



# Genome-wide identification of MITE-derived microRNAs and their targets in bread wheat

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## Resumen

Background: Plant miRNAs are a class of small non-coding RNAs that can repress gene expression at the post-transcriptional level by targeting RNA degradation or promoting translational repression. There is increasing evidence that some miRNAs can derive from a group of non-autonomous class II transposable elements called Miniature Inverted-repeat Transposable Elements (MITEs). Results: We used public small RNA and degradome libraries from *Triticum aestivum* to screen for microRNAs production and predict their cleavage target sites. In parallel, we also created a comprehensive wheat MITE database by identifying novel elements and compiling known ones. When comparing both data sets, we found high homology between MITEs and 14% of all the miRNAs production sites detected. Furthermore, we show that MITE-derived miRNAs have preference for targeting degradation sites with MITE

insertions in the 3' UTR regions of the transcripts. Conclusions: Our results revealed that MITE-derived miRNAs can underlay the origin of some miRNAs and potentially shape a regulatory gene network. Since MITEs are found in millions of insertions in the wheat genome and are closely linked to genic regions, this kind of regulatory network could have a significant impact on the post-transcriptional control of gene expression.

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