



New Record of Indian Whiting *Sillago indica* (McKay, Dutt & Sujatha, 1985) (Actinopterygii: Sillaginidae) from the Iranian coast of the Oman Sea

Seyedeh Narges Mirhadi¹, Mohammad Sadegh Alavi-Yeganeh^{1*}, Hashem Khandan Barani² & Manoochehr Nasri³

¹Department of Marine Biology, Tarbiat Modares University, Nur, Iran

²Department of Aquatic Sciences, Hamoun International Wetland Institute, Research Institute of Zabol, Zabol, Iran

³Department of Fisheries, Faculty of Natural Resources, Lorestan University, Khorramabbad, Iran

Abstract: The present study reports the first record of *Sillago indica* from the Iranian coast of the Oman Sea. Sixteen specimens were collected with beach seine during sampling in Chabahar Bay. The obtained detailed information on the morphometric and meristic characters is compared with previous records of *S. indica*. Morphological characters matched the previous description of this species. Molecular confirmation of the species identification was carried out using the partial mitochondrial cytochrome oxidase subunit I gene (COI). Genetic results revealed a 0.181–0.231 K2P distance with other sillaginid species. The identified haplotypes were identical with conspecific haplotypes in GenBank.

Key words: Sillaginidae, New record, Chabahar Bay, COI

Introduction

The family Sillaginidae comprises small to moderate demersal marine fish species occurring in tropical and subtropical areas of the western Pacific and Indian Oceans (McKAY 1985, NELSON et al. 2016). The members of this family have commercial and recreational exploitation in their distribution range (McKAY 1992, GRAY & KENNEL 2003). The Sillaginidae taxonomy is complex and species-specific morphological data are restricted because of similarities and overlapping distributions (CHENG et al. 2021). The structure of the swim bladder is a key taxonomic character in sillaginids, which is commonly used to classify species and genera (CHENG et al. 2021). At present, five genera (*Sillago*, *Sillagino-*

podys, *Sillaginops*, *Sillaginopsis* and *Sillaginodes*) and forty species of sillaginids are recognised as valid (KAGA 2013, CHENG et al. 2021, SAHA et al. 2022). The genus *Sillago*, represented by c. 32 species, differs from other genera of the family in having two posterior extensions of the swim bladder (McKAY 1992, KAGA 2013). Several studies in recent years have provided additional information, describing new species and reviewing the geographic distribution of this genus (XIAO et al. 2021, SAHA et al. 2022, YU et al. 2022). Three species of *Sillago*, including *S. arabica*, *S. attenuata* and *S. sihama* (McKAY 1992, ALAVI-YEGANEH et al. 2016) and one species of *Sillaginopodys*, i.e., *S. chondropus* (KHANDAN BARANI et al. 2023) have been reported from the Iranian coasts of the Oman Sea.

