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Genetic Analysis of Bacterial Blight Resistance in Seventy-Four Cultivars of Rice, *Oryza sativa* L.

G.S. Sidhu, G.S. Khush and T.W. Mew
International Rice Research Institute, Manila (Philippines)

Summary. The genetics of resistance to bacterial blight, *Xanthomonas oryzae* (Uyeda and Ishiyama) Dowson, for 74 cultivars of rice, *Oryza sativa* L., was studied. The PX061 isolate of bacterial blight from the Philippines was used for inoculation of parental and hybrid populations. Single dominant genes at the *Xa 4* locus convey resistance in 38 cultivars. Of these, 18 are resistant at all stages of plant growth and thus have the $Xa\ 4^a$ allele for resistance. However, 20 are susceptible up to maximum tillering stage but are resistant at booting and flowering stages. These cultivars have the $Xa\ 4^b$ allele for resistance. Thirty-two cultivars have single recessive genes for resistance which are allelic to *xa 5*.

The resistance in 'DV85', 'DV86' and 'DZ78' is conditioned by two genes. At maximum tillering stage *xa 5* conveys resistance. However, at later growth stages an additional dominant gene, designated *Xa 7* in 'DZ78', also gives resistance. The dominant genes of 'DV85' and 'DV86' are probably allelic to *Xa 7*. *Xa 7* segregates independently of *Xa 4*, *xa 5* and *Xa 6*, however like *Xa 6*, it conveys resistance at booting and post-booting stages only.

The resistance in 'PI 231129' is conditioned by a single recessive gene, designated *xa 8*. It also segregates independently of *Xa 4*, *xa 5* and *Xa 6*.

Key words: *Xanthomonas oryzae* (Uyeda and Ishiyama) Dowson – dominant gene – recessive gene – germ plasm bank – allelic relationships

Introduction

The genetics of resistance to bacterial blight, *Xanthomonas oryzae* (Uyeda and Ishiyama) Dowson, in some rice cultivars was investigated in Japan and three dominant genes, *Xa 1*, *Xa 2* and *Xa 3*, for resistance to Japanese isolates of the bacterium were identified (Sakaguchi 1967; Ezuka et al. 1975). Three genes *Xa 4*, *xa 5* and *Xa 6* for resistance to Philippine isolates of the bacterium have also been identified (Petpisit et al. 1977; Olufowote et al. 1977; and Sidhu and Khush 1978). Two alleles at the *Xa 4* locus are known. $Xa\ 4^a$ conveys resistance at all the stages of plant growth, however plants having $Xa\ 4^b$ are resistant at the booting and post-booting stages only (Librojo et al. 1976). Cultivars with *xa 5* show resistance at all stages of plant growth while *Xa 6* conveys resistance at booting and post-booting stages (Olufowote et al. 1977; Sidhu and Khush 1978). *Xa 4*, *xa 5* and *Xa 6* have been utilized in the rice improvement programs at IRRI and elsewhere. Our research was to identify additional genes to convey resistance to bacterial blight.

Materials and Methods

The rice cultivars used in the study are listed in Table 1. 'Taichung Native 1' (TN1) is a dwarf, bacterial blight susceptible cultivar and was used as a susceptible parent in the crosses. 'IR22' is an improved plant-type cultivar and is homozygous for *Xa 4*, for resistance. 'IR1545-339' is also an improved plant-type selection and is homozygous for *xa 5*, for resistance. 'Malagkit Sungsong' and 'Zenith' are tall cultivars and both carry *Xa 6* for resistance. 'IR22', 'IR1545-339', 'Malagkit Sungsong' and 'Zenith' were used in crosses for allele tests. The 74 test cultivars were selected from the IRRI germplasm bank on the basis of their resistant reaction to the PX061 isolate of bacterial blight. Some of the test cultivars are resistant at all stages of growth whereas others are resistant at the booting and post-booting stages only (Table 1).

