**MITOGENOME ANNOUNCEMENT**

The complete mitochondrial genome of *Phyllidiella pustulosa* (Cuvier, 1804) (Nudibranchia, Phyllidiidae)

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**ABSTRACT**

In the present study, the complete mitogenome of a dorid nudibranch *Phyllidiella pustulosa* was sequenced and analyzed. The complete mitochondrial genome of *P. pustulosa* was 14,717 bp in length, containing 13 protein coding genes, two ribosomal RNA genes, and 22 tRNA genes. Phylogenetic analysis according to protein coding genes revealed that *P. pustulosa* has a close relationship with *Phyllidia ocellata*. This is the first complete mitochondrial genome record for the genus *Phyllidiella*.

*Phyllidiella pustulosa* is a common phyllid nudibranch distributed in the Indo-West Pacific region. Characteristics for morphological identification include elongated, ovate body shape and pink clustered tubercles on a black dorsum (Brunckhorst 1993). However, a phylogenetic analysis based on partial cytochrome C oxidase subunit I (*cox1*) gene has indicated that *P. pustulosa* is potentially a species complex (Stoffel et al. 2016). The mitochondrial genome with multiple markers is a useful tool for species identification. Therefore, the complete mitogenome of *P. pustulosa* might be helpful to discriminate its complex.

The *P. pustulosa* sample was collected in May 2013 from Dodu-dong, Jeju island, Korea (33°31'19.1" N – 126°27'04.3" E) through scuba diving. The sample was preserved in 97% ethanol and deposited in the Department of Biotechnology, Sangmyung University, Korea (SMU00012) for further analysis. The DNA of *P. pustulosa* was extracted from the foot of the specimen using E.Z.N.A.® Mollusc DNA Kit (Omega Bio-tek, Norcross, GA, USA). Paired end reads of mitogenome were generated by Illumina Miseq sequencing system (San Diego, CA, USA). Paired end reads were targeted for reconstructing the complete mitogenome by MITObim (Hahn et al. 2013). The circular sequence was annotated using MITOS web server (Bernt et al. 2013) and Geneious 9.1 software (Kearse et al. 2012).

The size of the complete mitogenome of *P. pustulosa* (GenBank accession number: MK279705) was 14,717 bp. Similar to the other nudibranchs, it contained 13 protein-coding genes (PCGs), 22 transfer RNA genes, and 2 ribosomal RNA genes. Nucleotide content of the mitogenome consisted of 30.3% A, 15.1% C, 17.5% G, and 37.1% T. The longest protein coding gene was *nd5* (1683 bp) while the shortest protein coding gene was *atp8* (156 bp). The sizes of 12S rRNA and 16S rRNA genes were 758 bp and 1244 bp, respectively. The tRNA gene lengths ranged from 56 bp (tRNA-Ser 2) to 71 bp (tRNA-Arg and tRNA-Cys).

Among PCGs, ten genes started with ATG codon, two genes (*nd3* and *nd4l*) started with ATA codon, and one gene (*nd6*) started with ATT codon. It should be noted that there were 11 genes terminated with TAA and only two genes (*cox3* and *nd5*) terminated with TAG. In total, 13 genes were encoded on L-strand, including four PCGs (*atp6*, *atp8*, *cox3*, and *nd3*), one rRNA gene (12S rRNA) and eight tRNA genes (tRNA-Gln, tRNA-Leu 2, tRNA-Asn, tRNA-Arg, tRNA-Glu, tRNA-Met, tRNA-Ser 2, and tRNA-Thr).

The phylogenetic position of *P. pustulosa* was constructed based on amino acid sequences of 12 PCGs (*atp8* gene, etc.).
excluded). The result showed that *P. pustulosa* formed a clade with *Phyllidia ocellata* in the suborder Doridina (Figure 1). The previous molecular phylogeny study based on 16S rRNA and *cox1* gene suggested the similar relationship between the *Phyllidiella* and *Phyllidia* genera (Stoffel et al. 2016). In addition, phylogenetic tree according to *cox1* from the previous study demonstrated that there are different clades inside *P. pustulosa* (Stoffel et al. 2016). Our study provides the mitogenome of *P. pustulosa* from Korean waters. To confirm the *P. pustulosa* species complex, more mitogenomes from different geographic localities should be added.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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