

The complete mitochondrial genome of *Chionodraco hamatus* (Notothenioidei: Channichthyidae) with phylogenetic consideration

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ABSTRACT

The complete mitochondrial genome of *Chionodraco hamatus* was obtained, which was 17 457 bp in length. This genome consists of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and a putative control region. Of the 37 genes, 28 were encoded by heavy strand, while 9 were encoded by light strand. Overall base composition of mitogenome is estimated to be 26.38% for A, 17.44% for G, 26.00% for T, 30.18% for C, respectively, with a slight A + T bias (52.38%). The phylogenetic analysis based on 13 concatenated protein-coding genes suggested that *C. hamatus* as a sister species to *Chionodraco myersi* was clustered in family *Chionodraco*. The complete mitochondrial genome sequence of *C. hamatus* could provide a basic data for the studies on evolution for low temperature adaptability, population structure, molecular systematic, stock evaluation and conservation genetics.

ARTICLE HISTORY

Received 3 December 2015
Revised 26 December 2015
Accepted 30 December 2015

KEYWORDS





Chionodraco hamatus;
evolutionary relationships;
gene order; genome
structure; mitochondrial
genome

Chionodraco hamatus, an important Antarctic fish species of family Channichthyidae, is widely distributed in the High Antarctic zone all around the continent (Kock 2005). These fish families have developed unique physiological features that allowed them to survive in the Antarctic seawater that reaches temperatures near to -2°C . They produce anti-freeze glycoproteins that prevent tissues freezing (Bargelloni et al. 1994). Moreover, as an extreme adaptation, the Channichthyidae showed the complete absence of haemoglobin and of functional blood erythrocytes (Ruud 1954). Within this family, 11 genera and 15 species are currently recognized, with the large majority of these genera being monospecific. One of the few exceptions is the genus *Chionodraco* for which three species have been described, namely *C. hamatus*, *Chionodraco myersi* and *Chionodraco rastrospinosus* (Eastman & Eakin 2000). But most researchers based their identification primarily on the occurrence and distribution of adults fish (Moteki & Ishimaru 2008). In addition, the origin of this group is ambiguous due to the lack of a fossil record although they are thought to have originated from an ancestor of the sub-order Percoidei (Buonocore et al. 2006). The complete mitochondrial genome sequence of *C. hamatus* could provide a basic data for the studies on above. So far, no complete mitogenome sequence information of *C. hamatus* is available.

Adult fish of *C. hamatus* was collected near Zhongshan Station (68°10'N 70°10'E) after freezing at -80°C it was transported to East China Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences for storage and DNA extraction.

In this study, we obtained the complete mitochondrial genome sequence of *C. hamatus*, and submitted it into the GenBank database with an accession number KT921282. This mitochondrial genome is 17 457 bp in length and contained 13 protein-coding genes, 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes and a putative control region. Among the 37 genes, 28 were encoded by heavy strand, while 9 were encoded by light strand just as in other teleosts. What differentiated was that the gene arrangement and genome structure were diverse from most teleosts, even from the sister species *C. myersi*. The NADH dehydrogenase subunit 6 (ND6) gene and the adjacent tRNA^{Glu} were not lost but had been translocated to between tRNA^{Thr} and tRNA^{Pro} from their canonical location between ND5 and cytochrome b genes. The overall base composition of this genome is 26.38% for A, 17.44% for G, 26.00% for T, 30.18% for C, respectively, with a slight higher A + T content (52.38%).

Two kinds of start codons (ATG and GTG) were identified in 13 protein-coding genes; 5 genes ended with TAA, whereas 8 genes had incomplete stop codons TA or T. The length of the total protein-coding genes was 11 444 bp, and the base composition was 23.68% for A, 30.63% for C, 17.63% for G and 28.06% for T. The length of the two rRNA genes was 2639 bp, with the overall base composition of 31.68% for A, 25.54% for C, 21.52% for G and 21.26% for T. The length of 22 tRNA genes was 1593 bp, with the overall base composition of 29.69% for A, 24.67% for C, 21.09% for G, 24.54% for T. The non-coding region was 1810 bp in length, its overall

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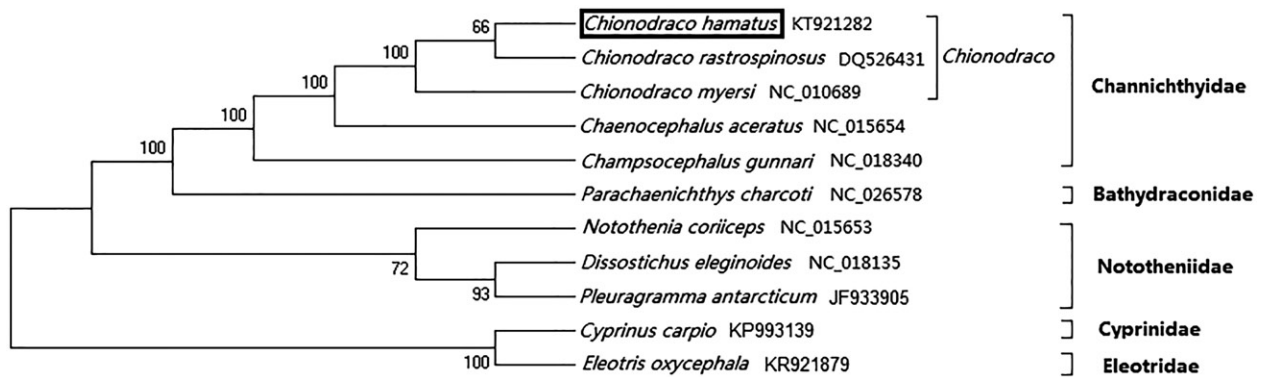


Figure 1. Phylogenetic position of *Chionodraco hamatus* within suborder Notothenioidei based on 13 protein-coding genes using neighbour-joining method. *C. hamatus* is highlighted with a box. The ND6 was not included in the protein-coding genes of *Chionodraco rastrispinosus* and *Chionodraco myersi* analysed here.

base composition is 28.34% for A, 32.43% for C, 13.48% for G, 25.75% for T. The putative control region was 1349 bp in length, longer than non-Antarctic fishes. Furthermore, only two typical domains including termination-associated sequences (TAS and ETAS) and central conserved sequence block (CSB-E) were detected in the putative control region by comparing with the mitochondrial genomes of other species. The phylogenetic position of *C. hamatus* within suborder Notothenioidei was reconstructed based on 13 concatenated protein-coding genes using the neighbour-joining method (some mitochondrial genomes without ND6). The phylogenetic tree (Figure 1) shows that *C. hamatus* first clustered as a monophyletic group with *C. rastrispinosus*, then together with other three fishes in family Channichthyidae, forming a big branch. Besides, another three fishes in family Nototheniidae formed a big sister branch as well.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This work was

supported by the Chinese National Antarctic Research Expedition (CHINARE2014-01-06).

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