CHARACTERIZATION OF NEW GENES REQUIRED FOR THE NEGATIVE REGULATION OF VULVAL INDUCTION, INCLUDING THE NEW CLASS B SYNMUV GENE *LIN-61*

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The regulation of vulval induction in *C. elegans* provides a useful model system for the study of genetic and molecular mechanisms involved in signal transduction, transcriptional repression and cell-fate determination. Previous work has defined two classes of genes (A and B) that act redundantly to negatively regulate the adoption of vulval cell fates by vulval precursor cells. The elimination of a member of both gene classes results in a synthetic multivulva (synMuv) phenotype. The class B synMuv genes include genes similar to members of the mammalian Rb signaling pathway. By contrast, determination of the molecular nature of the known class A synMuv genes has thus far yielded relatively little insight into the mechanism of their function (see abstract by Davison and Horvitz).

The mutation *sy223* (a generous gift from Paul Sternberg) defines a new class B synMuv gene, *lin-61*. We have found that this gene, located on LG I, encodes a protein weakly similar to *Drosophila* Polycomb group members, and more strongly similar to predicted proteins of unknown function from *C. elegans* and human. Three alleles of *lin-61* are currently under study, each of which contains a point mutation in the C-terminus of the putative protein product. We are currently seeking a null allele of this gene. RNAi of *lin-61* produces embryonic lethality both in a synMuv A (*lin-15A(n767*)*)* and in a wild-type background, suggesting that the gene has an essential function in addition to its role in the inhibition of vulval induction.

In addition to the analysis of *lin*-61, we are also attempting to identify new class A synMuv genes. Previous screens to isolate class A genes would not have recovered synMuv mutations that also cause sterility or maternal-effect lethality. For this reason, we are now performing a clonal screen to seek alleles of new class A synMuv genes as well as new alleles of known genes. Beginning with a strain containing a strong *lin-15B* allele, *n744,* we have screened more than 10,000 genomes and isolated more than 20 mutants that display a Muv phenotype. Complementation testing and mapping of these mutants is currently underway.