**Enhancer regulation underlying phenotypic variation in Drosophila**

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This research looks at enhancer variation in the brains of female, virgin fruit flies of several natural isolates of Drosophila. Enhancers are non-coding regions of DNA that determine the expression of genes, which means that this research is focused on variation at the regulatory level. Specifically, the purpose of the research is to look at how this type of variation underlies phenotypic differences between the strains, in other words, differences in their observable characteristics. The general idea behind the project is that if variation at the regulatory level is important for evolution in phenotypic characteristics, then we should see variability in enhancer usage between the natural isolates. In other words, if variation in which enhancers are active (in open chromatin) underlies variation in observable characteristics between the different strains of Drosophila, then the different strains should have differences in which non-coding DNA is in open chromatin confirmation.

Even though there has been quite a bit of research into the effects of protein variation on phenotypic characteristics, very little is known about how variation at the regulatory level affects these characteristics. The findings of this project could give us an insight into the degree to which the two aforementioned types of variation (at the protein-coding and regulatory level) have an impact on evolution. The general purpose of the research is therefore to create a database of active chromatin in several strains of Drosophila so that comparisons can be made.

Though this research includes both an in-lab and bioinformatics component (the latter means using coding and software to analyze data), our work this summer was mainly focused on the in-lab part. This included dissecting the flies and extracting the DNA from their brains, and then performing several more procedures to achieve purified DNA samples in collections, or 'libraries'. This technique to assess genome-wide accessibility of chromatin, in other words to assess which non-coding regions of DNA are accessible to 'to work', is called ATAC-SEQ. After several steps during this process, the quality of the samples was checked using bio-analysis. These quality controls were the reason many samples did not make it into the DNA libraries.

Further steps of the research would include the bioinformatics portion of the lab, in which the actual database is being constructed and a comparison in enhancer usage is made. Though we did not see any final results during the summer, we were able to collect several samples that were good enough to go through the stage of library quantification and that could therefore in the future be used during bioinformatics and could contribute to the data set on enhancers in Drosophila.

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