



Regulation of Gene Expression & Transposable Elements

July 8, 2021

Background: The processes leading to the emergence of novel phenotypes remain a central question in Biology. In the recent years, the role of Transposable Elements (TEs) in adaptive evolution has received an increased focus. One of the major mechanisms by which TEs can lead to adaptive evolution is their impact on the regulation of gene expression. Eusociality, one of the major evolutionary transitions, has arisen independently in many animal clades especially in insects. Despite several attempts to understand the genomic basis of eusocial transition, evidence are disparate among its different origins. Nevertheless, a trend emerged demonstrating that eusocial transition was accompanied by an increased capacity of gene regulation.

Eusociality has a monophyletic origin in Blattodea (cockroaches and termites) contrary to hymenopterans. Such monophyletic origin of Eusociality represents a great advantage to investigate the underlying evolutionary processes of eusocial transition. Within this project, we will take advantage of the gene expression and genome data in termites and cockroaches to investigate if the insertion of TEs within genomes has an impact on the subsequent regulation of gene expression and may have aided the eusocial transition in Blattodea.

Objectives: The project is planned to identify and categorize TEs in each genome species, their proximity with genes and identify differential TE insertions close to genes with differential expression among castes in eusocial but not in solitary blattodeans and vice versa.

Requirements:

- Interest in genome evolution
- Basic knowledge of gene expression and regulation
- Basic knowledge of command line and scripting
- Ability to work independently

Methods: TE insertions within the genome of termites and cockroaches next to genes will be evaluated with BEDtools. After categorization of TEs near genes, differential expression of those genes among castes in termites and cockroaches will be gathered from available data. The different TE families inserting near differentially expressed genes among castes in termites but not in cockroach and vice-versa will be compared using linear model packages in R.

Supervision: Dr. Bertrand Fouks, b.fouks@uni-muenster.de, Molecular Evolution and Bioinformatics Group (<http://bornberglab.org/>).