

Article

New Record of *Saurida micropectoralis* Shindo & Yamada, 1972 (Aulopiformes: Synodontidae) in the Southern Red Sea and Evidence of Range Expansion to East Africa

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Abstract

The shortfin lizardfish *Saurida micropectoralis* is recorded here for the first time from Jizan, Southern Red Sea, based on morphological and molecular analyses. This species closely resembles both *S. tumbil* and *S. lessepsianus*. However, *S. micropectoralis* is characterized by translucent whitish pelvic fins (vs. dusky in *S. tumbil*), indistinct blackish spots on the upper margin of the caudal fin (vs. distinct black spots (6–8) in *S. lessepsianus*), a short pectoral fin that never reaches the origin of the pelvic fin (vs. reaching a little beyond the base of the pelvic fin in *S. lessepsianus*), three rows of teeth on the outer palatines (vs. two rows in *S. lessepsianus*) and a pale whitish stomach and intestine (vs. greyish or black anteriorly in *S. lessepsianus*). Molecular analyses based on COI haplotypes confirmed the species-level identification but also revealed the existence of four distinct lineages across the species distribution range. The COI data revealed a clear geographic partitioning of haplotypes, indicating restricted gene flow and suggesting the presence of four cryptic species or, at minimum, independent evolving evolutionary units within *Saurida micropectoralis*. Populations of the shortfin lizardfish are well established in the Southern Red Sea and belong to a genetic lineage reported along the East African coast (Madagascar, Mozambique and Tanzania) and India.

Keywords: DNA barcoding; integrative taxonomy; shortfin lizardfish

Key Contribution: This study applied comprehensive morphological and molecular analyses confirming the occurrence of the shortfin lizardfish *S. micropectoralis* in the Southern Red Sea, which expands its geographical range towards the Red Sea and the east coast of Africa. Genetic data reveal clear geographic structuring of haplotypes, consistent with the existence of four cryptic species within what is currently recognized as *S. micropectoralis*. Populations of the shortfin lizardfish established in the Southern Red Sea belong to a genetic lineage reported along the East African coast (Madagascar, Mozambique and Tanzania) and India.



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1. Introduction

The fishes in the family Synodontidae, known as lizardfishes (so-named because of their heads that superficially resemble those of lizards), are found in tropical and sub-tropical marine waters throughout the world [1–3]. They usually occur on soft muddy

or sandy bottoms, although some species are found associated with shallow reef areas on continental shelves [2,3]. There are currently 83 valid species in this family belonging to four valid genera [4], of which *Saurida* Valenciennes, 1850 contains 26 species [5]. Fischer and Bianchi [2] listed five species of the genus in the Western Indian Ocean (Fishing Area 51): *S. gracilis* (Quoy & Gaimard, 1824); *S. longimanus* Norman, 1939 and *S. nebulosa* Valenciennes in Cuvier & Valenciennes, 1849; *S. tumbil* (Bloch, 1795); and *S. undosquamis* (Richardson, 1848). Russell [3] described *S. golanii* Russell, 2011 as a new *Saurida* species from the deep waters of the Gulf of Aqaba in the Northern Red Sea. Bogorodsky et al. [6] recorded the occurrence of *S. longimanus* in the Red Sea for the first time. Russel et al. [7] re-identified *S. undosquamis* to be *S. lessepsianus* Russell, Golani & Tikochinski, 2015 as a new endemic species to the Red Sea. Therefore, Golani and Fricke [8] listed five *Saurida* species in the Red Sea: *S. golanii*, *S. gracilis*, *S. lessepsianus*, *S. longimanus* and *S. tumbil*.

In their survey, Bogorodsky et al. [6] predicted a continuous increase in the number of new records from the Southern Red Sea due to the recent expansion of fish populations from the northwestern Indian Ocean. They estimated the expected number of demersal species in Jizan (Southern Red Sea) using the species accumulation curve for the survey of trawled fishes in the Jizan area and found that it could increase from 85 to 122 species by increasing the number of fishing trawls from 12 to 50 trawls. Moreover, there have been further new records recently for *Acanthocybium solandri* (Cuvier, 1832), *Kajikia audax* (Philippi, 1887) [9] and *Triacanthus biaculeatus* (Bloch, 1786) [10] from the Red Sea. Furthermore, the endemic Red Sea parrotfish *Scarus collana* Ruppell, 1835 expanded its range out to the southern coast of India [11].

During sample collection of *Saurida* species from trawl catches at the Jizan landing site (Southern Red Sea), specimens of suspected species such as *S. tumbil* and *S. lessepsianus* were obtained. After detailed examination of the specimens, we confirmed the identity as *S. micropectoralis* Shindo & Yamada, 1972 [12], based on morphological characteristics. In addition, some specimens were used for DNA barcoding to confirm the identification, which also recognized the species as *S. micropectoralis*, which is known to be restricted to the Indo-West Pacific waters [1]. This study aims to document for the first time the occurrence of this species in the Red Sea and to examine species delimitation among *Saurida* specimens collected in the Red Sea in comparison with those known from the broader region.

2. Materials and Methods

Specimens of lizardfish were collected from the demersal trawls commercial catch landed at Jizan, Southern Red Sea, Saudi Arabia, during 2021. The trawling operations in Jizan (Figure 1) are usually conducted at fishing grounds varying in depth from 10 to 40 m using trawl nets of about 50 m length constructed of multi-monofilament polyethylene netting panels and with a cod end mesh size of 40 mm [13]. The samples were kept in ice-cooled boxes and transferred directly to the fish Laboratory in the Marine Biology Department, Faculty of Marine Sciences, King Abdulaziz University, Jeddah. The specimens of *Saurida* species were sorted, and those of the shortfin lizardfish *S. micropectoralis*, greater lizardfish *S. tumbil* (the most abundant congeneric species) and *S. lessepsianus* were separated for examination. Morphometrics and meristic data of 26 specimens of *S. micropectoralis* ranging in standard length from 202.0 to 315.0 mm were recorded following the methods used by Shindo and Yamada [12], Inoue and Nakabo [14] and Russell et al. [7]. A digital Vernier caliper was used to take measurements to the nearest 0.01 mm. Voucher specimens were preserved in formalin and later transferred to 70% ethanol before being deposited in the fish collections of the King Abdulaziz University Marine Museum (KAUMM), Jeddah, Saudi Arabia (KAUMM-547).

