



Meta-analysis of constitutive QTLs for disease resistance in maize and its synteny conservation in the rice genome

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ABSTRACT. We collected data regarding 340 disease resistance quantitative trait loci (QTLs) from the maize genomic database (MaizeGDB). We constructed an integrated linkage map and analyzed this map by using the BioMercator 2.1 software with IBM2 2008 Neighbors genetic linkage map as a reference. We used a meta-analysis method to identify five “consensus” synthetic resistance QTLs located on maize chromosomes 1, 3, 6, and 10, with map intervals of 5.14, 9.00, 28.50, 1.73, and 33.34 cM, respectively. The gene and marker sequences within the five “consensus” QTLs were downloaded from the MaizeGDB website. We identified eight resistance gene analogs (RGAs), through comparison of these sequences with the resistance genes of other members of Poaceae by using the online BLASTx software. On the basis of comparative mapping between the maize genetic map and the rice physical map, 54 rice and 44 maize resistance genes were projected onto the maize IBM2 2008 Neighbors genetic linkage map by using a synteny conservation approach. Additionally, 15 resistance genes in the “consensus” QTL regions were found in

two “consensus” QTLs on chromosomes 3 and 6; these resistance genes included rp3, scmv2, wsm2, RG3, RG16, RG36, RG51, RG53, scmv1, mdm1, RG5, RG8, RG10, RG14, and RG29. Our results provide valuable information for fine-mapping QTL, gene cloning, and molecular breeding for resistance in maize.

Key words: Maize; QTL for disease resistance; Meta-analysis; Integrated linkage map; Comparative mapping; Genetic map