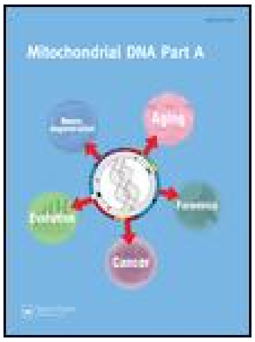

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Mitochondrial DNA Part A
DNA Mapping, Sequencing, and Analysis

ISSN: 2470-1394 (Print) 2470-1408 (Online) Journal homepage: http://www.tandfonline.com/loi/imdn21

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To cite this article: Jae Soon Oh, Seunghyun Kang, Do Hwan Ahn, Mi-Kyeong Kim, Hyoungseok Lee, Young Min Chi & Hyun Park (2016) Complete mitochondrial genome of the Antarctic dragonfish, Parachaenichthys charcoti (Notothenioidei: Bathydraconidae), Mitochondrial DNA Part A, 27:5, 3151-3152, DOI: 10.3109/19401736.2015.1007309

To link to this article: http://dx.doi.org/10.3109/19401736.2015.1007309

Mitochondrial DNA

http://informahealthcare.com/mdn
ISSN: 2470-1394 (print), 2470-1408 (electronic)

Mitochondrial DNA Part A, 2016; 27(5): 3151–3152

DOI: 10.3109/19401736.2015.1007309

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Antarctic dragonfish, *Parachaenichthys charcoti* (Notothenioidei: Bathydraconidae)

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Abstract

The complete mitochondrial genome of the Antarctic dragonfish, *Parachaenichthys charcoti* (Vaillant, 1906), is described, representing the first complete mitochondrial genome sequence of the family Bathydraconidae. The mitochondrial genome is 18,202 base pairs in length and encodes 13 protein-coding genes, 23 tRNAs, 2 rRNAs and 2 control regions. The overall base composition is A: 25.8%, T: 25.3%, G: 17.9% and C: 31.0%, with an A:T content of 51.1%. The complete mitochondrial genome sequence will be useful for phylogenetic, evolutionary and functional studies of Antarctic Notothenioids.

Keywords

Antarctic fish, complete mitochondrial genome, *Parachaenichthys charcoti*

History

Received 23 December 2014
Revised 30 December 2014
Accepted 10 January 2015

The fish fauna of the Southern Ocean is dominated by a single lineage belonging to the perciform suborder Notothenioidei (Eastman, 2005), consisting of 132 species and 8 families (Eakin et al., 2009). Among these, three non-Antarctic families, the Bovichthidae, Pseudaphritidae and Eleginopidae, diverged before the isolation and glaciation of the Antarctic continental shelf (Baluskin, 1992). The remaining five Antarctic families, the Nototheniidae, Harpagiferidae, Artedidraconidae, Bathydraconidae and Channichthyidae, consisting of 104 species, are restricted to the cold waters of Antarctica (Near et al., 2004). These Antarctic fishes have evolved unique physiological and morphological attributes suited to this extreme environment; for example, they produce antifreeze glycoproteins (Chen et al., 1997) but lack heat-shock protein responses (Hofmann et al., 2005), hemoglobin (Eastman et al., 1993) and a functional swim bladder (Eastman et al., 1993; Klingenberg & Ekau, 1996).

The monophyly of Notothenioidei was well-established in previous phylogenetic analyses using mitochondrial and nuclear genes (Chen et al., 2003; Dettai & Lecointre, 2004, 2005; Dettai et al., 2012; Smith et al., 2007) and morphological characteristics (Hastings, 1993). To date, only three whole mitogenome sequences from Antarctic fishes have been registered in the GenBank database: *Pleuragramma antarcticum* (NC_015652) (Lee et al., 2014a), *Chaenocephalus aceratus* (NC_015654) (Lee et al., 2014b) and *Notothenia coriiceps* (NC_015653) (Oh et al., 2014).

Table 1. Mitogenome organization of *P. charcoti*.

