

Analysis of the Role of MicroRNAs in the Control of *C. elegans* Aging

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MicroRNAs (miRNAs) constitute a 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 miRNAs are critical regulators of gene expression in diverse biological processes, including developmental timing, cell-fate specification, cell proliferation and differentiation. The first miRNAs 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 miRNAs also control aging. The genetic basis of *C. elegans* aging has been studied extensively, and a number of genes that define conserved regulatory pathways that affect lifespan have been characterized. To identify miRNAs that might function in the regulation of the aging process, we screened our collection of miRNA mutants for those abnormal in aging. We analyzed deletion alleles of 95 miRNA genes for abnormalities in lifespan and the response to heat stress. This analysis identified *mir-71* as a miRNA gene that is required for normal lifespan and stress responses, since worms lacking *mir-71* are short-lived and hypersensitive to heat shock and oxidative stress. We are currently investigating the possible role of *mir-71* in the control of *C. elegans* aging.

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