Acta Ichthyologica et Piscatoria 53, 2023, 137–145 | DOI 10.3897/aiep.53.103343

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ACTA ICHTHYOLOGICA ET PISCATORIA

# A new record of *Upeneus pori* (Actinopterygii: Syngnathiformes: Mullidae) from the South China Sea: Integrating morphology and DNA barcoding

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**Academic editor:** Jolanta Kiełpińska ♦ **Received** 11 March 2023 ♦ **Accepted** 29 August 2023 ♦ **Published** 2 October 2023

**Citation:** Luo Z, Yi M, Gu S, Lin H-D, Yan Y (2023) A new record of *Upeneus pori* (Actinopterygii: Syngnathiformes: Mullidae) from the South China Sea: Integrating morphology and DNA barcoding. Acta Ichthyologica et Piscatoria 53: 137–145. https://doi.org/10.3897/aiep.53.103343

## Abstract

This study constitutes the first record of the Por's goatfish, *Upeneus pori* Ben-Tuvia et Golani, 1989, from the South China Sea. This fish had formerly only been reported in the western Indian Ocean. Six specimens of *U. pori* collected from the South China Sea were identified through comparisons of morphology and molecular analysis. *Upeneus pori* and *Upeneus tragula* Richardson, 1846 are very similar. The difference is that the former has seven spines in the first dorsal fin, lacks any spots or blotches on its body, and exhibits white or creamy white barbels. The latter has eight spines in the first dorsal fin, exhibits black spots on its body, and displays orange-colored barbels, along with different caudal fin patterns. Pairwise genetic distance computation demonstrated that *U. pori* exhibits a very low genetic distance from sequences of the other three recorded *U. pori* species found in the type locality of Israel, Red Sea, as documented in GenBank. These findings provide compelling evidence of the Por's goatfish's presence in the South China Sea.

## Keywords

*COI*, morphometry, novel distribution, south coast of China, taxonomy

## Introduction

The family Mullidae is composed of 100 species and six genera (Fricke et al. 2023) that are distributed in the Atlantic, Indian, and Pacific oceans and rarely found in brackish waters (Uiblein and Gouws 2014; Chen and Zhang 2015; Nelson et al. 2016). The mullids are otherwise known as goatfishes and have two independently moving hyoid barbels that contain chemical receptors used for detecting sand or holes in the reef to search for bottom-dwelling invertebrates. Until recently, the family Mullidae had been affiliated with the order Perciformes. Since 2022 it has been placed in Syngnathiformes (see Nash et al. 2022), which is accepted by (Fricke et al. 2023). A total of twenty-eight species of goatfishes, representing three genera (*Mulloidichthys*, *Parupeneus*, and *Upeneus*), have been recorded in China (Cheng et al. 1962; Shen 1993; Randall 2001). With the highly exhibited diversity of the goatfishes, the genus *Upeneus* Cuvier 1829 was revised by Lachner (1954), but only ten species were known at that time. Subsequently, Uiblein and Heemstra (2010) studied and verified the morphological characteristics of

26 species of *Upeneus* and summarized the taxonomy of this genus. They pointed out that 25 of the 26 species could be separated into four taxonomic groups (*japonicus* group, *tragula* group, *moluccensis* group, and *vittatus* group). Later, an increasing number of new species of *Upeneus* were described and new records of known species were reported worldwide using alpha taxonomy alone or in combination with barcoding approaches. To date, the number of valid species of the genus *Upeneus* has reached 47 species (Fricke et al. 2023) and there are seven taxonomic groups (*japonicus* group, *tragula* group, *moluccensis* group, *stenopsis* group, *margarethae* group, *suahelicus* group, *pori* group) (Uiblein and Maclaine 2021). The majority of these discoveries were concentrated in the Indian and Atlantic oceans (Yamashita et al. 2011; Nicolaidou et al. 2012; Uiblein and Lisher 2013; Bos 2014; Uiblein and White 2015; Uiblein et al. 2016, 2017, 2019, 2020; Deidun et al. 2018; Uiblein and Motomura 2021).

Since the discovery of *Upeneus quadrilineatus* Cheng et Wang, 1963, from the East China Sea, neither new species nor new records of *Upeneus* have been reported from this body of water. As recently as 2019, a new species *Upeneus heterospinus* Uiblein et Pavlov, 2019 was described, based on the material collected from the South China Sea (Uiblein et al. 2019). Thus, the following nine goatfishes of the genus *Upeneus* have been recorded in China: *Upeneus tragula* Richardson, 1846; *Upeneus vittatus* (Forsskål, 1775); *Upeneus subvittatus* (Temminck et Schlegel, 1843); *Upeneus sulphureus* Cuvier, 1829; *Upeneus moluccensis* (Bleeker, 1855); *Upeneus japonicus* (Houttuyn, 1782); *Upeneus luzonius* Jordan et Seale, 1907; *U. quadrilineatus*; and *U. heterospinus*. According to research related to the diversity and distribution of goatfishes in the western Pacific by Jiao and Chen (2000), the biodiversity of goatfish plummets from southern to northern waters in the China Sea. These authors also considered that the destruction of coral reefs has led to a sharp decline in fish production and some common species are difficult to find.

