

Genetics of Resistance to Bacterial Spot

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Bacterial spot is an economically important disease of tomato (*Solanum lycopersicum* L.) that is caused by as many as four species of *Xanthomonas*. Resistance has been identified in several accessions and breeding lines which are closely related to the cultivated tomato. These include resistance from Hawaii breeding lines 7998 and 7981, which may trace to introgressions from *S. pimpinellifolium*; resistance from *S. lycopersicum* var. *cerasiforme* accession PI 114490; and resistance from *S. pimpinellifolium* accessions such as PI 128216. We will review progress in developing genetic markers to facilitate simultaneous genetic dissection and breeding for resistance in crosses to close relatives of the cultivated tomato. Quantitative resistance to race T1 was identified from Hawaii 7998 by using marker-trait association analysis in intraspecific crosses. A single locus on chromosome 5, *Rx3*, explained 41% of the phenotypic variation for resistance in replicated field trials. Marker-assisted selection was utilized to combine *Rx3* in coupling phase with *Pto*, a single, dominant gene that confers resistance to bacterial speck race 0 (caused by *Pseudomonas syringae* pv. *tomato*). Resistance to both spot and speck was successfully combined and verified in field trials. Accession PI 114490 appears to resist multiple races of bacterial spot. We utilized single marker-trait analysis in an Inbred Backcross (IBC) population derived from PI 114490, FL 7600, and OH 9242 to identify a locus on chromosome 11 that explained 16.6%, 13.7%, 56.5%, and 29.4% of the variation for resistance to races T1, T2, T3, and T4, respectively. Both PI 114490 and FL 7600 alleles contributed to resistance relative to the OH 9242 allele. The PI 114490 allele conferred the highest level of resistance to T2 strains while the FL 7600 allele was most effective against T1 strains. A PI 114490 allele on chromosome 1 was associated with resistance to T2, T3 and T4 strains, explaining up to 11% of the variation. Resistance to T2 strains from QTL on chromosomes 1, 3, and 11 were confirmed in subsequent crosses. To characterize resistance to race T3 from PI 128216 (*S. pimpinellifolium*), we developed an IBC population from a cross to the *S. lycopersicum* breeding line OH 88119. Marker-trait analysis indicates that two major loci from PI 128216 contribute to a T3 mediated HR response following greenhouse inoculation. We are seeking to verify these results in subsequent crosses. Our results indicate progress in simultaneous introgression, selection, and genetic characterization using inbred backcross population designs. At the same time, there remains a need to develop population structures that allows us to pyramid resistance while retaining desirable field characteristics.