



Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Antarctic bullhead notothen, *Notothenia coriiceps* (Perciformes, Nototheniidae)

Jae Soon Oh^{1*}, Do Hwan Ahn^{2,3*}, Jongkyu Lee², Jungeun Choi², Young Min Chi¹, and Hyun Park^{2,3}

¹Division of Biotechnology, College of Life Sciences, Korea University, Seoul, Republic of Korea, ²Division of Polar Life Sciences, Korea Polar Research Institute, Yeosu-gu, Incheon, South Korea, and ³Polar Sciences, University of Science & Technology, Yuseong-gu, Daejeon, Korea

Abstract

The complete sequence of the mitochondrial genome of *Notothenia coriiceps* was obtained by genome assembly. The complete sequence was determined to be 18,347 base pairs in length and to contain 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 2 control regions. Of the thirteen protein-coding genes, two genes (*cox1* and *atp6*) had GTG start codons, and six genes (*nad2*, *cox2*, *cox3*, *nad3*, *nad4*, and *cytb*) had incomplete stop codons that require the post-transcriptional addition of A bases. The base composition of the mitogenome was 26.3% A, 27.6% T, 17.5% G, and 28.5% C.

Keywords

Antarctic, complete mitochondrial genome, *Notothenia coriiceps*

History

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Antarctic fish have experienced extraordinary evolutionary episodes in the cold environment of the Southern Ocean for ~34 million years (Clarke et al., 1992; Eastman et al., 1993). Notothenioids are a clade of acanthomorph teleost fishes that contain approximately 129 species (Eastman, 2005) and dominate the Antarctic fish fauna, representing 77% of the species diversity, 92% of the number of individuals, and 91% of the biomass (Eastman & Hubold, 1999). Their rate of endemism is 97% at the species level (Eastman et al., 1993). Research interest in Antarctic fishes is partly due to their physiological and anatomical adaptations to life in cold waters. A number of studies have investigated the general mitochondrial functionality and capacities in Antarctic fish (Hardewig et al., 1999; Urschel & O'Brien, 2008, 2009; Weinstein & Somero, 1998) as key functional traits in thermal acclimatization and adaptation, as they mediate the integration of molecular adaptations into higher functional levels and reflect the energy demands of cells, tissues, and organisms under given environmental conditions (Pörtner, 2002). As a result, considerable progress has been made in understanding the molecular phylogenetics of the Notothenioidae.

Most previous phylogenetic analyses of notothenioids using DNA sequence data have relied exclusively on mtDNA gene sequences (Bargelloni et al., 1994, 2000; Cziko et al., 2006; Derome et al., 2002; Near, 2004; Near et al., 2003). From the perspective of comparative mitogenomics, complete mitogenome

Table 1. Mitogenome organization of *N. coriiceps*.