## Materials and methods

Six specimens of fishes visually representing a species of the genus *Upeneus* were collected from the local fish markets in coastal cities near the northwestern South China Sea (Fig. 1). All specimens were caught by bottom trawling. Detailed collection information is given in Table 1. According to the key morphological characteristics provided by Ben-Tuvia and Golani (1989), these specimens were examined, identified, and deposited in the College of Fisheries, Guangdong Ocean University. We performed a morphometric examination on six samples according to the measurement and counting method by Uiblein and Heemstra (2010) and compared them with paratypes from the Red Sea described by Ben-Tuvia and Golani (1989). Standard length (SL) and other measurements were made

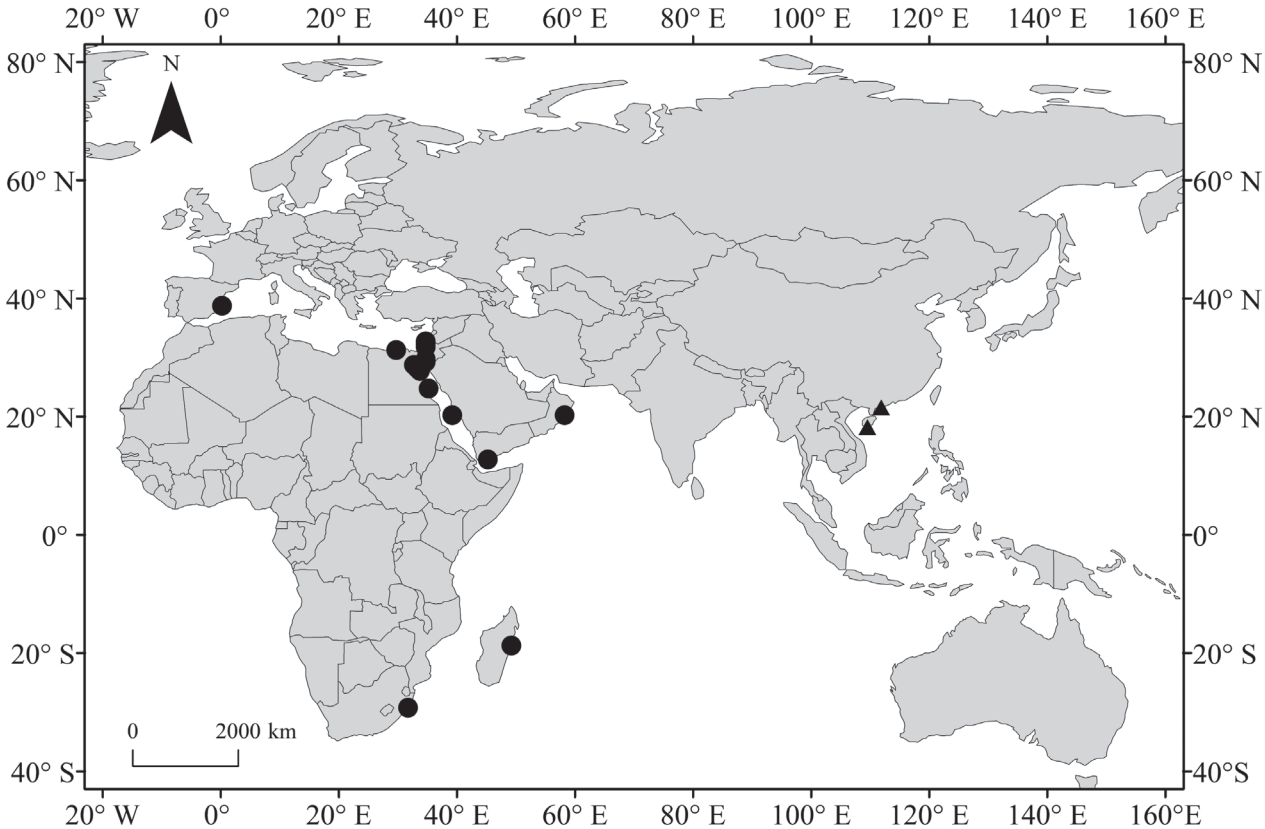


**Figure 1.** Distribution records for *Upeneus pori* in the world's oceans. The triangles indicate records added in this study and the circles denote historical records.

