



Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the South Polar Skua *Stercorarius maccormicki* (Charadriiformes, Stercorariidae) in Antarctica

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Abstract

The South Polar Skua, gull-like seabirds is the most fascinating Antarctic seabirds that lay two eggs at sites free of snow and ice and predominantly hunt pelagic fish and penguins. Blood samples of the South Polar Skua *Stercorarius maccormicki* was collected during the summer activity near King Sejong station in Antarctica. The complete mitochondrial DNA sequence of *S. maccormicki* was 16,669 bp, showing conserved genome structure and orientation found in other avian species. The control region of *S. maccormicki* was 93- and 80 bp shorter compared to those of *Chroicocephalus saundersi* and *Synthliboramphus antiquus* respectively. Interestingly, there is a (CAACAAACA)₆ repeat sequence in the control region. Our results of *S. maccormicki* mt genome including the repeat sequence, may provide useful genetic information for phylogenetic and phylogeographic histories of the southern skua complex.

Keywords

Antarctica, complete mitochondrial genome, simple sequence repeat, South Polar Skua, *Stercorarius maccormicki*

History

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The South Polar Skua (*Stercorarius maccormicki*) is the most fascinating Antarctic seabirds that are closely related to gulls. They are abundant around the Antarctic coastline but can be found as far as the North Pacific and Atlantic Oceans (Eklund, 1961). The South Polar Skua breeds around the Antarctic coast and on the offshore South Shetland Islands; they lay two eggs at sites free of snow and ice and predominantly hunt pelagic fish and penguins (Kim et al., 2010). They have been the subject of research in the Antarctic for decades because phylogenetic history of the Southern Hemisphere seabird group, including South Polar Skua

and Brown Skua, is thought to reflect the Antarctic glaciation. However, frequent hybridizations amongst different southern taxa (e.g. between Brown Skua and South Polar Skua, between Chilean and Falkland Skua or between South Polar Skua and Chilean Skua) make it difficult to analyze their population divergence, speciation and classification (Ritz et al., 2008).

As mitochondrial DNA information has revealed the presence of hybrids and significant gene flow between populations of different southern taxa (Reinhardt et al., 1997; Ritz et al., 2008), larger-scale information such as that pertaining to full structure

Table 1. Mitochondrial genome organization of *S. maccormicki*.

Gene/region	Position		Size		Codons		Intergenic sequence
	Start	Finish	No. of nt	No. of aa	Initiation	Termination	
<i>Cox1</i>	1	1548	1548	516	GTG	AGG	–6
<i>trnS2^{UGA}</i>	1616	1543	74				2
<i>trnD</i>	1619	1687	69				1
<i>Cox2</i>	1689	2369	681	227	ATG	TAA	4
<i>trnK</i>	2374	2443	70				1
<i>Atp8</i>	2445	2615	171	57	ATG	TAA	–7
<i>Atp6</i>	2609	3289	681	227	ATG	TAA	2
<i>Cox3</i>	3292	4074	783	261	ATG	T	0
<i>trnG</i>	4075	4145	71				–1
<i>Nad3</i>	4145	4493	349	106	ATC	TAA	8
<i>trnR</i>	4502	4569	68				1
<i>Nad4L</i>	4571	4864	294	98	ATG	TAA	–4
<i>Nad4</i>	4861	6237	1377	459	ATG	T	1
<i>trnH</i>	6239	6308	70				0

(continued)

Table 1. Continued

Gene/region	Position		Size		Codons		Intergenic sequence
	Start	Finish	No. of nt	No. of aa	Initiation	Termination	
<i>trnS1^{GCU}</i>	6309	6373	65				–1
<i>trnL1^{UAG}</i>	6373	6444	72				0
<i>Nad5</i>	6445	8256	1812	604	ATG	AGA	15
<i>Cytb</i>	8272	9411	1140	380	ATG	TAA	6
<i>trnT</i>	9418	9487	70				12
<i>trnP</i>	9571	9500	72				21
<u><i>Nad6</i></u>	10,111	9593	519	173	ATG	TAG	3
<u><i>trnE</i></u>	10,185	10,115	71				0
<i>CR</i>	10,186	11,271	1086				0
<i>trnF</i>	11,272	11,342	71				0
<i>rrnS</i>	11,343	12,323	981				0
<i>trnV</i>	12,324	12,396	73				0
<i>rrnL</i>	12,397	13,994	1598				0
<i>trnL2^{UAA}</i>	13,995	14,068	74				8
<i>Nad1</i>	14,077	15,051	975	325	ATG	AGG	0
<i>trnI</i>	15,052	15,125	74				8
<u><i>trnQ</i></u>	15,204	15,134	71				–2
<i>trnM</i>	15,203	15,272	70				0
<i>Nad2</i>	15,273	16,310	1038	346	ATA	TAG	1
<i>trnW</i>	16,312	16,384	73				0
<u><i>trnA</i></u>	16,453	16,385	69				2
<u><i>trnN</i></u>	16,529	16,456	74				2
<u><i>trnC</i></u>	16,598	16,532	67				–1
<u><i>trnY</i></u>	16,668	16,598	71				1
							77

Stop codons were not included; Underlined genes/tRNAs are reverse transcribed; nt, nucleotide; aa, amino acid.

and sequences of mt genome is required to assess breeding success and frequency of hybridization as well as phylogeography of the skua complex.

Blood and tissue samples of the South Polar Skua was collected during summer field trip to King Sejong Station in Antarctica (62°13'26.67" S, 58°47'32.85" W) in 2012 and 2013. After extraction of total genomic DNA by using DNeasy Blood & Tissue Kit (Qiagen, Hilden, Germany), DNA was sequenced using Illumina sequencing genome analyzer (Macrogen, Seoul, Korea) and gene assembly and annotation were performed by following the methods of Kim et al. (2013).

The complete mt genome of *S. maccormicki* was 16,669 bp (accession no. KM401546) and it contained the typical set of 13 protein-coding genes (PCGs), 2 rRNA genes, 22 tRNAs, and a control region (CR) (Table 1). The nucleotide composition of the entire *S. maccormicki* mt genome consisted of 30.9% A, 24.4% T, 30.8% C, 13.8% G and 55.3% AT content. While most genes use a common start and stop codon, *Cox1* began with GTG and ended with AGG whereas *Nad5* ends with AGA. The genome structure and orientation were identical to those of avian species previously published; however mt genome sequences of *S. maccormicki* differ in length from those of closely related species *Chroicocephalus saundersi* and *Synthliboramphus antiquus* mt genomes (Ryu & Hwang, 2012). The *S. maccormicki* mt genome was 56- and 61 bp shorter than those of *C. saundersi* (16,725 bp) and *S. antiquus* (16,730 bp), respectively, although the intergenic regions were longer (29 and 22 bp) than those of *C. saundersi* (48 bp) and *S. antiquus* (55 bp), respectively. These length discrepancies were mainly due to the CR because *S. maccormicki* CR is 93- and 80 bp shorter compared to those of *C. saundersi* (1179 bp) and *S. antiquus* (1166 bp). Interestingly, the CR of *S. maccormicki* contains (CAACAAACAA)₆ repeat sequences. The presence of simple sequence repeats was usually associated with heteroplasmy and varies within and between populations

(Mundy et al., 1996; Ritchie & Lambert, 2000). Therefore, the *S. maccormicki* genome including the repeat sequence, may provide useful genetic information for phylogenetic and phylogeographic histories of the southern skua complex.

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 Basic Research Program of the Korea Polar Research Institute (PE14020).

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