Isozyme Genotype of Major Cultivar Groups Resistant to Bacterial Blight in Asian Rice

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Summary

Isozyme types were determined for six cultivar groups carrying different resistance to rice bacterial blight in Asia. The temporarily proposed Isozyme genotypes would be associated with the differentiation of the reaction of resistance. The predominant type of the Java 14 group was Isozyme type VI-1, and type II-4 was involved as the second predominant type. The majority of the DZ 192 group belonged to type II-1 and II-2. A newly assigned TN 1 group consisted of Isozyme type I and VI. The predominant occurrence of I-1 and I-2 was common among the TKM 6, Cas 209, Mond Ba and TN 1 groups. However, frequent involvement of IM-1 and IM-2 were specific to the TKM 6 group. The frequent presence of I-4 and I-5 was the characteristic of the Cas 209 and Mond Ba groups. Based on these observations the ecotypic diversity of each group was discussed.

Key Words : bacterial blight, ecotype diversity, isozyme classification, *Oryza sativa* L, resistance, *Xanthomonas oryzae*, gene-for-gene evolution.

Introduction

The intraspecific variation of cultivated rice, *Oryza sativa* L, has been a matter of importance for rice breeding and genetics. Many classifications of rice variation have been proposed based on morphological and physiological characteristics including Indica-Japonica classification (Kato 1930, Matsuo 1952, Morinaga 1954, Ting 1957, Oka 1958, Morishima and Oka 1981, Nakagahra *et al.* 1986), and classifications based on isozyme analysis (Second 1982, Nakagahra 1978, Katayama *et al.* 1982, Glaszmann 1987b). The gene-for-gene co-evolution (Flor 1956) is another aspect of the study of the evolution of rice. Genes for resistance may have played a crucial role in suppressing rice diseases from the primitive era of cultivation due to the absence of other effective control methods.

Bacterial blight (BB) caused by *Xanthomonas oryzae* (Swing *et al.* 1990) is one of the most serious diseases of rice. Since the first report of this disease in Japan (Tagami and Mizukami 1962), the 18 genes have been

identified as resistant to BB (Report of committee on gene symbolization convened by Kinoshita 1995). Among them, four major BB resistant groups based on their reaction pattern to Philippine races were found to be predominant and distributed widely in Asia (Ogawa and Khush 1989, Ogawa *et al.* 1991). The following genes confer resistance to BB races in each cultivar group : *Xa-3* in the Java 14 group, *Xa-4* in the TKM 6 group, *xa-5* in the DZ 192 group, and *Xa-10* in the Cas 209 group. In addition to these major groups, there are somewhat smaller groups known as the Mond Ba, DV 85, Makhmal Mehi and BJ 1 sub-groups. Our recent study observed that a 5th major group, namely TN 1 group (*Xa-14*), is also distributed predominantly in Asia. Thus, bacterial blight resistant rice was divided into five major groups. A close relationship between these BB resistant groups and ecotype diversity has been shown by applying the isozyme classification of Glaszmann (1987a). The Isozyme type related to the TN 1 group was still obscure. Furthermore, a preliminary survey of cultivars belonging to each BB resistant group in Myanmar suggested that further diversities existed within the same Isozyme type (Endo *et al.* 1997). This study deals with the fine analysis of Isozyme genotypes related to five major BB resistant groups in Asian native cultivars, including the newly formed TN 1 group as well as the Mond Ba sub-group having both *Xa-4* and *Xa-10*.

Materials and Methods

Rice cultivars screened for BB resistance to Philippine races were determined their genotypes for five isozyme loci ; *Pgi-1* and *Pgi-2* of phosphoglucose isomerase, and *Amp-1*, *Amp-2* and *Amp-3* of aminopeptidases. The material cultivars consisted of 224 in the Java 14 group, 160 in the TKM 6 group, 380 in the DZ 192 group, 171 in the Cas 209 group, 41 in the Mond Ba sub-group, 141 in the TN 1 group, and totally 1117 cultivars were subjected to analysis (Table 1). Upon the analysis of isozymes, four to six grains per cultivar were germinated in darkness and the crude extract of young plumules was examined for isozymes. When two alleles were observed jointly in the same sample, this was treated as having both alleles on the locus after replicated analysis.

