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Genetic Mapping of Broad-Spectrum QTLs and Strain-Specific Major QTL for Resistance to *Ralstonia solanacearum* in Eggplant Using GBS

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The Solanaceae family includes major agricultural crops cultivated worldwide such as tomato, potato, pepper and eggplant. Production of these crops in tropical and subtropical areas is limited by *Ralstonia solanacearum*, the causal agent of the bacterial wilt disease. This pathogen represents a threat for crops due to its large host range, its persistence in fields and its extensive genetic diversity. The species complex of *R. solanacearum* is divided into four phlotypes, which all are able to wilt eggplant. Seeking for efficient and stable resistance to bacterial wilt, an intraspecific population of 178 eggplant recombinant inbred lines (RILs) was evaluated for resistance to *R. solanacearum* strains belonging to phlotypes I, IIA, IIB, and III. In addition of 162 AFLP and SSR markers, genotyping-by-sequencing (GBS) of the RILs provided 661 SNPs used to construct a dense genetic map anchored to the physical map of tomato. Quantitative Trait Loci (QTL) analysis showed the presence of a major QTL (*ERs1*) specifically associated with resistance to phlotype I strains on the chromosome 9 of eggplant. Two broad-spectrum QTLs were also identified on chromosome 2 and chromosome 5. Although less efficient than *ERs1*, these QTLs were found to partially control strains belonging to phlotype I, IIA and III. Molecular markers linked to QTLs will be very useful for breeding resistance to *Ralstonia solanacearum* in eggplant. The anchored map will also help to identify candidate genes underlying the so far identified resistance factors.

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