

Thirty-one potential miRNAs that belong to 16 miRNA families were discovered from more than 324 000 EST sequences of apple (*Malus domestica*). In addition, precise sequences, especially terminal nucleotides of the 16 apple miRNAs (mdo-miRNAs) in 16 families were validated by miR-RACE, a newly developed method for the determination of the potential miRNAs predicted computationally. The expression of these 16 microRNAs could be detected in apple young leaf, old leaf, young stem, flower bud, flower and developing fruits by quantitative RT-PCR (qRT-PCR) and some of them showed tissue-specific expression. Fifty-six potential targets were identified for the 16 apple miRNAs, most of which were transcription factors that play important roles in apple development. Twelve target genes were experimentally verified by qRT-PCR, with some exhibiting different expression trends from their corresponding microRNAs, indicating the cleavage mode of miRNAs on their target genes.