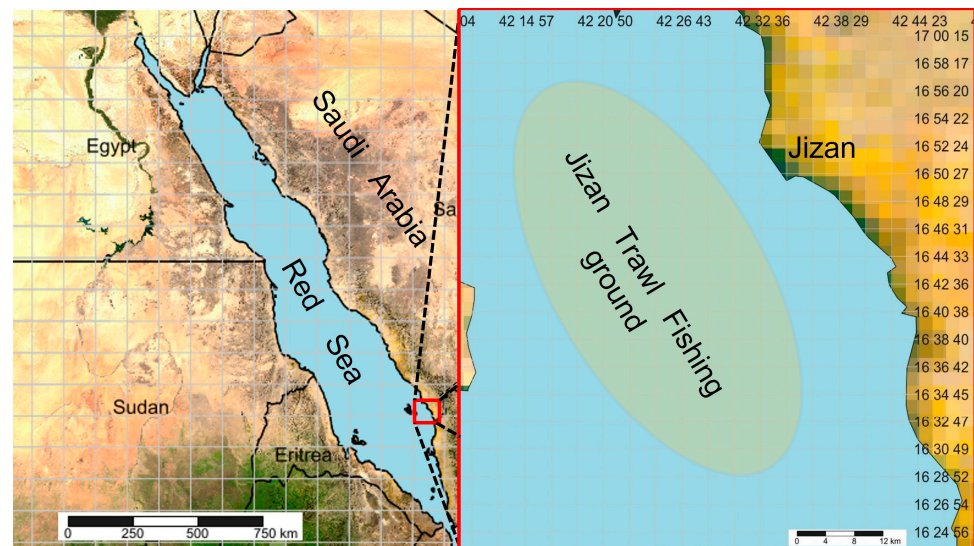


Figure 1. Map showing the fishing grounds for demersal trawling in Jizan, Red Sea (the map was generated using SimpleMappr [15]).

2.1. Genetic Analysis

Four *Saurida* specimens collected from the Southern Red Sea and morphologically identified as *S. tumbil* (two specimens) and *S. micropectoralis* (two specimens) were subjected to DNA barcoding for species confirmation. Total genomic DNA was extracted from tissue samples and preserved in 99% Ethanol using the PureLink Genomic DNA Mini Kit (Invitrogen), following the manufacturer's instructions. A -655 bp fragment from the 5' region of the mitochondrial cytochrome c oxidase subunit I (COI) gene was amplified using the primer pairs FishF1/FishR1 and FishF2/FishR1 (Ward et al.) [16], following the protocol of Ward et al. [16]. The PCR protocol was as follows: an initial denaturation at 98 °C for five minutes, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 57 °C for 30 s, and extension at 72 °C for 1 min, with a final extension at 72 °C for five minutes. PCR products were sent to GENOSCREEN (Lille, France) for Sanger sequencing. The resulting sequences were trimmed, quality-checked and aligned using MEGA 7 software. Cleaned sequences were uploaded to the Barcode of Life Data System (BOLD) in the publicly accessible project REDBF, where they were automatically assigned to Barcode Index Numbers (BINs) using the RESL species delimitation algorithm.

2.2. Haplotype-Based ML Analysis

To investigate the phylogenetic relationships among *Saurida* specimens collected in the Red Sea and species known from the region (*S. tumbil*, *S. gracilis*, *S. lessepsianus* and *S. longimanus*; *S. golanii* was excluded due to the unavailability of COI sequences), we reconstructed a Maximum Likelihood (ML) tree using all available sequences in the BOLD system (consultation on 9 July 2025) and sharing a common portion of 542 bp (Table S1). The analysis also included all available sequences representing three BINs (BOLD: AAB1858, BOLD: ADC6985 and BOLD: ADC8274) from BOLD assigned to *S. micropectoralis* to validate the morphology-based identification of two Red Sea specimens. BINs were generated using the Refined Single Linkage (RESL) algorithm [17], an automated species delimitation method integrated into BOLD Systems, which clusters COI sequences based on sequence similarity and genetic distance. While more complex species delimitation models (e.g., GMYC, ABGD, ASAP, PTP and mPTP) can offer additional insights, the BIN system is a standardized, widely used approach for primary molecular species delimitation in DNA barcoding studies. BINs are not formal species descriptions and should not be considered strictly equivalent to species boundaries; however, they represent robust operational units

generated from standardized algorithms (RESL) that, in most cases, closely correspond to described species [17]. They therefore provide reliable working hypotheses of species limits, particularly useful in cases of cryptic diversity, although their interpretation requires caution. Because specimen misidentification is common among *Saurida* species (as evidenced by the occurrence of different species names within the same BINs), species names assigned to each BIN were primarily inferred from sequences regarded as references, i.e., those corresponding to specimens identified by recognized fish taxonomists. The distinct assignment of *S. micropectoralis* sequences to separate BINs is consistent with the existence of cryptic diversity, which we further explored using both phylogenetic and haplotype-based methods. The genetic distances between BINs were also estimated using MEGA7 [18] under the Kimura 2-parameter (K2P) model, which is the standard metric in DNA barcoding studies and facilitates direct comparisons with previous taxonomic and barcode-based assessments.

Phylogenetic inference was conducted using IQ-TREE v1.6.12 [19]. The best-fit nucleotide substitution model was identified using ModelFinder [20], which selected the TIM3+F+I+G4 model under the Bayesian Information Criterion (BIC). To assess the reliability of the inferred phylogenetic relationships, node support was tested using the bootstrap method with 1000 ultrafast bootstrap replicates, implemented in UF-Boot2 [21]. The tree was rooted using sequences from three *Synodus* species, selected as the outgroup following prior taxonomic classifications and phylogenetic evidence supporting their position relative to *Saurida*. Branch lengths represent the number of nucleotide substitutions per site.

The geographic structure of *S. micropectoralis* genetic diversity was further examined by analyzing all COI sequences available in the BOLD library (consultation on 9 July 2025) assigned to four Barcode Index Numbers (BINs): BOLD: AAB1858, BOLD: ADC6984, BOLD: ADC6985 and BOLD: ADC8274. These sequences were retrieved from the BOLD database to ensure comprehensive coverage of the species' genetic diversity. To visualize the relationships and infer potential geographic structuring among haplotypes, a Minimum Spanning Tree (MST) [22] was constructed using the software POPART [23]. This method allows the depiction of the genetic distance between haplotypes by minimizing the total branch length, thereby providing insights into the phylogeographic patterns of *S. micropectoralis* populations across their distribution range. The final distribution map of the species (complex) of *S. micropectoralis* was generated using SimpleMappr [24] based on either barcode information or observation from the Global Biodiversity Information Facility [25].

