

Progress Toward Validation and Isolation of Novel Genetic Factors Controlling Lycopene Content in a *S. pimpinellifolium* × *S. lycopersicum* RIL Population

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Numerous epidemiological and intervention studies have indicated that dietary intake of lycopene-rich food may result in a decreased incidence of certain cancers. Fresh tomatoes and tomato-based products are the leading sources of dietary lycopene, a major tomato carotenoid and a potent natural antioxidant. As such, the identification of genetic factors which regulate high fruit lycopene content is imperative. To facilitate this endeavor, identification of genetic sources of high fruit lycopene content, genetic factors controlling lycopene content, lycopene assays that are rapid, accurate, high-throughput and low-cost, and production of robust, reliable phenotypic data are all essential. Here we report a genetic analysis of fruit lycopene content in a genetically mapped RIL population developed from a cross between a *Solanum pimpinellifolium* accession, with exceptionally high fruit lycopene content, and a *S. lycopersicum* breeding line. The RIL population was grown under field conditions in four years (F₇ – F₁₀) and fruit lycopene was analyzed using HPLC, spectrophotometric and colorimetric assays. Using the data obtained from each lycopene assay and using simple, composite and multiple interval mapping analyses, we have identified new major QTLs which affect lycopene content in this population. These QTLs do not correspond to known map positions of carotenoid biosynthetic genes. In order to study the QTLs further, we have initiated a marker-assisted backcross program to develop near-isogenic lines (NILs) in the cultivated tomato genetic background for two of the QTLs. We will discuss our QTL analyses, our rapid and accurate spectrophotometric method of lycopene measurement and the status of NIL development.