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Unravelling organelle genome evolution architecture using RNA-sequencing data

Background: Mitochondria genomes vary from 11 Mb to 6 kb, while plastids can vary from 1 Mb to 30 kb. Non-coding DNA accounts for most of this size variation, but the mechanistic and evolutionary reasons for that are still unknown. Next generation sequencing has generated unprecedented amounts of genomic and transcriptomic data that can be used for organelle genome evolution studies. However, most of these data is used only for the study of cell nucleus. Therefore, I decided to use these untapped data source to investigate the transcription of organelle genomes in plastid-bearing protists.

Methods: I mapped the transcriptomes over the genomes of 116 protist species using the algorithm Bowtie 2 through the software Geneious.

Results/Discussion: 77 out of 116 species had their organelle genomes entirely recovered from transcripts. These genomes come from diverse protists and vary immensely in size and structure, which allowed me to determine the transcriptomic architecture of organelle genomes regardless of their nature.

Conclusions: RNA-seq data generated for cell nucleus studies can be used to investigate organelle genome transcription. Even though organelle genomes can exhibit large portions of non-coding DNA, these regions are still transcribed and might play a role in post-transcription regulation. Here, I will argue how RNA-seq data can be used to explore this field and how transcription can interfere in the genome size evolution.

Interdisciplinary reflection: My work combines Biodiversity and Molecular Evolution to investigate the evolution of organelle genomes and speciation, which ultimately will help us better manage protist-rich ecosystems.