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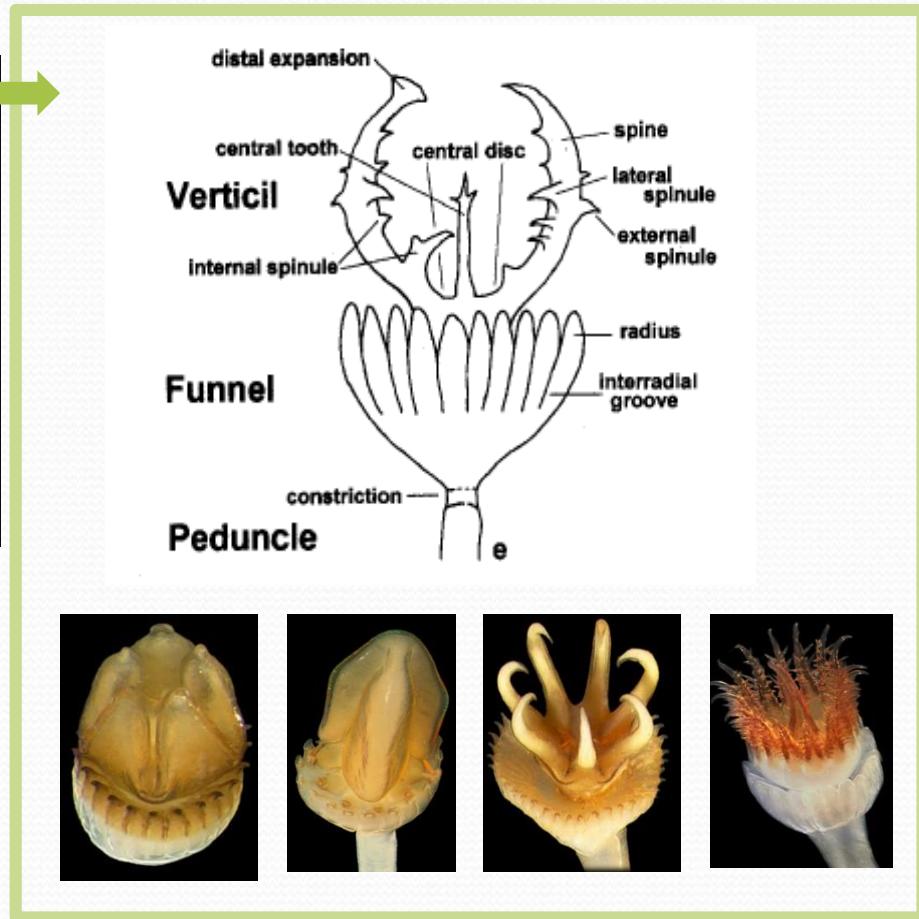
# CO1 barcoding and novel mitochondrial genome of *Hydroides* (Serpulidae)

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# Genus *Hydroides* Gunnerus, 1768

- The largest genus with > 100 nominal species
- Complex two-tiered operculum



# Troubles bothering taxonomists

- Difficult to identify some species due to
  - High variability of opercula structure in one species



- Incomplete taxonomic descriptions in earlier studies
- Unsuccessful attempts to develop any molecular identification tools within *Hydroides*