3. Results

Genus: *Saurida* Valenciennes, 1850

Species: *Saurida micropectoralis* Shindo & Yamada, 1972, [12]

English Common name: Shortfin Lizardfish

(Figure 2, Table 1)

The general morphology and color of the fresh specimens of *S. micropectoralis* collected from the Southern Red Sea are shown in Figure 2. The body is elongate and cylindrical, with a lizard-like head and adipose fin, as in all species of the *Saurida* genus. The color of the back (dorsal) and upper sides is brown or coppery brown. The color of the lower sides (two scale rows below the lateral line with melanophores) is paler brown. The belly (ventral side) is silvery white. Faint darker blotches (9 to 10) are found along the lateral line, and faint black dots are present along the upper edge of the caudal fins (Figures 2 and 3). The pectoral fin is very short; its tips do not reach the origin of the pelvic fin or the P-D line (between the origins of the pelvic and dorsal fins) (Figure 4). The upper portion of the inner face of the pectoral fins is dark. The inner surface of the operculum is yellowish or

grey, and the pelvic fin is unpigmented (Figure 5A). The stomach and intestine are pale whitish (Figure 6).



Figure 2. General morphology (view of the left side) of *S. micropectoralis* collected from the Southern Red Sea deposited at King Abdulaziz University Marine Museum (KAUMM-547).

From the range and mode of meristic data of *S. micropectoralis* provided in Table 1, no fins have spines; there are 12 dorsal fin rays (11–12); 9 pelvic fin rays; 14 pectoral fin rays (14–15); 11 anal fin rays (10–12); 57 pored lateral-line scales (56–59); 4.5 transverse scales above the lateral line (Figure 7A) and 5.5 transverse scales below the lateral line with two scale rows of them with melanophores (Figure 7B); 20 predorsal scales (19–22); 11 preadipose scales (10–12); three rows of teeth on the outer palatine anteriorly (3–4); and one patch of six (2–10) teeth on the vomer (Figure 8).

Table 1. Morphometric and meristic data of *S. micropectoralis* recorded in the Red Sea (26 specimens: 202.0–315.0 SL; n = 26).

	Morphometrics (% Standard Length)		Mean $\pm$ SD
	Min	Max	
Predorsal length	40.0	43.3	41.8 $\pm$ 0.8
Preadipose length	79.3	83.1	81.2 $\pm$ 0.9
Preanal length	69.3	72.2	70.9 $\pm$ 0.9
Preanal fin length	73.2	76.3	74.7 $\pm$ 0.7
Prepectoral length	21.1	24.1	22.5 $\pm$ 0.8
Prepelvic length	34.6	37.7	36.2 $\pm$ 0.8
Head length	22.0	23.7	22.6 $\pm$ 0.7
Body depth	12.8	15.0	14.2 $\pm$ 0.5
Body width	12.9	16.6	14.6 $\pm$ 1.1
Interpelvic width	9.4	10.3	9.7 $\pm$ 0.4
Pectoral fin length	10.7	13.3	11.9 $\pm$ 0.7
Pelvic fin length	14.6	17.3	16.5 $\pm$ 0.8
Length of 2nd dorsal ray	16.3	20.9	18.1 $\pm$ 1.3
Length of last dorsal ray	3.2	7.5	4.6 $\pm$ 0.8
Length of dorsal fin base	11.9	13.8	12.6 $\pm$ 0.5
Length of 2nd anal ray	8.6	11.0	10.0 $\pm$ 0.6
Length of last anal ray	4.0	5.9	5.1 $\pm$ 0.6
Length of anal fin base	7.8	9.8	8.8 $\pm$ 0.6
Length of caudal peduncle	14.6	16.9	15.9 $\pm$ 0.9
Depth of caudal peduncle	5.4	6.4	5.9 $\pm$ 0.3
Width of caudal peduncle	5.7	7.0	6.5 $\pm$ 0.3
Morphometrics: % head length and (%SL)			
Snout length	17.9 (3.6)	29.8 (5.7)	22.2 $\pm$ 3.3 (4.7 $\pm$ 0.6)

Table 1. Cont.

	Morphometrics (% Standard Length)		Mean $\pm$ SD
	Min	Max	
Eye diameter	15.8 (3.5)	25.5 (4.5)	18.9 $\pm$ 2.5 (4.0 $\pm$ 0.3)
Snout width	25.9 (6.4)	35.7 (8.1)	32.3 $\pm$ 2.6 (7.1 $\pm$ 0.4)
Interorbital width	17.6 (4.6)	25.2 (5.6)	22.9 $\pm$ 1.8 (5.1 $\pm$ 0.3)
Postorbital length	57.4 (12.5)	64.3 (14.6)	62.3 $\pm$ 2.0 (13.7 $\pm$ 0.6)
Upper jaw length	56.9 (12.7)	75.2 (16.5)	67.5 $\pm$ 4.5 (15.0 $\pm$ 1.2)
Meristics	Min	Max	Mode
No. of dorsal fin rays	11	12	12
No. of pectoral fin rays	14	15	14
No. of pelvic fin rays	9	9	9
No. of anal fin rays	10	12	11
Pored lateral-line scales	56	59	57
Transverse scales above lateral line	4.5	4.5	4.5
Transverse scales below lateral line	5.5	5.5	5.5
Scale rows below LL with melanophores	2	2	2
Predorsal scales	19	22	20
Preadipose scales	16	19	18
Postadipose scales	10	12	11
No. rows of palatine teeth anteriorly	3	4	3
No. vomerine teeth	2	10	6

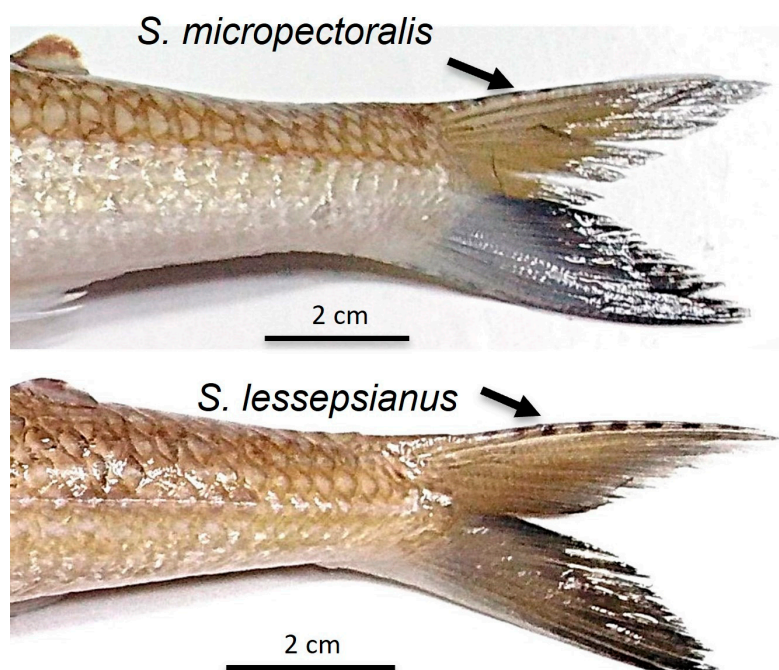


Figure 3. Upper edges of the caudal fin with indistinct blackish spots in *S. micropectoralis* and distinct black spots (usually 6 or 8) in *S. lessepsianus*.

