



ÖKOLOGISCHES KOLLOQUIUM
des Instituts für Zoologie in person in room 0.024

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Host: H. Arndt

Neglected Kinetoplastid species and Kinetoplastid genome evolution

Kinetoplastids are a lineage of Euglenozoa famous for a number of bizarre and unique molecular features - their nuclear genomes have high gene density and very few canonical spliceosomal introns, nuclear genes are frequently arranged in polycistronic clusters; the mitogenome of kinetoplastids has extremely complex maintenance and organisation, containing an enormous amount of DNA.

Although a huge diversity of free-living Kinetoplastids was cultured and described, sequencing data available for the free-living lineages is usually limited to the marker region sequence, and functional studies are rarely carried out on rather inconvenient non-model free-living species.

As a result, some critical nodes on Metakinetoplastina phylogeny remain unresolved, phylogeny itself so far relying mainly on 18S rRNA gene sequences; little is known about the origin and evolution of both mitochondrial and nuclear genome organisation and function, main evolutionary studies on the lineage thus far focused only on metabolic pathways and origin of parasitism.

We try to test if the reduction in the number of introns and denser gene arrangement could be the result of natural selection for reduced nuclear genome size, which, in turn, can be connected massive increase in mitogenome size and complexity.

In the presentation, we will cover some methodological aspects of how we:

- 1) isolate and cultivate a broad variety of Kinetoplastids
- 2) to produce transcriptomic (and plan on producing genomic) data for the isolates we obtained in culture
- 3) develop a method to estimate mitochondrial and nuclear DNA content based on fluorescent DNA staining and microscopy.

and how the combination of sequencing and imaging data can be used to answer a variety of questions connected with the evolution and function of the bizarre traits of Kinetoplastids.

We will also review some preliminary results obtained from the combination of methods, which could, in the future, help to shed light on:

- 1) unresolved nodes Metakinetoplastina phylogeny
- 2) diversity of organisation and sizes of nuclear and mitogenomes of Kinetoplastids
- 3) possible evolutionary adaptations that might be interpreted in the context of nuclear and mitogenome (co)-evolution in the lineage