# A difficult road: CO1 Barcoding of *Hydrodoides*

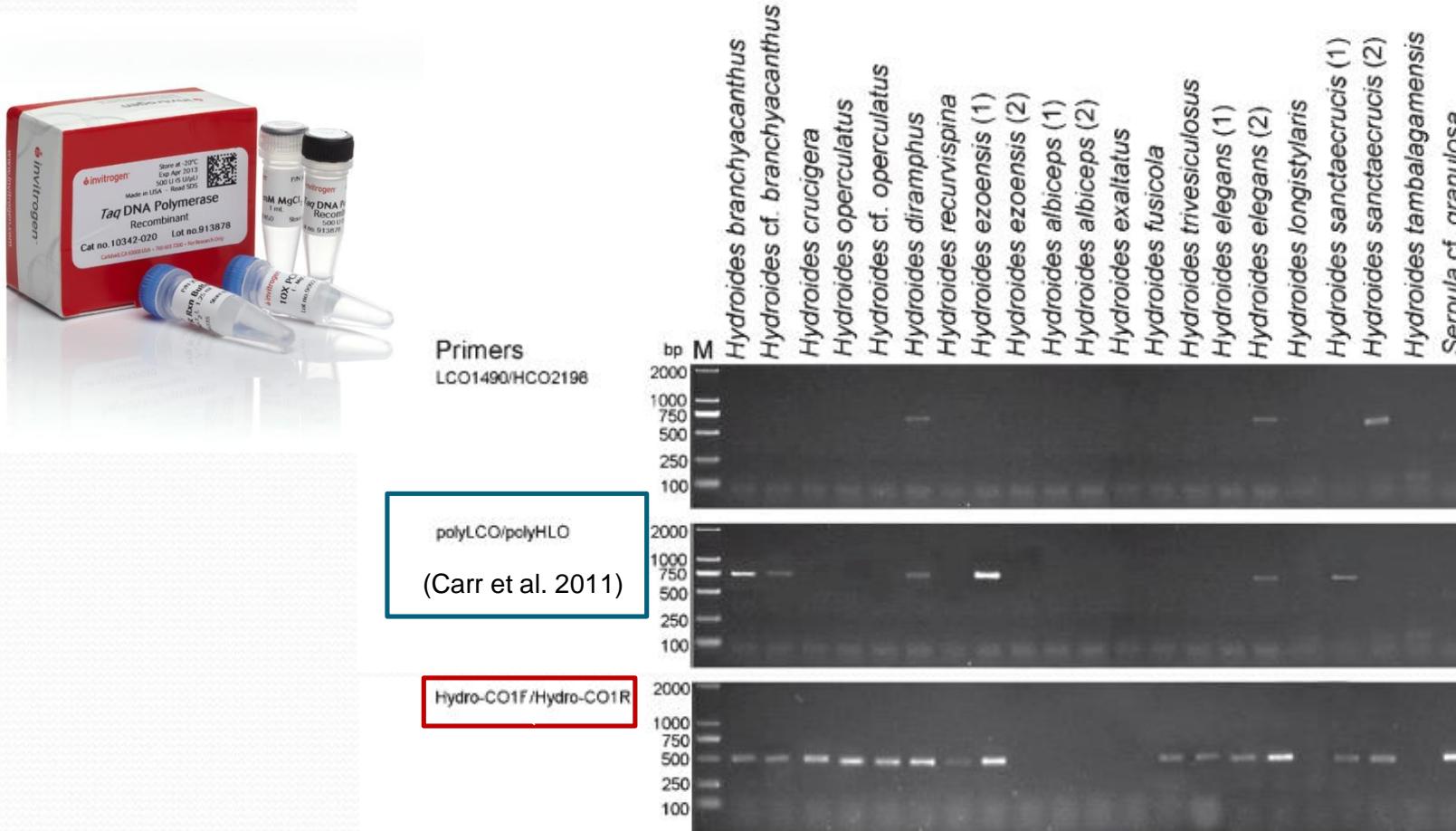
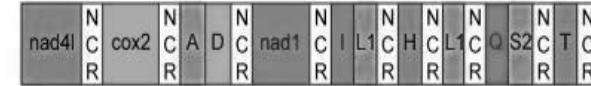
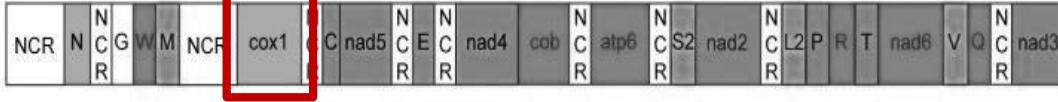


Fig. 1. Gel images of PCR amplicons for 20 *Hydrodoides* specimens and one *Serpula* specimen using LCO1490/HCO2198, polyLCO/polyHCO and Hydro-CO1F/Hydro-CO1R, respectively. 'M' denotes molecular size ladder in base pairs. The specimen labels are also shown in Table 1. (Sun et al. 2012)

