuss the genetic variation in blast resistance in rice accessions and the present situation of rice varieties in Bangladesh in terms of their relationships between 4 ecotypes, between Japonica and Indica Groups, and between landraces and improved cultivars.

**Materials and Methods**

**Plant materials**

Rice accessions comprising 284 landraces and 50 improved varieties from Bangladesh, 25 DVs and a susceptible check variety (the Chinese Japonica Group cultivar Lijiangxintuanheigu [LTH]) were used to investigate the genetic variation in resistance to blast disease (Supplemental Table 1). The Bangladesh rice accessions were conserved in the Rice Gene Bank, Bangladesh Rice Research Institute (BRRI), Gazipur, Bangladesh. A total of 23 monoclonal lines carrying 21 resistance genes (Kobayashi et al. 2007, Tsunematsu et al. 2000) and 2 near isogenic lines (Telebanco-Yanoria et al. 2010) were used as the DVs. To postulate the presence of specific resistance genes in the accessions, the patterns of reaction of the accessions to SDBIs, which were selected in Japan (Hayashi 2005), Bangladesh (Khan et al. 2016) and Kenya (unpublished), were compared to patterns of reaction to the 25 DVs.

**DNA extraction and genotyping of rice accessions using SSR markers**

To clarify the differentiations of genome chromosomes among rice accessions, 74 SSR markers distributed over the 12 rice chromosomes were used (Supplemental Table 2). All SSR markers were selected from a public database (http://www.gramene.org). Whole genomic DNA was extracted from a young leaf of each accession following the method of Dellaporta et al. (1983) with little modification. Leaf tissue was ground in 200 µL of DNA extraction buffer with zirconium beads in a 2 mL micro tube. Next, 34 µL of 5 M potassium acetate was added, mixed well and incubated on ice for 5 min. The sample was then centrifuged for 10 min at 15,000 rpm. The supernatant (100 µL) was collected in a 1.5 mL micro tube and 100 µL of isopropanol was added, mixed gently and incubated at room temperature for 15 min. The sample was then centrifuged for 15 min at 15,000 rpm. The supernatant was discarded and the DNA washed with 70% ethanol. Finally, the DNA was dried and dissolved in 100 µL of sterile water and the harvested DNA preserved at −20°C. The DNA working sample was prepared for PCR by 20 times dilution with sterile water.

PCR was performed in 10 µL of a PCR mixture containing 0.7 µL sterile water, a total of 1 µL forward primer (2 µM) and reverse primer (2 µM), 5 µL of 2x Quick Taq HS DyeMix (Toyobo Co., Ltd., Osaka, Japan) and 3.3 µL DNA working sample concentrated to about 5–10 ng/µL. PCR amplification was performed with the following profile: 94°C for 2 min, and 40 cycles of 30 s at 94°C, 30 s at 50–67°C and 1 min at 68°C. To detect polymorphisms, the amplified products were separated by electrophoresis on 3% agarose gels in 1× TAE buffer at 150 V and 500 mA for 50–60 min and the DNA fragment was detected with ethidium bromide.

**Inoculation and evaluation of blast disease, and postulation of resistance gene(s)**

A total of 20 SDBIs (11 from Bangladesh [Khan et al. 2016], 1 from Kenya [unpublished] and 8 from Japan [Hayashi 2005]) for which pathogenicities have already been clarified, were used to evaluate the degree of infection and to postulate the resistance gene(s) harbored in the rice accessions. Three seeds of each accession were sown in plastic cell trays (14 × 32 cells; cells 16 mm diameter, 25 mm deep) and grown to the 4th- to 5th-leaf stage in a greenhouse at 25°C. Border lines of each seedling tray were
sown with US-2 (a universal susceptible check to blast disease) to avoid any border effect. The spore concentration of each SDBI was standardized to 30–50 × 10<sup>4</sup> spores/mL, and 80 mL of the suspension was sprayed onto each tray with a fine sprayer 21 days after seeds were sown. The degree of infection of each seedling was evaluated at 7 days after inoculation. The reaction to blast isolates was scored on a scale of 0–5 following the method of Hayashi and Fukuta (2009). Each of the isolates was evaluated twice, to minimize experimental error.

