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ConGenOmics short visit scientific report

My visit to Dr. Christopher Wheat's laboratory at Stockholm University facilitated my learning techniques necessary to complete the analytical portion of my project on the conservation genomics of the Bay Checkerspot Butterfly, *Euphydryas editha bayensis*. Throughout the two-week visit, I worked on a dataset of male dragonfly (*Ladona fulva*) genomic DNA pooled by flight performance. This dataset is analogous to the one I will obtain for *E. editha*. I first constructed a library of 48 candidate central metabolic genes based on the corresponding protein sequences found in the proteome of a closely related species. I used these protein sequences to search the genome of *Ladona fulva* for corresponding genetic sequences, then searched reads pooled by flight metabolic rate for genetic variation correlated to flight performance. I found a high degree of nonsynonymous variation in glyceraldehyde 3-phosphate dehydrogenase that is correlated to flight performance. The coverage at this site is half the average coverage of the genome, and thus appears to be sex-linked. Outside this gene, little variation was found segregating the two pools. I will continue to collaborate with the Wheat lab to validate and publish these results.

I also learned techniques to complete de novo genome assembly that I will use to construct a draft genome of *E. editha*. I created a "best practices" document detailing the steps necessary for genome assembly and analysis of pool seq data using a program called Mespa (currently under development by the Wheat lab). This document will be used as a guide for training subsequent students in pool seq techniques.

Once the *E. editha* data returns from the core facility, I will complete the same analyses I used for *Ladona fulva* to search for candidate genes correlated with flight performance. If candidate genes are found, primers will be developed and

used to amplify target genes for sequencing. Existing samples of *E. editha* and *Euphydryas gillettii* will be used to validate the candidate genes. The pool seq analyses and subsequent validation will be published in a scientific journal.