MicroRNAs (miRNAs) play an important role in post-transcriptional gene regulation that involved various biological and metabolic processes. Many extensive studies have been done in model plant species, to discover miRNAs' regulating expression of their target genes and analyze their functions. But, the function of Poncirus trifoliata miRNAs has not been properly investigated. In this study, we employed the 5' rapid amplification of cDNA ends (RLM-RACE) and the newly developed method called poly (A) polymerase-mediated 3' rapid amplification of cDNA ends and RNA ligase-mediated (PPM-RACE), which mapped the cleavage site of target mRNAs and detected expression patterns of cleaved fragments that could in turn indicate the regulatory functions of the miRNAs on their target genes. Furthermore, the spatiotemporal expression levels of target genes were analyzed by qRT-PCR, with exhibiting different expression trends from their corresponding miRNAs, thus indicating the cleavage mode of miRNAs on their target genes. The expression patterns of miRNAs, their target mRNAs and cleaved target mRNAs in different organs of juvenile and adult trifoliate orange were studied. The results showed that the expression of miRNAs and their target mRNAs was in a trade-off trend. When the miRNA expression was high, its corresponding target mRNA expression was low, while the cleaved target mRNA expression was high; when the miRNA expression was low, its target mRNA expression was high, while the expression of cleaved target mRNAs follows that of the miRNA. The validation of the cleavage site of target mRNAs and the detection of expression patterns of cleaved fragments can further broaden the knowledge of small RNA-mediated regulation in P. trifoliate.