

A New Deep-water Species of *Saurida* (Pisces: Synodontidae) from the South China Sea and Central Philippines

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A new species of lizardfish, *Saurida weijeni* sp. nov., from deep water of the outer slope of the North Macclesfield Bank (Zhongsha), South China Sea, and Guimaras Island, Western Visayas region of the Philippines, is described and figured. The new species is distinguished by the following combination of characteristics: dorsal fin with 11–12 rays; pectorals with 13–15 rays; lateral-line scales 49–52; transverse scale rows above the lateral line 3½, below the lateral line 5½; pectoral fins moderately long (extending to or just beyond a line from origin of pelvic fins to origin of dorsal fin); 2 rows of teeth on outer palatines; 0–3 teeth on vomer; tongue with about 3–4 rows of teeth posteriorly; 47–49 vertebrae; caudal peduncle compressed (depth greater than width); anterior part of stomach dusky or black, posterior extension pale whitish, intestine black. *Saurida weijeni* sp. nov. is genetically distinct from all other species of *Saurida*.

Key words: *Saurida weijeni* sp. nov., Macclesfield Bank (Zhongsha), Guimaras Island, Western Visayas region, Philippines

BACKGROUND

The lizardfish genus *Saurida* (family Synodontidae) comprises about 25 species found in tropical and subtropical seas world-wide (Fricke et al. 2024). They commonly occur on continental shelves associated with soft, muddy, or sandy bottoms in depths usually to about 200m, although some species are associated with shallow reef areas.

In the Western Central Pacific, 11 species of *Saurida* are reported (Russell 1999) and 7 species are known from the South China Sea (Russell 2000). Sampling of trawl catches during a survey of the

tropical deep-sea benthos of the Macclesfield Bank area (ZhongSha 2015 expedition) in the South China Sea (Fig. 1) in depths of 162–343 m, has yielded an additional new species. Other specimens, subsequently collected from Cabalagnan Fish Port, Guimaras Island, Western Visayas, Philippines (Fig. 1), were found to be the same undescribed species. Further investigation showed this species has been previously misidentified from the South China Sea as *S. umeyoshii* Inoue and Nakabo 2006 (Wang et al. 2014) but is genetically distinct from that species.

The specimens examined in this study belong to the *Saurida undosquamis* species group characterised

by Inoue and Nakabo (2006) as having dark dots on the upper margin of the caudal fin, pectoral fin exceeding origin of pelvic fin, anterior rays of dorsal fin neither elongate nor filamentous, predorsal length greater than distance between dorsal-fin and adipose-fin origins, 46–55 pored lateral-line scales, and vomer with 0–8 teeth. Specimens collected from the North Macclesfield Bank and Guimaras Island differ morphologically as well as genetically from other species in the *undosquamis* group and are described herein as a new species.

MATERIALS AND METHODS

Specimens from Macclesfield Bank were collected from trawl catches during a survey of the tropical deep-sea benthos of the Macclesfield Bank area (ZhongSha 2015 expedition) under the auspices of MUSORSTOM (a survey organized by the Muséum national d'Histoire naturelle and ORSTOM - Office de la Recherche Scientifique et Technique Outre-Mer – Head of Mission: Wei-Jen Chen, National Taiwan University) between 22 July 2015 and 1 August 2015. Specimens

collected from Cabalagnan Fish Port, Guimaras Island, Western Visayas, Philippines were collected during a survey undertaken by the University of the Philippines Visayas as part of a broader project to establish a *COI* gene-sequence library for marine fishes of the Western Visayas region of the Philippines.

Specimens are deposited in the Muséum national d'Histoire naturelle (MNHN), Paris; Museum and Art Gallery of the Northern Territory (NTM), Darwin; National Taiwan University Museum (NTUM), Taipei; and the Museum of Natural Sciences, University of the Philippines Visayas, Miagao Iloilo, Philippines (UPVMI).

