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Taxonomic account of misidentified *Saurida lessepsianus* Russell, Golani and Tikochinski, 2015 from the east coast of India (Bay of Bengal)

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Abstract

The objective of the current study was to tackle the problem of incorrect identification regarding *Saurida lessepsianus*. In prior research conducted along the eastern coast of India, it had been mistakenly labeled as *Saurida undosquamis* due to their similar physical characteristics. Through a comprehensive analysis involving both morphological and genetic data, this study serves to establish that the species referred to as *S. undosquamis*, identifiable by its upper caudal fin with distinctive black spots, along the eastern coastline of India (Bay of Bengal), is in fact *S. lessepsianus*. The misidentification arose from the assumption that the presence of black dots on the upper lobes of the caudal fin was a unique feature of *S. undosquamis,* which was later found that this trait is shared among certain species within the same genus. This underscores the necessity for applying the accurate scientific nomenclature to species, as precision in taxonomy is fundamental for effective conservation and management efforts. Consequently, this study significantly expands the documented range of *S. lessepsianus* to encompass the east coast of India (Bay of Bengal), in addition to its previously recognized habitats in the Mediterranean/Red Sea region and the eastern Arabian Sea.

Keywords:
Saurida lessepsianus, Bay of Bengal, *Saurida undosquamis*

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Introduction

The genus *Saurida* Valenciennes, 1850 is one of the four genera of the lizardfish family Synodontidae (order: Aulopiformes), which are widespread in tropical and subtropical regions of the world. The species of *Saurida* can be differentiated from other genera of the family by having cylindrical body with 9 pelvic fin rays of subequal length i.e., inner rays of pelvic fin slightly longer than outer rays (Russell, 2022). Richardson (1848) described *Saurida undosquamis* (Richardson, 1848) from north-western Australian Coast with the following morphological characters like two rows of palatine teeth with no teeth on vomer, tip of pectorals reaches far as dorsal ray, pelvic fin placed before dorsal fin, about 57 scales on lateral line and a series of small brown spots on the upper caudal fin ray.

Further studies pointed that more than one species was being identified under the name *S. undosquamis*. Yamada and Ikemoto (1979) identified two geographically segregated morphotypes of "*S. undosquamis*" in the East China Sea. Later, Yamada (1986) referred them as S-type and N-type of *S. undosquamis* based on morphological and ecological features. Yamaoka et al. (1989) carried out biochemical-genetic analysis and found that the genetic divergence between the S and N types of *S. undosquamis* justified their separation as distinct species. The study also suggested that the S type of *S. undosquamis* might be more closely related with *S. wanieso* than the N type.

Inoue and Nakabo (2006) assessed the taxonomic validity of *S. undosquamis* throughout its distribution in the Indo-West Pacific region and reported morphological variation between samples collected from North-West Indian Ocean and West Pacific Ocean. They introduced the term "*S. undosquamis* group" to encompass all *Saurida* species which are characterised by dark dots on the upper edge of the caudal fin, pectoral fins long and reaching beyond origin of pelvic fins, first rays of dorsal fin not elongate, and pre-dorsal length greater than distance between the origins of dorsal-fin and adipose-fin and moderately large scales on the body with 46–55 pored scales on the lateral line. Based on their study on "*S. undosquamis* group", they recognized four species as valid in the Indo-West Pacific region; *Saurida umeyoshii* Inoue & Nakabo, 2006; *Saurida macrolepis* Tanaka, 1917; *Saurida undosquamis* Richardson, 1848, and *S. longimanus* Norman, 1939. The taxonomic identification of species within the genus *Saurida* has been a daunting task due to overlapping morphological characters, which has led to widespread misidentification.

