



Interspecific Reproductive Barriers in Tomato (IRBT) Meeting Abstracts

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Cytogenetic characterization of species hybrids in the tomato clade

Stephen M. Stack, Patricia Bedinger, and Paul Covey

¹Biology Department, Colorado State University, Fort Collins, CO

The tomato clade ($2n = 2x = 24$) includes ten recognized species that exhibit different levels of interspecies compatibility. Tomato (*Solanum lycopersicon*) accepts pollen from two more distantly related members of the clade *S. pennellii* and *S. habrochaites* (unilateral incompatibility) that are more closely related to each other than to tomato. F_1 hybrids between tomato and *S. pennellii* and between tomato and *S. habrochaites* are fertile and regularly form twelve chiasmate bivalents at metaphase I. However, spreads of synaptonemal complexes (SCs) during pachytene reveal mismatched elements in the hybrids. First, the length of some bivalents is different enough that foldback loops are formed and/or ends are mismatched. This may be due to differences in genome size since SC lengths are proportional to genome sizes, and the tomato genome is 20% smaller than the genome of *S. pennellii*. In addition, kinetochores do not match for as many as five of the hybrid bivalents. This suggests heterozygosity for pericentric inversions, and indeed, inversion loops are sometimes observed in early pachytene. All three species have pericentric heterochromatin, and tomato and the two hybrids have distal recombination nodules, indicating that crossing over occurs primarily in distal euchromatin and rarely in pericentric heterochromatin. This suggests that most of the distal euchromatin is syntenic between the three species and inversions are largely confined to pericentric heterochromatin. Because synaptic partner trades were not observed, translocations may not have occurred in the tomato clade.