*Corresponding author: malavi@modares.ac.ir

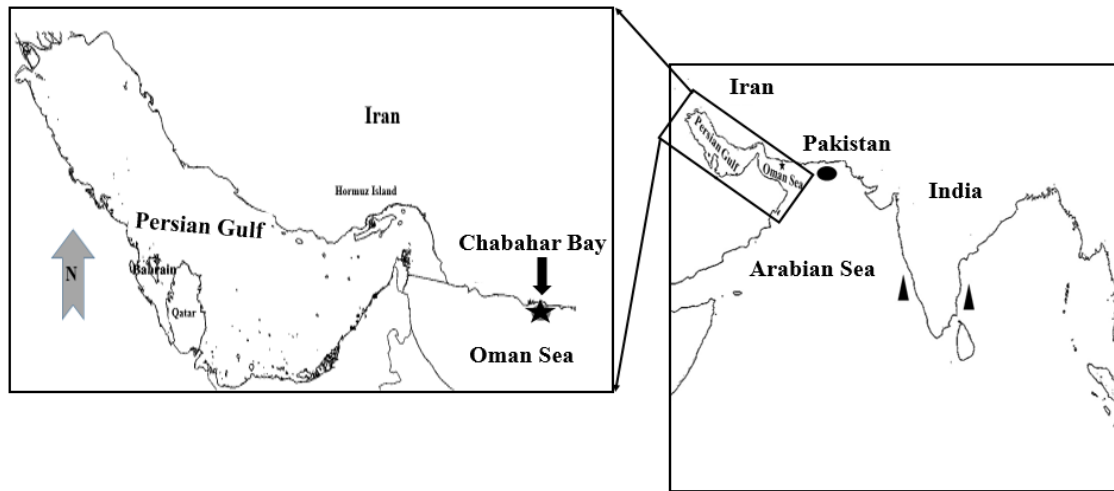


Fig. 1. Sampling site of *Sillago indica* from the northern coast of the Oman Sea, Chabahar Bay. Legend: New distribution (Chabahar Bay), Northern Arabian Sea coast of Pakistan (PANHWAR et al. 2018), East and west coasts of India (McKAY 1992)

This paper reports the first documented record of *S. indica* from the Iranian waters of the Oman Sea, providing morphometrical and meristic data. In addition, molecular analysis using the mitochondrial COI gene sequence was carried out in order to support the findings based on morphology.

Materials and Methods

Sampling

Fish samples were directly collected by local fishermen and fishery surveys along the coast of Chabahar Bay, north of the Oman Sea, during occasional sampling in 2019–2020 (Fig. 1). Three specimens were fin-clipped for molecular analysis. All specimens were catalogued at the Tarbiat Modares University aquatic animal collection (TAC1229F).

Morphological analysis

Taxonomical identification of specimens was done based on MCKAY (1985; 1992). Seventeen morphometric measurements were taken using a digital caliper (0.01 mm accuracy) and seven meristic characters were studied using a stereomicroscope and x-ray photos (for counting vertebrae). Morphological data were compared with the available data on *S. indica* (XIAO et al. 2016).

Genetic analysis

Cytochrome oxidase subunit I (COI) fragments were amplified to confirm the identification of *S. indica*. Total genomic DNA extraction and polymerase chain reaction (PCR) followed the protocols of GAO et al. (2011). The primers used were as follows: Fish F1: 5'-TCAACCAACCACAAAGACATTGGCAC-3'

and Fish R1: 5'-TAGACTTCTGGGTGGCCAAA-GAATCA-3' (WARD et al. 2005). Three sequences obtained from *S. indica* in this study were submitted to GenBank with the following accession numbers: PP031953-5. Other haplotypes from other sillaginid species, including *S. aeolus*, *S. asiatica*, *S. attenuata*, *S. mengjialensis*, *S. panhwari*, *S. shaoi* and *S. sihama*, were used for phylogenetic tree reconstruction and calculating genetic distances. Sequences were edited and aligned using the Chromas Ver. 2.6.6 and Mafft Ver. 7.505. MEGA Ver. 7.0 and MrBayes Ver. 3.2.7. were used to estimate the genetic distances (Kimura 2-parameter model) and construct a Bayesian tree (G+I model), respectively. The COI haplotype of *Kyphosus vaigiensis* was selected as outgroup.

Result

Diagnosis

Sillago indica is distinguished by dorsal-fin rays X–XI, I+20–22, anal fin rays II (21–23); scales in lateral line 69–75, scales above lateral line 5–6; total vertebra 34 in number (Table 1). The swim bladder has two anterior extensions and two posterior extensions with a lacuna between them; the duct-like process begins is at the termination of the swim bladder and is between the base of the two posterior extensions.

Description

General body features were shown in Fig. 2. Morphometric and meristic characters of the 16 collected specimens from the Northern Oman Sea (Chabahar Bay) are presented in Tables 1 and 2. The body is elongated, slightly conical anteriorly and tubular posteriorly. All the morphometric measurements and meristic

Table 1. Morphometric and meristic characteristics of 16 specimens of *Sillago indica* from the north of Oman Sea in comparison with previous published data (XIAO et al. 2016). Standard and head lengths are abbreviated as SL and HL, respectively.