All the 74 test cultivars were crossed with 'TN1' and the reactions to bacterial blight of the F_1 and F_2 populations from these crosses were evaluated to determine the mode of inheritance of resistance. When F_2 data did not give a good fit to monogenic control of resistance, the reactions of F_3 populations from crosses with 'TN1' were studied.

The cultivars that showed monogenic recessive segregation for resistance were crossed with 'IR1545-339', and the F_1 progenies from these crosses were evaluated to determine allelic relations of recessive genes with *xa 5*. The cultivars that showed monogenic

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Table 1. Rice cultivars used in a 1977 study to identify additional genes for resistance to bacterial blight

Cultivar	IRRI Acc. No.	Origin
Taichung Native 1 (TN1)	105	Taiwan
IR22	11356	IRRI
IR1545-339	32624	IRRI
Malagkit Sungsong[a]	755	Philippines
Zenith[a]	4038	U.S.A.
Aus 32	28895	Bangladesh
Aus 251	29043	,,
Aus 449	29230	,,
DB 3	8361	,,
DD 48	8620	,,
DD 100	8649	,,
DF 1	8365	,,
DL 5	8593	,,
DNJ 142	8426	,,
DV 29	8816	,,
DV 32	8818	,,
DV 52	8828	,,
DV 85	8839	,,
DV 86	8840	,,
DV 139	8870	,,
DZ 78	8555	,,
Kaliboro 600	29367	,,
Pankhiraj	24139	,,
ADT25[a]	5151	India
ARC 5756	20220	,,
Bilekagga 36	19927	,,
CO21[a]	6396	,,
Hema	–	,,
K116-69-10	36798	,,
KH998	16948	,,
Kolongi Bao	24135	,,
M.C.M. –2	19301	,,
Perunel 0.69-18[a]	19581	,,
PI 180060-1	3687	,,
Taothabi[a]	13746	,,
Vella Peruvazha 0.68-12[a]	19588	,,
Bageri	16193	Nepal
Bakai	23806	,,
Bangaluwa	16268	,,
Devarasi	16173	,,
Dudhi	16256	,,
Lal Ahu	16121	,,
Lalaka Gadur	16255	,,
Lal Sar	16185	,,
Maturi	16187	,,
Matury	16190	,,
Nakhi	16254	,,
Rerm Bilash	16273	,,
Sajani	16177	,,
Sokan Dhan	16250	,,
Tally	16146	,,
Bathkiriel	15212	Sri Lanka
Halsudu Heenati[a]	15599	,,
Halsuduwee[a]	15723	,,
Kirikunda[a]	15558	,,
Mahamawee[a]	15213	,,
Malalwariyan[a]	15203	,,
Murunga Balawee[a]	15725	,,
Murungawee[a]	15498	,,
No. 20	15606	,,
Patchaiperumal[a]	15681	,,
Perum Karuppan[a]	15513	,,
Race[a]	15706	,,
Rathu Heenati[a]	15609	,,
Sudumalawee[a]	15218	,,
Wanni Dahanala	15721	,,
Yakadawee[a]	15293	,,
Back Gi Cheong Byeo[a]	19695	Korea
Chukei No. 314	–	,,
Gui do	19745	,,
Patong 32	13843	Malaysia
Tolil 14	13836	,,
Ngane Tia	13010	Laos
Nam Sakouy	11617	,,
Pakheng	12996	,,
Kalimodu 50	19338	Sierra Leone
Nam Sagui 19	11462	Thailand
PI 231129	11114	U.S.A.
Lua Ngu[a]	16852	Vietnam

[a] Susceptible at seedling stage but resistant at booting and flowering stages

dominant segregation for resistance were crossed with 'IR22'. The F_1 and F_2 populations from those crosses were evaluated to determine the allelic xrelationships of dominant genes for resistance with *Xa 4*. The cultivars that appeared to have genes different from *Xa 4* or *xa 5* were crossed with either 'Malagkit Sungsong' or 'Zenith' and F_1 and F_2 populations of those crosses were evaluated to determine the allelism with *Xa 6*.

