



Differential expression of microRNAs may regulate pollen development in *Brassica oleracea*

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ABSTRACT. MicroRNAs (miRNAs) are a class of non-coding endogenous negative regulators that regulate gene expression at both the transcriptional and post-transcriptional levels. However, little is known about the expression characteristics of miRNAs during pollen development in *Brassica oleracea*. In this study, five known and three novel miRNAs were identified and their expression patterns were compared in the flower buds of *B. oleracea* using stem-loop reverse transcription polymerase chain reaction (RT-PCR) and quantitative real-time PCR. The results revealed that the eight miRNAs were constantly expressed during pollen development but exhibited different expression patterns during the five developmental stages of the flower buds between the cytoplasmic male sterile (CMS) line and its fertile maintainer. The highest miRNA expression levels occurred at the uninucleate microspore stage in the fertile line *Bo01-12B* and at the bicellular pollen stage in the CMS line *Bo01-12A*. Potential target genes for the miRNAs were predicted and analyzed, and suggested that miRNAs are involved in the regulation of target genes related to pollen development.

The results of this study further our understanding of the regulatory role of miRNAs in pollen development.

Key words: miRNA; Expression pattern; Flower bud; Male sterility