A Genetic Study of Genes that Regulate the Larval Foraging Behavior in *Drosophila melanogaster*

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Abstract: A General Overview of the Project

Is human behavior controlled by predetermined by an individual's genetic makeup or is it a product of the environment? This is a question that has been asked every millennia and has gone unanswered for much of history. Recently, the scientific method along with genetics have been used to answer this question. Studying genes that regulate behavior of modal organisms such as the *Drosophila melanogaster*, has provided some important insights into answering this question.

The purpose of this thesis is to use genetic techniques to investigate the genes that regulate the **larval foraging behavior** in *Drosophila melanogaster*. **Larval foraging refers to the way in which the larva of** *Drosophila melanogaster* acquire food. The larval foraging behavior is used as a model behavior in *Drosophila* to understand how behavior is controlled in other animals. The hope is that what is learned in this project can be

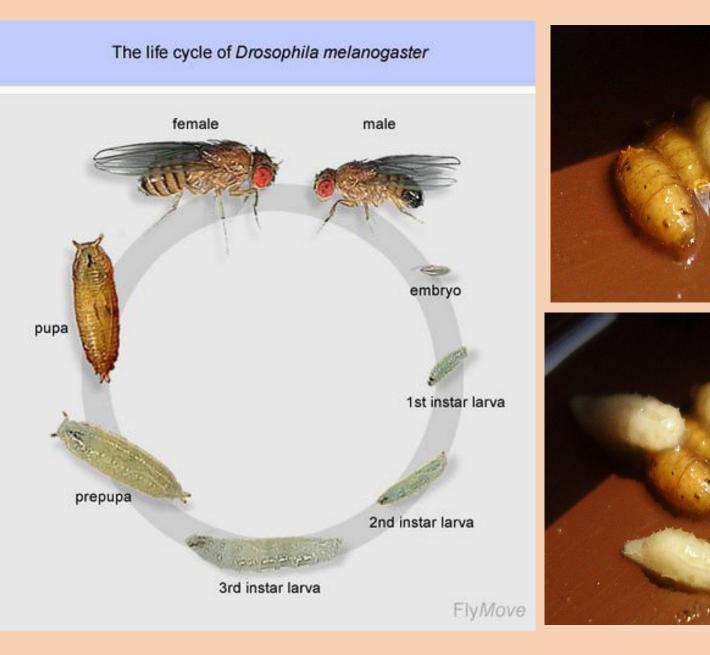
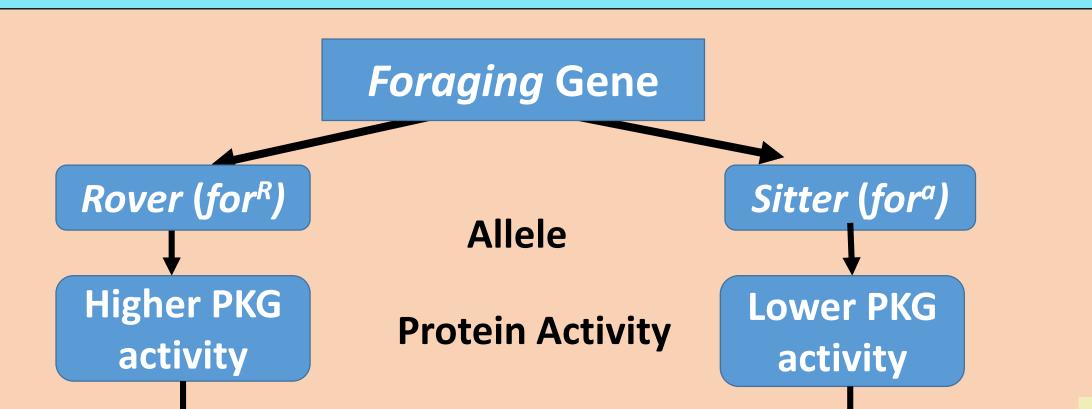


Figure 1: The Life Cycle of Drosophila melanogaster. The foraging behaviour referred to in this report is that of the 3rd instar larva. Image from flymove. http://upload.wikimedia.org/wikipedia/commons /a/a3/Fruit_fly_pupae_01.jpg

Results of Lifespan Assays

#1: The Effect of Foraging alleles on Lifespan

There are two known genes that control the larval foraging behavior. The first one is termed the *foraging* (*for*) gene. *For* encodes a **cGMP-dependent protein kinase** (PKG) protein in *Drosophila melanogaster*. There are two alleles for the *for* gene. Having **Rover** (*for*^{*R*}) alleles produces a higher PKG activity in cell and is associated with moving longer distances in larval form. The **Sitter** (*for*^{*S*}) allele produces a lower PKG activity and is associated with shorter distance movement. This report discovered the difference in lifespan between organisms containing rover alleles and sitter alleles. **This report found that rover** (*for*^{*R*}) allele provided a longer lifespan. This was confirmed with ectopic expression of foraging gene in transgenic flies using GAL4/UAS system.



