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Evaluation of Myanmar Rice Germplasms for Resistance to Bacterial Blight

By

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Abstract

Pathogenic diversity of *Xanthomonas oryzae* pv. *oryzae* from four major rice growing divisions of Myanmar was investigated. One hundred and thirty two isolates: 28 isolates from Ayeyarwady Division, 17 from Yangon Division, 42 from Bago Division and 45 from Mandalay Division, collected during 2004 and 2005 rice growing seasons were very diverse in virulence on 12 near-isogenic lines each of which carrying a specific resistance gene, *Xa 1*, *Xa 2*, *Xa 3*, *Xa 4*, *xa 5*, *Xa 7*, *xa 8*, *Xa 10*, *Xa 11*, *xa 13*, *Xa 14*, or *Xa 21*. The isolates were classified into 19 races based on their virulence. Among 19 races, Race 17 which consisted of 21.97% of the test isolates, was not only the most predominant race but also prevalent in 4 major rice growing divisions of Myanmar. It was also virulent on most of the differentials except IRBB 13 and IRBB 21. Race 7 and Race 11 fell into the second and third position in terms of predominance, respectively. However, Race 11 was found in four major rice growing divisions except Yangon Division, and Race 7 was detected in Bago and Mandalay Divisions only. Similarly, most of the other races found in one or two divisions were not detected in other divisions. The most predominant race in one division was also different from that of other divisions.

Pathogenic diversity of four selected isolates collected from Hmawbi, Bogale, Paukkhaung and Kyaukse was confirmed by computer-assisted image analysis method in quantifying disease severity. The virulence of each of the four isolates on three near-isogenic lines, IRBB 3, IRBB 7 and IRBB 13 each carrying a specific resistance gene *Xa 3*, *Xa 7*, and *xa 13*, respectively, was qualitatively different from that of other isolates. One hundred and thirty-four Myanmar rice germplasms obtained from Seed Bank, Department of Agricultural

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Research, Yezin, were evaluated for their resistance to the representative isolates of four races. The test rice germplasms were divided into four groups, Group A, B, C and D, based on their reaction to four isolates. Two rice germplasms namely Mya Wut Yi and Talay were belonged to Group D and resistant to three representative isolates of the three most predominant races detected in four major rice growing divisions of Myanmar.

Introduction

Myanmar is an agricultural country, and agricultural sector is the backbone of its economy. Rice is the principal human food resource and primary foreign exchange earner of Myanmar. It is being widely grown throughout the country occupying an area of about 6.0 million ha and sharing about 50% of the total crop sown area. Based on isozyme polymorphism, Nakagahra (1978, 1987) proposed that the center of genetic diversity of rice was situated in an area consisting of northern part of Myanmar, Laos and Yunnan Province of China. Seed bank was established in Yezin, Myanmar in 1990. It is the national centre of plant genetic resources in the country which has been collecting, introducing, characterizing, evaluating and conserving diverse plant genetic resources. One of the main objectives of Seed Bank is to ensure the effective utilization of germplasms in breeding programs so as to contribute to agricultural development in Myanmar (CARI, 2001). Rice, its wild relatives and some major crops have mainly been focused and now more attention is paid to minor crops and wild plants. Rice diseases, insect pests and weeds are major constraints for increasing productivity of rice. Approximately 74 pathogens are associated with rice and 16 diseases are economically important (Roger *et al.* 1991). Among them, bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* is one of the major constraints in rice production. Yield losses in severely infected field ranged from 20 to 30%, and may on rare occasions be up to 50% (Ou 1985).

Some chemicals have been developed to control the disease. However, none of them has been fully effective under very severe conditions (Noda *et al.* 1996). As chemical control may have an adverse effect on the environment and is costly, growing resistant cultivars is the most safe and feasible control measure against the disease (Ezuka and Kaku 2000). To develop resistant varieties by hybridization, identification of resistant donors is the first step. In the early stage of research on bacterial blight of rice, specific differentiation of virulence in the pathogen, *Xanthomonas oryzae* pv. *oryzae*, was not known. So the resistance of rice cultivars was evaluated simply by inoculating a single bacterial isolate. Nowadays, the existence of races in *X. oryzae* pv. *oryzae* is an established fact that is accepted by all the researchers working on bacterial blight of rice (Ezuka and Kaku 2000).

To control bacterial blight of rice based on host resistance, determination on pathogenic diversity of *X. oryzae* pv. *oryzae* is a prerequisite. Evaluation of resistance in rice germplasms and incorporation of the resistant genes into improved varieties may then be investigated. The present study was, therefore, conducted with the following objectives:

1. to determine the pathogenic diversity of *Xanthomonas oryzae* pv. *oryzae* from major rice growing divisions of Myanmar,
2. to examine the distribution of races of *X. oryzae* pv. *oryzae* in different rice growing regions,
3. to identify Myanmar rice germplasms resistant to different races of *X. oryzae* pv. *oryzae* and
4. to provide resistant donors for rice breeding program for bacterial blight resistance.

