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Confirmation of hilsa shad (*Tenualosa ilisha*) in Vietnamese waters: a morphological and genetic analysis

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Abstract

One specimen of tropical shad was caught from the Giang Thanh River, Kien Giang province, Vietnam in a survey on 16 October 2022. We identified the specimen as the hilsa shad, *Tenualosa ilisha* Hamilton, 1822 using morphological analysis, and further validated by its cytochrome oxidase subunit I (COI) sequence. The specimen was 418 mm long, 1428 g in weight, with a head length of 29.0% and pectoral fin length of 31.1% of its standard length. Notably, the presence of 34 scutes, a higher gill raker count and a caudal fin length within the moderate range for *Tenualosa* species distinguished it from *T. macrura, T. toli* and *T. reevesii*. The COI sequence of the sample matched closely to the *T. ilisha*. The results confirm that *T. ilisha* still endures Vietnamese water, where it was thought to be extinct. Climate change and Indo-Pacific Ocean currents may introduce expansion of distribution area of the *T. ilisha*. Further studies on distribution of the *T. ilisha* and other *Tenualosa* species and their dynamics are needed.

Introduction

The aquatic ecosystems of Southeast Asia harbour a rich biodiversity (Koh and Sodhi, 2010; Liu, 2013; Hughes, 2017), with various fish species contributing significantly to the region's ecological and economic dynamics (Todd *et al.*, 2010; Pomeroy *et al.*, 2019). *Tenualosa ilisha* is a highly valued fish species in South Asia and some Middle Eastern countries (Hossain *et al.*, 2019a; Hossain *et al.*, 2019b), where it has economic, cultural and ecological significance (Khan *et al.*, 2020; Bandara and Wijewardene, 2023). They are anadromous fish and migrate from marine to freshwater environments for spawning (Bhaumik, 2015a; Hossain *et al.*, 2016; Asaduzzaman *et al.*, 2019b; Asaduzzaman *et al.*, 2020). However, the distribution and population status of *T. ilisha* in different regions is poorly understood, especially in the Vietnamese water, where it was thought to be extinct due to overfishing, habitat degradation and climate change (Blaber *et al.*, 2023).

Previous studies on *T. ilisha* focused on its biology, ecology and fisheries management in the Bay of Bengal and the Persian Gulf (Bhaumik, 2017; Hossain *et al.*, 2019a, 2019b), where it is more abundant and accessible (Bhaumik, 2015a; Sarker *et al.*, 2023). However, consistent, reliable data on the occurrence, abundance and genetic diversity of *T. ilisha* in the South China Sea is lacking. Moreover, only one study documented the existence of *T. ilisha* in Vietnamese water but without support data (Nguyen and Nguyen, 1994; Turan *et al.*, 2004). We aimed to survey *T. ilisha* in Vietnamese water and confirm the sampled species using both morphological and molecular data.

Materials and methods

We set up six trawling trips and surveyed from offshore to the estuary area of the Giang Thanh River, Kien Giang Province, Vietnam (Figure 1). Temperature and salinity were determined using a conventional CTD profiler (Compact-CTD Lite, JFE Advantech, accuracy \pm 0.03) (Miyata *et al.*, 2016). Only one individual of *Tenualosa* species was captured on 16 October 2022 (Figure 2). Morphometric characters of the specimen were measured following a methodology outlined in a previous study (Arai and Amalina, 2014).

Fin and tissue samples were preserved in 96% ethanol for subsequent analysis. DNA was extracted using an Ezup Column Animal Genomic DNA Purification Kit (Sangon, Shanghai, China). Cytochrome oxidase subunit I (COI) gene was amplified using standard COI gene primers designed for the Clupeiformes in our lab (COI-F GGAGCTACAATCCGCCGCCTA and COI-R GGTTCGATTCCTYCCTTTCTCGTT). Each PCR reaction contained 2.0 μ l of DNA sample, 2.5 μ l of each 10 μ M of each primer, 50 μ l of the QIAGEN Taq PCR Master Mix and 43 μ l of distilled water. The PCR reaction condition was as follows: initial denaturation: 94°C for 5 min; 32 cycles of 94°C for 30 s, primer annealing at 62.9°C for 30 s and extension at 72°C for 1 min; with a final extension at 72°C for 7 min. Finally, the PCR products were analysed by using 1.5% agarose gel electrophoresis with Biotium – Gel Red. The sequences were



Figure 1. Collection sites of the Tenualosa specimen in the Kien Giang province of Vietnam. A black circle on the map indicates the sampling location.

determined through Sanger sequencing at Sangon Biotech. Chromatographs were used to check and edit sequences, which were assembled using Codon Code Aligner software (Centerville, MA, USA).