Subsequently, studies were carried out in different parts of the world to resolve the taxonomic ambiguity. Russell *et al*. (2015) reported that *Saurida lessepsianus* Russell, Golani & Tikochinski, 2015 from the Red Sea and Mediterranean Sea was being misidentified as *S. undosquamis*. A new species, *Saurida tweddlei* Russell, 2015 was reported from the Mascarene Plateau, Western Indian Ocean, which was also earlier misidentified as *S. undosquamis* (Russell, 2015). *Silpa et al. (2021) confirmed that the species* earlier diagnosed as *S. undosquamis* from the west coast of India (Arabian Sea) is *S. lessepsianus*. However, the previous study was restricted to the western coast and could not extended to the eastern coast of India (Bay of Bengal) due to COVID-19 pandemic. The present study aims at identifying the abundantly available *Saurida species* with dotted caudal along east coast of India by using an integrated approach incorporating morphological and molecular tools.

Materials and methods

In the present study, a total of 75 samples were collected from three locations: Tuticorin (30) [8° 45' 22.68'' N &78° 10' 44.76'' E] in Tamil Nadu, Visakapthanam (30) [17° 41' 8.16'' N & 83° 13' 6.6'' E] in Andhra Pradesh and Gopalpur (15) [19° 15' 42.79'' N & 84° 53' 40.60'' E] in Odisha along the east coast of India (Bay of Bengal).

The samples were collected between February – March 2022, from commercial trawls operated at the depths of 100–200 m. The collected individuals were

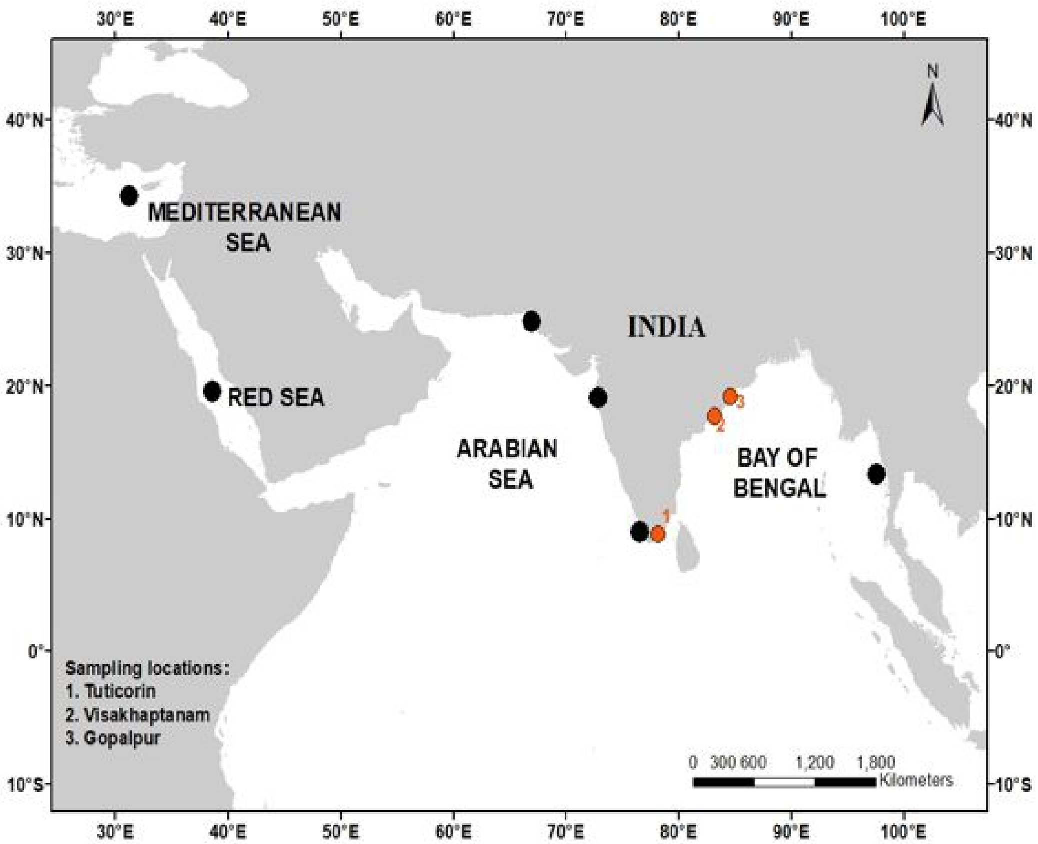

Fig 1. Present distribution of *Saurida lessepsianus*. Red dot indicates the present sampling sites along the East coast of India; Black dots depict the previous confirmed distribution.