**Table 1.** Information on the *COI* sequences and collection in this study.

| Species | Specimen No. | Sampling location | Coordinates | Accession No. | Source |
|---|---|---|---|---|---|
| *U. pori* | GOU103674 | South China Sea, China | 18.238°N, 109.509°E | GAF | |
| | GOU103676 | South China Sea, China | 18.238°N, 109.509°E | MW922385 | This study |
| | GOU103678 | South China Sea, China | 18.238°N, 109.509°E | MW922386 | This study |
| | GOU104100 | South China Sea, China | 21.572°N, 111.832°E | MW922387 | This study |
| | GOU104101 | South China Sea, China | 21.572°N, 111.832°E | GAF | |
| | GOU104102 | South China Sea, China | 21.572°N, 111.832°E | MW922388 | This study |
| | UpPo14A | Israel | | KM538630 | GenBank |
| | Upor | Egypt | | LC572156 | GenBank |
| | 1059 | Turkey | | KY176690 | GenBank |
| | P. 14829 | Israel | 31.799°N, 34.608°E | KF564319 | GenBank |
| *U. sulphureus* | FSCS045-06 | Guangdong, China | 20.42°N, 109.84°E | EF607609 | GenBank |
| | BW-A11206 | Indonesia | 8.80°S, 116.48°E | JN313348 | GenBank |
| *U. subvittatus* | NS587 | Nansha Island, China | 5.317°N, 111.667°E | KY372338 | GenBank |
| | NS586 | Nansha Island, China | 5.317°N, 111.667°E | KY372339 | GenBank |
| *U. quadrilineatus* | BW-A6880 | Jawa Timur, Indonesia | 8.21667°S, 111.067°E | GU674207 | GenBank |
| | BW-A6879 | Indonesia | 8.21667°S, 111.067°E | GU674208 | GenBank |
| *U. moluccensis* | TR1879EK | Turkey | 8.81°N, 78.14°E | KC501840 | GenBank |
| | CIFE:FGB UM-01 | India | 8.81°N, 78.14°E | KJ920110 | GenBank |
| *U. japonicus* | ASIZP0078749 | Taiwan | | KT718279 | GenBank |
| | HMJ6 | Shizuoka Japan | 34.667°N, 138.333°E | JF952884 | GenBank |
| *U. tragula* | GBMIN131725-17 | Phu Quoc, Vietnam | | KX887496 | GenBank |
| | FSCS209-06 | Guangdong, China | 20.92°N, 110.54°E | EF607611 | GenBank |
| *Mullus argentinae* | HRCB:53038 | Sao Paulo, Brazil | 26.352°S, 45.139°W | JQ365451 | GenBank |
| *Parupeneus multifasciatus* | IRD BMF-162.2 | Maluku, Indonesia | 3.6876°S, 128.183°E | MN870495 | GenBank |

GAF = *COI* gene amplification failure.

with dial calipers from Shanghai Shenhan Measuring Tools Co., Ltd. with an accuracy of 0.1 mm.

Muscle tissues (50 mg) were stored in a 95% alcohol solution and in a –20°C freezer for later study. DNA was extracted by a Rapid Animal Genomic DNA Isolation Kit (Sangon Biotech, Inc., Shanghai, China). Using the universal primers FishF1 and FishR1, the *COI* gene was amplified (Ward et al. 2005). PCR was carried out in a 25 μL reaction mixture containing 12.5 μL of *Taq* PCR Master Mix (Sangon Biotech, Inc., Shanghai, China), 2 μL of $MgCl_2$, 5 μL of DNA template, 1 μL of forward, and reverse primer and 3.5 μL of ultrapure water. The thermal regime consisted of denaturation for three min at 95°C, followed by 33 cycles of 45 s at 92°C, 45 s at 50°C and one minute at 72°C, with post-extension at 72°C for ten min. Then, the temperature was maintained at 4°C. The PCR products were sequenced by Sangon Biotech Co., Ltd. (Shanghai) using an ABI PRISM 3730 DNA sequencer (Applied Biosystems, Foster City, CA, USA) with the BigDye Terminator kit (Applied Biosystems).

Sequence alignment and manual editing were performed using Sequencher 5.4.5 software. Four sequences were obtained and utilized to search for homologous sequences using BLAST on the NCBI website (Altschul et al. 1990) and then deposited in GenBank under accession numbers MW922385 to MW922388. The Maximum Likelihood (ML) method tree of 22 sequences was performed by the software PhyloSuite v.1.2.2 (Zhang et al. 2020), of which two sequences were downloaded from GenBank as out-group sequences: *Parupeneus multifasciatus* (Quoy et Gaimard, 1825), MN870495 and *Mullus argentinae* Hubbs et Marini, 1933, JQ365451. The HKY+G4+F model was selected for the best-fit model using the BIC criterion by ModelFinder (Kalyaanamoorthy et al. 2017). Maximum Likelihood phylogenies were inferred using IQ-TREE (Nguyen et al. 2015) with the HKY+G4+F model for 5000 ultrafast (Minh et al. 2013) bootstraps, as well as the Shimodaira–Hasegawa-like approximate likelihood-ratio test (SH-aLRT) (Guindon et al. 2010). The Kimura two-parameter model (K2P) model was used to calculate intra- and interspecific genetic distances of the genus *Upeneus*. Information on the *COI* sequences of *Upeneus* is provided in Table 1.

## Results

The collected specimens represented a single species, *Upeneus pori*, which was confirmed using morphological methods as well as DNA barcoding.

## Taxonomy

### Family Mullidae Rafinesque, 1815
### Genus *Upeneus* Cuvier, 1829

### *Upeneus pori* Ben-Tuvia et Golani, 1989

(Figs. 2 and 3; Table 2)

**Morphological characteristics.** The morphometric measurements are shown in Table 2. Head medium, obtuse, and conical; body laterally compressed and elongated; maxilla slightly longer than the mandible; cordiform teeth present in both jaws, palatine, and vomer; single complete lateral-line on each body side; snout slightly inferior; body with rhomboidal ctenoid scales; two separate dorsal-fins; two barbels on the chin; upper lobe of the caudal fin larger than the lower lobe.

