

ANALYSIS OF GENE EXPRESSION IN *DROSOPHILA*

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Limited life span and senescence are near-universal phenomena, and are quantitative traits controlled by genetic and environmental factors whose interactions both limit life span and generate variation in life span between individuals, populations and species. Recently, there has been considerable progress towards understanding the environmental factors and genetic pathways that regulate life span across diverse taxa. For example, caloric restriction generally extends life span, reproduction shortens longevity, and genetic analyses have implicated the insulin signaling pathway in regulating life span across diverse taxa. However, there is great variation in life span and rate of aging within populations of humans and other organisms. In contrast to the wealth of accumulating knowledge regarding the loci and pathways regulating life span, little is known about the genes causing naturally occurring variation in longevity. Are these a subset of the genes identified by analysis of mutations, or will analysis of naturally occurring variation for life span uncover additional loci and novel pathways? We have mapped quantitative trait loci (QTLs) affecting variation in life span in *Drosophila* with high resolution by linkage to molecular markers. At least 17 QTLs affect variation in life span between the wild type Oregon and 2b strains, and 14 QTLs on the third chromosome alone affect variation in life span between Old strains selected for postponed senescence and their Base population unselected controls. QTLs are, however, not genes, but genomic intervals bounded by molecular markers containing one or more genes affecting variation in life span. The challenge is to map QTLs to the level of individual genes. We have quantified whole genome transcript profiles of males and females from Oregon, 2b, two Old selection lines and one Base population selection line for young and old flies. We used analyses of variance to partition variation of the expression data into sources attributable to Age, Sex, Genotype, and all interactions. We will present results of these analyses. Candidate genes affecting life span correspond to those whose transcript abundance changes with age, while candidate genes corresponding to QTL are those that lie within the QTL regions, and for which the Genotype term is significant.