

Abstract

Rice blast resistant QTLs were mapped using composite interval mapping with six races IB1, IB45, IB49, IB54, IC17, and ID1 of *Magnaporthe oryzae* in a recombinant inbred line (RIL) population derived from a cross of the moderately-susceptible japonica cultivar Lemont with the moderately-resistant indica cultivar Jasmine 85. Disease reactions of 227 RILs were evaluated using a category scale of ratings from 0, representing the most resistant, to 5, representing the most susceptible. The category data we collected were used for mapping resistant QTLs. A total of eight QTLs responsible for different degrees of phenotypical variation ranging from 5.2 to 26.5% were identified on chromosomes 3, 8, 9, 11, and 12.

Introduction

Resistance to blast conditioned by minor genes are thought to be more durable and effective. These minor genes known as quantitative trait loci (QTL) with different resistant effects are located on different chromosomal regions, some of them located at or near the major blast resistance genes known as *Pi*-genes. In the southern US, rice cultivars with high yielding and good quality have been deployed with blast resistance conditioned by some of these resistant QTLs. These cultivars carrying resistant QTLs have been widely grown because they offer better yield potentials than rice cultivars carrying *Pi*-genes in the Southern USA.

The objective of the present study is to identify resistant QTLs from two US rice cultivars, Jasmine 85 and Lemont for marker assisted breeding programs in the USA.

Materials & Methods

A population consisting of 227 RILs from the cross of Lemont with Jasmine 85 (LJRILs) were used in this study. Twelve common races of *M. oryzae* (Plant Disease, 93:639-644) were used to screen disease reactions of rice to the pathogen. Six resistant races of IB1, IB45, IB49, IB54, IC17, and ID1 were used. Disease inoculation was based on a standard method (Genetics, 127:87-101). Seedlings were inoculated in a bag at the spore concentration of 5-15x10⁶ spores/mL. At 24 hrs after incubation, seedlings were returned back to a greenhouse for additional six days to allow disease development. Disease reactions were evaluated one week after inoculation with the pathogen.

A disease rating system described by Valent (1997) was modified. Disease reaction was evaluated on a scale of 0 to 5, where 0 indicates no visible lesion; and 5 indicates that lesions were greater than 50% of the leaf area.

The mean of blast severity for the LJRIL was used for the composite interval mapping (CIM). QTL analysis was performed using Windows QTL Cartographer version 2.5 with the default CIM control parameters: model 6 of standard model, five control markers, 10 cM of window size, and forward regression method. The LOD threshold of ≥ 2.4 was used to declare the presence of a putative QTL. Additive effect and percentage of variation explained by individual infection category - QTL were estimated.

Results & Summary

- Jasmine 85 was resistant to IB1, IB49, IC17, ID1 and Lemont susceptible to these races; whereas Lemont was resistant to IB45 and IB54 and Jasmine 85 susceptible to both of them. Thus, IB1, IB49, IC17, and ID1 were used to identify resistant factors from Jasmine 85; and IB45 and IB54 used to identify resistance factors from Lemont.
- The typical category data as frequency distribution of disease reactions to each race are summarized in Fig.1. Disease reactions of most individuals to all races were determined to be infection type 0.
- QTL in Lemont.** Two resistance factors were identified for IB45 and IB54 (Table, Fig. 2). The major resistance factor *qBLAST11* in Lemont to both races IB45 and IB54 were mapped between SSR markers RM206 and RM224, closer to RM224 on chromosome 11, accounting for 26.5% and 19.6% of disease reactions, respectively.
- QTL in Jasmine 85.** Two resistance factors to the race IB49 of *M. oryzae* were identified in Jasmine 85 (Table, Fig. 2). *qBLAST8-1* was mapped between RM6863 and RM72, closer to RM1148 on chromosome 8 and *qBLAST12* was mapped between RM247 and RM277, closer to OSM89 on chromosome 12. They accounted for 6.68% and 9.7% of disease reactions, respectively.
- The most important merit for this study was that disease reactions were evaluated using individual races of blast fungus under greenhouse conditions instead of classic field plot experiments.