The four specimens barcoded and morphologically identified as *S. micropectoralis* or *S. tumbil* were assigned by BOLD to two distinct BINs: BOLD: AAB1858 and BOLD: AAE4219, respectively. BIN BOLD: AAB1858 includes eight specimens identified as *Saurida* cf. *micropectoralis*, five as *S. micropectoralis* (including one identified by Barry Russell), one as *S. undosquamis*, one as *S. tumbil* and two others that were unidentified. In contrast, BIN BOLD: AAE4219 comprises 40 specimens identified as *S. tumbil* and 8 unidentified specimens. In BOLD, two additional BINs were associated with the species name *S. micropectoralis*: BOLD: ADC6985 and BOLD: ADC8274. Phylogenetic reconstruction (Figure 9)

revealed a close genetic proximity among these three BINs, together with BIN BOLD: ADC6984 (comprising specimens initially identified as *S. tumbil*, Table S1), with pairwise divergences ranging from 2% to 4% (Table S2). While the three BINs assigned to *S. gracilis* were clearly separated and represented the most divergent lineage within the dataset, the phylogenetic relationships among the remaining *Saurida* species recorded in the Red Sea were not well resolved.

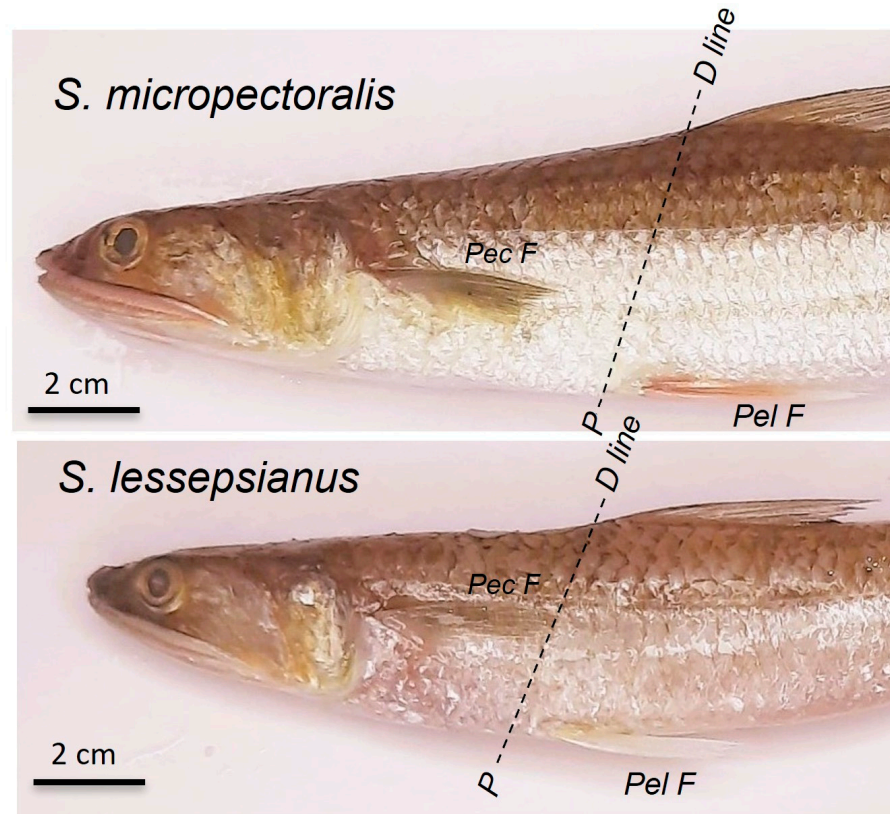


Figure 4. The pectoral fin of *S. micropectoralis* does not reach the P-D line (between the origins of the pelvic and dorsal fins) and that of *S. lessepsianus* is moderately long, just reaching or a little beyond the base of pelvic fin.

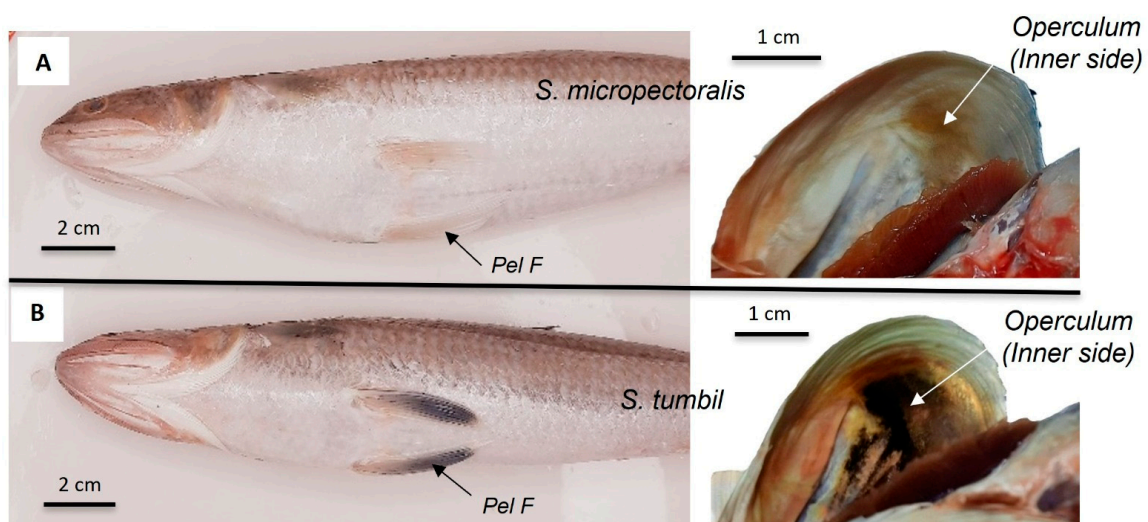


Figure 5. *Saurida micropectoralis* (A) with unpigmented pelvic fin (left) and yellowish or grey inner surface of the operculum (right) versus (B) dark pelvic fin (left) and dark grey inner surface of the operculum (right) in *S. tumbil*.