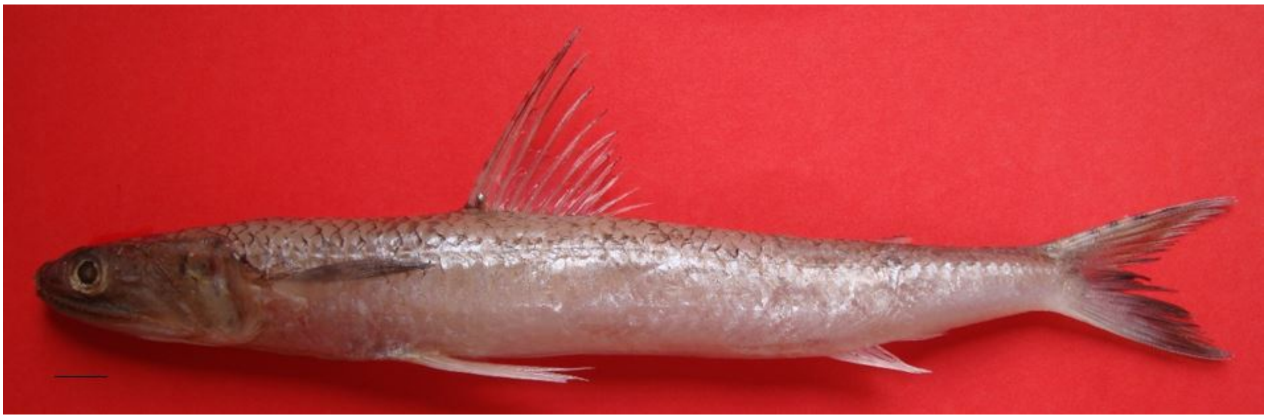

Fig 2. Images of *Saurida lessepsianus*, fresh specimen collected from Visakhapatnam fishing in Andhra Pradesh; SL 213 mm

carried to the laboratory in insulated ice box where they were cleaned and photographed. Morphometric and meristic characters were obtained following Russell *et al*. (2015). We utilized a digital Vernier caliper with a precision level of 0.1mm to conduct measurements, and in addition, we documented meristic counts. Morphometric traits were expressed as percentage of standard length (*SL*) for body measurements and head length (*HL*) for head measurements.

For molecular analysis, muscle tissue was taken from under the skin of the caudal peduncle region using a sterile scalpel and forceps. The tissues were preserved in 95% alcohol in properly labelled vials. DNA extraction was carried out by following the protocol devised by Green & Sambrook (2017) with some modifications. The quality and quantity of the isolated DNA was measured using Nano Drop Spectrophotometer. As proposed by Hebert *et al*. (2003), a part of the protein-coding mitochondrial gene, 658 bp fragment of cytochrome C oxidase subunit I (COI) was amplified by using a set of primers (FishF1 and FishR1) (Ward *et al.,* 2005). The PCR thermal regime consisted of initial denaturation of 2 min at 94 °C followed by 35 cycles of 45 sec at 94 °C, 45 sec at 52 °C and 45 sec at 72 °C and final extension of 5 min at 72 °C. The PCR products were then gel purified and sequenced in both directions using the Sanger sequencing technique. The quality of sequence was assessed by examining the Phred score (threshold value >30) of each base using FinchTV software. The good quality sequences were submitted to GenBank with accession numbers OR234585-94.

