Title
Investigating genetic interactors of *nejire*, the *Drosophila melanogaster* CREB-binding protein, using RNA interference

Key words
Dendrite, Drosophila, RNA interference, Transcription factors, Genetics

Authors
Joshua Lott, Sarah Clark

Introduction
The nervous system is a highly complex array of different cell types that requires an efficient method of integration to function as a single system. Dendrites provide this integration by allowing each cell to receive synaptic information from other cells. Dendritic abnormalities can drastically alter neural network connectivity, and can cause significant neurological impairment such as is seen in Down's syndrome, Fragile X syndrome, and autism spectrum disorders. Transcription factors, genes which control the expression of other genes, have been shown to play a role in determining dendritic morphology in *Drosophila* sensory neurons. The transcription factor *nejire*, the *Drosophila* CREB-binding protein, plays a role in the determination of dendritic complexity. In this study RNA interference (RNAi) is used to examine a number of genes that have been bioinformatically determined to be potential interactors of *nejire*.

Methods
RNAi is expressed in isolated neurons of the *Drosophila Melanogaster* sensory nervous system using the *Gal4-UAS* binary expression system. Confocal microscopy is used to visualize the neurons of interest in the living subject; then a tracing program is used to quantify the neuronal morphology so that neurons expressing RNAi can be compared to neurons in which the typical expression of *nejire* has been altered.

Results
Of the eleven genes investigated using RNAi, four (*Relish, slow border cells, Arginine Methyltransferase 4, and charlatan*) showed an increase in dendritic complexity. Two genes (*Rpd3 and Medea*) showed a decrease in complexity. One gene (*Smad on X*) showed an increase in complexity with one RNAi line and a decrease in complexity with a different RNAi line.

Conclusion
The genes which demonstrated an effect on dendritic complexity will be examined further using advanced techniques including mass spectrometry and RNA sequencing. These methods will determine which of those genes interact specifically with *nejire* in pathways that play a role in the determination of dendritic complexity.