

Phinyarat Kongprakhon 2009: Identification of Genomic Locations of Quantitative Trait Loci for Leaf and Neck Blast (*Pyricularia grisea*) in Rice and Barley. Doctor of Philosophy (Genetics), Major Field: Genetics, Department of Genetics. Thesis Advisor: Associate Professor Nitsri Sangduen, Ph.D. 91 pages.

*Pyricularia grisea* is the most destructive and cosmopolitan fungal pathogen of rice and it can also cause disease on other agriculturally important cereals. We determined the number, location, and interaction of QTL associated with resistance to *P. grisea* isolates obtained from rice (THL142 and THL222) and barley (TH16 and THL80) in leaf (LB) and neck blast (NB). We used mapping population of rice (IR64 x Azucena), barley (BCD47/Baronesse) and isogenic lines BISON. On rice IR64 was highly resistant, and Azucena was highly susceptible, to all four isolates. The numbers of resistant vs. susceptible progeny suggest that the resistance of IR64 is determined by two or three genes with additive effects in LB and NB. Five QTL were detected, one each on chromosomes 2, 8, 9, 11 and 12. On barley Baronesse was highly resistant, and BCD47 was susceptible, to all four isolates. The numbers of resistant vs. susceptible progeny suggest that the resistance of Baronesse is determined by one gene with additive effects in LB and two or three genes in NB. Four QTL were detected, one each on chromosomes 1H, 4H, and 7H. The results of the QTL analysis support interpretation of the phenotypic frequency distributions regarding the number of genes determining resistance to the four isolates in rice and barley population. We used isogenic lines BISON to validate resistance gene in barley. BCD12, BCD47, BISON1H, and BISON1H+4H+5H showed susceptibility to all blast isolates. Baronesse, BISON4H, BISON5H, BISON7H, BISON1H+4H, and BISON1H+5H showed resistance to all blast isolates. To compare the phenotypic data with the graphical genotype, we focused only on the region of chromosome 1H containing the major QTL. From previous studies reported this region coincident with *R* genes which confer resistance to many pathogens that causes disease to barley. In addition to we established co-linearity of gene order between 23.5 cM region of barley chromosome 1H containing *Mla* and a 510 kb region at the end of short arm of rice chromosome 5. These results indicate that a defined region on the short arm of barley chromosome 1H, including *Mla*, harbors genes conferring qualitative and quantitative resistance to multiple pathogens.

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