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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Antarctic barnacle *Lepas australis* (Crustacea, Maxillopoda, Cirripedia)

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Abstract

We present the complete mitochondrial genome of the Antarctic barnacle *Lepas australis* (Cirripedia, Thoracica, Lepadidae). The genome sequence is 15,502 bp in size. Except for *CO1*, 12 protein-coding genes (PCGs) start with an ATN initiation codon (ATA, ATG, ATC and ATT). Twelve PCGs were terminated with TAA or TAG stop codon, whereas *ND1* possessed an incomplete termination codon (T– –). We compared the mitogenome structure of *L. australis* to those of other cirripeds and a typical arthropod *Homarus americanus*. The PCGs in the *L. australis* mtgenome showed a typical gene arrangement, identical to the arthropod pattern in other cirriped genomes. However, at least 8 tRNA genes were translocated and 2 tRNA genes were inverted in the coding polarity. Unique differences in *L. australis* mtgenome included translocation of *trnS2*, *trnD* and *trnI*. These results are useful for understanding the phylogenetic relationships among cirripedians, and additional mtgenome information of barnacles including the polar species would allow exploration of the thoracican relationships and mtgenome modifications in the barnacle evolution.

Keywords

Antarctic barnacle, Cirripedia, complete mitochondrial genome, *Lepas australis*

History

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Lepas australis (Darwin, 1851) is the most common goose barnacle in the subantarctic region. This species is most frequently encountered attached to floating objects such as driftwood, buoys, bulk kelps, or other artefacts. Antarctic ecosystems are believed to be isolated, but Antarctic- and subantarctic fur seals regularly cross the Antarctic Polar Front (APF) along with their obvious parasites, goose barnacles. Recent studies report that goose barnacles are important passengers of floating bulk kelp from the subantarctic region to mainland New Zealand, providing valuable information for estimation of the duration of kelp-rafting by their body size for trans-oceanic origin studies (Fraser et al., 2010). Mitochondrial DNA sequences were successfully applied to identify the genetic variation between intra/inter-species and the gene flow patterns for phylogenetic and biogeographic studies. In this study, we sequenced the complete mitochondrial genome of *L. australis* (Cirripedia, Thoracica, Lepadidae) and the sequence structure was compared with that of four other species of Thoracica with reference to a linearized representation of each mitochondrial genome (Begum et al., 2004; Kim et al., 2011; Lim & Hwang, 2006) (Figure 1).

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The specimens were collected from the kelp rafts in the intertidal zone of Marian cove (62°12′38″S, 58°45′48″W) near King Sejong Station during the activity performed in summer 2012 in Antarctica. The complete mtgenome of *L. australis* was 15,502 bp in length (accession no. KM017964), containing the typical set of 13 protein-coding genes (PCGs), 2 rRNA genes, 22 tRNAs, and a control region (CR). The nucleotide composition of the entire *L. australis* mtgenome was 33% A, 34.5% T, 18.2% C, and 14.2% G and 67.5% A + T content. Except for *CO1*, whose start codon is AAA instead of the ATN initiation codon that is mostly used in metazoan mitochondrial PCGs (Shen et al., 2009), most genes in *L. australis* use common start codon. Twelve PCGs were terminated with TAA or TAG stop codon, whereas *ND1* had an incomplete termination codon (T– –). *Lepas australis* seemed to have a longer CR of 444 bp between *rrnS* and *trnS2* as compared to CRs of other four cirripeds (263–370 bp). The 22 tRNA genes ranged from 57 ($trnS1^{UCU}$) to 75 (*trnK*) nucleotides in length.

The PCGs in all cirriped mtgenomes including *L. australis* showed the typical arthropod ground pattern except for *ND5-ND4L* inversion in *M. volcano*. However, at least 8 tRNA genes were translocated and 2 tRNA genes were inverted in the coding polarity in *L. australis* mtgenome. In addition, it showed the conserved tRNA blocks, *R-N-A-E-S1* like other cirriped mtgenomes, instead of the basal arthropod pattern *A-R-N-S1-E-F* (Dowton et al., 2003). Interestingly, *L. australis* mtgenome had *trnD* located between *trnL2-CO2* in contrast with 7 other cirripeds. Moreover, unique differences in *L. australis* mtgenome were the positions of *trnS2* and *trnI*. The *trnS2* was located after *Cytb* in all 7 cirripeds known to have a typical arthropod pattern, but *L. australis trnS2* was located after CR. Instead, *trnI* was