To test whether the species delimitation based on morphology is supported by genetic evidence, COI mtDNA sequences from GenBank belonging to *genus Saurida* were downloaded and examined along with the eight sequences from the present study. The sequences were properly trimmed and aligned to their homologous position using the Clustal W program. The pairwise intra-specific and inter-specific genetic distance values were calculated by Kimura two parameter (K2P) model. A neighbour-joining tree was generated to provide a graphic representation of divergence pattern between species with 100 pseudo simulations. All the above-mentioned molecular analyses were carried out in Molecular Evolutionary Genetic Analyses (MEGA11) software.

Results and discussion

For the current study, a total of 75 specimens with size range of 140.0 - 269.4 mm standard length was examined for morphometric and meristic traits. The specimens were submitted to Aquatic Biodiversity Repository and Museum, ICAR-CIFE, Mumbai, India under registration number CF1TN0148. Based on the morphometric, meristic and molecular results obtained, the sample collected was identified as *Saurida lessepsianus* Russell, Golani & Tikochinski, 2015.

Systematics

Order: Aulopiformes

Family: Synodontidae

Genus: *Saurida* Valenciennes, 1850
Species: *Saurida lessepsianus* Russell, Golani & Tikochinski, 2015

Common name: Lessepsian lizardfish

Diagnostic Characters: Body elongated, usually cylindrical with lizard-like pointed and depressed head, compressed extreme posterior region and a well-developed forked caudal fin with pointed lobes. Eye circular, placed laterally with wide interorbital distance, overlaid with fleshy adipose eyelid anteriorly and posteriorly. Body covered with large cycloid scales, slightly deciduous, scales on lateral-line slightly raised forming a ridge. Large mouth with deep cleft, slightly longer upper jaws, having numerous sharp teeth arranged in rows on both jaws, tongue and palatines. Palatine teeth grouped into two distinct series: long outer series with teeth in two rows and short inner series with few undefined rows; outer palatine teeth merge anteriorly but is set apart by vomer which is

Table 1. Morphometric characters of *Saurida lessepsianus* collected during the presently study compared with previous studies. Cranial measurements are expressed in percentage of head length (H*L*); Body measurements are expressed in percentage of SL

	Present study (n=75)		*S. lessepsianus* (n=40) (Silpa et al., 2021)		*S. lessepsianus* (n=37) (Russell et al., 2015)		*S. undosquamis* (n=8) (Inoue & Nakabo, 2006)	
Morphometric trait	**Range**	**Mean± SD**	**Range**	**Mean ± SD**	**Range**	**Mean ± SD**	**Range**	**Mean**
Standard length [mm]	140.0-269.4	-	112.1–236.5	-	108.0-282.2	-	112.1–358.0	-
Pre-dorsal length	40.5-44.5	42.4 ± 0.9	42.61–46.61	44.22 ± 0.38	40.3–45.0	42.6 ± 1.2	41.1–43.1	42.2
Pre-adipose length	79.4-83.4	81.2 ± 0.9	53.50–84.69	79.50 ± 2.93	76.9–83.2	80.9 ± 1.4	79.5–81.8	80.6
Pre-anal length	55.7-76.2	72.3± 2.1	48.67–76.77	71.74 ± 2.60	67.2–77.1	71.9 ± 1.9	70.5–73.4	71.8
Pre-anal fin length	72.6-76.9	74.4± 1.0	75.11–79.45	77.22 ± 0.51	65.0–79.3	74.8 ± 2.5	72.9–76.1	74.8
Pre pectoral length	24.1-27.7	25.6± 1.1	25.65–27.98	26.68 ± 0.20	23.4–28.7	25.7 ± 1.2	24.1–26.7	25.5
Pre pelvic length	36.3-40.9	39.2± 1.3	36.05–41.71	39.49 ± 0.58	35.4–42.6	38.8 ± 1.6	35.8–38.9	37.4
Head length	20.7-24.7 24.8	23.0± 0.9	19.21–26.05	24.40 ± 0.61	22.5–26.5	24.4 ± 1.0	23.2–25.5	
Body depth	12.0-16.8 12.5	14.1± 1.4	14.42–20.65	17.19 ± 0.53	10.4–17.2	13.3 ± 1.5	11.7–13.5	
Body width	11.3–15.1	13.2 ± 0.3	11.67–15.05	13.72 ± 0.33	10.9–15.6	13.0 ± 1.3	11.4–14.6	13.2
Inter-pelvic width	5.7-8.9	7.8± 0.3	5.06–8.68	7.58 ± 0.34	7.6–9.5	8.4 ± 0.5	7.6–8.6	8.2
Pectoral fin length	12.2-18.3	14.8± 1.0	12.77–17.63	15.04 ± 0.43	11.5–17.0	14.2 ± 1.3	13.4–14.5	13.9
Pelvic fin length	14.2-18.0	16.2± 0.9	14.81–18.11	16.77 ± 0.30	14.2–18.6	16.6 ± 0.8	16.7–20.0	18.1
Length of 2nd dorsal ray	16.6-22.8	20.2± 1.3	15.91–23.17	20.14 ± 0.74	16.0–21.5	19.8 ± 1.1	16.5–20.3	18.7
Length dorsal fin base	12.8-15.7	14.0± 0.8	12.83–14.54	14.03 ± 0.17	12.5–16.6	14.4 ± 1.0	11.7–13.2	12.6
Length of anal-fin base	5.8-12.1	10.1± 0.8	5.94–10.96	9.58 ± 0.43	5.5–12.4	10.0 ± 1.2	8.6–10.3	9.6
Depth of caudal peduncle	5.5-7.0	6.5± 0.39	5.57–7.45	6.51 ± 0.20	5.7–7.1	6.4 ± 0.3	5.9-7.2	6.4
Eye diameter	15.3-23.2	19.1±2.1	14.21–25.34	18.58 ± 0.92	18.4–25.6	21.4 ± 1.9	15.3-22.9	19.6

