200. Functional analysis of the micro RNA genes of *C. elegans*

Eric Miska[*], Ezequiel Alvarez-Saavedra[*], Allison Abbott[§], Nelson C. Lau[#], David P. Bartel[#], Victor Ambros[§] and Bob Horvitz[*]

[*] HHMI and Dept. Biology, MIT, Cambridge, MA 02139, USA
[§] Dept. Genetics, Dartmouth Medical School, Hanover, NH, 03755, USA
[#] Whitehead Institute for Biomedical Research and Dept. Biology, MIT, Cambridge, MA 02142, USA

The heterochronic genes *lin-4* and *let-7* encode unusually small (21-22nt) non-protein coding regulatory RNAs[1,2]. Strains carrying a mutation in either of these genes display retarded development, with some cell lineages having an altered temporal pattern of cell division and differentiation. *lin-4* and *let-7* inhibit translation of target genes that when mutated lead to an opposing phenotype, precocious development and early expression of some cell lineages.
Recently, molecular and bioinformatic approaches identified many genes encoding small RNAs in *C. elegans*, *Drosophila* and mammalian cell lines[3,4,5,6]. All of these genes encode 21-25nt RNAs derived from longer transcripts that contain partially double-stranded RNAs. These small RNAs, termed microRNAs (miRNAs, *mirs*), define a large, new class of genes.
We have identified over 100 miRNAs in *C. elegans* to date, a subset a subset of which is conserved in *Drosophila* and mammals. To understand the biological functions of miRNAs, we decided to generate mutations in the majority of these genes. Using a library of *C. elegans* mutants and automated liquid handling, we are screening for deletion strains. In parallel, we are seeking to establish the temporal and spatial expression patterns of these genes.

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