The resistance genes present in each rice accession were postulated based on their patterns of reaction to 20 SDBIs in comparison to the patterns of reaction of the DVs and LTH. It was assumed that the pattern of reaction of each rice accession was the result of at least a single resistance gene in one chromosome region, such as Pik, on chromosome 1; Pik-s, on chromosome 2; Pik-m, Pik-t, and Pik-5 on chromosome 6; Pia, Pia-2, Pia-t, Pia-3, and Pia-5 on chromosome 11; or Pita, Pita-2, Pita-12, Pita-t, Pita-19, or Pita-20 on chromosome 12.

**Data analyses**

Cluster analysis with Ward’s hierarchical method (Ward 1963) and JMP 11.2 (JMP 11.2 for Windows, 2014; SAS Institute, Inc., Cary, NC, USA) were used to classify marker polymorphisms and reaction data with respect to blast isolates into groups. The relationships between these groups and rice ecotypes were also evaluated. To clarify the genetic variation in rice accessions, we calculated the average number of alleles per locus, gene diversity, heterozygosity (H) and polymorphic information content (PIC) by using PowerMarker 3.25 (Liu and Muse 2005). Resistance diversity index was calculated by using Simpson’s diversity index (Simpson 1949). The index value varies from 0 to 1, where 0 represents no diversity and 1 is maximum diversity.

**Table 1. Relationships between ecotypes and 3 polymorphism groups in 334 rice accessions**

<table>
<thead>
<tr>
<th>Rice ecotype&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Cluster groups classified based on polymorphic data of SSR markers</th>
<th>Genetic diversity&lt;sup&gt;b&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Cluster groups classified based on polymorphic data of SSR markers</td>
<td></td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>II</td>
</tr>
<tr>
<td></td>
<td>Ia</td>
<td>Ib</td>
</tr>
<tr>
<td>Aus</td>
<td>7 (8.0)</td>
<td>42 (47.7)</td>
</tr>
<tr>
<td>Aman</td>
<td>48 (30.0)</td>
<td>1 (0.6)</td>
</tr>
<tr>
<td>Boro</td>
<td>4 (8.2)</td>
<td>12 (24.5)</td>
</tr>
<tr>
<td>Jhum</td>
<td>1 (3.2)</td>
<td>18 (58.1)</td>
</tr>
<tr>
<td>Others</td>
<td>1 (16.7)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>Total</td>
<td>61 (18.3)</td>
<td>73 (21.9)</td>
</tr>
<tr>
<td>Genetic diversity</td>
<td>0.37</td>
<td>0.33</td>
</tr>
</tbody>
</table>

<sup>a</sup>Aus: upland, rainfed (duration of cultivation: March–August); Aman: lowland, rainfed (June–December); Boro: lowland, irrigated in dry winters (November–May); Jhum: slash-and-burn agriculture in hill regions (May–September); and Others: Nipponbare and 5 improved varieties released in Bangladesh. The Japonica Group cultivar ‘Nipponbare’ was classified into polymorphism cluster I, and the Indica Group Aus cultivar ‘Kasalath’ was classified into polymorphism subcluster Ia.

<sup>b</sup>A total of 334 accessions including landraces (n = 284) and improved varieties (n = 50) were used to investigate the polymorphism patterns of 74 SSR markers.

<sup>c</sup>Genetic diversity was determined on the basis of polymorphic data of SSR markers by PowerMarker 3.25 (Liu and Muse 2005).
Variation in resistance

Using SDBIs revealed distinct variations in resistance in the rice accessions. Specific reactions were found to SDBIs from Bangladesh and Kenya, and almost all accessions were resistant to the isolates from Japan (Fig. 1). Based on the reaction data, the accessions plus the DVs and LTH were classified into 4 resistance groups, A1, A2, B1 and B2 (Fig. 1, Supplemental Table 1).

