

Complete mitochondrial genome of Staghorn damselfish, *Amblyglyphidodon* *curacao* (Perciformes, Pomacentridae)

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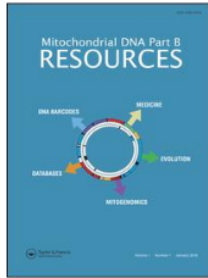
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Complete mitochondrial genome of Staghorn damselfish, *Amblyglyphidodon curacao* (Perciformes, Pomacentridae)

Hyun-Woo Kim^{a,b} , Sinar Pagi Sektiana^{a,c}, Md. Jobaidul Alam^{a,d}  and Sapto Andriyono^{a,e} 

^aInterdisciplinary Program of Biomedical, Mechanical and Electrical Engineering, Pukyong National University, Busan, Republic of Korea; ^bDepartment of Marine Biology, Pukyong National University, Busan, Republic of Korea; ^cAquaculture Technology Study Program, Sekolah Tinggi Perikanan, Jakarta, Indonesia; ^dDepartment of Fisheries, Ministry of Fisheries and Livestock, Dhaka, Bangladesh; ^eDepartment of Marine, Fisheries and Marine Faculty, Universitas Airlangga C Campus Jl. Mulyorejo Surabaya, East Java, Indonesia

ABSTRACT

The complete mitochondrial genome of the Staghorn damselfish, *Amblyglyphidodon curacao* was determined by next-generation sequencing (NGS) platform. The circular mitochondrial genome of *A. curacao* (16,612 bp) encoded the 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 2 non-coding regions (origin of light strand replication (*OL*) and the control region (*D-Loop*)). All the tRNAs have typical clover-leaf structures except for tRNA-Ser. Phylogenetic analysis based on the currently reported mitochondrial genomes in Pomacentridae showed that *A. curacao* was most closely related to *Amphiprion frenatus*. The complete mitogenome sequence of *A. curacao* would provide essential genetic information of Pomacentrinae related to them for their scientific management in the coral-reef ecosystem in Indonesian waters.

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Next generation sequencing; damselfish; complete mitogenome; coral-reef fish



Although the pomacentrids represent the greatest diversity and abundance of fish species inhabiting around coral reef zone (Meekan et al. 1995), the documentation of their genetic information is still lacking, especially in subfamily Pomacentrinae. Based on FishBase (fishbase.org), there are currently 11 recognized species in this genus *Amblyglyphidodon* but no mitochondrial genome information is currently documented. *Amblyglyphidodon curacao* also known as a staghorn damsel inhabits the tropical and subtropical coral reefs as one of the ecologically important components (Allen 1991). We here report the complete mitochondrial genome of *A. curacao* firstly in genus *Amblyglyphidodon*.

The specimen was collected from the coastal water at Thousand islands, Jakarta, Indonesia (5°44'41.03"S, 106°35'36.97"E), which stored at Sekolah Tinggi Perikanan, Jakarta, Indonesia. Species identification of the specimen was confirmed by both its morphological characteristics and DNA sequence identity in the COI region to the GenBank database (KF929588). Mitochondrial DNA was extracted by a commercial kit (Abcam, Cambridge, UK), followed by the fragmentation of the purified mitochondrial DNA into smaller sizes (~350 bp) by Covaris M220 Focused-ultrasonicator (Covaris Inc., Woburn, MA, USA). A library for sequencing was constructed by TruSeq[®] RNA library preparation kit V2 (Illumina Inc., San Diego, CA, USA) and its quality and quantity were analyzed by 2100 Bioanalyzer (Agilent Technologies, Santa

Clara, CA, USA). DNA sequencing was performed by MiSeq sequencer (Illumina, San Diego, CA, USA) and the complete mitogenome of *A. curacao* was assembled by Geneious v 11.0.2 (Kearse et al. 2012).

