

**Original Research**

DOI : <http://doi.org/10.22438/jeb/43/1/MRN-1975>

## Description of a new species of queenfish, *Scomberoides pelagicus* from Indian seas

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Received: 12.05.2021

Revised: 26.07.2021

Accepted: 27.09.2021

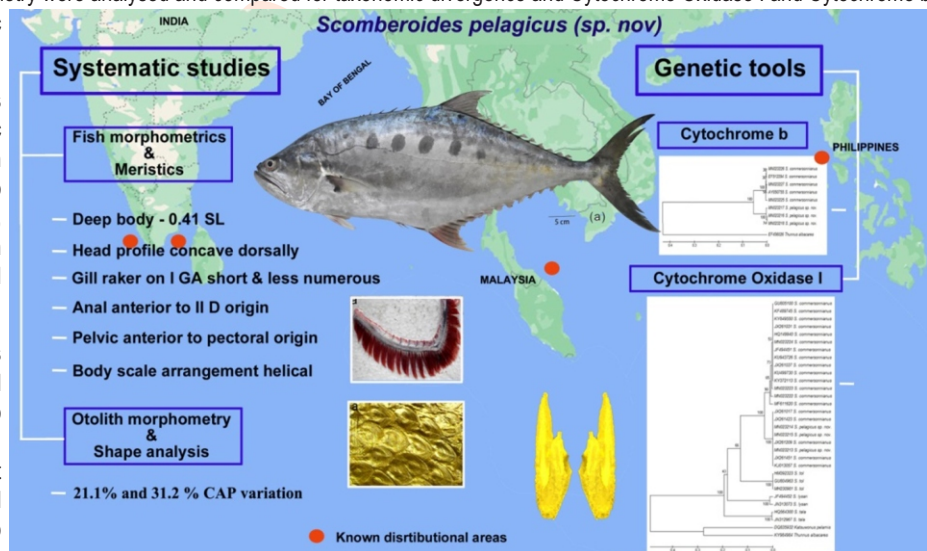
### Abstract

**Aim:** The study was carried out to ascertain whether morphotype of *Scomberoides commersonianus* (Talang queenfish) existing along the Indian coast is a new species or not.

**Methodology:** Talang queenfish and the morphotype were tested for their uniqueness using systematic and molecular tools. The morphometric and meristic details including otolith morphometry were analysed and compared for taxonomic divergence and Cytochrome Oxidase I and Cytochrome b gene sequences for quantifying genetic divergences.

**Results:** The systematic analysis indicated significant morphometric differences between both. The otolith morphometry and phylogeny also confirmed the divergence between them, and qualified the morphotype as an independent species status and named *Scomberoides pelagicus* sp. nov.

**Interpretation:** The new species is distinct by deep ovate body, concave dorsal head profile, anal fin origin anterior to second dorsal fin and pelvic to pectoral fin, helical arrangement of body scale and stout and less numerous gill rakers on the first gill arch. The phylogeny as on Cytochrome b and Cytochrome Oxidase 1 sequences are very distinct, with 11.2% and 2.0% divergence respectively. Their known distributional range are peninsular region of Indian coast, Malaysian region of the South China Sea and Manila Bay, Philippines.



**Key words:** Deep bodied queenfish, Genetic divergence, Otolith morphometry, Phylogeny, *Scomberoides pelagicus*, Talang queenfish

**How to cite :** Abdussamad, E.M., A. Gopalakrishnan, K.G. Mini, S. Sukumaran, P.R. Divya, T.B. Rethesh, A.A. Muhammed, N.V. Dipti, A.R. Akhil, T. Thomas and K.D. Jacob: Description of a new species of queenfish, *Scomberoides pelagicus* from Indian seas. *J. Environ. Biol.*, **43**, 105-114 (2022).

## Introduction

Carangidae, one of the largest teleost fish families (Order Perciformes), is represented by over 140 species belonging to 32 genera and have wide distribution throughout the Western Indian and Western Pacific Oceans (Bianchi, 1985; Nelson, 2006; Riede, 2004; Smith-Vaniz, 1984). Being highly diverse in body size and morphometry, their correct identification remain complicated (Smith-Vaniz, 1999). Lin and Shao (1999) while reviewing the carangids of Taiwan waters highlighted the taxonomic ambiguities in the family and cautioned possible mis-identifications. Seas around Indian sub-continent are rich in their diversity, supported by 60 species including four species of queenfishes in the genus *Scomberoides* (Pillai et al., 1987; Abdussamad et al., 2007, 2013, 2018). Queenfishes are cryptic, found mainly in inshore and offshore reef areas and estuaries (Griffiths et al., 2005). Globally, they are represented by four extant species viz., Talang or Giant queenfish, *Scomberoides commersonnianus*; Lesser queenfish, *Scomberoides lysan*; Barred queenfish, *Scomberoides tala* and Needle skin queenfish, *Scomberoides tol* and three fossil species; *Scomberoides spinosus* (Smirnov, 1936), *Scomberoides inensis* (Ohe and Furuhashi, 1977) and *Scomberoides maruoi* (Uyeno and Suda, 1991).

