# Insights on the mitochondrial genome of appendicularians



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**Project Aim:** To determine the sequence and structure of the mitochondrial genome of appendicularians.

# **Open questions**

Is editing widespread in Appendicularia? Is there an editing signal?
Is the mitochondrial genome circular, linear or partitioned?
Are genes spread out in different fragments that are then transpliced?
Which genes are encoded in the mitochondrial genomes?

## Editing in Oikopleura dioica and Fritillaria pellucida

mitogenomic poly-T correspond at RNA level to TTTTTT (6T) regions in O. dioica but to shorter TTTT (4T) regions in F. pellucida, suggesting species-specific RNA editing by deletion.

In *O. dioica* editing involves the removal of polyT at 6T sites





## RNA base probability around 6T sequence in O. dioica

Table 1: Amino acyl tRNA synthetase identified in the genomic assemblies of *Ciona intestinalis, Oikopleura dioica* and *Homo sapiens*.

For each species, green cells with a check mark indicate the successful identification of amino acyl tRNA synthetase homologue while red cells which indicate their putative absence. The division of amino acyl tRNA synthetase into "single eukaryotic lineage", "cytosolic" and "mitochondrial" follows [26].

		Ciona	Oikopleura	Ното
Single	A	$\checkmark$	$\checkmark$	$\checkmark$
	G	$\checkmark$	$\checkmark$	$\checkmark$
eukaryotic	Н	$\checkmark$	$\checkmark$	$\checkmark$
lineage	Q	$\checkmark$	$\checkmark$	$\checkmark$
Cytosolic	C	$\checkmark$	$\checkmark$	$\checkmark$
	D	$\checkmark$	$\checkmark$	$\checkmark$
	E/P	$\checkmark$	$\checkmark$	$\checkmark$
	FA	$\checkmark$	$\checkmark$	$\checkmark$
	FB	$\checkmark$	$\checkmark$	$\checkmark$
	Ι	$\checkmark$	$\checkmark$	$\checkmark$
	K	$\checkmark$	$\checkmark$	$\checkmark$
	L	$\checkmark$	$\checkmark$	$\checkmark$
	Μ	$\checkmark$	$\checkmark$	$\checkmark$
	Ν	$\checkmark$	$\checkmark$	$\checkmark$
	R	$\checkmark$	$\checkmark$	$\checkmark$
	S	$\checkmark$	$\checkmark$	$\checkmark$
	Т	$\checkmark$	$\checkmark$	$\checkmark$
	V	$\checkmark$	$\checkmark$	$\checkmark$





\* The presence of mt-PheRS in organisms that lost tRNAPhe has been explained by structural constraint [25, 26].

partial mitochondrial gene together with nuclear genes. For example:



### Conclusions

- Editing at poly T sites exists both in Fritillariidae and Oikopleuridae.
- MinION data support the organization of the genome predicted based on rRNA sequences, however the MinION data contain many reads encompassing both nuclear and mitochondrial genes suggesting that rearrangements may have occur during library formation.
- We show that the mitochondrial genome of Oikopleura encodes only one tRNA (*trnM*).

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