Methods of counting and measuring follow Shindo and Yamada (1972) and Inoue and Nakabo (2006). The following additional characteristics, not previously used, were also assessed: number of teeth rows on the tongue (counted as the number of teeth across the width of the posterior part of the tongue); depth and width of the caudal peduncle; and colour of the stomach and intestine (see Fishelson et al. 2012). Body length measurements are Standard Length (SL), measured from the tip of the snout, including the upper lip, to the



Fig. 1. Map of South China Sea showing locations at which *Saurida weijeni* sp. nov. was collected. Red stars - Macclesfield Bank and Cabalagnan Fish Port, Guimaras Island, Philippines (Map credit: Nations Online Project).

posterior end of the midlateral portion of the hypural plate; Head Length (HL) measurements are from the tip of the snout to the posterior edge of the operculum. Measurements were taken with digital calipers to the nearest 0.1 mm. Vertebral counts were taken from radiographs.

Proportional measurements were calculated as the

percentage of SL or HL (Table 1). In the description, measurements and counts for the holotype are given first; those for the paratypes, where different from the holotype, are enclosed in parentheses. Institutional codes generally followed Sabaj (2020).

For DNA barcoding, total DNA was extracted from muscle tissue preserved in 99.5% ethanol,

Table 1. Morphometric and meristic data of the holotype (169.6 mm SL) and 11 paratype specimens (126.2–223.4 mm SL) of *Saurida weijeni* sp. nov.

Morphometrics (% SL)	Holotype	Paratypes (n = 11) mean (range)
Predorsal length	41.8	42.5 (38.0–44.8)
Preadipose length	81.3	80.1 (74.1–83.4)
Preanal length	72.9	73.0 (69.9–76.1)
Preanal-fin length	75.0	75.7 (74.0–79.1)
Prepectoral length	26.7	27.2 (25.6–29.6)
Prepelvic length	37.9	39.1 (37.2–41.1)
Head length (HL)	26.7	25.8 (24.3–27.2)
Body depth	12.0	14.1 (11.3–17.3)
Body width	14.9	13.7 (11.4–15.4)
Interpelvic width	9.0	8.6 (7.9–9.3)
Pectoral-fin length	16.1	15.9 (14.6–16.9)
Pelvic-fin length	17.4	17.7 (16.2–18.8)
Length of 2nd dorsal ray	18.5	18.8 (17.8–19.5)
Length of last dorsal ray	6.1	5.9 (5.5–6.7)
Length dorsal-fin base	13.2	13.3 (12.6–15.0)
Length of 2nd anal ray	-	8.4 (7.1–9.3)
Length of last anal ray	5.7	5.6 (4.4–6.7)
Length of anal-fin base	8.6	10.5 (9.0–11.5)
Length of caudal peduncle	14.4	14.3 (10.4–16.8)
Depth of caudal peduncle	5.7	5.5 (4.0–6.5)
Width of caudal peduncle	4.6	4.9 (3.0–6.1)
Morphometrics (% HL)		
Snout length	22.6	22.1 (19.1–23.8)
Eye diameter	19.4	21.3 (18.3–23.4)
Snout width	24.9	25.0 (22.2–29.4)
Interorbital width	20.7	20.9 (19.1–23.6)
Post orbital length	60.5	62.4 (54.8–98.6)
Upper jaw length	67.6	69.2 (67.0–77.0)
Meristics		
Dorsal fin	12	11–12
Pectoral fin	14	13–15
Pelvic fin	9	9
Anal fin	11	10–11
Pored lateral-line scales	52	49–52
Transverse scales above lateral line	3.5	3.5
Transverse scales below lateral line	5.5	5.5
Scale rows below lateral line with melanophores	2.5	2–3
Predorsal scales	20	17–19
Preadipose scales	16	14–16
Postadipose scales	13	10–12
No. vertebrae	49	47–49
No. rows of palatine teeth anteriorly	2	2
No. of vomerine teeth	0	0–2
No. teeth rows across tongue	4	3–4