The COI gene sequence was lodged in NCBI as *T. ilisha* OR088067. The COI sequence was compared with the sequences of other *Tenualosa* for species identification using BLAST. The sequence obtained in this study also was aligned to other *Tenualosa* species (KX786670.1, KY751995.1, Nc 016682.1, NC 016719.1, MK572252.1) with *Gudusia chapra* (MK572252.1) as the outgroup using the MUSCLE algorithm. A neighbour-joining tree (NJ tree) was reconstructed under the Kimura 2-Parameter model selected by using MEGA XI (Mello, 2018).

Results

The water parameters at the sampling location: temperature ranged from 28.4 to 31.7° C and salinity from 25.0 to 28.0 ppt. The specimen was 418 mm in length and 1428 g in weight, showing a size-weight correlation within its species (Nima *et al.*, 2020). It had a head length of 29.0% and pectoral fin length of 31.1% of its standard length, indicative of its unique body proportions (Salini *et al.*, 2004; Hossain *et al.*, 2022). Notably, the presence of 34 scutes aided in species identification (Tint *et al.*, 2019). The specimen showed a higher gill rakers count of 283, and a caudal fin length within the moderate range for *Tenualosa* species (Table 1), distinguishing it from *T. macrura*, *T. toli* and *T. reevesii*.



Figure 2. Photograph showing the *Tenualosa ilisha* (418 mm in TL) collected in Vietnam.

The amplified COI gene of the specimen was 1532 bp in length and 98.76% match with *T. ilisha* sequences in GenBank (NC_016682.1). The reconstructed phylogenetic tree confirmed that the Giang Thanh River specimen is a *T. ilisha* (Figure 3). A close relationship between *T. ilisha* and *T. toli* was supported by a 100% bootstrap value.

Discussion

Prior research suggested that the T. ilisha was extinct in the South China Sea (Arjunaidi et al., 2016; Blaber et al., 2023). The discovery of them in Vietnamese Giang Thanh River suggests a broader migratory pattern or habitat adaptation within the Indo-Pacific region. The T. ilisha is an indigenous anadromous fish in the Indo-Pacific (Brierley and Kingsford, 2009; Hossain et al., 2019a), inhabiting the coasts, estuaries and rivers of southern Asia countries (Sahoo et al., 2018; Ghosh et al., 2022). Its habitat preferences include extensive continental shelves (Hossain et al., 2016; Dwivedi, 2019), monsoonal influences, significant precipitation and runoff (Naskar et al., 2017; Leal Filho et al., 2022), surface temperatures of 20-30°C (Kundu et al., 2020), seasonally shifting currents (Hossain et al., 2019b), moderate organic productivity (Sarker et al., 2016) and coastal waters with lower salinity (Mohindra et al., 2023). The water conditions at the sampling location are suitable for the T. ilisha's growth and survival (Fernandes et al., 2016; Das et al., 2020; Dalpadado et al., 2021). This finding is significant as it suggests that the Giang Thanh River could serve as a previously unrecognized habitat or migration pathway for this species. Nonetheless, further studies are essential to assess the population size, genetic variation and ecological impact of the T. ilisha in Vietnamese water.

