Sequence and phylogenetic analysis of the complete mitochondrial genome for the grey stingfish *Minous monodactylus* (**Scorpaeniformes**: **Synanceiidae**)

Hyun-Woo Kim\(^a\)\(^b\), Md. Jobaidul Alam\(^a\), Ah-Ran Kim\(^a\), Hyun Park\(^c\) and Sapto Andriyono\(^a\)\(^d\)

\(^a\)Interdisciplinary Program of Biomedical, Mechanical and Electrical Engineering, Pukyong National University, Busan, Republic of Korea;\(^b\)Department of Marine Biology, Pukyong National University, Busan, Republic of Korea;\(^c\)Korea Polar Research Institute, Korea Ocean Research and Development Institute, Incheon, Republic of Korea;\(^d\)Fisheries and Marine Faculty, C Campus Jl. Mulyorejo, Universitas Airlangga, Surabaya, Indonesia

**ABSTRACT**

The mitochondrial genome sequence of *Minous monodactylus* (16,459 bp) was determined by the MiSeq platform for the first time in the genus *Minous*. It encoded the 37 genes (13 protein-coding genes, 22 tRNAs, and two ribosomal RNAs) and two conserved noncoding regions; control region (**D**-loop) and the origin of light strand (**OL**). Twenty-eight genes were encoded on the heavy (**H**) strand, while eight tRNAs and **ND6** genes were on the light (**L**) strand. According to the phylogenetic analysis with other complete mitogenomes from order **Scorpaeniformes**, *M. monodactylus* was clustered with *Synanceia verrucosa* as family **Synanceiidae** with 81% sequence identity.

The grey stingfish, *Minous monodactylus* (**Scorpaeniformes**: **Synanceiidae**) is a venomous demersal marine fish species, which inhabits the bottoms of the continental shelf (Yamada et al. 1995). It is widely distributed in the Indo-West Pacific region including East Africa, Red Sea, Indonesia, and Japan (Eschmeyer and Hallacher 1979). Although 12 species are currently reported in genus *Minous* based on the FishBase (http://www.fishbase.org), no complete mitochondrial genome in the genus is documented. We here report the mitochondrial genome of *M. monodactylus*, which was collected from Korean water as the first mitogenome sequence in the genus *Minous*.

The specimen of *M. monodactylus* was collected during a regular EEZ fish survey (32°03′28.3″N, 125°05′58.6″E) by the

---

**CONTACT** Sapto Andriyono sapto.andriyono@gmail.com Department of Marine, Faculty of Fisheries and Marine, Universitas Airlangga, Surabaya, East Java, 60115, Indonesia

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
National Institute of Fisheries Science (NIFS) in 2013. The specimen was confirmed by both the morphological characteristics and its COI sequence identity with GenBank database (KP330538). The specimen and its DNA were stored at Pukyong National University, Korea and its mitochondrial genome were determined by next-generation sequencing (NGS) technique. The mitochondrial DNA extracted by the commercial purification kit (Abcam, Cambridge, UK) was fragmented into smaller sizes (~350 bp) by Covaris M220 Focused-Ultrasonicator (Covaris Inc., Woburn, MA). A library was constructed by TruSeq® RNA library preparation kit version 2 (Illumina Inc., San Diego, CA), which was further sequenced by MiSeq sequencer (Illumina Inc., San Diego, CA). Geneious® version 11.0.2 (Kearse et al. 2012) was used for mitogenome assembly, and phylogenetic analysis was conducted by MEGA version 7.0 program with minimum evolutionary (ME) algorithm (Kumar et al. 2016) (Figure 1).

The circular mitochondrial genome of *M. monodactylus* (MK433297) was 16,459 bp in length, which encodes the canonical 37 genes (13 protein-coding genes, 22 tRNAs, and two ribosomal RNAs). The A + T contents were 55.5%, which was higher than G + C composition (44.5%). Twenty-eight genes were located on the heavy (H) strand, while nine were located on the light (L) strand. The control region (*D-Loop*) was located between *tRNA-Pro* and *tRNA-Phe* while origin of light strand (*OL*) was located between *tRNA-Asn* and *tRNA-Cys*. Except for *COX1* (GTG), ATG was predicted as the start codon in all the protein-coding genes. The incomplete stop codon (T<sup>C</sup>C/C<sup>G</sup>TA<sup>C</sup>/C<sup>G</sup>) was identified in six genes including *ND2*, *COX2*, *COX3*, *ND3*, *ND4*, and *Cyt b*. Three tRNA clusters (IQM, WANCY, and HSL) were conserved. Except for in *tRNA-Ser<sup>GTC</sup>* which lacks the dihydrouridine (DHU) arm, the typical cloverleaf secondary structures were predicted in all the tRNAs according to the result by ARWE software (Canbäck and Laslett 2008).

The mitogenome of *M. monodactylus* showed the highest sequence identity (81%) to *Synanceia verrucosa* (KP789313), the only synanceiid mitogenome sequence in the GenBank database. The phylogenetic analysis with mitogenomes in *Scorpaeniformes* also showed that two synanceiid species, *S. verrucosa*, and *M. monodactylus* were clustered together distinct from those in the others. Additional mitogenome sequences should be supplemented to have better knowledge about the evolutionary relationship in the family *Synanceiidae*.

**Disclosure statement**

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

**Funding**

This work was supported by the educational grant of LPDP (BUDI-LN batch I 2016).

**ORCID**

Hyun-Woo Kim http://orcid.org/0000-0003-1357-5893
Sapto Andriyono http://orcid.org/0000-0002-3594-8147
Md. Jobaidul Alam http://orcid.org/0000-0002-2566-1636

**References**

Canbäck B, Laslett D. 2008. ARWEN: a program to detect tRNA genes in metazoan mitochondrial nucleotide sequences. Bioinformatics. 24: 172–175.

Eschmeyer WN, Hallacher LE. 1979. The scorpionfish genus Minous (*Scorpaenidae*, Minoinae) including a new species from the Indian Ocean. Proceedings of the California Academy of Sciences/California Academy of Sciences; Material sin tematizar Bibliografıa: p.470–473.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28: 1647–1649.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol. 33: 1870–1874.

Yamada U, Shirai S, Irie T. 1995. Names and illustrations of fishes from the East China Sea and the yellow sea: Japanese Chinese Korean. Tokyo, Japan: Overseas Fishery Co-operation Foundation.