using the GF-1 Nucleic Acid Extraction Kit (Vivantis Technologies Sdn. Bhd, Malaysia) and PureLink™ Genomic DNA Mini Kit (Invitrogen) extraction kits, according to the manufacturer's protocols. The partial Cytochrome Oxidase subunit I (*COI*) gene was amplified using the primers designed by Ward et al. (2005) (Fish F1–5'-TCAACCAACCACAAAGACATTGGCAC-3' and Fish R1–5'-TAGACTTCTGGGTGGCCAAAGAATCA-3'). The PCR thermo-cycling conditions used are as follows: 95°C for 2 mins (initial step), 35 cycles at 94°C for 30 sec (denaturation), 54°C for 30 sec (annealing), 72°C for 40 sec (extension), and 72°C for 10 min (final extension). The PCR products were visualized on 1% agarose gels. Sequencing of the samples was performed at Macrogen Inc. (South Korea). Sequence data was deposited in GenBank and Bar Code of Life Data System (BOLD), the accession numbers and metadata of all evaluated DNA sequences are summarized in table S1. Forward and reverse sequences were checked, trimmed, and assembled into contigs using Unipro UGENE software (Okonechnikov et al. 2012). The sequences determined here were aligned using Multiple Sequence Comparison by Log-Expectation (MUSCLE) software (Edgar 2004) as implemented in MEGA version 10.2.4 (Stecher et al. 2020). From the aligned sequences, the best evolutionary model was found using MEGA, the Kimura 2-parameter model with invariant sites (K2P+I) being selected by the Bayesian Information Criterion. Pairwise nucleotide genetic distances were calculated using the Kimura 2-parameter model (K2P; Kimura 1980) in MEGA. A maximum likelihood tree was reconstructed using MEGA, and node support measured using nonparametric bootstrapping with 1,000 replications. *COI* sequences from taxonomically verified and vouchered *Saurida* spp. specimens (Furuhashi et al. 2022) were included in the analysis, while the *COI* sequence of *Harpadon nehereus*, which belongs to the same subfamily as *Saurida*, was included as an outgroup.

RESULTS

Saurida weijeni Russell, Malay and Cabebe-Barnuevo sp. nov.

Common name: Wei-Jen's lizardfish

(Figs. 2–4, Table 1)

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Saurida umeyoshii (not of Inoue and Nakabo 2006): Wang et al. 2014: 1399 (South China Sea).

Holotype: NTUM 17606, sample id. No.

WJC 5756, 233.3 mm SL, South China Sea, outer slope of North Macclesfield Bank, *ZhongSha 2015* Trawl Survey Station CP CP4147, 16°09.83'N, 114°15.25'E–6°08.15'N, 114°17.97'E, 259–343 m, Wei-Jen Chen, RV *Ocean Researcher 1*, 26 July 2015.

Paratypes: Eleven specimens, 126.2–223.4 mm SL. NTUM 17604, sample id. No. WJC 5713, 166.7 mm SL, South China Sea, outer slope of North Macclesfield Bank, *ZhongSha 2015* Trawl Survey Station CP4146, 16°07.60'N, 114°18.83'E–16°09.29'N, 114°16.23', 232–314 m, Wei-Jen Chen, RV *Ocean Researcher 1*, 26 July 2015. NTUM 17605, sample id. No. WJC 5714, 169.6 mm SL, same data as preceding. NTM S.18814–001, sample id. No. WJC 5757, 188.2 mm SL, South China Sea, outer slope of North Macclesfield Bank, *ZhongSha 2015* Trawl Survey Station CP4147, same data as holotype. NTM S.18815–001, 3: sample id. No. WJC 5786, 202.7 mm SL, sample id. No. WJC 5787, 218.3 mm SL, sample id. No. WJC 5788, 171.2 mm SL, South China Sea, outer slope of North Macclesfield Bank, *ZhongSha 2015* Trawl Survey Station CP4148, 16°08.60'N, 114°17.22'E–16°07.33'N, 114°19.21'E, 218–281 m, Wei-Jen Chen, RV *Ocean Researcher 1*, 26 July 2015. MNHN 2022-0330, 3: sample id. No. WJC 5832, 136.7 mm SL; sample id. No. WJC 5833, 133.4 mm SL; sample id. No. WJC 5834, 126.2 mm SL, South China Sea, outer slope of North Macclesfield Bank, *ZhongSha 2015* Trawl Survey Station CP4149, 16°06.54'N, 114°20.05'E–16°06.75'N, 114°22.97'E, 162–165 m, Wei-Jen Chen, RV *Ocean Researcher 1*, 26 July 2015. UPVMI–01361, sample id. No. BAR-829, 205.6 mm SL, Philippines, Guimaras Island, Western Visayas, Cabalagnan Fish Port, purchased 29 November 2020. UPVMI–01362, sample id. No. BAR-830, 223.45 mm SL, same data as preceding.