The PX061 isolate, which is representative of the Philippine isolates of the bacterial pathogen, was used for the inoculation of parental and hybrid populations. The hybrid progenies from the crosses of cultivars resistant at all growth stages were inoculated at the maximum tillering stage. The hybrid progenies from the crosses of cultivars resistant at booting and post-booting stages were inoculated at the booting stage. 'TN1' and resistant parents were grown with the hybrid populations as checks. Plants were inoculated by the clipping technique described by Kauffman et al. (1973) with a bacterial suspension of about 10^9 cells/ml. The bacterial pathogen was cultured by the modified Wakimoto's method (Karganilla et al. 1973).

Disease scores were taken 2 weeks after inoculation following the standard system of Kauffman et al. (1973). The F_1 and F_2 populations were scored on an individual plant basis. In the F_3 families individual plants were scored and each family was then classified as resistant, segregating or susceptible.

Results

Inheritance of Resistance

The bacterial blight reactions of F_1 and F_2 populations from the crosses of test cultivars with 'TN1' are listed in

Table 2. The F_1 progenies of 33 cultivars showed a susceptible reaction and the F_2 populations of those hybrids segregated in the ratio of 3 susceptible to 1 resistant plants, thereby indicating that the 33 cultivars have single recessive genes for resistance. The F_1 progenies of the remaining 41 cultivars crossed with 'TN1' were resistant, indicating that those cultivars have dominant genes for resistance.

The F_2 progenies from the crosses of 38 cultivars segregated in the ratio of 3 resistant to 1 susceptible thus showing that those cultivars have single dominant genes for resistance.

The F_2 data from the crosses of three cultivars ('DV85', 'DV86' and 'DZ78') with 'TN1' did not fit the 3:1 or 1:3 ratio expected for monogenic control of resistance. Moreover, the F_1 progenies of the three cultivars crossed with 'TN1' were susceptible at the maximum tillering stage but resistant at the flowering stage (Table 2). The F_3 progenies of the crosses were therefore evaluated for resistance at maximum tillering stage and flowering stage. At maximum tillering stage the F_3 families segregated in a ratio of 1 resistant: 2 segregating: 1 susceptible (Table 3) and within the segregating families there were more susceptible than resistant plants. Since F_1 hybrids of the three cultivars were susceptible at the maximum tillering stage, a single recessive gene apparently confers resistance at this stage in those cultivars. However, because the F_1 hybrids of the three cultivars with 'TN1' were resistant at the flowering stage, at least one dominant gene for resistance must also be present in them.

The classification of the same families at the flowering stage into resistant, segregating and susceptible groups agreed with 7:8:1 ratio (Table 3) expected for two independently segregating genes. Thus, at the flowering stage the resistance in 'DV85', 'DV86' and 'DZ78' is governed by one recessive and one dominant gene.

Allele Tests

The F_1 populations from the crosses of 'IR1545-339' with cultivars showing monogenic recessive inheritance were examined. All the populations, with the exception of the 'PI 231129' cross, were resistant, indicating that all the cultivars, except 'PI 231129', have the same recessive gene (*xa 5*) as 'IR1545-339'. The F_1 progeny of 'IR1545-339' × 'PI 231129' was susceptible. In the F_2 population of this cross, inoculated at the flowering stage, there were 249 resistant and 279 susceptible plants, approximating the 7:9 ratio ($X^2 = 2.49$) expected for two independently segregating recessive genes. Similarly, among the F_3 families of the cross (inoculated at the flowering stage) there were 48 resistant, 65 segregating, and 7 susceptible families. That classification agrees with 7:8:1 ratio ($X^2 = 0.79$) expected for digenic segregation in the cross. These data indicater that the recessive gene that confers resistance in 'PI 231129' is independent of *xa 5*.

