

The unexpected relationships within *Haliclystus* (Cnidaria: Staurozoa)

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Staurozoa is a unique group of jellyfish that has undergone significant taxonomic revisions over the past two decades. Despite this, the phylogenetic relationships within this group remain poorly understood. The most numerous and problematic genus within this group is *Haliclystus*, which contains 13 known species. Some of these species' validity is questionable. The current study aims to investigate the diversity and phylogenetic relationships of *Haliclystus* in the Northern and Far Eastern seas using morphological and molecular methods.

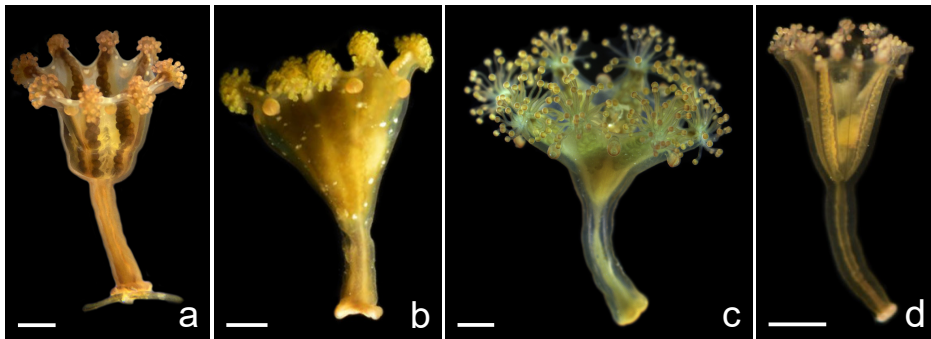


Fig. 1. Living specimens of *Haliclystus*: (a) *H. borealis*, (b) *H. tenuis*, (c) *H. auricula*, (d) *Haliclystus* sp. Rud23-043. Photo credit: Irina Ekimova (a, b, d), Valeriia Khabibulina (c). Scale bars: 1 mm.

Fig. 2. Molecular phylogenetic reconstruction of the genus *Haliclystus* based on the COI (591 bp), Bayesian inference. Numbers from the left indicate bootstrap support from Maximum Likelihood (BS), numbers on the right — posterior probabilities (PP) from Bayesian Inference, dash — unsupported clades. Bold font marks sequences obtained in this work.