Materials and Methods

Determination on Pathogenic Diversity of *Xanthomonas oryzae* pv. *oryzae* from Major Rice Growing Divisions of Myanmar

One hundred and thirty-two isolates of *X. oryzae* pv. *oryzae* collected from 27 townships of 4 major rice growing divisions of Myanmar (Figure 1) during 2004 and 2005 rice growing seasons were evaluated for their virulence on differential varieties. Diseased leaf samples of bacterial blight of rice were collected from diseased fields of different locations. Isolation of the pathogen was done as soon as possible after the leaf samples were collected. Proposed international differential rice varieties for *X. oryzae* pv. *oryzae* (Ogawa 1993) namely IRBB 1, IRBB 2, IRBB 3, IRBB 4, IRBB 5, IRBB 7,IRBB 8, IRBB 10, IRBB 11, IRBB 13, IRBB 14 and IRBB 21, each carrying a specific resistance gene *Xa1*, *Xa2*, *Xa3*, *Xa4*, *xa5*, *Xa7*, *xa8*, *Xa10*, *Xa11*, *xa13*, *Xa14*, and *Xa21*, respectively, were used for determination of pathogenic diversity of *X. oryzae* pv. *oryzae*. TN 1 was tested as a checked variety.

Thirty-day old seedlings of each test variety were transplanted individually in one row plot at 30 x 30 cm spacing. The plants were grown up to panicle initiation to booting stage in accordance with the normal cultivation practices. The flag leaves or the uppermost fully expanded leaves of five tillers were inoculated by clipping method at 90 days after sowing. The experiment was laid out on a strip plot design with three replications. Disease recording was done 21 days after inoculation (DAI) according to the IRRI's Standard Evaluation System for Rice (IRRI, 1988). Percent leaf area infected on inoculated leaves was visually estimated. Disease reactions of the rice varieties to the bacterial isolates were determined based on

disease scores. The variety was ranked as resistance (R) if the disease score was 3 or less and susceptible (S) if it was more than 3.

Confirmation on Pathogenic Diversity *of Xanthomonas oryzae* pv*. oryzae*

Pathogenic diversity of *X. oryzae* pv. *oryzae* was confirmed by computer-assisted image analysis method in quantifying disease severity. Four isolates of *X. oryzae* pv. *oryzae* designated as 04107, 04172, 0505 and 0530 which were representative isolates of Race 14, 11, 17, and 7, respectively, were tested to confirm the pathogenic diversity of the pathogen.

Three near-isogenic lines namely IRBB 3, IRBB 7 and IRBB 13 each carrying a specific resistance gene *Xa 3*, *Xa 7*, and *xa 13*, respectively, were selected as differentials based on the results of previous experiment. IRBB 21 and TN 1 were used as resistant check and susceptible check variety, respectively. The plants were grown up to 90 days after sowing. The same inoculation method was again employed here as in the previous experiment. The experiment was laid out on a strip plot design with four replications. Disease severity (percent leaf area infected) was measured 21 days after inoculation by computer-assisted image analysis method.

Total leaf area and infected leaf area of the inoculated leaves were measured by computer-assisted image analysis method and percent leaf area infected was calculated. The inoculated leaves were detached from the plant and made flat by applying pressure with a hot iron. The leaves were then mounted on white cards with 30 cm x 22 cm area, scanned and saved as digital images with 1.2 million pixels resolution. To determine the percentage of leaf area infected, colour threshold method was applied using SigmaScan Pro 5.0 (SPSS Inc.) image analysis software. Image of the inoculated leaves appeared on the image window of SigmaScan Pro 5.0 was duplicated. An overlay in red colour was applied to defined measurement parameters for the infected portions. Colour threshold method was applied comparing with the original image of the leaves. Then infected leaf area was measured using the Measurements / Measure Objects tab. The area of the infected portions was obtained on the data work sheet (Plate 1 A, B, C, D & E). To measure the total leaf area, the original image of the leaves was duplicated again, and the entire portion of the duplicated image of the leaves was determined using fill mode as mentioned above. Total leaf area was shown on another data work sheet (Plate 1 F).

Evaluation of Myanmar Rice Germplasms for Resistance to Different Races of *Xanthomonas oryzae* pv. *oryzae*

Totally, 134 indigenous rice germplasms from 14 states and divisions of Myanmar, obtained from Seed Bank, Department of Agricultural Research, Yezin, were tested for resistance to different races of *X. oryzae* pv. *oryzae*. The plants were grown up to 90 days after sowing.

The representative isolates of 4 races, Race 14, 11, 17, and 7, of *X. oryzae* pv. *oryzae* designated as 04107, 04172, 0505, and 0530, respectively, were tested for their virulence on indigenous rice germplasms. Inoculum preparation for each isolate and inoculation to the test germplasms were carried out as described in the previous experiment. The experiment was laid out on a strip plot design with four replications. Evaluation for resistance of each germplasm was done at 21 DAI according to Standard Evaluation System for Rice (IRRI 1988).

