

Research Article

First record on the occurrence of long fingered gurnard *Lepidotrigla longimana* (Scorpaeniformes: Triglidae) from Bangladesh

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ABSTRACT

This study confirmed the presence of triglid fish *Lepidotrigla longimana* Li (1981) for the first time in Bangladesh waters. Four individuals of this species were collected from Cox's Bazar (21.77 N 91.62 E) on 5 October 2018 as bycatch. The species was taxonomically identified through the traditional morphometric method, which was further validated by a molecular approach based on partial cytochrome c oxidase subunit I (COI) sequences (DNA barcodes). The total length was three times the head length and 4.1 times the body height. The head length was 2.5 times larger than the snout length and 3.2 times the eye diameter. The number of scales on the lateral line was 60. A smaller blue spot is present on the inner side of the pectoral fin. The average K2P distances of the COI sequence within species were 0.53. The sequences clustered together under a single clade in the Maximum likelihood (ML) tree. Morphometric, meristic, and molecular data thus confirmed the species as *L. longimana*.

Introduction

Lepidotrigla Günther (1860), the most diverse genus of the family Triglidae, are small fishes less than 200 mm in standard length and are commonly known as gurnards or sea robins. They are found in the Bay of Bengal, the Andaman Sea off Myanmar (Gomon and Kawai, 2018), and temperate and tropical waters of the eastern Atlantic, Indian, and Western Pacific oceans (Richards, 1992). Richards and Saksena (1977) revised the genus *Lepidotrigla* from the Western Indian Ocean and noted the difficulty of diagnosing it. The presence of two species *L. bispinosa* and *L. piloptera*, has been documented so far from Bangladesh waters (Fanning et al., 2019; Singha et al., 2019). Due to its small size, muddy flavor, and highly bony muscles, the species is non-targeted and has low market

demand. But a recent study attempted the production of bioactive peptides from this species for their abundant protein content (Hu et al., 2022).

Ahmed et al. (2021) have mentioned the presence of this species on the Bangladesh coast, and here in this paper, we describe this gurnard fish, *Lepidotrigla longimana* Li (1981) based on morphometric and molecular approach.

Material and Methods

Sampling and morphological analysis

Four specimens of *L. longimana* were collected on 5 October 2018 from Cox's Bazar (21.77 N 91.62 E) off the coast of the Bay of Bengal. The fishermen caught it during fishing as bycatch along with the fishes of the genus *Nemipterus*

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(Threadfin bream). The specimens were carried to the lab with ice in a coolbox for further analysis. Following Li's (1981) and Richards's (1992) guideline, the specimens were examined. The length was measured in cm scale. A small portion of muscle was taken for DNA extraction and tagged the specimen with a voucher ID (DUZM_MF_159C, DUZM_MF_159C.2, DUZM_MF_159C.3, DUZM_MF_159C.4).

DNA extraction and amplification by PCR

The extraction of genomic DNA was performed by Monarch® Genomic DNA Purification Kit, USA, following the manufacturer's protocol. PCR amplification of the target MT-COI gene and purification of amplified PCR products were performed following Ahmed et al. (2021) and Datta et al. (2020). Approximately 658 bp was amplified from the 5' regions of the MT-COI gene using the primers FishF2 5'TCGACTAATCATAAAGATATCGGCAC3' and FishR2 5'ACTTCAGGGTGACCGAAGAATCAGAA3' (Ward et al., 2005). The quality amplicons were viewed by the Nanodrop spectrophotometer (NanoDrop™ One Microvolume UV-Vis Spectrophotometer).

Sequencing and Phylogenetic Analysis

The sequencing was performed in First BASE Laboratories SdnBhd, Malaysia. CHROMAS

software was used to view the raw sequences and edited manually using MUSCLE. BLAST verified the sequence, and only the best matches with more than 96% similarity were submitted to the NCBI GenBank. Analyses were performed by MEGA X software (Kumar et al., 2018). The Maximum-Likelihood (ML) phylogenetic tree was constructed using the K2P model (Kimura, 1980).

