

# IN SILICO IDENTIFICATION, CHARACTERIZATION AND PHYLOGENETIC ANALYSIS OF miRNAs IN WILD PEPPER

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## Abstract

*Capsicum annuum* var. *glabriusculum* is a species of wild pepper with perennial and woody growth that due to its organoleptic characteristics is used in food as a flavoring. It is an important source of germplasm for the *Capsicum* genus, especially when used as a source of genes for resistance to disease. Due to human invasion, inadequate harvests and environmental degradation, their survival is threatened. Recently, the plant transcriptome has received attention from the scientific community to identify which miRNAs are regulating gene expression. The miRNAs are a class of small non-coding RNAs which length ranges from 20 to 24 nucleotides, and perform regulatory function in the organism. This class of small RNAs is involved in several biological functions, such as cell proliferation, apoptosis, and stress response. The objective of this work was to identify, characterize and analyze phylogenetically, putative miRNAs of *Capsicum annuum* var. *glabriusculum* and their orthologs. We searched for the probable mature miRNAs and precursors using miRBase. Pre-miRNAs were characterized as to their structural and thermodynamic characteristics. The conservation and alignment analyzes were performed using ClustalX 2.1 and RNAalifold. The secondary structures of the pre-miRNAs were obtained by RNAfold. Phylogenetic analysis of *C. annuum* var. *glabriusculum* pre-miRNAs and their orthologs using MEGA v5.2 was also performed. From the analysis, 101 putative miRNA families were obtained, and the families MIR-160, MIR-162, MIR-164, MIR-390, MIR-393 and MIR-828 showed high conservation in Solanaceae. It is worth mentioning that the targets of these families were described. The phylogenetic analysis of these miRNA families showed high conservation within their families and the phylogenetic distribution corroborated with the plant life tree. When comparing the secondary structures of the orthologs with the precursors it was evident that the pre-miRNAs are also conserved, mainly within the family Solanaceae. Thus, the obtained results amplify the understanding of the miRNA pathway in wild *Capsicum annuum* var. *glabriusculum* opening space for new inquiries regarding the regulation of gene expression in this species.

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