Chloroplast and nuclear phylogenomics reveals concordant phylogenetic structure in wild tomatoes (Solanum sect. Lycopersicon, Solanaceae)

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Introduction

Tomato is one of the most important crops worldwide with 177 million tonnes covering 4.7 million ha (FAOSTAT 2016). Compared to other crops it has seriously narrow genetic basis due to selection for a limited set of traits during its domestication (Rodriguez et al. 2011). To prevent genetic erosion and to enrich the tomato gene pool breeding tapped into the diversity provided by wild relatives of the tomato clade (Solanum sect. Lycopersicon). This group consisting of 13 inter-crossable diploid (2n = 2x = 24) species under extensive taxonomic studies (see Peralta et al. 2008), is an important source of traits and genes for tomato improvement. Virtually all resistance genes introgressed to the tomato gene pool originate from crop wild relatives (CWR) (Ebert and Schafflter 2015). New disease resistance alleles are reported from tomato wild relatives at a rate of about one per year since 1982. For example a recent study reported that Galapagos tomato (S. galapagense S.C. Darwin & Peralta) has a broad spectrum of resistance against sap sucking insects (Vosman et al. 2018). In the present study we utilized high-throughput illumina sequencing data to gather a transcriptome based nuclear matrix and to assemble complete plastid genome sequences for all species of the core tomato clade (Solanum sect. Lycopersicon). We compare the genome organization, structure and phylogenetic relationships based on these data and investigate incongruences found between nuclear and plastid genomic trees.

Methods

Chloroplast Genomes

Nuclear Transcripts

Transcriptome Assembly

Gene Annotation

Gene Alignment Matrix Construction

Maximum Likelihood and Parsimony Phylogeny of Chloroplast and Nuclear Matrix

Incomplete Lineage Sorting assessment using gene trees from Chloroplast and Nuclear matrix

Polytomies assessment and rate heterogeneity assessment across the Solanaceae

Network fitting across the Solanaceae

Trimming Alignment

Independent Phylogenetic Assessment of Solanaceae positioning

Phylogenetic Concordance across Chloroplast and Nuclear matrix

Results and discussion

Our study allowed us to construct the first interspecific analysis including all species of wild tomatoes based on entire plastid sequences and compare genomic rearrangements with congeneric taxa. We found that plastome based trees provide strong support for two major groups in the tomato clade with S. pennelli and S. habrochaites in two distinct groups with the rest of the species. On the other hand, these two species form a clade in a basal position as compared with other tomato species in the phylogenetic analyses based on nuclear genes. This topological incongruence observed might be caused by the chloroplast capture event. In this process, a new combination of nuclear and chloroplast genomes were formed through inter-species hybridization and subsequent backcrosses with S. pennelli and S. habrochaites. Cross-species transfer of the chloroplast from one species to another has been reported among hybridizing plant groups, but it has not been hypothesised previously in Solanaceae.

References