First of all, Isozyme types were determined based on the combination of alleles at 5 isozyme loci, following

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Table 1. Origin of rice cultivars used for the isozyme analysis

Country of origin	No. of cultivars belonging to each BB resistant group						Total
	Java 14 (<i>Xa-3</i>)	TKM 6 (<i>Xa-4</i>)	DZ 192 (<i>Xa-5</i>)	Cas 209 (<i>Xa-10</i>)	Mond Ba (<i>Xa-4+10</i>)	TN 1 (<i>Xa-14</i>)	
Japan	24	1					25
Korea	5						5
PROC ¹⁾	5					62	67
Taiwan	4					5	9
Vietnam		3	1	26			30
Cambodia				3	1		4
Laos	2	6					8
Thailand	4	3			1	7	15
Malaysia	2			1		47	50
Myanmar	1	36	9	51	4		101
Philippines	9	1		4		6	20
Indonesia	93	8	2	2	1	3	109
Bangladesh	38	27	273	26	20	2	386
Nepal	1		14	12	2		29
India	1	22	74	42	11	5	155
Pakistan		1	3	1			5
Sri Lanka	1	41	1	3		3	49
Others	34	11	3	0	1	1	50
Total	224	160	380	171	41	141	1117

¹⁾ PROC : People's Republic of China

the methodology established by Glaszmann (1987a, 1987b). Secondly, allelic frequency of respective loci was examined to find the difference of allele presence in each BB resistant group. Upon the computation of allele frequency, cultivars having two different alleles (heterozygote or a mix of different homozygotes on a subjected locus) were treated as having both alleles with even-by-even balance. Thirdly, in order to further analyze the diversity of Isozyme types, the dominant isozyme combination of 5 loci within possible combinations was examined to detect any skew from independent allele-conjunction of 5 loci, following the methodology described in Endo *et al.* (1997).

Results

Determination of Isozyme types for BB resistant groups in Asia

Of 1117 cultivars examined, the balance of respective Isozyme types consisted of Isozyme type I (43 %), type II (31 %), and type VI (16 %), which covered 90 % of the total cultivars (Table 2). Among this balance, the newly formed TN 1 group was found to have either type I or type VI. The Java 14 group involved almost all the Isozyme types except for type III. The majority of the Java 14 group belonged to type VI, followed by a minor occurrence of types II and V. In contrast to the Java 14 group, the majority of the DZ 192 group belonged to type II, and two small types ; I and III were also nested

to this group. All the cultivars of the TKM 6 group consisted of type I and intermediate types (IM) only. Most of the cultivars in the Cas 209 group belonged to type I, and a few occurred in types II, III, and V. The Mond Ba sub-group were placed in type I mostly. Thus, different Isozyme types were associated with respective BB resistant groups as was pointed out by Ogawa *et al.* (1991).

Allelic frequencies of isozyme loci between BB resistant groups

Pgi-1 locus (Chromosome 3)

Of 4 alleles reported for *Pgi-1* locus, *Pgi-1*¹ and *Pgi-1*² were predominant, and *Pgi-1*³ and *Pgi-1*⁴ were involved only in the Java 14 group (Table 3). All cultivars having *Pgi-1*⁴ were present in Korean cultivars. Among the two predominant alleles, more than 90 % of *Pgi-1*² was present in both the Java 14 and DZ 192 groups, whereas the TKM 6, Cas 209, Mond Ba and TN 1 groups tended toward *Pgi-1*¹. Thus, *Pgi-1*² was the allele to differentiate the Java 14 and DZ 192 groups from the TKM 6, Cas 209, Mond Ba and TN 1 groups.

