

# Bacterial Blight Quantitative Resistance in Rice (*Oryza sativa L.*)



Lincoln Mandal<sup>1\*</sup>, Sunil Kumar Verma<sup>2</sup>, Saugata Sasmal<sup>3</sup> and Jawahar Lal Katara<sup>4</sup>

<sup>1</sup>Department of Agriculture and Biotechnology, CG, India

<sup>2</sup>Department of Genetics and Plant Breeding, CARS, India

<sup>3</sup>Krishi Vigyan Kendra, IGKV, India

<sup>4</sup>Department of Plant Biotechnology, National Rice Research Institute, India

Submission: November 30, 2017; Published: February 27, 2018

\*Corresponding author: Lincoln Mandal, Department of Agriculture and Biotechnology, CG, Raipur-492012, India, Email: lincolndbt@gmail.com

## Abstract

Bacterial blight disease, caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), is one of the most serious diseases in rice producing areas. The durable and broad resistance of plants was found to be usually governed by multiple genes or quantitative trait loci (QTLs). The quantitative trait loci were mapped for bacterial blight resistance in rice by various researchers almost on all chromosomes. QTLs mapped will facilitate the isolation of novel Bacterial blight resistance genes and their utilization in rice resistance breeding through marker-assisted selection.

## Introduction

The Bacterial leaf blight caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) [1,2] is one of the most destructive diseases of rice throughout the world [3]. The presence of complete resistance and partial resistance to *Xanthomonas oryzae* pv. *oryzae* in rice has been reported [4,5]. The resistance of rice to specific *Xanthomonas oryzae* pv. *oryzae* races is governed by both major R genes with a qualitative effect that condition complete resistance (CR) and polygenes with a quantitative effect

(quantitative trait loci, QTL) that condition partial resistance (PR) [6,7]. The durable and broad resistance of plants was found to be usually governed by multiple genes or quantitative trait loci (QTLs) [8].

## Quantitative Trait Loci

The Quantitative Trait Loci were mapped for bacterial blight resistance in rice by many researchers using various mapping population [7,9-13] shown in Table 1.

**Table 1:** QTLs mapped using various population using *Xoo* strains in rice.

Xoo Strains	Origin	QTL Localization Chromosome	QTL Name	LOD Score	Closely Linked Marker/ Interval	Additive Effect	PVE (%)	References
MA11	Mali	1	<i>qABB-1</i>	5.068	RM129	1.7	13.4	Djedatin et al. [13]
		7	<i>qABB-7</i>	16.006	RM125	3.2	36.6	
		11	<i>qABB-11</i>	4.666	RM144	1.5	12.4	
BA14	Burkina Faso	7	<i>qABB-7</i>	13.943	RM125	3.5	33.4	
		11	<i>qABB-11</i>	4.68	RM144	1.8	12.8	
BA13	Burkina Faso	11	<i>qABB-11</i>	5.728	RM144	2.5	15.3	
NA18	Niger	9	<i>qABB-9</i>	4.359	RM242	2.3	12.9	
		10	<i>qABB-10</i>	3.606	RM294A	-2.23	10.8	
		11	<i>qABB-11</i>	6.03	RM144	2.7	17.4	
PX086	Philippines	5	<i>qBB-5</i>	4.209	RM440	-1.68	11.5	
		8	<i>qBB-8-2</i>	4.957	RM281	-2.16	13.4	
		12	<i>qBB-12</i>	4.869	RM512	1.9	13.2	
PX061	Philippines	4	<i>qBB-4</i>	3.403	RM252	-1.7	10	
		11	<i>qABB-11</i>	36.78	RM144	7.3	67.9	