Table 2. Meristic data of specimens examined in this study.

	Present study (n=74)		**S. *lessepsianus* (n=40) Silpa *et al.,* 2021)**		**S. *lessepsianus* (n=37) (Russell *et al.,* 2015)**	
	Mode	**Range**	**Mode**	**Range**	**Mode**	**Range**
Dorsal fin rays	12	11-12	11	11-12	12	11-12
Pelvic fin rays	9	-	9	-	9	-
Pectoral fin rays	14	13-15	14	13-15	14	13-15
Anal fin rays	11	10-12	11	11-12	11	10-12
Lateral line scales	49	47-51	49	48-51	50	47-51
Pre-dorsal scales	16	15-20	15	15-19	17	14-20
Transverse scale (above LL)	4½	-	4½	-	4½	-
Transverse scale (below LL)	5½	-	5½	-	5½	-
Vertebrae	47	44-47	47	44-47	47	44-47

LL: Lateral line

toothless or bears 1 - 2 teeth. Teeth on outermost row is visible even when mouth is closed. A roughly triangular shaped dorsal fin placed midway on back, followed by a short adipose dorsal fin, moderately wide anal fin, ventral fin with nearly equal rays placed anterior to dorsal fin, pectoral fin placed adjacent to opercular margin.

The morphometric data is enlisted in Table 1. The pectoral fin moderately long, 15.8% (13.2-18.3%) of SL as it reaches just before or just beyond line drawn between origin of pelvic fins and dorsal fin. The base of dorsal fin (mean 15.0% SL) longer than that of anal fin (mean 10.1% SL); adipose fin is placed above posterior half of anal fin. Deeply forked caudal fin with equal upper and lower lobes in length.