Diagnosis: A moderately large species of *Saurida*, with the following combination of characters: dorsal fin with 11–12 rays; pectorals with 13–15 rays; lateral-line scales 49–52; transverse scale rows above lateral line 3½, below lateral line 5½; pectoral fins moderately long, reaching beyond a line from origin of pelvic fins to origin of dorsal fin; 2 rows of teeth on outer palatines; 0–2 teeth on vomer; tongue with about 3–4 rows of teeth posteriorly; caudal peduncle rounded (depth about equal to width); anterior part of stomach dusky or black, posterior extension pale whitish, intestine black; leading edge of upper lobe of caudal fin with 3–6 black spots.

Description: Counts and proportional measurements of the type series are provided in Table 1. Dorsal-fin rays 12 (11–12); pectoral-fin rays 14 (13–15); pelvic-fin rays 9; anal-fin rays 11 (10–11). Pored lateral-line scales 52 (49–52); transverse scale rows above lateral line 3½, transverse scale rows below lateral line 5½, scale rows below lateral line with melanophores 2½

(2–3); predorsal scales 20 (17–19); pre-adipose scales 16 (14–16); post-adipose scales 13 (10–13). Vertebrae 49 (47–49).

Body elongate and cylindrical, somewhat depressed on head and compressed on caudal peduncle, the latter with slightly raised lateral line scales, forming a slight ridge; scales large, cycloid, deciduous; scales present on cheek and opercle. Snout rounded when viewed from above. Nostrils located about midway between snout tip and anterior margin of orbit; anterior nostrils a little larger than posterior, anterior one with a broad dermal flap posteriorly. Eye circular, directed laterally, covered with fleshy adipose eyelid anteriorly and posteriorly. Interorbital region broad, slightly concave.

Mouth very large, the gape extending well beyond posterior margin of eye. Teeth on jaws numerous, small, canine-like, generally in four rows, outermost teeth smallest, innermost longest, visible when mouth closed; similar teeth on the palate, tongue and branchial arches; palatine teeth in two separate series: teeth of outer series long, in two rows, with anterior teeth longer, teeth of inner series short, in about six poorly defined rows; outer palatine series converge anteriorly but separated by vomer which is toothless (or with 0–2 teeth); tongue

short, spatulate, fleshy, with triangular shaped patch of teeth, in about 4 (3–4) rows posteriorly; lower jaw slightly shorter than upper jaw and fits into groove between teeth at tip of upper jaw; gill rakers absent, branchial arches each with about 4 rows of teeth, those on the inside largest.

Origin of dorsal fin just anterior to midpoint of distance from snout to adipose fin origin; base of dorsal fin longer than that of anal fin; adipose fin above posterior half of anal fin; anus just anterior to origin of anal fin; pectoral fins moderately long, 16.1% (14.6–16.6%) in SL, tip of pectoral fin reaching beyond a line from base of pelvic fin to origin of dorsal fin (P–D line); pectoral and pelvic fins with long and pointed axillary scales, those of pelvic a little shorter; caudal fin deeply forked, upper and lower lobes about equal.

