MicroRNA regulates gene expression during fruit development in pineapple

Abstract

MicroRNAs (miRNA) are small RNAs approximately 21-24 nucleotides in size. They function by regulating gene expression of various plant tissues such as leaf, root and embryo through the mechanism of RNAi silencing. Numerous reports have been published of the role of miRNA in regulating fruit development in tomato, a model organism for fruit development and ripening in climacteric fruits. However, there is a dearth of information on its role in non-climateric fruits, such as pineapple. This paper aims to firstly, isolate and characterize miRNAs in pineapples, and secondly, to reveal differentially expressed miRNA profiles between pineapples and tomatoes. MicroRNAs from a mature green pineapple were isolated using an optimized small RNAs concatamerization and cloning method. 150 clones were sequenced resulting in the identification of a total of 1,706 small RNAs. These small RNAs were screened for conserved microRNAs from other plant species using the miRBase online database. The small RNAs were also screened for differentially expressed miRNAs between pineapple and tomato using the Tomato Functional Genomics Database (TFGD). Twelve conserved microRNA families were identified as regulators of fruit development in pineapples. The most abundant was miR157, which had 58 copies out of the total small RNA pool. This was followed by miR396 (6), miR164 (3), miR166 (3), miR319 (3), miR827 (3), miR159 (2), miR171 (2), miR156 (1), miR162 (1), miR395 (1), and miR529 (1). However, the TFGD search revealed that only miR529 and miR827 were absent in tomato. This may be indicative of the differences in the mechanism of regulation by microRNA between climacteric and non-climacteric fruits.