Pgi-2 locus (Chromosome 6)

With regard to the *Pgi-2* locus, the Java 14 and Mond Ba groups tended to have *Pgi-2*¹, while the DZ 192 group had mostly *Pgi-2*³ (Table 3). The TKM 6, Cas 209 and TN 1 groups involved both *Pgi-2*¹ and *Pgi-2*² in similar proportion. The Mond Ba sub-group tended towards *Pgi-1*¹. The frequency of the Mond Ba sub-group was rather closer to Isozyme type VI than type I, although most of the cultivars in this sub-group belonged to Isozyme type I. Other than these three dominant alleles, *Pgi-2*⁴ was involved in the Java 14 and Cas 209 groups due to the presence of Isozyme type V. It seems that *Pgi-2*¹ is related to the Java 14 and Mond Ba groups, and *Pgi-2*³ to the DZ 192 group. The remaining *Pgi-2*² thus seemed related to the TKM 6, Cas 209 and TN 1 groups. These results suggest that genotypes belonging to the same Isozyme type I are different depending upon BB resistant groups.

Table 2. Isozyme types of Asian rice cultivars resistant to bacterial blight

Isozyme types ¹⁾	Cultivar groups having resistance to different races of BB						Total No.
	Java 14 (<i>Xa-3</i>)	TKM 6 (<i>Xa-4</i>)	DZ 192 (<i>Xa-5</i>)	Cas 209 (<i>Xa-10</i>)	Mond Ba (<i>Xa-4+10</i>)	TN 1 (<i>Xa-14</i>)	
I	9	133	21	161	39	121	484
II	20		323	1	1		345
III			15	1			16
IV	2						2
V	13			3		1	17
VI	160		1			18	179
I. M. ²⁾	20	27	20	5	1	1	74
Total	224	160	380	171	41	141	1117

¹⁾ Classification of Isozyme type refers to Glaszmann (1987b)

²⁾ I. M. is the group of intermediates

Amp-1 locus (Chromosome 2)

Of 7 alleles reported for *Amp-1* locus, *Amp-1*¹ and *Amp-1*² were predominant (Table 3). The third frequent allele was *Amp-1*⁴ and present mostly in the Cas 209 and Mond Ba groups. Another minor occurrence of *Amp-1*³ was present in the Java 14 group mostly. No *Amp-1*⁵ was observed. The dominance of *Amp-1*¹ was clear in the Java 14 and TN 1 groups, while *Amp-1*² was predominant in the DZ 192 group. The presence of *Amp-1*² was higher in the TKM 6 group than the Cas 209 and Mond Ba groups.

Amp-2 locus (Chromosome 8)

With regard to *Amp-2* locus, recently reported null allele (*Amp-2*⁰; Vaughan and Juliano 1992) was present in only 10 cultivars out of a total 1117, and most of them belonged to the Java 14 group (Table 3). This result as well as the close relation of the Java 14 group to Isozyme type VI suggested the additional involvement of *Amp-2*⁰ in Isozyme type VI. The *Amp-2*³ was also minor and present in Chinese cultivars of the TN 1 group. The most dominant allele of this locus was *Amp-2*² followed by *Amp-2*¹. As a total, the Java 14 group involved *Amp-2*¹ with high frequency, whereas *Amp-2*² was dominant in other groups. These differences suggest a clear genetic diversity of the Java 14 group on this locus.

Amp-3 locus (Chromosome 6)

The dominant alleles of *Amp-3* locus were rather limited being either *Amp-3*¹ or *Amp-3*² (Table 3), although the number of alleles reported for this locus was very polymorphic. The heterozygous *Amp-3*¹/*Amp-3*² genotype was often observed particularly in Isozyme types I and VI. Many of these heterozygous type I originated from the countries of Indo-China, and heterozygous type VI from Indonesia. Although this heterozygous genotype was difficult to treat as a real heterozygote or the mix of different homozygotes, the frequent presence of the heterozygous genotype seemed a characteristic of Isozyme type I and VI as was pointed out by Glaszmann (personal communication). Among the other minor alleles, the *Amp-3*⁶ was present in DZ 192 group due to the involvement of Isozyme type III (Table 2). Another minor allele, *Amp-3*³, was present in the TN 1 group, and most of them were Chinese cultivars. Including a third minor *Amp-3*⁴, the Java 14 group seemed the most polymorphic. As a whole, the *Amp-3*¹ was dominant in the Java 14 and TN 1 groups, and the cultivars of the DZ 192 group mostly had *Amp-3*². The difference between the TKM 6, Mond Ba and Cas 209 groups was not clear.