The allelic relationships of the recessive gene of 'PI 231129' with *Xa 4* and *Xa 6* were examined by studying the F_1 and F_2 populations of 'IR22' × 'PI 231129' and

Table 2. Classification of F_1 and F_2 plants for bacterial blight resistance from crosses of 'TN1' with resistant cultivars

Cross	Reaction of F_1 progenies		Reaction of F_2 populations			
	Maximum tilbring	Flowering stage	Resistant (no.)	Susceptible (no.)	x^2 3:1	x^2 1:3
TN1 × Aus 32	S	S	154	436	–	0.38
TN1 × Aus 251	S	S	84	251	–	0.00
TN1 × Aus 449	S	S	130	437	–	1.30
TN1 × DB 3	S	S	132	371	–	0.40
TN1 × DD 48	S	S	129	331	–	2.60
TN1 × DD 100	S	S	115	331	–	0.13
TN1 × DF 1	S	S	100	341	–	1.26
TN1 × DL 5	S	S	96	348	–	2.63
TN1 × DNJ 142	S	S	102	340	–	0.86
TN1 × DV 29	S	S	113	349	–	0.06
TN1 × DV 32	S	S	106	350	–	0.75
TN1 × DV 52	S	S	101	333	–	0.68
TN1 × DV 85	S	R	222	126	23.31	–
TN1 × DV 86	S	R	123	101	48.21	–
TN1 × DV 139	S	S	79	212	–	0.62
TN1 × DZ 78	S	R	144	110	45.40	–
TN1 × Kaliboro 600	S	S	104	343	–	0.78
TN1 × Pankhiraj	S	S	109	315	–	0.10
TN1 × ADT 25	S	R	415	131	0.29	–

Table 2 (cont.)

Cross	Reaction of F_1 progenies		Reaction of F_2 populations			
	Maximum tilbring	Flowering stage	Resistant (no.)	Susceptible (no.)	x^2 3:1	x^2 1:3
TN1 X ARC 5756	S	S	141	374	–	1.73
TN1 X Bilekagga 36	MR	R	177	73	2.50	–
TN1 X CO 21	S	R	365	113	3.11	–
TN1 X Hema	R	R	496	168	0.04	–
TN1 X K 116-69-10	R	R	325	87	3.30	–
TN1 X KH998	R	R	497	166	0.00	–
TN1 X Kolongi Bao	MR	R	370	110	0.11	–
TN1 X M.C.M. 2	MR	R	366	112	0.63	–
TN1 X Perunel 0.69-18	MS	R	232	75	0.56	–
TN1 X PI 180060-1	S	S	113	308	–	0.75
TN1 X Taothabi	MS	MR	326	99	0.49	–
TN1 X Vella peruvazha 0.68-12	MS	MR	331	84	5.06	–
TN1 X Bageri	S	S	96	268	–	0.36
TN1 X Bakai	MR	MR	181	66	0.39	–
TN1 X Bangaluwa	S	S	112	398	–	2.51
TN1 X Devarasi	S	S	75	259	–	0.77
TN1 X Dudhi	S	S	80	231	–	0.08
TN1 X Lal Ahu	S	S	101	319	–	0.20
TN1 X Lalaka Gadur	S	S	101	260	–	1.70
TN1 X Lal Sar	S	S	93	259	–	0.37
TN1 X Maturi (Acc. 16187)	S	S	77	259	–	0.75
TN1 X Matury (Acc. 16190)	S	S	84	255	–	0.00
TN1 X Nakhi	S	S	88	271	–	0.04
TN1 X Rerm Bilash	S	S	85	219	–	1.41
TN1 X Sajani	S	S	84	218	–	1.26
TN1 X Sokan Dhan	S	S	87	213	–	2.56
TN1 X Tally	MS	MS	97	260	–	0.89
TN1 X Bathkiriel	MR	R	273	102	0.96	–
TN1 X Halsudu Heenati	MS	R	250	75	0.71	–
TN1 X Halsuduwee	MS	R	301	115	1.52	–
TN1 X Kirikunda	MS	R	278	75	2.65	–
TN1 X Mahamawee	MS	R	351	132	1.39	–
TN1 X Malalwariyan	MS	R	261	62	5.80	–
TN1 X Murunga Balawee	MS	R	302	79	3.69	–
TN1 X Murungawee	MS	R	389	106	3.07	–
TN1 X No. 20	MR	R	171	44	2.35	–
TN1 X Patchaiperumal	MS	R	324	96	1.02	–
TN1 X Perum Karuppan	MS	R	414	126	0.80	–
TN1 X Race	MS	R	273	78	0.13	–
TN1 X Rathu Heenati	MS	R	364	99	3.23	–
TN1 X Sudumalawee	MS	MR	205	49	4.36	–
TN1 X Wanni Dahanala	MR	R	260	99	1.27	–
TN1 X Yakadawee	MS	MR	245	74	0.52	–
TN1 X Back Gi Cheong Byeo	MS	R	269	81	0.64	–
TN1 X Chukei No. 314	R	R	327	97	1.00	–
TN1 X Gui do	R	R	319	95	0.93	–
TN1 X Patong 32	MR	R	491	139	3.02	–
TN1 X Tolil 14	MS	MS	105	309	–	0.00
TN1 X Nagane Tia	MR	R	179	66	0.49	–
TN1 X Nam Sakouy	R	R	351	108	0.25	–
TN1 X Pakheng	R	R	320	84	3.82	–
TN1 X Kalimodu 50	MS	R	174	69	1.49	–
TN1 X Nam Sagui 19	R	R	348	98	2.17	–
TN1 X PI 231129	S	MS	132	298	–	7.44
TN1 X Lua Ngu	MS	R	675	225	0.00	–