The modal value and range of meristic characters of *S. lessepsianus*: Dorsal-fin rays 12 (11–12); pectoral-fin rays 14 (13–15); anal-fin rays 11 (11–12); lateral-line scales 49 (47–51); transverse scales above and below lateral line 4½ and 5½, respectively; pre-dorsal scales 16 (15–20); vertebrae 47 (44–47); two rows of palatine teeth (Figure 3); no teeth on vomer; 4–6

Fig 3. Upper jaw of *Saurida lessepsianus*
(a) outer palatines with two rows of teeth anteriorly
(b) inner palatines with 5–6 rows of teeth

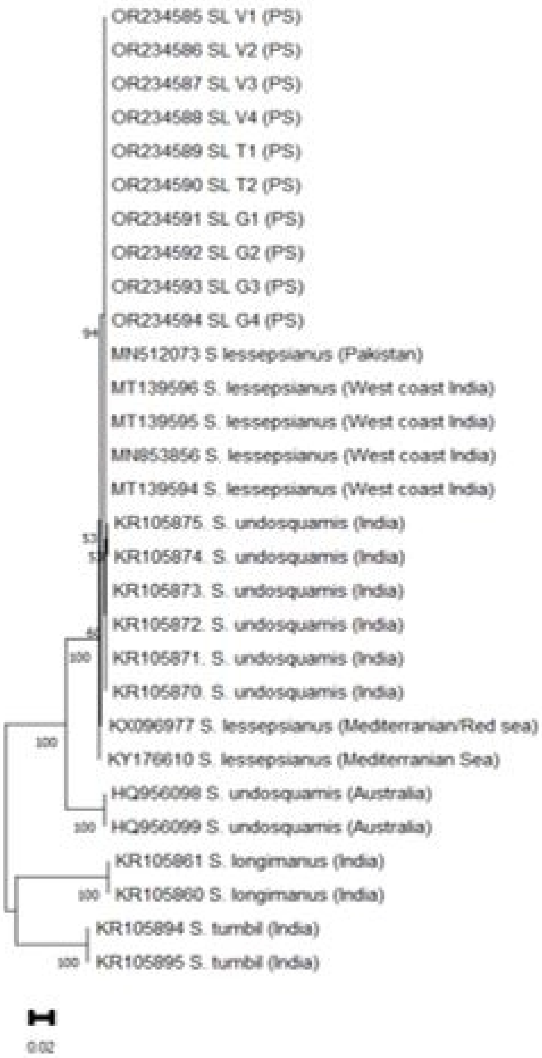

Fig 4. Neighbour-joining tree of selected species of genus *Saurida constructed using the COI gene. The values above the nodes represent the bootstrap values. (PS - Present study)*

tooth rows on tongue. These values are compared with other studies (Table 2)

Colour: back and upper part of trunk brown while lower sides and belly pale or silvery; 8–10 brownish elongated blotches often visible along lateral line; dorsal fin pale with 5–10 indistinct black dots on first two dorsal rays; translucent adipose fin with blackish spot anterodorsally; upper margin of caudal fin with 3–8 (usually 6 - 7) distinct black spots, posterior edge and lower lobe of caudal fin with anthracite grey margins; upper part of pectoral fin dusky; pelvic fins and anal fin translucent. Stomach greyish or black anteriorly and white posteriorly (Figure 4), with white intestine.

The molecular analysis unequivocally demonstrated that the species examined in the present study as well as previously identified as *S. undosquamis* from Indian waters, shares a common clade with *Saurida lessepsianus* specimens from the Red Sea, Mediterranean Sea, and Arabian Sea. In contrast, *S. undosquamis* specimens (HQ956098-99 from Australia) formed a distinct, separate clade (Fig. 5). The pair-wise genetic distance values among the clades *S. undosquamis* and *S. lessepsianus* are 7.69% indicating that they are two different species (Table 3).

The significant outcome of this research is the confirmation that *Saurida lessepsianus* observed along the east coast of India (Bay of Bengal) is indeed a distinct taxon separate from previously classified *S. undosquamis*. Russell *et al*. (2015) described *S. lessepsianus* from the Red Sea and the Mediterranean Sea based on the following combination of characters: elongated cylindrical body with a depressed head; large mouth with 2 rows of teeth on outer palatines and 0–2 rows of teeth on vomer; long pectoral fin reaching line between origin of pelvic fins and dorsal fin; vertebrae 47–51; pored lateral-line scales 44–47; stomach greyish to black anteriorly and white or pale posteriorly.