Gene	Start	End	Direction	Length	Start codon	Stop codon
<i>nad1</i>	1	975	+	975	ATG	TAA
<i>tRNA^{Ile}</i>	980	1049	+	70		
<i>tRNA^{Gln}</i>	1049	1120	–	72		
<i>tRNA^{Met}</i>	1120	1188	+	69		
<i>nad2</i>	1189	2234	+	1046	ATG	TA–*
<i>tRNA^{Trp}</i>	2235	2305	+	71		
<i>tRNA^{Ala}</i>	2307	2375	–	69		
<i>tRNA^{Asn}</i>	2377	2449	–	73		
<i>tRNA^{Cys}</i>	2484	2550	–	67		
<i>tRNA^{Tyr}</i>	2551	2620	+	70		
<i>cox1</i>	2622	4172	+	1551	GTG	TAA
<i>tRNA^{Ser}</i>	4173	4243	–	71		
<i>tRNA^{Asp}</i>	4245	4315	+	71		
<i>cox2</i>	4318	5008	+	691	ATG	T––*
<i>tRNA^{Lys}</i>	5009	5082	+	74		
<i>atp8</i>	5084	5251	+	168	ATG	TAG
<i>atp6</i>	5230	5925	+	696	GTG	TAG
<i>cox3</i>	5958	6742	+	785	ATG	TA–*
<i>tRNA^{Gly}</i>	6743	6812	+	70		
<i>nad3</i>	6813	7161	+	349	ATG	T––*
<i>tRNA^{Arg}</i>	7162	7230	+	69		
<i>nad4l</i>	7231	7527	+	297	ATG	TAA
<i>nad4</i>	7521	8901	+	1381	ATG	T––*
<i>tRNA^{His}</i>	8902	8970	+	69		
<i>tRNA^{Ser}</i>	8971	9037	+	67		
<i>tRNA^{Leu}</i>	9042	9114	+	73		
<i>nad5</i>	9115	10,953	+	1839	ATG	TAG
<i>cytb</i>	11,246	12,386	+	1141	ATG	T––*
<i>tRNA^{Thr}</i>	12,387	12,458	+	72		
<i>Control region I</i>	12,459	13,381	+	923		
<i>nad6</i>	13,382	13,906	–	525	ATG	TAG
<i>tRNA^{Glu}</i>	13,907	13,975	–	69		
<i>tRNA^{Pro}</i>	14,043	14,112	–	70		
<i>Control region 2</i>	14,113	15,492	+	1380		

*These authors contributed equally to this work

Correspondence: Hyun Park, Division of Polar Life Sciences, Korea Polar Research Institute, Yeosu-gu, Incheon 406840, South Korea. E-mail: hpark@kopri.re.kr (H. Park).

Young Min Chi, Division of Biotechnology, College of Life Sciences, Korea University, Seoul, Republic of Korea. E-mail: ezeg@korea.ac.kr (Y.M. Chi)

(continued)

Table 1. Continued

Gene	Start	End	Direction	Length	Start codon	Stop codon
<i>tRNA^{Phe}</i>	15,493	15,560	+	68		
<i>rrnS</i>	15,561	16,508	+	948		
<i>tRNA^{Val}</i>	16,509	16,580	+	72		
<i>rrnL</i>	16,581	18,273	+	1693		
<i>tRNA^{Leu}</i>	18,274	18,347	+	74		

*The asterisks represent the premature stop codons which require the post-transcriptional addition of A bases.

information from diverse Antarctic fishes is necessary for understanding the evolution of Antarctic fish species. However, only two whole mitogenome sequences from Antarctic fishes are presently registered in the GenBank database: *Pleuragramma antarcticum* (NC_015652; Lee et al., 2014a) and *Chaenocephalus aceratus* (NC_015654; Lee et al., 2014b).

In this study, to better understand the evolution of Antarctic fishes, we determined the complete mitochondrial genome sequence of *Notothenia coriiceps*, which can be exploited in phylogenetic studies using comparative genomics. Samples were collected from the sea near Barton Peninsula, King George Island, West Antarctica (62°14' S, 58°47' W), from December 2009 through January 2010. Genomic DNA was sequenced using a GS-FLX system and the total sequence information was assembled using Newbler software (Roche, Basel, Switzerland). The assembled mitochondrial genome was completed with specifically designed primers and the long PCR method. The complete sequence of the mitochondrial genome of *N. coriiceps* was 18,347 base pairs in length and has been registered in the GenBank database (accession number NC_015653). The sequence contained 13 protein-coding genes (PCGs), 22 tRNA genes, 1 large (*rrnL*) and 1 small (*rrnS*) ribosomal RNA genes, as seen in most metazoans (Table 1). The start and stop codons were divergent in several genes. For example, *cox1* and *atp6* had GTG start codons, while six genes, *nad2*, *cox2*, *cox3*, *nad3*, *nad4*, and *cytb*, had incomplete stop codons that require the post-transcriptional addition of A bases. The base composition of the mitogenome was 26.3% A, 27.6% T, 17.5% G, and 28.5% C.

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 Antarctic organisms: Cold-adaptation mechanism and its application grant (PE14070) funded by the Korea Polar Research Institute (KOPRI).

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