Colour of fresh specimens (Figs. 2, 3): Top of head and back dark brown or coppery brown, some scales narrowly edged with black, forming a variegated pattern; paler 2–3 scale rows below lateral line, ventral surface silvery white; dorsal fin translucent, leading edge with 6 (3–5) indistinct spots; adipose fin dusky on outer half of fin; caudal fin translucent, leading edge of upper lobe with 5 (4–5) blackish spots, outer part of lower lobe dusky; pectoral fins dusky, base of



Fig. 2. *Saurida weijeni* sp. nov. Holotype NTUM 17606 (WJC 5756), 233.3 mm SL, South China Sea, North Macclesfield Bank showing freshly caught colours (Photo credit: W-J Chen).



Fig. 3. *Saurida weijeni* sp. nov. Paratype UPVMI-01361 (BAR-829), 205.6 mm SL, Philippines, Guimaras Island, Western Visayas, Cabalagnan Fish Port showing freshly caught colours (Photo credit: RA Cabebe-Barnuevo).

fin translucent; pelvic fins and anal fin translucent. Peritoneum pale whitish; anterior part of stomach dusky or black, posterior extension pale whitish, intestine black.

Colour in alcohol (Fig. 4): Brown on back, paler below lateral line, pigment extending to about 2½ (2–3) scale rows below lateral line; pectoral fins dusky over outer two thirds of fin; pelvic fins pale; dorsal, caudal and anal fins pale, anterior margin dorsal fin with indistinct spots; upper leading edge of upper lobe of caudal fin with 6 (3–5) spots, lower lobe of fins dusky on outer half; adipose fin dusky on outer half. Peritoneum whitish; anterior part of stomach dusky or black, posterior extension pale, intestine black.

Etymology: Named in honour of Professor Wei-Jen Chen, Institute of Oceanography, National Taiwan University, who collected this species during an exploratory fish survey of the Macclesfield Bank area of the South China Sea. The name *weijeni* is treated here as a noun in the genitive case (ICZN 1999, Article 31.1). The common English name Wei-Jen's lizardfish is proposed for this species.

Distribution: *Saurida weijeni* sp. nov. has only been recorded from the South China Sea and from Cabalagnan Fish Port, Guimaras Island, Western Visayas, Philippines (Fig. 1). Specimens collected from the outer slope of the North Macclesfield Bank, South China Sea, were trawled in depths of 162–343 m. The Macclesfield Bank (Zhongsha) lies east of the Paracel Islands, southwest of Pratas Island and north of the Spratly Islands, and comprises many entirely submerged banks, seamounts, and shoals in the South China Sea. It is about 130 km long from southwest to northeast, and about 70 km wide at its broadest part (Huang et al. 2020; United States National Geospatial-Intelligence Agency 2020). With an ocean area of 6,448 km² it is one of the largest submerged atolls of the world. In general, the central lagoon is very deep, with depths up to 100 m and outside of the banks, depths quickly drop to more than 1000 m. Specimens collected from Cabalagnan Fish Port, Guimaras Island, Western Visayas, in the Philippines lacked information

on fishing gear, collection depth, or specific locality, but were presumably fished in deeper water from either Guimaras Strait or the Sulu Sea.

Genetic analysis: *COI* sequence fragments of 544 base pairs were recovered from twelve specimens of *Saurida weijeni* sp. nov. Two *COI* haplotypes were observed, with the sequence from Macclesfield Bank differing at two nucleotide positions from the haplotype from the Philippines (intraspecific K2P genetic difference = 0.37%). Notably, the haplotype from the Philippines is identical to GenBank sequence KM189365.1 from the South China Sea, identified as *Saurida umeyoshii* by Wang et al. (2014) in their study of the complete mitochondrial genome of that species. Unfortunately, a request to the corresponding author of this study for a photograph and/or the voucher specimen of KM189365.1 for verification was unsuccessful and it seems that their specimen was misidentified. Incorrect species identification in public sequence databases such as GenBank is a growing problem (Hung et al. 2017) and this case further emphasises the importance of accurate taxonomic identification and/or verification using museum voucher specimens in DNA barcoding and systematic studies.

