The microRNA *mir-71* Is Involved in the Regulation of Longevity and Stress Responses in *C. elegans*

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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. We identified *mir-71* as a miRNA gene required for normal lifespan and stress responses, since worms lacking *mir-71* are short-lived and hypersensitive to heat shock and oxidative stress. *mir-71* is likely involved in the control of *C. elegans* aging, since *mir-71* adults undergo an early decline of locomotion and pharyngeal pumping, two physiological behaviors that normally decline with age. We are currently performing site-of-action studies to identify the tissues in which *mir-71* functions to regulate lifespan and stress responses, and we are investigating the possible role of *mir-71* in the pathways that are known to control *C. elegans* aging.

Poster
Session topic: I. Physiology, a. Aging and stress
Second session topic: IV. Gene Regulation and Genomics, b. Mechanisms and function of RNA interference and small RNAs
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