

## Original Article

# First record of *Favonigobius gymnauchen* (Bleeker, 1860) (Teleostei: Gobiidae) in the north-western Indian Ocean: Evidence for potential taxonomic diversity

Fatah Zarei<sup>1</sup>, Hamid Reza Esmaili<sup>1\*</sup>, Seyed Hassan Hashemi<sup>2</sup>

<sup>1</sup>Ichthyology and Molecular Systematics Research Laboratory, Zoology Section, Department of Biology, School of Science, Shiraz University, Shiraz, Iran.

<sup>2</sup>Department of Environment, Bandar Abbas, Hormuzgan Province, Iran.

**Abstract:** A single specimen of *Favonigobius gymnauchen* was captured from the Iranian coast of the Persian Gulf, north-western Indian Ocean. Species identification was performed based on sequence analysis of the mitochondrial COI barcode region. This significant record from the northern Persian Gulf, adds a new species to the gobiid fauna of the north-western Indian Ocean and represents the easternmost documentation of the species. The presence of a deep phylogeographic break between the Indian Ocean and the West Pacific groups of haplotypes suggests the potential existence of hidden taxonomic diversity, hereby highlighting the necessity of a comprehensive morphological and molecular analysis of the sharp-nosed sand gobies from the two oceans.

*Article history:*

Received 5 January 2023

Accepted 1 April 2023

Available online 25 April 2023

*Keywords:* Gobioidae, Distribution, DNA barcoding, Persian Gulf, Sharp-nosed sand goby.

## Introduction

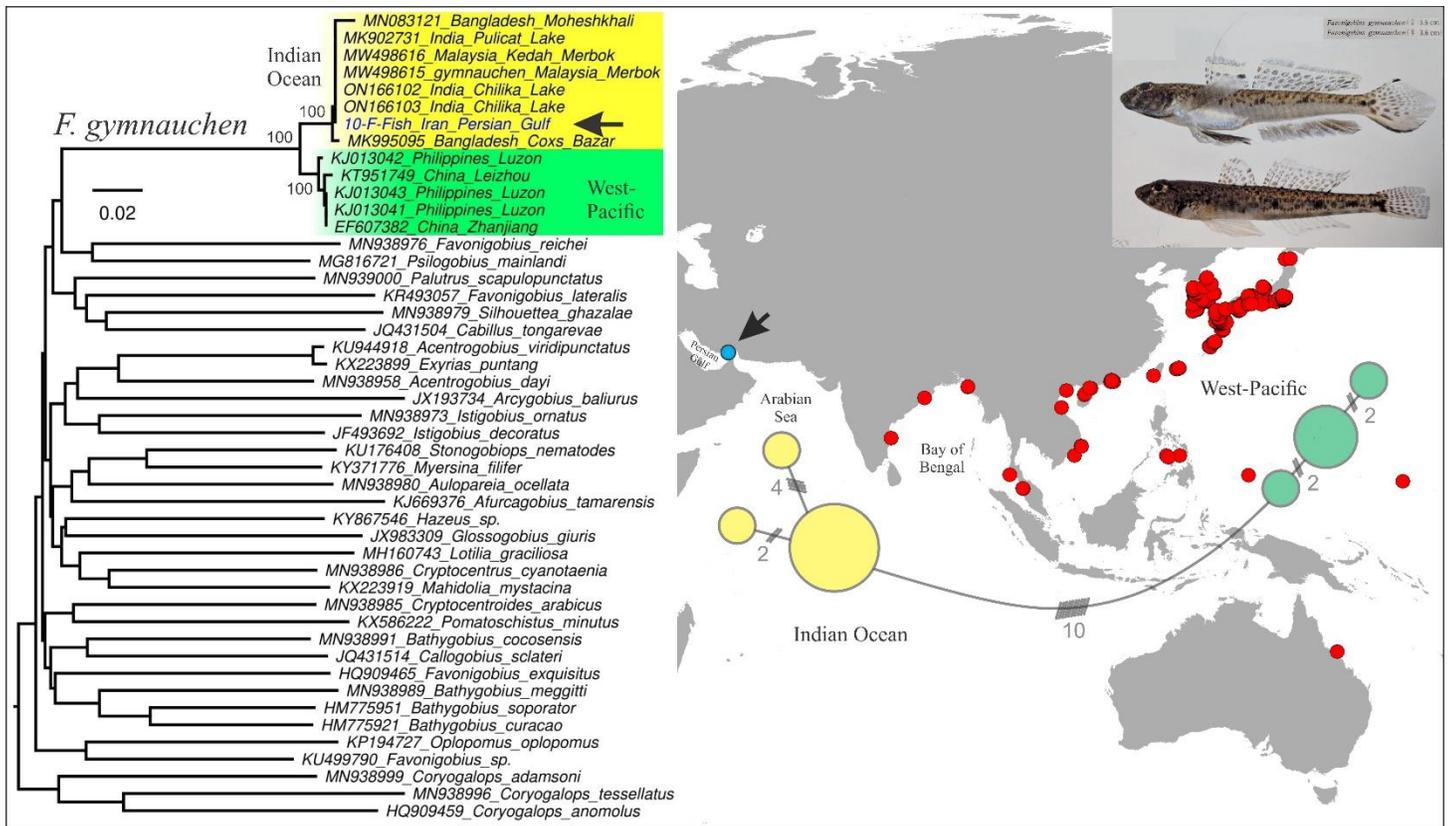
Gobiidae is the largest fish family with some 1974 recognized species (Fricke et al., 2022). While gobiids are found both in marine and freshwater environments throughout the world (Nelson et al., 2016), a few other fish families having more than a thousand valid species are strictly freshwater fishes. Among fish, they are unparalleled for their ability to adapt to microhabitats and specialize in novel ecological niches, leading to rapid speciation and adaptive radiations (Patzner et al., 2011). Gobiids of the northern Indian Ocean have not been thoroughly studied yet, mainly due to their low economic importance, small sizes, cryptic appearance, poor geographic sampling, and distributions in difficult-to-sample habitats. Recent systematic observations in this region resulted in the description of a few new species (Kovačić et al., 2020; Zarei et al., 2022) and new records (e.g., Sadeghi and Esmaili 2019; Sadeghi et al., 2017, 2019; Ghanbarifardi and Lagzian, 2019; Al Jufaili et al., 2022), suggesting a rich but yet unexplored gobiid fauna for the region.