S = Susceptible, MS = Moderately susceptible, MR = Moderately resistant, R = Resistant

Table 3. Classification of F_3 families from crosses of 'TN1' with 'DV 85', 'DV 86' and 'DZ 78' for bacterial blight resistance

Cross	Stage of inoculation	F_3 families (no.)			
		Resistant	Segregating	Susceptible	x^2
TN1 X DV 85	Maximum tillering	46	114	40	4.28[a]
	flowering	104	84	12	5.69[b]
TN1 X DV 86	Maximum tillering	26	55	19	1.98[a]
	flowering	51	44	5	2.18[b]
TN1 X DZ 78	Maximum tillering	32	51	17	4.65[a]
	flowering	52	41	7	3.47[b]

[a] x^2 for 1:2:1 expected ratio
[b] x^2 for 7:8:1 expected ratio

'PI 231129' × 'Malagkit Sungsong'. As expected, the F_1 progeny of 'IR22' × 'PI 231129' was resistant and in the F_2 population of the cross there were 479 resistant and 79 susceptible plants. The proportion of resistant and susceptible plants agrees with the 13:3 ratio ($X^2 = 4.0$) expected for independent segregation of one dominant and one recessive gene. The F_1 hybrid 'PI 231129' × 'Malagkit Sungsong', when inoculated at booting stage, was susceptible and in the F_2 population of the cross inoculated at the same stage there were 202 resistant and 248 susceptible plants. As pointed out by Sidhu and Khush (1978), *Xa 6* shows recessive gene action when the segregating populations are inoculated at the booting stage. Thus the number of resistant and susceptible plants in the F_2 populations of the 'PI 231129' × 'Malagkit Sungsong' cross agrees with the 7:9 ratio ($X^2 = 0.27$) expected for two independently segregating recessive genes. These data therefore show that the recessive gene of 'PI 231129' segregates independently of *Xa 4*, *xa 5*, and *Xa 6*.

The F_1 hybrids of 'IR22' with cultivars having single dominant genes were resistant. Similarly, no susceptible plants were observed in any of the F_2 populations from those crosses (Table 4). It is therefore obvious that the cultivars have allelic genes at the *Xa 4* locus. Eighteen of the cultivars are resistant at all stages of plant growth and thus have $Xa\,4^a$ for resistance. Twenty are resistant at the booting and post-booting stages and have $Xa\,4^b$ for resistance.