Diagnosis

L. longimana closely resembles to *L. venusta* Fowler (1938). Both throat and breast are covered with scales. Pectoral fin rays are long and finger-like and reach the origin of the anal fin. A dark spot is present on the anterior dorsal fin where in posterior is absent. The species can be separated from *L. venusta* by the number of scales on the lateral line. The number of scales on the lateral line is 60 in the former species and 52-54 in the latter. A smaller blue spot is present on the inner side of the pectoral fin in *L. longimana*.

Results & Discussion

Description

The color of the body and head is red, and the ventral side is lighter. The center of the inner surface of the chest is long and blue (Fig. 1). The throat and breast are covered with scales, dorsal fin with 9 spines and 14 rays. A dark black spot is



Fig. 1. *Lepidotrigla longimana* (10 cm), family Triglidae, voucher ID DUZM_MF_159C.2, collection date: 5-October-2018, place: Cox's Bazar (21.77 N 91.62 E)

present on the anterior and posterior dorsal fin without a spot (Fig. 1). The pectoral fin is long and finger-like and reaches the origin of the anal fin with 11 and 3 free rays. A smaller central blue spot is present on the inner side of the pectoral fin. The total length is 3 times of the head length and 4.1 times the body height (Table 1). The head length is 2.5 times larger than the snout length and 3.2 times the eye diameter. A total of 60 scales are present on the lateral line.

Table 1. Morphometric data of the specimens of *Lepidotrigla longimana* (DUZM_MF_159C to 159C.4)

Measurements (cm)	Present study (N=4)	Li (1981)
Total length (TL)	9.5	
Body height	2.3	
Standard length (SL)	7.5	
Head length (HL)	3.2	
Eye diameter (ED)	1.0	
Inter orbital length (IOL)	0.7	
Snout length (SnL)	1.3	
Pectoral length (PL)	3.0	
Free pectoral length (FPL)	1.7	
Caudal Fin length (CFL)	2.0	
Caudal peduncle length (CPL)	1.2	
Caudal peduncle depth (CPD)	0.4	
HL/SnL	2.5	2.1-2.6
HL/ED	3.2	3-3.5
TL/HL	3.0	2.9-3.3
TL/BH	4.1	4-4.8
Counts		
Dorsal fin	IX+14	IX+1-14
Anal fin	15	15
Pectoral fin	11+ 3 free	11+ 3 free
Ventral fin	I+5	I+5
Caudal fin		
Scales in lateral line	60	60

Molecular analysis

The generated three partial sequences of the COI gene with an average of 634 bp of the three specimens were submitted to the NCBI database with assigned accession numbers MN083140, MN083141, and MN083142. The species was confirmed through BLAST search having 99% query coverage and 95.59% identity with the pre-existing JQ681320 and 95.53% with KP266831, which validated the morpho-taxonomic identification of the species. The mean nucleotide base frequencies were T: 27.17%, C: 33.00%, A:22.18%, and G: 17.66%. GC content analysis showed that the average GC was 50.66% and AT 49.34%. The GC contents were found at the first, second, and third codon positions at 57.17%, 42.43%, and 52.36%, respectively. The K2P distance within species was 0.53. The nearest species were found, *L. hime*, which was 5.33% distant from *L. longimana*, and *L. abyssalis* was the distant species (Table 2). Phylogenetic analyses showed that highly similar species formed a distinctive clade.

Table 2. Genetic divergence (% K2P distance) of *L. longimana* with other species

Species	Interspecies Distance %
<i>L. longimana</i> <i>L. hime</i>	5.33
<i>L. kishinouyi</i>	5.63
<i>L. dieuzeidei</i>	5.66
<i>L. bispinosa</i>	6.30
<i>L. alata</i>	6.61
<i>L. argus</i>	7.66
<i>L. multispinosa</i>	7.70
<i>L. cavillone</i>	7.84
<i>L. mulhalli</i>	9.39
<i>L. abyssalis</i>	12.04

A total of 22 sequences of 12 species were used, where three were from the present study, and the rest were retrieved from NCBI Genbank. *Pterygotrigla hemisticta* was used as an outer genus of triglidae family. *L. longimana* formed a distinctive clade with a bootstrap value of 98 in

the phylogenetic tree, and other species formed clades as of their similarities (Fig. 2). Classical taxonomy based on morphometric and meristic characters along with DNA barcoding confirms the species as *L. longimana*.

