

## Abstract/Session Information for Program Number 705C

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Functional analysis of the microRNA genes of *C. elegans*. **Ezequiel A. Alvarez-Saavedra**<sup>1</sup>, Eric A. Miska<sup>1</sup>, Allison L. Abbott<sup>2</sup>, Nelson C. Lau<sup>3</sup>, David P. Bartel<sup>3</sup>, Victor Ambros<sup>2</sup>, Bob Horvitz<sup>1</sup>. 1) HHMI, Dept. Biology, MIT, Cambridge, MA; 2) Dept. Genetics, Dartmouth Medical School, Hanover, NH; 3) Whitehead Institute for Biomedical Research and Dept. Biology, MIT, Cambridge, MA.

The heterochronic genes *lin-4* and *let-7* encode small (21-22 nt) non-protein coding regulatory RNAs that inhibit translation of their target genes. Recently, a large number of genes with similar characteristics in plants, *C. elegans*, *Drosophila* and mammals have been identified. All of these genes encode 21-25 nt RNAs that are derived from longer transcripts, which form partially double-stranded RNAs. These small RNAs, termed microRNAs, define a large new class of genes. To determine the biological functions of microRNAs, we are attempting to generate deletion mutations of most if not all *C. elegans* microRNA genes. By screening a library containing  $7 \times 10^6$  mutagenized genomes with the aid of an automated liquid handling system, we have obtained 34 strains which in total carry deletions in 40 microRNA genes. The number of microRNA genes in the *C. elegans* genome is at least 100.

We began our program of microRNA deletions by targeting those that are evolutionarily conserved (e.g. *mir-1*, *mir-2*), that are in clusters (e.g. *mir-35* to *mir-41*, *mir-42* to *mir-44*), that have expression patterns that vary during development (e.g. *mir-34*, *mir-49*), or that are related in sequence (e.g. *mir-52*, *mir-53*). We have begun phenotypic analysis of these mutants (see abstract by Miska *et al.*).

In addition, we have analyzed the expression patterns of some of the 40 microRNA genes for which we have deletion strains by fusing upstream sequences from the microRNAs to GFP. The temporal expression patterns are consistent with those of developmental northern.

**Session Information****Session Title:** GENE EXPRESSION**Session Type:** POSTER, **Session Time:** Monday-Wednesday**Location:** ACKERMAN GRAND BALLROOM**Abstract Information****Poster Board Number:** 705C, **Presentation Time:** WED, JULY 2, 2003 3:00-4:30PM**Title:** FUNCTIONAL ANALYSIS OF THE MICRORNA GENES OF C. ELEGANS.**Author:** ALVAREZ-SAAVEDRA,EZEQUIEL A. ;\* MISKA,ERIC A. ; ABBOTT,ALLISON L. ; LAU,NELSON C. ; BARTEL,DAVID P. ; AMBROS,VICTOR ; HORVITZ,BOB.**Keywords:** KW07:69 - GENE EXPRESSION (TRANSCRIPTION/RNA PROCESSING/TRANSLATIONAL CONTROL/PROTEIN DEG); MICRORNA[Print](#) [Close window](#)