Along the Indian coast, all the four extant species co-exist and supports an important year round commercial fisheries and they fetches good local demand. They are caught by a variety of gears, especially hooks and lines and drift gillnets. The routine fishery and taxonomic monitoring indicates occurrence of a distinct morphotype for Talang queen fish along the region. Although the morphotype resembles the latter in certain aspects, it is very distinct in the morphology, body colouration and skin characteristics. Literature scan indicates scarcity of recent works and information on the taxonomic review of queen fishes, barring a comparative revision of *Scomberoides* and other carangid groups, including their phylogenetic position (Smith-Vaniz and Staiqer, 1973) and description of two fossil species, *S. inensis* (Ohe and Furuhashi, 1977) and *S. maruoi* (Uyeno and Suda, 1991) respectively from Kyoto and Tottori in Japan. In recent days, DNA barcoding is widely employed to precisely resolve the taxonomic ambiguities of overlooked species and for species confirmation (Zemlak et al., 2009). Otoliths of fish possess species specific morphology, and researchers consider it as a reliable alternate taxonomic tool (Nolf, 1985; Tuset et al., 2003; Joshi et al., 2012; Karahan, et al., 2014; Libungan et al., 2015; Libungan and Pálsson, 2015; Abdussamad et al., 2015; 2016; Qamar et al., 2016; Azam and Naeem 2021).

Otolith morphometry and shape analysis is also used in food and feeding studies of Predatory fishes for prey identification (Škeljo and Ferri, 2012). To scientifically resolve the observed ambiguity issues of queenfish identity, a detailed taxonomic review employing conventional systematics, otolith morphometrics and molecular tools were attempted. Samples representing extant species, including the morphotype forms the

primary material for the study. The systematic details of the morphotype was examined and compared with that of the extant species and the available details of fossil species. The article describes the extent of taxonomic and phylogenetic divergence between each, and how the morphotype differ from extant and fossil species.

Present work is important as among the more than 15,000 described marine species, fishes are increasingly threatened of marine lives owing to their increasing role in human food chain (Zemlak et al., 2009). Realizing that natural resources are declining at a faster pace and may have adverse consequences on human well-being and survival, public awareness on the need to conserve biodiversity has also growing. Policy makers, scientists and conservationists across the globe has made it a priority to advance policies and knowledge for this purpose. To serve this purpose information on overlooked species/resources, correct identification of species, updated taxonomic classification and grouping is the basic requirement.

## Materials and Methods

The study was carried out during 2010-2019 using materials collected from commercial fish landings. Unsorted samples consisting of all size groups were collected from different locations along the coast. The specimens were sorted as per Fischer and Bianchi (1984) and morphometric measurements, meristic counts and colour descriptions were made following the standard protocols (Hubbs and Lagler, 1958; Haedrich, 1967; Fischer, 2013). A total of 105 specimens of the morphotype, 84 of *S. commersonnianus* and 30 each of other species were analysed in the study. Size of the specimens used ranged between 280 and 984mm standard lengths (SL) for the morphotype and 186 and 1,288mm SL for *S. commersonnianus*. The size ranges of other species were 138-462, 187-562 and 202-513 mm SL respectively for *S. tol*, *S. tala* and *S. lysan*. Since, preliminary analysis of morphometric and meristic data indicate no significant differences ( $P > 0.05$ ) between sexes, pooled data were used for all analysis. The morphotype was also compared with the fossil species using information gathered from the earlier reports (Smirnov, 1936; Smith-Vaniz and Staiqer, 1973; Ohe and Furuhashi, 1977; Uyeno and Suda, 1991).

Sagittal otoliths were extracted and high-resolution digital images were captured for image analysis as suggested in Green et al. (2009) and Abdussamad et al. (2019). Shape analysis was conducted using Shape R software package, on R platform and the extent of shape variations were measured and quantified (Škeljo and Ferri, 2012; Karahan et al., 2014; Libungan et al., 2015). The wavelet coefficients were analysed using Canonical Analysis of Principal Co-ordinates to distinguish between species (Libungan and Pálsson, 2015). Student's t-test was performed in order to determine the difference between otolith length, width, area and perimeter of both species. Phylogenetic analysis were conducted following the standard protocols and procedures

(Miller *et al.*, 1988; Sambrook and Russel, 2001; Folmer *et al.*, 1994a, 1994b; Hall, 1999; Samonte *et al.*, 2000). The COI sequences of morphotype were aligned with sequences of *S. commersonnianus*, *S. tol*, *S. lysan* and *S. tala* using Clustal W in MEGA 6. Phylogenetic tree was constructed using Unweighted Pair-Group Method with Arithmetic Mean (UPGMA) method with 1000 bootstraps and tree topology was confirmed by Maximum Likelihood, Maximum Parsimony and Neighbour-Joining methods (Rozas *et al.*, 2006). The phylogenetic trees were rooted using sequences of *Thunnus albacares* and *Katsuwonus pelamis* retrieved from National Center for Biotechnology Information (NCBI), GenBank. Genetic divergences between the species were estimated using Kimura 2P distance values in MEGA 6. Genetic divergence between *S. commersonnianus* and its morphotype was also determined by Cytb gene, with *T. albacares* as the out-group.