XF89b	Taiwanese	6	<i>qBBR06.1</i>	13.2	RM6395-RM412	-1.13	9.58	Tseng et al. [12]
		8	<i>qBBR08.1</i>	15.04	RM1376-RM8020	-1.2	11.04	
		11	<i>qBBR11.1</i>	26.6	RM27051-ID111102	-1.64	21.1	
P2(PX086), P3(PX079), P4(PX071), P5(PX0112), P6 (PX099), P7 (PX0280), P8 (PX0145), P9 (PX087), P10(PX0124) and C4(ZHE173)	Philippines/China	1	<i>qBBR1</i>	10.1	RM128	4.89	21.5	Han et al. [11]
		3	<i>qBBR3</i>	6.2	R03D158	3.73	12.3	
		5	<i>qBBR5</i>	17.8	RM6972	7.36	39.2	
PX0611 (race 1), PX085 (race 2), PX079 (race 3), PX071 (race 4), PX0112 (race5), PX099 (race 6) PX0145 (race 7), PX0280 (race 8), PX0339 (race 9) and PX0341 (race 10)	Philippines	1	<i>QBbr1a</i>	4.56	RM84			Li et al. [7]
		1	<i>QBbr1b</i>	6.06	RM23			
		1	<i>QBbr1c</i>	1.97	RG381			
		1	<i>QBbr1d</i>	5.43	RM104			
		2	<i>QBbr2a</i>	3.7	RM211			
		2	<i>QBbr2b</i>	4.95	RM27			
		2	<i>QBbr2c</i>	2.85	RG654			
		3	<i>QBbr3a</i>	1.98	RG100			
		3	<i>QBbr3b</i>	3.66	RM282			
		3	<i>QBbr3c</i>	3	RM16			
		3	<i>QBbr3d</i>	2.45	RZ337A			
		3	<i>QBbr3e</i>	2.93	RZ448			
		3	<i>QBbr3f</i>	5.64	RM227			
		4	<i>QBbr4a</i>		RM307			
		4	<i>QBbr4b</i>	2.26	RM252			
		4	<i>QBbr4c</i>	4.74	RM317			
		4	<i>QBbr4d</i>	4.49	RG143			
		5	<i>QBbr5a</i>		RG556			
		5	<i>QBbr5b</i>	6.7	RM163			
		5	<i>QBbr5c</i>	4.77	RZ70			
		6	<i>QBbr6a</i>		RM3			
		6	<i>QBbr6b</i>	3.7	RG433			
		7	<i>QBbr7a</i>		RG769			
		7	<i>QBbr7b</i>	4.5	RM234			
		7	<i>QBbr7c</i>	4.58	RZ978			
		8	<i>QBbr8a</i>	2.9	RZ143			
		8	<i>QBbr8b</i>	3.51	RM223			
9	<i>QBbr9a</i>	2.56	RZ422					
9	<i>QBbr9b</i>	5.54	RZ12					
9	<i>QBbr9c</i>	3.11	RM215					
10	<i>QBbr10</i>	5.04	RM228					
11	<i>QBbr11a</i>	4.53	RZ638					
11	<i>QBbr11b</i>	4.33	RM120					
11	<i>QBbr11c</i>	4.59	RM21					

CR4, CX08, CR6	China	2	<i>Pi-q5</i> ,		RG520/ RZ476a			Li et al. [9]
			<i>Pi-2</i>					
		3	<i>QSbr3a</i>		C515/ RG348			
		3	<i>QSbr3b</i>		RG482/ CD0795			
		4	<i>Xa1</i> ,		RG214/Ph			
			<i>Xa2</i>					
		4	<i>Bph-3</i> ,		RZ69/ RG190			
			<i>Glh</i>					
		8	<i>Pi-11(t)</i>		G104/ G1314a			
		9	<i>QSbr9a</i>		RG451/ RZ404			
		10	<i>QSbr10</i>		RG1094f/ C16			
		11	<i>Xa 4</i>	61.1 43.0 36.1	Xa4 (RZ536/ G2132b)		65.2 55.2 52	
		11	<i>QSbr11</i>		RG1022/ RZ525			
		12	<i>Pi-q6</i> ,		RG91Q/ RG341			
	<i>Pi-4(t)</i>							

### Importance

The QTLs mapped will facilitate the isolation of novel Bacterial blight resistance genes and their utilization in rice resistance breeding [11]. The new information on genes and QTLs for resistance to bacterial blight will be useful for controlling the disease [13]. The molecular mapping of QTL results provide a suitable source of potential disease resistance genes and establish a system for improving rice bacterial blight resistance through marker-assisted selection [12]. The race specificity of partial resistance (PR) and its strong genetic overlap with complete resistance (CR) indicate that partial resistance (PR) is essentially “weaker” complete resistance (CR) [7]. A high level of durable resistance to *Xoo* may be achieved by the cumulative effects of multiple QTLs, including the residual effects of “defeated” major resistance genes [9].