The complete mitochondrial genome of *A. curacao* (MH995533) was 16,612 bp in length, which consisted of 13 protein-coding genes, 22 tRNAs, 2 ribosomal RNAs (12S and 16S), and non-coding regions including putative control region *D-Loop* (842 bp) and origin of light strand replication *OL* (30 bp). The three tRNA clusters (IQM, WANCY, and HSL) were also well conserved (Satoh et al. 2016). Secondary structure prediction result by ARWEN (Laslett and Canbäck 2008) showed that all the tRNAs have typical clover-leaf structures except for tRNA-Ser. The non-coding region *D-Loop* was identified between tRNA-Pro^(TGG) and tRNA-Phe^(GAA) while the *OL* was between tRNA-Asn^(GTC) and tRNA-Cys^(GCA) at WANCY cluster. The protein-coding region was initiated with ATG except for COX1 gene which initiated by GTG. Incomplete stop codons were identified in ND2, COX2, ATP6, COX3, ND3, ND4, ND5, and Cyt b genes.

The phylogenetic analysis of *A. curacao* with the currently reported mitogenome in family Pomacentridae was constructed by MEGA7 with minimum evolution algorithm (Kumar et al. 2016). *Amblyglyphidodon curacao* was clustered with those in subfamily Pomacentrinae including *Stegastes flavilatus* and *Abudefduf vaigiensis*, which is distinct from those in subfamily Amphiprioninae (Figure 1). However,

CONTACT Sapto Andriyono  sapto.andriyono@gmail.com  Interdisciplinary Program of Biomedical, Mechanical and Electrical Engineering, Pukyong National University, Busan, 48513, Republic of Korea

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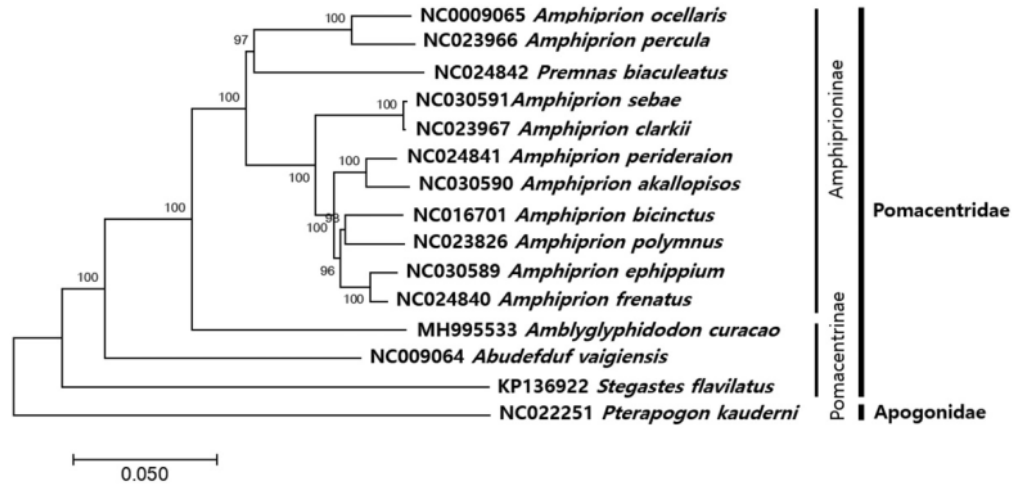


Figure 1. Phylogenetic tree of *Amblyglyphidodon curacao* within Pomacentridae. Phylogenetic tree of *Amblyglyphidodon curacao* complete genome was constructed by MEGA7 software with Minimum Evolution (ME) algorithm with 1000 bootstrap replications. Each scientific name followed by GenBank Accession numbers and furthermore *Pterapogon kauderni* (NC022511) family of Apogonidae as an outgroup.

A. curacao showed the highest sequence identity to *Amphiprion frenatus* (87%) among the currently identified mitogenomes in family Pomacentridae and more mitogenome information of subfamily Pomacentrinae should be supplemented to provide the basic information about the genetic structure within the family Pomacentridae.

Disclosure statement

The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the manuscript.

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ORCID

Hyun-Woo Kim <http://orcid.org/0000-0003-1357-5893>
Md. Jobaidul Alam <http://orcid.org/0000-0002-3594-8147>

Sapto Andriyono <http://orcid.org/0000-0002-2566-1636>

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