

Evolutionary history of TEs associated with newly expressed ORFs

Background

Transposable elements (TEs) or jumping DNA can contribute sequence and regulatory signals to new transcripts. In *Drosophila melanogaster*, some transcripts containing newly expressed open reading frames (neORFs) overlap or lie near TEs. This project asks whether these associated TE copies are less or more diverged than comparable copies elsewhere in the genome. The answer could help distinguish associations involving recent TE activity from those involving older retained sequences.

TE near a neORF transcript



Conceptual example of proximity, not results. Overlapping TEs are analysed separately; divergence is not a direct insertion date.

The project

You will use existing data from one *Drosophila* line to compare TE copies overlapping or near neORF-containing transcripts with background copies matched by family where possible and by genomic context. Direct overlap and proximity will be analysed separately, using a small set of annotation workflows. Kimura divergence from the family consensus will provide an approximate indicator of evolutionary history, rather than a direct insertion date.

Expected outcome

A reproducible analysis and figures showing whether divergence differences persist after accounting for TE family composition and annotation choice.

Possible MSc thesis extension

Extend the comparison to additional lines and TE families and investigate selected insertions in corresponding genomic regions across lines.

Methods

Genomic interval analysis, TE divergence data, matched comparisons, statistical testing and 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

1. 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.
2. Van Oss & Carvunis (2019). De novo gene birth. *PLoS Genetics* 15:e1008160.
3. Lebherz et al. (2024). DNA Transposons Favor De Novo Transcript Emergence Through Enrichment of Transcription Factor Binding Motifs. *Genome Biology and Evolution* 16:evae134. doi:10.1093/gbe/evae134.
4. Lebherz et al. (2026). Attention note: Data reanalysis DNA Transposons Favor de novo Transcript Emergence Through Enrichment of Transcription Factor Binding Motifs. *Research Square* [Preprint]. doi:10.21203/rs.3.rs-9616708/v1.