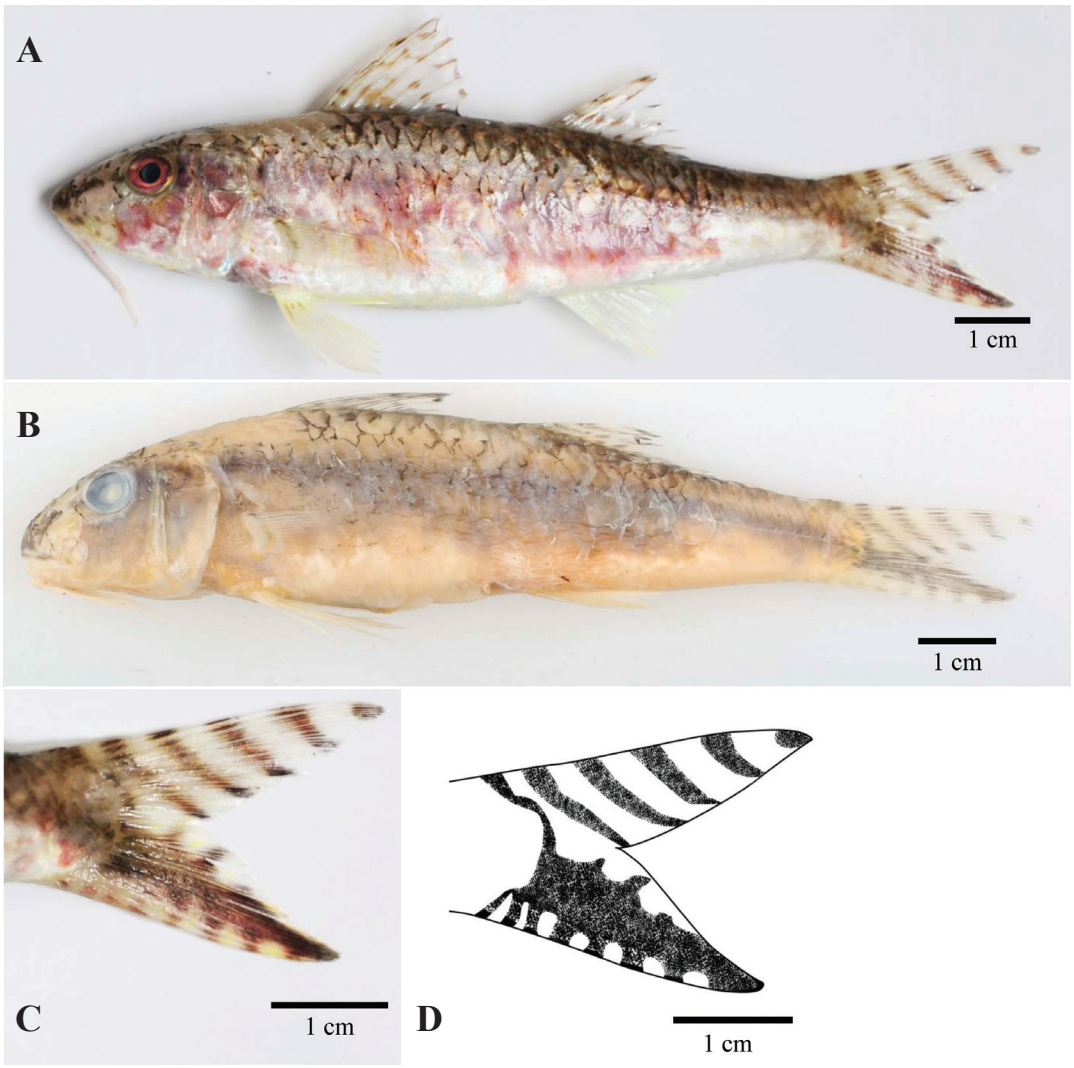


**Figure 2.** *Upeneus pori*, 106 mm SL, GOU104100, (**A**) fresh specimen; (**B**) preserved specimen; (**C**) caudal-fin characteristics; (**D**) drawing of caudal-fin patterns.

