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JAW miRNAs regulate plant development

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MicroRNAs (miRNAs) and small interfering RNAs (siRNAs) have been isolated from all complex eukaryotes examined to date. Plant mRNA cleavage is mechanistically analogous to that involving siRNAs, is initiated by miRNAs, and can mediate posttranscriptional regulation. The mechanisms regulating CIN expression - a member of the TCP family of DNA-binding proteins - have been unclear, but even in wildtype (WT) plants, distinct RNA patterns are observed as a result of differential transcription or alterations in transcript stability. In the August 20 *Nature*, Javier Palatnik and colleagues at [The Max Planck Institute for Developmental Biology](#) identify a miRNA-producing locus that regulates cleavage of several TCP genes involved in leaf development. Their findings demonstrate for the first time the direct involvement of miRNA cleavage in a plant biological process (*Nature* 2003, DOI:10.1038/nature01958,).

Palatnik et al. examined the global expression profile for an *Arabidopsis thaliana* mutant *jaw-D* (phenotypically similar to the snapdragon *cin* mutant) using duplicate Affymetrix arrays representing over 24,000 genes. Alignment of four TCP genes with reduced expression levels in the mutant plants revealed a seven amino acid motif conserved at the RNA level - the JAW locus. This motif was absent from TCP genes with WT levels of expression. miRNA-resistant versions of TCP4 (mTCP4) were generated by altering the miRNA sequence within the JAW locus while conserving the amino acid sequence. Transformants exhibited a number of common developmental defects, indicating that miRNA-mediated posttranscriptional regulation of TCP4 plays a role in normal plant development. Overexpression of exogenous TCP2, mTCP2, and TCP4 produced no phenotypic effects. However, overexpressing exogenous mTCP4 resulted in defects similar to those observed following endogenous expression of mTCP4.

"The complex relationship between related miRNAs on the one hand and overlapping sets of potential targets on the other hand indicates that the miRNA regulatory network is similarly intricate compared with transcriptional networks in which families of related DNA-binding proteins control overlapping sets of target genes. Global transcript analysis, together with miRNA overexpression and the engineering of miRNA-resistant target genes, as implemented in our study, should be powerful tools for dissecting the miRNA regulatory network in plants," conclude the authors.

References

1. RNA silencing: the genome's immune system

2. Bishop CL: Leaf curvature gene *The Scientist*, February 28, 2003., [<http://www.the-scientist.com/news/20030228/03/>]
3. *Nature*, [<http://www.nature.com>]
4. The Max Planck Institute for Developmental Biology, [<http://www.eb.tuebingen.mpg.de>]