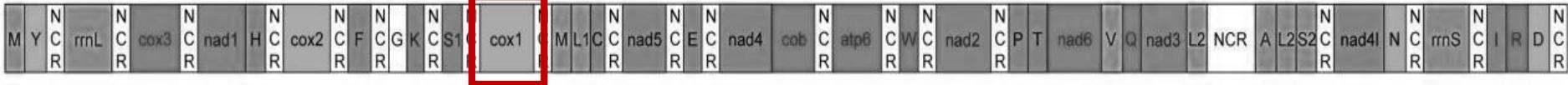
- Taxon-specific primers work only on 17 species
- No further reference sequences for new primer design

# Mitochondrial genomes of *Hydroides* spp.

# *Hydroides dirampha*



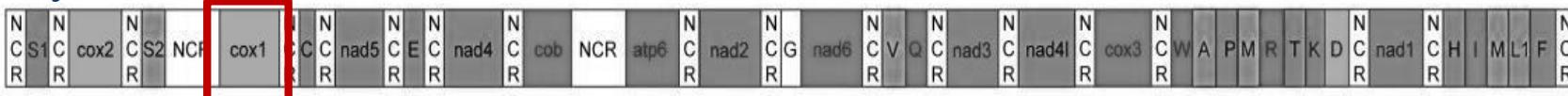
# *Hydroides elegans*



# *Hydroides ezoensis*



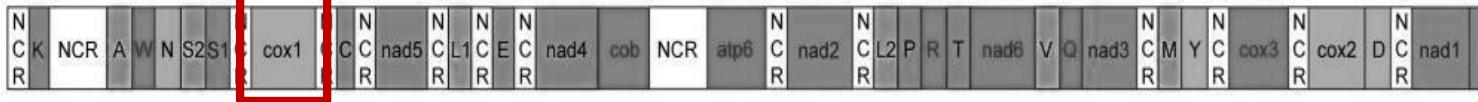
