

Transposable elements in insects

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Transposable Elements (TEs) are genetic elements present in most of the eukaryotic genomes. They produce repetitive landscapes in the eukaryotic genomes known as “mobilome”. The distribution and abundance of these families within genomes vary widely. TEs are related to big differences in DNA content in eukaryotic genomes. Particularly, in insects, genome sizes vary from less than 100 megabases (mb) to larger than 10 gigabases (Gb). Also, some genomes harbor few albeit vary numerous families like the human genome, while other contain numerous families with less individual copy numbers like insects such as *Drosophila melanogaster* or *Anopheles gambiae*.

An archetypal TE family might be composed of a diverse cloud of genetic copies resulting in a complex dynamic.

We have been studying *in silico* the distribution, abundance and evolution of the mobilomes present in several insect genomes and transcriptomes. Particularly, we have analyze the genomes of important vectors of infectious diseases such as *Anopheles gambiae*, *Aedes aegypti*, *Rhodnius prolixus* and we are now analyzing the expression profile of these elements in the transcriptome of *An. funestus*.

We used combined strategies based on different Blast programs to identify and characterize the repetitive elements present in these genomes and transcriptome and presented all the gathered information in an easy and accessible manner: as hyperlinked spreadsheets presenting the obtained results. This platform can also serve for analysis of TEs in other sequenced genomes or transcriptomes, allowing for comparative purposes.

Biography

RDFM has completed a Ph.D. in Public Health at the National School of Public Health/FIOCRUZ, Rio de Janeiro, Brazil and has now a posdoctoral position at the same institution. She has been working with the identification, characterization and evolution of transposable elements in several insect genomes.

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