Gene	Start	End	Direction	Size	Start codon	Stop codon
nad1	1	975	+	975	ATG	TAA
$tRNA^{Ile}$	980	1049	+	70		
$tRNA^{Gln}$	1049	1120	–	72		
$tRNA^{Met}$	1120	1188	–	69		
nad2	1189	2235	+	1047	ATG	TAA
$tRNA^{Trp}$	2235	2305	+	71		
$tRNA^{Ala}$	2307	2375	–	69		
$tRNA^{Asn}$	2377	2449	–	73		
$tRNA^{Cys}$	2491	2559	–	69		
$tRNA^{Tyr}$	2560	2629	–	70		
cox1	2631	4181	+	1551	GTG	TAA
$tRNA^{Ser}$	4182	4252	–	71		
$tRNA^{Asp}$	4254	4324	+	71		
cox2	4327	5025	+	699	ATG	AGA
$tRNA^{Lys}$	5018	5091	–	74		
atp8	5093	5260	+	168	ATG	TAA
atp6	5251	5934	+	684	ATG	TAA
cox3	5958	6743	+	786	ATG	TAA
$tRNA^{Gly}$	6743	6811	+	69		
nad3	6812	7162	+	351	ATG	TAA
$tRNA^{Arg}$	7161	7229	+	69		
nad4l	7230	7526	+	297	ATG	TAA
nad4	7547	8905	+	1359	ATG	AGG
$tRNA^{His}$	8900	8969	+	70		
$tRNA^{Ser}$	8970	9036	+	67		
$tRNA^{Leu}$	9041	9113	+	73		
nad5	9114	10,952	+	1839	ATG	TAA
cytb	11,000	12,196	+	1197	ATG	TAA
$tRNA^{Thr}$	12,141	12,212	+	72		
$tRNA^{Pro}$	12,580	12,649	–	70		
Control region I	12,650	13,557		908		

(*continued*)

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Table 1. Continued

Gene	Start	End	Direction	Size	Start codon	Stop codon
nad6	13,558	14,082	–	525	ATG	AGG
tRNA^{Glu}	14,083	14,151	–	69		
Control region II	14,290	15,351		1062		
tRNA^{Phe}	15,352	15,419	+	68		
tRNA^{Phe}	15,352	15,419	+	68		
rrnS	15,420	16,366	+	947		
tRNA^{Val}	16,367	16,438	+	72		
rrnL	16,440	18,127	+	1688		
tRNA^{Leu}	18,129	18,202	+	74		

In this study, we determined the complete mitochondrial genome sequence for *Parachaenichthys charcoti*, which is one of the 16 species in the Bathydraconidae family. It is hoped that these data will facilitate research on the phylogeny of the Nototheniodei. Specimens of *P. charcoti* were collected by scuba divers from the northern Antarctic Peninsula Marian Cove (62°14′S, 58°47′W) near King Sejong station in January of 2013 from depths of 20–30 m. Genomic DNA was extracted using a DNeasy Tissue Kit (Qiagen, Valencia, CA) then sequenced using the MiSeq platform (Illumina, San Diego, CA) and assembled using the Celera Assembler (ver. 8.0) (Myers et al., 2000). The assembled mitochondrial genome was completed using specific primers and the long PCR method. The complete mitochondrial genome of *P. charcoti*, which consists of an 18,202-bp circular molecule, has been registered in the GenBank database (accession number: KP300644). The overall base composition is A: 25.8%, T: 25.3%, G: 17.9% and C: 31.0%, with an A:T content of 51.1%. The genome contains 13 protein-coding, 23 tRNA and 1 large (*rrnL*) and 1 small (*rrnS*) ribosomal RNA genes (Table 1). Most of the start codons in the protein-coding genes begin with ATG, with the exception of *cox1*, which begins with GTG. *nad4* and *nad6* had AGG stop codons, and *cox2* had AGA stop codons.

Declaration of interest

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

This work was supported by an Antarctic Organisms: Cold-adaptation Mechanism and Its Application grant (PE15070), funded by the Korea Polar Research Institute.