# *Hydroides homoceros*



## *Hydroides minax*



# *Hydroides operculata*



## *Hydroides pseudouncinata*

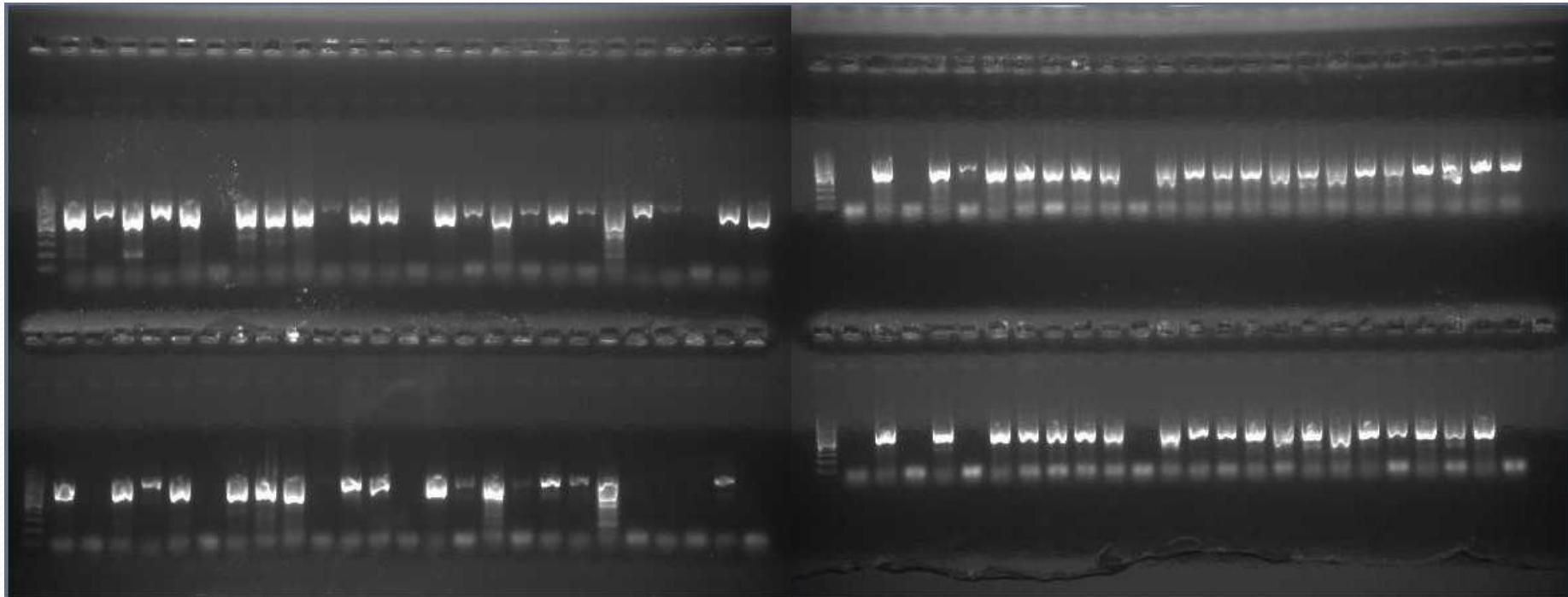


# *Hydroides sanctaecrucis*

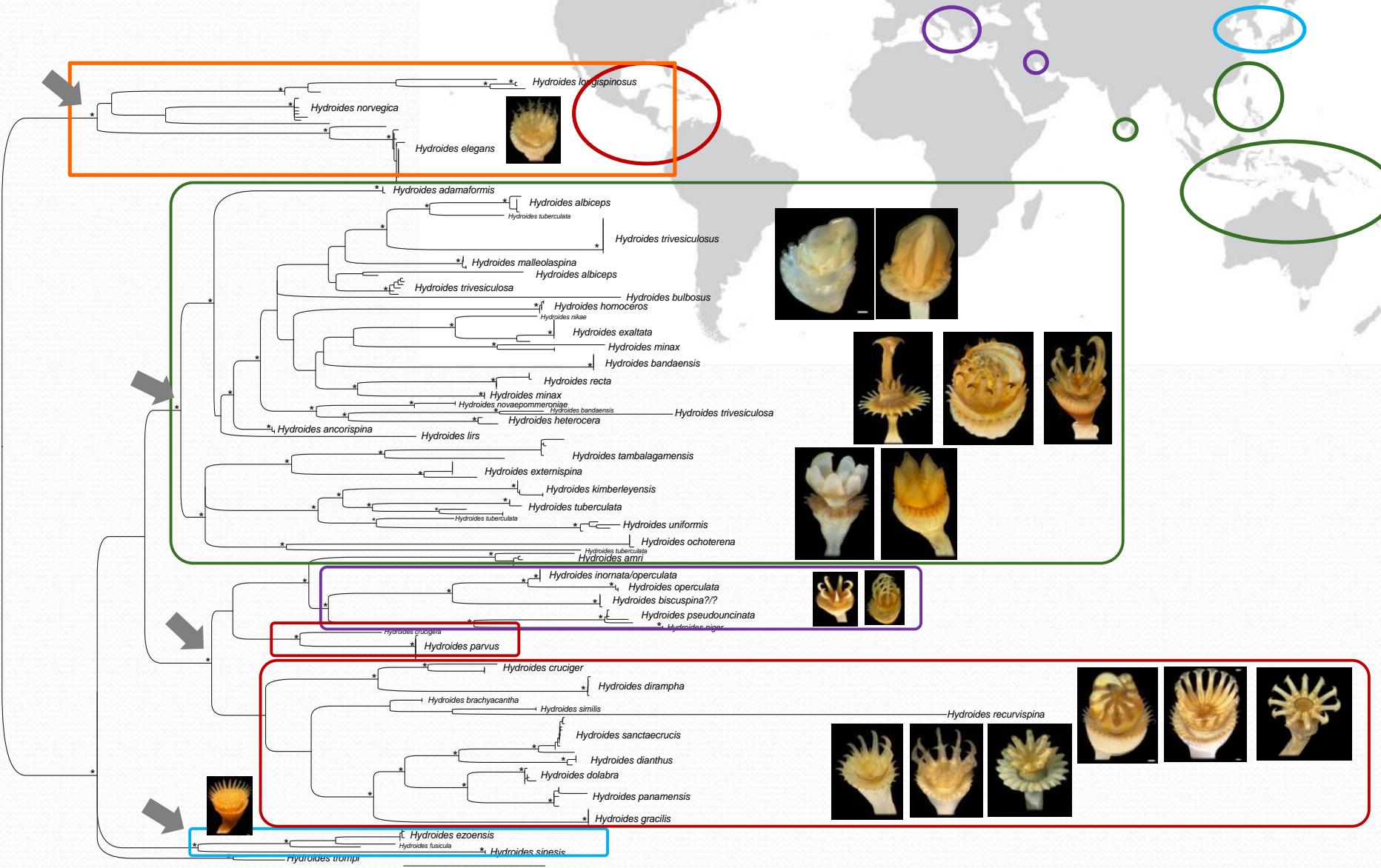


# Testing of new primers

- Covers around 600 bp of CO1 barcoding region
- Works on all 45 tested species
- A database with 278 sequences of 45 *Hydroides* species world wide