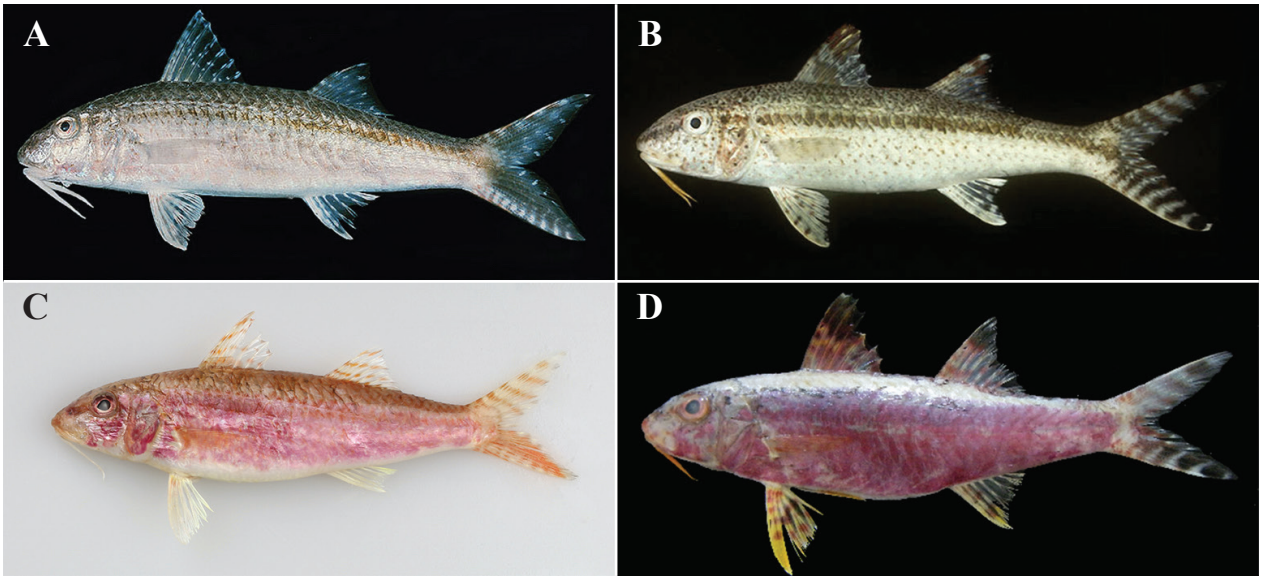


**Figure 3.** Comparison between *Upeneus pori* and *Upeneus tragula*. (**A**) *Upeneus pori*, fresh, 114 mm SL; (**B**) *Upeneus tragula*, fresh, 216 mm SL, (**C**) *Upeneus pori*, dead, 102 mm SL, GOU103678, this study; (**D**) *Upeneus tragula*, dead, 145.4 mm SL. Photos A and B by Randall JE (1997). Randall's tank photos. Collection of 10,000 large-format photos (slides) of dead fishes. Published in Froese and Pauly (2023). Photo D by Sahat Ratmuangkhwang; published in Froese and Pauly (2023).

**Table 2.** Presently reported ($n$ = 6) morphometric measurements of *Upeneus pori* compared with the data of the paratypes in Ben-Tuvia and Golani (1989) ($n$ = 22).

| Character | *Upeneus pori* | | | |
|---|---|---|---|---|
| | Presently reported study | | Ben-Tuvia and Golani 1989 | |
| | Range | Mean | Range | Mean |
| SL [mm] | 101.1–114.1 | 105 | 74–125 | |
| | In % SL | | | |
| Body depth | 24.4–26.4 | 25.2 | 21.8–25.9 | 23.9 |
| Body width | 14.3–17.2 | 15.8 | | |
| Head length | 23.7–27.1 | 25.8 | 25.8–29.2 | 27.8 |
| Snout length | 7.4–10.0 | 8.3 | 9.7–12.1 | 10.9 |
| Orbit diameter | 5.4–6.7 | 6.3 | 6.4–8.5 | 7.2 |
| Interorbital width | 7.6–8.0 | 7.8 | 6.6–8.1 | 7.4 |
| Upper jaw length | 6.0–10.7 | 8.6 | | |
| Lower jaw length | 5.4–9.1 | 7.6 | | |
| Predorsal length | 29.8–35.2 | 32.6 | 32.0–38.2 | 35.6 |
| Prepelvic length | 27.7–29.3 | 28.8 | | |
| Preanal length | 63.3–65.4 | 64.6 | | |
| Prepectoral length | 25.9–29.9 | 27.5 | | |
| First dorsal-fin height | 17.7–20.5 | 19.4 | 17.1–20.1 | 18.6 |
| Second dorsal-fin height | 13.5–16.8 | 15.1 | 13.0–16.9 | 15.1 |
| Pectoral fin length | 16.8–21.1 | 20.0 | 18.3–21.3 | 19.6 |
| Pelvic fin length | 13.8–18.2 | 17.4 | 16.5–20.5 | 18.3 |
| Anal fin height | 13.7–16.5 | 15.5 | 12.7–15.6 | 13.8 |
| Caudal peduncle depth | 9.9–10.9 | 10.2 | 9.4–11.1 | 10.0 |
| Caudal peduncle length | 21.0–25.2 | 23.1 | 21.9–27.8 | 25.6 |
| Barbels length | 16.7–18.1 | 17.2 | 15.3–20.1 | 17.1 |
| Meristic counts | | | | |
| Dorsal fin rays | VII, 9 | | VII, 9 | |
| Anal fin rays | I-6–7 | | I-7 | |
| Pectoral fin rays | 14 | | 14–15 | |
| Lateral line scales | 29–31 | | 29–30 | |
| Scales above lateral line | 2 | | | |
| Scales below lateral line | 4–5 | | | |
| Total developed gill rakers | 3–5 + 13–14 | | | |
| Total gill rakers | 6–7 + 17–19 | | 6–8 + 18–20 | |

SL = standard length.

**Color.** Mainly based on recently deceased specimens (Fig. 2A). Dorsally darkened, head and sides reddish-brown, belly whitish; mid-lateral body with faint brownish-red bar running from snout to base of caudal fin in fresh fish; barbels white or creamy white; first and second dorsal-fins with 3–4 sets of reddish-brown spots running horizontally; pectoral fins cream-colored to transparent; pelvic fins creamy-white and base of fins with several yellow marks; anal fin rays whitish with transparent membranes; upper lobe of caudal fin with 4–5 oblique reddish-brown stripes intersecting rays; middle part of lower lobe of caudal fin with wide reddish-brown band extending from base of caudal fin to tip of lower lobe; 3–4 red-brown stripes above wide band; 6–7 stripes with same color below wide band and all stripes approximately perpendicular to wide band; fluorescent yellow spots between stripes on both lobes of caudal fin, sometimes vague (Figs. 2C and 2D). The preserved specimens are dorsally dark-brown; all fins retain original spots, bars, or stripes; mid-lateral sides with faint dark grey bar (Fig. 2B).