Species of the gobiid genus *Favonigobius* Whitley, 1930, belonging to the *Gobiopsis*-lineage *sensu* Agorreta et al. (2013) of the subfamily Gobiinae with nine currently recognized species, are found in the seas and freshwaters environments of the Indo-Pacific. The sharp-nosed sand goby, *Favonigobius gymnauchen* (Bleeker, 1860) is mainly distributed in the West Pacific region (Fricke et al., 2022), however, a few georeferenced COI barcodes deposited in the GenBank confirm its presence in the coastal habitats of India, Bangladesh, and Malaysia in the Bay of Bengal (Fig. 1). The present study for the first time records it from the Iranian waters of the Persian Gulf, which adds a new species to the fish fauna of the north-western Indian Ocean. We investigate the new record's phylogenetic placement based on the mitochondrial COI, and preliminary discuss the species' phylogeographic pattern in the Indo-West Pacific.

## Materials and Methods

On October 2017, one goby specimen was collected

\*Correspondence: Hamid Reza Esmaili  
E-mail: hresmaili@shirazu.ac.ir



**Figure 1.** Left: Phylogenetic placement (ML) of the *Favonigobius gymnauchen* COI haplotype sampled from the Persian Gulf basin, Iran (marked with a black arrow). Right: Point distribution map of *F. gymnauchen*: red circles indicate previous records (Froese and Pauly, 2022; GBIF, 2022; GenBank, 2022), whereas the blue circle (marked with a black arrow) represents the new record from the Persian Gulf, Iran (Arabian Sea basin). The MJ haplotype network on the map for the six COI haplotypes observed in 13 *F. gymnauchen* specimens shows a deep phylogeographic break (10 mutational steps) between the Indian Ocean (yellow circles) and the West Pacific (green circles) groups of haplotypes. Species figures: male (upper) and female (lower) *F. gymnauchen* (after Masuda et al., 1984).

