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First record of *Mugilogobius chulae* (Smith 1932), (Gobiiformes: Oxudercidae) from the Andaman Islands, India

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Abstract

This study constitutes first record of *Mugilogobius chulae* from the South Andaman Islands based on seven specimens collected from a shrimp pond. The species was confirmed based on integrated taxonomy. Three COI gene sequences were generated, and the genetic analysis suggests a raw pairwise sequence distance of 7.0–7.5%, indicating a species complex or inter-species gene variations due to geographical isolation.

Key words: *Insular, Goby, Mangrove, Diversity, New report.*

Introduction

The Andaman and Nicobar (ANI), an archipelago situated in the Bay of Bengal, between 6°45′ N-13°41′ N and 92°12′ E-93°57′ E is biodiversity hotspots for plants, terrestrial and aquatic fauna. This archipelago possesses some endemic freshwater fish like *Aplocheilus andamanicus*, *Microphis insularis* and *Sicyopterus garra*. The earliest ichthyological work are known from the work of Day (1870), Annandale and Hora (1925), Mukerji (1935), Herre (1939, 1940 & 1941), Koumans (1940), Sen (1975), Starmühlner (1978). This was followed by Talwar (1990), Rao *et al*., (2000), Vijay and Priya (2009), Devi (2010), Rajan and Sreeraj (2013), Rajan *et al*., (2013), Rajan and Sreeraj (2014 a, b and c), Kumar *et al*., (2016), and in the recent times from the works of Praveenraj *et al*., (2017a, b, c, d, 2018 & 2022). The fish fauna of ANI still remains unexplored and new records and new species continues to get discovered. During a visit to shrimp pond located at South Andaman District, specimens of *Mugilogbius chulae* were collected. The present work serves to report *M. chulae* as a new distributional record to the ANI based on integrated taxonomy.

Materials and methods

Specimens of *Mugilogobius chulae* were collected from a shrimp farm besides a mangrove patch located at South Andaman Islands (11°43’03.0”N 92°40’08.8”E). Collected specimens were maintained in an aquarium for photography and subsequently euthanized with clove oil and fixed in 10% formalin for further study. Measurements were made with a digital caliper to accuracy of 0.1 mm, and the meristic counts were taken with an aid of stereo zoom microscope under a transmitted light following Hubbs and Lagler (1958) and Larson (2001). Vertebrae were counted from one cleared and stained specimen (CIARI/FF-24, 26.0 mm SL). Only the larger specimen of *M. chulae* (~20 mm SL) was used for measurements, while the smaller specimens (n=3) were used for DNA studies.

Genetic analysis

Total genomic DNA was isolated from three small specimens using the DNeasy Blood & Tissue KitsTM (Qiagen, Germany) following manufacturer’s guidelines. The mitochondrial cytochrome c oxidase unit I (COI) partial gene (650 bp) was amplified using the PCR conditions and primers described in Ward *et al*., (2005). The resulting PCR products were purified and sequenced in forward and reverse directions using an ABI 3500 DNA analyser (Eurofins Pvt. Ltd., Bangalore). Sequence quality was assessed by examining the Phred score of each base using FinchTV software. The open reading frame of the sequence was confirmed using the NCBI ORF finder tool (https://www.ncbi.nlm.nih.gov/orffinder/). The final COI gene sequences obtained were submitted to NCBI GenBank under the accession numbers PQ269304-306 (n=3). Sequence alignment was performed using Clustal-W, integrated with MEGA XI Tamura *et al*., (2021). Sequences were trimmed at the ends to ensure uniform length, and genetic distance values were estimated using MEGA XI. Maximum likelihood tree was constructed using mitochondrial CO1 gene sequences in IQ-TREE 2 software Minh *et al.,* (2020) aiding best-fit model (HKY+F+G4) according to BIC score using ModelFinder Kalyaanamoorthy *et al*., (2017) and ultrafast bootstrap (UFBoot, 20000 replicates) Hoang *et al.,* (2018). Tree image was visualized using Interactive Tree of Life v6 Letunic and Bork (2024).

Results

Mugilogobius chulae

Material examined: CIARI/FF-124, 4 ex., 17.2–26.8 mm SL, 2 ♂ (26.0 & 26.8 mm SL), 2♀ (17.2 & 23.3 mm SL); 11.7175 N, 92.6691 E, Brindaban Village, South Andaman Islands; collected by J. Praveenraj and team**,** 5.3. 2024.

