# Structural Duplications and tRNA Expansions in mtDNA of *M. diorchis* and *R. parvicaudatus*

## Introduction

Parasitic flatworms - the cestode *Microsomacanthus diorchis* and the trematode *Renicola parvicaudatus* populate seagulls at White Sea region.

The mitochondrial genome is a reliable genetic marker for taxonomic identification due to its rapid evolution, maternal inheritance, and lack of recombination.

## Goal

Assemble and annotate the mitochondrial genomes of *R. parvicaudatus* and *M. diorchis*.

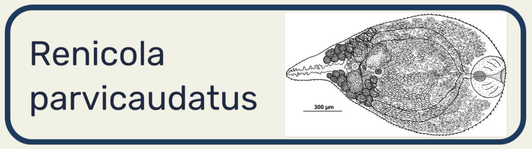
## Take-home messages

- tRNA Expansion (*R. parvicaudatus*): The repetitive region in *R. parvicaudatus* mtDNA accommodates several additional tRNA copies. We propose that locus expansions originated through replication slippage or imperfect DNA repair and were fixed by positive selection for parasitic adaptation. Future comparative genomic analyses will test this model.
- Genome Architecture & Markers (*M. diorchis*): The divergent non-coding region in *M. diorchis* exhibits substantial intraspecific diversity, serving as a promising population marker despite overall mtDNA synteny with closely related species.

SMTB

Sabancı Üniversitesi

# Methods




# Results

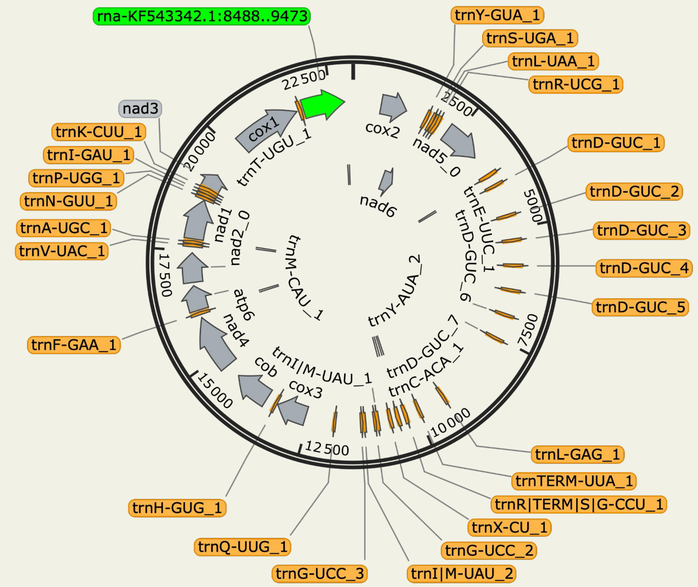



Figure 1. Map of the *R. parvicaudatus* mitochondrial genome. The genome spans 22,989 bp and encodes standard mitochondrial protein-coding genes (grey), rRNA genes (green), and tRNA genes (orange). Analysis of the unannotated region ("dark matter") in the *R. parvicaudatus* mitogenome revealed repeats that represent additional copies of tRNA genes.

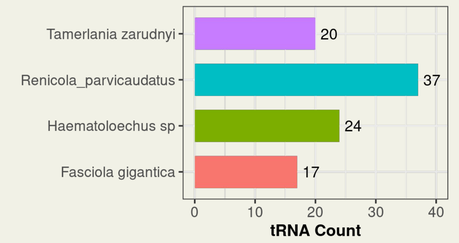



Figure 2. Comparison of tRNA gene copy numbers across closely related trematode species. The *R. parvicaudatus* mitogenome contains twice as many tRNA genes as related taxa.

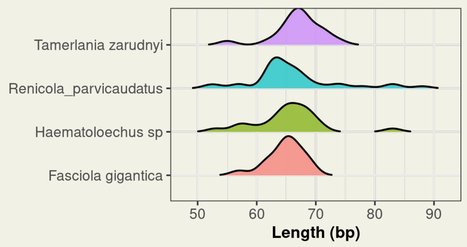



Figure 3. Length comparison of *R. parvicaudatus* tRNA genes. tRNA genes in *R. parvicaudatus* tend to be shorter than those of closely related trematode species.

# Methods




Illumina data

↓

Assembly with GetOrganelle

↓

Annotation with MITOS2, LiftOff

↓

Visualization in SnapGene

# Results

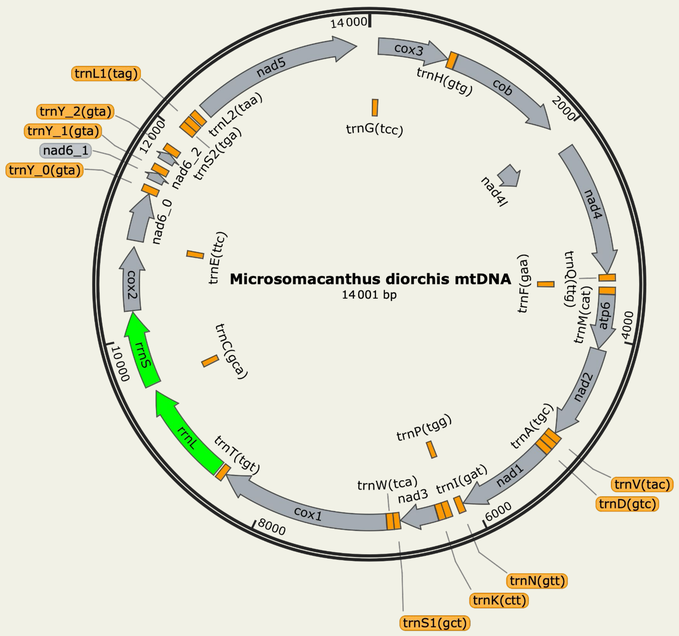



Figure 4. Map of the *M. diorchis* mitochondrial genome. The genome spans 14,001 bp and encodes standard mitochondrial protein-coding genes (grey), rRNA genes (green), and tRNA genes (orange). All expected genomic features were identified in the newly assembled genome.

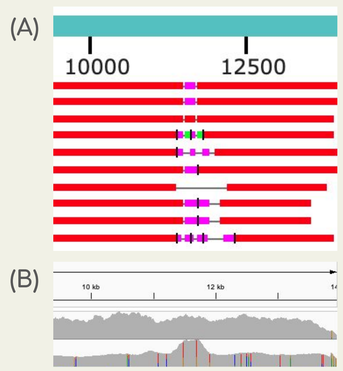



Figure 5. Variations in the M. diorchis mitogenome. (A) BLAST search revealed high sequence similarity (>95% query coverage with ~80% sequence identity with other flatworms). (B) An IGV view comparing an individual specimen (Sample 1) against a multi-individual pooled sample 2 highlights a duplication event accompanied by single nucleotide polymorphisms (SNPs) in the pooled sample.


## Acknowledgements

We thank Maud Borensztein and Christel Picard for reagents, Anna Solovyova for providing data, Lev Levanov and Alesia Levanova for cells and plasmids, Anna Perederina for help and support in the experimental work, SMTB for organisation.