using a hand net from the Iranian coast of the Persian Gulf (Fig. 1). A sample of pectoral fin tissue was taken from this specimen and stored in 96% ethanol for genetic analysis. The voucher specimen was preserved in formaldehyde (10%), and deposited in the Zoological Museum of Shiraz University, Collection of Biology Department (ZM-CBSU). Total DNA was extracted from the fin clip according to a salt method protocol described in Bruford et al. (1992). Following Zarei et al. (2021) and using a Bioer XP Thermal Cycler (Bioer Technology Co. Ltd., Hangzhou, China), the mitochondrial cytochrome C oxidase subunit I (COI) barcode region was amplified using a primer pair Fish-BCL and Fish-BCH (Baldwin et al., 2009). Following purification with the ExoSAP-IT® (usb) kit, the PCR product was Sanger sequenced with BigDye® Terminator v3.1 Cycle Sequencing Kit (Applied

Biosystems, Foster City, CA) on an ABI PRISM 3730xl DNA Analyzer (Applied Biosystems, Foster City, CA) by the Faghihi Lab., Shiraz, Iran.

BioEdit 7.1 (Hall, 1999) was used to read and edit the new DNA chromatogram, while ClustalW procedure in Mega 7 (Kumar et al., 2016) was used for sequence alignment. The new COI sequence is deposited in the GenBank (OQ892260). A total of 46 COI sequences representing 35 gobioid species from different lineages were obtained from GenBank. After alignment with the new haplotype sequence from the Persian Gulf, the COI dataset was analyzed using the maximum likelihood (ML) method in Mega. PopART 1.7 (Leigh and Bryant, 2015) was used to investigate the phylogeographic depth. To delineate putative species, (i) a statistical parsimony (SP) network based on a 95% connection probability threshold was estimated in TCS 1.21 (Clement et al.,

2000), and (ii) an Assemble Species by Automatic Partitioning analysis (ASAP; Puillandre et al., 2021) was performed through its web interface (<https://bioinfo.mnhn.fr/abi/public/asap/asapweb.html>) using Kimura (K80) ts/tv (=0.2). Furthermore, cutoff value of 2% K2P sequence divergence for COI was used as an indicator of distinct species (Ward, 2009).

## Results

The *Favonigobius* specimen recorded from the Persian Gulf, phylogenetically grouped with *F. gymnauchen* (Fig. 1). The sequence analysis of a 615 bp fragment of the COI region detected 20 variable nucleotide sites, including 8 singletons and 12 parsimony informative sites between 13 examined *F. gymnauchen* specimens from the Indo-West Pacific region, leading to the definition of 6 haplotypes. Corroborating the ML phylogeny, the median-joining haplotype network shows that the three haplotypes from the Indian Ocean localities (i.e., Persian Gulf and Bay of Bengal) are separated from the three West Pacific haplotypes from China and Philippines by 10 mutational steps (Fig. 1). The two lineage are separated by 2.4% K2P genetic distance in the sequence of COI barcode, i.e., larger than the conventional threshold proposed for COI in fish (i.e., 2%; Ward, 2009) as an indicator of distinct species. The Statistical Parsimony (SP) and Assemble Species by Automatic Partitioning (ASAP; the partition with the highest ASAP-score) analyses found support for only one species in the *F. gymnauchen* clade. The partition with the second-best ASAP-score however, found support for two putative species in the *F. gymnauchen* clade, corresponding to the Indian Ocean and West Pacific subclades.

## Discussion

*Favonigobius gymnauchen* is well known from the West Pacific (Fricke et al., 2022), and there are few unpublished GenBank records from the Bay of Bengal, northeastern Indian Ocean. This significant record from the Iranian waters of the Persian Gulf,

adds a brand new species to the gobiid fauna of the northwestern Indian Ocean and represents the easternmost documentation of the species. Our results validated two deeply diverged lineages within the range of *F. gymnauchen*: one lineage in the Indian Ocean and a second lineage in the West Pacific.