Description

See Fig. 1 for general appearance and Table 1 for morphometry details. Body slender and elongated, oval in cross section anteriorly and compressed, less so anteriorly. Head wider than deep, broad and depressed in males. Eyes large, located dorso-laterally. Mouth sub-terminal with upper jaw slightly extending just over lower jaw, with fleshy lips; cheeks muscular. Scales on body ctenoid. Cheek without scales, opercular and pectoral fin base with cycloid scales. Prepelvic with cycloid scales. Belly with patches of ctenoid scales under pelvic region. Sides with ctenoid scales extending forward in narrow wedge to behind pectoral fin, extending above its base. Genital papilla in male elongated, flattened, narrowing to pointed tip; in female, short, rounded with blunt tip. Position of second dorsal fin opposite to origin of anal fin. Caudal fin rounded. First spine of first dorsal fin long and produced as filament, its length 115% of HL and 30% of SL. First dorsal fin with 4–5 spines, second dorsal and anal fin with 1 spine and 7 soft rays. Pectoral with 15 rays, and caudal fins with 14–16 rays. Longitudinal scales 26–31, transverse scales 8, caudal scales 8, predorsal scales 10–15, total vertebrae 26 (10 precaudal, 16 caudal vertebrae).

Table 1: Morphometry of *Mugilogobius chulae* (n=4)

Morphometric characters (n=4)		
Standard length (mm)	17.2–26.8	
Character	**Range**	**Mean±SD**
Head length in SL	26.4–30.0	28.3±1.6
Head width in HL	69.4–73.9	70.9±2.1
Body depth in SL	18.4–23.3	20.3±2.1
Caudal-peduncle length in SL	19.1–27.4	23.6±3.6
Caudal – peduncle depth in SL	11.9–13.9	13.3±0.9
Snout length in HL	17.1–29.0	24.7±5.3
Eye width in HL	22.8–30.5	27.3±3.3
Jaw Length in HL	35.5–55.0	47.4±8.3
Interorbital length in HL	23.1–36.5	29.5±5.5
Pectoral Length in SL	15.7–20.9	19.0±2.3
Pelvic length in SL	14.3–18.2	16.5±1.6
Caudal Length in SL	27.2–28.8	28.1±0.8
Longest D1 spine in SL	18.3–29.6	26.2±5.3

Colouration in life: Body grayish to golden yellow (Fig. 1). Snout dark gray with a golden yellow tinge. Inter-orbital region black. First dorsal fin greyish brown with a black spot in the middle 2nd to 5th fin spines bordered by bluish margin anteriorly covering, anterior fin margin yellow, a white filament produced in the first spine. Second dorsal fin base pale brown, followed by translucent yellow mid fin and yellowish white anterior margin. The membrane covering 1st spine to 5th ray is with a combination of yellow and white. Caudal fin translucently grayish with yellow sub-margin, its rays black; basal margin with two spots on dorsal and ventral portion. Anal fin translucently grayish with white narrow margin. Pectoral fins translucent yellow. Body overall greyish brown with 6 black transverse bars, first one incomplete, originating prior to the first dorsal fin base and in line with the pectoral fin base; second bar complete, originating in the middle of first dorsal fin and extending up to belly followed by incomplete 3rd and complete 4th, 5th and 6th bars all extending ventrally. Posterior portion of head with an incomplete bar. Peritoneum white. In male, scales on sides darkened around margins, appearing marbled.

Figure 1: ***Mugilogbius chulae,*** **colouration of live specimens, CIARI/FF-124, A. Male, 26.8 mm SL, B. Female, 23.3 mm SL.**

Figure 2: ***Mugilogobius chulae,*** **colouration in preservative, CIARI/FF-124, male, 26.8 mm SL.**

In preservative: (Fig. 2) Overall body pale gray with black bars. All fins dark gray, except pectoral fin hyaline. Yellow colour on fins replaced by pale white.

