



## Mitochondrial DNA Part B Resources

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## Characterization of the complete mitochondrial genome of *Amphioplus laevis* (Ophiuroidea, Amphiuroidae) with phylogenetic analysis

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### ABSTRACT

The complete mitochondrial genome of *Amphioplus laevis* was 16,084 bp in length (Genbank accession: MN276320). It contained 13 protein-coding genes, 2 ribosomal RNA and 22 transfer RNA. The GC contents of *A. laevis* was 37.59%. The gene order was similar with species in the same family. Phylogenetic relationships within known ophiuroids reconstructed by 13 protein-coding mitochondrial genes, which showed that it was mostly related to *Amphipholis squamata*, corresponding to the gene order. These results could provide a novel insight to the phylogeny of Ophiuroidea.

### ARTICLE HISTORY

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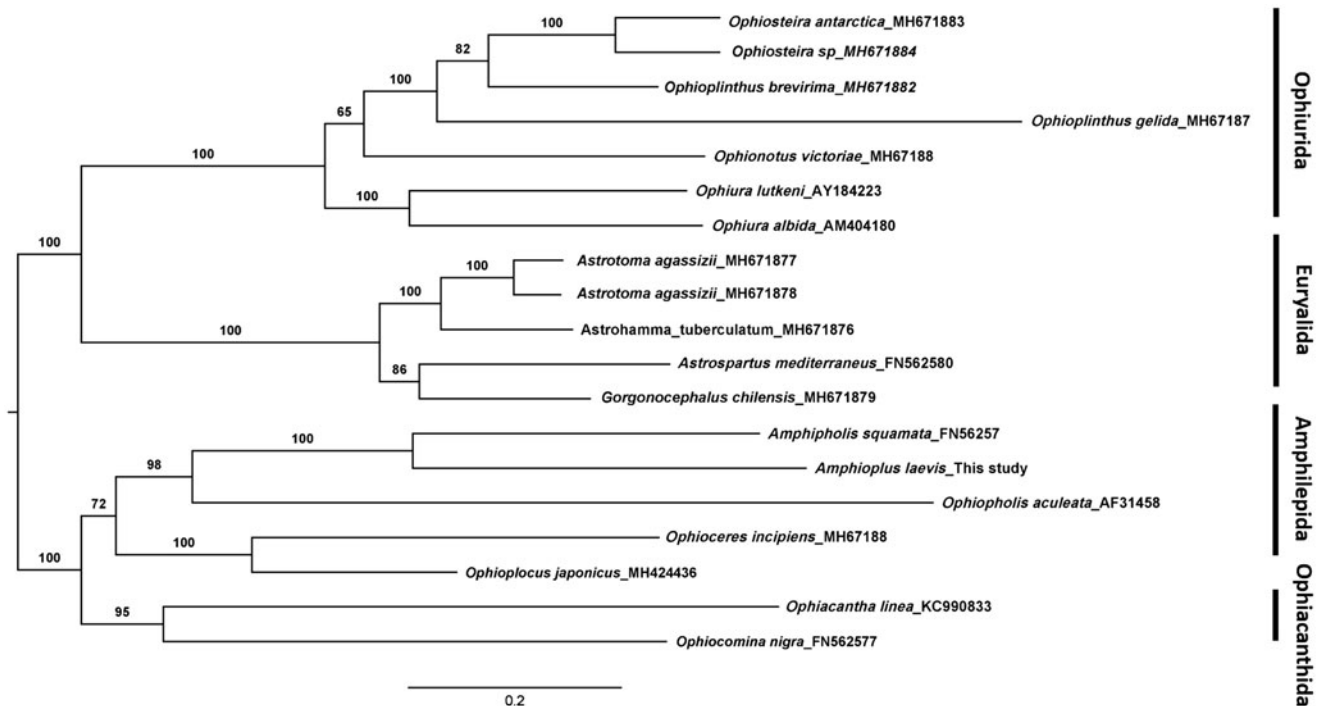
### KEYWORDS

mitochondrial genome;  
Ophiuroid; phylogeny



*Amphioplus laevis*, belonging to Amphilepidida, Ophiuroidea, is very common species in Indo-West Pacific region and play an important role in biogeochemical cycles. This species is also potentially prolific sources for marine drugs. Some sample were collected from South Yellow Sea (33.0032°N, 123.5013°E) and the tissue was stored in Key laboratory of

Science and Engineering for Marine Ecology and Environment, First Institute of Oceanography, MNR (NO. FIO-ECH-H289).

The whole genome was sequenced on the Illumina HiSeq 2500 Sequencing Platform (Illumina, Hayward, CA, USA) by Novogene corporation (Beijing, China) and assembled using



**Figure 1.** The Maximum Likelihood tree of 13 protein-coding mitochondrial genes in 19 ophiuroids. Number at each branch, bootstrap probability. Number after the species name, Genbank accessions.

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SPAdes 3.6.1 (Bankevich et al. 2012). Mitochondrial genomic fragments were queried using a BLAST algorithm-based search against other available Ophiuroidea mitogenomes in GenBank and Price (Ruby et al. 2013) and MITObim v1.8 (Hahn et al. 2013) were used to fill the gaps. The mitochondrial reads were collected by bowtie2 (Langmead and Salzberg 2012) and reassembled. The circular structure of the mitochondrial genome was verified using Bandage (Wick et al. 2015) and then submitted to Genbank (Genbank accession: MN276320).

The gene structure is same with other known Ophiuroids, containing 13 protein-coding genes, 2 ribosomal RNA genes, and 22 transfer RNA genes (Perseke et al. 2013; Galaska et al. 2019). The length of 13 protein-coding gene was 11,367, which occupied 70.67% of the whole mitochondrial genome. The overall base component is A 31.60%, T 30.20%, G 15.90%, and C 22.40%. The GC contents of this mitochondrial genome was 37.59%. The gene order of *A. laevis* was almost same with *Amphiopholis squamata*, except the order of *tRNA<sup>M</sup>*.

Phylogenetic relationships among *A. laevis* and 18 known mitochondrial genomes of brittle stars (Figure 1) were reconstructed using the Maximum Likelihood method by IQTREE (Nguyen et al. 2015). The results showed that *A. laevis* was most closed to *A. squamata*. This phylogenetic result was corresponding to the gene order, which indicated a conserved relationship in family Amphiuridae. Those results provided details for further studies on the phylogeny of Ophiuroidea.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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