## Analysis of the Role of microRNAs in C. elegans Aging

*Konstantinos Boulias, Ezequiel Alvarez-Saavedra, Ala Berdichevsky, Bob Horvitz*
**HHMI, Dept. Biology, MIT, Cambridge, MA 02139 USA**

MicroRNAs constitute a recently discovered class of small (20-24 nt) non-coding RNAs found in C. elegans, Drosophila, plants, mammals and other organisms. Studies over the past few years indicate that microRNAs are critical regulators of gene expression in diverse biological processes, including developmental timing, cell-fate specification, cell proliferation and differentiation. The first microRNAs discovered were lin-4 and let-7, which control the timing of developmental processes in C. elegans. Since aging can be regarded as a temporally regulated developmental process, it is plausible that microRNAs also control aging. The genetic basis of C. elegans aging has been studied extensively and genes that define conserved regulatory pathways that affect lifespan have been characterized.

To identify microRNAs that might function in the regulation of the aging process, we are using microarrays that contain all known C. elegans microRNAs to determine microRNA expression patterns during aging. In parallel, we are analyzing deletion alleles of 92 microRNA genes to identify microRNA mutants with an abnormal aging phenotype. To this end, we are assessing lifespans and the accumulation of a lipofuscin-like intestinal pigment, a well-characterized marker of aging, for each strain.

**Contact:** boulias@mit.edu
**Lab:** Horvitz