
72. Structural diversity of a lycopene beta-cyclase gene segment in wild and cultivated *Solanum* (section *Lycopersicon*) accessions with distinct mature fruit colors

Maria Esther de N.Fonseca, Ana Heloneida Araújo and Leonardo Silva Boiteux
EMBRAPA-Vegetable Crops, Brasília-DF, Brazil
Email: leonardo.boiteux@embrapa.br

A very important step in the carotenoid pathway is the cyclization of lycopene to produce the pigments alpha-carotene and beta-carotene. This step is mediated by lycopene cyclases, which expression is crucial for defining fruit color as well as pigment composition and content. A heterologous PCR approach was employed to isolate alleles of the chromoplast-specific lycopene beta-cyclase (CYCB) gene from wild and cultivated tomatoes. An effective PCR protocol was established by testing DNA template samples from distinct germplasm accessions with a primer pair designed to selectively target conserved regions present in the available CYCB sequences. This PCR optimization allowed the amplification of 1219 out 1666 bp of CYCB in ten taxa: *S. galapagense*, *S. cheesmaniae*, *S. peruvianum*, *S. chilense*, *S. neorickii*, *S. habrochaites*, *S. pennellii*, *S. pimpinellifolium*, *S. lycopersicum* var. *cerasiforme* and *S. lycopersicum*. The sequence similarity between the putative wild species CYCB genomic amplicons with the mRNA sequence available on GenBank indicates this gene is intronless. A total of 42 single nucleotide polymorphisms (SNPs) were detected when comparing *S. lycopersicum* (AF 254793) sequence with six accessions of five taxa. Higher frequency of SNP polymorphisms was found in green-fruited species (25 in *S. neorickii*, 18 in *S. peruvianum* and nine in *S. pennellii*). A smaller number of SNPs was found in yellow-fruited (four in *S. cheesmaniae*) and red-fruited species (three in *S. pimpinellifolium* and none in the *S. lycopersicum* 'Santa Clara'). A phylogenetic tree based upon this gene segment was in agreement with previous taxonomic studies using the granule-bound starch synthase gene. Sequence analyses of the amplicons obtained via heterologous PCR indicated robustness and selectiveness of the primers allowing SNP detection as well as the potential employment of this strategy to isolate CYCB-like amplicons in other species within the genus *Solanum*.