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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Antarctic icefish, *Chaenocephalus aceratus* (Perciforms, Channichthyidae)

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Abstract

The complete sequence of the mitochondrial genome of the Antarctic icefish *Chaenocephalus aceratus* was determined to be 17311 bp in length, and to contain 13 protein coding genes (PCGs), 22 tRNA genes and 2 rRNA genes. The total A + T content is 52.8%. The notothenioid-exclusive ND6/tRNA^{Glu} translocation was observed in the mitogenome of *C. aceratus*. Generally, the order and contents of the other genes are identical with those of other fishes. Antarctic icefishes, the only vertebrates which do not have hemoglobins, have evolved to survive sub-freezing temperature. Therefore, the whole mitogenome sequences of *C. aceratus* will provide the insights into resolving the evolutionary history of icefish.

Keywords

Antarctic, *Chaenocephalus aceratus*, complete mitochondrial genome

History

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Antarctic fish fauna is unique for two reasons of high degree of endemism and a single dominant taxonomic group by the perciform suborder Notothenioidei (Eastman, 2005). Following the separation of the Antarctica from the continent and the development of the circumpolar currents, the decreasing water temperature and the expansion of glaciers resulted in extinction of most ancient fish fauna. The suborder Notothenioidei, however, has filled the available niches in isolated marine environment and undergone a remarkable diversification by adaptive radiation (Eastman & McCune, 2000; Mintenbeck et al., 2012). The analysis of mitochondrial DNA sequences suggests that the major radiation of Antarctic nototheteniods began ~21 MYA and that Channichthyidae, the most diversified notothenioid family, might appear at the boundary between Miocene and Pliocene (8-2MYA) (Bargelloni et al., 2000). Antarctic icefishes, which belong to the family Channichthyidae perciformes suborder Notothenioidei, are the only vertebrates which do not have hemoglobin in their blood resulted from genetic mutations in the globin loci (Near et al., 2006; Ruud, 1954). The loss of hemoglobin has been considered as a molecular adaptation to compensate for the increased fluid viscosity by low temperature or to reduce the metabolic energy to carry oxygen under hyperoxidative environment (Egginton, 1996; Mintenbeck et al., 2012). The molecular evidences which show the evolutionary clade of the family have been identified by phylogenetic analyses using nuclear and mitochondrial DNA. However, studies on the molecular phylogenetic evolution of the Notothenioidei species have been dependent on the sequence variation of a single gene (Bargelloni et al., 2000; Lautrédou et al., 2012; Near & Cheng, 2008; Near et al., 2004). In this study, we report the complete mitochondrion genome sequences of *Chaenocephalus aceratus*, one of the 16 species of Antarctic channichthyidae icefish, which could be exploited for the comparative mitogenomics.

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The samples were collected from the sea near Barton Peninsula, King George Island, West Antarctica (62°14′S, 58°47′W) from December 2009 to January 2010. We sequenced the genomic DNA of *C. aceratus* using NGS technologies GS-FLX system and assembled with Newbler (Roche, Basel, Switzerland). The assembled mitochondrial genome was completed with the Long-PCR method. The complete sequence of the mitochondrial genome of *C. aceratus* was found to be 17,311 bp in length and registered in GenBank (accession number: NC_015654). It contains 13 protein coding genes, 22 tRNA genes and 2 rRNAs, as are found in most metazoans (Table 1). The recently found notothenioid-exclusive translocation of ND6/tRNA^{Glu} (Zhuang & Cheng, 2010) was also observed in the

Table 1. Mitogenome organization of *C. aceratus*.

Gene	Start	End	Direction	Size	Start codon	Stop codon
ND1	1	975	+	975	ATG	TAA
tRNA-Ile	980	1049	+	70		
tRNA-Gln	1049	1120	−	72		
tRNA-Met	1120	1188	+	69		
ND2	1189	2234	+	1046	ATG	TA–*
tRNA-Trp	2235	2305	+	71		
tRNA-Ala	2307	2375	−	69		
tRNA-Asn	2377	2449	−	73		
tRNA-Cys	2485	2551	−	67		
tRNA-Tyr	2552	2619	−	68		
COX1	2621	4171	+	1551	GTG	TAA
tRNA-Ser	4172	4242	−	71		
tRNA-Asp	4244	4314	+	71		
COX2	4317	5007	+	691	ATG	T––*
tRNA-Lys	5008	5081	+	74		
ATP8	5083	5250	+	168	ATG	TAG
ATP6	5229	5924	+	696	GTG	TAA
COX3	5962	6746	+	785	ATG	TA–*
tRNA-Gly	6747	6816	+	70		

(*continued*)

Table 1. Continued

Gene	Start	End	Direction	Size	Start codon	Stop codon
ND3	6817	7165	+	349	ATG	T–-*
tRNA-Arg	7166	7234	+	69		
ND4L	7235	7531	+	297	ATG	TAA
ND4	7525	8905	+	1381	ATG	T–-*
tRNA-His	8906	8974	+	69		
tRNA-Ser	8975	9041	+	67		
tRNA-Leu	9046	9118	+	73		
ND5	9119	10,960	+	1842	ATG	AGA
Cytb	11,066	12,206	+	1141	ATG	T–-*
tRNA-Thr	12,207	12,278	+	72		
ND6	12,452	12,976	–	525	ATG	AGG
tRNA-Glu	12,977	13,045	–	69		
tRNA-Pro	13,084	13,153	–	70		
tRNA-Phe	14,458	14,525	+	68		
12S rRNA	14,526	15,472	+	947		
tRNA-Val	15,473	15,544	+	72		
16S rRNA	15,545	17,237	+	1693		
tRNA-Leu	17,238	17,311	+	74		
Misc-features						
Non-coding region	12,279	12,451		173		
Control region	13,154	14,457		1304		
Repeat region	13,771	14,238		358		

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

mitogenome of *C. aceratus*. The base composition of mitogenome is 26.6% A, 26.2% T, 17.4% G and 29.8% C. The divergent start codons and stop codons were found in several genes. For example, *C. aceratus* uses GTG as a start codon for COX1 and ATP6, and AGA and AGG as stop codons for ND5 and ND6, respectively. In addition, 6 PCGs (6/13; ND2, COX2, COX3, ND3, ND4 and Cytb) have an incomplete stop codons that require the post-transcriptional addition of A bases.

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 Functional Genomics on Polar Organisms grant (PE13020) funded by Korea Polar Research Institute (KOPRI).

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