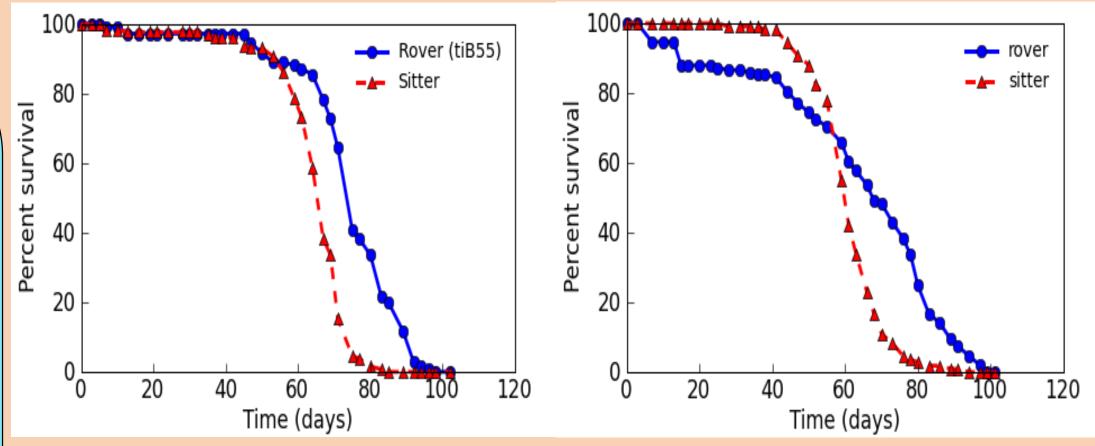
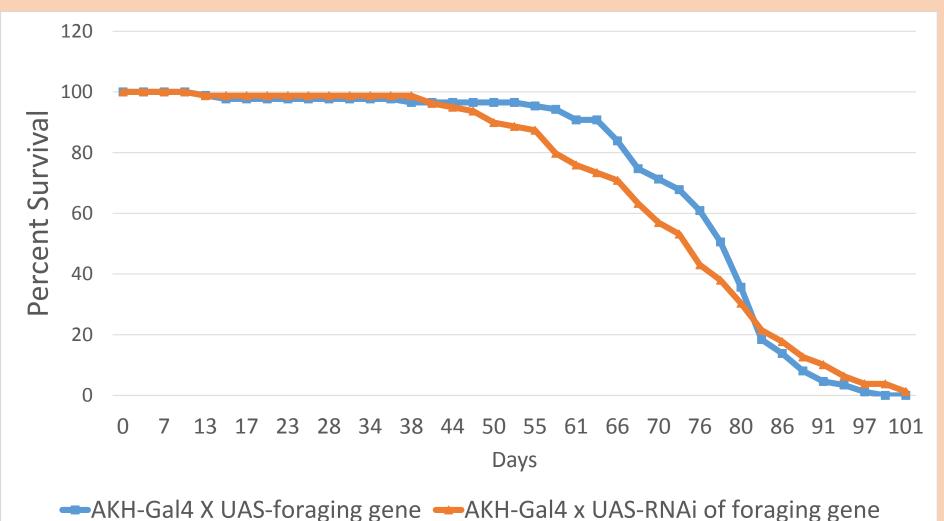
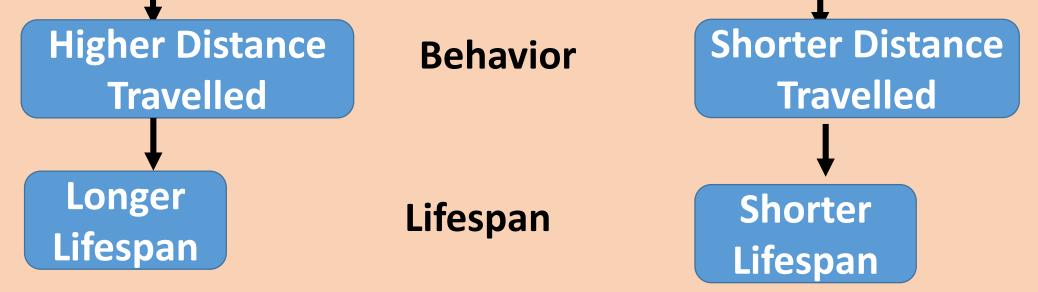


