The complete mitochondrial genome of *Haloa japonica* (Pilsbry, 1895) (Cephalaspidea, Haminoeidae)

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**ABSTRACT**

*Haloa japonica* is a bubble snail species in the family Haminoeidae. In the present study, the complete mitochondrial genome of *H. japonica* was decoded and analyzed. With the size of 13,797 bp, the mitogenome of *H. japonica* is the shortest among all known mitogenomes of the order Cephalaspidea. Overall base-pair composition of the mitogenome was 69% A–T and 31% C–G. The phylogenetic tree showed a clade of *H. japonica* and other species in the family Haminoeidae.

*Haloa japonica*, previously known as *Haminoea japonica* (WoRMS Editorial Board 2020), is a bubble snail with native distribution in Japan and Korea. Moreover, non-native populations were reported in different regions of the world (Gosliner and Behrens 2006). The schistosome parasite found in *H. japonica* is involved in human cercarial dermatitis (Brant et al. 2010). Therefore, the spread of *H. japonica* could negatively impact human health. However, it has been challenging to detect *H. japonica* populations in non-native regions due to difficulties in the identification of *H. japonica* and its related species (Hanson et al. 2013). Mitogenome is widely used for resolving phylogenetic and taxonomic complications. The complete mitogenome is necessary for discrimination of *H. japonica* with its related species.

The sample of *H. japonica* was collected from Jeju Island, Korea (33°28′59.45″N, 126°22′26.73″E) in May 2013. The sample (voucher number: SMU00051) was deposited in the Department of Biotechnology, Sangmyung University, Korea. The procedure of mitogenome sequencing and annotation for *H. japonica* was presented in the previous study (Do et al. 2019). For phylogenetic analysis, the mitogenomes of cephalaspidean species were retrieved from GenBank. The phylogenetic analysis using amino acid sequences of 13 protein-coding genes (PCGs) was performed by MEGA X (Kumar et al. 2018) with the neighbor-joining method. The

**Figure 1.** Phylogenetic position of *H. japonica* in the order Cephalaspidea. The mitogenome of *H. japonica* is marked with a black spot. Two species from the order Nudibranchia *Chromodoris annae* and *Phyllidia ocellata* are used as the outgroup.

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bootstrap method (×1000 replicate) was used to calculate statistical support.

The total length of the *H. japonica* mitogenome (GenBank accession number: MN911170) was 13,797 bp, with 13 PCGs, 2 ribosomal RNA genes, and 22 tRNA genes. This is the shortest size among all recorded mitogenomes of the order Cephalaspidea. The main reason of the short length could be the compact structure of the mitogenome. Accordingly, there were up to 28 overlapping regions found in the mitogenome. The base-pair composition of the *H. japonica* mitogenome included 69% A–T and 31% C–G. Among 37 genes of the mitogenome, there were 24 genes encoded on the H-strand and 13 genes encoded on the L-strand. The gene order of the *H. japonica* mitogenome is similar to the mitogenomes of *Smaragdinella calyculata* and *Bullacta exarata*, which also belong to the family Haminoeidae (Worms Editorial Board 2020).

Of 13 PCGs, eight genes initiated with ATG (*atp8*, *atp6*, *cob*, *cox3*, *nd1*, *nd4*, *nd5*, and *nd6*) and five remaining genes initiated with ATT (*cox1*, *cox2*, *nd2*, *nd3*, and *nd4l*) codons. For stop codon, seven genes terminated with TAA (*atp8*, *atp6*, *cob*, *cox1*, *nd1*, *nd4l*, and *nd6*), three genes terminated with TAG (*cox2*, *nd2* and *nd5*) and three genes had incomplete termination with T- (*cox3*, *nd3* and *nd4*).

The phylogenetic analysis revealed three species in the family Haminoeidae are clustered together, and *H. japonica* is closest to *Smaragdinella calyculata* (Figure 1). This pattern is consistent with the report on the relationship of the family Haminoeidae (Oskars et al. 2019). Our study presented the mitogenome of *H. japonica* and it is the third record for the family Haminoeidae. Mitogenome sequencing for other haminoeid species are recommended to resolve taxonomic difficulties for this group.

**Disclosure statement**

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

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