

Complete mitochondrial genome analysis of *Aquilonastra batheri* (Echinodermata, Asteroidea, Valvatida)

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ABSTRACT

In this study, we determined the complete mitochondrial genome sequences of *Aquilonastra batheri*. This is the first study on mitochondrial genome sequencing of the genus *Aquilonastra* belonging to the family Asterinidae, order Valvatida, and class Asteroidea. The complete mitogenome of *A. batheri* was 16,463 bp and consisted of 13 protein-coding genes (PCGs), 22 tRNAs, and two rRNAs. The orders of PCGs and rRNA genes were identical to those of nine recorded mitogenomes of asteroids. The phylogenetic tree determined by the maximum likelihood method revealed that *A. batheri* was clearly grouped with *Patiria pectinifera*, which belongs to the family Asterinidae.

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A sea star genus *Aquilonastra* was removed from the genus *Asterina* in 2004, based on a molecular and morphological revision (O'Loughlin and Waters 2004). A total of 31 species of the genus *Asterina* have been reported to date worldwide, and these species have extensive distribution, from Korea to Australia and Maldives, Arabian Sea, Red Sea, Indonesia, and Papua New Guinea (Clark 1921; O'Loughlin and Rowe 2006; Shin 2010; O'Loughlin and Bribiesca-Contreras 2015, 2017). *Aquilonastra batheri* is a common species found in the shallow water of Jeju-do, whose morphological characteristics are as follows: small sized (>30 mm), oral side flattened, with various marked irregular patterns on the aboral side (Shin 2010).

Specimens were collected by SCUBA diving at a depth of 21 m from the Munseom Island, Jeju-do in Korea (33°13'38"N, 126°34'08"E) on 29 March 2018. Specimens were deposited in the Marine Echinoderm Resources Bank of Korea (Seoul, Korea). The method of mitochondrial DNA extraction and amplification, next-generation sequencing (NGS), and genomic library conformed with those in the study by Lee and Shin (2018). Phylogenetic analyses of the dataset were performed using the maximum likelihood (ML) method with PhyML 3.1 (Guindon et al. 2010). The best-fit substitution was estimated using jModelTest 2.1.1 (Guindon and Gascuel 2003; Darriba et al. 2012) for the nucleotide dataset of 13 protein-coding genes (PCGs). For ML analyses, PhyML were used with the GTR+G model of substitution for the nucleotide dataset. Bootstrap resampling was performed using the rapid option with 1,000 iterations.

The complete mitogenome of *A. batheri* (GenBank accession No. MH507076) was 16,463 bp and contained 13 PCGs, 22 tRNA genes, and two rRNA genes. The order and direction

of the genes were identical to those of the other nine complete mitogenomes of asteroid species. Eleven PCGs contained an ATG initiation codon (methionine), with the exception of NADH4L (ATC, isoleucine) and NADH3 (ATT, isoleucine). The TAA codon was the termination codon of nine PCGs, with the exceptions of COX2, NADH2, NADH5 (TAG), and CytB (Phenylalanine (TTC)+T).

To examine the phylogenetic relationships, the ML method was used based on the nucleotide sequences of 13 PCGs obtained from ten asteroids, including *A. batheri* (Figure 1), with two ophiuroids, *Astrospartus mediterraneus* (NC_013878) and *Ophiura luetkenii* (NC_005930), which were used as outgroups. In the phylogenetic tree, the ten asteroid mitogenomes were clearly divided with two ophiuroids (Figure 1). *Aquilonastra batheri* formed a distinct monophyly with *Patiria pectinifera* (NC_001627), which belonged to the family Asterinidae. Furthermore, they distinctly formed a monophyletic clade with *Acanthaster brevispinus* (NC_007789) and *A. planci* (NC_007788), which belongs to the identical order Valvatida (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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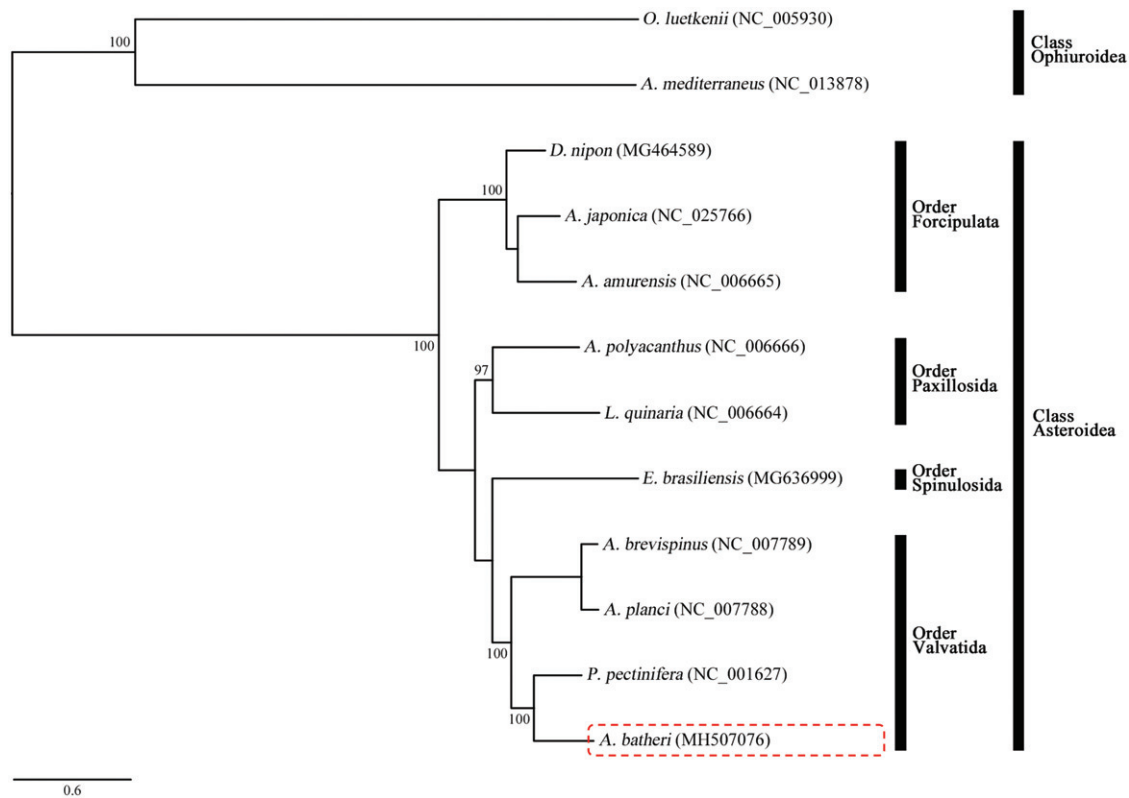


Figure 1. Phylogenetic tree constructed using the maximum likelihood (ML) method based on the nucleotide sequences of the complete mitogenomes of *Aquilonastra batheri* (MH507076) and eight other asteroids. The bootstrap values indicated on each node are >70.

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