Because resistance at the maximum tillering stage in 'DV85', 'DV86' and 'DZ78' is apparently governed by a single recessive gene, the reactions of F_1 hybrids and F_2 populations from the crosses of those cultivars with 'IR1545-339' were studied. The F_1 hybrids were resistant at maximum tillering as well as at later stages. The F_2 populations, consisting of 405, 392 and 506 plants from the crosses 'IR1545-339' × 'DV85', 'IR1545-339' × 'DV86' and 'IR1545-339' × 'DZ78', respectively, were all resistant. These data confirm that 'DV85', 'DV86' and 'DZ78' each has *xa 5* for resistance.

Table 4. Classification for reaction to bacterial blight of F_2 populations from the crosses of 'IR22' with varieties having single dominant genes for bacterial blight resistance

Cross	F_2 plants (no.)	
	Resistant	Susceptible
IR22 X ADT 25	300	0
IR22 X Bilekagga 36	369	0
IR22 X CO 21	312	0
IR22 X Hema	500	0
IR22 X K 116-69-10	417	0
IR22 X KH 998	310	0
IR22 X Kolongi Bao	592	0
IR22 X M.C.M. 2	618	0
IR22 X Perunel 0.68-18	463	0
IR22 X Taothabi	375	0
IR22 X Vella Peruvazha 0.68-12	450	0
IR22 X Bakai	243	0
IR22 X Bathkiriel	375	0
IR22 X Halsudu Heenati	444	0
IR22 X Halsuduwee	439	0
IR22 X Kirikunda	307	0
IR22 X Mahamawee	228	0
IR22 X Malalwariyan	435	0
IR22 X Murunga Balawee	328	0
IR22 X Murungawee	416	0
IR22 X No. 20	518	0
IR22 X Patchaiperumal	412	0
IR22 X Perum Karuppan	549	0
IR22 X Race	392	0
IR22 X Rathu Heenati	532	0
IR22 X Sudumalawee	450	0
IR22 X Wanni Dahanala	399	0
IR22 X Yakadawee	500	0
IR22 X Back Ai Cheong Byeo	450	0
IR22 X Chukei No. 314	378	0
IR22 X Gui do	274	0
IR22 X Patong 32	500	0
IR22 X Nagane Tia	593	0
IR22 X Nam Sakouy	352	0
IR22 X Pakheng	278	0
IR22 X Kalimodu 50	464	0
IR22 X Nam Sagui 19	720	0
IR22 X Lua Ngu	500	0

Table 5. Classification for bacterial blight reaction at flowering stage of F_1 and F_2 plants and F_3 families from crosses of 'IR22' with 'DV 85', 'DV 86' and 'DZ 78'

Cross	F_1	F_2 (no.)			F_3 families (no.)			
		Resistant	Susceptible	x^2 61:3	Resistant	Segregating	Susceptible	x^2 37:26:1
IR22 X DV 85	Resistant	607	23	1.50	66	33	1	2.68
IR22 X DV 86	Resistant	336	26	5.04	86	51	0	3.11
IR22 X DZ 78	Resistant	927	59	3.71	59	41	0	1.58

The allelic relationships of dominant genes for the resistance of 'DV85', 'DV86' and 'DZ78' with *Xa 4* were examined by studying the reaction of F_1, F_2 and F_3 populations of crosses of those cultivars with 'IR22'. The F_1 hybrids were resistant whereas the F_2 data agreed with the 61 resistant to 3 susceptible ratio (Table 5) expected for independent segregation of two dominant and one recessive gene. Similarly, classification of F_3 families into resistant, segregating, and susceptible groups showed a close fit to the 37:26:1 ratio (Table 5) expected for independent segregation of two dominant and one recessive gene. These observations suggest that the dominant gene in each of the cultivars 'DV85', 'DV86' and 'DZ78' is independent of *Xa 4*.

