

# Genome-wide identification and *in silico* characterization of microRNAs and their targets in *Ananas comosus* L.

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Pineapple (*Ananas comosus* (L.) Merr.) is an economically important tropical fruit and the most important crop in the Bromeliaceae family. Due to pineapple's close proximity to crops of the Poaceae family such as rice, corn, sugar-cane and wheat, the investigation of regulatory and developmental elements in this specie is useful for crops enhancement programs. One of the key regulatory elements are microRNAs (miRNAs). They are small non coding RNAs (approximately 21 to 24 nucleotides in length) that negatively regulates gene expression by guiding a RNA-induced silencing complex (RISC) to a complementary target messenger RNA (mRNA) and directly promote post-transcriptional gene silencing. In this work we identified and characterized the mature miRNAs, precursor miRNAs and target genes in the genome and transcriptome of *A. comosus* using a series of Bioinformatics steps. Firstly, we applied a robust and adapted algorithm described by de Souza Gomes et al., (2011) to the genome of *A. comosus*. Following steps including homology searches, secondary structure prediction, and minimal free energy evaluation, the algorithm identified 277 putative mature miRNAs and their respective precursors. Then, all of those sequences were manually evaluated considering their homology results to known and conserved miRNA sequences, thermodynamic and structure characteristics of pre-miRNAs, and phylogenetic analyses. After the manual curation the remaining 102 miRNAs and their precursors were classified. Then we performed de novo assembly of the transcriptome from single-ended reads of pineapple's apical meristem and roots using the software Trinity. The web-tool psRNATarget, available at <http://plantgrn.noble.org/>, was used to identify miRNA's target sequences on these transcriptomes. The 102 identified miRNAs in pineapple had 575 target transcripts in meristem samples and 582 targets in roots. A better characterization of the miRNAs and their target genes will help the understanding of how tissue-specific gene regulation controls the pineapple's development and physiology.

Financial support: CAPES and CNPq