Results and Discussion

Pathogenic Diversity of *Xanthomonas oryzae* pv. *oryzae* in 4 Major Rice Growing Divisions of Myanmar

One hundred and thirty-two isolates of *X. oryzae* pv. *oryzae* collected from four major rice growing divisions of Myanmar: 28 isolates from Ayeyarwady Division, 17 from Yangon Division, 42 from Bago Division and 45 from Mandalay Division, were very diverse in virulence on differentials, 12 near-isogenic lines. The bacterial isolates were classified into 19 races based on their virulence on the differentials. All isolates tested were virulent on TN 1 but avirulent on IRBB 21. Virulence of these isolates on other differentials varied with the combination of the differentials and races (Table 1).

Table 1. Pathogenic diversity[x] of 132 isolates of *X. oryzae* pv. *oryzae* from 4 major rice growing divisions of Myanmar on 12 near-isogenic lines

Races	No. of isolates	Differential varieties													Isolates (%)
		IRBB 21	IRBB 7	IRBB 13	IRBB 3	IRBB 4	IRBB 1	IRBB 5	IRBB 14	IRBB 10	IRBB 2	IRBB 8	IRBB 11	TN 1	
1	11	R	R	R	R	R	R	R	R	R	R	R	R	S	8.33
2	1	R	R	R	R	R	R	R	R	R	R	S	S	S	0.76
3	1	R	R	R	R	R	R	R	R	S	R	R	S	S	0.76
4	1	R	R	S	R	R	R	R	R	R	R	R	S	S	0.76
5	1	R	R	S	R	R	R	R	R	R	R	S	S	S	0.76
6	1	R	R	S	R	R	R	R	R	R	S	S	S	S	0.76
7	24	R	R	S	R	R	S	S	S	S	S	S	S	S	18.18
8	11	R	R	S	R	S	S	S	S	S	S	S	S	S	8.33
9	1	R	R	S	R	S	S	S	S	S	S	S	R	S	0.76
10	2	R	R	S	S	R	S	S	S	S	S	S	S	S	1.52
11	16	R	R	S	S	S	S	S	S	S	S	S	S	S	12.12
12	1	R	R	S	S	S	S	S	S	S	S	S	R	S	0.76
13	4	R	S	R	R	R	S	S	S	S	S	S	S	S	3.03
14	3	R	S	R	R	S	S	S	S	S	S	S	S	S	2.27
15	2	R	S	R	S	R	S	S	S	S	S	S	R	S	1.52
16	9	R	S	R	S	R	S	S	S	S	S	S	S	S	6.82
17	29	R	S	R	S	S	S	S	S	S	S	S	S	S	21.97
18	3	R	S	S	R	R	S	S	S	S	S	S	S	S	2.27
19	11	R	S	S	S	S	S	S	S	S	S	S	S	S	8.33

[x]R = Resistant, 0 to 12 % leaf area infected
S = Susceptible, 13 to 100 % leaf area infected

Race Composition of the Test Isolates

Of 132 isolates of *X. oryzae* pv. *oryzae* tested in this study, 11 were classified as Race 1 and this race was virulent only on TN1 but a virulent on other differentials. On the other hand, another 11 isolates belonged to Race 19; it was virulent on all of the differentials except IRBB 21. Among 19 races, Race 17 which accounted for 21.97% of the test isolates was the most predominant race. This race was also virulent on most of the differentials except IRBB 13 and IRBB 21. Race 7 was the second-most predominant race; it comprised 18.18% of the test isolates. The virulence of Race 7 and Race 8 on the differentials was similar to each other except the virulence on IRBB 4. Race 11 which contained 12.12% of the test isolates was the third-most predominant race. This race was also avirulent only on two differentials, IRBB 7 and IRBB 21. Most of the other races consisted of only one or two isolates (Table 1). Thus, the three most predominant races, i.e. Race 7, 11, and 17, occupied 52.57% of the test isolates, and these races were virulent on 8 to 10 differentials each carrying a specific resistance gene. In other words, most of the resistant genes tested were defeated by the predominant races. Therefore, most of the currently available sources of major resistance genes are unlikely to provide effective control against the predominant races which currently exist in four major rice growing divisions of Myanmar.

Distribution of Races in Four Major Rice Growing Divisions

Among the races classified in this study, Race 17 was the most predominant one. It was found in all of the four major rice growing divisions, 3.03%, 4.55%, 8.33% and 6.06% of the test isolates in Ayeyarwady, Yangon, Bago and Mandalay Divisions, respectively. Therefore, Race 17 was not only the most predominant but also prevalent race in four major rice growing divisions of Myanmar. However, the second-most predominant race, Race 7, was found in only two major rice growing divisions, Bago and Mandalay Divisions. On the other hand, the third-most predominant race, Race 11, was not detected in Yangon Division. Similarly, some of the other races detected in one or two divisions were not found in other divisions (Table 2).

