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# Role of the *Methuselah* Gene on the Aging of *D. Melanogaster*

Aging is a phenomenon that occurs among most organisms, yet much about the cellular basis of aging remains unknown. Specifically, the stem cell population is of interest because it persists throughout the lifetime of the organism and thus is more susceptible than somatic cells to accumulated cell damage. It has been shown that aging is associated with a decreased rate of germline stem cell division. However, flies with a homozygous mutation for the methuselah (*mth*) gene do not show this decreased rate of division. Interestingly, *mth* mutants also show an increased life span and are resistant to the oxidative stress caused by reactive oxygen species accumulated over time. While methuselah is known to be a pro-aging gene, its functional site is not known. In order to localize the functional site of the methuselah gene, we are examining three possible cell types in the testis of *Drosophila melanogaster*. Specifically, we are using flies with a mutant background for *mth* and expressing wild-type methuselah selectively in the hub, cyst, and germline stem cells. The cell types in which *mth* function is required to induce stem cell cycle changes will be determined through the analysis of germline stem cell division rate and lifespan.