The F_1 and F_2 populations from the crosses of 'Zenith' with 'DV85', 'DV86' and 'DZ78' were evaluated for resistance to determine the allelic relationship of the dominant resistance genes of 'DV85', 'DV86' and 'DZ78' with *Xa 6*. The inoculations were done at the flowering stage. All the F_1 hybrids were resistant. In the F_2 population of 'Zenith' x 'DV85', there were 335 resistant and 20 susceptible plants. The F_2 population of 'Zenith' x 'DV86' exhibited 326 resistant and 10 susceptible plants. The F_2 population of 'Zenith' x 'DZ78' produced 351 resistant and 23 susceptible plants. These data agree with the 61:3 ratio expected for independent segregation of two dominant and one recessive gene. The results show that the dominant gene for resistance present in each of the cultivars 'DV85', 'DV86' and 'DZ78' are also independent of *Xa 6*.

Discussion

Of the 74 cultivars analyzed, 38 have single dominant genes for resistance that are allelic to *Xa 4*. Thirty-two cultivars have single recessive genes for resistance that are allelic to *xa 5* for resistance. Of the 38 cultivars having dominant genes at the *Xa 4* locus, 18 have the $Xa\,4^a$ allele whereas 20 have $Xa\,4^b$ (Table 6). Resistance in three cultivars analyzed ('DV85', 'DV85' 'DZ78') is conditioned by *xa 5* at the maximum tillering stage, whereas at flowering and later growth stages it is conferred by *xa 5* as well as by an additional dominant gene that segregates independently of *Xa 4*, *xa 5* and *Xa 6*. According to the International Rules of Nomenclature (Int. Rice Commision 1959), we have designated the dominant gene of 'DZ78' as *Xa 7*. Cultivar 'PI 231129' has a single recessive gene for resistance that segregates independently of *Xa 4*, *xa 5* and *Xa 6*. This gene is designated *xa 8*. The allelic relationships of *Xa 7* to the dominant genes for resistance in 'DV85' and 'DV86' are not known. However, 'DV85', 'DV86' and 'DZ78' are morphologically similar and perhaps from a common stock; in all probability the three cultivars have *Xa 7*.

So far, five different genes for resistance to Philippine isolates of bacterial blight are known. All the known cultivars with *Xa 5*, with the exception of 'Tolil 14', are from the Indian subcontinent. 'Tolil 14' is from Malaysia and might have been introduced from the Indian subcontinent. Cultivars with *Xa 4* analyzed in our investigation and earlier ones (Librojo et al. 1976; Olufowote et al. 1977; Petpisit et al. 1977) are more widely distributed. *Xa 6* seems to be confined to the Philippine germ plasm (Sidhu and Khush 1978). 'DZ78' having *Xa 7* and 'PI

Table 6. Bacterial blight resistant cultivars analyzed in this study and the resistance genes possessed by them

Cultivars	Resistance gene
Aus 32	*xa 5*
Aus 251	*xa 5*
Aus 449	*xa 5*
DB 3	*xa 5*
DD 48	*xa 5*
DD 100	*xa 5*
DF 1	*xa 5*
DL 5	*xa 5*
DNJ 142	*xa 5*
DV 29	*xa 5*
DV 32	*xa 5*
DV 52	*xa 5*
DV 85	*xa 5* + ?[a]
DV 86	*xa 5* + ?[a]
DV 139	*xa 5*
DZ 78	*xa 5* + *Xa 7*
Kaliboro 600	*xa 5*

Table 6 (cont.)