Table 2. Distribution (percentage of isolates) of races of *Xanthomonas oryzae* pv. *oryzae* in different locations

Race	Location (Division)				
	Ayeyarwady	Yangon	Bago	Mandalay	Total
17	3.03	4.55	8.33	6.06	21.97
7	-[x]	-	5.30	12.89	18.18
11	7.58	-	3.79	0.76	12.12
1	6.06	-	0.76	1.52	8.33
8	-	0.76	2.27	5.30	8.33
19	2.27	3.79	2.27	-	8.33
16	-	-	5.30	1.52	6.82
13	-	-	-	3.03	3.03
14	-	0.76	-	1.52	2.27
18	-	1.52	-	0.76	2.27
10	-	-	1.52	-	1.52
15	-	-	1.52	-	1.52
2	0.76	-	-	-	0.76
3	-	-	0.76	-	0.76
4	1.76	-	-	-	0.76
5	-	0.76	-	-	0.76
6	-	-	-	0.76	0.76
9	-	0.76	-	-	0.76
12	0.76	-	-	-	0.76

[x] - Not detected

If the same race occurs in all locations, as Race 17 detected in all of the four major rice growing divisions, screening for resistance could be carried out with the common race. However, when different races occur in different locations, it makes screening more complicate. It means that screening for resistance has to be done with different races due to differences in pathogen population among locations.

Confirmation on Pathogenic Diversity *of Xanthomonas oryzae* pv*. oryzae*

Virulence of four isolates of *X. oryzae* pv. *oryzae,* 04172, 0505, 0530 and 04107 on four near isogenic lines, IRBB 3, IRBB 7, IRBB 13 and IRBB 21, and TN 1 were tested. Computer-assisted image analysis method was applied to measure disease severity. It was observed that disease severity (% leaf area infected) on the test varieties inoculated with four bacterial isolates showed highly significant differences among the varieties and among the isolates. The interaction between the varieties and the isolates was also highly significant (Table 3).

Table 3. Analysis of variance for disease severity (% leaf area infected) measured by computer-assisted image analysis method on five rice varieties inoculated with four isolates of *Xanthomonas oryzae* pv. *oryzae*

Source of variation	Degree of freedom	Sum of squares	Mean squares	Observed F
Replication	3	106.19	35.40	1.42 ns
Variety	4	45559.23	11389.81	457.72 **
Error (a)	12	298.61	24.88	-
Isolate	3	2219.58	739.86	21.95 **
Error (b)	9	303.42	33.71	-
Variety x Isolate	12	31992.51	2666.04	44.74 **
Error (c)	36	2145.45	59.60	-
Total	79	82624.98	-	-

CV (a) = 13.4%; CV (b) = 15.5%; CV (c) = 20.7%
**: significant at 1% level; ^{ns}: not significant

Zadoks and Schein (1979) indicated that interaction is the mathematical way of describing the biologic phenomenon called physiologic specialization. They stated that when there is interaction, some varieties differentiate between the pathogen isolates and likewise these pathogen isolates differentiate between the varieties. The results of the present investigation, therefore, suggested that there was a distinct differential interaction between the variety-isolate combination and proved the pathogenic diversity among the test isolates of *X. oryzae* pv. *oryzae.*

Four isolates of *X. oryzae* pv. *oryzae* were distinctly different in their pathogenicity on three near isogenic lines namely IRBB 3, IRBB7 and IRBB 13. Isolate 04172 was virulent on

IRBB 3 and IRBB 13 but avirulent on IRBB 7 whereas another isolate, 04107 was avirulent on IRBB 3 and IRBB 13 but virulent on IRBB 7. On the other hand, Isolate 0505 was virulent on IRBB 3 and IRBB 7 but avirulent on IRBB 13. However, the virulence of the isolate 0530 on the three near isogenic lines was reverse to that of isolate 0505. All of the isolates were virulent on TN 1 and avirulent on IRBB 21 (Table 4, 5, Fig 2, and Plate 2, 3). According to these results, the virulence of each isolate on the test varieties was qualitatively different from that of other isolates. This kind of differences in pathogenic capacity could be accounted for in screening and breeding programs for bacterial blight resistance.

Table 4. Disease severity (% leaf area infected) measured by computer-assisted image analysis method on five rice varieties inoculated with four isolates of *Xanthomonas oryzae* pv. *oryzae*[x].

Bacterial isolates	Rice varieties				
	IRBB 3	IRBB 7	IRBB 13	IRBB 21	TN 1
04172	58.33 a B[y]	2.38 b C	53.80 b B	5.13 a C	77.72 ab A
0505	60.10 a B	58.64 a B	7.77 c C	8.96 a C	86.36 a A
0530	10.12 b C	6.98 b C	67.63 a B	8.91 a C	84.06 ab A
04107	6.02 b C	56.39 a B	5.36 c C	7.06 a C	75.19 b A

CV (a) = 13.4 %; CV (b) = 15.5 %; CV (c) = 20.7 %
[x] Inoculated 90 days after sowing and measured 21 days after inoculation
[y] Means followed by the same letter are not significantly different at 5%LSD . Small letters indicate comparison of means in each column while capital letters indicate comparison in each row.

