

First Record of an Ilyophine Eel from the Southern Ocean (Anguilliformes, Synphobranchidae)

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Background:

A single *Ilyophis* eel specimen was trawled in the Kong Haakon VII Sea off Dronning Maud Land at a depth of 1500 meters during the 2019 joint expedition of the Institute of Marine Research (Norway), the University of Bergen (Norway), the Arctic University of Norway, the University of Science and Technology (Norway) and the Stellenbosch University (South Africa) onboard the Norwegian research vessel Kronprins Magnus Haakon.

Taxonomy:

We tentatively identify the specimen as *Ilyophis* cf. *maclainei* based on an integrative taxonomic approach. Phylogenetic analysis of mitochondrial COI places the Antarctic specimen in a clade of sequences deposited in BOLD as *Ilyophis* sp., *I. cf. brunneus* and *I. brunneus*. Morphological data show overlaps in some morphometric and meristic characters with *I. brunneus* and the recently described *I. maclainei* for which no genetic samples are currently available. Our analysis reveals taxonomic issues within *I. brunneus* and the need for increased sampling and a worldwide taxonomic review of *I. brunneus*. The specimen is now housed at the ichthyological collection of the University Museum Bergen, Norway (ZMUB). The full mitochondrial genome will be deposited in Genbank as resource for future phylogenetic, barcoding, and eDNA studies.

Key words:

cutthroat eels, Ilyophinae, *Ilyophis brunneus*, *Ilyophis maclainei*, integrative taxonomy, cytochrome oxidase I, Antarctic

Significance:

This is the first record of the genus *Ilyophis* in the Southern Ocean.



Figure 1: *Ilyophis* cf. *maclainei* ZMUB 23883: a) Left lateral view of the freshly collected fish after death. b) right lateral view of the ethanol preserved specimen. White line in front of the anal pore is a plastic string holding the specimen for photographing c) Arrangement of lateral scales. d) Anal opening.

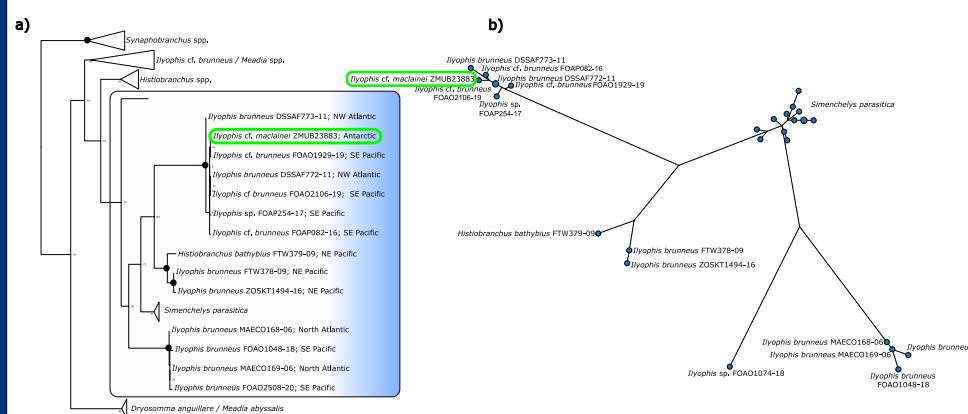


Figure 2: a) Maximum Likelihood based phylogenetic reconstruction with bootstrap support indicated at nodes, full support indicated by black dots based on 100 replicates and cytochrome oxidase I data. Estimate performed under the GTR Gamma substitution model. *Synphobranchus* spp. chosen as outgroup sequences. Framed taxa indicate sequences used for the haplotype network reconstruction in b) based on the Jukes Cantor model. Black dots on lines connecting haplotypes indicate mutational steps; unique haplotypes dominate. Sample numbers indicated after species names.

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