

Identifying Enhancers of Drop Dead (*drd*)

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In the model organism *Drosophila melanogaster*, our goal is to identify the function of the gene *drd*. It is currently known that the *drd* gene sequence located on the X chromosome of *D. melanogaster* encodes a membrane protein. It has been observed that flies homozygous for a mutated allele of this gene, *drd*^{lwf}, exhibit five recognizable phenotypes: small body size (seen in adults), neurodegeneration, shortened life span, female sterility, and improper food movement through the gut. Since the function of *drd* is unknown, we plan to conduct a screen to indentify genes that interact with *drd* and deduce from the findings the function of *drd*.

The phenotypic marker of shortened life span was used to identify enhancers of *drd* in a series of survival curves with less severe alleles of *drd* – *drd*^{CB6275}, *drd*^{G3}-and deficiencies spanning the second chromosome. Positive enhancing regions produced an increase in the rate of death that is normally seen in either *drd*^{CB627} or *drd*^{G3}. Data from genetic crossing schemes corroborate the enhancing effects of three large deficiency regions: Df(2R)Jp1 (3518), Df(2R)X1(1702), and Df(2L)drm-P2 (6507). Of these regions, 6507 and 3518 have been further narrowed down to a specific gene and smaller deficiencies respectively. It has been found that the gene *sister of odd and bowl* (*sob*), a transcription factor, found in the 6507 deficiency region has some potential enhancing effects on *drd*. Furthermore, three smaller deficiencies in the region 3518 have shown significant enhancing activity of *drd*^{G3}. In the upcoming semester, the smaller deficiencies in the 3518 region will be examined in smaller components such as individual genes and deficiencies with both alleles.