Table 5. Disease reactionx of five rice varieties to four isolates of Xanthomonas oryzae pv. oryzaey

Rice varieties	Bacterial isolates			
	04172	0505	0530	04107
IRBB 3	S	S	R	R
IRBB 7	R	S	R	S
IRBB 13	S	R	S	R
IRBB 21	R	R	R	R
TN 1	S	S	S	S

[x] R = Resistant (Disease score 3 or less)
S = Susceptible (Disease score more than 3)
[y] Inoculated 90 days after sowing and measured 21 days after inoculation

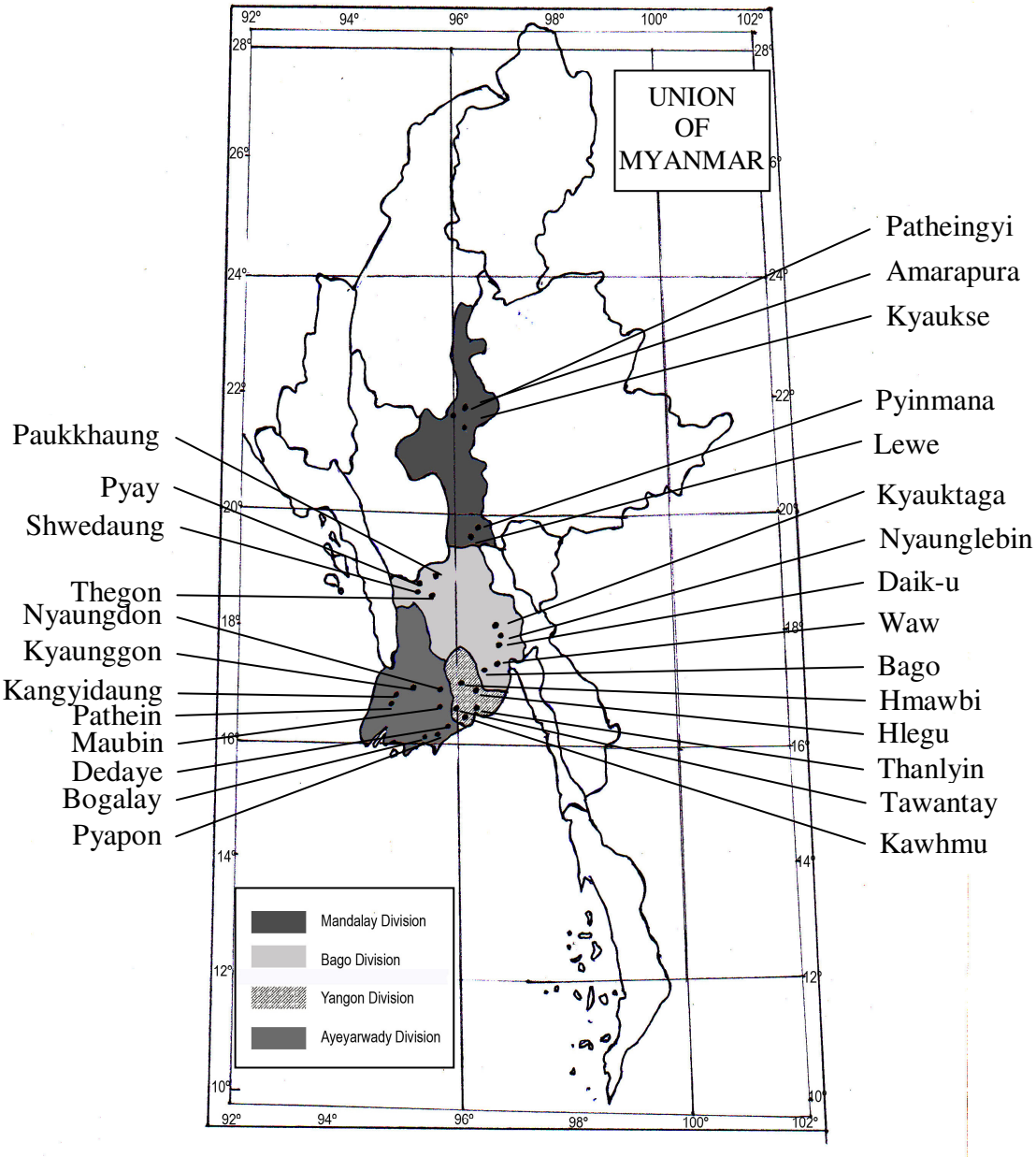


Figure 1. Collection sites (townships) of test isolates of *X. oryzae* pv. *oryzae*