The specimen has a shorter head and longer tail than *T. toli* and *T. reevesii*, similar head length and caudal fin length to *T. macrura*, but higher in the number of gill rakers than *T. toli* and *T. macrura* (Table 2). This variation possibly reflects its wide geographic range, ecological diversity, feeding habits and preferences (Borah *et al.*, 2022; Sarker *et al.*, 2023). These differences can distinguish *T. ilisha* from *T. macrura*, *T. toli* and *T. reevesii*, which often get confused due to their similar appearance

Table 1. Morphometric measure and meristic characters of the *T. ilisha* specimen

Character	Range
Body weight (B)	1428 g
Morphometric (mm)	
1. Total length (TL)	418
2. Fork length (FL)	357
3. Standard length (SL)	347
4. Pelvic fin length (PVFL)	33
5. Pectoral fin length (PFL)	54.7
6. Caudal fin length (CFL)	107
7. Predorsal length (PDL)	144
8. Preanal length (PAL)	234
9. Prepectoral length (PPCL)	63
10. Prepelvic length (PPVL)	142
11. Length of dorsal fin base (LDFB)	136
12. Length of anal fin base (LAFB)	138
13. Mouth height (MH)	46
14. Upper jaw length (UJL)	47
15. Lower jaw length (LJL)	39
16. Length of caudal peduncle (LAFB)	51
17. Depth of caudal peduncle (DCP)	35
18. Body depth (BD)	111
19. Body width (BW)	56
20. Snout length (SNL)	27
21. Eye diameter (ED)	23
22. Head length (HL)	76
23. Girth	305
24. HL% of SL	29%
25. CFL% of SL	31%
26. PVFL% of SL	9.51%
Meristic	
27. Dorsal fin ray (DFR)	18
28. Anal fin ray (AFR)	20
29. Pectoral fin ray (PCFR)	15
30. Pelvic fin ray (PVFR)	9
31. Prepelvic scutes (PrePVSC)	19
32. Postpelvic scutes (PostPVSC)	17
33. Total number of scutes (TSC)	34
34. Gill raker on lower arch of the first-gill arch	283

TL, total length; SL, standard length; g, grams.

and overlapping distribution (Bhaumik, 2015b). However, morphological identification alone may not be sufficient or accurate, and molecular genetic analysis is often needed to confirm the species identity and phylogenetic relationships of *Tenualosa* species.

Although *T. ilisha* is found in Bruneian and Malaysian waters (Azri *et al.*, 2020), only one record *T. ilisha* was found in Vietnam in 1994, with no supported data (Nguyen and Nguyen, 1994). The complexity of visually identifying *Tenualosa* species needs molecular genetic analysis for validation. The confusion in

morphological identification among these species can be attributed to their genetic similarities and differences (Rahman *et al.*, 2018; Abdullah *et al.*, 2021; Afrand *et al.*, 2023). The BLAST analysis revealed that the *T. ilisha* sample from Kien Giang closely matched the Indian hilsa species, with a 2708 score reflecting a high gene sequence similarity. The 98.76% query cover confirms extensive sequence overlap, suggests a significant genetic link and a common evolutionary background between the two populations. The NJ tree (Figure 3) also suggested that the Kien Giang sample is *T. ilisha*.

The phylogenetic analysis indicated *T. ilisha* and *T. toli* are closely related (Figure 3), as evidenced by a 10,000 bootstrap value, suggesting a strong genetic link between the two species. This close relationship implies they share similar appearances and structures, which leads to confusion when naming them based solely on morphology. On the other hand, *G. chapra*, the outgroup species, appears to be distantly related to *T. ilisha*, and shows significant genetic divergence (Egana *et al.*, 2018; Milec *et al.*, 2022). This genetic distance helps to clarify the evolutionary lineage of *T. ilisha* and its separation from the outgroup species (Sarker *et al.*, 2021; Sultana *et al.*, 2022).

The low genetic diversity and the presence of admixed individuals without precise grouping could further contribute to the morphological confusion (Jorde and Wooding, 2004; Slovák et al., 2012; Holm et al., 2018; Garmendia et al., 2022). Recent studies highlighted the low genetic variation within T. ilisha populations, suggesting a single panmictic population with admixture from other populations (Sarker et al., 2021). Moreover, the genetic population structure of T. ilisha is influenced by its highly migratory nature (Mohindra et al., 2019; Habib et al., 2022; Sultana et al., 2022). The presence of distinct genetic barriers, limited gene flows and complex evolutionary processes has resulted in a significant population genetic and phylogeographic structure for T. ilisha (Asaduzzaman et al., 2019a; Habib et al., 2022). The genetic relationships and evolutionary history of T. ilisha are complex and influenced by various factors, including migration patterns, genetic diversity and population structure (Asaduzzaman et al., 2019a, 2020). These factors play a crucial role in the morphological similarities and differences observed among Tenualosa species and have important implications for their identification and conservation.