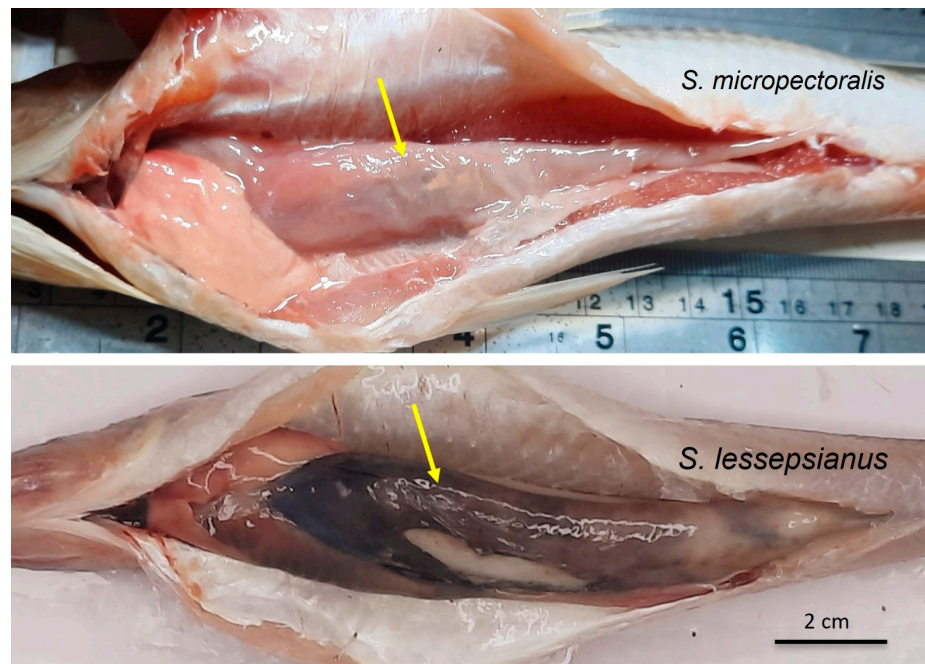


Figure 6. An unpigmented stomach in *S. micropectoralis* versus grey to dark stomach anteriorly in *S. lessepsianus*.

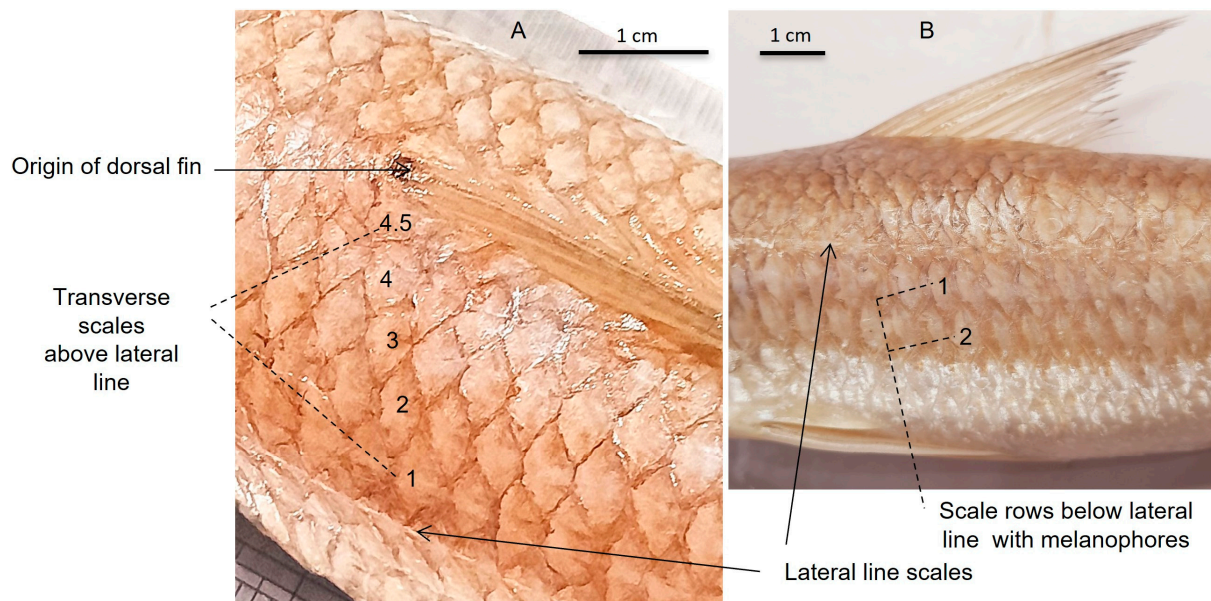


Figure 7. Transverse scale rows above lateral line (A) and scale rows below LL with melanophores (B) in *S. micropectoralis* collected from Jizan fisheries, Saudi Arabia.

The Minimum Spanning Tree analysis of the four BINs assigned to *S. micropectoralis* (BOLD: AAB1858, BOLD: ADC6984, BOLD: ADC6985 and BOLD: ADC8274) revealed a clear phylogeographic structure (Figure 10). BIN BOLD: AAB1858, which includes the Red Sea specimens, also contains sequences from India and the southwestern Indian Ocean, notably from Mozambique, Tanzania and Madagascar. The haplotypes within BOLD: AAB1858 formed a distinct cluster, separate from those of BINs BOLD: ADC6984, BOLD: ADC6985 and BOLD: ADC8274, which were composed of specimens from geographically restricted areas in the Indo-Pacific. The genetic distances and branching patterns between these BINs, despite their close proximity in the phylogenetic reconstruction (Figure 9), support the existence of geographically structured lineages.

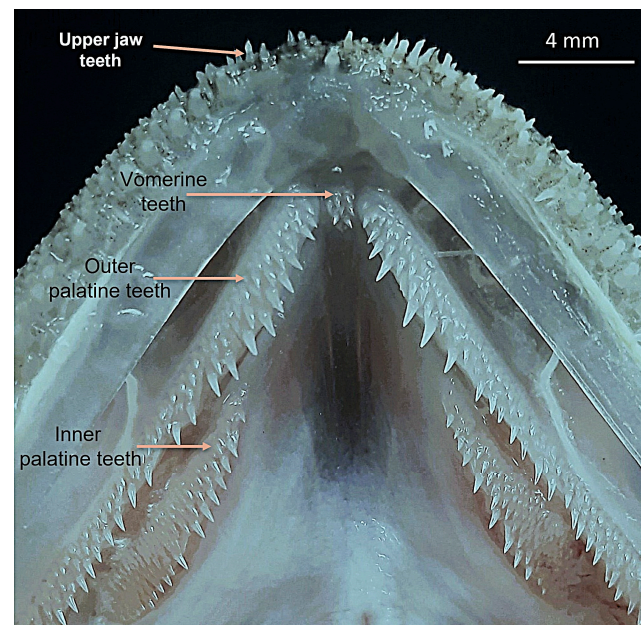


Figure 8. Upper jaw showing outer palatines with three rows of teeth and vomerine series of 10 teeth in *S. micropectoralis* collected from Jizan fisheries, Saudi Arabia.

