Data in Brief

The complete mitochondrial genome of the Antarctic stalked jellyfish, *Haliclystus antarcticus* Pfeffer, 1889 (Staurozoa: Stauromedusae)

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**Abstract**

In present study, the complete mitogenome sequence of the Antarctic stalked jellyfish, *Haliclystus antarcticus* Pfeffer (Staurozoa: Stauromedusae), has been sequenced by next-generation sequencing method. The assembled mitogenome comprises of 15,766 bp including 13 protein coding genes, 7 transfer RNAs, and 2 ribosomal RNA genes. The overall base of Antarctic stalked jellyfish constitutes of 26.5% for A, 19.6% for C, 19.8% for G, 34.1% for T and show 90% identity to Sessile Jelly, *Haliclystus sanjuanensis*, in the northeastern Pacific Ocean. The complete mitogenome of the Antarctic stalked jellyfish, contributes fundamental and significant DNA molecular data for further phylogeography and evolutionary analysis for seahorse phylogeny. The complete sequence was deposited in DBJ/EMBL/GenBank under accession number KU947038.

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overall base of Antarctic stalked jellyfish has 26.5% of A, 19.6% of C, 19.8% of G, 34.1% of T and matches 90% identity to Sessile Jelly, Haliclystus sanjuanensis, in the northeastern Pacific Ocean.

The protein coding and tRNA genes of Antarctic stalked jellyfish mitogenome were predicted by using DOGMA [5], ARWEN [6] and MitoAnnotator [7] tools. Some ambiguous annotation sites are manual checked. All protein-coding genes were encoded on H-strand with exception for COX1. All tRNA genes were encoded on H-strand with exception for tRNA-Ser, tRNA-Leu, and tRNA-Phe. All the 13 mitochondrial protein-coding genes share the start codon ATG, except for NAD2, NAD3, NAD4L, COX1, COX3, ATP6, and ATP8 for NAD3 and NAD4L (Both with ATA start codon). It also important to note that NAD2, NAD3, NAD4L, COX1, COX3, ATP6, and ATP8 all have the same stop codon (TAA), while others are terminated with exception for COX1. All tRNA genes were encoded on H-strand manually checked. All protein-coding genes were encoded on H-strand.

To validate the phylogenetic position of H. antarcticus, we used MEGA6 [8] software to construct a Maximum likelihood tree (with 500 bootstrap replicates) containing complete mitogenomes of 6 Cnidaria species. Hydra oligactis derived from Hydrozoa was used as outgroup for tree rooting. Result shows H. antarcticus can be grouped with H. sanjuanensis and Craspedacusta sowerbyi in a monophyly with high bootstrap value supported (Fig. 1). In conclusion, the complete mitogenome of H. antarcticus was decoded for the first time in this study and provides essential and important DNA molecular data for further phylogenetic and evolutionary analysis for jellyfish.

Conflict of interest
Authors declare no conflicts of interest in this study. The authors are responsible for the published content and manuscript compilation.

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Fig. 1. Molecular phylogeny of Haliclystus antarcticus and other Cnidaria species based on complete mitogenome. The complete mitogenomes is downloaded from GenBank and the phylogenetic tree is constructed by maximum likelihood method with 500 bootstrap replicates. The gene’s accession number for tree construction is listed as follows: Hydra oligactis (NC_010214), Craspedacusta sowerbyi (JN53332), Haliclystus sanjuanensis (JN700944), Haliclystus antarcticus (KU947038), Aurelia aurita (NC_008446), Cassiopea frondosa (NC_016466) and Chrysaora quinquecirrhia (NC_020459).