**Sequence analysis of the *COI* gene.** The mean sequence of some mitochondrial cytochrome C oxidase (*COI*) genes, collected from fish specimens examined in the presently reported study, was 690 nucleotide sites. The base frequencies of A, C, T, and G of twenty *COI* sequences were 22.2%, 29.4%, 29.4%, and 19.0%, respectively and the A + T content (51.6%) was greater than the C + G content (48.4%). The intraspecific genetic distance ranged from 0% to 1.58% and the interspecific genetic distance ranged from 8.87% to 19.36% (Table 3). The interspecific genetic distance was much greater than the intraspecific genetic distance. According to the results of the maximum likelihood tree (Fig. 4), *Upeneus sulphureus*, *U. subvittatus*, *U. quadrilineatus*, *U. moluccensis*, *U. japonicus*, and *U. tragula* clustered and separated from *U. pori* with high bootstrap values and SH-aLRT values, respectively, indicating significant differentiation amongst them, of which the sequences in this study (GOU103676, GOU103678, GOU104100, and GOU104102) were clustered with the sequences (KM538630, LC572156, KY176690, and KF564319) distinguished as *U. pori* in the Red Sea area from GenBank with high SH-aLRT and ultrafast bootstrap values (97/99). The genetic distance (Table 4) shows that the *U. pori* collected in the South China Sea and the *U. pori* from the Red Sea belong to the species range.

## Discussion

*Upeneus pori* was first reported in the Mediterranean by Kosswig (1950) as *U. tragula*. Then, Ben-Tuvia and Golani (1989) re-examined the specimens and suggested there was a new species of the genus *Upeneus* in the Red Sea and named the new one *Upeneus pori* in recognition of Professor Francis Dov Por's contribution to the field of the Lessepsian migration of organisms. Before this time, many scholars misidentified *U. pori* for other species of *Upeneus* (see Ben-Tuvia 1953, 1966; George and Athanassiou 1966, 1967). Although few resources of *U. pori* were investigated in the Chinese waters, we observed *U. pori* was often mingled with *U. tragula* for sale in the local fish markets. The reason for the above is that there is still a lack of systematic classification of *Upeneus* species in China. At the same time, some *Upeneus* species

**Table 3.** Interspecific (bottom half of matrix) and intraspecific (bold diagonal) sequence divergences of 7 species of *Upeneus*, corrected using the Kimura two-parameter (K2P) model.

| | *U. japonicus* | *U. pori* | *U. tragula* | *U. sulphureus* | *U. subvittatus* | *U. quadrilineatus* | *U. moluccensis* |
|---|---|---|---|---|---|---|---|
| *U. japonicus* | **0.0039** | | | | | | |
| *U. pori* | 0.1328 | **0.0000** | | | | | |
| *U. tragula* | 0.1089 | 0.0950 | **0.0000** | | | | |
| *U. sulphureus* | 0.1821 | 0.1751 | 0.1600 | **0.0098** | | | |
| *U. subvittatus* | 0.1936 | 0.1759 | 0.1686 | 0.1250 | **0.0019** | | |
| *U. quadrilineatus* | 0.1645 | 0.1705 | 0.1555 | 0.1048 | 0.1072 | **0.0000** | |
| *U. moluccensis* | 0.1930 | 0.1675 | 0.1679 | 0.1285 | 0.0887 | 0.1012 | **0.0158** |

**Table 4.** Pairwise genetic distance calculated using the K2P model between the *COI* gene sequences of *Upeneus pori* from the South China Sea (this study) and the 12 sequences of different species of *Upeneus* from GenBank.

| Group | Sequence | Group | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |
| 1 | GOU103676_*U. pori*_SCS | | | | | | | | | | | | | | | | | | | |
| 2 | GOU103678_*U. pori*_SCS | 0.0000 | | | | | | | | | | | | | | | | | | |
| 3 | GOU104100_*U. pori*_SCS | 0.0000 | 0.0000 | | | | | | | | | | | | | | | | | |
| 4 | GOU104102_*U. pori*_SCS | 0.0000 | 0.0000 | 0.0000 | | | | | | | | | | | | | | | | |
| 5 | KM538630_*U. pori*_RS | 0.0000 | 0.0000 | 0.0000 | 0.0000 | | | | | | | | | | | | | | | |
| 6 | LC572156_*U. pori*_RS | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | | | | | | | | | | | | | | |
| 7 | KY176690_*U. pori*_RS | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | | | | | | | | | | | | | |
| 8 | KF564319_*U. pori*_RS | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | | | | | | | | | | | | |
| 9 | EF607609_*U. sulphureus*_SCS | 0.1751 | 0.1751 | 0.1751 | 0.1751 | 0.1751 | 0.1751 | 0.1751 | 0.1751 | | | | | | | | | | | |
| 10 | JN313348_*U. sulphureus*_IDOW | 0.1751 | 0.1751 | 0.1751 | 0.1751 | 0.1751 | 0.1751 | 0.1751 | 0.1751 | 0.0098 | | | | | | | | | | |
| 11 | KY372338_*U. subvittatus*_SCS | 0.1746 | 0.1746 | 0.1746 | 0.1746 | 0.1746 | 0.1746 | 0.1746 | 0.1746 | 0.1274 | 0.1250 | | | | | | | | | |
| 12 | KY372339_*U. subvittatus*_SCS | 0.1772 | 0.1772 | 0.1772 | 0.1772 | 0.1772 | 0.1772 | 0.1772 | 0.1772 | 0.1250 | 0.1226 | 0.0019 | | | | | | | | |
| 13 | GU674207_*U. quadrilineatus*_IDOW | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1037 | 0.1060 | 0.1084 | 0.1060 | | | | | | | |
| 14 | GU674208_*U. quadrilineatus*_IDOW | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1705 | 0.1037 | 0.1060 | 0.1084 | 0.1060 | 0.0000 | | | | | | |
| 15 | KC501840_*U. moluccensis*_IDAW | 0.1699 | 0.1699 | 0.1699 | 0.1699 | 0.1699 | 0.1699 | 0.1699 | 0.1699 | 0.1344 | 0.1222 | 0.0897 | 0.0920 | 0.1010 | 0.1010 | | | | | |
| 16 | KT718279_*U. moluccensis*_SCS | 0.1651 | 0.1651 | 0.1651 | 0.1651 | 0.1651 | 0.1651 | 0.1651 | 0.1651 | 0.1348 | 0.1226 | 0.0854 | 0.0876 | 0.1013 | 0.1013 | 0.0158 | | | | |
| 17 | KJ920110_*U. japonicus*_SCS | 0.1303 | 0.1303 | 0.1303 | 0.1303 | 0.1303 | 0.1303 | 0.1303 | 0.1303 | 0.1742 | 0.1847 | 0.1922 | 0.1896 | 0.1620 | 0.1620 | 0.1927 | 0.1878 | | | |
| 18 | JF952884_*U. japonicus*_JAW | 0.1353 | 0.1353 | 0.1353 | 0.1353 | 0.1353 | 0.1353 | 0.1353 | 0.1353 | 0.1794 | 0.1900 | 0.1976 | 0.1949 | 0.1671 | 0.1671 | 0.1981 | 0.1932 | 0.0039 | | |
| 19 | KX887496_*U. tragula*_SCS | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.1625 | 0.1574 | 0.1699 | 0.1673 | 0.1555 | 0.1555 | 0.1677 | 0.1065 | 0.1682 | 0.1113 | |
| 20 | EF607611_*U. tragula*_SCS | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.0951 | 0.1625 | 0.1574 | 0.1699 | 0.1673 | 0.1555 | 0.1555 | 0.1677 | 0.1065 | 0.1682 | 0.1113 | 0.0000 |