Group A1 comprised 77 accessions, including 9 DVs for resistance genes Pia, Pib, Pit, Pi3, Pi5(t), Piz, Piz-t, Pi12(t) and Pi20(t). The Japonica Group rice cultivar ‘Nipponbare’ and the Indica Group cultivar ‘Kasalath’ were also classified into this group. The mean disease score of this group was 2.9. Group A2 (n = 19), which included LTH and 14 DVs for resistance genes Pish, Pii, Pik-s, Pik-m, Pi1, Pik-h, Pik, Pik-p, Pi7(t), Pi7a (2), Pita (2) and Pi19(t), was the most susceptible group, with mean disease score of 3.4. Resistance group B1 was the largest comprising 165 accessions (45.8% of the total), including 2 DVs for resistance genes Piz and Piz-5. Accessions in this group showed the highest resistance among the 4 groups, with mean disease score of 1.8. Resistance group B2 included 99 accessions without any DV, and the mean disease score was 2.3. Therefore, the most susceptible group was A2, which included LTH and many DVs, followed in order by A1, B2 and B1.

We investigated the relationships between resistance groups and ecotypes in Bangladesh (Table 2). Some remarkable differences between ecotypes were found in the frequencies of their occurrence in resistance groups. Most of the Aus accessions were classified into groups A1 and B2, whereas most of the Aman accessions were classified into group B1, and most of the Boro and Jhum accessions were classified into groups B1 and B2. These results suggested that Aus had a wide variation in blast resistance and that Aman comprised mostly resistant cultivars. The values of diversity in resistance varied among the 4 ecotypes, with the highest diversity found in Aus (0.67) followed by Boro (0.60), Aman (0.58) and Jhum (0.53).

Relationships between resistance groups and polymorphism groups

Unique relationships were found between the resistance groups (A1, A2, B1 and B2) and the polymorphism cluster groups (I, Ia and IIb) (Table 3). Accessions classified into polymorphism cluster I fell mostly into resistance group B1, accessions classified into polymorphism subcluster Ia fell mostly into resistance groups A1 and B2, and accessions classified into polymorphism subcluster IIb fell mostly into resistance group B1. Each polymorphism group had different frequencies of these resistance groups. Polymorphism subcluster Ia, which had high frequencies of accessions in resistance groups A1 and B2, showed the highest resistance diversity (0.64) among the 3 polymorphism groups, followed by polymorphism subcluster IIb (0.61) and polymorphism cluster I (0.44). These results indicated that cluster I had a high frequency of accessions falling into resistance group B1, but that the genetic diversity of resistance was lower than that of cluster II.

Postulation of blast resistance genes in rice accessions

Resistance genes in accessions were postulated by comparing reaction patterns with those of the DVs. The frequencies of expected blast resistance genes varied markedly among the accessions and also among the 4 disease resistance groups (A1, A2, B1 and B2). Each of the 23 genes in the DVs, with the exception of Pi19(t), was resistant to at least one of the SDBIs. The DV for Pi19(t) was susceptible to all of the SDBIs used. Thus, the presence of Pi19(t) could not be estimated in the genetic background of the rice accessions. At least one Pik allele was found in many Bangladesh
Table 2. Relationships between rice ecotypes and 4 disease resistance groups against standard differential blast isolates

<table>
<thead>
<tr>
<th>Rice ecotype</th>
<th>A1 (%)</th>
<th>A2 (%)</th>
<th>B1 (%)</th>
<th>B2 (%)</th>
<th>Total</th>
<th>Resistance diversity$^d$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aus</td>
<td>31 (35.2)</td>
<td>1 (1.1)</td>
<td>26 (29.5)</td>
<td>30 (34.1)</td>
<td>88 (100.0)</td>
<td>0.67</td>
</tr>
<tr>
<td>Aman</td>
<td>28 (17.5)</td>
<td>3 (1.9)</td>
<td>92 (57.5)</td>
<td>37 (23.1)</td>
<td>160 (100.0)</td>
<td>0.58</td>
</tr>
<tr>
<td>Boro</td>
<td>7 (14.3)</td>
<td>0 (0.0)</td>
<td>25 (51.0)</td>
<td>17 (34.7)</td>
<td>49 (100.0)</td>
<td>0.60</td>
</tr>
<tr>
<td>Jhum</td>
<td>1 (3.2)</td>
<td>0 (0.0)</td>
<td>16 (51.6)</td>
<td>14 (45.2)</td>
<td>31 (100.0)</td>
<td>0.53</td>
</tr>
<tr>
<td>Others</td>
<td>10 (31.3)</td>
<td>15 (46.9)</td>
<td>6 (18.8)</td>
<td>1 (3.1)</td>
<td>32 (100.0)</td>
<td>0.65</td>
</tr>
<tr>
<td>Total</td>
<td>77 (21.4)</td>
<td>19 (5.3)</td>
<td>165 (45.8)</td>
<td>99 (27.5)</td>
<td>360 (100.0)</td>
<td>0.67</td>
</tr>
</tbody>
</table>