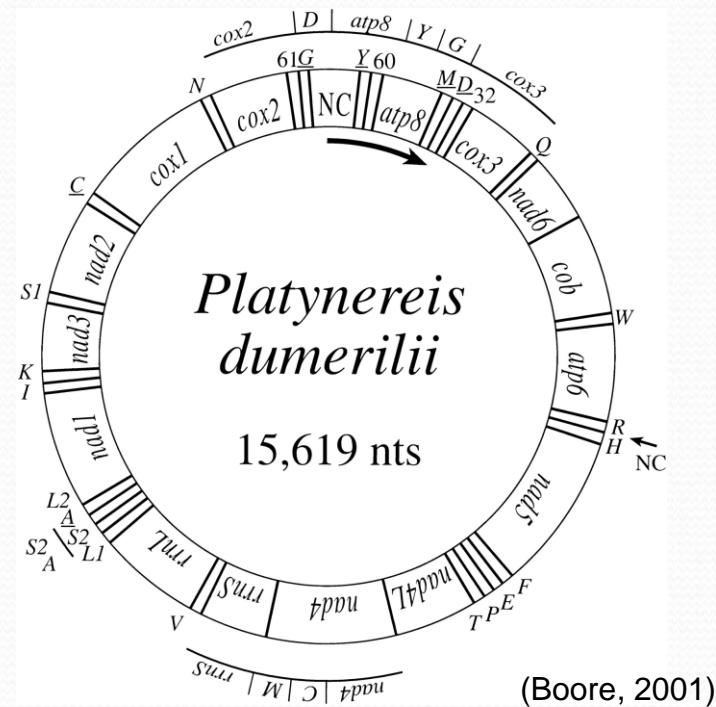


# Geographic relationship indicated by barcoding data



# Conserved polychaete mitochondrial genome

- Circular
- Around 16kb in size
- 37 genes: 13 protein-coding genes, 2 ribosomal RNAs and 22 transfer RNAs
- One long control region
- Putatively conserved gene order of protein-coding genes and rRNA.



(Boore, 2001)



