Examining Enhancers and PREs In Relation to Gene Expression in the Eyes Absent Gene Within Drosophila melanogaster Reyna N. Parker, Class of 2020

Drosophila melanogaster, commonly known as the fruit fly, has been used throughout genetics research due to its quick reproductive capabilities and rapid life cycle. Fruit flies have a similar genetic makeup to many other organisms, including humans. One of these similar genes is the eyes absent gene, also known as the Eya gene. The Bateman lab has conducted much research with this particular gene as its focus. The Eya gene is responsible for eye development across all seeing animals. The Drosophila compound eye is composed of individual photoreceptor cells called ommatidium. Mutations that completely disrupt the transcription of the Eya gene leads to Drosophila phenotypes that lack a compound eye. When the Eya gene is expressed in other tissues, it produces an ectopic eye.

Gene transcription occurs when the gene regulatory elements, enhancers and promoters, loop together in a process known as DNA looping (Tian et al., 2019). This interaction between the enhancer and promoter initiates gene transcription, but other regulatory elements can disrupt this interaction to silence gene transcription. Recently, the Bateman lab has discovered such silencing elements, known as Polycomb Response Elements, (PREs). PREs work by recruiting other proteins that physically prevent DNA looping between the enhancer and the promoter. This summer we used immunohistochemistry and Polymerase Chain Reactions (PCRs) to identify and compare the different relationships between PREs and enhancers and how they affect gene transcription.

The Eya gene has three different enhancers and two PREs upstream of the promoter (Weasner et al., 2016). We used a LacZ reporter gene to develop four different constructs. The LacZ reporter gene allowed us to take specific parts of the Eya gene and observe gene expression more simplistically. Constructs were developed by removing the part of the Eya gene that only had enhancer 1 and the PRE that was closest to it. These specific DNA sequences were then attached to the LacZ reporter gene, thus isolating one PRE and one enhancer. We made three different genetic constructs. The first two constructs, #1 and