

Complete mitochondrial genome analysis of *Sakuraeolis japonica* (Baba, 1937) (Mollusca, Gastropoda, Nudibranchia)

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ABSTRACT

In this study, a complete mitochondrial genome of a nudibranch species, *Sakuraeolis japonica* was sequenced and analyzed. The mitochondrial genome size is 15,059 bp with 28.1% A, 14.9% C, 19.3% G, and 37.7% T nucleotide distributions. This is the eighth record for complete mitochondrial genome of the Nudibranchia and first record for the genus. Furthermore, phylogenetic relationship of *S. japonica* in the Nudibranchia was investigated by using protein-coding genes of complete mitochondrial genome. The present study suggests that *S. japonica* belongs to the family Facelinidae and it is placed in monophyletic Nudibranchia. The closest species to *S. japonica* are *Chromodoris magnifica* and *Chromodoris quadricolor* that belong to the family Chromodorididae.

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Sakuraeolis japonica (Baba, 1937) is an aeolid nudibranch species. Previously, it had six synonym names but although the genus *Sakuraeolis* has not been verified, current accepted name of the species is *S. japonica* (WoRMS Editorial Board, 2016). Even though there are more than 2000 valid species of nudibranchs known, there is only eight complete mitochondrial sequence information of them declared in the GenBank. Phylogenetic relationship of the nudibranchia should be accomplished with more compensative mitogenome data.

In this study, *S. japonica* was collected from Donghae, Korea (37°34'4"N, 129°7'15"E) by scuba diving. The specimen (Marine Biodiversity Institute of Korea Accession number MABIK MO00157623) was preserved in 97% ethanol and DNA was extracted from foot. Paired end reads generated from a mitochondrial enriched genomic library and sequences were

assembled and annotated by using MITObim (Hahn et al. 2013) and MITOS (Bernt et al. 2013), respectively. Furthermore the complete mitochondrial genome data of the Nudibranchia species were retrieved from the GenBank and 12 protein-coding genes (*ATP8* excluded) of the species used for the analysis of phylogenetic relationship of Nudibranchia. Phylogenetic tree reconstructed by MEGA 6 (Tamura et al. 2013) with maximum-likelihood analyses based on mtREV with Freqs (+F) model. Bootstrap method used 1000 replicates to know statistical support.

The size of mitochondrial genome of *S. japonica* is 15,059 bp (GenBank accession number KX610997). This is the longest mitogenome within known complete mitogenome of the Nudibranchia species. The nucleotide composition of the genome is 28.1% A, 14.9% C, 19.3% G, and 37.7% T with

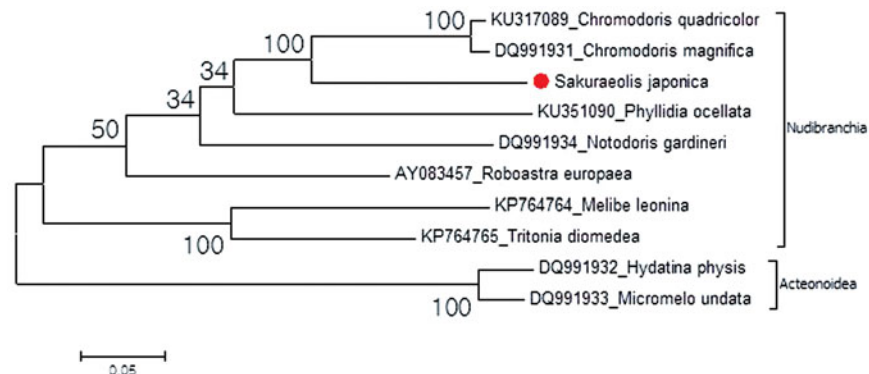


Figure 1. Phylogenetic tree of *S. japonica*. Two species which belong to Heterobranch superfamily Acteonoidea were used as outgroup.

65.0% AT content in the protein-coding regions. It has been known that the shorter protein-coding sequences have the higher AT content because of the structure of stop codons (Wuitchick & Karrer 1999) and *S. japonica* has five protein-coding genes with TAA as stop codon while seven coding genes with incomplete T-- as stop codon. The mitochondrial genome is composed of 13 protein coding, 2 ribosomal RNA, and 22 tRNA genes and the gene order is same to the other nudibranch mitochondrial genomes. There are five overlapping regions ranging from 1 to 5 bp and there are 29 intergenic sequences. The longest intergenic sequence is 451 bp and located between *COI* and *tRNA-Val*. Besides, there are more comparatively long intergenic sequences located between *12s rRNA* and *tRNA-Met* (251 bp), *ATP6* and *tRNA-Arg* (262 bp), and *NAD5* and *NAD1* (173 bp). These noncoding regions allow complete mitogenome of *S. japonica* to be the longest within mitogenomes of the known Nudibranchia species.

The phylogenetic tree (Figure 1) suggests that *S. japonica* is placed in the monophyletic Nudibranchia and a clade including *Chromodoris magnifica* and *C. quadricolor*, which are the closest species to *S. japonica* is shown. Previous molecular study suggested that the family Facelinidae is paraphyletic or polyphyletic. Since this is the first record for the family, we cannot analyze this hypothesis (Carmona et al. 2013). The present study provides additional data for molecular Nudibranchia phylogeny.

Disclosure statement

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