Xth International Symposium on Thysanoptera and Tospoviruses

Asilomar Conference Grounds
May 16th through May 20th, 2015

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Functional marker assisted-selection and genetic variability of Sw-5bgene in multi-tospovirus resistant Solanum (section Lycopersicon) germplasm accessions using locus-specific primers

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The most important breeding source for *Tospovirus* resistance reported in tomatoes thus far is the *Sw*-5 locus, which was introgressed into cultivated *Solanum lycopersicum* L. accessions from an unidentified *S. peruvianum* L. accession. This locus contains at least five paralogues (denoted *Sw*-5a through *Sw*-5e), of which *Sw*-5bis the effective copy involved with the resistance response to distinct *Tospovirus* species. A polymorphic amplicon was found encompassing a sequence region of the functional *Sw*-5b gene, resulting in a specific, co-dominant polymorphism between germplasm accessions with and without this copy. The objective of the present work was to evaluate the conservation of this *Sw*-5b-specific polymorphism in a range of wild tomato species and breeding lines aiming to identify potential allelic variation of the locus in accessions of *Solanum* (section *Lycopersicon*) germplasm. A subset of accessions previously identified as having wide spectrum resistance against four Tospovirus species (*Tomato spotted wilt virus*, *Tomato chlorotic spot virus*, *Groundnut ringspot virus*, and *Chrysanthemum stem necrosis virus*) was also included in the evaluation. Three distinct amplicon patterns were observed with two of them being associated with susceptible accessions. Distinct insertion/deletion events were associated with these amplicon size differences. These indels generated multiple allele variants in the wild species. However, minor sequence variation was observed among *S. peruvianum* accessions, thus representing distinct *Sw*-5b alleles. The only exception was *S. peruvianum* 'PI 128660',which individual plants displayed either one SNP or they were 100% identical to the original *Sw*-5b gene.