The Isozyme genotypes of BB resistant cultivar groups based on the allelic combinations of five isozyme loci

Theoretically, it is possible for various combinations of alleles on 5 loci to consist of Isozyme type I to VI. However, some alleles are specific to particular groups showing different BB resistance (Table 3). Of 1117 cultivars, 67 different combinations of 5 loci were

Table 3. Allelic frequencies of five isozyme loci among BB resistant groups

Isozyme Locus	Allele	Allelic frequency (%) of each BB resistant group						Total
		Java 14 (Xa-3)	TKM 6 (Xa-4)	DZ 192 (Xa-5)	Cas 209 (Xa-10)	Mond Ba (Xa-4+10)	TN 1 (Xa-14)	
<i>Pgi-1</i>	1	3	93	6	83	95	85	43
	2	9.5	8	94	17	5	15	57
	3	< 0.5 ¹⁾	—	—	—	—	—	< 0.5
	4	1	—	—	—	—	—	< 0.5
<i>Pgi-2</i>	1	87	53	4	44	80	41	41
	2	3	48	4	52	17	59	25
	3	9	—	92	2	2	—	33
	4	1	—	—	2	—	—	1
<i>Amp-3</i>	0	1	—	< 0.5	1	—	—	< 0.5
	1	67	50	6	64	48	76	44
	2	25	49	90	34	52	18	52
	3	1	1	—	—	—	5	1
	4	4	—	—	1	—	1	1
	5	< 0.5	—	< 0.5	—	—	—	< 0.5
<i>Amp-2</i>	0	1	—	4	1	—	—	2
	1	4	—	< 0.5	—	—	—	1
	2	89	3	5	4	—	13	22
	3	5	98	95	96	100	83	76
<i>Amp-1</i>	0	1	—	—	—	—	4	1
	1	—	—	1	—	—	1	< 0.5
	2	94	82	20	78	76	96	64
	3	1	13	78	2	2	—	29
	4	3	1	—	1	—	1	1
	5	1	4	1	19	22	3	5
<i>Amp-1</i>	6	—	—	—	—	—	—	—
	6	1	1	—	1	—	—	< 0.5

¹⁾ The mark < 0.5 in the table shows less than 0.5 % presence, and the mark — stands for no presence.

observed, and highly frequent presence of a particular allelic combination was indicated for each BB resistant group as summarized in Fig. 1. For instance, with Isozyme type II, the co-presence of *Amp-1*² and *Amp-2*² was predominant in the DZ 192 group, while the co-presence of *Amp-1*¹ and *Amp-2*¹ was peculiar to Isozyme type II of the Java 14 group. Similarly the presence of *Pgi-1*¹ was unique to BB resistant groups belonging to Isozyme type I. The *Amp-1*⁴ seemed to associate with the Cas 209 and Mond Ba groups. Thus, totally 22 Isozyme genotypes were proposed temporarily and the frequency distribution of the 22 types are shown in Fig. 1.

The most frequent Isozyme genotype of Java 14 group was VI-1 (148 of 224 cultivars). The co-presence of *Amp-1*¹ and *Amp-2*¹ was common in VI-1, II-4, IM-2 and IM-6. Isozyme genotypes having this allele combination accounted for 85 % of the total in the Java 14 group.

