

ELUCIDATION OF TRANSCRIPTION REGULATION IN AGING OF *DROSOPHILA MELANOGASTER*

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Aging is a biological process almost universal to eukaryotic organisms. The parallel genetic studies in yeast, worms, flies, and mice have implicated similar genes involved in lifespan extension in organisms ranging from yeast to mice. A number of genes also exhibit changes in transcription levels with both aging and oxidative stress, and the mutations in many genes that increase lifespan confer tolerance to oxidative stress. These findings suggest that it is important to elucidate the regulatory system of the gene expression related to aging and oxidative stress in a wide range of organisms. Previous experiments indicated that two highly diverged animals, the nematode *Caenorhabditis elegans* and the fruit fly *Drosophila melanogaster*, implement a shared adult-onset expression program of genes involved in mitochondrial functions. Several transcription factors were identified, which may regulate expression of the common genes. To study function of these genes involved in aging of *Drosophila melanogaster*, double-stranded RNA (dsRNA) were used to generate loss- or reduction-of-function phenotype in fly S2 cells. After dsRNA treatment, survival of S2 cells was analyzed by exposure to hydrogen peroxide as an oxidative stress to elucidate whether each candidate transcription factor is related to the aging. We found that S2 cells with loss-of-function of one transcription factor were more sensitive to hydrogen peroxide compared to control. Additional analyses of more than 10 other transcription factors are currently being completed.