### Results and Discussion

The morphometric and phylogenetic variations between extant species of the queenfishes and the morphotype were very distinct (Table 1, Fig. 1). Since, the morphotype had shown

certain degree of resemblance only with *S. commersonnianus*, in-depth comparisons were made only between them (Table 2, Fig. 2). The morphotype has a relatively deeper body (0.41 SL at anal origin) than the latter (0.32 SL). The origin of anal and pelvic fins in the former were respectively anterior to second dorsal and pectoral origin whereas they were in the same line in the latter. Dorsal profile of the head and nape was distinctly concave above the eye in morphotype and it was smooth convex in *S. commersonnianus*. Gill rakers on the first gill arch were less numerous (10-11) and short-stout in the former, whereas it was 14-16 and elongate-narrow in the latter (Fig. 2). Anterior ascending limb of lateral line was wavy in morphotype (Fig. 2<sub>2a</sub>) and lateral line scales were more numerous (226-236). Anterior ascending limb smooth in *S. commersonnianus* (Fig. 2<sub>2b</sub>) and lateral line scales were comparatively less numerous (217-228). Body scale arrangement was helical in the former and overlapping in the latter (Fig. 2<sub>3</sub>).

Head and body were silvery white and light greenish dorsally. Laterally body possesses 5 to 8 light medium vertically elliptical blotches above lateral line, first two touches or intersect lateral line. In the absence of detailed systematic details for fossil

**Table 1:** Comparative morphometrics as ratio of the standard length of the extant species in the genus *Scomberoides* from Indian seas

Characteristics	<i>S. pelagicus</i> sp. nov (n=105)	<i>S. commersonnianus</i> (n=84)	<i>S. lysan</i> (n=30)	<i>S. tala</i> (n=30)	<i>S. tol</i> (n=30)
<b>a. Morphometrics</b>					
Total Length (TL)	1.27	1.26	1.26	1.25	1.23
Fork Length (FL)	1.11	1.1	0.98	1.09	1.10
Standard Length (SL)	1	1	1.00	1.00	1.00
Head Length (HL)	0.21	0.21	0.20	0.19	0.20
Snout Length	0.05	0.05	0.06	0.05	0.06
Snout to 1 <sup>st</sup> Dorsal origin	0.31	0.3	0.29	0.28	0.28
Snout to 2 <sup>nd</sup> Dorsal origin	0.54	0.52	0.51	0.51	0.50
Snout to Anal fin origin	0.5	0.52	0.50	0.45	0.47
Snout to Pectoral origin	0.23	0.22	0.22	0.20	0.21
Snout to Pelvic origin	0.21	0.22	0.22	0.18	0.22
Depth at 1 <sup>st</sup> Dorsal origin	0.36	0.27	0.23	0.26	0.21
Body depth at 2 <sup>nd</sup> dorsal origin	0.39	0.32	0.00	0.00	0.00
Depth at Anal fin origin	0.41	0.32	0.27	0.33	0.24
Maximum body depth	0.41	0.32	0.27	0.33	0.24
<b>Body Shape</b>	<b>Oblong, more deep and compressed</b>	<b>Oblong elongate and compressed</b>	<b>Oblong, more deep and compressed</b>	<b>Oblong elongate and compressed</b>	<b>Oblong elongate and compressed</b>
<b>Shape of body blotches</b>	<b>Vertically elliptical</b>	<b>Round</b>	<b>Near round blotches</b>	<b>Vertically Elongate stripe</b>	<b>Round</b>
<b>b. Meristic counts (numbers)</b>					
Lateral line scales	229	222			
GR* on upper lobe of IGA**	2	4 – 5	8	4	7
GR* on lower lobe of IGA**	8-9	10-11	17	8	17
Total GR* on IGA**	10-11	14-15	25	12	24
Body spots: Rows	1	1	2	1	1

**Table 2:** The range and mean of morphometric as ratios with SL and meristic details of *S. pelagicus* sp. nov and *S. commersonianus* from Indian seas