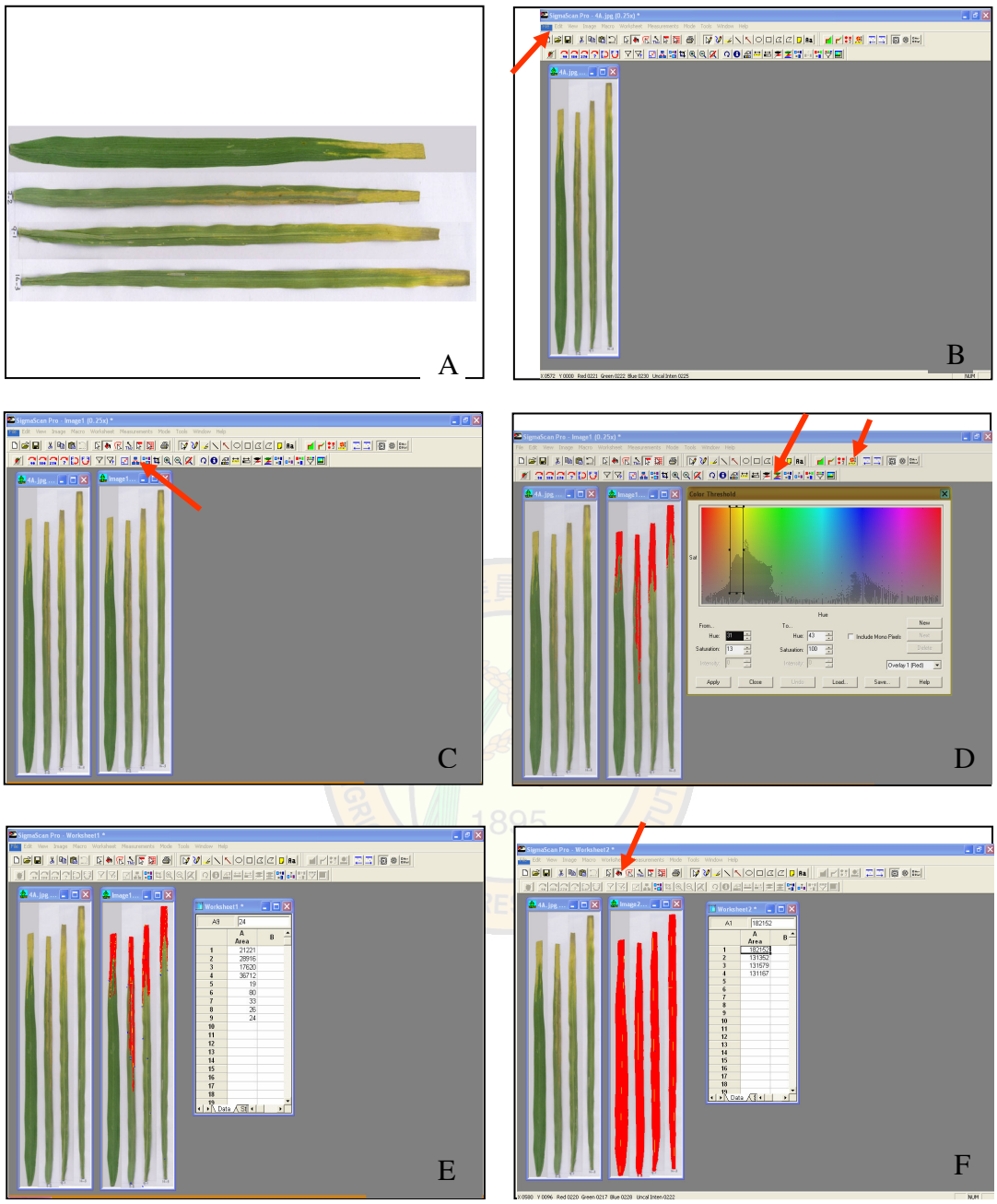


Plate 1. Measuring infected and total leaf areas of inoculated leaves by computer-assisted image analysis method

A. Inoculated leaves, on which % leaf area infected is to be measured
B. Opening the file; image of the leaves appeared on the image window of Sigma Scan Pro 5.0
C. Duplication of the image of leaves to be measured
D. Overlaying with red colour on the infected portion of the duplicated image of leaves using fill mode; colour threshold method was applied to measure the infected area
E. Measuring the infected leaf area; the area was shown on the data work sheet
F. Measuring the total leaf area; the original image of the leaves was duplicated again, the entire portion of the duplicated image of the leaves was defined using fill mode, and total leaf area was shown on another data work sheet

