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## DNA sequences and morphological variation in *Lophiodes iwamotoi* Ho, Serét & Shao, 2011 based on new material from New Caledonia

HSUAN-CHING HO<sup>1,2,4</sup> & WEI-JEN CHEN<sup>3</sup>

<sup>1</sup>National Museum of Marine Biology & Aquarium, Pingtung, Taiwan, no. 2, Houwan Rd., Checheng, Pingtung, Taiwan.  
E-mail:ogcoho@gmail.com

<sup>2</sup>Institute of Marine Biodiversity & Evolutionary Biology, National Dong Hwa University; No. 2, Houwan Rd., Checheng, Pingtung, Taiwan

<sup>3</sup>Institute of Oceanography, National Taiwan University, No.1, Sec. 4 Roosevelt Rd. Taipei 10617, Taiwan

<sup>4</sup>Corresponding author

### Abstract

Iwamoto's anglerfish *Lophiodes iwamotoi* is recorded from New Caledonia for the first time. Study of molecular features further support the validity of the species. Molecular sequence data from the cytochrome c oxidase subunit-I and Rhodopsin loci, along with morphological variation are provided, as well as information on its fresh coloration.

**Key words:** Pieces, Teleostei, Lophiiformes, Lophiidae, New Caledonia

### Introduction

Ho *et al.* (2011) documented the species of the family Lophiidae from the South Pacific Ocean, recognizing seven valid species and describing two new species from Polynesia. One of these, *Lophiodes iwamotoi* Ho, Serét & Shao, 2011 was described on the basis of five specimens collected from the Savannah Seamount of Polynesia at depths of 706–710 m in 1977. These specimens, despite being in good condition, were strongly faded due to long-term preservation.

Recently, the authors examined fish specimens collected during the 39-day exploratory cruise (campaign: EXBODI) by the R/V *Alis* deployed by the French Oceanographic Fleet on seamounts off New Caledonia, in which nine lophiid specimens were recognized. Among them, four are identified as *L. iwamotoi*. Of the remaining five, three were identified as *L. mutilus* (Alcock 1894) and two as *Lophiomus setigerus* (Vahl 1797).

The purpose of the present work is to record this recently described species and its congeners represented in the New Caledonian ichthyofauna. A molecular comparison was undertaken to obtain further data regarding the validity of the species. We discuss this DNA sequence data as well as morphological variation in *L. iwamotoi*, and provide fresh color information on this species for the first time (Fig. 1).

### Material and methods

Nine lophiid specimens were included in the morphological and molecular examination. Whole genomic DNA was extracted from fin clips or muscle tissue of specimens using the Qiagen DNeasy extraction kit (Qiagen, Valencia, CA) according to manufacturer's instructions. Fragments of two protein-coding genes (cytochrome c oxidase subunit-I [COI] and rhodopsin [Rhod]) located in mitochondrial and nuclear genomes, respectively, were amplified and sequenced for this study. Protocols for collecting molecular data follow those outlined in Ward *et al.* (2005) for COI and Chen *et al.* (2003) for Rhod. Collected DNA sequences were deposited in NCBI GenBank (see Fig. 2 for the accession numbers of the corresponding gene sequences). Compiled sequences were manually aligned based on the inferred amino acid translation using Se-Al v2.0a11 (available at <http://tree.bio.ed.ac.uk/software/seal/>).