

Eccentricities of mitochondrial genomes across diplomonids

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Diplomonids are marine micro-eukaryotes that belong to the phylum Euglenozoa, together with their extensively studied sister group, the kinetoplastids, and the well-known euglenids. Traditionally considered a small and insignificant flagellate group, diplomonids are now being recognized as one of the most diverse and most abundant eukaryotes in the world's oceans (1).

Coincidentally, diplomonids also feature a most unusual genome architecture, gene structure, and gene expression in their mitochondrial organelle. Specifically, we discovered that the mitochondrial genome of the type species *Diplonema papillatum* is composed of hundreds of small circular chromosomes each carrying a piece of a gene. In addition to systematic fragmentation, mitochondrial genes are further encrypted by nucleotide deletions and substitutions (2).

We will briefly present how exactly these broken genes are expressed in *D. papillatum*, involving a unique type of trans-splicing and three different types of RNA editing. Yet, the main topic of our report will be the comparison of mitochondrial gene structure and expression across a broad range of diplomonids: the established taxa *D. papillatum*, *D. ambulator*, *Diplonema* sp. 2, and *Rhynchopus euleeides*, and four additional species newly isolated from the Sea of Japan that associate in phylogenetic analyses with either the *Diplonema/Rhynchopus* or the *Hemistasia* clades (3). Based on this comparison, we will address the question of how widespread and diverse mtDNA eccentricities are across diplomonids, and whether it has reached its climax in *D. papillatum* or goes even beyond that in other members of the clade.

References

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