Interspecific Reproductive Barriers in Tomato (IRBT) Meeting Abstracts

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Abs # P35021

Self-Incompatibility Factors in Unilateral Incongruity in Tomato

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Self-Incompatibility (SI), wherein self pollen is rejected by styles, is widespread in plants and functions to prevent inbreeding. In gametophytic SI, RNases encoded at the S-locus (S-RNases), are the female SI determinant. Other factors in addition to S-locus genes are required for SI, including the asparagine-rich HT-family proteins. Interspecific pollen rejection is less well understood than intraspecific SI. Often interspecific pollinations are only successful in one direction; this phenomenon is known as unilateral incongruity or incompatibility (UI). The role of SI proteins in UI appears to be complex. In tomato, genetic studies of *Solanum pennellii* X *S. lycopersicum* and *S. habrochaites* X *S. lycopersicum* crosses have directly implicated the S-locus in UI. However, there are clear examples in the tomato clade where UI is S-RNase independent. The experiments reported here examine the mode of pollen tube rejection in interspecific crosses and assess the role of SI genes in UI in wild tomato species. We find that there are at least two modes of interspecific pollen rejection; rapid (in the upper 15% of the style) and slow (in the lower half of the style). Neither mode of interspecific pollen rejection depends on high levels of S-RNases. Two HT-family genes, HT-A and HT-B, are tightly linked and map to a UI QTL on Chromosome 12. While the HT-A gene appears to be functional in all wild tomato accessions tested, the HT-B gene contains a point mutation that should eliminate expression in all tested accessions of *S. habrochaites*, regardless of whether plants were self-compatible or self-incompatible.

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Abs # P06004:

Identification of Interspecific Reproductive Barriers in Tomato Through Comparative Proteomics

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The molecular mechanisms that establish and maintain reproductive barriers between related species of higher plants are not currently known. This is an important question since manipulation of interspecific barriers could ease the transfer of desirable traits, such as resistance to abiotic and biotic stresses, or nutritional value, from wild to domesticated species. Since cases of unsuccessful pollination can be associated with failure of the pollen tube to grow through the stylar cell walls and reach the embryo sac, it is hypothesized that extracellular proteins and transmembrane proteins, derived from both pollen and pistil, may be critical compatibility determinants. We plan to use iTRAQ-based comparative proteomics to characterize these protein populations, using a number of Solanum species as a model system and a series of backcross introgression lines. This technique allows the simultaneous identification and relative quantification of many hundreds of proteins presented in each tissue. The proteomic analyses will be complemented by pyrosequencing of cDNA populations from the same tissues, collectively providing insights into the pollen and style proteomes and transcriptomes.