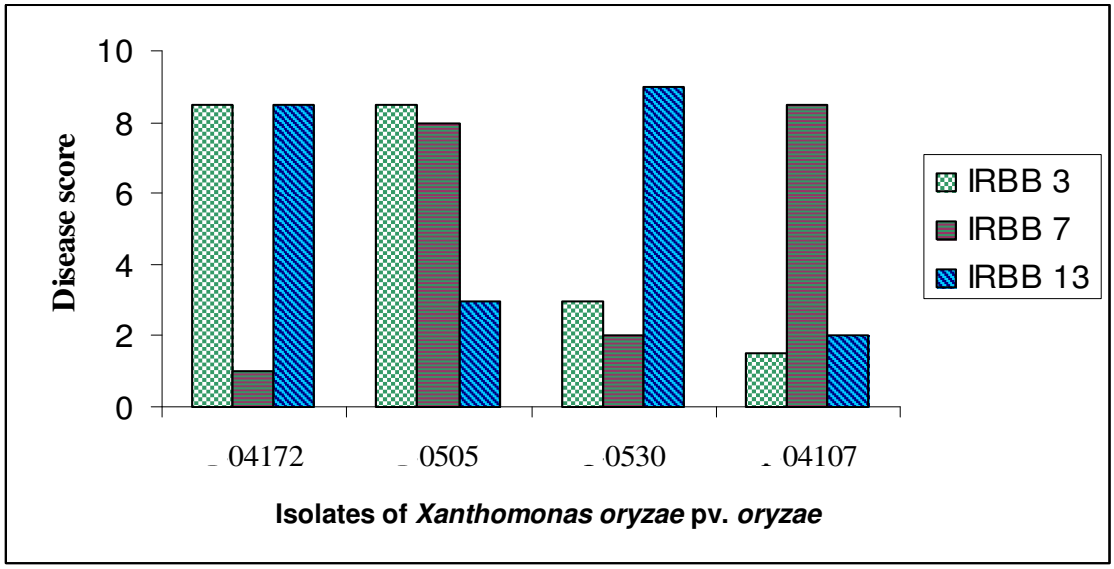


Figure 2. Virulence of four isolates of *Xanthomonas oryzae* pv. *oryzae* on three near isogenic lines

Evaluation of Myanmar Rice Germplasms for Resistance to Different Races of Xanthomonas *oryzae* pv. *oryzae*

Indigenous rice germplasms of Myanmar were evaluated for resistance to four Myanmar races of *X. oryzae* pv. *oryzae*. On the basis of reaction patterns to representative isolates of four races, 134 rice germplasms were categorized into four varietal groups, Group A, B, C and D.

Seventy-eight rice germplasms included in Group A were susceptible to all of the representative isolates of four races. In Group B, there were 50 rice germplasms and they were resistant to Race 11, but susceptible to other three races. Only 4 and 2 rice germplasms belonged to Group C and D, respectively. Four rice germplasms of Group C, Khae Saba, Van Lai Phal, Ant Baw and Baw Gyi, were resistant to two races, Race 7 and 11. Mya Wut Yi and Taylay, which belonged to Group D, were resistant to three races, Race 7, 11 and 17 (Table 6 and 7).



Plate 2. Disease reaction of IRBB 21 and TN 1 to fourisolates of *Xanthomonas oryzae* pv. *oryzae*

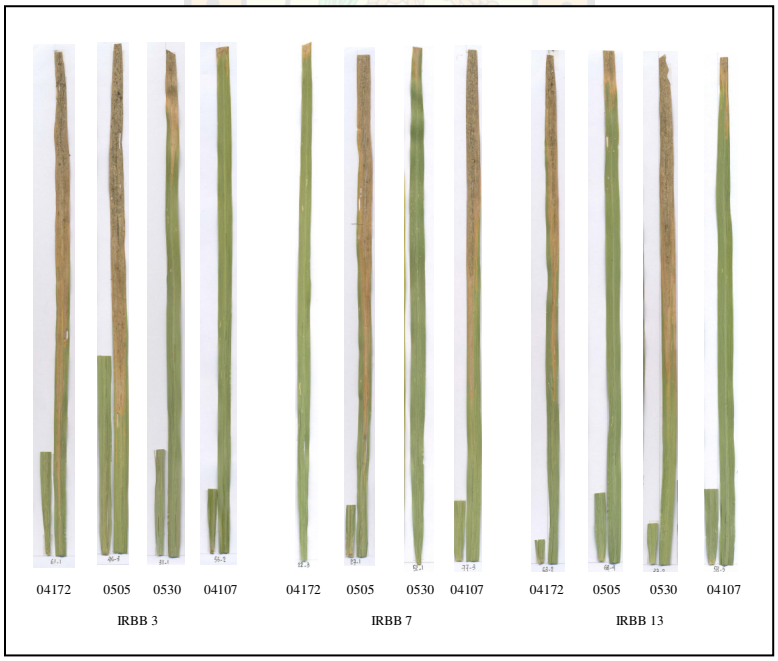


Plate 3. Disease reaction of three near-isogenic lines, IRBB 3, IRBB 7 and IRBB 13 to four isolates of *Xanthomonas oryzae* pv. *oryzae*

Table 6. Grouping of 134 Myanmar rice germplasm on the basic of reaction patterns to four isolates* of *Xanthomonas oryzae* pv. *oryzae*