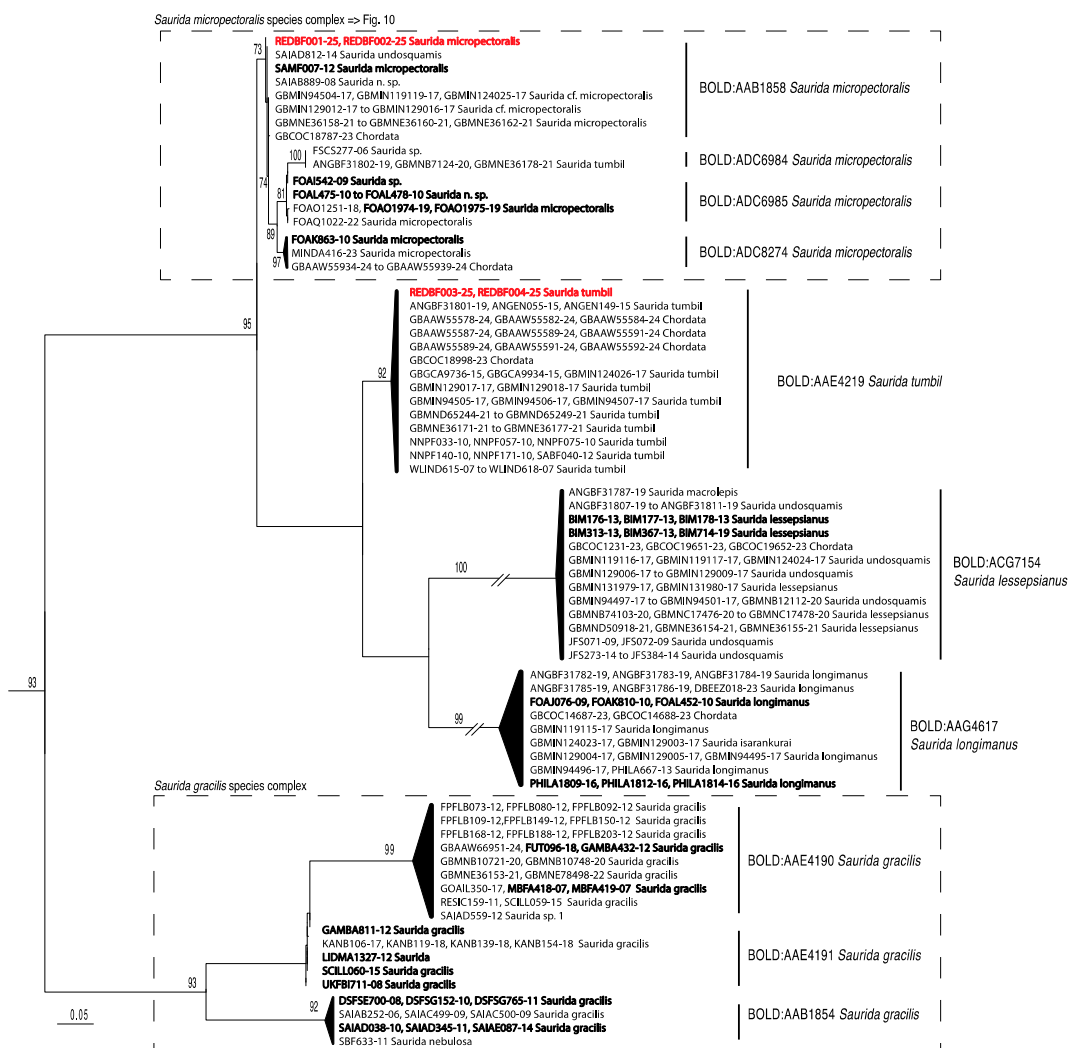


Figure 9. Maximum Likelihood phylogenetic tree of *Saurida* and related taxa reconstructed with IQ-TREE v1.6.12 [18]. Analyses were conducted on an alignment of 198 sequences (542 bp, COI gene),

including 340 constant sites (62.7%), 181 parsimony-informative sites, and 197 distinct site patterns. The best-fit substitution model selected by ModelFinder [19] according to BIC was TIM3+F+I+G4, with 60.8% invariable sites and a gamma shape parameter $\alpha = 1.258$. Branch support values represent SH-aLRT (%) / ultrafast bootstrap (UFBoot, 1000 replicates [20]), and only bootstrap values $\geq 70\%$ are shown. A total of 45 near-zero internal branches (<0.0018) were detected and should be interpreted with caution. The log-likelihood of the best ML tree was -3556.62 , with an AIC of 7491.24, AICc of 7695.28 and BIC of 8303.05. The tree was rooted with three *Synodus* sequences: *Synodus synodus* (HM390092), *S. intermedius* (GU225496) and *S. foetens* (MT455807). Sequences obtained from specimens collected in the Red Sea are shown in red. On the right side of the tree, the Barcode Index Numbers (BINs) assigned by the BOLD system are indicated, together with the most probable species identity that should be considered. A complete list of sequences used in the phylogeny is provided in Supplementary Table S1. Specimen codes (from BOLD) and species names in bold correspond to specimens identified by taxonomists (Diane E. Pitassy, Barry Russell, Phillip C. Heemstra, Jeff Williams, Allan D. Connell, Nir Stern, Jeff Williams, Kent E. Carpenter and William White; see Table S1). A complete list of sequences used in the phylogeny is provided in Table S1.