In the DZ 192 group, II-1 was predominant (251 of 380 cultivars), followed by II-2 and II-3. Consequently, 85 % of cultivars belonged to II-1, II-2 or II-3, and little presence of II-4 was the characteristic of the DZ 192 group. The predominant II-1 was characterized as the co-presence of *Amp-1*² and *Amp-2*². This combination was common in IM-1 and IM-4. Thus, the stem

g: Isozyme genotypes tentatively proposed

Isozyme genotype	Allele of each loci				
	Pgi-1	Pgi-2	Amp-3	Amp-2	Amp-1
I-1	1	2	-	2	1
I-2	1	1	-	2	1
I-3	2	-	-	2	1
I-4	1	-	-	2	4
I-5	2	-	-	2	4
II-1	2	3	2	2	2
II-2	2	3	2	1	2
II-3	2	3	2	2	1
II-4	2	3	2	1	1
III	2	3	6	2	2
IV	2	1	6	1	1
V-1	2	1	-	1	1
V-2	2	1	-	1	4
VI-1	2	1	-	1	1
VI-2	Others				
IM-1	1	-	-	2	2
IM-2	1	-	-	1	1
IM-3	2	3	-	-	-
IM-4	2	non 3	-	2	2
IM-6	2	-	-	1	1
IM-7	2	-	-	0	1
IM-8	Others				

Fig. 1. Frequency distribution of cultivars belonging to each Isozyme genotype.

a: Java 14 group having *Xa-3*b: TKM 6 group having *Xa-4*c: DZ 192 group having *xa-5*d: Cas 209 group having *Xa-10*e: Mond Ba sub-group having both *Xa-4* and *Xa-10*f: TN 1 group having *Xa-14*

g: Tentative isozyme genotypes

In Fig. 1-a, b, c, d and e, the genotypes having *Amp1*⁴ were shown by a white bar, and otherwise shown by a black bar. The numbers in the figure show No. of cultivars when the frequency beyond the scale.

In Fig. 1-g, the mark-stands for any alleles other than specified. Tentative genotypes were formed based on the frequent presence of alleles in each isozyme type shown in Table 3, and based on the specificity of each BB group.

types related to the DZ 192 group had the co-presence of *Amp-1*² and *Amp-2*².

The TKM 6, Cas 209 and Mond Ba groups were similar in terms of the dominance of Isozyme type I, and the I-1 and I-2 were the most dominant genotypes commonly in this Isozyme type I (Fig. 1). However, the Mond Ba sub-group differed from other two groups in the frequent presence of *Pgi-2*¹ (Table 3): a more frequent occurrence of I-2 than I-1 (Fig. 1). Both the Cas 209 group and the Mond Ba sub-group involved *Amp-1*⁴ with higher frequency than TKM 6 group, hence I-4 and I-5 were present more frequently in the Cas 209 group and the Mond Ba sub-group (Fig. 1). The presence of IM-1 and IM-2 was rather specific to the TKM 6 group.

The TN 1 group was similar to the TKM 6, Mond Ba and Cas 209 groups: I-1 and I-2 were predominant (Fig. 1). Within Isozyme type VI, VI-1 was dominant. This trend was the same to the presence of VI-1 in the Java 14 group.

Discussion

The five major BB resistant groups were not subjected to the classification originally, but were only the result of screening BB resistance of native cultivars collected at the International Rice Research Institute (IRRI) and in Japan (Ogawa *et al.* 1991). Randomly selected cultivars covering most Asian countries were provided, and resistant cultivars were selected based on the reaction to Philippine races of BB. The genes resistant to BB races were further analyzed genetically, and the property of cultivar grouping based on the reaction of BB resistance was proved for the cultivars of Myanmar (Endo *et al.* 1992). Thus, BB resistant genes become the criterion to set up BB resistant cultivar groups.