Cultivars	Resistance gene
Pankhiraj	*xa 5*
ADT 25	*Xa 4*^{b}
ARC 5756	*xa 5*
Bilekagga 36	*Xa 4*^{a}
CO21	*Xa 4*^{b}
Hema	*Xa 4*^{a}
K116-69-10	*Xa 4*^{a}
KH 998	*Xa 4*^{a}
Kolongi Bao	*Xa 4*^{a}
M.C.M. 2	*Xa 4*^{a}
Perunel 0.69-18	*Xa 4*^{b}
PI 180060-1	*xa 5*
Taothabi	*Xa 4*^{b}
Vella Peruvezha 0.68-12	*Xa 4*^{b}
Bageri	*xa 5*
Bakai	*Xa 4*^{a}
Bangaluwa	*xa 5*
Devarasi	*xa 5*
Dudhi	*xa 5*
Lal Ahu	*xa 5*
Lalaka Gadur	*xa 5*
Lal Sar	*xa 5*
Maturi	*xa 5*
Matury	*xa 5*
Nakhi	*xa 5*
Rerm Bilash	*xa 5*
Sajani	*xa 5*
Sokan Dhan	*xa 5*
Tally	*xa 5*
Bathkiriel	*Xa 4*^{a}
Halsudu Heenati	*Xa 4*^{b}
Halsuduwee	*Xa 4*^{b}
Kirikunda	*Xa 4*^{b}
Mahamawee	*Xa 4*^{b}
Malalwariyan	*Xa 4*^{b}
Murunga Balawee	*Xa 4*^{b}
Murungawee	*Xa 4*^{a}
No. 20	*Xa 4*^{a}
Patchaiperumal	*Xa 4*^{b}
Perum Karuppan	*Xa 4*^{b}
Race	*Xa 4*^{b}
Rathu Heenati	*Xa 4*^{b}
Sudumalawee	*Xa 4*^{b}
Wanni Dahanala	*Xa 4*^{a}
Yakadawee	*Xa 4*^{b}
Back Gi Cheong Byeo	*Xa 4*^{b}
Chukei No. 314	*Xa 4*^{a}
Gui do	*Xa 4*^{a}
Patong 32	*Xa 4*^{a}
Tolil 14	*xa 5*
Nagane Tia	*Xa 4*^{a}
Nam Sakouy	*Xa 4*^{a}
Pakheng	*Xa 4*^{a}
Kalimodu 50	*Xa 4*^{b}
Nam Sagui 19	*Xa 4*^{a}
PI 231129	*xa 8*
Lua Ngu	*Xa 4*^{b}

[a] 'DV 85' and 'DV 86' each has two genes. One of them is *xa 5*. Allelic relations of the other are not known

231129', which has *xa 8* for resistance, are from Bangladesh and the U.S.A., respectively.

Literature

Ezuka, A., Horino, O.; Toriyama, K.; Shinoda, H.; Morinaka, T.: Inheritance of resistance of rice variety Wase Aikoku 3 to *Xanthomonas oryzae*. Bul. Tokai-kinki Nat. Agric. Exp. Sta. **28**, 124-130 (1975)

International Rice Commission. Genetic symbols for rice recommended by the International Rice Commission. IRC Newsletter. **8**, 1-16 (1959)

Karganilla, A.; Natural, M.P.; Ou, S.H.: Comparative study on the different media for *Xanthomonas oryzae*. Philippine Agric. **57**, 141-152 (1973)

Kauffman, H.E.; Reddy, A.P.K.; Hsieh, S.P.Y.; Merca, S.D.: An improved technique for evaluating resistance of rice varieties to *Xanthomonas oryzae*. Plant Dis. Rep. **56**, 537-541 (1973)

Librojo, V.; Kauffman, H.E.; Khush, G.S.: Genetic analysis of bacterial blight resistance in four varieties of rice. Sabrao J. **8**, 105-110 (1976)

Olufowote, J.O.; Khush, G.S.; Kauffman, H.E.: Inheritance of bacterial blight resistance in rice. Phytopathology **67**, 772-775 (1977)

Petpisit, V.; Khush, G.S.; Kauffman, H.E.: Inheritance of resistance to bacterial blight in rice. Crop Sci. **17**, 551-554 (1977)

Sakaguchi, S.: Linkage studies on the resistance to bacterial leaf blight, *Xanthomonas oryzae* (Uyeda et Ishiyama) Dowson, in rice. Bul. Nat. Inst. Agric. Sci. Japan. Ser. D. **16**, 1-18 (1967)

Sidhu, G.S.; Khush, G.S.: Dominance reversal of a bacterial blight resistance gene in some rice varieties. Phytopathology **68**, 461-463 (1978)

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Dr. G.S. Khush
Plant Breeder and Head
Plant Breeding Department
International Rice Research
Institute
P.O. Box 933, Manila
(Philippines)