Morphometric measurements (mm)	<i>S. pelagicus</i> sp. nov.			<i>S. commersonianus</i>		
	Mean	Min.	Max.	Mean	Min.	Max.
Total Length (TL)	1.27	1.23	1.31	1.26	1.20	1.36
Fork Length (FL)	1.11	1.10	1.14	1.10	1.07	1.12
Standard Length (SL)	1.00	1.00	1.00	1.00	1.00	1.00
Head Length (HL)	0.21	0.19	0.23	0.21	0.19	0.23
Snout Length	0.05	0.04	0.06	0.05	0.03	0.08
Snout to 1 <sup>st</sup> Dorsal origin	0.31	0.30	0.33	0.30	0.27	0.33
Snout to 2 <sup>nd</sup> Dorsal origin	0.54	0.51	0.57	0.52	0.50	0.56
Snout to Anal fin origin	0.50	0.49	0.52	0.52	0.50	0.55
Snout to Pectoral origin	0.23	0.21	0.25	0.22	0.20	0.25
Snout to Pelvic origin	0.21	0.18	0.23	0.22	0.20	0.24
Depth at 1 <sup>st</sup> Dorsal origin	0.36	0.32	0.40	0.27	0.25	0.28
Body depth at 2 <sup>nd</sup> dorsal origin	0.39	0.34	0.42	0.32	0.25	0.35
Depth at Anal fin origin	0.41	0.35	0.45	0.32	0.25	0.35
Maximum body depth	0.41	0.35	0.45	0.32	0.25	0.35
Upper jaw (maxillary) length	0.13	0.12	0.14	0.13	0.11	0.14
Shape of lateral spots	Vertically elliptical			Round		
Body Shape	Oval and compressed			Oblong and compressed		
Meristic counts	<i>S. pelagicus</i> sp. nov.			<i>S. commersonianus</i>		
	Mean	Min.	Max.	Mean	Min.	Max.
Lateral line scales	229	226	232	222	217	226
GR* on upper lobe of IGA**	2	2	2	4-5	4	5
GR* on lower lobe of IGA**	8-9	8	9	10-11	10	11
Total GR* on IGA**	10-11	10	11	14-15	14	16

\* GR-Gill rakers, \*\* IGA-First gill arch

species, researchers considered standard length-body depth (SL/BD) ratio as key character for comparison of species (Smirnov, 1936; Smith-Vaniz and Staiquer, 1973; Ohe and Furuhashi, 1977 and Uyeno and Suda, 1991). Among the described species *S. maruoi* had the deepest body with a SL/BD ratio of 3.2 (Table 3). In the present comparison, the ratio was smallest (2.56) for the morphotype, indicating them as the deepest bodied species, confirming distinctness of the morphotype from other members of the genera. The posterior of the sagittal otolith was smooth and round in the morphotype and mostly bifurcated in the latter (Fig. 2<sub>4</sub>). Otoliths shape analysis also indicated significant variations ( $P < 0.01$ ) between them. The morphometric variables viz., length, width, area and perimeter of the otolith were large in the morphotype compared to *S. commersonianus* and are statistically significant ( $P < 0.01$ ). The anterior region generally peaked with well-defined and pointed rostrum and anti-rostrum in both. But the sulcus acusticus part in the morphotype was slightly narrow than that of *S. commersonianus*. The major difference in average shapes could be observed in the parastrostrum at 0 to 45°, excisura major at 135 to 210° and postrostrum at 320 to 360°, with the postrostrum being the most variable. In the morphotype, postrostrum region was more broad and rounded and ostium and cauda were larger as compared to *S. commersonianus*.

**Table 3:** Key characters of the extant and fossil species of the genera *Scomberoides* for comparison (\*Data from Smith-Vaniz and Staiquer, 1973 and Uyeno and Suda, 1991) SL-standard length, BD-body depth

Species	SL/BD*	SL/BD Present estimate
<i>S. lysan</i>	3.2-3.6	3.70
<i>S. tala</i>	3.7	3.03
<i>S. tol</i>	4.4	4.17
<i>S. commersonianus</i>	3.5	3.13
<i>S. pelagicus</i> sp. nov	-	2.56
<i>S. spinosus</i>	4.5	-
<i>S. inensis</i>	3.8	-
<i>S. maruoi</i>	3.2	-

The first and second Catabolite Activator Protein (CAP) axes explained 21.1% and 31.2 % of the variation in otolith morphology between them (Fig. 3). CAP analysis successfully allocated individuals into two groups according to the shape. A significant difference could be detected in the scatter plots also. Several reports on description of new species and stocks using otolith morphology has been available (Nolf, 1985; Tuset et al., 2003; Duarte-Neto et al., 2008, Joshi et al., 2012; Abdussamad et



