

The complete mitochondrial genome of *Anneissia pinguis* (Crinoidea, Articulata, Comatulidae), from South Korea

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ABSTRACT

In this study, the complete mitochondrial genome sequence of *Anneissia pinguis* was examined by next-generation sequencing analysis. The complete mitogenome of *A. pinguis* has 15,912 bp in length and 37 genomes consist of 13 protein-coding genes (PCGs), 22 tRNAs, 2 rRNAs, and 1 control region (D-loop). Both gene orders and characteristics were in accordance with other species belonging to the phylum Echinodermata. Phylogenetic analysis revealed the establishment of molecular taxonomic relationship in class Crinoidea based on complete mitogenome.

ARTICLE HISTORY

Received 28 September 2020
Accepted 28 February 2021

KEYWORDS

Crinoidea; mitogenome;
Anneissia pinguis; phylogeny

Genus *Anneissia* belonging to the order Comatulida of the subclass Articulata has been accepted within the nine species of genus *Oxycomanthus* Hoggett, Birtles & Vail, 1986 by Summers et al. (2014). For now, the genus *Anneissia* consists of nine species. Among them, in Korea, only three species had been reported, and *Anneissia pinguis* (AH Clark 1909) was not recorded yet. We provide the complete mitogenome of *A. pinguis* (MW008594) for contributing to the establishment of the evolutionary relationship of crinoids.

The specimen was collected in Jeju Island, Korea (33°41'05.0"N, 127°28'02.0"E) by trawling, at a depth of 89 m on 31 October 2017, and identified based on the morphological studies (Clark 1909; Gislén 1922). Voucher specimens (MERBK-C-20203247) and mitochondrial DNA (mt-DNA) samples were deposited in storage and freezer (−80 °C) of Marine Echinoderm Resources Bank of Korea (Philjae Kim, swubio@naver.com, Seoul, Korea), respectively. For isolating the mitochondria, gonad was used as a tissue sample. The mitochondria isolation method and whole experiment steps were conformed to the description by Song et al. (2016). The mitochondria were isolated using Mitochondria Isolations Kit (Qiagen, Germany), and mitochondrial DNA (mt-DNA) was extracted by DNeasy Blood and Tissue Kit (Qiagen, Germany). For NGS, mt-DNA was amplified with REPLI-g Mitochondrial DNA Kit (Qiagen, Germany) and Exonuclease-Resistant Random Primer (Thermo Fisher Scientific, USA). The NGS analysis was conducted by Illumina Hiseq 4000 (platform (Illumina Inc., USA). The complete mitogenome was reconstructed by Geneious prime 2019.0.4. The phylogenetic analysis was conducted with the mitogenomes dataset of nine

Echinodermata, including *A. pinguis*. The best-fit substitution model was estimated using jModelTest 2.1.1 (Guindon and Gascuel 2003).

The complete mitogenome of *A. pinguis* (MW008594) is composed 15,912 bp of nucleotide. The genome is consists of 13 PCGs, 22 tRNA genes, 2 rRNA genes, and 1 control region (D-loop). The gene arrangement was in accord with other crinoids, except *Antedon mediterranea* (NC_010692). In all PCGs, the most common initiation codon is 'ATG,' except for ND4L, and ND5 started with 'GTG.' The most common termination codon is 'TAA' (ND4L, COX2, ATP8, ATP6, COX3, ND3, ND6, ND2), then is 'TAG' (COX1, ND5, ND1). Rest of the four PCGs (ND4, CytB) have incomplete terminal codon 'T—.' The mitochondrial base composition is 24.8% A, 46.6% T, 11.6% C, and 17% G.

