Fine Mapping of a Gametophytic Factor Controlling Unilateral Incompatibility in Tomato

Wentao Li and Roger T. Chetelat

C. M. Rick Tomato Genetics Resource Center, Department of Plant Sciences, University of California,

Davis, CA 95616, USA

Unilateral incompatibility or incongruity (UI) is a pollen rejection phenomenon, typically occurring in the style, that prevents hybridization of related species in one direction -- most often when a self-incompatible species is pollinated by a self-compatible one (the 'SI × SC rule'). Among the wild relatives of tomato, virtually all of the green-fruited species – whether SI or SC – reject pollen of Solanum lycopersicum by UI. Of significance to breeders, UI effectively prevents transfer of the maternally-inherited cytoplasmic genomes, which might encode useful traits such as CMS. The wild nightshade S. lycopersicoides (SI) rejects pollen of cultivated tomato by UI, as does the F1 S. lycopersicum × S. lycopersicoides hybrid. Pollen of S. pennellii, on the other hand, is compatible with styles of S. lycopersicoides and its hybrids with tomato; we previously demonstrated that up to three gametophytic factors, located on chromosomes 1, 6 and 10, determine pollen compatibility or incompatibility. The chromosome 1 factor maps at or near the S locus, suggesting pollen-S may be the gene underlying this locus. The chromosome 6 factor, herein referred to as ui6.1, acts in concert with the S-linked product: pollen must carry the pennellii alleles at both loci to overcome UI on S. lycopersicum × S. lycopersicoides hybrids. To fine map ui6.1, we genotyped approx. 7,000 progeny of S. pennellii-derived bridging lines carrying the chromosome 1 and 6 factors. The frequency of recombination around ui6.1 was highest in progeny of plants heterozygous for long introgressions, and in products of female meioses. The recombinant plants were phenotyped by pollination onto styles of S. lycopersicum × S. lycopersicoides hybrids to determine compatibility. In this way, the ui6.1 locus was mapped to an interval of less than 20 kb, which, by sequence analysis, contains two genes. The expression of these genes in different tissues is being studied in order to determine if either one is a likely candidate for ui6.1. This research is part of an NSF Plant Genome Program grant on Interspecific Reproductive Barriers in tomato.