SCS = South China Sea, RS = Red Sea, IDOW = Indonesian waters, IDAW = Indian waters, JAW = Japanese waters.

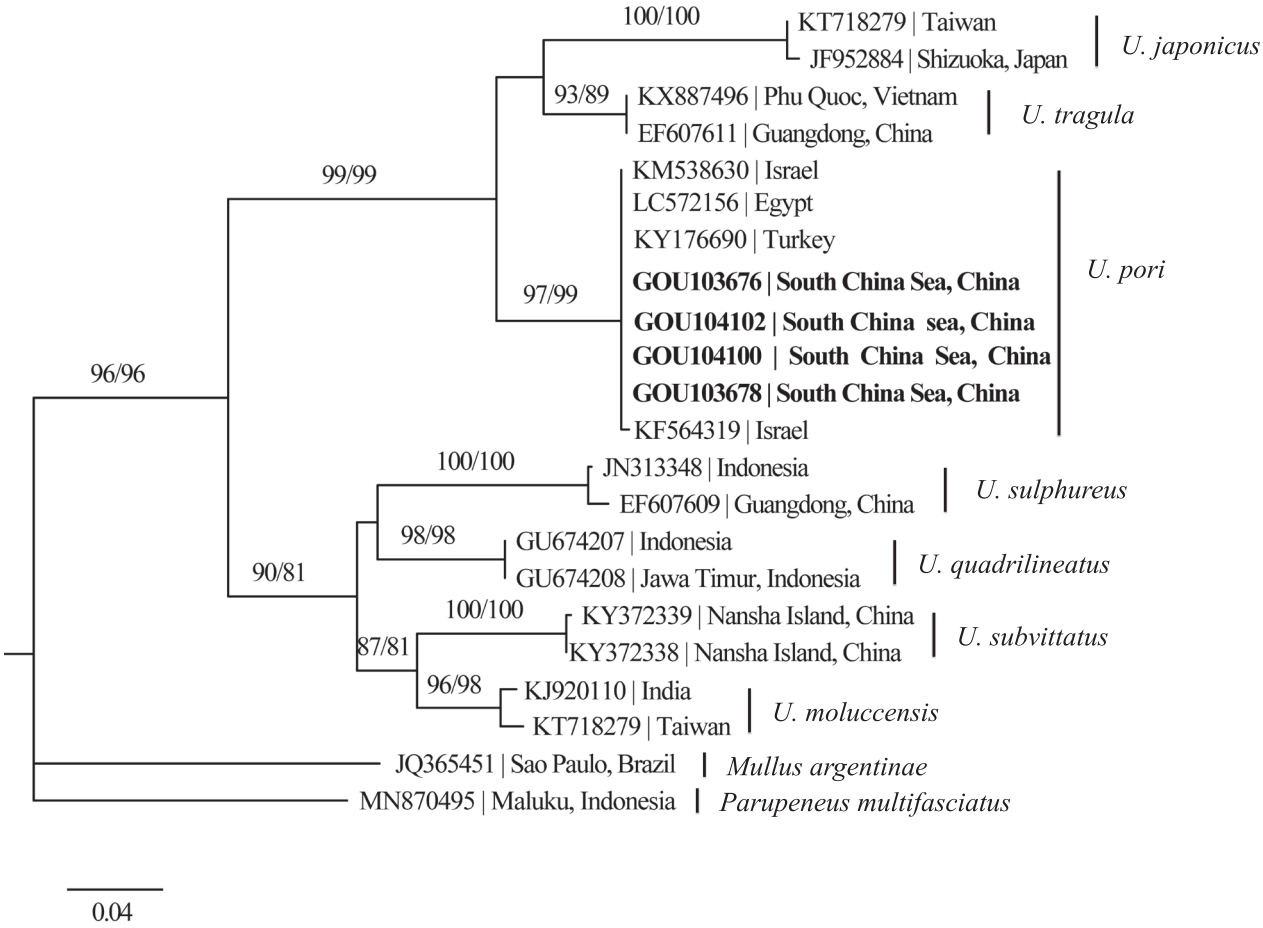


**Figure 4.** Maximum Likelihood phylogenetic tree of *Upeneus pori*, based on DNA sequences of the mitochondrial *COI* gene (bold fonts for sequences of this study, not bold for previous research). Numbers on the branches indicate the Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) and ultrafast bootstrap support (only values above 70% are displayed).

exhibit a similar body color after death (Figs. 3C and 3D), which can lead observers to believe it is the same fish. In addition, due to the lack of resources, it is highly likely to be ignored as another species and considered to be *U. tragula*. Here are different diagnoses between *U. pori* and *U. tragula* (Figs. 2A, 2C, and 2D; Figs. 3A and 3B; Table 5):

- barbels color: white or creamy-white vs. yellow barbels, but may be pale brown or orange in fresh fish;
- body pattern: without any spots or blotches vs. slightly darker above the lateral line, with irregular red, brown, or black spots and/or blotches;
- first dorsal-fin: seven spines, without blotch around tip, vs. eight spines, with a large blotch around tip;
- caudal-fin: different pattern shown in Uiblein and Heemstra (2010).

**Table 5.** Key features that distinguish *Upeneus pori* from *Upeneus tragula*.

| Distinguishing key features | *Upeneus pori* | *Upeneus tragula* |
|---|---|---|
| Barbels color | Creamy-white | Yellow; pale brown/orange (fresh fish) |
| Body pattern | No spots or blotches | With irregular red, brown or black spots and/or blotches |
| First dorsal-fin | VII; no blotch around tip | VIII; with a blotch around tip |

Uiblein and Heemstra (2010) established four taxonomic groups for separating morphologically similar species within the same group. They included 25 of the 26 species recorded in China, being separated in *japonicus* group, *tragula* group, *moluccensis* group, and *vittatus* group, which were distinguished by the differences in the number of spines in the first dorsal-fin, gill rakers, pectoral-fin rays, and stripes of the caudal-fin. *Upeneus pori* belonged to the *japonicus* group, as suggested by Uiblein and Heemstra (2010). New species and new records were gradually recorded, resulting in the taxonomic status of *Upeneus* being altered. The *vittatus* group was divided into the *stenopsis* group (Uiblein and Causse 2013) and the *suahelicus* group (Uiblein and Gouws 2015), causing *U. vittatus* to be ungrouped and the *vittatus* group to be cancelled. Uiblein et al. (2019) reported that *Upeneus margarethae* Uiblein et Heemstra, 2010; *Upeneus mouthami* Randall et Kulbicki, 2006; and *Upeneus