



## Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

**Complete mitochondrial genome of the Antarctic silverfish, *Pleuragramma antarcticum* (Perciformes, Nototheniidae)**

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**Abstract**

The complete sequence of the mitochondrial genome of *Pleuragramma antarcticum* was obtained from the assembled genome data. The complete sequence was determined to be 18,460 bp in length, containing 13 protein coding genes, 22 tRNA genes, 2 rRNA genes, 2 control regions and a repeat. The general order and contents of the genes are identical with those of other fishes. The Antarctic notothenioid-specific translocation of ND6/tRNA<sup>Glu</sup> exists in the mitogenome. *Pleuragramma antarcticum* is the only pelagic species which dominates Antarctic fish fauna by more than 90%. Thus, the whole mitogenome sequences of *P. antarcticum* will provide the basis to understand the deep phylogeny of the Antarctic species.

**Keywords**

Antarctic, complete mitochondrial genome, *Pleuragramma antarcticum*

**History**

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The Antarctic silverfish, *Pleuragramma antarcticum* (notothenioid), inhabit thermally isolated Antarctic Ocean where temperature is close to the freezing point of seawater at  $-1.9^{\circ}\text{C}$  with little seasonal variation. *Pleuragramma antarcticum* is an endemic species which is widely distributed and dominates in fish biomass by 90% in coastal water of South polar sea (Eastman, 1985; Hubold & Ekau, 1990). It is one of few pelagic species of the suborder Notothenioidei, living in water column in all developmental stages from egg to adult (Vacchi et al., 2004). Because of its wide distribution and high biomass, the Antarctic silver fish has been considered as a key species in the Antarctic marine food web. It serves as important nutrition sources for upper predators such as penguins, skuas, seals or other fishes, linking between lower and upper trophic levels in Antarctic marine ecosystem (Bottaro et al., 2009; La Mesa et al., 2004). To successfully inhabit in the pelagic zone of Antarctic sea waters, *P. antarcticum* has evolved life-history strategies based on a set of ecological, physiological and morphological adaptations, such as stage-specific specialized behaviors, possession of AFGPs (anti-freezing glycoproteins) and neutral buoyancy (La Mesa & Eastman, 2012).

In this study, to better understand the evolution of the Antarctic fishes, we report the complete mitochondrion genome sequences of *P. antarcticum*, which can be exploited in a phylogenetic study using comparative genomics. The samples were collected from the sea near Barton Peninsula, King George Island, West Antarctica ( $62^{\circ}14'S$ ,  $58^{\circ}47'W$ ) from December 2009 to January 2010. Genomic DNA was sequenced by GS-FLX system and assembled with a Newbler (Roche, Basel, Switzerland). The assembled mitochondrial genome was completed with Long-PCR method. The complete sequence of the mitochondrial genome of *P. antarcticum* was found to be 18,460 bp in length and registered

in GenBank database (accession number: NC\_015652). It contains 13 protein coding genes (PCGs), 24 tRNA genes, 16S rRNA and 12S rRNA, as in most metazoan (Table 1). The Antarctic notothenioid-exclusive translocation of ND6/tRNA<sup>Glu</sup> (Zhuang & Cheng, 2010) was also found in the mitogenome

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

Gene	Start	End	Direction	Size	Start codon	Stop codon
ND1	1	975	+	975	ATG	TAG
tRNA-Ile	980	1049	+	70		
tRNA-Gln	1120	1049	-	72		
tRNA-Met	1120	1188	+	69		
ND2	1189	2235	+	1047	ATG	TAA
tRNA-Trp	2235	2305	+	71		
tRNA-Ala	2375	2307	-	69		
tRNA-Asn	2449	2377	-	73		
tRNA-Cys	2552	2485	-	68		
tRNA-Tyr	2622	2553	-	70		
COX1	2624	4174	+	1551	GTG	TAA
tRNA-Ser	4245	4175	-	71		
tRNA-Asp	4247	4317	+	71		
COX2	4320	5010	+	691	ATG	T--*
tRNA-Lys	5011	5084	+	74		
ATP8	5086	5253	+	168	ATG	TAA
ATP6	5232	5927	+	696	ATG	TAA
COX3	5957	6742	+	786	ATG	TAA
tRNA-Gly	6742	6811	+	70		
ND3	6812	7162	+	351	ATG	TAG
tRNA-Arg	7161	7229	+	69		
ND4L	7230	7526	+	297	ATG	TAA
ND4	7520	8900	+	1381	ATG	T--*
tRNA-His	8901	8969	+	69		
tRNA-Ser	8970	9036	+	67		
tRNA-Leu	9041	9113	+	73		
ND5	9114	10,952	+	1839	ATG	TAA
CytB	11,013	12,153	+	1141	ATG	T--*
tRNA-Thr	12,154	12,225	+	72		

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(continued)

Table 1. Continued

Gene	Start	End	Direction	Size	Start codon	Stop codon
tRNA-Pro	12,294	12,225	–	70		
Control region I	12,295	13,484	+	1190		
Repeat region	13,341	13,432	+	92		
ND6	14,009	13,485	–	525	GTG	AGG
tRNA-Glu	14,078	14,010	–	69		
tRNA-Thr	14,144	14,215	+	72		
tRNA-Pro	14,284	14,215	–	70		
Control region II	14,285	15,603	+	1319		
tRNA-Phe	15,604	15,671	+	68		
12S rRNA	15,672	16,619	+	948		
tRNA-Val	16,620	16,691	+	72		
16S rRNA	16,692	18,386	+	1695		
tRNA-Leu	18,387	18,460	+	74		

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

sequence of *P. antarcticum*. The start codons and stop codons were divergent in several genes. For example, COX1 gene has a GTG start codon and the ND6 has a GTG start codon and an AGG stop codon. In addition, three genes – COX2, ND4 and CytB – have incomplete stop codons that require the post-transcriptional addition of A bases. The base composition of the mitogenome is 25.4% A, 26.7% T, 18.5% G and 29.3% 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 Functional Genomics on Polar Organisms grant (PE13020) funded by Korea Polar Research Institute (KOPRI).

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