Discovery of precursor and mature microRNAs and their putative gene targets using high-throughput sequencing in pineapple (Ananas comosus var. comosus)

Abstract

MicroRNAs (miRNAs) are a class of small, endogenous non-coding RNAs that negatively regulate gene expression, resulting in the silencing of target mRNA transcripts through mRNA cleavage or translational inhibition. MiRNAs play significant roles in various biological and physiological processes in plants. However, the miRNA-mediated gene regulatory network in pineapple, the model tropical non-climacteric fruit, remains largely unexplored. Here, we report a complete list of pineapple mature miRNAs obtained from high-throughput small RNA sequencing and precursor miRNAs (pre-miRNAs) obtained from ESTs. Two small RNA libraries were constructed from pineapple fruits and leaves, respectively, using Illumina's Solexa technology. Sequence similarity analysis using miRBase revealed 579,179 reads homologous to 153 miRNAs from 41 miRNA families. In addition, a pineapple fruit transcriptome library consisting of approximately 30,000 EST contigs constructed using Solexa sequencing was used for the discovery of pre-miRNAs. In all, four pre-miRNAs were identified (MIR156, MIR399, MIR444 and MIR2673). Furthermore, the same pineapple transcriptome was used to dissect the function of the miRNAs in pineapple by predicting their putative targets in conjunction with their regulatory networks. In total, 23 metabolic pathways were found to be regulated by miRNAs in pineapple. The use of high-throughput sequencing in pineapples to unveil the presence of miRNAs and their regulatory pathways provides insight into the repertoire of miRNA regulation used exclusively in this non-climacteric model plant.