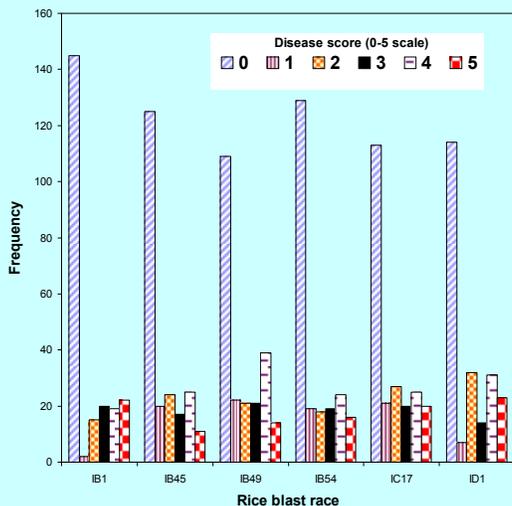


Fig. 1. Frequency distribution of disease reactions of 227 recombinant inbred lines from the cross of Lemont (LMNT) and Jasmine 85 (JSMN) assayed in greenhouse for blast resistance.

Summary of quantitative trait loci (QTLs), physical locations, nearby known *R* genes and percentage of phenotypical variation.

QTL	Chrom.	Race of <i>M. oryzae</i>	Marker interval	Nearest marker locus	Chrom. location (MB)	Location of nearby known blast <i>R</i> genes (MB)	LOD value	Phenotypic variation (%)	Additive effect
<i>qBLAST3</i>	3	IB45	RM251-RM338	RM282	12.4	IE1k resistance	3.4	5.17	-0.45
<i>qBLAST8-1</i>	8	IB49	RM6863-RM72	RM1148	4	<i>Pi36</i> (2)	4.3	6.69	0.45
<i>qBLAST8-2</i>	8	IC17	RM310-RM72	RM72	6.8	Sheath blight resistance	4.5	7.22	0.48
<i>qBLAST9-1</i>	9	IB54	RM257-RM108	RM257	17.7		3.3	4.64	0.47
<i>qBLAST9-2</i>	9	IC17	RM257-RM107	RM108	17.9	NBS-LRR	4.3	7.62	0.52
<i>qBLAST9-3</i>	9	IC17	RM107-RM245	RM215	21.2		2.9	4.49	0.42
<i>qBLAST11</i>	11	IB45	RM206-RM224	RM224	27.8	<i>Pikm/Pik</i> (28.4)	16.4	26.53	-0.87
		IB54	RM206-RM224	RM224	27.8		11.8	19.60	-0.79
<i>qBLAST12</i>	12	IB1	RM6998-OSM89	OSM89	7.9	<i>Pi-ta</i> (10.6)	3.3	5.44	0.46
		IB49	RM247-RM277	OSM89	7.9		5.9	9.70	0.57
		ID1	RM247-RM277	OSM89	7.9		5.7	10.18	0.64

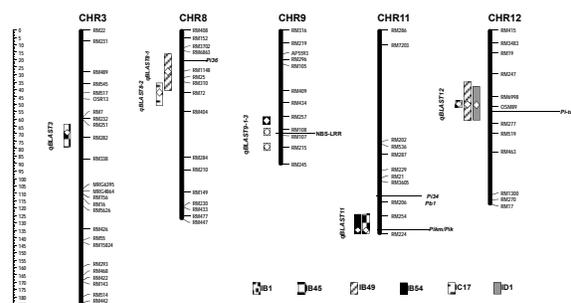


Fig. 2. Chromosomal locations of the blast-QTLs mapped in this study and estimated locations of the blast-QTLs and previously mapped major *R* genes. The genetic distances of SSR markers in cM are shown on the left side of the chromosomes.

Acknowledgements

We thank Michael Lin for assistance in greenhouse evaluation of blast disease reactions and Melissa Jia for assistance in genotyping of LJRILs.