# A genetic screen to identify the roles of human genes in *Drosophila*

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## Introduction

- *Drosophila* has been identified as a valuable model organism for human disease models due to its highly conserved genome (Roote and Prokop, 2013).
- A majority of the genes in the *Drosophila* genome are involved in the development of the fly eye. This makes it easy for studying the effects of altered gene expression since it will typically change the phenotype of the fly eye (Iyer et al., 2016).
- GMR-Gal 4 *Drosophila melanogaster* is commonly used to target expression of transgenes due to the ease of determining changes in expression by evident morphological changes in the eye phenotype (Ray and Lakhotia, 2015).
- Using *Drosophila* as a model organism, we aim to test over one thousand human genes to determine if they have any interference in the fly tissue eye development.

## Methods

- The GMR-Gal4 *Drosophila melanogaster* and the UAS lines containing human genes from Bloomington *Drosophila* Stock Center were cultured using standard fly food.
- Virgin female GMR-Gal4 flies and UAS-human gene males flies were placed in a single vial with standard fly food and a small amount of yeast for each cross visualized in Figure 1. The P1 generation was removed from the vial once pupae were seen on the walls.
- The progeny were preliminarily analyzed using a simple light microscope to determine if the cross produced a morphological change on the *Drosophila* eye. No further testing or analysis occurred if there was no change in the eye phenotype.
- Progenies with abnormal eye tissue were photographed with a light microscope and a scanning electron microscope. Figure 2 shows the results with major phenotypic changes. Images of the eye for a control GMR-Gal4 *Drosophila melanogaster* were also used for comparison.
- To avoid any bias, only Bloomington ID numbers were used in the screen project. After the phenotypic observations, the ID of the Bloomington stock were then entered int FlyBase to obtain the genotype and analyze the alleles.

## Figures

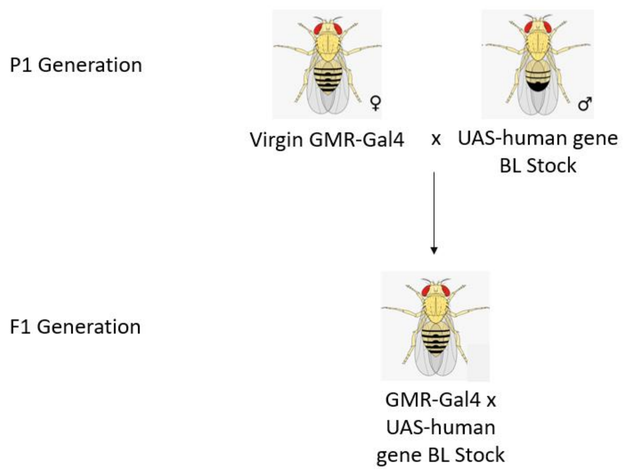


**Figure 1.** *Drosophila melanogaster* cross scheme of GMR-Gal4 with the UAS-human gene Bloomington stock. Each stock has its own ID number correlating to a specific human gene.

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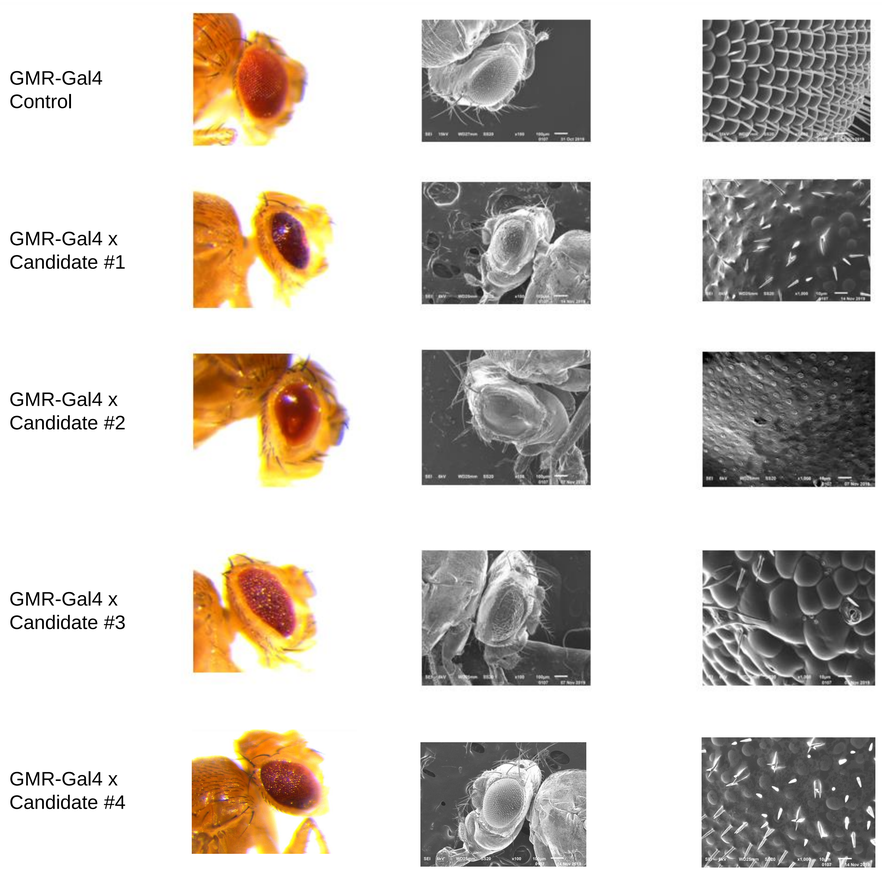


**Figure 2**. Photos acquired using a light microscope and SEM microscope of the progeny for the GMR-Gal4 Drosophila melanogaster crossed with various UAS-human gene Bloomington *Drosophila melanogaster*.

## Results

- Many of the crosses resulted in progenies with reduced eye size and thinned sides. Some had no change in eye size or shape but would have changes in the structure of the eye.
- Some crosses resulted in the loss of eye bristles, typically in a disorganized fashion as well. Others would be entirely absent of eye bristles.
- Crosses with ommatidia apoptosis would have ommatidia absent for the whole eye or only in parts of the eye. The amount of ommatidia apoptosis would also be random, where the same eye would have different sizes of ommatidia.

## Conclusion.

- The use of the GMR-Gal4 *Drosophila melanogaster* allow us to easily determine there was interference caused by the introduction of human genes in the genome.
- The majority of the crosses produced no morphological change in the *Drosophila* eye suggesting that most of the human genes did not influence enough of the gene expression to create an altered eye phenotype.
- Some of the crosses created progenies with lost eye bristles, extra eye bristles, eye bristles not forming on the edge of the eye, ommatidia apoptosis on the whole eye or only on the center of the eye, rough eye phenotype, reduction of eye size, merged ommatidia and ommatidia disorganization.
- Our method allows for hundreds of human genes to be tested very easily and quickly. We also are able to identify which human genes will be of interest to test further with and analyze how the gene affects and alters the gene expression.
- Further testing is required to accumulate more data to use and find the correlation for which human genes cause abnormal tissue formation.
- When the preliminary testing is completed with more data collected, we will be able to find the signaling network and relation for the human genes that interfered with the gene expression.

## References

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Jia lab website: https://sites.google.com/site/jialab2017/home