

Development of a 13-SNP Multiplex Assay for I-2, Mi, Sw-5, Tm-2, and Ve of 5 Disease Resistance Loci in Tomato

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Marker assisted selection (MAS) has become very important and useful in the selection of disease resistance genes in tomato (*Solanum lycopersicum*, syn. *Lycopersicon lycopersicum* & *Lycopersicon esculentum*). Single nucleotide polymorphism (SNP), because of its abundance and high-throughput scoring potential is becoming a powerful tool in genome mapping, association studies, diversity analysis, and tagging of important genes in plant genomics. The objective of this research was to develop multiplex SNP assays for MAS of multiple disease resistance genes in tomato. Gene-derived SNP markers were found for the five loci, I-2 of Fusarium wilt (*Fusarium oxysporum* f. sp. *Lycopersici*) resistance, Mi of root-knot nematode (*Meloidogyne incognita*, *M. javanica*, and *M. arenaria*) resistance, Sw-5 of tomato spotted wilt virus (TSWV) resistance, Tm-2 of tomato mosaic virus resistance, and Ve of *Verticillium* wilt (*Verticillium dahliae* and *V. albo-atrum*) resistance. One 13-SNP multiplex assay, consisted of one SNP for I-2, one SNP for Mi, two SNPs for Sw-5, three SNPs for Tm-2 locus, and six SNPs for Ve locus, was developed and verified to be useful in identifying and selecting the five loci of tomato disease resistance in different tomato germplasm.