



# Transposable Elements families & Functional Categories

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**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. Eusociality, one of the major evolutionary transition, 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. Blattodean genomes, contrary to hymenopterans, contain a large amount of TEs and previous evidence suggests their importance to aid gene duplication underlying eusocial adaptation (Harrison et al. 2018). TEs are not uniform and are composed of different classes (DNA transposons & RNA transposons) and families (e.g. LTR, SINE, LINE) and segregate in different regions of the genome (Lu et al. 2020).

**Objectives:** This project aims to further our understanding of the role of TEs in adaptive evolution in Blattodea, by categorizing TE classes and families, their segregation in the genome, and investigate if TEs segregating near genes are linked with specific functions.

**Requirements:**

- Interest in genome evolution
- General knowledge of biological processes
- 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, the function of each gene will be assigned using pfam and GO annotations. Association between TE insertion and gene function will be evaluated using topGO R package.

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