References

Baluskin AV. (1992). Classification, phylogenetic relationships, and origins of the families of the Suborder Notothenioidei (Perciforms). J Ichthyol 32:90–110.

Chen L, Devries AL, Cheng C-HC. (1997). Evolution of antifreeze glycoprotein gene from a trypsinogen gene in Antarctic notothenioid fish. Proc Natl Acad Sci USA 94:3811–16.

Chen W-J, Bonillo C, Lecointre G. (2003). Repeatability of clades as a criterion of reliability: A case study for molecular phylogeny of Acanthomorpha (Teleostei) with larger number of taxa. Mol Phylogenet Evol 26:262–88.

Dettai A, Berkani M, Lautredou A-C, Couloux A, Lecointre G, Ozouf-Costaz C, Gallut C. (2012). Tracking the elusive monophyly of nototheniid fishes (Teleostei) with multiple mitochondrial and nuclear markers. Mar Genomics 8:49–58.

Dettai A, Lecointre G. (2004). In search of notothenioid (Teleostei) relatives. Antarct Sci 16:71–85.

Dettai A, Lecointre G. (2005). Further support for the clades obtained by multiple molecular phylogenies in the acanthomorph bush. C R Biol 328:674–89.

Eakin RR, Eastman JT, Near TJ. (2009). A new species and a molecular phylogenetic analysis of the Antarctic fish genus Pogonophryne (Notothenioidei: Artedidraconidae). Copeia 4:705–13.

Eastman JT. (2005). The nature of the diversity of Antarctic fishes. Polar Biol 28:93–107.

Eastman JT, Pratt D, Winn W. (1993). Antarctic fish biology: Evolution in a unique environment. San Diego: Academic Press.

Hastings P. (1993). Relationships of the fishes of the perciform suborder Notothenioidei. A history and atlas of the fishes of the Antarctic Ocean. Carson City: Foresta Institute for Ocean and Mountain Studies.

Hofmann GE, Lund SG, Place SP, Whitmer AC. (2005). Some like it hot, some like it cold: The heat shock response is found in New Zealand but not Antarctic notothenioid fishes. J Exp Mar Biol Ecol 316:79–89.

Klingenberg CP, Ekau W. (1996). A combined morphometric and phylogenetic analysis of an ecomorphological trend: Pelagization in Antarctic fishes (Perciformes: Nototheniidae). Biol J Linn Soc 59: 143–77.

Lee JE, Lee HS, Lee JK, Choi JE, Park H. (2014a). Complete mitochondrial genome of the Antarctic silverfish, *Pleuragramma antarcticum* (Perciformes, Nototheniidae). Mitochondrial DNA. [Epub ahead of print]. doi:10.3109/19401736.2013.861443.

Lee JE, Lee HS, Lee JK, Jo J, Choi JE, Park H. (2014b). Complete mitochondrial genome of the Antarctic icefish, *Chaenocephalus aceratus* (Perciforms, Channichthyidae). Mitochondrial DNA. [Epub ahead of print]. doi:10.3109/19401736.2013.861444.

Myers EW, Sutton GG, Delcher AL, Dew IM, Fasulo DP, Flanigan MJ, Kravitz SA, et al. (2000). A whole-genome assembly of *Drosophila*. Science 287:2196–204.

Near TJ, Pesavento JJ, Cheng, CHC. (2004). Phylogenetic investigations of Antarctic notothenioid fishes (Perciformes: Notothenioidei) using complete gene sequences of the mitochondrial encoded 16S rRNA. Mol Phylogenet Evol 32:881–91.

Oh JS, Ahn DW, Lee J, Choi J, Chi YM, Park, H. (2014). Complete mitochondrial genome of the Antarctic bullhead notothen, *Notothenia coriiceps* (Perciformes, Nototheniidae). Mitochondrial DNA. [Epub ahead of print]. doi: 10.3109/19401736.2014.947603.

Smith WL, Craig MT, Quattro J. (2007). Casting the percomorph net widely: The importance of broad taxonomic sampling in the search for the placement of serranid and percid fishes. Copeia 2007:35–55.