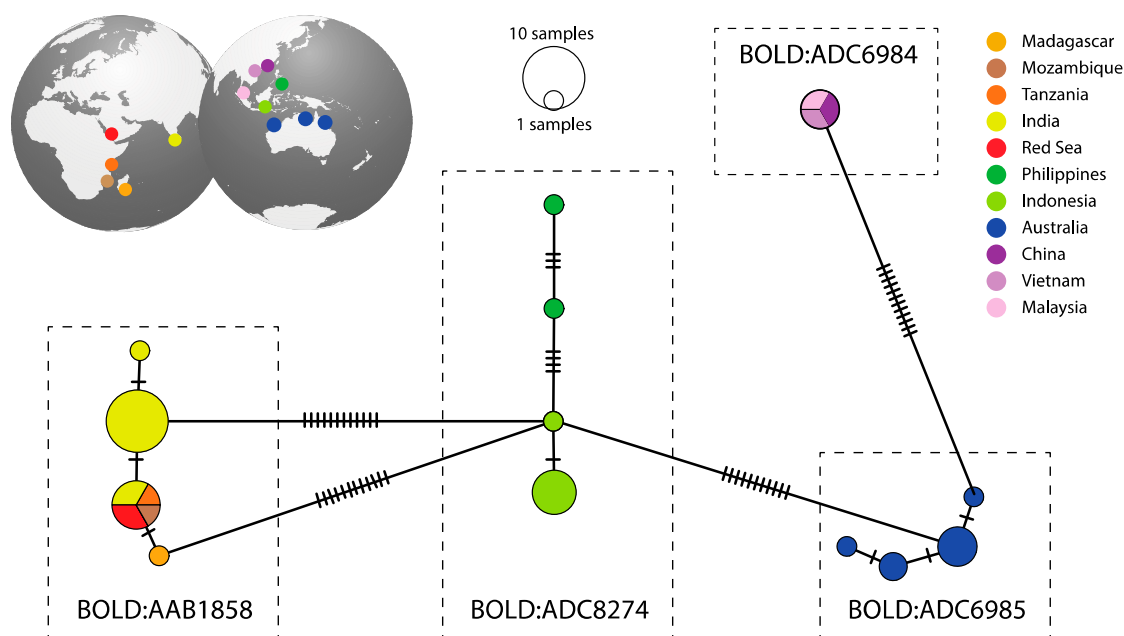


Figure 10. Minimum Spanning Tree (MST) based on all available COI sequences assigned to the BINs BOLD: AAB1858, BOLD: ADC6984, BOLD: ADC6985 and BOLD: ADC8274, associated with *S. micropectoralis*, including the two sequences obtained from the Red Sea in the present study. Each circle represents a unique haplotype, and the size of the circles is proportional to the number of individuals sharing the same haplotype. Colors indicate the geographic origin of the sequences. Hatch marks on the connecting lines represent the number of mutational steps between haplotypes. The MST illustrates the genetic relationships and phylogeographic structure of *S. micropectoralis* across its distribution range.

4. Discussion

Of the five *Saurida* species recorded in the Red Sea by Golani and Fricke [8], only *S. golanii* is endemic to the deep water (200–500 m depth) of the Gulf of Aqaba, Northern Red Sea [3,25]. The other four species, *S. tumbil*, *S. gracilis*, *S. lessepsianus* and *S. longimanus*, are widespread in the Western Indian Ocean and the Red Sea. Although *S. lessepsianus* is identified as a new species in the Northern Red Sea for the previously recorded species *S. undosquamis*, Silpa et al. [26] and Zohra et al. [27] confirmed the occurrence of this species (misidentified as *S. undosquamis*) in the Arabian Sea and Bay of Bengal. The present study

confirms the presence of *S. micropectoralis* in the Red Sea and the east African coast based on morphological and DNA barcoding. This record increases the number of *Saurida* species in the Red Sea to six species and expands the geographical range of the shortfin lizardfish towards the east coast of Africa. The previous distribution of this species is known to be restricted to the Indo-West Pacific, including the Andaman and South China seas [1], south to the Arafura Sea [28], to the Northern of Bay of Bengal [29] and to the southern Japanese waters [30]. This is the first record of *S. micropectoralis* in the Red Sea and the eastern African coast of the Indian Ocean.

The morphometric and meristic data recorded in the present study for *S. micropectoralis* are in agreement with those of the original description of the species in the south China Sea [12], as well as the description from the southern Japanese waters by Miyahara et al. [30] (Table 2). *Saurida micropectoralis* can be distinguished from other species recorded in the Red Sea by diagnostic characters listed in Table 3. The specimens of *S. micropectoralis* collected from the Southern Red Sea during the present study differed from the most common congeneric species, *S. tumbil*, by having an unpigmented pelvic fin, dark blotches on the flanks, indistinct black bars on the upper edges of caudal fin and a very short pectoral fin never reaching the pelvic fin origin (vs. a dark pelvic fin, no dark blotches on the flanks, no indistinct black bars on the upper edges of caudal fin and a short pectoral fin that may or may not just reach to the pelvic fin origin). *Saurida micropectoralis* can be distinguished from both *S. lessepsianus* and *S. longimanus* by having a very short pectoral fin never reaching the pelvic fin origin (moderately long and longer pectoral fin in *S. lessepsianus* and *S. longimanus*, respectively, reaching the pelvic fin origin), indistinct black spots (6–8 distinct black spots in *S. lessepsianus*) on the upper edges of the caudal fin, three rows of teeth on the outer palatine, a whitish stomach and intestine, and 55–58 lateral-line scales (two rows of teeth, grey to dark stomach (anteriorly) and 46–51 lateral-line scales in *S. lessepsianus* and *S. longimanus*). Moreover, *S. golanii* lacks blotches on the flanks and black bars on the upper edges of caudal fin. In addition, the species (*S. golanii*) is characterized by a dark stomach anteriorly and a dark intestine, a very long pectoral fin reaching well beyond the pelvic fin origin and 53–56 lateral-line scales. *Saurida gracilis* can be distinguished very easily from other *Saurida* species including *S. micropectoralis* by having different body colors, all fins with dark bars and spots, the presence of one or two teeth rows on the outer palatine and only 3.5 scale rows above the lateral line.

The present study provides clear morphological evidence for the occurrence of *S. micropectoralis* in the Red Sea, a region well outside its currently recognized distribution as reported in the Catalog of Fishes (consulted 28 July 2025). According to this source, the species is distributed along the east coast of India, Bangladesh, Myanmar and the Andaman Islands, extending eastward to the Philippines and Papua New Guinea, northward to China and southward to northern Australia. If confirmed, this observation would represent a major range extension, as shown in Figure 11. Notably, the DNA barcodes obtained from the Red Sea specimens were assigned to BIN BOLD: AAB1858, which also includes sequences from specimens collected in India, Mozambique, Tanzania and Madagascar. Like the Red Sea, the southwestern Indian Ocean has not been traditionally recognized as part of the species' distribution range [31]. Interestingly, most specimens grouped under BIN BOLD: AAB1858 have been registered in BOLD as either *S. micropectoralis* or *Saurida* cf. *micropectoralis*, suggesting that the presence of this species outside its documented range may have already been noted, albeit informally. Furthermore, the DNA barcoding results revealed two additional lineages among specimens morphologically identified as *S. micropectoralis*. The assignment of these lineages to distinct BINs, combined with their allopatric distributions, suggests the possible existence of closely related sister species. This highlights the need for further taxonomic investigation to determine whether these lineages

represent cryptic species or distinct taxa for which diagnostic morphological criteria have been underestimated.

Table 2. Comparative morphometric and meristic measurements of *S. micropectoralis*.

