

Whole Genome Sequencing of a Begomovirus-Resistant Tomato Inbred Reveals Introgressions from Wild *Solanum* Species

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The low cost of next generation sequencing (NGS) technology and the availability of a large number of well annotated plant genomes has made sequencing technology useful to breeding programs. With the published high quality tomato reference genome of the processing cultivar Heinz 1706, we can now utilize NGS technology for rapid and efficient investigation of tomato germplasm with interesting phenotypes. Comparative analysis of genomes of among cultivated tomatoes and with wild species contributing genetic variation can help identify desirable genes, such as those conferring disease resistance. Here, we present the first whole genome sequence of the tomato inbred, Gh13, which has a begomovirus resistance gene, Ty3, introgressed from a wild tomato species. Next generation re-sequencing and assembly revealed regions of high SNP density between Gh13 and Heinz 1706 sequences, and regions with small gaps in genome coverage (up to 20 kb) in the Gh13 genome sequence. The putative origin of introgressions was identified by comparison of the Gh13 sequences from regions of high SNP density with sequences from *S. pimpinellifolium*, *S. chilense*, and *S. habrochaites*. Several introgressions on chromosome 11 were identified as *S. pimpinellifolium*, and an introgression on chromosome 6, which corresponded to the Ty3 region, was from a source close to *S. chilense*. Other uncharacterized introgressions were present in other genomic locations. This methodology can be used to discover introgressions for elucidating the history of tomato breeding, for the development of marker technologies associated with important phenotypes, and for identification of novel variation for the improvement of tomato and other crops.