

Characterization and Genetic Mapping of Disease Resistance Genes to TSWV and Leaf Spots and Development of Molecular Markers for Breeding Selection

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We developed a recombinant inbred line population from the cross between SunOleic 97R and NC94022, named as the S-population, and improved the genetic map for identification of quantitative trait loci (QTLs) for resistance to TSWV and leaf spots. The improved genetic linkage map for the S-population had 248 marker loci with a marker density of 5.7 cM/loci. The analysis using the improved genetic map and multi-season (2010-2013) phenotypic data resulted in the identification of 76 QTLs with phenotypic variance explained (PVE) from 3.47 to 30.15%. Of the 76 QTLs, 13 QTLs were identified for resistance to TSWV, 43 QTLs for early leaf spot (ELS) and 20 for late leaf spot (LLS), which included four, 11, and six major QTLs (PVE larger than 10%) for each disease resistance, respectively. A total of nine major genomic regions (MGR) were found to have QTLs controlling more than one disease resistance. The identified QTLs and resistance gene-rich MGRs will facilitate further discovery of resistance genes and development of molecular markers for these important diseases..

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