randalli* Uiblein et Heemstra, 2011 differed from other *tragula* group species in the first dorsal-fin tip without dark pigmentation, total gill rakers 21–25 and 28–30 lateral-line scales so a new taxonomic group was proposed—the *margarethae* group. Uiblein and Maclaine (2021) proposed reclassifying *U. pori*, originally part of the *japonicus* group, into the newly established *pori* group. This reclassification is based on the limited distribution range exhibited by members of the *pori* group, as well as their shared coloration and morphological characteristics. These features distinguish them from other members of the *japonicus* group. As for Chinese records, they include the *margarethae* group (*U. heterospinus*), *japonicus* group (*U. japonicus*), *moluccensis* group (*U. moluccensis*, *U. quadrilineatus*, and *U. sulphureus*), *stenopsis* group (*U. subvittatus*), *tragula* group (*Upeneus sundaicus* (Bleeker, 1855), *U. luzonius*, and *U. tragula*), and ungrouped (*U. vittatus*). In this study, we have identified *U. pori*, a member of the *pori* group, which is recorded in China for the first time.

## Conclusion

This study has a certain reference value for the taxonomy of the genus *Upeneus* in the coastal areas of China. For further research and an in-depth understanding of the taxonomy and phylogeny of *Upeneus* within China's regional distribution, it is necessary to collect sufficient samples in various Chinese waters and provide detailed morphological characteristics. Apart from morphology, molecular analysis enables us to collect more knowledge about the taxonomy and phylogeny of *Upeneus*, which also contributes to coastal ecosystem management measures and provides the basis for the protection of local species diversity.

The presently reported study confirms a new record of *Upeneus pori* from the South China Sea, based on morphological characteristics and DNA barcodes and this record expands the distributional range of *U. pori* in the world's oceans and enriches the species composition and biodiversity of the South China Sea. This study also emphasizes that it is essential to increase taxonomic studies to survey the South China Sea with its high species diversity to better protect species diversity and monitor marine fisheries in the South China Sea.

## Acknowledgments

We gratefully acknowledge the funding support under the Guangdong Basic and Applied Basic Research Foundation, Grant/Award Number: [2019B1515120064]; Southern Marine Science and Engineering Guangdong Laboratory (Zhanjiang), Grant /Award Number: [ZJW-2019-08]; Science and Technology Plan Projects of Guangdong Province, China, Grant/Award Number: [2018B030320006].

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