82. CHARACTERIZATION OF *lin-54* AND OTHER GENES THAT NEGATIVELY REGULATE *let-60* Ras SIGNALING DURING VULVAL DEVELOPMENT

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The synthetic multivulva (synMuv) class A and class B genes act redundantly to negatively regulate Ras signaling during vulval development. The class B synMuv genes encode proteins that likely function to target the histone deacetylase HDA-1 to specific DNA sequences. Some of the proteins involved in this proposed targeting, including LIN-35 RB, DPL-1 DP and EFL-1 E2F, are conserved in mammals, and a similar targeting function has been described for their mammalian counterparts. To better understand this conserved pathway, we cloned the class B synMuv gene *lin-54* and identified new synMuv genes in a genetic screen.

lin-54 was originally identified and mapped to a small region of LGIV by Jeff Thomas, a former graduate student in our laboratory. We cloned *lin-54* and found that it encodes a protein with two copies of a cysteine-rich domain. A similar domain is found in proteins in other species; however, the function of this domain is not understood. We observed partial maternal rescue of the Muv phenotype of *lin-54* mutants, indicating that maternally-provided *lin-54* can regulate the vulval cell fate specification decisions that occur during postembryonic development. However, the stage-specific ectopic expression of *lin-54* under the control of heat shock promoters indicated that *lin-54* need not function prior to vulval induction to regulate this process. In addition, we conducted in vitro protein interaction experiments using LIN-54 and other class B synMuv proteins. We will present preliminary data concerning these studies.

With graduate students Frank Stegmeier and Melissa Harrison, we screened approximately 6500 haploid genomes and recovered 95 new synMuv mutations. The mutations we assigned to complementation groups fall into three general classes: 1) mutations that affect new and previously characterized class B synMuv genes, 2) mutations that affect *ark-1*, *sli-1* and *gap-1*, genes that are thought to directly regulate Ras pathway components, and 3) mutations that synergize with class A and class B synMuv genes and define previously uncharacterized genes (see abstract by Ceol and Horvitz). We will present our characterization of these new mutations.