$^a$ Aus: upland, rainfed (duration of cultivation: March–August); Aman: lowland, rainfed (June–December); Boro: lowland, irrigated in dry winters (November–May); Jhum: slash-and-burn agriculture in hill regions (May–September); and Others: Japonica group cultivar ‘Nipponbare’, 25 differential varieties (DVs), the susceptible check variety Lijiangxintuanheigu (LTH) and 5 improved varieties released in Bangladesh.

$^b$ In addition to the 334 accessions, 25 DVs and LTH were included.

$^c$ A total of 20 blast isolates from Bangladesh ($n = 11$), Kenya ($n = 1$) and Japan ($n = 8$) were used for the evaluation of resistance.

$^d$ Resistance diversity index was calculated by using the method of Simpson (1949).

Table 3. Relationships between resistance groups and polymorphism groups

<table>
<thead>
<tr>
<th>Polymorphism group</th>
<th>A1 (%)</th>
<th>A2 (%)</th>
<th>B1 (%)</th>
<th>B2 (%)</th>
<th>Total</th>
<th>Resistance diversity$^d$</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>7 (11.5)</td>
<td>1 (1.6)</td>
<td>44 (72.1)</td>
<td>9 (14.8)</td>
<td>61 (100.0)</td>
<td>0.44</td>
</tr>
<tr>
<td>II</td>
<td>28 (38.4)</td>
<td>0 (0.0)</td>
<td>14 (19.2)</td>
<td>31 (42.5)</td>
<td>73 (100.0)</td>
<td>0.64</td>
</tr>
<tr>
<td>a</td>
<td>33 (16.5)</td>
<td>3 (1.6)</td>
<td>105 (52.5)</td>
<td>59 (29.5)</td>
<td>200 (100.0)</td>
<td>0.61</td>
</tr>
<tr>
<td>b</td>
<td>61 (22.3)</td>
<td>3 (1.6)</td>
<td>119 (43.6)</td>
<td>90 (33.0)</td>
<td>273 (100.0)</td>
<td>0.65</td>
</tr>
<tr>
<td>Sum</td>
<td>9 (34.6)</td>
<td>15 (57.7)</td>
<td>2 (7.7)</td>
<td>0 (0.0)</td>
<td>26 (100.0)</td>
<td>0.54</td>
</tr>
<tr>
<td>Others$^e$</td>
<td>77 (21.4)</td>
<td>19 (5.3)</td>
<td>165 (45.8)</td>
<td>99 (27.5)</td>
<td>360 (100.0)</td>
<td>0.67</td>
</tr>
<tr>
<td>Total</td>
<td>77 (21.4)</td>
<td>19 (5.3)</td>
<td>165 (45.8)</td>
<td>99 (27.5)</td>
<td>360 (100.0)</td>
<td>0.67</td>
</tr>
</tbody>
</table>

$^a$ A total of 360 accessions including landraces ($n = 284$) and improved varieties ($n = 50$), 25 differential varieties (DVs) and susceptible check variety Lijiangxintuanheigu (LTH), were used to investigate blast resistance.

$^b$ A total of 20 blast isolates from Bangladesh ($n = 11$), Kenya ($n = 1$) and Japan ($n = 8$) were used for the evaluation of resistance.

$^c$ Resistance diversity index was calculated by using the method of Simpson (1949).

$^d$ Others = Susceptible check variety LTH and 25 DVs (No data of SSR marker polymorphism studies).

$^e$ Genetic diversity was determined based on the polymorphic data of SSR markers by PowerMarker 3.25 (Liu and Muse 2005).

Discussion

Using polymorphism data of 74 SSR markers and reactions of resistance to 20 SDBIs from Bangladesh, Japan and Kenya, we clarified the genetic variation in 334 Bangladesh rice accessions, including landraces and improved cultivars, covering 4 major ecotypes (Aus, Aman, Boro and Jhum). In addition, for the postulation of resistance genes in the rice accessions, their patterns of resistance were compared with those of other reported resistance genes in 25 DVs.

