The mitochondrial genome analysis of *Protaeolidiella atra* Baba, 1955 from Korea

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**ABSTRACT**

*Protaeolidiella atra* is an aeolid nudibranch found in Korean and Japanese waters. This study presents the complete mitochondrial genome of *P. atra* from Korea. The mitogenome size of *P. atra* was 14,445 bp, including 27.3% A, 39.3% T, 14.8% C, and 18.6% G. Identical to other nudibranchs, there were 13 protein-coding genes, 2 rRNA genes, and 22 tRNA genes in the mitogenome of *P. atra*. The result of the phylogenetic analysis indicated that *P. atra* is closest to *Sakuraeolis japonica*.

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In 1955, Baba described *Protaeolidiella atra* for the first time based on samples collected from Japan (Baba 1955). Even though *P. atra* and *Pleurolidia juliae* were once considered to be conspecific, morphological and molecular pieces of evidence proved that they are two distinct species (Carmona et al. 2015). *Protaeolidiella atra* was previously regarded as a primitive species of the family Aeloidiidae. However, the differences in morphology and specialized diet of *P. atra* compared to other members of the family have resulted in a long debate on the phylogenetic position of this species (Carmona et al. 2015). Currently, *P. atra* and *P. juliae* are accepted as only two species of the family Pleurooliidae (WoRMS Editorial Board 2020). Decoding and analysis of the *P. atra* mitogenome might be useful for the understanding of its phylogenetic relationships.

In this study, *P. atra* was sampled from Ulleungdo island, Korea (37°32′20.40″N, 130°50′19.82″E) in August 2013. The collected sample (voucher number: SMU00041) was preserved in absolute ethanol and maintained in the Department of Biotechnology, Sangmyung University, Korea. Following DNA extraction, Next-generation sequencing was conducted on Miseq system (Illumina, San Diego, CA), and the paired-end reads were assembled by MITObim (Hahn et al. 2013). The mitogenome sequence was annotated using the MITOS web server (Bernt et al. 2013) with the support of ARWEN (Laslett and Canbäck 2008) for tRNA search.

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The phylogenetic position of *P. atra* was determined based on amino acid sequences of protein-coding genes (PCGs). The tree of *P. atra* and related species was reconstructed with the neighbor-joining method in MEGA X (Kumar et al. 2018).

The size of the complete mitogenome of *P. atra* (GenBank accession number: MN911169) was 14,445 bp with nucleotide composition: 27.3% A, 39.3% T, 14.8% C, and 18.6% G. Nine of the 13 PCGs were encoded on the H-strand (cob, *cox1*, *cox2*, *nd1*, *nd2*, *nd4*, *nd4l*, *nd5*, and *nd6*) while four remaining PCGs were encoded on the L-strand (*atp6*, *atp8*, *cox3*, and *nd3*). The sizes of PCGs were in the range of 153 bp (*atp8*) to 1680 bp (*nd5*). Of the 22 tRNA genes, the sizes varied from 54 bp (*tRNAThr*) to 69 bp (*tRNAGly*). For rRNA genes, 12S rRNA gene was 721 bp in length and encoded on the L-strand while 16S rRNA gene was 1140 bp in length and encoded on the H-strand.

There were 18 overlapping regions with the longest region found between *tRNAIle* and *nd2* (40 bp). In addition, 18 intergenic regions were detected, ranging from 1 to 240 bp and the longest region was located between *tRNAHis* and *tRNACys*.

The phylogenetic tree showed the position of *P. atra* in the suborder Cladobranchia (Figure 1). *Protaeolidiella atra* formed a clade with *Sakuraeolis japonica*, and they were sister to *Hermissenda emurai* (Figure 1). This study provided the first mitogenome record for the family Protaeolidiellidae. Additional data from *Pleurolidia juliae* and different species of the superfamily Aeolidioidea is necessary to reveal insight into the phylogenetic position of *P. atra*.

**Disclosure statement**

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

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**References**

Baba K. 1955. Opisthobranchia of Sagami Bay supplement. Iwanami Shoten, Tokyo. 59 pp.

Bernt M, Donath A, Juhling F, Externbrink F, Florentz C, Fritzsch G, Putz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2):313–319.

Carmona L, Pola M, Gosliner TM, Cervera L. 2015. *Protaeolidiella atra* Baba, 1955 versus *Pleurolidia juliae* Burn, 1966: one or two species? Helgol Mar Res. 69(2):137–145.

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads—a baiting and iterative mapping approach. Nucleic Acids Res. 41(13):e129.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549.

Laslett D, Canbäck B. 2008. ARWEN: a program to detect tRNA genes in metazoan mitochondrial nucleotide sequences. Bioinformatics. 24(2):172–175.

WoRMS Editorial Board. 2020. World Register of Marine Species; [Accessed 2020 Jan 03]. http://www.marinespecies.org.