A NOVEL FAMILY-BASED SEQUENCING APPROACH FOR NON-MODEL ORGANISMS TO ELUCIDATE REGULATORY NETWORKS

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In the fields of ecology and evolution, *-omics* (i.e genomics, transcriptomics, proteomics, etc…) approaches provide information about molecular interactions between regulators and their targets associated with a given phenotype, but have mainly been applied in model organisms (*Drosophila, Arabidopsis, Mus*) that lack important ecological context. In this project we aim to apply genomic approaches to better understand phenotypes of organisms whose ecological context is also well understood. The tools developed here can thus be applicable to other non-model organisms, such as endangered or invasive species, which are challenging to study in the laboratory.

The wood tiger moth (*Arctia plantaginis*) (fig.1) is a chemically defended moth in which the males have either white or yellow hind wings and females are orange-red. In this project we aim to determine the molecular regulatory mechanisms underpinning the colour polymorphism. Integrating knowledge from these different regulatory levels (i.e. molecule-molecule, predator-prey, and mating preferences) will allow elucidating their interplay in determining the overall fitness of the different phenotypes.

We apply a novel combination of alternative genome assembly methods, gene expression, and analyses of open chromatin to better understand gene regulatory networks underlying natural polymorphisms. We will pioneer a family-based trio sequencing approach that allows for the assembly of two haploid genomes from a single offspring individual. This project will demonstrate the potential to go from genome sequence to regulatory network analysis in a non-model organism within a single project.

Specifically we investigate **1)** If the colour polymorphism is controlled by a super gene locus, its genomic structure and how are the alleles related to other closely related *Arctia* species? **2)** What are the gene regulatory networks controlled by the alternative supergene alleles? and **3)** How is the architecture of open chromatin involved in regulation of gene networks different between the alternative morphs

This project collaborates closely with the research group of professor Chris Jiggins from Cambridge university and Professor Richard Durbin from Welcome Sanger Institute.

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