Development of Strategies to Manage Rice Blast Disease in the USA

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Summary

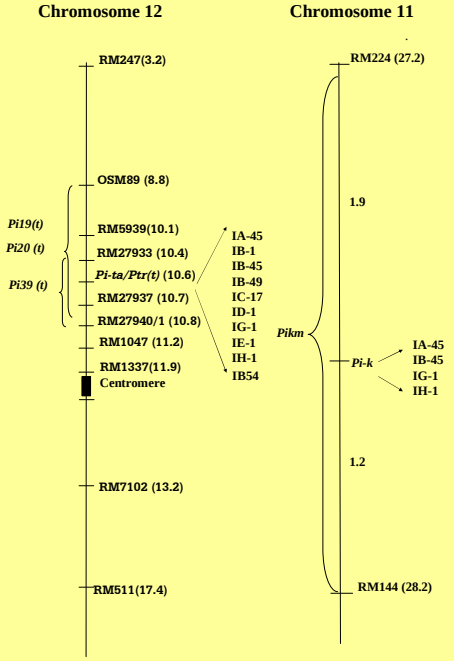
Rice blast disease has been a serious threat to stable rice production in the southern USA. Blast disease has caused yield losses for decades. Severity of blast epidemics has always been influenced by a combination of the following three factors: 1) rice cultivars deployed with different combination of major and minor resistance (*R*) genes, 2) weather conditions during rice growing stages, particularly high relative humidity before and during heading, and 3) race composition of field pathogen populations. In the USA, successful deployment of rice degree days, known as the "DD-50" program, erratic irrigation (shallow flood, intermittent flooding, furrow irrigation, pivot irrigation attempts) and improved varieties carrying both major and minor *R* genes have greatly contributed to the effectiveness of blast management.

Progress and Recent Accomplishments

Since the Fourth International Rice Blast Conference held in Changsha, map positions, resistance spectra, DNA sequence variation, and evolution of the six most commonly used blast *R* genes, *Pi-ta*, *Pi-b*, *Pi-kh/s(m)*, *Pi42(t)*, *Pi43(t)*, *Pi-z(t)* and eight blast resistant QTLs in the US have been investigated. Progress will be presented by **Costanzo, Lee, Dai, Roy-Chowdhury, Wang, Liu, Zhou, Reddyvari-Channarayappa, and Zhai**. Additional accomplishments are listed below:

1. A resistant spectrum of the *Pi-ta* and *Pi-k* gene in the US was determined (Fig. 1). The *Pi-ta* gene was found to confer resistance to 10 races of the US blast fungus and *Pi-k* confers resistance to 4 races of blast fungus**.**
2. Through a combination of DNA sequencing, genetic crosses and pathogenicity assays a large linkage block at the *Pi-ta* region was identified. Genotyping of selected rice germplasm and six mapping populations revealed that such a linkage block is a result of the combination of selection of blast resistance, recombination suppression, and segregation distortions (Fig. 2).
3. A total of 182 mono - and digenic rice lines with different combinations of *Pi-ta*, *Pi-kh* and *Pi-ks* and agronomic traits have been created to facilitate the genetic studies of epistatic interactions of yield, yield components, and blast resistance (Table 1).

Fig 1. *Pi-ta* Confers Resistance to 10 US Races, *Pi-k* Confers Resistance to 4 US Races of Blast Fungus

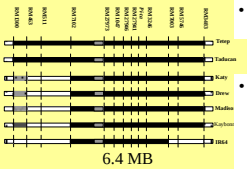


Jia et al., Plant Disease 93: 639-644, 2009.

Fig 2. A Large Linkage Block at the *Pi-ta* Locus

A. Linkage block under selection in indica and japonica crosses

B. Linkage block under no selection



- The block size is less than 1 megabase in a cross of indica with indica rice.
- The block size is 8 megabase in a cross of indica with japonica rice suggesting a potential role of incompatibility of an indica and japonica cross.

Jia, Heredity 103: 333-339, 2009

Table 1. Ranges of Characteristics of Mono - and Digenic Lines Containing Different Blast *R* Genes†

Characteristics	Range of traits in mono- and digenic lines containing different blast *R* genes			
	Pi-ta + *Pi-k*^{s}	*Pi-k*^{s}	*Pi-ta* + *Pi-k*^{h}	*Pi-k*^{h}
Heading Days (day)	72-158	68-99	73-104	70-100
Plant Height (cm)	76-132	80-126	86-131	83-123
Seed Length (cm)	0.87-1.05	0.90-1.7	0.90-1.4	0.91-1.1
Seed Width (cm)	0.22-0.27	0.23-2.8	0.20-0.27	0.2-0.27
Ratio	3.91-4.22	3.57-4.40	3.36-4.7	3.53-4.71
Weight (g) /100 kernels	1.78-2.69	1.74-2.76	1.7-2.53	1.83-2.54

Jia and Moldenhauer, J. of Plant Registration 103: 333-339, 2010 (cover)

Future Directions

1.Clone additional components in the *Pi-ta* mediated resistance responses using both genetic and biochemical approaches;
2.Understand the molecular mechanisms of recombination suppression;
3.Develop strategies for marker assisted breeding to reduce linkage block.

References

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