The present results of isozyme analysis confirmed the diversity of the Isozyme types in cultivars belonging to different BB resistant groups. The Isozyme types proposed by Glaszmann (1987a) are the monitor of genotypes associated with various ecotypes of rice. Therefore, the difference of Isozyme genotype obtained among BB re-

sistant cultivar groups may be ascribed to the genetic diversity of BB resistant groups. In fact, it was suggested for Myanmar that different Isozyme genotypes tended to correspond to different phenotypes of rice cultivars (Endo *et al.* 1997). From these points of view, the difference of Isozyme genotypes shown for respective BB resistant groups may suggest a pre-existing linkage between BB resistance gene and respective isozyme genes which are particularly predominant to the corresponding BB resistant groups.

Characteristics of BB resistant cultivar groups

Java 14 group

The Java 14 group consisted of the most polymorphic genotypes among the BB resistant groups, and the majority occurred in the VI-1. Historically, *Xa-3* was included both in IRRI differentials and Japanese differentials, and due to the wide spectrum of the gene as well as the unstable expression of resistance at seedling stage, many different names were assigned such as *Xa-3*/*Xa-w* (Ezuka *et al.* 1975, Petpisit *et al.* 1977), *Xa-6* (Sidhu and Khush 1978) and *xa-9* (Singh *et al.* 1983). Then, a series of revised genetic analysis united the nomenclature as *Xa-3* (Ogawa *et al.* 1990a, Ogawa *et al.* 1990b, Ogawa *et al.* 1990c). The resistance on lesion suppression is always accompanied by brownish symptoms unlike the expression of other genes: *Xa-4*, *xa-5*, *Xa-10* and *Xa-14*. This unique and wide spectrum of resistance of *Xa-3* may be attributable to the polymorphic presence of Isozyme types in the Java 14 group. Most cultivars of this group have a few tiller, reach flowering before September in Japan, and white grains are popular (data not shown). According to Glaszmann (1988), Isozyme type VI distributes at high elevation in south Asia, in upland areas of southeast Asia, and is predominant in temperate east Asia, including Bulu in Indonesia and Keng in China, clearly corresponding with Japonica in a sense of Oka (1958). The distribution of the Java 14 group mostly overlapped with the distribution of Isozyme type VI such as from Bangladesh, Indo-china, the Philippines to Indonesia as well as to China and Japan (Ogawa *et al.* 1991, Table 1). These characteristics of the Java 14 group may be an indication of a tight connection between *Xa-3* and the Isozyme type having *Amp-1*¹ and *Amp-2*¹, hence the VI -1 as a predominant genotype.

TKM 6 group

The *Xa-4* was firstly identified in an IRRI variety (Petpisit *et al.* 1977). It is also known that cultivars having *Xa-4* are frequent in so-called Indica. The present results confirm that the most frequent types are the I-1 and I-2. The Isozyme type I corresponds to Indica in the sense of Oka (1958), and is one of the most polymorphic groups in Asia (Glaszmann 1987a, 1988). The following ecotypes are included in Isozyme type I: Aman in Bangladesh, Tjereh in Indonesia, Hsien in China. On the other hand, the TKM 6 group widely distributes from

Bangladesh, India and southward to Sri Lanka (Ogawa *et al.* 1991, Table 1). Most IM types of this group originated from Sri Lanka, where both Isozyme type I and Isozyme type II were dominant. Thus, the distribution of the TKM 6 group was included in the distribution of Isozyme type I. The stem genotypes of the TKM 6 group seemed to be the I-1 and I-2 having *Pgi-1*¹ in common.

DZ 192 group

The cultivars of the DZ 192 group seemed uniform, and mostly belonged to the II-1, followed by the II-2 and II-3. The spectrum of *xa-5* resistance is also wide like the Java 14 group, however the recessive mode of inheritance is unique. Many cultivars of DZ 192 group involved colored brown-rice, and reached flowering before September in Japan. The distribution of this gene is mostly limited to the Indian sub-continent (Khush 1977, Ogawa *et al.* 1991, Table 1). The Isozyme type II mostly occurs in Aus in Bangladesh and India (Glaszmann 1988). From this point of view, it is most likely that the genetic diversity of the DZ 192 group is closely linked with the Aus ecotype having the combination of *Amp-1*² and *Amp-2*² (II -1).

