## BIOINFORMATICS SEMINAR

## **Bioinformatics of Tiny Regulatory RNAs**

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## Abstract

MicroRNAs (miRNAs) are an abundant class of small RNAs that are thought to regulate the expression of protein-coding genes in plants and animals. miRNAs are present in many (if not most) animals, and several labs, including ours, have found large numbers of miRNA genes by cloning ~22-nucleotide RNAs from worms, flies or mammals. Together with the Burge lab, we have developed computational methods that find additional genes by looking for characteristic features of miRNA precursors together with their sequence conservation in related genomes. The computational analysis identifies most of the cloned miRNAs and also some others that are difficult to clone because they are expressed at low levels or in only certain cells or conditions. It also enables estimates of the total number of miRNA-coding genes in the human and Caenorhabditis elegans genomes, indicating that nearly 1% of the genes in these genomes code for miRNAs and that the majority of the miRNAs in these genomes have been identified. Only about 20 miRNAs have been reported so far in plants. Nonetheless, there is arguably a broader understanding of their regulatory roles and biochemical functions than for animal miRNAs. This is because the regulatory targets of plant miRNAs (unlike those of animal miRNAs) can be convincingly predicted simply by identifying mRNAs with near-perfect complementarity. These targets are predominantly members of transcription-factor gene families involved in developmental patterning or cell differentiation. The targeting of developmental transcription factors suggests that many plant miRNAs function during cellular differentiation to clear key regulatory transcripts from daughter-cell lineages.

> Monday May 5, 2003 11:00 a.m. – 1:00 p.m. (Talk starts at 11:30) Building NE43, Room 941 Refreshments at 11am in NE43-941 (LCS, 200 Tech Square, Cambridge, MA)



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