



Mapping quantitative trait loci for sheath blight disease resistance in Yangdao 4 rice

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ABSTRACT. Rice sheath blight (ShB), which is caused by *Rhizoctonia solani*, has become the most serious rice disease in China. Yangdao 4, a cultivar with partial resistance to ShB, was crossed with Lemont, a susceptible cultivar, to develop mapping populations that were used to analyze quantitative trait loci (QTL) that confer resistance to ShB. QTL analysis were performed in 3 environments (E1-E3) using 2 F₂ and 1 F_{2:3} populations, respectively. Three traits were recorded to evaluate ShB resistance, including disease rating (DR), lesion height (LH), and percentage of lesion height (PLH). Based on field evaluation of ShB resistance and the 2 genetic maps constructed, we identified a total of 8 QTLs for DR (4 in E1, 4 in E2, and 3 in E3), 6 QTLs for LH (1 in E1, 3 in E2, and 2 in E3), and 7 QTLs for PLH (1 in E1, 4 in E2, and 2 in E3). Sixteen of the ShB-QTLs co-localized as 6 clusters on chromosomes 3, 7, 11, and 12. Four of the 6 clusters contained ShB-QTLs that were detected in 2 environments, while the other 2 clusters with ShB-QTLs were detected in 1 environment. Three ShB-QTLs (*qSBD-3-2*, *qSBL-3-1*, and *qSBPL-3-1*) were delimited to a 581-kb region flanked by markers D333B and D334 on chromosome 3. The resistance alleles of

Yangdao 4 at the *qSBD-3-2* locus decreased DR by 0.68 and 0.79 in E2 and E3, respectively.

Key words: Quantitative trait locus; Rice (*Oryza sativa* L.); Sheath blight (ShB); ShB-resistant cultivars