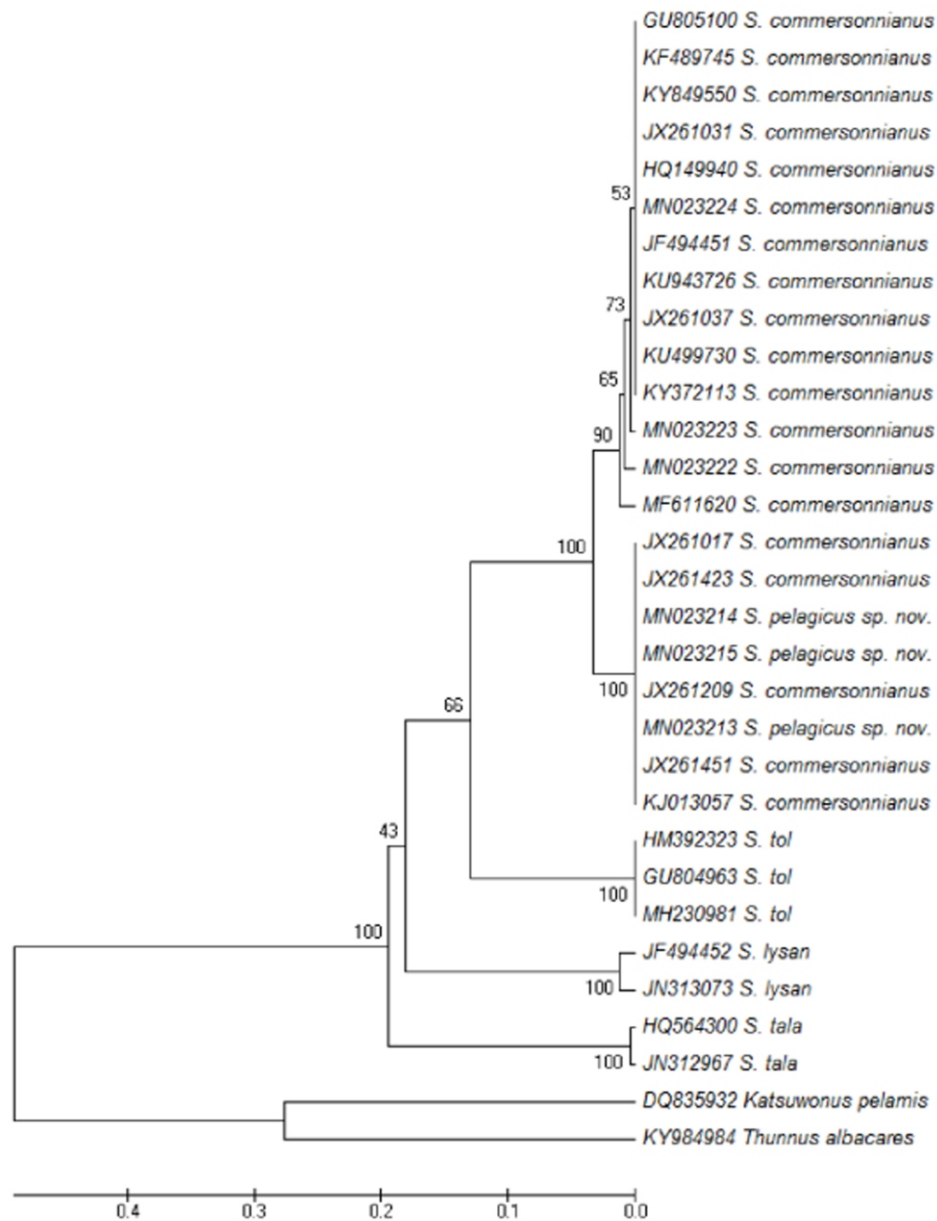
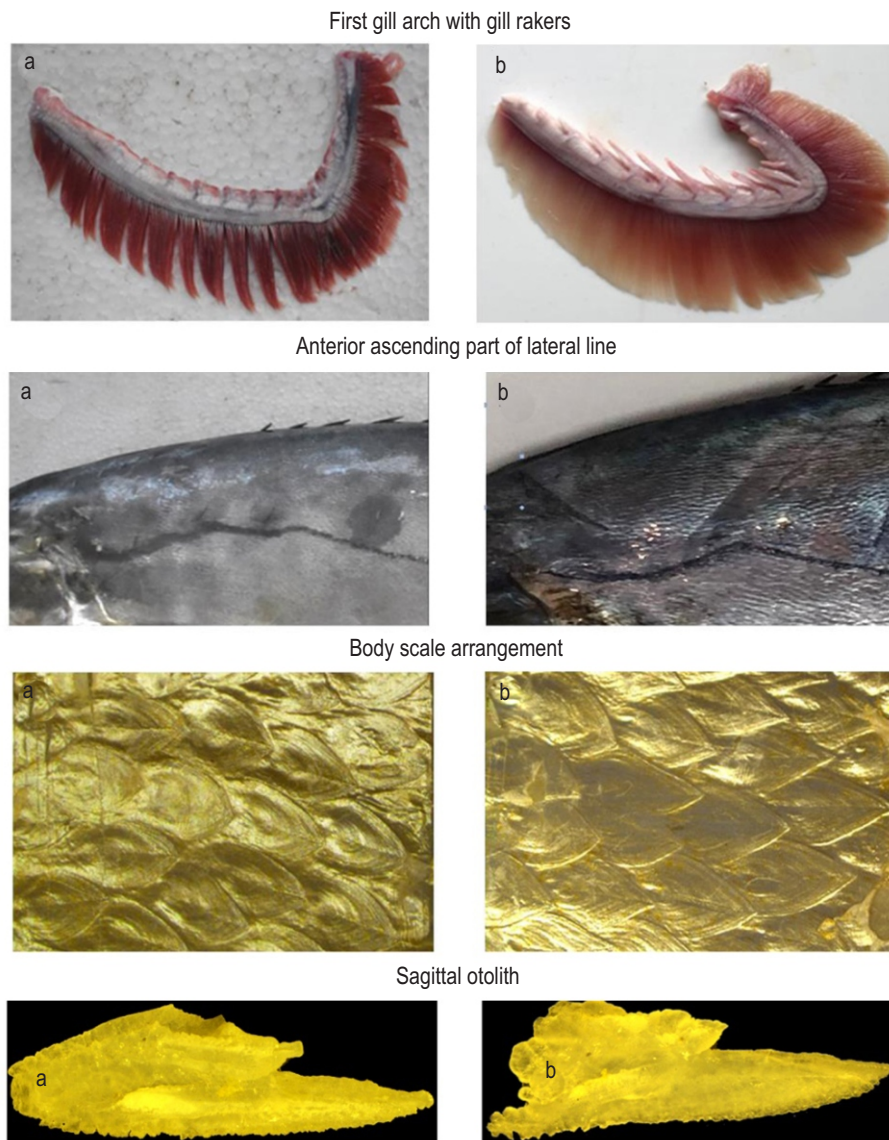


