

## IN BRIEF

# MicroRNA Evolution in the Genus *Arabidopsis*

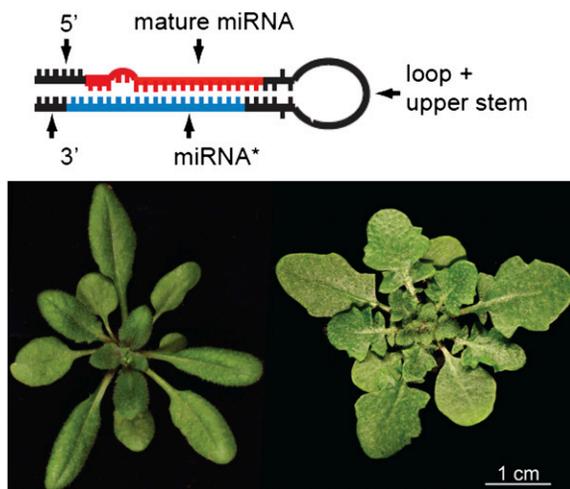
MicroRNAs (miRNAs), a plentiful class of small RNAs in plants, are processed from single-stranded RNA precursors that form imperfect stem-loop foldback structures (reviewed in Voinnet, 2009; see figure). The resulting 20- to 24-nucleotide miRNAs are involved in posttranscriptional down-regulation of genes whose transcripts are targeted based on sequence complementarity. *MIRNA* genes, the loci that encode the RNA precursors, fall into two main categories in plants (reviewed in Axtell and Bowman, 2008; Axtell, 2008). The first includes several *MIRNA* families that are deeply conserved among plant lineages and are highly expressed. miRNAs from this category participate in processes ranging from development to responding to biotic and abiotic stresses. By contrast, *MIRNA*s in the much larger, second category are not broadly conserved and, in general, are expressed at much lower levels. What roles, if any, most miRNAs from this category play in plants are not clear (reviewed in Axtell, 2008).

Now, **Fahlgren et al. (pages ■■■)** and **Ma et al. (pages ■■■)** independently have taken

advantage of the newly sequenced genome of *Arabidopsis lyrata*, a close relative of *Arabidopsis thaliana* (see figure), for a systematic analysis of miRNA evolution. Among other things, both groups found that genes from more widespread (conserved) *MIRNA* families showed sequence divergence between the two *Arabidopsis* species mainly in the loop, 5' ends, and 3' ends of the foldback. The relatively low divergence in the miRNA region is consistent with purifying selection due to the requirement for complementarity to target genes. The miRNA\* region (see figure), which must retain its complementarity to the mature miRNA for the foldback to form, also would be expected to face evolutionary constraints in a functional miRNA. By contrast, *MIRNA* genes in the less conserved category were more diverged and were divergent even in the miRNA region, consistent with neutral evolution of these younger genes. This is suggestive of a lack of functionality because divergence in the miRNA region would presumably cause the loss of target complementarity and therefore would not be expected in a functional miRNA.

Fahlgren et al. also examined *MIRNA* loci in the context of genome rearrangements between the two species and provide strong evidence supporting the idea that *MIRNA*s in plants arise from inverted repeats. Analyses from both articles show that, despite the existence of some near-ubiquitous miRNAs among green plants, many *MIRNA* families are changing rapidly. Fahlgren et al. estimate the rate of flux to be from 1.2 to as high as 3.3 genes per million years. Furthermore, Ma et al. found that regions of the genome that produce high amounts of short interfering RNA also are dynamic. Together, these articles provide a comprehensive comparison of miRNA in these species and demonstrate the power of information from closely related species to clarify evolutionary mechanisms.

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A schematic view (top) of the stem-loop foldback of a *MIRNA* locus is shown (from Ma et al., 2010). The bottom photograph shows *A. thaliana* on the left and *A. lyrata* on the right (photo courtesy of Josh Cuperus, Oregon State University).

## REFERENCES

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