Considering that the West Pacific lineage includes sequences close to the type locality of *F. gymnauchen* (i.e., Tokyo, Japan; Bleeker, 1860), it is possible that the Indian Ocean lineage may represent a yet undescribed species depending on the outcome of additional sampling, and an integrative morphological and molecular analysis. The geographic distribution of these two lineages suggests a significant phylogeographic break at the Sunda Shelf barrier. This phylogeographic break was also documented for several marine fish (Rocha et al., 2007), including blenniids *Omobranchus punctatus* (Mehraban et al., 2021), *O. ferox* and *O. elongates* (Gibbs et al., 2018), and the Japanese threadfin bream, *Nemipterus japonicas* (Farivar et al., 2017). Similar phylogeographic patterns have also been documented for macroalgae (Wichachucherd et al., 2014), and bivalves (Mahidol et al., 2007). This concordance in the geography of gene-tree partitions across multiple genes and co-distributed taxa implicates a shared historical biogeographic factor—allopatric divergence driven by the effect of Sunda Shelf Barrier—in shaping intraspecific genealogies.

## Acknowledgment

Shiraz University and Department of the Environment are acknowledged for financial and logistic supports.

## References

- Agorreta A., San Mauro D., Schliewen U., Van Tassell J.L., Kovačić M., Zardoya R., Rüber L. (2013). Molecular phylogenetics of Gobioidae and phylogenetic placement of European gobies. *Molecular Phylogenetics and Evolution*, 69(3): 619-633.
- Al Jufaili S.M., Esmaili H.R., Sayyadzadeh G.,

- Masoumi A.H., Larson H.K. (2022). Redescription of the goby *Glossogobius tenuiformis* Fowler, 1934 (Teleostei: Gobiidae) and assignment of Oman *Glossogobius* populations: a morpho-molecular approach. *Zootaxa*, 5133(4): 543-554.
- Baldwin C.C., Mounts J.H., Smith D.G., Weigt L.A. (2009). Genetic identification and color descriptions of early life history stages of Belizean *Phaeoptyx* and *Astrapogon* (Teleostei: Apogonidae) with comments on identification of adult *Phaeoptyx*. *Zootaxa*, 26: 1-22.
- Bleeker P. (1860). Zesde bijdrage tot de kennis der vischfauna van Japan. *Acta Societatis Regiae Scientiarum Indo-Neerlandicae*, 8: 1-104.
- Bruford M.W., Hanotte O., Brookfield J.F.Y., Burke T.A. (1992). Single locus and multilocus DNA fingerprinting. In: A. Hoelzel (Ed.). *Molecular genetics analysis of populations: a practical approach*. Oxford University Press. New York. pp: 225-269.
- Clement M., Posada D., Crandall K.A. (2000). TCS: a computer program to estimate gene genealogies. *Molecular Ecology*, 9(10): 1657-1659.
- Farivar S., Jalil-Piran Z., Zarei F., Hosseinzadeh Sahafi H. (2017). Intraspecific phylogeography of the Japanese threadfin bream, *Nemipterus japonicus* (Perciformes: Nemipteridae), from the Persian Gulf and Indo-West Pacific: a preliminary study based on mitochondrial DNA sequence. *Iranian Journal of Fisheries Sciences*, 16(2): 587-604.
- Fricke R., Eschmeyer W.N., van der Laan R. (2022). Eschmeyer's catalog of fishes: genera, species references. Available from: [www.calacademy.org/scientists/projects/eschmeyers-catalog-of-fishes](http://www.calacademy.org/scientists/projects/eschmeyers-catalog-of-fishes). Retrieved 12/26/2022.
- Froese R., Pauly D. (2022). FishBase. Available from: [www.fishbase.org](http://www.fishbase.org). Retrieved 12/26/2022.
- GBIF. (2022). Global Biodiversity Information Facility. Available from: [www.gbif.org](http://www.gbif.org). Retrieved 12/26/2022.
- GenBank. (2022). GenBank. Available from: [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov). Retrieved 12/26/2022.
- Ghanbarifardi M., Lagzian M. (2019). Molecular phylogeny of gobies (Teleostei, Gobiidae) from Iranian water bodies with a new record. *Russian Journal of Marine Biology*, 45: 385-392.
- Gibbs S., Hundt P.J., Nelson A., Egan J.P., Tongnunui P., Simons A.M. (2018). Systematics of the combtooth blenny clade *Omobranchus* (Blenniidae: Omobranchini), with notes on early life history stages. *Zootaxa*, 4369(2): 270-280.
- Hall T.A. (1999). BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series*, 41: 95-98.
- Kovačić M., Sadeghi R., Esmaili H.R. (2020). New species of *Silhouettea* (Teleostei: Gobiidae) from Qeshm Island, Iran and the DNA barcoding of the Persian Gulf and Oman Sea gobies. *Zootaxa*, 4750(1): 49-66.
- Kumar S., Stecher G., Tamura K. (2016). MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution*, 33(7): 1870-1874.
- Leigh J.W., Bryant D. (2015). Popart: full-feature software for haplotype network construction. *Methods in Ecology and Evolution*, 6(9): 1110-1116.
- Mahidol C., Na-Nakorn U., Sukmanomon S., Taniguchi N., Nguyen T.T. (2007). Mitochondrial DNA diversity of the Asian moon scallop, *Amusium pleuronectes* (Pectinidae), in Thailand. *Marine Biotechnology*, 9: 352-359.
- Mehraban H., Zarei F., Esmaili H.R. (2021). A prelude to the molecular systematics and diversity of combtooth blennies (Teleostei: Blenniidae) in the Persian Gulf and Oman Sea. *Systematics and Biodiversity*, 19(5): 438-452.
- Masuda H., Amaoka K., Araga C., Uyeno T., Yoshino T. (1984). *The fishes of the Japanese Archipelago*, Vol. 2. Tokai University Press, Japan. 437 p.
- Nelson J.S., Grande T.C., Wilson M.V. (2016). *Fishes of the World*. John Wiley & Sons. Hoboken, New Jersey. 752 p.
- Patzner R.A., Van Tassell J.L., Kovačić M., Kapoor B.G. (2011). *The biology of gobies*. CRC Press, Enfield, NH. 685 p.
- Puillandre N., Brouillet S., Achaz G. (2021). ASAP: Assemble species by automatic partitioning. *Molecular Ecology Resources*, 21(2): 609-620.
- Rocha L.A., Craig M.T., Bowen B.W. (2007). Phylogeography and the conservation of coral reef fishes. *Coral Reefs*, 26: 501-512.
- Sadeghi R., Ebrahimi M., Esmaili H.R. (2019). Tessellate goby, *Coryogalops tessellatus* Randall, 1994 (Teleostei: Gobiidae), an additional fish element for the Iranian marine waters. *FishTaxa*, 4: 25-30.
- Sadeghi R., Esmaili H.R. (2019a). First documentation of an uncommon goby genus and species, *Palutrus*