Fig. 1: UPGMA tree based on COI sequences of queenfish species from Indian seas.

al., 2015; 2016; Qamar *et al.*, 2016). They considered it as a reliable taxonomic tool and is also gaining importance in the prey identification from gut remains of predatory fishes. Molecular variation is evident from partial sequence information of COI and Cytb genes. The sequences of partial region of COI and Cytb genes of the morphotype and *S. commersonnianus* were deposited in NCBI, GenBank with the accession numbers MN023213-MN023230. The phylogenetic tree constructed of the morphotype, *S. commersonnianus*, *S. tol*, *S. lysan* and *S. tala* resulted in distinct species-specific clades with significant bootstrap (Fig. 1). A total of 650 base pairs of aligned

sequences were compared. COI sequences of *S. commersonnianus* previously deposited in NCBI GenBank were also found to form two distinct clades in the phylogenetic tree, with majority of the sequences in the first clade and few in the second clade. Sequences of the morphotype from the present study clustered with the second minor clade indicating that the minor clade comprised individuals of the morphotype described in the present study.

The other sequences of minor clade were from the Malaysian region of the South China Sea (JX261451; JX261423;



**Fig. 2:** Morphological distinctness of (a) *S. pelagicus* sp. nov. from (b) *S. commersonianus* from Indian seas.

JX261017; JX261209) and Manila Bay, Philippines (KJ013057), indicating wider distribution for the morphotype in the Indo-Pacific waters. The tree topology of COI sequences was similar when phylogenetic analyses were carried out using maximum likelihood, maximum parsimony and neighbour joining methods. K2 P values between species in COI gene indicated 2.0, 6.9, 8.5 and 10.3 % divergence between the morphotype and *S. commersonianus*, *S. tol*, *S. lysan* and *S. tala*, respectively. A total of 1100 base pairs of aligned sequences of Cytb gene were studied in both the morphotype and *S. commersonianus*. Similar results were obtained when phylogenetic tree was constructed using Cytb sequences with distinct clustering among species with significant bootstrap values (Fig. 4). Cytb sequences of the

morphotype clustered separately from *S. commersonianus* and other species indicating their distinctiveness. K<sub>2</sub>P value between both indicated 11.2% divergence. Incidence of addition of new species to the phylum through genetic studies has been discussed by Cawthorn *et al.* (2012). Genetic divergence at COI indicated distinctness of all previously reported species of *Scomberoides* from the morphotype. Genetic divergence between the morphotype and *S. commersonianus* was 2.0 %. Following the 10x thumb rule by Hebert *et al.* (2003) and average intra specific distance being 0-0.002, the morphotype can be considered as a separate species.

Genetic divergence at Cytb gene level was much higher,

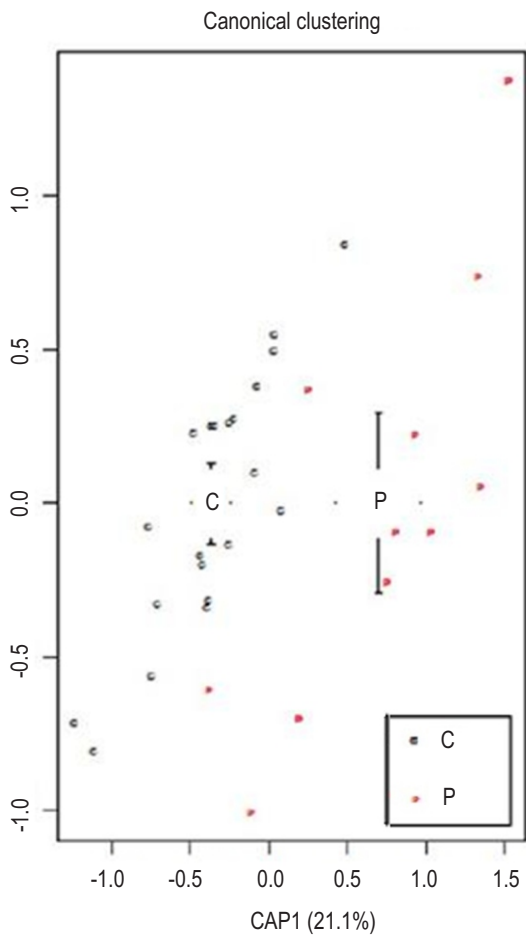


Fig. 3: Canonical scores for discriminating axes 1 (CAP1) and 2 (CAP2) for *S. pelagicus* sp. nov. (P) and *S. commersonianus*

