

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Antarctic amphipod
Gondogeneia antarctica (Crustacea, amphipod)

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Abstract

The complete sequence of the mitochondrial genome of the Antarctic amphipod *Gondogeneia antarctica* was determined to be 18,424 bp in length, and to contain 13 protein-coding genes (PCGs), 22 tRNA genes, and large (*rrnL*) and small (*rrnS*) rRNA genes. Its total A + T content is 70.1%. The *G. antarctica* mitogenome is the largest known among those of crustaceans, due to the existence of two relatively large intergenic non-coding sequences. The PCG arrangement of *G. antarctica* is identical to that of the ancestral pancrustacean ground pattern, although the tRNA arrangement differs somewhat. The complete mitogenome sequences of 68 species of pancrustacea have been added to the NCBI database, only 4 of which represent complete mitogenome sequences from amphipods. This is the first report of a mitogenome sequence of an Antarctic amphipod, and provides insights into the evolution of crustacean mitochondrial genomes, particularly in amphipods.

Keywords: Antarctic, *Gondogeneia antarctica*, complete mitochondrial genome

Amphipods (class Malacostraca) are important members of the macrofaunal community in aquatic environments, and are a vital link in food webs, feeding on smaller plankton and being consumed by larger predators such as fish (Hop et al. 2000). Amphipods in Antarctica exhibit a high degree of endemism, with nearly 40% of genera and 90% of species being endemic (Knox and Lowry 1977). The amphipod *Gondogeneia antarctica* (Chevreux 1906) belongs to the family Pontogeneiidae and is an abundant species in the sublittoral zone of West Antarctica, accounting for about 61% of amphipods in the sublittoral zone of Admiralty Bay (Jazdzewski et al. 2001). Several studies on the importance of this endemic species have focused on potential sentinel species for Antarctic environmental changes, such as the impact of solar ultraviolet radiation (Obermuller

et al. 2005, 2007; Gomes et al. 2009). Specimens of *G. antarctica* were collected from intertidal zones in Marian Cove and on Barton Peninsula, King George Island, West Antarctica (62°14'S, 58°47'W) between 2009 and 2010. Genomic DNA was extracted using a DNeasy Tissue Kit (Qiagen, Valencia, CA, USA). The partial sequences of *cox1*, *cytb*, and *nad5* were initially determined using a pyrosequencing database for this species (unpublished data). The nucleotide sequences for each of the partial gene fragments were then used to design specific primers for long PCR amplification. The complete sequence of the mitochondrial genome of *G. antarctica* (GenBank accession number: JN827386) was found to be 18,424 bp in length, and to contain 13 protein-coding genes (PCGs), 22 tRNA genes, and large (*rrnL*) and small (*rrnS*) ribosomal RNA subunits genes, as are found in

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Table I. Mitogenome organization of *G. antarctica*.

Gene	Location*	Size (bp)	Start codon	Stop codon	Intergenic nucleotides†	Anti-codon
<i>cytb</i>	1–1155	1155	ATG	TAA		
tRNA ^{Ser}	1139–1201	63			–16	TGA
<i>nad1</i>	(1228–2145)	918	ATT	TAA	27	
tRNA ^{Cys}	(2181–2240)	60			36	GCA
tRNA ^{Phe}	(2239–2298)	60			–1	GAA
tRNA ^{Tyr}	2328–2386	59			30	GTA
tRNA ^{Gln}	(2390–2451)	62			4	TTG
tRNA ^{Leu}	(2451–2515)	65			0	TAG
<i>rrnL</i>	2507–3610	1104			–8	
tRNA ^{Val}	(3558–3618)	61			–2	TAC
<i>rrnS</i>	3611–4465	855			–7	
tRNA ^{Ile}	5705–5767	63			1240	GAT
tRNA ^{Met}	5767–5830	64			0	GAT
<i>nad2</i>	5885–6682	798	ATT	TAA	55	
tRNA ^{Trp}	7078–7145	68			396	TCA
tRNA ^{Gly}	8977–9040	64			1832	TCC
<i>cox1</i>	9098–10,594	1497	ATG	TAA	58	
tRNA ^{Leu}	10,699–10,760	62			105	TAA
<i>cox2</i>	10,760–11,437	678	ATA	TAA	0	
tRNA ^{Asp}	11,550–11,613	64			113	GTC
tRNA ^{Lys}	11,612–11,673	62			–1	TTT
<i>atp8</i>	11,712–11,867	156	ATT	TAA	39	
<i>atp6</i>	11,861–12,532	672	ATG	TAA	–6	
<i>cox3</i>	12,532–13,320	789	ATG	TAA	0	
<i>nad3</i>	13,346–13,681	336	ATA	TAA	26	
tRNA ^{Ala}	13,679–13,740	62			–2	TGC
tRNA ^{Ser}	13,738–13,789	51			–2	TCT
tRNA ^{Asn}	13,787–13,850	64			–2	GTT
tRNA ^{Glu}	13,855–13,918	64			5	TTC
tRNA ^{Arg}	13,921–13,981	61			3	TCG
<i>nad5</i>	(13,978–15,678)	1701	ATT	TAA	–3	
tRNA ^{His}	(15,678–15,739)	62			0	GTG
<i>nad4</i>	(15,683–17,056)	1374	ATG	TAA	–56	
<i>nad4L</i>	(17,050–17,346)	297	ATG	TAG	–6	
tRNA ^{Thr}	17,802–17,863	62			456	TGT
tRNA ^{Pro}	(17,862–17,922)	61			–1	TGG
<i>nad6</i>	17,925–18,424	500	ATG	TA‡	0	

* Parentheses denote that the gene is encoded on the light strand; † Numbers correspond to the nucleotides separating genes. Negative numbers indicate overlapping nucleotides between adjacent genes; ‡ Truncated termination codon.

most metazoans (Table I). Of the 37 genes, 11 (4 PCGs and 7 tRNA genes) are on the heavy strand, and 26 on the light strand. Three overlaps between PCGs and five overlaps between PCGs and tRNA genes were identified in the mitogenome of *G. antarctica*. The *G. antarctica* mitogenome is the largest known among those of crustaceans, due to the existence of two relatively large intergenic non-coding sequences. The average mitochondrial genome size of 68 known pancrustaceans (crustaceans + hexapoda) is 15,725 bp. The size expansion of two non-coding regions, one between the *nad2* and *cox1* genes and the other between the *rrnS* and *nad2* genes, was notable. These regions contain two tRNA genes, and two tRNA genes and putative control region, respectively. This is presumably one of the causes for the mitogenome being so large. The nucleotide composition of the strand encoding most of the proteins in the *G. antarctica* mitogenome (the light strand) was

34.8% A (6420 bases), 35.3% T (6501), 19.3% C (3549), and 10.6% G (1954). The total A + T content is 70.1%. Seven of the 13 PCGs in the *G. antarctica* mitogenome started with the orthodox ATG initiation codon, four with an ATT codon, and two with an ATA codon. Putative translation stop codons for 11 of 13 genes are TAA (the *nad4L* gene employs a TAG codon and the *nad6* gene a truncated TA termination codon). The PCG arrangement of *G. antarctica* is identical to that of the ancestral pancrustacean ground pattern (Boore et al. 1995, 1998), although differences exist in the tRNA gene arrangement.

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