The dataset for phylogenetic analysis included 13 PCGs of eight crinoids, and one asteroid (*Asterias amurensis*, AB183559) was used as an outgroup. The maximum-likelihood (ML) analysis was conducted using PhyML 3.1 with GTR+I+G model with 1000 replication of bootstrap assembling (Guindon et al. 2010). In the ML tree, *A. pinguis* formed a monophyletic clade in the crinoid group (Figure 1). In the molecular analysis based on complete mitogenome information, all crinoids that we compared were well distinguished at the species-level. The newly obtained mitogenome in this study will be used as a genomic resource, and be contributed to further evolutionary studies of Echinodermata based on molecular evidence.

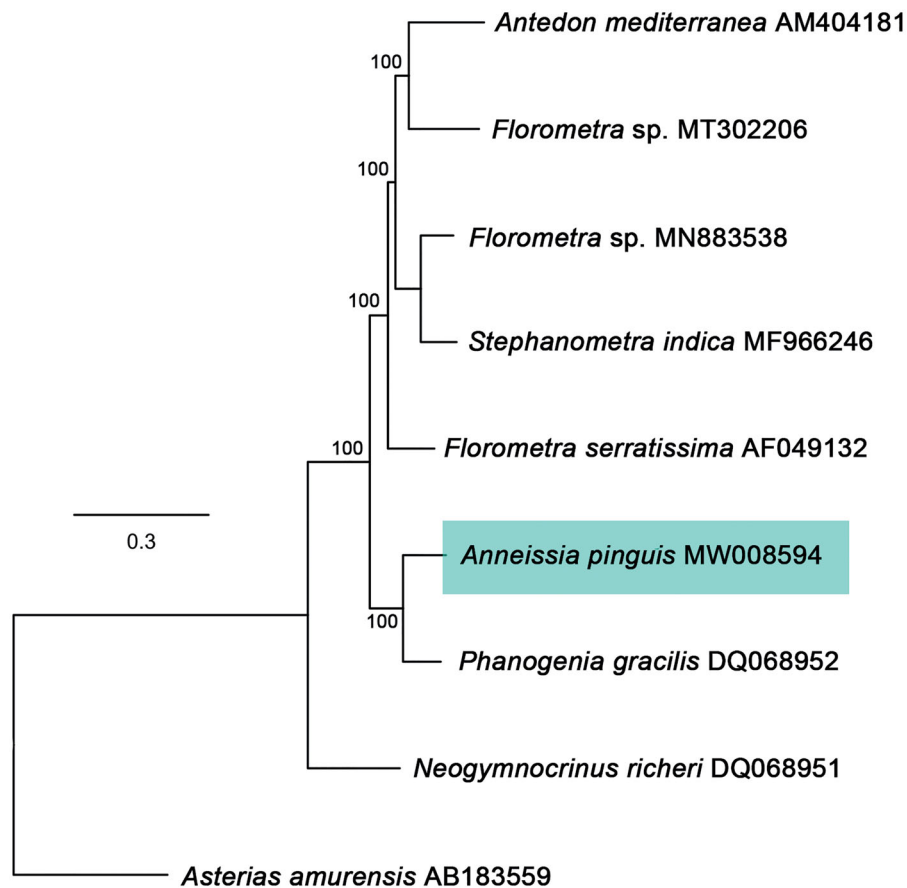


Figure 1. Phylogenetic tree inferred by maximum-likelihood using of 13 protein coding genes of nine echinodermata mitochondrial genomes, including *A. pinguis* (MW008594). Bootstrap support values based on 1000 replicates are displayed on each node as >70.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

This study was supported by the project titled 'Improvement of Management Strategies on Marine Disturbing and Harmful Organisms' funded by the Ministry of Oceans and Fisheries, Korea [20190518] and a grant from the National Institute of Biological Resources (NIBR), which was funded by the Ministry of Environment of the Republic of Korea [NIBR202002204].

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov/>) under the accession no. MW008594. We submitted our sequence through Sequin software (<https://www.ncbi.nlm.nih.gov/Sequin>),

therefore we have no associated BioProject, SRA, and Bio-Sample numbers in this study.

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