

## Complete mitochondrial genome of the Antarctic crocodile icefish, *Chionodraco hamatus* (Perciformes: Channichthyidae)

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### ABSTRACT

Antarctic icefish *Chionodraco hamatus* is an ideal model for studying cold adaptation mechanisms. The complete mitochondrial genome of *C. hamatus* was sequenced in this study. The genome sequence is 17373 bp in length, which comprises 13 protein-coding genes, 22 tRNAs, two rRNAs and a control region. The overall base composition is A: 26.25%, T: 26.05%, G: 17.49% and C: 30.21%, with an A:T content of 52.3%. The phylogenetic analyses based on the concatenated nucleotide sequences of all the genes and control region supported a relatively close relationship with *Parachaenichthys charcoti*. The complete mitochondrial genome sequence will be useful for evolutionary and functional studies of Antarctic Notothenioids.

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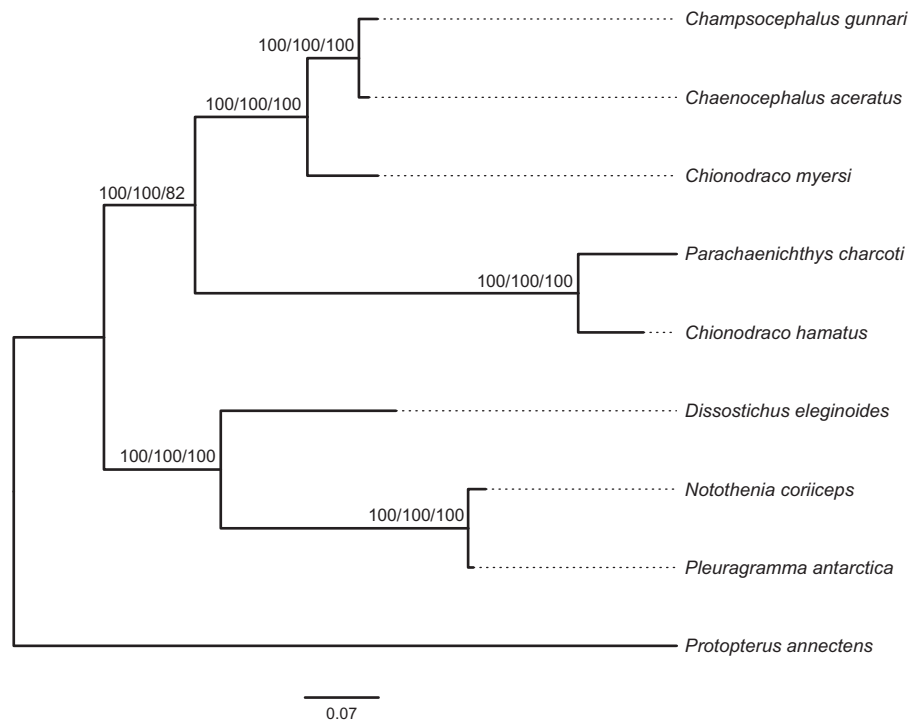
*Chionodraco hamatus*;  
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The icefish *Chionodraco hamatus* (Perciformes: Channichthyidae) is an endemic Antarctic teleost, which is the most abundant channichthyidae. As *C. hamatus* evolved in the persistently cold and oxygen-rich water, they acquired unique adaptations at the morphological, physiological and biochemical level. For example, as a result of adapting to oxygen-rich water, *C. hamatus* has white blood because it lacks haemoglobin and functionally active erythrocytes (Pellegrino et al., 2004). *C. hamatus* is an ideal model for studying cold adaptation (Marino et al., 2007; Buonocore et al., 2012; Rizzello et al., 2013; Xu et al., 2015). The complete mitochondrial genome sequence will be useful for evolutionary and functional studies of Antarctic Notothenioids. In this study, the complete mitochondrial genome of *C. hamatus* was determined. Fish sample was collected from Prydz Bay, Antarctica (69°22'S, 76°22'E).

The complete mitogenome of *C. hamatus* was 17373 bp in length (accession no. KU341409), with an overall base composition of 26.25% A, 17.49% C, 30.21% G and 26.05% T. The circular genome contains 13 protein-coding genes, 22 tRNA genes, two rRNA genes and one control region (CR or D-loop). Most of its mitochondrial genes are encoded on the heavy strand except for NADH dehydrogenase subunit 6 (ND6) and eight tRNA genes (*tRNA-Gln*, *tRNA-Ala*, *tRNA-Asn*, *tRNA-Cys*, *tRNA-Tyr*, *tRNA-Ser*, *tRNA-Glu* and *tRNA-Pro*), which were encoded on the light strand. Twelve of the 13 protein-coding genes started with ATG, while COI utilized GTG.

Eight of the 13 protein-coding genes ended with complete (TAA) or incomplete (T) stop codons. *ATPase8*, *ND5* and *ND6* stopped with TAG, AGA and AGG, respectively. *ND2* and *COX3* stopped with incomplete (TA) stop codons. The 22 tRNA genes range from 67 bp to 74 bp in size. The 12S and 16S rRNA genes were 947 bp and 1691 bp, respectively. D-loop was 1125 bp in length.

To investigate the phylogenetic relationship among Antarctic Notothenioids, we downloaded the mitochondrial genome sequences of seven currently available Notothenioids, including *Chionodraco myersi* (accession no. NC\_010689), *Chaenocephalus aceratus* (NC\_015654), *Champscephalus gunnari* (NC\_018340), *Pleuragramma antarctica* (NC\_015652), *Parachaenichthys charcoti* (NC\_026578), *Notothenia coriiceps* (NC\_015653) and *Dissostichus eleginoides* (NC\_018135), together with African lungfish *Protopterus annectens* (NC\_018822) as an outgroup species. The concatenated nucleotide sequences of 13 protein-coding genes, 22 tRNAs, two rRNAs and the D-loop of nine species were aligned with the CLUSTALW program (Thompson et al., 2002) and refined by eye. Phylogenetic trees were reconstructed with the concatenated nucleotide alignment using MEGA6 (Tamura et al., 2013) for neighbour-joining, maximum likelihood and maximum parsimony methods. Tree topology was evaluated by 1000 bootstrap replicates. Different methods give the same tree topology, and the result indicates that *C. hamatus* mitogenome is close to that of *P. charcoti* (Figure 1).



**Figure 1.** Phylogenetic tree of Antarctic Notothenioids, with African lungfish *Protopterus annectens* as an outgroup. The topology of phylogenetic tree was inferred from neighbour-joining, maximum-likelihood and maximum parsimony methods. Bootstrap supports for each analysis are indicated above the nodes

## Disclosure statement

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