

Marker Assisted Breeding for Tomato Begomovirus Resistance

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Another begomovirus resistance gene *Ty-3* was recently mapped to a marker interval of 7 cM on the long arm of chromosome 6, ~15 cM apart from the partially dominant gene *Ty-1*. Recently, we identified 30 recombinants from a population of 717 F₂ progeny. Linkage analysis delimits the *Ty-3* gene to a shorter marker interval from cLEG-31-P16 to PG9 (~5 cM). Homozygous sub-recombinant inbred lines (subRILs) have been identified from these recombinants and advanced breeding lines genotyped in the previous seasons. Disease severity indexes (DSI) for the subRILs infected with begomovirus supported the map position of the *Ty-3* gene. In addition, the DSI also indicated *Ty-1* was absent in *Solanum chilense* accession LA2779-derived lines, although they carry an introgression spanning both *Ty-1* and *Ty-3* regions. Evaluation of begomovirus resistance among the subRILs in replicated trails will validate the *Ty-3* gene position on the linkage map and allow construction of a high-resolution map. Most resistant breeding lines and commercial hybrids originating from other tomato wild species including *S. habrochaites*, *S. peruvianum*, and *S. pimpinellifolium* carried alien introgressions spanning the *Ty-3* region, suggesting that these wild species most likely also contain begomovirus resistance alleles at the *Ty-3* locus. In addition, a higher resolution map of another major begomovirus resistance gene *Ty-2* has also been constructed, which delimits the *Ty-2* gene to a much smaller interval. A fourth potential resistance gene on a different region on chromosome 6 was also explored using numerous approaches. Begomovirus genes could be pyramided into elite breeding lines and hybrids with the assistance of molecular markers to maximize utilization of existing genes and provide improved durable resistance.