Discussion

Mugilogobius chulae Smith (1932) was described from Kohi Samui, Gulf of Siam, Thailand. The species is known to be restricted to the south-east Asian archipelago; ranging from estuaries in the southernmost islands of Japan, Hong Kong, Thailand, Sri Lanka, Singapore, Malaysia, Borneo, Philippines and Indonesia, with Palau being its easternmost point of distribution Larson (2001). From the Indian sub-continent the species was also recorded from Sri Lanka. However, till date its presence in the regions between south-east Asian Archipelago and the Indian sub-continent was not recorded. The present record constitutes the first report of *M. chulae* from the Andaman Island, India (Fig. 3.). Previously, only *M. tigrinus* was known to be distributed in the Andaman Islands reported by Praveenraj *et al*., (2017). The record of *M. chulae* from Andaman Islands reveals its extended distribution towards northeast of the Indian Ocean. From the mainland of India, only two species of *Mugilogobius* were reported till date, *viz*. *M. tigrinus* and *M. rambaiae* Moulitharan *et al.,* (2023); Sreeraj *et al.,* (2024 a & b); in addition to that, the present record of *M. chulae* constitute an addition to the genus *Mugilogobius* species diversity. Genetic analysis based on COI sequences of *M. chulae* from the Andaman Islands revealed a pairwise sequence divergence of 7.0–7.5% among the specimens, suggesting the presence of a species complex or significant interspecific genetic variation likely driven by geographic isolation. Maximum likelihood tree also suggests that *M. chulae* is a species complex involving atleast 3-4 cryptic species (Fig. 4). Therefore, future works involving integrated taxonomy of the specimens across its distributional range may reveal new species from this complex.

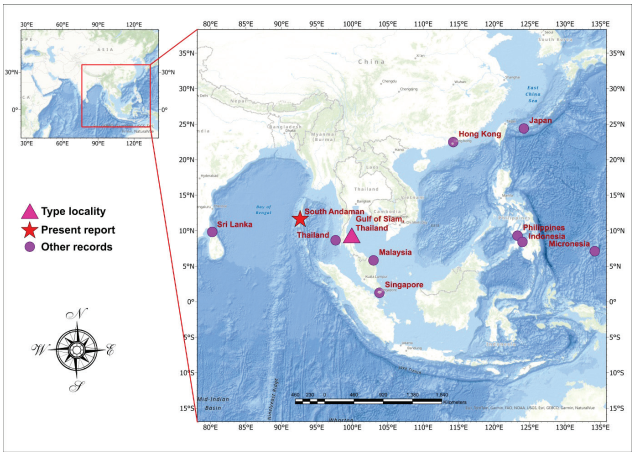

Figure 3: Distribution and present record of *Mugilogobius chulae* in South East Asia, and Indian subcontinent.

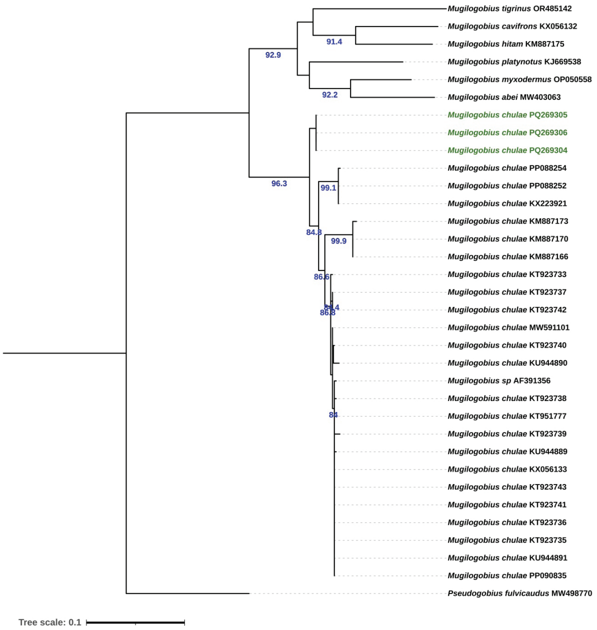

Figure 4: The maximum likelihood tree of *Mugilogobius chulae,* and the related species were plotted with the model of BIC: HKY+F+G4 with 20000 bootstrap replicates, based on mitochondrial COI gene sequences (bp). Each node represents branch support values.

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Author contributions

JP: Data preparation, molecular analysis and original draft preparation; MK, CR, NM: Morphological study and plates preparation; RKS, KS: field sampling and critical analysis. All authors read and approved the final manuscript.

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Data availability

The genetic data generated from this study are deposited in the NCBI GenBank and are accessible to workers. The data that support the findings of this study are available on request from the corresponding author.

Declarations

Conflict of interest

The authors declare that there is no conflict of interest among the authors regarding the publication.

Ethical approval

The species examined in this study are not listed under any schedule or protection category of the Wild Life (Protection) Act, 1972, Government of India. DNA isolation was performed using tissue obtained from the small dead specimens. Therefore, ethical clearance certification was not required.

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