11.2%. Avise (2004) discussed the possible use of combinations of molecular markers like Cytb to resolve ambiguities in cases of low resolution at COI level. The small genetic divergence of morphotype at the COI level indicates the possibility that it may be a recently evolved species as opined by Tamura *et al.* (2013). However, their wider and discontinuous distribution along the Malaysian region of the South China Sea and Manila Bay, Philippines as indicated by the DNA sequences in NCBI, GenBank (Jaafar *et al.*, 2012), established them as an existing species that has long been overlooked as *S. commersonianus* and may not be the result of recent localised evolution. The morphotype, being systematically and phylogenetically qualified for an independent species was named *Scomberoides pelagicus* sp. nov. with reference to their predominantly pelagic habitat (Fig. 5). Their existing vernacular names are “Vellaikatta” in Tamil and ‘Polavatta’ in Malayalam and the proposed common name is ‘deep bodied queenfish’. Along the Indian coast, *S. pelagicus* sp. nov. is found only along the southern coast, with major distribution and abundance along the Gulf of Mannar and Central Kerala, respectively, along the southeast and southwest coasts. Comparison of COI sequences available with NCBI GenBank shows wide distributional range for them along the Malaysian region of the South China Sea and Manila Bay, Philippines.

**Description of type specimens**

Genus: *Scomberoides* Lacepede 1801

Species: *Scomberoides pelagicus* sp. nov.

Authors: Abdussamad, Retheesh and Gopalakrishnan

**Type specimens:** Three voucher specimens, the holotype (Voucher No. CMFRI DNR No.: GB 31.24.21.5, 606 mm SL; GenBank accession numbers MN023213) and a pair of paratypes (i. Voucher No. CMFRI DNR No.: GB 31.24.21.6, 376

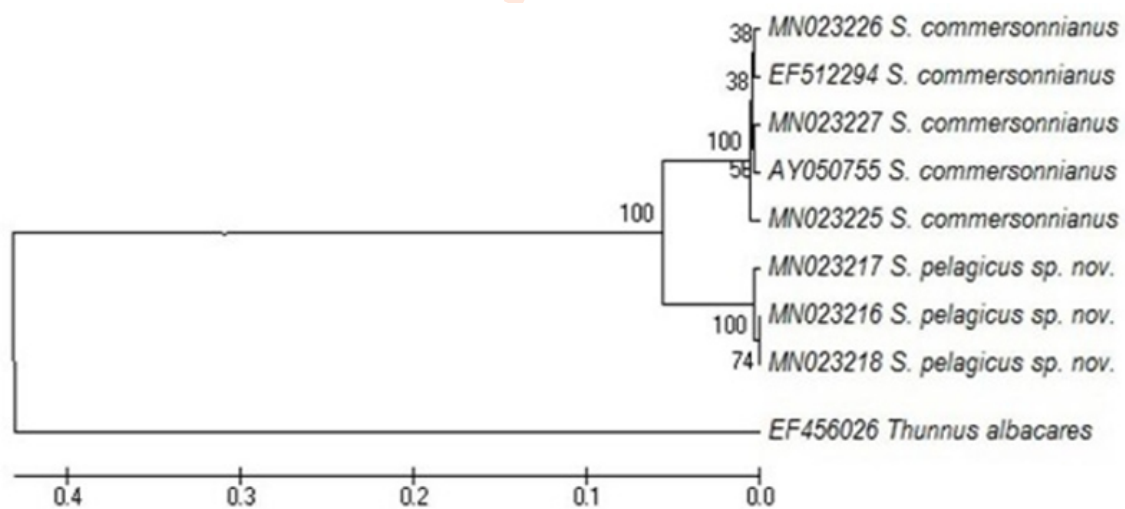


Fig. 4: UPGMA tree based on Cytochrome-b sequences of *S. pelagicus* sp. nov. and *S. commersonianus*.