Parameter	Present study (n = 16)	XIAO et al. (2016) (n = 72)
Standard length, mm	92.8-126.16	139.2-192.4
As % of SL		
Head length	27-29	27.5–32.4
Snout length	11.3-13.1	11.1-14.2
Body depth	16-19.6	-
First dorsal fin base	20.1-23	19.3-23.7
Second dorsal fin base	35.2-37.8	33.9-38.0
Anal fin base	33.4-37.4	31.8-37.1
Caudal peduncle length	5.76-9.34	8.9-11.7
Caudal peduncle depth	6.02-7.5	6.6-8.9
Pre dorsal length	33.6-36.2	-
Pre anal length	53.1-56.9	-
Pre pelvic length	29.36-4.95	-
Pectoral fin length	12.7-15.8	14.4-19.1
Pelvic fin length	13.9-16.7	14.1-17.9
As % of HL		
Snout length	40.03-3.48	-
Eye diameter	14.70-2.10	-
Post orbital length	32.01-1.93	-
Meristic Character		
Dorsal fins	X-XI-, I, 20_22	X-XI,I,20-22
Anal fins	II,21–23	II, 21-23
Pectoral fin rays	16-17	16-17
Pelvic fin rays	I,5	I,5
Scales above/below lateral line	5-6/10-11	5-6/10-12
Lateral line scales	69-75	68-71
Vertebrae (in total)	34	33-35 (mostly 34)

Table 2. Comparison of some morphological characteristics of *Sillago indica* and four other sillaginid species inhabiting the Northern Oman Sea

Parameter	<i>Sillago indica</i> ^a	<i>Sillago sihama</i> ^b	<i>Sillago arabica</i> ^c	<i>Sillago attenuata</i> ^c	<i>Sillaginopodys chondropus</i> ^{d&c}
Dorsal fins rays	X–XI, I, 20–22	XI, I, 20–23	XII–XIII, I, 19–21	XII–XIII, I, 22–24	XI, I, 21–22
Anal fin rays	II, 21–23	II, 21–23	II, 22–24	II, 18–20	II, 20–22
Scales in lateral line	68–71	68–72	75–80	73–75	66–80
Scales above/below lateral line	5–6/10–11	5–6/10–12	-	-	4–5, 8–10
Vertebrae	34	34	38–40	37–39	-
Snout Length / HL (%)	40.03–43.48	-	33–35	-	35.6±3.1

Notes: a. Present study; b. DIVYA et al. (2021); c. MCKAY (1985, 1992); d. KHANDAN BARANI et al. (2023).



Fig. 2. *Sillago indica* from the northern coast of the Oman Sea, Iran

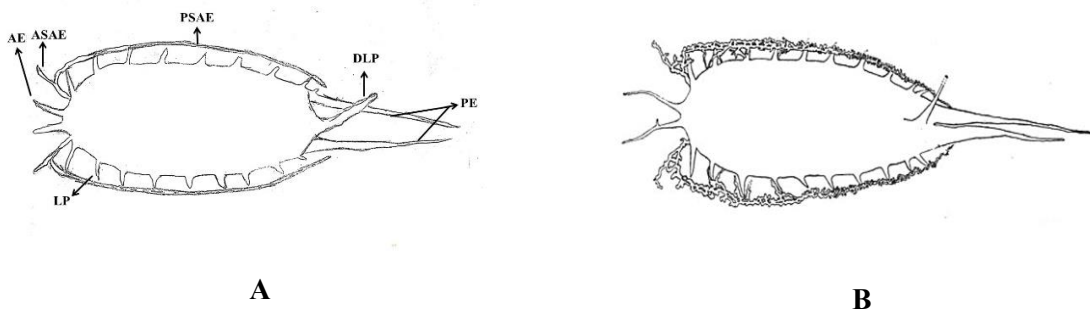


Fig. 3. Swim bladders of *Sillago indica* (A) and *S. sihama* (B). Abbreviations: AE, anterior extension; ASAE, anterior sub-extension of anterolateral extension; PSAE, posterior sub-extension of anterolateral extension; LP, lateral processes; DLP, duct-like process; PE, posterior extension.

counts were consistent with the previously reported data for *S. indica* (XIAO et al. 2016). This species is distinguished from the other members of *Sillago* in the Oman Sea by the following characteristics:

- from *S. arabica* and *Sillaginopodys chondropus*, by having a bigger head (40.03–43.48% SL in *S. indica* vs. 33.0% in *S. arabica* and 35.6±3.1% in *Sillaginopodys chondropus*);

- from *S. arabica* and *S. attenuata*, by having 34 vertebrae (38–40 in *S. arabica*, 37–39 in *S. attenuata*), less dorsal spines (X–XI in *S. indica* vs. XII–XIII in *S. arabica* and *S. attenuata*) and having 68–71 scales on lateral line (75–80 in *S. arabica*, 73–75 in *S. attenuata*).

