

Epigenetic Interplay: How Maternal and Paternal Effects Interact in Australian Crickets

Supervisory team:

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Project description:

Are you interested in learning more about insect molecular genetics while at the same time enriching your CV with key data science and other computational skills? This exciting project focuses on evolutionary computational models and experimental tests of nongenetic inheritance through fathers in the cricket *Teleogryllus oceanicus*.

While it is well known that mothers transfer – next to their genes – various nongenetic factors to their young (e.g., hormones, DNA methylation variants and small RNAs), fathers in most animals are thought to transfer nothing but genes to offspring. However, this view is now increasingly untenable given recent studies which show that fathers influence offspring phenotypes via DNA methylation or small RNAs. A clear example of such paternal influences occurs in the cricket *Teleogryllus oceanicus*, in which fathers transfer a spermatophore (a large clump of foam) to females during mating which affects offspring viability. The aim of this interdisciplinary project is to understand why and how paternal effects influence offspring phenotypes through a combination of computational modeling, selection experiments and RNA sequencing in *Teleogryllus oceanicus*.

Below we suggest three components of this project, but encourage the student to develop their own components according to their interests: Computational models of paternal effects: as we still have a limited understanding of whether paternal effects are a general phenomenon in the animal kingdom, this part of the project allows the student to learn computational techniques with which to model the evolution of paternal effects across a range of biological scenarios. Such models allow you to make general predictions about the ecological contexts and molecular mechanisms that are most conducive to paternal effects.

Selection experiments of paternal versus maternal effects and their interaction: with these computational predictions in hand, we then create selection lines of *Teleogryllus oceanicus* to assess how maternal and paternal effects interact. We can do so by artificially selecting for diverging spermatophore characteristics, so that lines become different in features such as spermatophore size and transcriptome profile. Using other lines, we can also artificially select for different characteristics of ova. Ultimately, by crossing spermatophore and ova selection lines, we can then achieve much-needed insight on how maternal and paternal effects interact in shaping the transcriptome and subsequent survival of the developing zygote.

Transcriptome bioinformatics: using state-of-the-art bioinformatics techniques we analyze the gene expression levels in spermatophores and ova of these selection lines to assess divergence in paternal versus maternal effects.