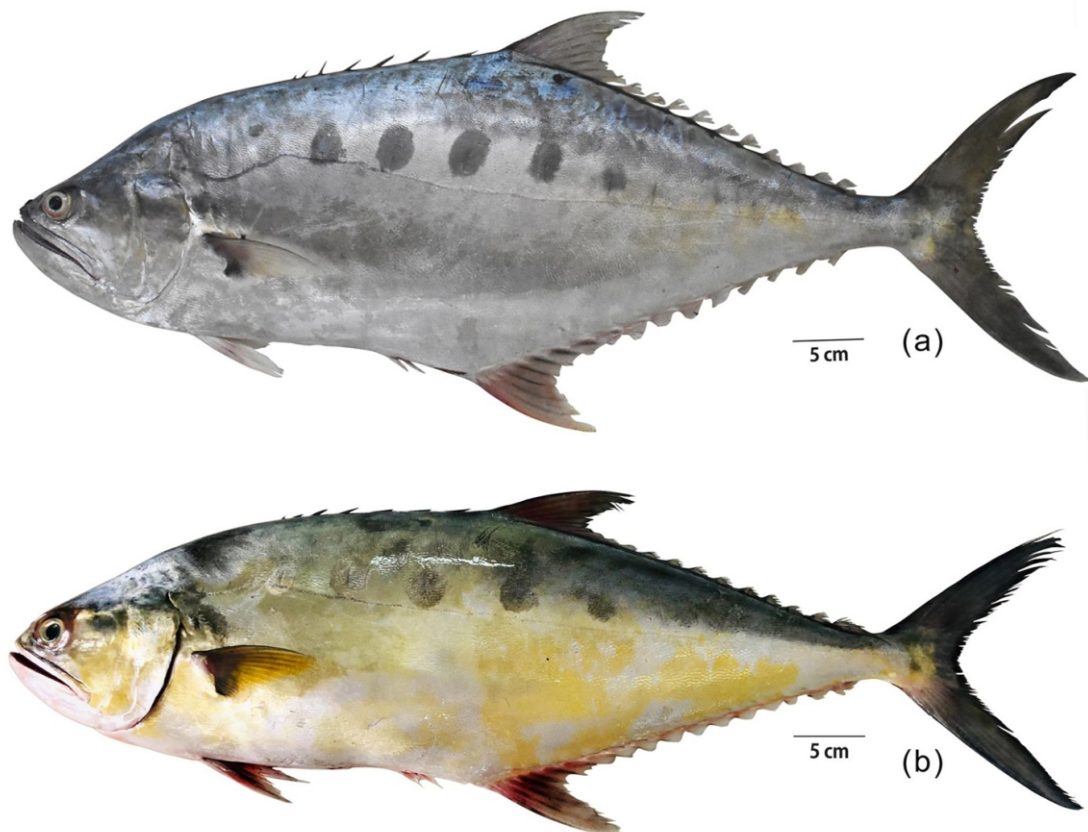


Fig. 5: (a) Deep bodied queenfish *S. pelagicus* sp. nov and (b) Talang queenfish, *S. commersonianus* from Indian seas.

mm SL, GenBank accession numbers MN023214 and ii. Voucher No. CMFRI DNR No.: GB 31.24.21.7, 280 mm SL GenBank accession numbers MN023215) of *S. pelagicus* sp. nov. were deposited with the Marine Biodiversity Referral Museum of ICAR-Central Marine Fisheries Research Institute (CMFRI), Kochi, India. The new species *S. pelagicus* sp. nov. is highly distinct in their morphometry, otolith morphology, genetic divergence, colour patterns, skin characteristics and body size. Their distinctive character are; deep ovate body, dorsal profile of head and nape concave, two distinct dorsal fins, first dorsal modified in to free spines, second dorsal origin above 3<sup>rd</sup> anal rays with its base length shorter than anal base length, pelvic origin anterior to pectoral origin, anterior ascending limb of lateral line wavy and maximum body depth (0.35–0.45 in SL) at anal origin. First dorsal fin VII; second dorsal fin I, 19 - 20; pectoral fin I, 18; pelvic fin I, 4; anal fin III, 18 - 19; gill rakers 10 – 11; body with relatively small lanceolate scales; lateral line scales 226-236; upper jaw length 0.12–0.14 in SL, reaching beyond the posterior margin of the eye; eyes moderate, 0.03–0.05 in SL; inter orbital area narrow, 0.06-0.08 in SL; sagittal otolith lean and thick, ventral margin almost straight and smoothly curved to a round posterior, antirostrum pointed. *S.*

*pelagicus* sp. nov is now the eighth species in the genera, *Scomberoides* and the fifth extant species. This finding adds to the biodiversity richness of the coast and positively to its biodiversity valuation.

#### Acknowledgments

Authors are grateful to A. Gopalakrishnan, Director, Central Marine Fisheries Research Institute (CMFRI), Kochi for support. R. Prathibha, Head, Pelagic Fisheries Division, CMFRI and P.P. Manojkumar, Scientist-in-charge, Tuticorin RC of CMFRI is also acknowledged for support and encouragement. Authors are also grateful to the Director, ICAR-NBFGR, for the technical support rendered by PMFGR Centre of NBFGR, Kochi.

#### Add-on Information

**Authors' contribution:** **A. Gopalakrishnan:** Molecular taxonomic studies including sampling design, phylogenetic analysis and interpretations; **K.G. Mini:** Otolith imaging, shape analysis and statistical interpretation of results; **S. Sukumaran, P.R. Divya:** Molecular taxonomic studies including sampling



design, phylogenetic analysis and interpretations; **T.B. Retheesh, A.A Muhammed, A.R. Akhil, T. Thomas:** Sample collection, taxonomic studies-morphometric and meristic analysis and literature collection; **N. V. Dipti, K. D. Jacob:** Otolith, extraction, imaging, otolith shape analysis.

**Research content:** The research content of manuscript is original and has not been published elsewhere.

**Ethical approval:** Not applicable

**Conflict of interest:** There is no conflict of interest among the authors contributed to this publication.

**Data from other sources:** Not applicable

**Consent to publish:** All authors agree to publish the paper in *Journal of Environmental Biology*.

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