Sillago indica is most similar to *S. sihama* in the meristic characters and colour pattern. However, their swim bladders are obviously different (Fig. 3).

Colour of fresh specimens

The body yellowish-brown dorsally and light-silver ventrally. Cheek slightly silver, with little black dots gathered on the anterior inferior part of eyes. Dorsal fins hyaline, with small dark spots on fin membrane. Pectoral and pelvic fins yellowish; no blotches on

base. Anal fin light-yellowish; small dark spots on fin membrane. Caudal fin yellowish-dusky.

Swim bladder

The swim bladder is large (Fig. 3). Two anterior extensions protruding to the end anteriorly on each side of the basioccipital over the auditory capsule. Two anterolateral extensions originating from anteriorly of the swim bladder, each one divided into two anterior and posterior subsections: anterior sub-extensions short, simple blind tubules; posterior one is kinked, long and thin, extending along abdominal wall and reaching to the roots of two posterior extensions. The entire lateral surface of the main body of the swim bladder has eight or nine lateral processes; the anterior three processes are stout and horn-like; the posterior five or six processes are rather small and triangular. Two posterior extensions penetrate into caudal region. The roots of two posterior extensions in the swim bladder of *S. indica* were non-adjacent and there was a lacuna between the two posterior extensions. The origin of the duct-like process was at the terminus of the swim bladder

Table 3. Genetic distances (K2P) among and within haplotypes of eight sillanigid species and the obtained haplotype of *S. indica* in the present study

	Species	1	2	3	4	5	6	7	8	9	10
1	<i>Sillaginopodys chondropus</i>	0.009									
2	<i>Sillago aeolus</i>	0.25	0.000								
3	<i>Sillago asiatica</i>	0.27	0.17	0.002							
4	<i>Sillago attenuata</i>	0.20	0.21	0.21	0.000						
5	<i>Sillago indica</i>	0.22	0.21	0.23	0.23	0.000					
6	<i>Sillago indica</i> (this study)	0.21	0.21	0.23	0.22	0.001	0.000				
7	<i>Sillago mengjialensis</i>	0.26	0.19	0.13	0.23	0.21	0.21	0.003			
8	<i>Sillago panhwari</i>	0.26	0.23	0.21	0.23	0.22	0.22	0.15	0.004		
9	<i>Sillago shaoi</i>	0.23	0.15	0.19	0.23	0.22	0.22	0.20	0.23	0.004	
10	<i>Sillago sihama</i>	0.20	0.20	0.18	0.27	0.17	0.18	0.18	0.19	0.20	0.000
		1	2	3	4	5	6	7	8	9	10