# Mitochondrial genome of *Hydroides* spp.

- Genome length

## *Hydroides dirampha*



## *Hydroides elegans* (~19 kb)



## *Hydroides ezoensis* (~ 18 kb)



### *Hydroides homoceros*



### *Hydroides minax*



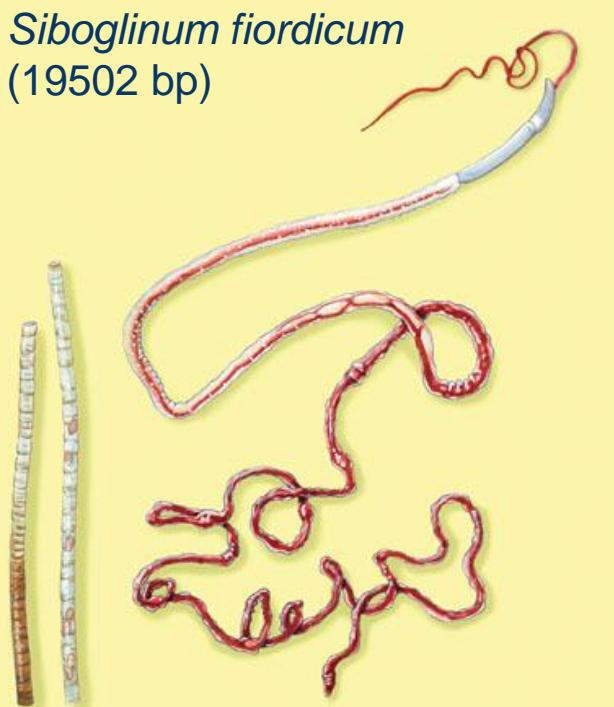
### *Hydroides operculata*



*Hydroides pseudouncinata*



## *Hydroides sanctae crucis*

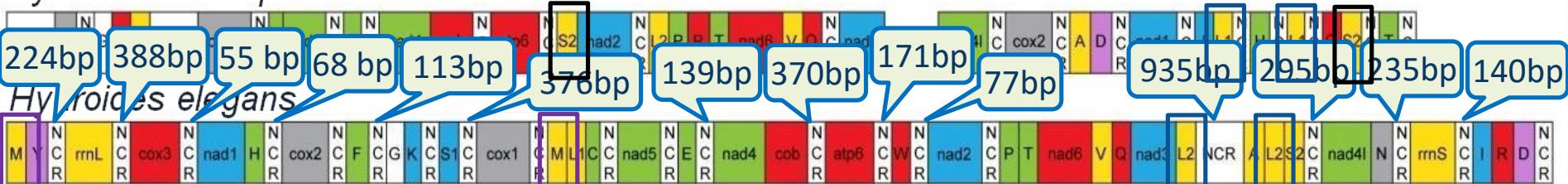


# Mitochondrial genome of *Hydroides* spp.

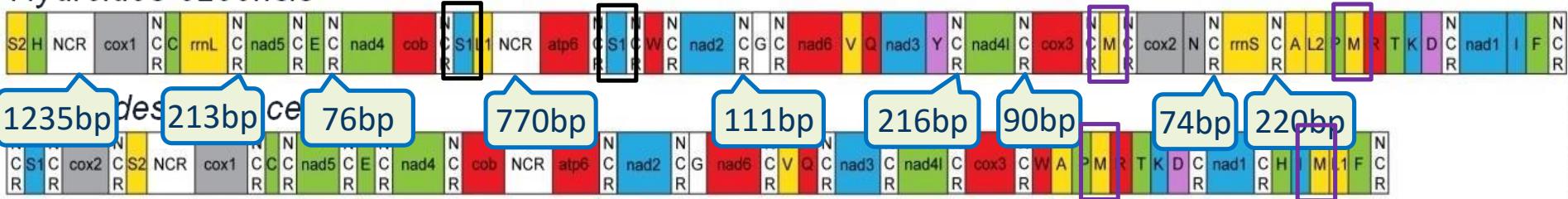
## Genome composition

- 12 protein-coding genes, missing atp8
  - Duplication events of tRNA
  - Multi non-coding regions (NCR)