Cas 209 group and Mond Ba sub-group

The cultivars having *Xa-10* were firstly noticed in a IRRI differential; Cas 209 only (Yoshimura *et al.* 1983), followed by the finding of many cultivars in Asia with a dominance shown for Myanmar (Endo *et al.* 1991). Thus, the cultivars having *Xa-10* were placed as the fourth major group designated as the Cas 209 group, then the Mond Ba sub-group, having both *Xa-10* and *Xa-4*, was nested to the Cas 209 group (Ogawa *et al.* 1991).

In the present analysis, the confirmed results show that both Cas 209 group and the Mond Ba sub-group consisted of Isozyme type I mostly. TKM 6, Cas 209 and Mond Ba groups were alike in the presence of I-1 and I-2. However, the difference between the Cas 209 group and the TKM 6 group was shown as was indicated for Myanmar: the frequent presence of cultivars having *Amp-1*⁴ (Endo *et al.* 1997). As a whole in Asia, the cultivars having *Amp-1*⁴ were mostly observed in Myanmar and neighboring countries. According to Glaszmann (1987a, 1988), the presence of *Amp-1*⁴ is minor in Asia and is limited to Isozyme types I and V, distributing along the Himalayas. The distribution of the Cas 209 group was mostly from Vietnam, Myanmar, India to Nepal (Endo *et al.* 1991, Ogawa *et al.* 1991, Table 1), which agreed well with the distribution of *Amp-1*⁴ in Asia. These Asian trends of the Cas 209 group supported the idea that the origin of the Cas 209 group and the Mond Ba sub-group is different from the TKM 6 group, and close links are due to *Amp-1*⁴.

TN 1 group

At first, *Xa-14* was identified in Taichung Native 1 (Taura *et al.* 1992), and the cultivars showing the same

resistant reaction were designated as the TN 1 group. The Isozyme types of the TN 1 group were first determined in the present paper. The results revealed that dominant occurrence was in Isozyme type I with a second small group as type VI. The majority was distributed in China, Taiwan to Malaysia, and most of type VI originated from China. Two ecotypes of Chinese cultivars are known as Hsein and Keng which correspond to Isozyme types I and VI, respectively (Glaszmann 1987a). Isozyme type VI of the TN 1 group seemed like Keng of China, while type I like Hsien. The cultivars of Malaysia were mostly belonged to Isozyme type I. As a whole in Asia, the dominance of Isozyme type I characterized the TN 1 group. The difference between the TN 1 group and the TKM 6, Cas 209, and Mond Ba groups was the joint presence of Isozyme types I and VI as well as geographic cline.

Genetic diversity of major BB resistant groups

The rice bacterial blight have been a serious epidemic disease in Asia and tremendous yield loss has occurred in the history of long cultivation (Ou 1985, Singh *et al.* 1977, Mew 1989). Probably the role of gene-for-gene evolution (Flor 1956, Adhikari *et al.* 1995) has played an important role in differentiating BB resistant groups in the long term history of rice cultivation. In fact, our recent DNA analysis provides evidence of genetic diversity among the BB resistant groups (unpublished data), and present results obviously show different Isozyme genotypes occurring among different BB resistant groups. Thus, single BB resistance genes seem closely linked with particular genotypes of rice.

The genes *Xa-3*, *Xa-4* and *Xa-10* locate on chromosome 11 (Report of committee on gene symbolization convened by Kinoshita 1995), whereas *xa-5* locates on chromosome 5, and *Xa-14* on chromosome 4. The five isozyme loci, on the other hand, locate on different chromosomes: *Pgi-1* on chromosome 3, *Pgi-2* and *Amp-3* on chromosome 6, *Amp-1* on chromosome 2, and *Amp-2* on chromosome 8. This dispersed nature of chromosome location never interprets the genotype diversity of BB resistant groups simply by genetic linkage, hence a likelihood can be placed on the motive of genetic diversity in BB resistant groups such that varietal groups characterized by particular genotypes were tightly associated with the origin of particular BB resistance.

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