



Identification and characterization of conserved microRNAs and their target genes in wheat (*Triticum aestivum*)

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ABSTRACT. MicroRNAs (miRNAs) are non-coding small RNAs that regulate gene expression by translational repression or transcript degradation. A large number of miRNAs have been identified from model plant species; however, the character of conserved miRNAs is poorly understood. We studied 42 miRNA families that are conserved within the plant kingdom, using the miRBase database. Some conserved miRNA families were found to be preferentially expressed in dicots relative to monocots, especially miR403, miR472 and miR479. Using an improved homology search-based approach and the conserved miRNAs as the query set, 34 conserved miRNAs and the miR482 family were identified in wheat. Forty-six wheat mRNAs were predicted as their putative target genes. Most conserved wheat miRNAs were found to retain homologous target interactions and have analogous molecular functions. The miR172 displayed a wheat-specific function and was found to have an additional target interaction with succinyl-CoA ligase.

We concluded that although miRNAs are conserved, the expression and function of some have drifted during long periods of plant evolution.

Key words: MicroRNAs; Wheat; Target genes; Conservation