Group	Varieties
A	Khao Kain, Magauk, Saba Ni, Khao Hlaing, Moe Thay, Kyaw Par Lae, Kha Yan Gyar, Chin Pa Chee, Khao Mon Moe Nae, Khao Mon Han Young, Lin Ban Chaw,Khao La Shae, Khao Pha Yaung, Bu Do Ya, Saba Khar, Khao Pae Law, Khao Maw Kyan, Ekare, Ekarin Kwa, Shwe Pyi Aye, Bu Har, Baria, Rel Beng, Dug Thin, Kalagyi, Kyaw Galay, Kari Let Yone, Lone Phyu, Yay Thu Ma, Shan Nyein, Kyun Shwe War, Nga Kauk Che, Sar Pa Si Chay, Nga Kyein Thee, Sa O Me, Ohn Ni Ma, Ya Khine Ma, Khao Saw, Khao Man Mu, Khao Kan, Let The Zaung, Pale Pyu, In Gyin Su, Kauk Latt Phyu, Shan Ma Lay, Pa Dee Pu, Pa Che Mwe Swe, A Pyo Daw Gyi, Kyauk Htu, Phwe Htaung Ni, Ye Tha, Sabani Hmwe, Ah Nauk Chaung, Yatha Lay Long Thwe, Nga Kywe Taung Pyan, Khun Na Ya Thee Dat, Nga Pya Yin, Bu Thout, San Gyi, Pin Shwe War, Kalar Htun, Sa Sar, Shwe Phyu, Thone Hnan Latt, Tha Htay Gyi, Ywet Thay, Mwe Swe, Okshit, Naung Aine, Taung Hteik Pan, Kauk Thwe Phyu, Thet Nu Bay Kyar, Nga Kyee Du Me, Let Yone, Kauk Thwe, Let Yone Gyi, Kywe Chae Manaing and Nga Yar Nga Se
B	Naung Tu, Let The Nu, Khao Lar Say, Nga Yar Gyaw, Kauk Kyi Saw, Shwe Pu, Yay Thu Ma, Epa Tine, Dawe Sein, Kala Lay, Ekare Phyu, Naga Yar, Mya Sein, Bahat Ni, Gauk Ya, Ah Nauk Thama, Khao San Haung, Khao Man Mon Tine, Khao Kyaine, Khao Kyauk Oun, Khao Mwe Naung, Khao Note Tit, Takade, Tay Lay, Shwe Bo Khun Ni, Ya Thae, Wun Htauk, Nga Sein Du Me, Shwe Chay Gyin, Paw La Khe, Thone Poke Ta Pote, Nga Kywe Phyu, Shwe Dinga, Aung Lan Daw, Pyi Daw Aye, Hnan War, Wa Ti Tun, Du Wa Pho, Ban Gauk, Man Nga Sein, Mee Kauk, Shwe Kyi Dauk, Kauk Sann, Shwe Kyi Nyo, Ngar Yar Kyaw, Baw Kyan, Ma Po Lay, Maung Nyo Sann, Balakyar and Phya Pon Thee Dat
C	Van Lai Phai, Ant Baw, Khae Saba and Baw Gyi
D	Mya Wut Yi and Talay

*: Representative isolates of 4 races, 04172, 0505, 0530, and 04107, i.e., races 11, 17, 7, and 14, respectively

Table 7. Disease reaction[x] of four groups of rice germplasms to four isolates of *Xanthomonas oryzae* pv. *oryzae*

Varietal group	No. of germplasms belong to each group	Isolates[y]			
		04172	0505	0530	04107
A	78	S	S	S	S
B	50	R	S	S	S
C	4	R	S	R	S
D	2	R	R	R	S

[x] R = resistant, 0 to 12% leaf area infected
S = susceptible, 13 to 100% leaf area infected
[y] Representative isolates of 4 races, 04172, 0505, 0530 and 04107, i.e., races 11, 17, 7, and 14, respectively

In order to develop bacterial blight resistant varieties, selection of appropriate donor parents which show broad spectrum of resistance is important for the breeding program. Thus, evaluation of introduced and indigenous rice germplasms for bacterial blight resistance is one of the primary tasks for rice genetic resources management and utilization. In the present study, 134 indigenous rice germplasms of Myanmar were evaluated for resistance to four Myanmar races of *X. oryzae* pv. *oryzae*. It was observed that, majority of the indigenous rice germplasms, i.e. 78 germplasms of Group A, were susceptible to four Myanmar races. On the other hand, 50 rice germplasms included in Group B were resistant to Race 11. This race was one of the three predominant races detected in this study and distributed in three major rice growing divisions, Ayeyarwady, Bago, and Mandalay Divisions. Therefore, these rice germplasms could be used as resistant donors in varietal improvement program for those divisions.

The discovery of pathogenic specialization led to the incorporation of different resistance genes into improved cultivars. Thus, modern breeding program paid an attention to develop rice varieties which are resistant to multiple races of *X. oryzae* pv. *oryzae*. In the present study, Khae Saba, Van Lai Phal, Ant Baw and Baw Gyi were resistant to Race 7 and 11, and Mya Wut Yi and Taylay were resistant to Race 7, 11 and 17. These three races were predominant races detected in four major rice growing divisions of Myanmar. It indicated that these six indigenous rice germplasms were potential donors for multiple race resistance in breeding program for bacterial blight in Myanmar.

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