Morphological and meristic examination (Table 1 & 2) of the specimens collected during present study showed resemblance with that of *S. lessepsianus* and differed from *S. undosquamis* on several characteristics. Some of the key distinguishing characters include the number of pored lateral line scales, vertebrae, teeth across the tongue and colour of stomach and intestine etc. are summarized in Table 4.

DNA barcoding has been shown to be a useful method for resolving taxonomic ambiguities in cryptic species (Polanco *et al.,* 2016**,** Pavan-Kumar *et al.* 2018). By evaluating the level of divergence in COI sequences between individuals, this method establishes species distinctions (Herbert *et al*., 2003). Consequently, individuals belonging to the same species exhibit lower divergence value (less than 3%) compared to those of different species regardless of their geographic origin. The analysis of COI sequences revealed minimum

Fig 5.Images of stomach of *Saurida lessepsianus*

divergence (ranging from 0.00 to 0.60 %) between the sequences obtained from the current study and those from Mediterranean Sea, Red Sea and India waters (Table 3). The phylogenetic tree (Figure 4) provides additional support to this finding by forming a single clade. Concurrently, it demonstrated the formation of separate clade for *S. undosquamis* and *S. lessepsianus* with significant genetic divergence of 7.74% between them.

One of the major reasons behind the wide spread misidentification of the species was due to the field-level identification which was primarily based on the presence of characteristic black dots on the second dorsal fin ray and upper margin of the caudal fin. However, this characteristic was later found to be common to both *S. lessepsianus*, *S. undosquamis*, and some other species of the genus. Earlier, *S. undosquamis* was thought to be a widely distributed in Indo-west Pacific, including the areas from Eastern Africa, the Red Sea, the Persian Gulf, all the way to Japan and Australia (Fisher & Bianchi, 1983). This species extended its range to the eastern Mediterranean Sea through Lessepsian migration facilitated by the Suez Canal (Ben-Tuvia, 1953). Tikochinski *et al.* (2013) recorded that populations of species with broad geographic distribution display sufficient level of genetic variation as to be considered a different taxon. Following the identification by Russell *et al*. (2015) that *S. undosquamis* from the Red Sea and Mediterranean Sea was *S. lessepsianus*, subsequent reports emerged indicating the same in Myanmar waters, Bay of Bengal (Psomadakis *et al.,* 2019), western coast of India, eastern Arabian Sea (Silpa *et al.,* 2021) and Pakistan waters, Northern Arabian Sea (Zohra *et al.,* 2022).

The nomenclature *S. undosquamis* is still being used in published literature and checklists in India to refer to *S. lessepsianus* (Chhandaprajnadarsini *et al.,* 2019, Mohanchander *et al.,* 2020). A phylogenetic tree constructed from sequences previously submitted to public sequence databases under both *S. undosquamis* and *S. lessepsianus* designations displayed a unified clade. Consequently, the specimens formerly recognized as *S. undosquamis* in India, as documented in both published literature and public sequence databases, may be reclassified under the new scientific name, *S. lessepsianus*. Rectifying this misclassification is of utmost importance, as adopting the accurate species name is essential for the implementation of effective conservation and management strategies. The outcomes of the current study reaffirm the presence of *S. lessepsianus* along the eastern coast of India, underscoring the urgency to revise the species designation accordingly.

Conclusion

Accurate species identification is of paramount importance for ecological studies and conservation initiatives. By employing a combination of morphological and molecular methods, the study successfully demonstrated the distinctiveness of *S. lessepsianus*, establishing it as a separate species from *S. undosquamis* along India's east coast. Consequently, this study expands the known distribution of *S. lessepsianus* to the east coast of India (Bay of Bengal) in addition to previously recognised presence in Mediterranean/Red Sea region and eastern Arabian Sea.

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Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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