Climate change significantly affects species distribution, as warmer temperatures and altered sea conditions disrupt marine ecosystems and migration (Harley et al., 2006; Brierley and Kingsford, 2009; Doney et al., 2012). The presence of Tenualosa in Vietnam's Kien Giang Sea is influenced by climate change (Mitra and Mitra, 2013), and ocean currents (Blaber, 2002; Habib et al., 2022). The occurrence of T. ilisha in Malay and Brunei (Roberd et al., 2019; Yakup et al., 2019; Azri et al., 2020) implies climate-driven range shifts explain its presence in the Kien Giang Sea. Genetic studies corroborate revealing the species' evolutionary links and possible migration routes (Asaduzzaman et al., 2019b, 2020). Closeness of India to the Kien Giang Sea suggests a dispersal path, aided by ocean currents serving as natural passageways. Comprehending these elements and their interactions is crucial for understanding the effects of climate change on marine life diversity and formulating effective preservation measures.

Conclusion

Our study confirmed the presence of T. *ilisha* in Vietnamese waters, a species once considered extinct locally. Utilizing the COI gene for molecular identification, we emphasize the necessity of refined molecular techniques testing uncertain morphological traits. The detection of T. *ilisha* indicates potential novel



Figure 3. Phylogenetic tree of four species of the *Tenualosa* genus based on cytochrome oxidase subunit I (COI) gene sequences and *Gudusia chapra* from the same family as the outgroup. The neighbour-joining (NJ) tree was reconstructed using K2P model with 10,000 replications for bootstrap analysis.

Table 2. Distinctive biological characters and geographical distribution of five Tenualosa species found in Indo-Pacific region (Yakup et al., 2019)

T. ilisha	T. toli	T. macrura	T. reevesii	T. thibaudeaui
Caudal fin moderate, 25– 31% of CFL % of SL	Caudal fin relatively short, 31–34% of CFL % of SL	Caudal fin long, 40–42% of CFL % of SL	Caudal fin moderate, 25–31% of CFL % of SL	Caudal fin moderate, about 25–30% of CFL % of SL
Gill rakers fine and numerous, about 100–250	Gill rakers fine but not numerous, 60–100	Gill rakers fine but not numerous, 60–75	Gill rakers fine and numerous, 80–250	Gill rakers fine and very numerous, 204–316
Indo-West Pacific	Indo-West Pacific	Western Central Pacific	Northwest Pacific	Mekong endemic, middle to the Delta

CFL % of SL, ratio of caudal fin length for standard length.

migratory routes, warranting further exploration of its movement and habitat choices, and reassessment of conservation tactics and the advocacy of sustainable fisheries to preserve its existence. Future research should target the ecological elements aiding endurance of *T. ilisha* in Vietnam and the development of collective management approaches with community, policy and research stakeholders.

Data availability. The data sets include morphological measurements and genetic sequences are available at NCBI: **OR088067** of *T. ilisha* specimen collected from Vietnamese waters.

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Author contributions. Vanthu Giap conceived the study, designed and coordinated the research, performed molecular genetic studies and sequence alignment and drafted the manuscript. Md Rashedur Rahman conducted molecular genetic experiments. Chenhong Li provided resources, reviewed and edited the manuscript, supervised the project and provided funding. All authors read and approved the final manuscript.

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Competing interest. None.

Ethical standards. The *Tenualosa ilisha* specimen was collected and examined under the ethical standards and guidelines of the Institute of Aquaculture, Nha Trang University, Vietnam, and in compliance with local regulations and permissions granted by the appropriate Vietnamese authorities. The specimen's welfare and conservation were prioritized, and all ethical considerations, particularly regarding handling and identification, met international standards.

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