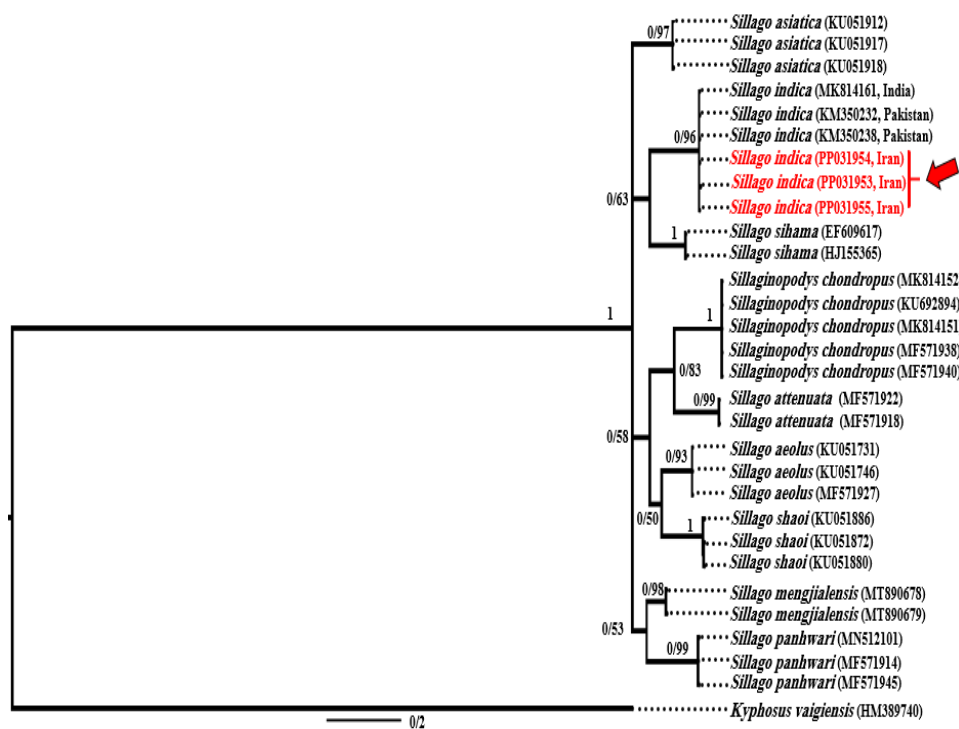


Fig 4. Bayesian analysis based on the mitochondrial cytochrome c oxidase subunit I (COI) sequences of species of the sillanigid species. Bayesian posterior probabilities are displayed at branch nodes. All reference sequences were obtained from GenBank with their accession numbers. The arrow is in front of identified haplotype from the north of Oman Sea in present study.

and between the roots of two posterior extensions. However, in the swim bladder of *S. sihama*, the roots of the two posterior extensions were adjacent and without a lacuna between them.

Molecular characters

Fragments of COI (655 bp) were sequenced from samples of *S. indica*. Genetic distances (K2P) within and among species are shown in Table 3. Genetic distances between the identified sequence and previous reported sequences from Pakistan (KM350232 and KM350238) and India (MK804161) were 0.001,

while genetic distances among other *Sillago* spp. were in the range of 0.181 to 0.231. In the constructed phylogenetic tree, all sequences of *S. indica* formed a monophyletic clade, which was in sister position with haplotypes of *S. sihama* (Fig. 4). All surveyed morphological and molecular characters confirmed the identification of the collected specimens as *S. indica*.

Discussion

The family Sillaginidae currently comprises 40 valid species (SAHA et al. 2022). Previous studies

have reported four species of the family Sillaginidae along the Iranian shores of the Persian Gulf and the Oman Sea: *S. arabica* and *S. attenuata* (subgenus *Parasillago*), *S. sihama* (subgenus *Sillago*), and *S. chondropus* (subgenus *Sillaginopodys*) (McKAY 1992, KHANDAN BARANI et al. 2023). Among them, *S. sihama* is the only one that spreads throughout the southern marine waters of Iran. The previous investigations have been exclusively based on morphological characters. Furthermore, very few studies have focused on the taxonomy of the Sillaginidae from the Chabahar Bay, Iran. The presence of *S. indica* in more than three sampling sites in Chabahar Bay indicates its abundance in the area. The information on sillaginid species in this area was based on external morphological characters, without any studies of the swim bladder structure or molecular markers. *Sillago sihama* is a complex species with the high intraspecific genetic diversity (CHENG et al. 2021). It was also observed in this study that *S. indica* is morphologically similar to *S. sihama* (Table 2) and least genetic distance appeared for *S. sihama* in comparison with *S. indica* (0.17–0.18 K2P distance; Table 3). Therefore, it seems that *S. indica* was hidden under the name *S. sihama* because of inaccurate identification and a lack of comprehensive study in the area. In agreement with our observation, XIAO et al. (2016) noted that *S. indica* had not been previously reported due to its resemblance to other species. These taxonomic ambiguities are related to the similarities in external morphological characters in this family (SAHA et al. 2022, YU et al. 2022). The swim bladder of *S. indica* is described in detail; it is similar to that of *S. sihama* but there are some notable differences.

In this study, a molecular method was also employed to confirm the morphological identification of species. Sequences of collected specimens from Indian sillago (*S. indica*) were grouped with other conspecific sequences (XIAO et al. 2016, DIVYA et al. 2021) and showed interspecific genetic distances with *S. sihama* and other *Sillago* spp. in the area. Genetic distances between *S. indica* and other species ranged from 0.18 to 0.23 (K2P distance) and the interspecific genetic distances were much greater than the intraspecific distances (0.000–0.001, K2P distance).

In conclusion, this study reports the first record of *S. indica* on the Iranian coast of the Oman Sea based on morphological and molecular data. The result will be helpful for understanding the fish fauna and distribution in the Oman Sea.

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