	Present Study (26 Specimens: 202–315 mm SL)	Miyahara et al., 2002 [30] (1 Specimen: 324 mm SL)	Shindo and Yamada, 1972 [12] (32 Specimens: 86–246 mm SL)
Morphometrics: As a percentage of standard length			
Predorsal length	40.0–43.3	43.4	42.0–44.9
Preanal fin length	73.2–76.3	75.9	75.6–79.7
Prepelvic length	34.6–37.7	37.6	36.7–40.5
Head length	22.0–23.7	23.7	24.1–26.7
Body depth	12.8–15.0	14.8	11.5–15.8
Pectoral fin length	10.7–13.3	12.0	10.8–12.9
Pelvic fin length	14.6–17.3	16.5	14.8–17.4
Length of longest dorsal ray	16.3–20.9	20.1	18.8–22.9
Length of dorsal fin base	11.9–13.8	14.0	-
Length of longest anal ray	8.6–11.0	10.4	-
Length of anal fin base	7.8–9.8	8.7	-
Length of caudal peduncle	14.6–16.9	15.3	-
Depth of caudal peduncle	5.4–6.4	6.3	-
Snout length	3.6–5.7	5.8	-
Eye diameter	3.5–4.5	3.8	3.66–5.46
Interorbital width	4.6–5.6	5.4	-
Upper jaw length	12.7–16.5	16.2	-
Meristics			
No. of dorsal fin rays	11–12	12	11–12
No. of pectoral fin rays	14–15	15	14–15
No. of pelvic fin rays	9	9	9
No. of anal fin rays	10–12	11	10–11
Pored lateral-line scales	56–59	55	56–58
Transverse scales above LL	4.5	5	5
Transverse scales below LL	5.5	6	-
Predorsal scales	20–22	22	20–21

Table 3. Diagnostic characteristics of the five *Saurida* species recorded in the Red Sea, excluding *S. gracilis*, which can be readily distinguished from the other species by its distinct body coloration and the presence of dark bars and spots on all fins.

Character	<i>S. golanii</i>	<i>S. lessepsianus</i>	<i>S. longimanus</i>	<i>S. micropectoralis</i>	<i>S. tumbil</i>
Position of the pectoral fin versus pelvic fin origin	Largely beyond	Slightly beyond	Well beyond	Not reaching	Just reaching
Bars on upper edges of caudal fin	Absent	Present (black spots)	Present (indistinct)	Present (faint dusky spots)	Absent
Blotches on flanks	Absent	Present	Present	Present	Absent
Stomach color	Dark anteriorly	Grey to dark anteriorly	Dark	Unpigmented	Unpigmented
Intestine color	Black	Unpigmented	Striped	Unpigmented	Unpigmented
Pelvic fin color	Unpigmented	Unpigmented	Unpigmented	Unpigmented	Dark
Outer series of palatine teeth	Three rows	Two rows	Two rows	Three rows	Three rows
No. of lateral-line scales	53–56	47–51	46–50	56–59	55–58

Based on the present study, more demersal fish species could be reported. Therefore, we recommend more demersal trawling surveys in the Red Sea to increase the probability of exploring more new species or records of demersal fish species as assumed and predicted by Bogorodsky et al. [6] from the analysis of the species accumulation curve. Further studies on the biology of *S. micropectoralis* in Jizan area are urgently required, as well as the phylogenetic relationship of the other species of the genus.

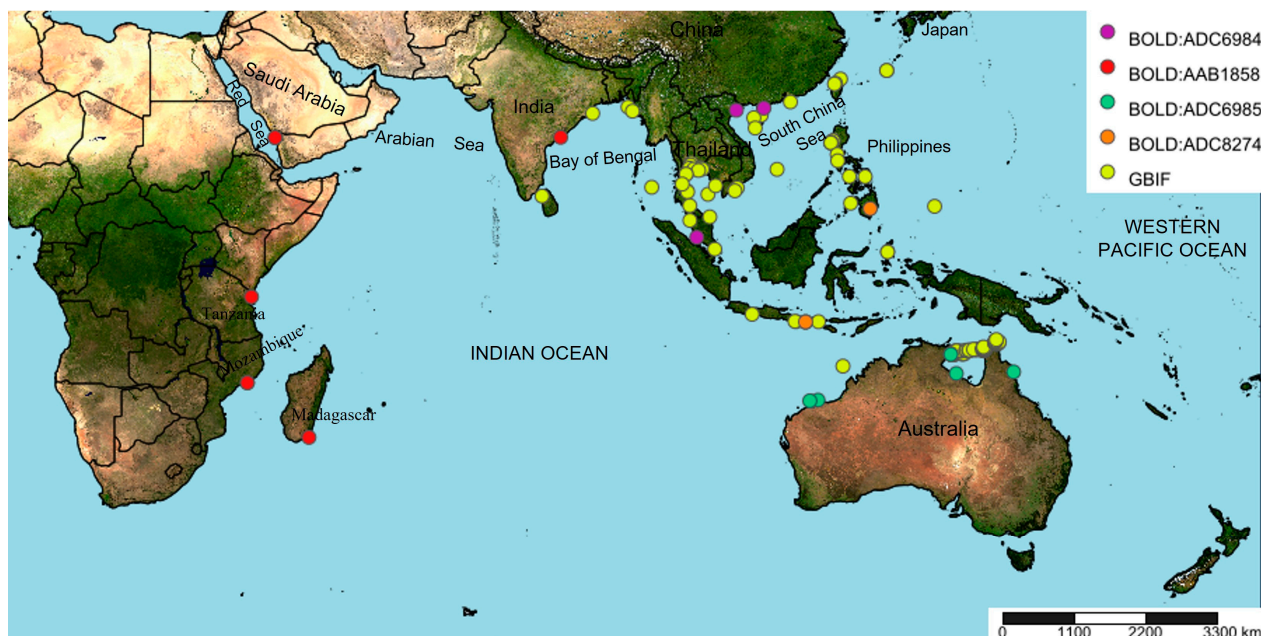


Figure 11. Distribution map of *S. micropectoralis* Shindo & Yamada (1972) [12] in the Indo-West Pacific. (the map was generated using SimpleMappr [15]).

5. Conclusions

Based on clear evidence from morphological and molecular analyses in this study, it is concluded that the shortfin lizardfish *S. micropectoralis* occurs in the Southern Red Sea, a region well outside its currently recognized distribution. The morphometric and meristic data recorded in the present study for *S. micropectoralis* are in agreement with those of the original description of the species in the south China Sea, as well as the description from the southern Japanese waters. Molecular analyses confirmed the species-level identification but also revealed the existence of four distinct lineages across the species distribution range. This record expands the geographical range of the species towards the Red Sea and the east coast of Africa and increases the number of *Saurida* species in the Red Sea to six species: *S. golanii*, *S. gracilis*, *S. lessepsianus*, *S. longimanus*, *S. tumbil* and *S. micropectoralis*. More trawling surveys are required to reveal the diversity of demersal species in the Southern Red Sea.

Supplementary Materials: The following supporting information can be downloaded at <https://www.mdpi.com/article/10.3390/fishes10090452/s1>, Table S1: List of COI sequences of *Saurida* spp. specimens used for phylogenetic reconstruction, with specimen information and accession numbers; Table S2: Estimates of Evolutionary Divergence over Sequence Pairs between and within Barcode Index Numbers of some *Saurida* spp. [32].

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