



Interspecific Reproductive Barriers in Tomato (IRBT) Meeting Abstracts

[Frontiers of Sexual Plant Reproduction III](#)

Tucson, AZ

October 2008

Oral Presentations

UNILATERAL INCONGRUITY IN TOMATO: ROLE OF SELF-INCOMPATIBILITY FACTORS

Paul A. Covey¹, Katsuhiko Kondo², Aruna Kumar², Lilli Welch¹, Esther van der Knaap³, Bruce A. McClure² and Patricia A. Bedinger¹

¹ Department of Biology, Colorado State University, Fort Collins CO 80523-1878

² Department of Biochemistry, 240A Bond Life Sciences Center, University of Missouri-Columbia, Columbia, MO 65211

³ Department of Horticulture and Crop Science, 217A Williams Hall, OARDC, 1680 Madison Ave, Wooster, OH 44691

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 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 have directly implicated the *S*-locus in UI. However, there are clear examples in the tomato clade where UI is SRNase independent. The mode of pollen tube rejection was examined in interspecific crosses to 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 that can be distinguished at the morphological level – rapid (in the upper 15% of the style) and slow (in the lower half of the style). Neither mode of interspecific pollen rejection necessarily 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.

ENDOCYTOSIS IN S-RNASE-BASED SELF-INCOMPATIBILITY

Bruce McClure, Christopher B. Lee, Sunran Kim, and Aruna Kumar

**Division of Biochemistry, Interdisciplinary Plant Group, Christopher S. Bond Life Sciences Center,
University of Missouri, 1201 East Rollins Street, Columbia, MO 65211 USA**

The genetics of S-RNase-based self-incompatibility (SI) are simple: a multiallelic S-locus determines compatibility, and individual pollen tubes are rejected if their S-haplotype matches either of the two S-haplotypes in the diploid pistil. However, the mechanism of pollen rejection has not proven to be this simple at the molecular and cellular levels. Although it is now established that S-RNase determines S-specificity in the pistil and the S-locus F-box (SLF) protein determines specificity in the pollen, it is also clear that these S-specificity determinants alone are not sufficient for SI. Several non-S-specific factors are required on the pistil side, and a number of pollen proteins that interact with SLF are probably also implicated in SI. Furthermore, there is a topological problem relating to how S-RNase from the pistil extracellular matrix (ECM) gains access to the cytoplasmic compartment. We have observed large amounts of S-RNase associated with pollen tube vacuoles and also that HT-B, a pistil factor known to be required for SI, appears to be degraded in compatible pollen tubes. While S-RNase sequestration could provide a mechanism for compatible pollen tubes to evade S-RNase cytotoxicity, the topological problem remains. A better understanding of how pistil ECM components move through the pollen tube endomembrane system will help resolve this problem. This talk will describe pollen proteins that bind to ECM components and that could be involved in endocytosis and retrograde transport in pollen tubes as well as evidence that uptake of pistil proteins occurs through fluid phase endocytosis.

Poster Abstract

P4-13

FINE MAPPING OF A POLLEN UNILATERAL INCOMPATIBILITY LOCUS IN TOMATO

Wentao Li & Roger T. Chetelat

**C. M. Rick Tomato Genetics Resource Center, Department of Plant Sciences,
University of California, Davis, CA 95616, USA**

In the Solanaceae, unilateral incompatibility (UI) is a stylar pollen rejection phenomenon that most often occurs when self-compatible species are used as pollen parents in crosses with related self-incompatible species (the 'SI x SC rule'). The wild tomato relative *Solanum lycopersicoides* is SI and rejects pollen of cultivated tomato, *S. lycopersicum*, by UI, as do pistils of hybrids between the two; pollen of *S. pennellii* can overcome this barrier. Our previous research identified three QTLs, located on chromosomes 1, 6 and 10, from *pennellii* that are required to overcome UI on diploid or sesquidiploid *lycopersicum* × *lycopersicoides* hybrids. The chromosome 1 factor maps to the same position as the S locus, suggesting it may be involved in pollen UI. The chromosome 6 gene, herein referred to as *ui6.1*, acts as a gametophytic factor in a two gene system involving the chrom. 1 QTL. Preliminary results show *ui6.1* is located on the short arm of chromosome 6. Fine mapping was initially impeded by suppressed recombination between *pennellii* and tomato chromosomes in this region. Previous studies demonstrated that recombination frequency is positively correlated with the length of the alien

segment. To exploit this relationship, recombinants were isolated from progeny of heterozygous substitution lines containing a long (80cM) segment derived from *pennellii*. So far, three BC populations of 3618 individuals have been genotyped. Recombination frequency in female gametes was much higher than in male gametes, and fortuitously relatively normal in the region of our target locus. In this fashion, the *ui6.1* factor was mapped to a 0.10 cM region with one crossover on one side and two crossovers on the other side. Physical mapping of this gene using BAC and cosmid libraries is in progress.