- scapulopunctatus* (de Beaufort, 1912) from the Persian Gulf (Teleostei: Gobiidae). Iranian Journal of Ichthyology, 6(3): 143-149.
- Sadeghi R., Esmaeili H.R. (2019b). Cocos frillgoby, *Bathygobius cocosensis* (Bleeker, 1854): an additional fish element for the Iranian marine waters (Teleostei: Gobiidae). International Journal of Aquatic Biology, 7(3): 117-122.
- Sadeghi R., Esmaeili H.R., Fricke R., Larson H. (2017). New geographical record and morphological features of the Indo-Pacific tropical sand goby, *Favonigobius reichei* (Bleeker, 1854) from Iranian coast of the Makran Sea (Teleostei, Gobiidae). Check List, 13(5): 641-645.
- Ward R.D. (2009). DNA barcode divergence among species and genera of birds and fishes. Molecular Ecology Resources, 9(4): 1077-1085.
- Wichachucherd B., Prathep A., Zuccarello G.C. (2014). Phylogeography of *Padina boryana* (Dictyotales, Phaeophyceae) around the Thai-Malay Peninsula. European Journal of Phycology, 49(3): 313-323.
- Zarei F., Al Jufaili S.M., Esmaeili H.R. (2022). *Oxyurichthys omanensis* sp. nov., a new Eyebrow Goby (Teleostei: Gobiidae) from Oman. Zootaxa, 5182(4): 361-376.
- Zarei F., Esmaeili H.R., Schliewen U.K., Abbasi K., Sayyadzadeh G. (2021). Mitochondrial phylogeny, diversity, and ichthyogeography of gobies (Teleostei: Gobiidae) from the oldest and deepest Caspian sub-basin and tracing source and spread pattern of an introduced *Rhinogobius* species at the tricontinental crossroad. Hydrobiologia, 848: 1267-1293.