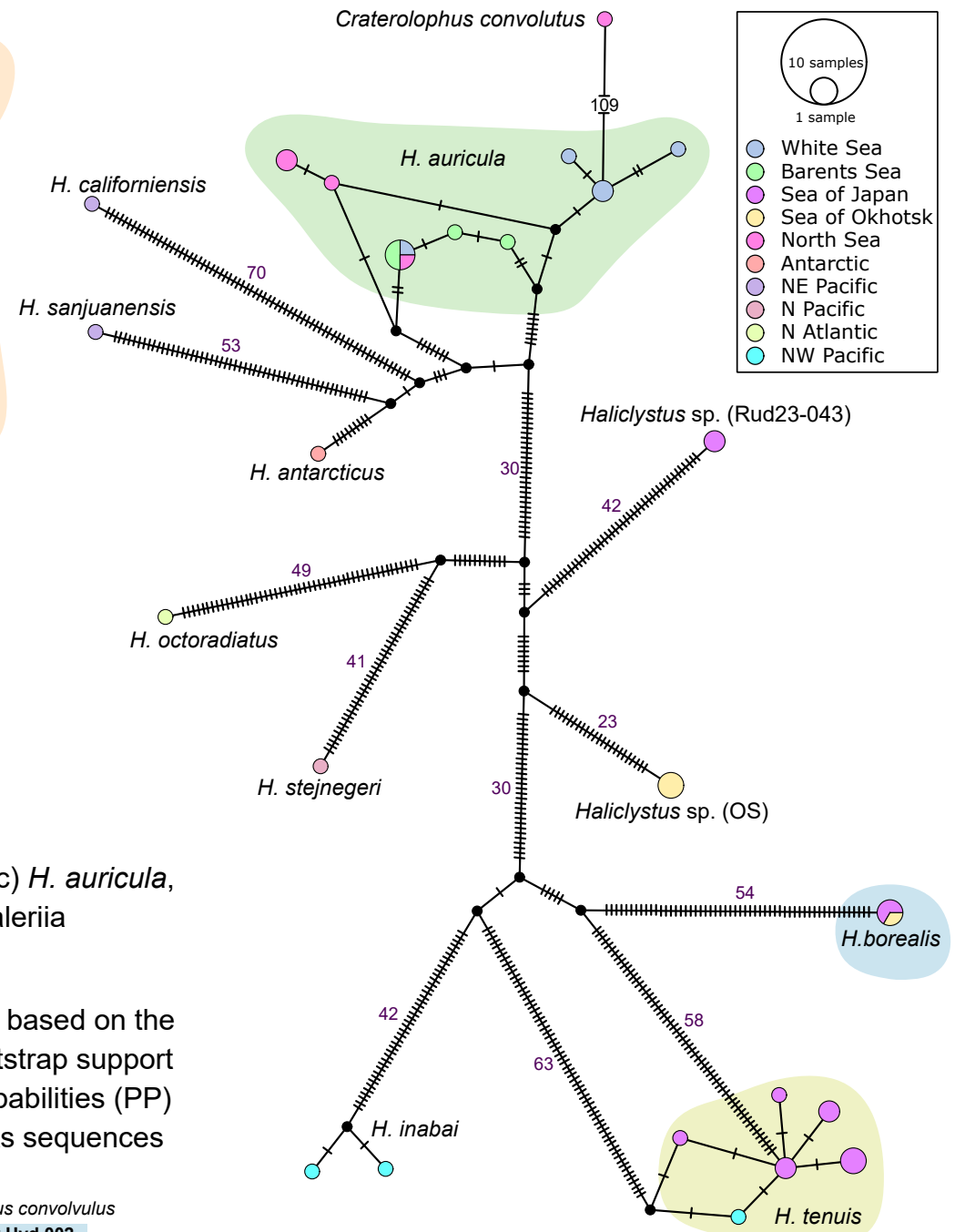
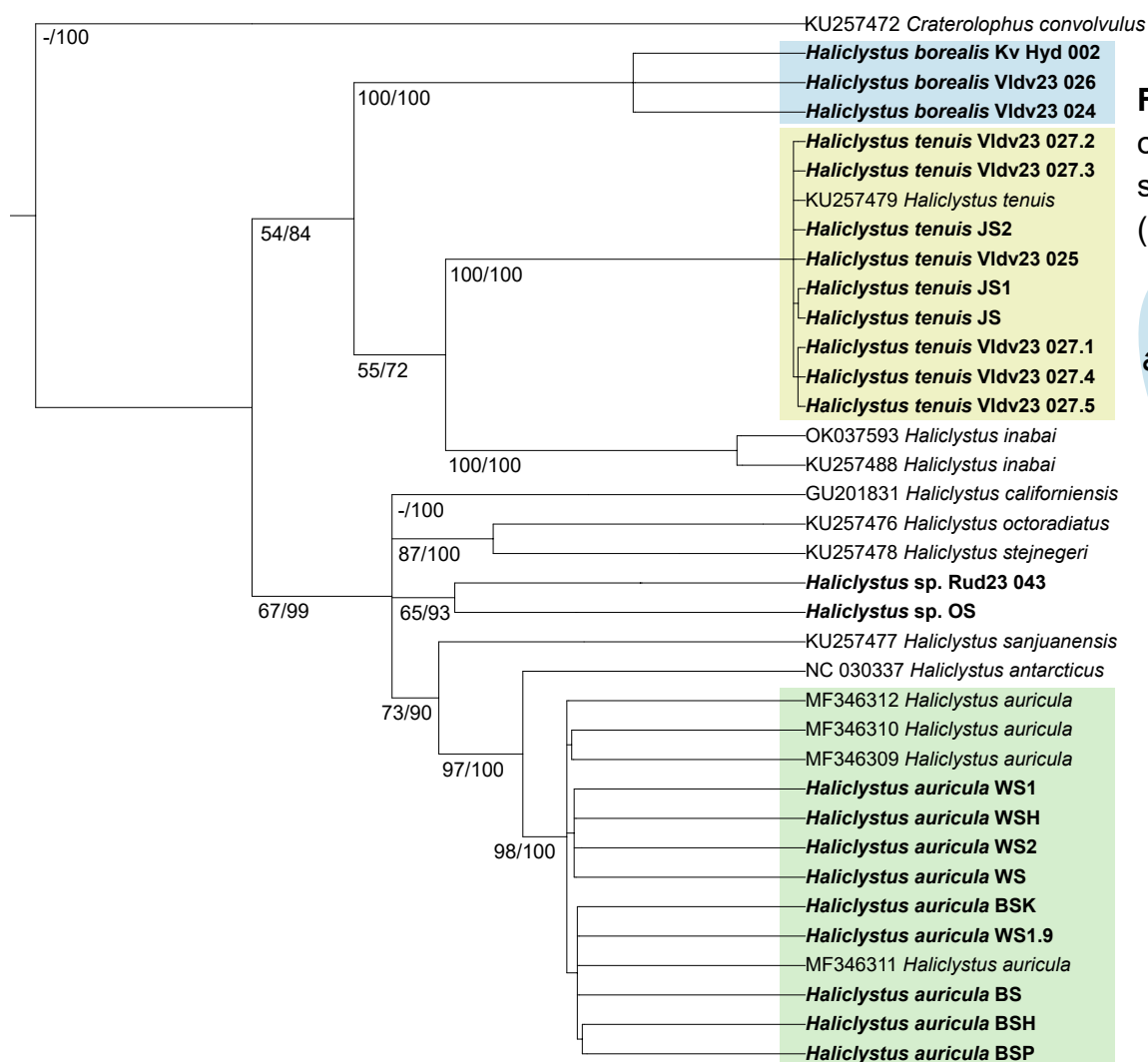


Fig. 3. COI haplotype network produced with TCS method. Colour of circles refers to the geographic origin of each haplotype, relative size of circles is proportional to the number of sequences included (shown in the legend).

All samples from the White and Barents seas form the *H. auricula* clade, together with samples from the North Sea. Some samples from the Sea of Japan and one sample from the Okhotsk Sea fall into the *H. borealis* clade. All other samples from the Sea of Japan belong to the *H. tenuis* clade. One Rud23 sample from the Sea of Okhotsk and one from the Sea of Japan, which have not yet been morphologically identified may correspond to poorly studied species, such as *H. salpinx* and/or *H. sinensis*, or potentially represent new species.

We are grateful for our colleagues who collected material: I. Ekimova, D. Grishina, A. Lyanguzova, G. Kremnev and D. Tumanov. The fieldwork was carried out at the MBS 'Belomorskaya' SPbU and Murmansk MBI of RAS. The research was performed using equipment of the 'Centre for Culture Collection of Microorganisms' of the Research Park of SPbU.