### References

- Ishiyama S (1922) Studies on bacterial blight of rice. Report of Agric Exp Station 45: 233-261.
- Swings J, Van Den Mooter M, Vauterin L, Hoste B, Gillis M, et al. (1990) Reclassification of the causal agents of bacterial blight *Xanthomonas campestris* pv. *oryzae* and bacterial leaf streak *Xanthomonas campestris* pv. *oryzicola* of rice as pathovars of *Xanthomonas oryzae* new species Ex Ishiyama 1922. Int J Syst Bacteriol 40: 309-311.
- Mew TW (1987) Current status and future prospects of research on bacterial blight of rice. Annu Rev Phytopathol 25: 359-382.
- Zhang Q, Mew TW (1985) Adult plant resistance of rice cultivars to bacterial blight. Plant Dis 69: 896-898.
- Parlevliet JE, Zadoks JC (1977) Integrated concept of disease resistance-new view including horizontal and vertical resistance in plants. Euphytica 26(1): 5-21.
- Koch MF, Parlevliet JE (1991) Genetic analysis of, and selection for, factors affecting quantitative resistance to *Xanthomonas campestris* pv. *oryzae* in rice. Euphytica 53(3): 235-245.
- Li ZK, Arif M, Zhong DB, Fu BY, Xu JL, et al. (2006) Complex genetic networks underlying the defensive system of rice (*Oryza sativa* L.) to *Xanthomonas oryzae* pv. *oryzae*. Proc Nat Acad Sci USA 103(21): 7994-7999.
- Johnson R (1984) A critical analysis of durable resistance. Annu Rev Phytopathol 22: 309-330
- Li ZK, Luo LJ, Mei HW, Paterson AH, Zhong DB, et al. (1999) A ‘defeated’ rice resistance gene acts as a QTL against a virulent strain of *Xanthomonas oryzae* pv. *oryzae*. Mol Gen Genet 261: 58-63.
- Sujatha K, Natarajkumar P, Laha GS, Mishra B, Rao KS, et al. (2011) Inheritance of bacterial blight resistance in the rice cultivar Ajaya and high-resolution mapping of a major QTL associated with resistance. Genet Res Camb 93(6): 397-408.
- Han X, Yang Y, Wang X, Zhou J, Zhang W, et al. (2014) Quantitative trait loci mapping for bacterial blight resistance in rice using bulked segregant analysis. Int J Mol Sci 15(7): 11847-11861.
- Tseng HY, Lin DG, Hsieh HY, Tseng YJ, Tseng WB, et al. (2015) Genetic analysis and molecular mapping of QTLs associated with resistance to bacterial blight in a rice mutant, SA042. Euphytica 205(1): 231-241.
- Djedatin G, Ndjiondjop MN, Sanni A, Lorieux M, Verdier V, et al. (2016) Identification of novel major and minor QTLs associated with *Xanthomonas oryzae* pv. *oryzae* (African strains) resistance in rice (*Oryza sativa* L.). Rice 9: 18.



This work is licensed under Creative Commons Attribution 4.0 License  
DOI: [10.19080/AIBM.2018.08.555738](https://doi.org/10.19080/AIBM.2018.08.555738)

**Your next submission with Juniper Publishers  
will reach you the below assets**

- Quality Editorial service
- Swift Peer Review
- Reprints availability
- E-prints Service
- Manuscript Podcast for convenient understanding
- Global attainment for your research
- Manuscript accessibility in different formats  
( Pdf, E-pub, Full Text, Audio)
- Unceasing customer service

**Track the below URL for one-step submission**

<https://juniperpublishers.com/online-submission.php>