Complete mitochondrial genome of the catophragmid barnacle *Catomerus polymerus* (Cirripedia, Thoracica, Balanomorpha, Catophragmidae)

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**ABSTRACT**

The family Catophragmidae is one of the lower balanomorphs from traditional and recent multiple mitochondrial and nuclear markers molecular analysis. Here, we characterized the first mitogenome of the catophragmid barnacle *Catomerus polymerus*, which was 15,446 bp in length with a 68.3\% AT content. The mitogenome had the typical pancrustacean gene arrangement, which was identical to the mitogenome configurations of the chthamalid *Octomeris* sp. and pachylasmatoid *Eochionelasmus ohtai*. On the mitogenic tree, the catophragmid *Catomerus polymerus* formed an independent branch that was basal to the members of the superfamilies Tetractiloidea and Balanoidea, which was inconsistent with previous findings.

Three superfamilies are recognized as the lower balanomorph barnacles from traditional and recent multiple mitochondrial and nuclear markers molecular analysis. Here, we characterized the first mitogenome of the catophragmid barnacle *Catomerus polymerus*, which was 15,446 bp in length with a 68.3\% AT content. The mitogenome had the typical pancrustacean gene arrangement, which was identical to the mitogenome configurations of the chthamalid *Octomeris* sp. and pachylasmatoid *Eochionelasmus ohtai*. On the mitogenic tree, the catophragmid *Catomerus polymerus* formed an independent branch that was basal to the members of the superfamilies Tetractiloidea and Balanoidea, which was inconsistent with previous findings.

In 14 January 2015, *C. polymerus* specimens were collected from Coledale Beach, Wollongong, Australia (34°17′5″ and 150°57′E). Genomic DNA extraction, sequencing, gene annotation, and phylogenetic analyses followed the methods of Kim et al. (2017, 2018). The specimen used for the mitogenome analysis has been deposited in the Biodiversity Research Museum of Academia Sinica, Taiwan (ASIZCR).

The complete mitogenome of *C. polymerus* was 15,446 bp in length (GenBank accession no. MH791045) and consisted of 13 protein-coding genes (PCGs), two ribosomal RNAs (rRNAs), 22 transfer RNAs (tRNAs), and a non-coding region. The gene organization followed the typical pancrustacean gene arrangement and was identical to that of the chthamalid *Octomeris* sp. (KJ754820) and pachylasmatoid *Eochionelasmus ohtai* (NC_036957). The trRNA arrangement differed slightly from that of the chthamalid *Notochthamalus scabrosus* (NC_022716), which possesses 21 trRNAs, while the chthamalid *Chthamalus antennatus* (NC_026730) had an unusual inverted gene arrangement between trRNA\(^{\text{Phe}}\) and ND2.

The base composition was 33.7\% A, 19.2\% C, 12.4\% G, and 34.6\% T. All of the PCGs had an ATN start codon, except COX1, for which the start codon was not determined. Most of the PCGs terminated with a complete stop codon (TAA or TAG), although COX3, ND3, and ND4 had incomplete stop codons (T-). The 16S and 12S rRNAs were 1312 bp (73.6\% AT content) and 749 bp (67.4\% AT content), respectively. The trRNA genes ranged from 58 to 70 bp in size. A 298-bp-long (80.9\% AT content) non-coding region was located between the 12S rRNA and tRNA\(^{\text{5Sr}}\).

Phylogenetic trees were constructed with the PCGs of 15 barnacles using maximum likelihood and Bayesian inference (Figure 1). Previous studies based on nuclear and partial mitochondrial genes recognized that Catophragmidae shares a common ancestor with Waikalasmatidae, Chionelasmidae, and Pachylasmidae, although this lacked high bootstrap support or Bayesian posterior probability (Pérez-Losada et al. 2014; Chan et al. 2017). However, on the mitogenic tree, the catophragmid *Catomerus polymerus* formed an independent branch and was located basal to the superfamilies Tetractiloidea and Balanoidea. Therefore, further mitogenic analysis of undetermined taxa of Waikalasmatidae and...
Pachylasmatidae is required to confirm the phylogenetic relationships and evolution of lower balanomorph barnacles.

**Disclosure statement**

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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