A total of 571 *COI* sequences from other *Saurida* species were retrieved from GenBank and the BOLD system (accessed March 19, 2024) and a preliminary maximum likelihood *COI* tree was reconstructed with all available sequences, including *S. weijeni* sp. nov. Initial screening to identify Operational Taxonomic Units (OTUs) based on a threshold of $\geq 3\%$ *COI* divergence in K2P distance (Ward et al. 2009) in this large and complex tree, showed *S. weijeni* sp. nov. to be genetically divergent from all other species of *Saurida*. The preliminary 'total' maximum likelihood *COI* tree of *Saurida* and its OTU's is the subject of continuing analysis by BCR that is beyond the scope of this paper. For this reason, only Western Pacific congeners of the *S. undosquamis* group (*S. fortis*, *S. macrolepis*, *S. umeyoshii*, *S. undosquamis*, *S. weijeni* sp. nov.) are included in the partial maximum likelihood *COI* tree that is presented here (Fig. 5), primarily to indicate



Fig. 4. *Saurida weijeni* sp. nov. Paratype UPVMI-01361 (BAR-829), 205.6 mm SL, colours after preservation (Photo credit: RA Cabebe-Barnuevo).

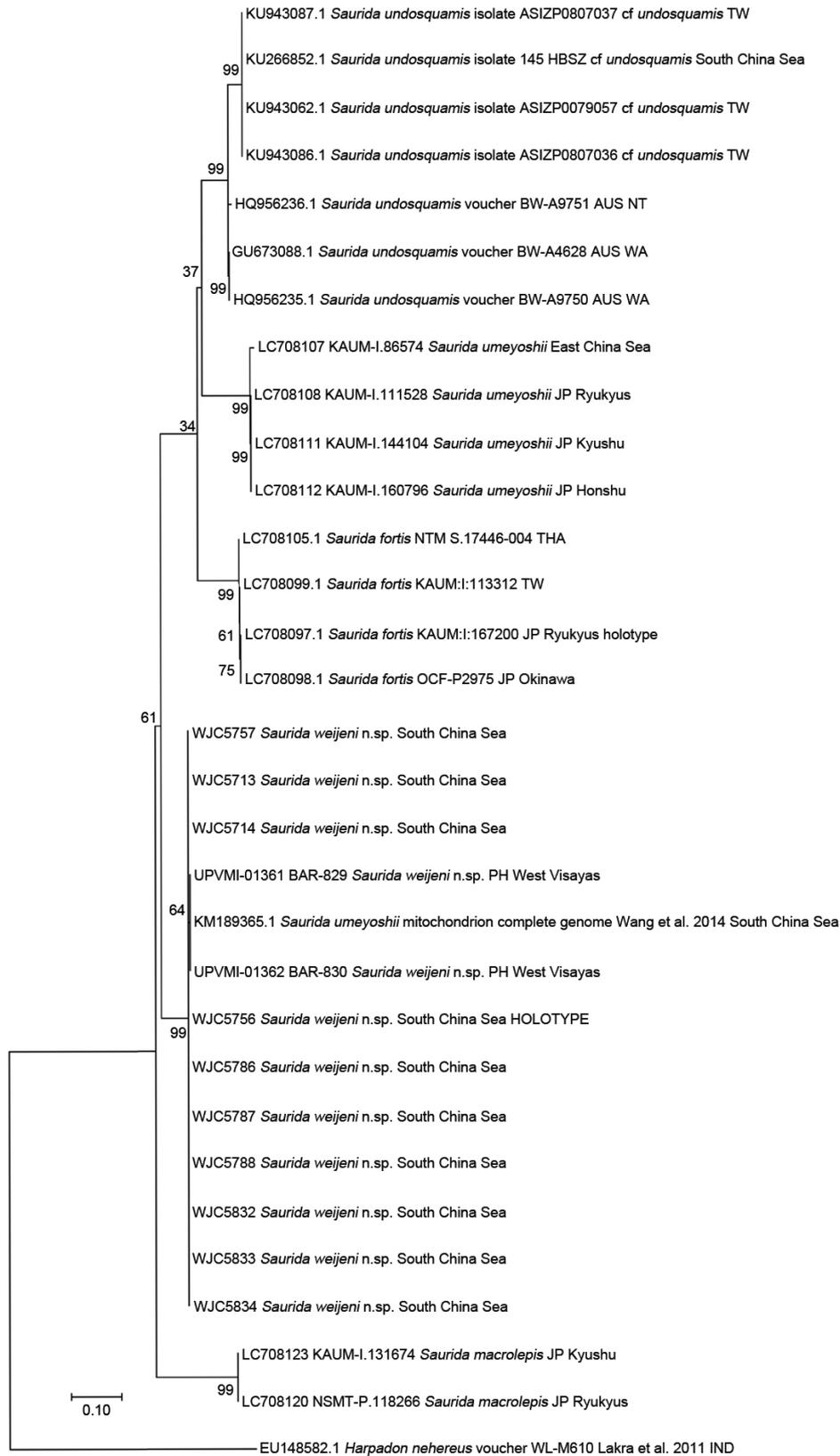


Fig. 5. Maximum likelihood tree based on mitochondrial *COI* DNA sequences. Numbers on the nodes represent bootstrap support values. Abbreviations: AUS NT = Australia, Northern Territory; AUS WA = Australia, Western Australia; IND = Indonesia; JP = Japan; PH = Philippines; THA = Thailand; TW = Taiwan.

K2P genetic differences rather than infer phylogenetic relationships.