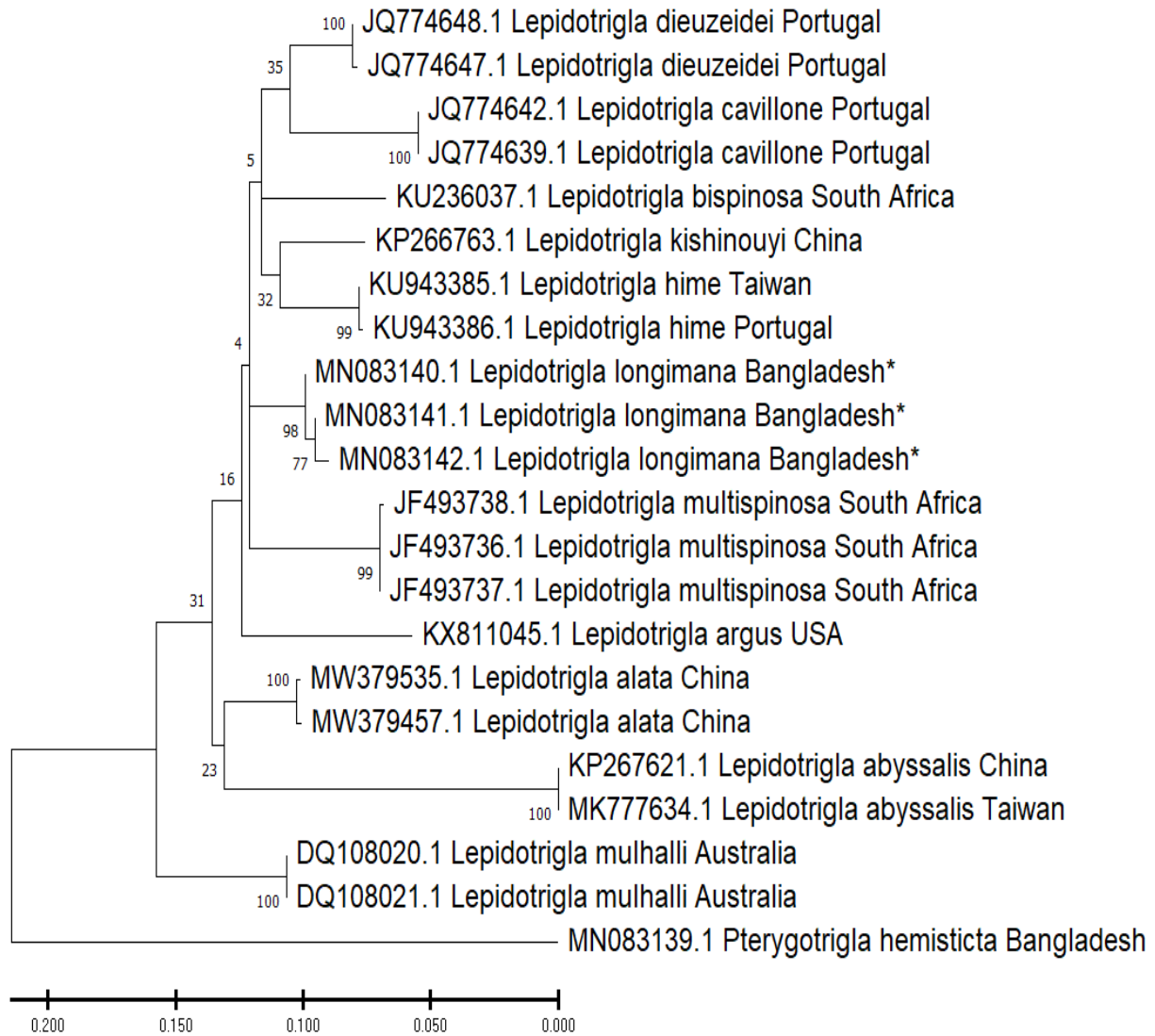


Fig. 2. Maximum Likelihood tree of the COI sequences showing the relationships among *Lepidotrigla longimana* with the pre-existing sequences of *Lepidotrigla* species of the NCBI GenBank. *Pterygotrigla hemisticta* was taken as an outgroup. (The sequences generated in this study are marked as Bangladesh*).

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