Prediction of microRNAs and miRNA pathway genes in *Solanum lycopersicum* and *Solanum pennellii*

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The cultivated tomato, *Solanum lycopersicum*, is one of the most important vegetable crops in global food and, next to the wild tomato *Solanum pennellii* are species widely used in developing cultivars. The study of the plant genomes has become a powerful tool to assist in the elucidation of the biological processes at the cellular level. One of the most important classes of small RNAs is microRNAs (miRNAs), acting on mRNA regulation in cells, inhibiting their translation and/or promoting its degradation. Computational methods have been applied extensively to identify novel miRNAs in different organisms. There are several proteins involved in the generation of miRNAs in plants, highlighting ARGONAUTE and DICER proteins which have key roles in the processing machinery of miRNAs. This study aimed to identify and characterize the genes involved in miRNA processing pathway as well as the miRNA molecules, their precursors and their target genes in the genome of *S. lycopersicum* and *S. pennellii* and also in next-generation sequencing. For the identification of the genes involved in miRNA pathway we used BLAST tools and reference genes available in NCBI, SolGenomics and Phytozomev11. We also performed domain and active site conservation analysis using PFAM and CDD databases and genome annotation files. The next-generation sequencing was held at Ion Personal Genome Machine®, using the Ion 318 chip. The targets of miRNAs were identified using the psRNATarget. We identified 65 proteins in the genome of *S. lycopersicum* and 109 in *S. pennellii* involved in small RNAs processing. Out of these proteins, 23 (*S. lycopersicum*) and 33 (*S. pennellii*) participate in the processing miRNAs pathway. In addition, we identified 342 different mature miRNAs, 226 precursor miRNAs distributed in 87 families, including 192 mature miRNAs not previously identified, belonging to 38 new families in *S. lycopersicum*. In *S. pennellii*, we found 338 mature miRNAs, 234 precursor miRNAs contained in 85 families. From the next generation sequencing, we identified 69 and 65 mature miRNAs distributed in 29 families and 28 in *S. lycopersicum* and *S. pennellii,* respectively. Furthermore, we identified 1310 different miRNA target genes in *S. lycopersicum* and 2772 in *S. pennellii*, suggesting important roles in plant development, regulation of hormonal response, defense against pathogens and other critical processes of biology, reproduction, and marketing of these species of tomato. Thus, our results expand the study of miRNAs in plants by providing new opportunities to understand essential in regulating processes based on miRNAs in tomato.