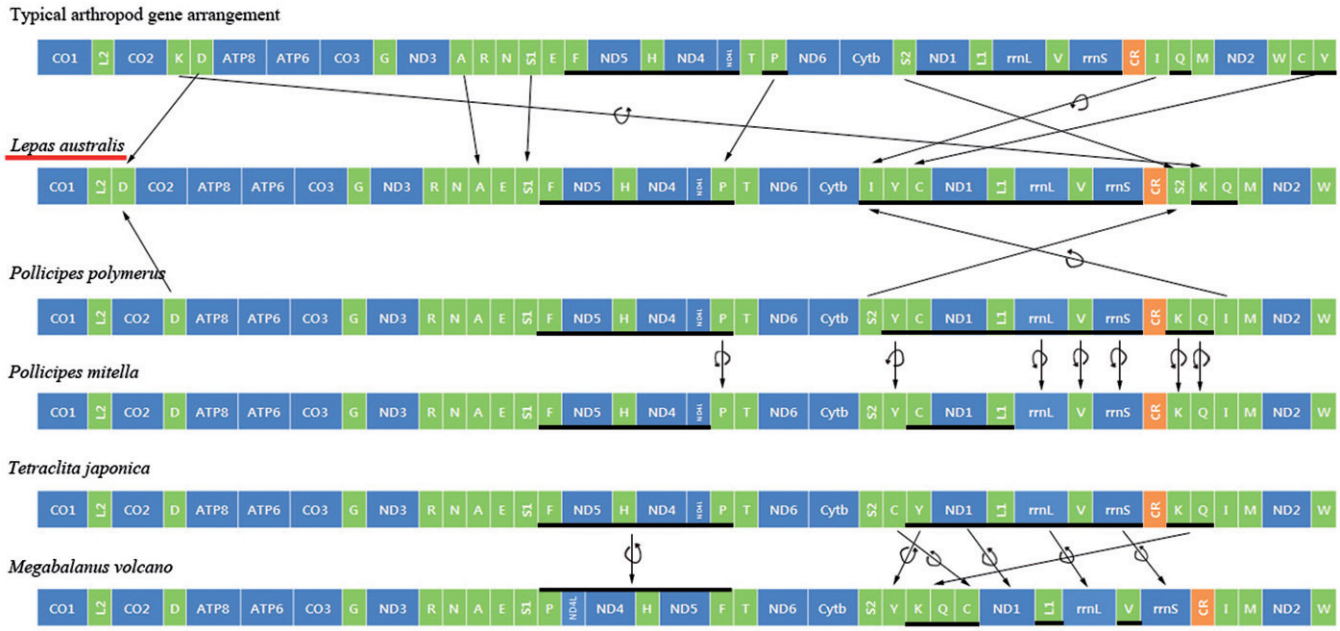

Figure 1. Comparison of the gene arrangements in cirriped mitochondrial genomes and typical arthropod (*Homarus americanus*). Mitochondrial genome gene arrangement of *Pollicipes polymerus* (Thoracica, Pedunculata), *P. mitella* (Thoracica, Pedunculata), *Tetraclita japonica* (Thoracica, Sessilia), *Megabalanus volcano* (Thoracica, Sessilia), and *Lepas australis* (Thoracica, Pedunculata) are shown. Underlines indicate the reverse polarity. The accession numbers of the genomes used for comparison were NC006293 (*M. volcano*), NC008974 (*T. japonica*), AY456188 (*P. polymerus*), and AY514042 (*P. mitella*).

translocated after *Cytb*, which was not observed in other cirripeds mtgenomes. These characteristic differences may be specific to the Lepadidae family or may have resulted from adaptation to the geographic range and the harsh environmental conditions. *Lepas australis* larvae provide an important food source for the grey-backed storm petrels and young fish at all other localities in the subantarctic ecosystem. Therefore, our data will facilitate the assessment of occurrences, diversification, and trans-oceanic dispersal of free-living larvae of polar barnacles. Additional mtgenome information of barnacles, including information on the polar species, would aid in the exploration of the thoracican relationships and mtgenome modifications in evolution of the barnacle.

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Declaration of interest

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