

SPP 2349 (GEvol): Genomic basis of evolutionary innovations.

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**Project title**

**The genomic basis of extreme sexual dimorphism in fireflies**

**Abstract:**

Fireflies are well known for their charismatic lighted mating signals. Less known, fireflies exhibit a fascinating variation in sexual dimorphism: some species show very mild sexual dimorphism whereas other species exhibit extreme sexual dimorphism. In species where extreme sexual dimorphism is present, females remain in a neotenic state with wing pads instead of fully developed wings. In some species the light organ is also sexually dimorphic, where males do not have a light organ but neotenic females do. Most importantly, this sexual dimorphism has evolved repeatedly across the firefly phylogeny.

Such strong variation in traits must be caused by underlying gene expression variation. Specifically, sexual dimorphism must be related to sex-biased gene expression. However, it is unknown how sex-biased gene expression evolves and if the same sex-biased genes are shared across the phylogeny. Furthermore, gene expression is most likely regulated by open chromatin accessibility. Nevertheless, the correlation between sex-biased open chromatin accessibility and sex-biased gene expression has not been shown previously.

In this project, we will study the evolutionary forces acting on gene expression using a phylogenetic framework. Only within a phylogenetic framework can we distinguish between all scenarios of gene expression evolution, for example, distinguishing directional selection from relaxed stabilizing selection. To address our questions, we will develop new methods and theory for the statistical analysis (Brownian motion and Ornstein-Uhlenbeck processes), specifically focusing on utilizing within-species variance in gene expression and sex-biased gene expression. Our novel methods will allow us to study the evolutionary forces acting on sex-biased gene expression, and if sex-biased gene expression is linked to extreme sexual dimorphism.

We will also generate the first homogeneous gene expression dataset (RNA-seq) for >10 species from at least 5 divergent genera, with multiple individuals per species and separated by body parts. Our study system, fireflies, is ideal for studying sex-biased gene expression evolution due to the repeated evolution of neoteny, but can be used as a reference and comparison to other non-sex-biased datasets too. Additionally, we will use ATAC-seq to generate chromatin accessibility data. With the ATAC-seq data, our project will produce novel insights into the correlation between gene expression evolution and chromatin accessibility evolution on a phylogenetic scale.

Taken together, our project will (a) generate a new comprehensive transcriptomic gene expression and chromatin accessibility dataset, (b) novel methods to study gene expression and chromatin accessibility evolution for multiple species and individuals across a phylogeny, (c) advance our understanding of genome evolution with regards to the molecular mechanism underlying sexual dimorphism. This knowledge will advance our understanding which genomic elements are driving innovations in insects, such as sexual dimorphism.