Glaszmann (1987) identified 6 isozyme groups in 1688 landraces of rice collected from Asia, including 99 from Bangladesh, and recognized the high diversity of Bangladeshi rice germplasms. But no Japonica Group accessions were included in that report. Ueno et al. (1990) reported that the accessions in Bangladesh were classified into Japonica and Indica Groups based on their KClO3 resistance, phenol reaction and apiculus hair length, and accessions of the Aman ecotype were included with high frequencies in both the Indica and Japonica Groups. Wang et al. (2013) surveyed 47 polymorphic SSR markers Bangladesh rice accessions and categorized them into 3 groups, Indica, Aus and Japonica Groups which included Aman and aromatic varieties. Rahman et al. (2016) also found differentiation of rice into Japonica and Indica Groups in Bangladesh, and found that aromatic rice accessions were categorized into the Japonica Group. Our results also showed the differentiation of Japonica Group rice cultivars in Bangladesh. Rice accessions in Bangladesh were mainly Indica Group cultivars, but several Japonica Group accessions were also included with...
low frequencies in the major 4 ecotypes. The frequency of Japonica Group accessions was higher in the Aman ecotype than the other 3 ecotypes, and the genetic diversity of Aman accessions was higher than those of the other 3 ecotypes based on polymorphism data of SSR markers (Table 1). Telebanco-Yanoria et al. (2008) indicated that rice in South Asia, including Bangladesh, maintained a high diversity of blast resistance in comparison with other areas of Asia and Africa, but genetic variations in the relationships between the 4 ecotypes in Bangladesh were not mentioned.

Accessions of Aus fell most frequently into resistance groups A1 and B2. Accessions of Aman fell most frequently into resistance group B1, and accessions of Boro and Jhum fell most frequently into resistance groups B1 and B2. Thus, the variation in resistance differed among the 4 ecotypes. The highest genetic diversity of resistance was found in Aus, and the diversity of resistance of Aman was similar to that of Boro and Jhum (Table 2). The results of genetic diversities clarified the differences in frequencies of resistance groups among the 4 ecotypes and the complex situation in Bangladesh.

In the relationships between the polymorphism cluster groups and the resistance cluster groups, polymorphism cluster I showed lower diversity in resistance than did cluster II, and resistance diversity tended to be lower in subcluster IIb than in subcluster Ila. Accessions of polymorphism cluster I fell most frequently into resistance group B1, accessions in polymorphism subcluster Ila fell most frequently into resistance groups A1 and B2, and accessions in polymorphism subcluster IIb fell most frequently into resistance group B1. Polymorphism subcluster IIb included many improved cultivars and subcluster Ila accessions fell with high frequency into resistance group B1 compared with subcluster Ila (Table 3). These findings indicate that cluster I (corresponding to Japonica Group cultivars) and subcluster IIb (including improved Indica Group cultivars) had high resistance but that diversity was low or limited compared with subcluster Ila. These results suggest that genetic improvement for resistance has induced low variation among rice cultivars in Bangladesh.

The resistance potential of Bangladesh rice accessions was comparatively higher against Japanese SDBIs than against SDBIs from Bangladesh and Kenya. The differences in the reactions to Bangladesh, Kenyan and Japanese blast isolates indicated the dramatic differentiations in the virulence of blast isolates, and the complex genetic mechanisms of resistance in Bangladesh accessions.

This study demonstrated clearly the differentiation and genetic variation in blast resistance in Bangladesh rice accessions by using SSR markers, reaction patterns to SDBIs, and their relationships with rice ecotypes. These findings indicate that different types of blast resistance are distributed among the rice accessions of the 4 ecotypes in Bangladesh, and indicate the complex composition of rice diversity. This information will be useful for a greater understanding of the differentiation and the components of blast resistance gene(s) in Bangladesh rice accessions, and will be helpful in forming the foundation for new strategies for the genetic improvement of rice varieties in Bangladesh.

Acknowledgements

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Literature Cited

Genetic variation in blast resistance in Bangladesh rice


