

TE associations with de novo genes in socially parasitic ants

Background

De novo genes originate from previously non-coding genomic regions and can contribute new genetic functions. Transposable elements (TEs) can provide sequence and regulatory elements that may facilitate the emergence of new genes. This project asks whether candidate de novo genes in socially parasitic ants are preferentially associated with TEs compared with other genes.

The project

You will use existing de novo gene candidates and TE annotations, initially focusing on *Temnothorax americanus* and its host *T. longispinosus*. You will quantify TE overlap within gene bodies and in fixed upstream and downstream regions and record TE class/family and orientation where appropriate.

De novo genes will be compared with background genes from the same genome, matched for relevant features such as gene length and local gene density. Direct overlap and nearby TE associations will be analysed separately to test whether any enrichment depends on genomic position.

Expected outcome

A reproducible analysis and figures showing whether de novo genes have stronger or different TE associations than comparable background genes, and which TE classes contribute most strongly to any pattern. The analysis will identify associations but will not assume that TEs caused de novo gene emergence.

Possible MSc thesis extension

Extend the analysis to additional parasite–host pairs and test whether TE associations with de novo genes are repeatedly observed across independent origins of social parasitism. Selected loci could then be examined in more detail to investigate whether particular TE sequences contributed coding or regulatory sequence to emerging genes.

Methods

Genomic interval analysis, matched comparisons, TE classification, permutation or resampling tests, and data visualisation in R or Python.

Requirements

- Interest in evolutionary genomics and willingness to learn command-line analysis and R or Python.
- Basic coding experience is helpful. Existing datasets will be provided.

Supervision

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Selected literature

- Harrison et al. (2025). Convergent Evolutionary Traces of Genomic Innovations and Depletions in Socially Parasitic Ants. *bioRxiv*. doi:10.1101/2024.12.31.630940
- Van Oss & Carvunis (2019). De novo gene birth. *PLoS Genetics* 15:e1008160.
- Grandchamp et al. (2023). Population genomics reveals mechanisms and dynamics of de novo expressed open reading frame emergence in *Drosophila melanogaster*. *Genome Research* 33:872–890.
- Lebherz et al. (2024). DNA Transposons Favor De Novo Transcript Emergence Through Enrichment of Transcription Factor Binding Motifs. *Genome Biology and Evolution* 16:evae134.
- Lebherz et al. (2026). Data reanalysis: DNA Transposons Favor de novo Transcript Emergence Through Enrichment of Transcription Factor Binding Motifs. *Research Square* [Preprint].