

MicroRNAs: unicellular organisms also have their share

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MicroRNAs (miRNAs) — a class of small RNAs with a role in the regulation of gene expression — had until now been found only in multicellular organisms. Now, Wang, Qi and colleagues provide the first report of miRNAs in a unicellular organism, the green alga *Chlamydomonas reinhardtii*, casting shadow on previous suggestions that miRNAs might have helped to drive evolution to a multicellular state.

To characterize the small-RNA pathways in *C. reinhardtii*, the authors cloned and sequenced the whole 18–28-nucleotide RNA fraction extracted during algal vegetative growth. More than 4,000 unique small RNAs perfectly

matched genomic sequences, indicating an unexpected complexity of putative RNAi processes in this organism. Two hundred small RNAs were predicted to derive from genomic sequences — either intronic or intragenic — that can potentially form the hairpin structures typical of miRNA precursors. About 20 of them were annotated as miRNAs on the basis of the presence of a corresponding sequenced miRNA* — that is, the strand pairing to a mature miRNA in the opposite arm of the precursor, the presence of which indicates that a miRNA is indeed processed from its stem-loop-structured precursor. The others were considered to be miRNA candidates. The expression of some of these miRNAs was confirmed by northern blot analysis.

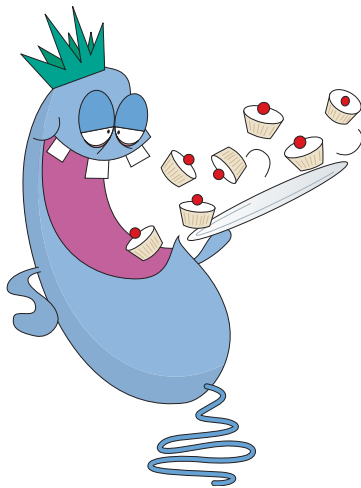
Using plant miRNA-prediction criteria, the authors identified more than 600 putative miRNA target sites among the annotated protein-coding transcripts and ESTs that are available for *C. reinhardtii*. Most of these lie in coding sequences — and some in untranslated regions — of genes involved in various processes. As in plants, the alga miRNAs seem to function by inducing cleavage of their target mRNAs, rather than by inhibiting translation, which is the common mechanism in animals. In fact, several miRNAs were shown to

induce cleavage of their predicted targets, both *in vitro* and *in vivo*, with a pattern that is characteristic of the RNA-induced silencing complex-mediated cleavage.

Although further studies are necessary to investigate miRNA functions in *C. reinhardtii*, the authors suggest a role in gametogenesis because few randomly selected miRNAs changed expression pattern during this process.

The discovery of miRNAs in a unicellular organism poses interesting evolutionary questions. Although miRNAs of *C. reinhardtii* and higher plants have common features that suggest the existence of a conserved machinery for miRNA production and function, they do not show sequence homology. So, did miRNAs evolve independently in unicellular and multicellular organisms, or are *C. reinhardtii* miRNAs evolutionary intermediates?

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ORIGINAL RESEARCH PAPER Zhao, T. *et al.* A complex system of small RNAs in the unicellular green alga *Chlamydomonas reinhardtii*. *Genes Dev.* **21**, 1190–1203 (2007)
FURTHER READING Bartel, D. P. & Chen, C. Z. Micromanagers of gene expression: the potentially widespread influence of metazoan microRNAs. *Nature Rev. Genet.* **5**, 396–400 (2004) | Chen, K. & Rajewsky, N. The evolution of gene regulation by transcription factors and microRNAs. *Nature Rev. Genet.* **8**, 93–103 (2007)