Figure 2 : Kaplan Meier survival curves from Rover (for^R/for^R) males and sitter (for) males. Both curves represent the same experiment that was repeated to using different rover and sitter alleles to provide more confidence in the result. In both cases, Rovers have a longer lifespan than sitters. Chi Squared Statistical test was performed to get restricted mean for direct comparison of average lifespan.





AKH Promoter GAL4 UAS Foraging Gene

→ Higher *foraging* expression
→ Higher PKG Activity
→ More Distance at foraging
→ Rover-like
→ Longer Lifespan



→Lower foraging expression
→Lower PKG Activity
→Less Distance at foraging
→Sitter-like
→Less Lifespan

Figure 3: Kaplan Meier survival curves from transgenic Drosophila melanogaster. The results show that the flies production a higher amount of the foraging gene product live slight longer than that producing less amount of PKG. Chi Squared Statistical test was performed to get restricted mean for direct comparison of average lifespan.

How Deletion mapping works and Results of Mapping experiment

#2: Mapping of Chaser Gene

The second gene controlling larval foraging is the **Chaser** (*Csr*) gene. A study from 1995 found that the Chaser gene is located in a region on the third chromosome containing **120,617 base pairs**. This region contains approximately **73 candidate genes**, therefore, the identity of the Chaser gene was hard to decipher in 1995. Technology has improved since then. In 2014, the second experiment of this thesis ran a successful deletion mapping experiment with newer/better deletions. **This experiment narrows down the Chaser gene to a region of approximately only 2700 nucleotides** and contains only **3 genes**. This report narrowed down the identity of the Chaser gene down to one of three possible genes.

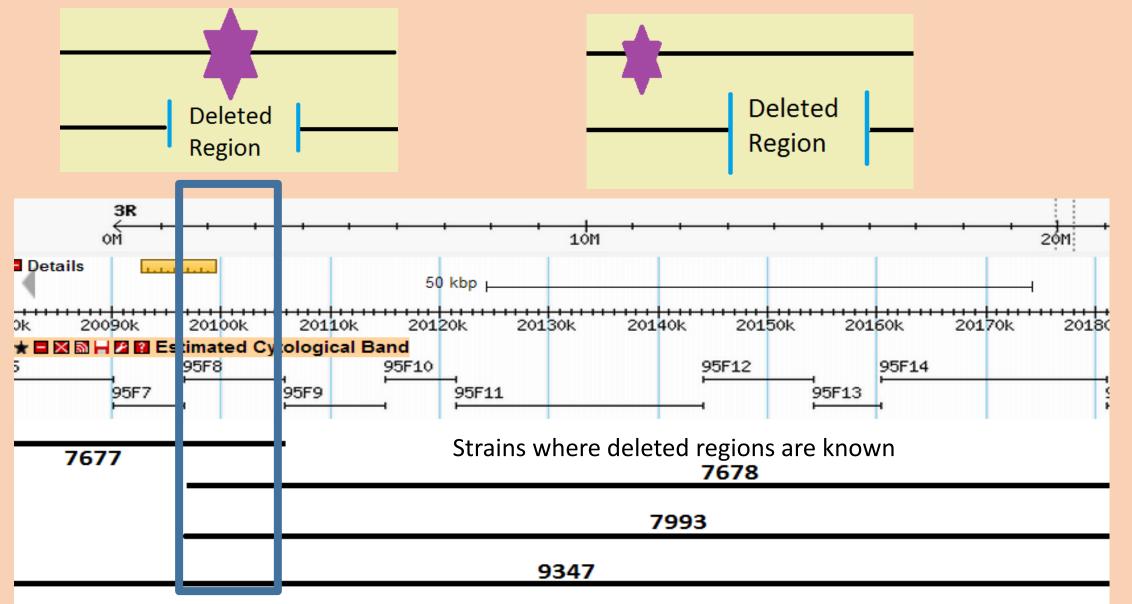


Figure 4: A deletion map created from the deletions that did not show complementation. The overlapping region of 95F8 is where chaser gene is likely to be.

This thesis was completed under the supervision of Dr. Arthur Hilliker Contact Email: jay_gajiwala@hotmail.com