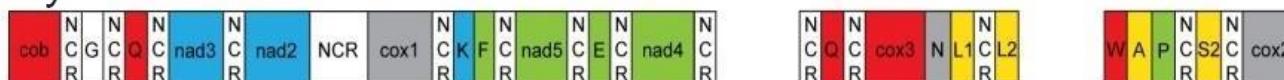
## *Hydroides dirampha*



## *Hydroides ezoensis*



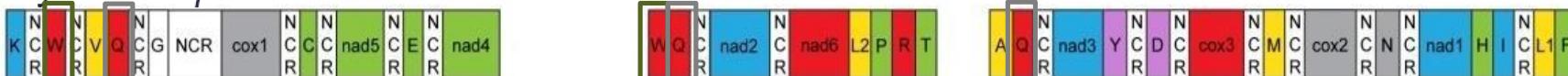
### *Hydroides minax*



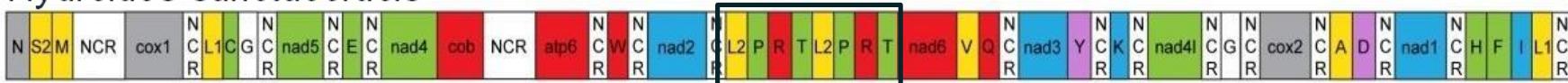
### *Hydroides operculata*



### *Hydroides pseudouncinata*



## *Hydroides sanctae crucis*

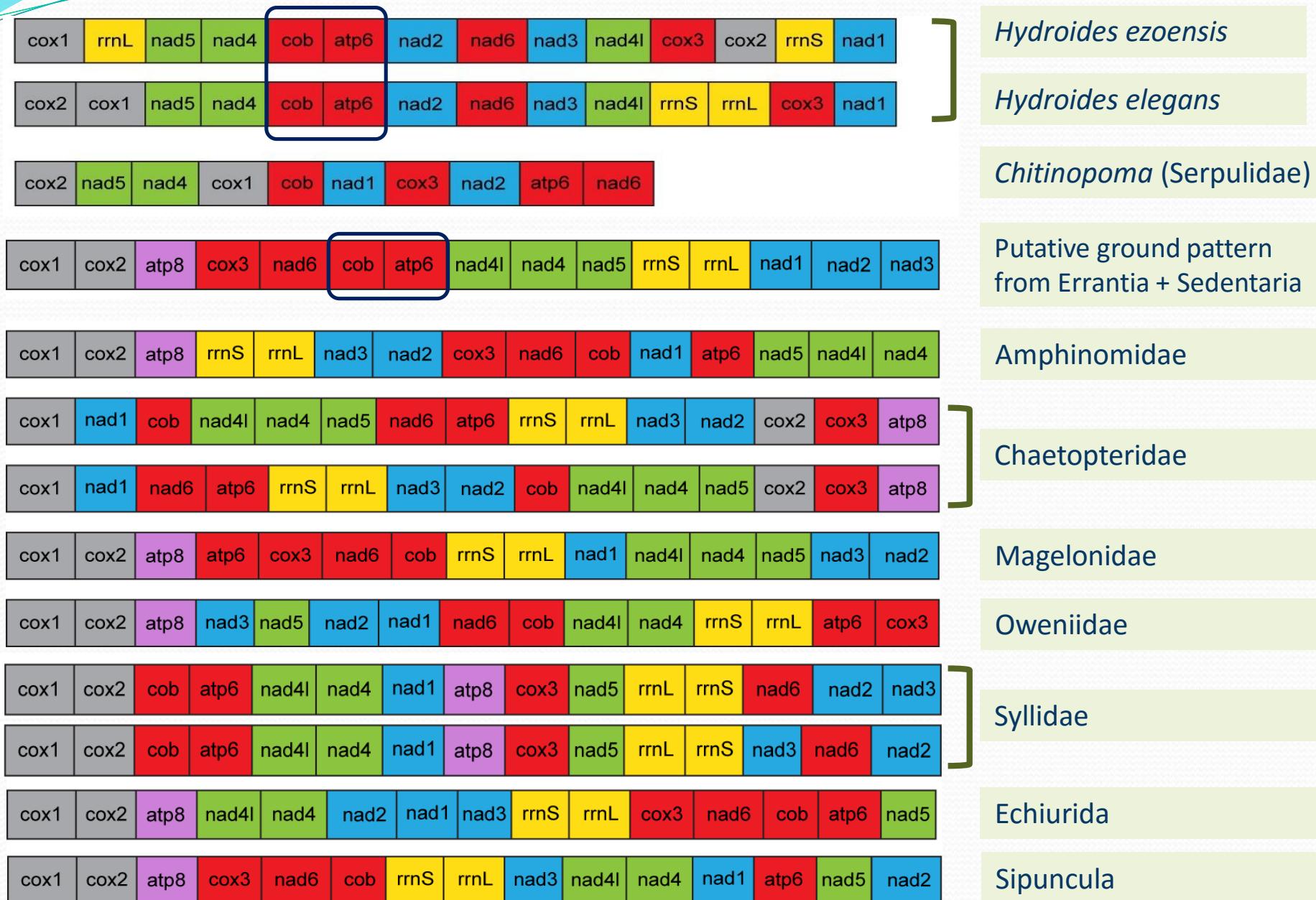


# Mitochondrial gene order and rearrangements of *Hydriodes* spp.

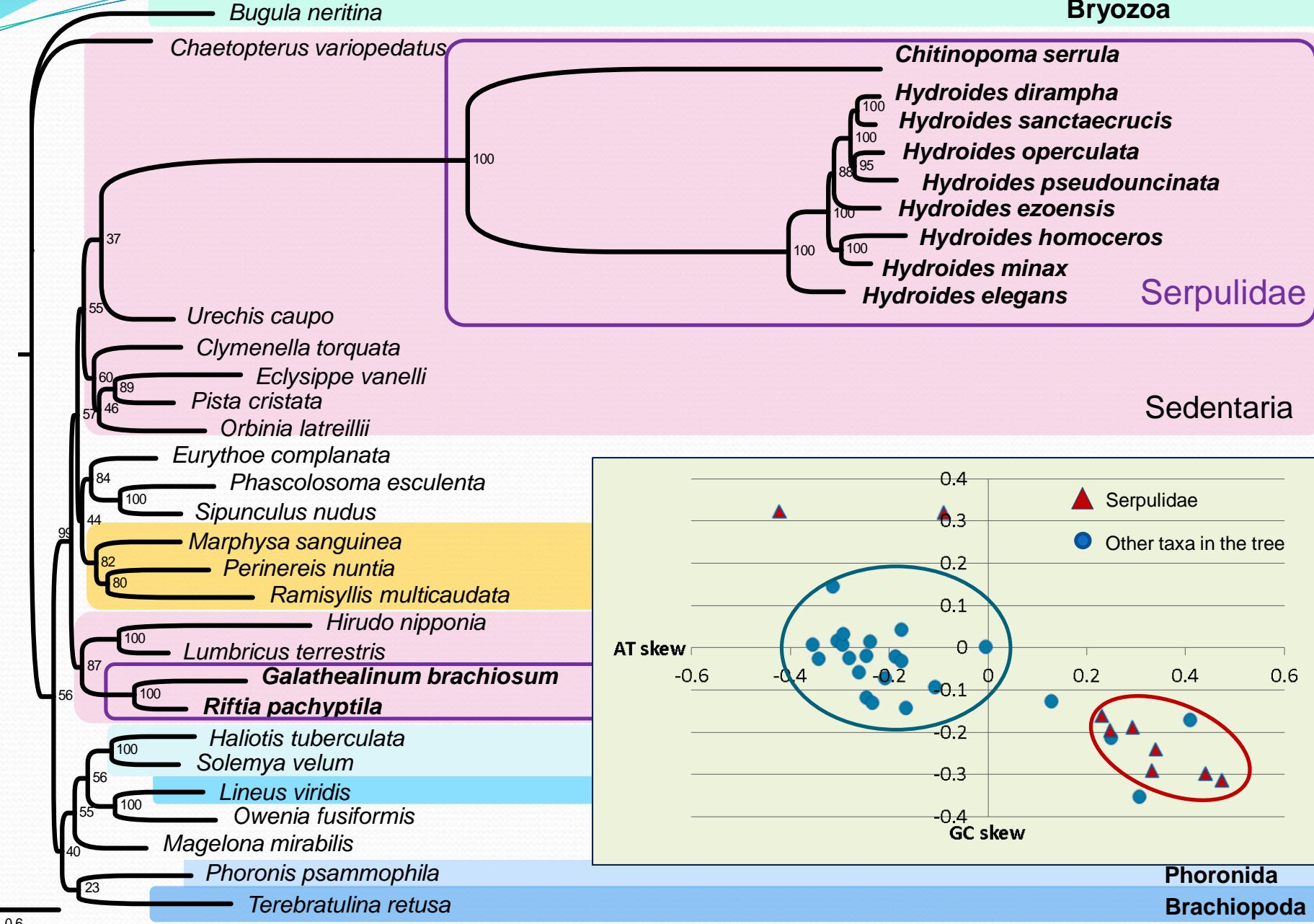
## *Hydroides dirampha*



# Comparison of gene order of Serpulids and the putative ground pattern from Annelida



# Phylogenetic relationship based on mitochondrial genome data



# Summary

- First CO1 Barcoding data of half species of the entire genus, reveals closer relationships among species of *Hydroides* from close geographic regions.
- Mitochondrial genomes of *Hydroides* show unusual large genome size, non-coding regions, gene order rearrangements, and high substitution rate.
- Phylogenetic analysis support the position of Serpulidae in Sedentaria.

# Thanks to:



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