Based on recent sequence data for the true *Saurida umeyoshii* (Furuhashi et al. 2022) interspecific K2P genetic difference between *Saurida weijeni* sp. nov., including KM189365.1, and *S. umeyoshii* is $13.1 \pm 0.1\%$. Average interspecific K2P genetic differences with other closely related congeners ranged from $10.5 \pm 0.7\%$ (*S. weijeni* sp. nov. vs. *S. undosquamis*) to $12.0 \pm 0.2\%$ (*S. weijeni* sp. nov. vs. *S. macrolepis*). A maximum likelihood tree based on *COI* sequences (Fig. 5) showed *S. weijeni* sp. nov. to be reciprocally monophyletic with *S. umeyoshii* and other *Saurida* species.

Comparative material: *Saurida fortis* (41 specimens, 120.0–499.8 mm SL): listed in Furuhashi et al. (2022), from Japan, Taiwan, and Thailand. *Saurida lessepsianus* (38 specimens, 108.0–282.2 mm SL): listed in Russell et al. (2015), from Red Sea and eastern Mediterranean Sea. *Saurida macrolepis* (10 specimens, 135.5–210.5 mm SL): BSKU 58129, 137.0 mm SL, BSKU 58130, 162.1 mm SL, BSKU 58131, 204.4 mm SL – Iburi fishing port, Tosa Bay, Kochi, Japan; NTUM 145372, 4: 176.5–210.5 mm SL – Iorigawa fishing port, Miyazaki, Japan; MUFS 25074, 135.5 mm SL; ZUMT 7478, 196.1 mm SL, ZUMT 7479, 192.6 mm SL – Tokyo Fish Market, Japan. *Saurida umeyoshii* (11 specimens, 216.8–332.0 mm SL): BSKU 32666, 255.0 mm SL, BSKU 33029, 332.0 mm SL, BSKU

33114, 281.8 mm SL, BSKU 33116, 244.8 mm SL, BSKU 33117, 232.4 mm SL, BSKU 33118 239.3 mm SL, BSKU 34325, 288.3 mm SL, BSKU 34326, 244.6 mm SL, BSKU 34327, 239.2 mm SL, BSKU 34328, 266.5 mm SL – Okinawa Trough, Japan; BSKU 85776, 216.8 mm SL – Mimase, Kochi, Japan. *Saurida undosquamis* (18 specimens, 162.6–346.6 mm SL): listed in Russell et al. (2015), from Northwestern Australia. *Saurida* cf. *undosquamis*: (6 specimens, 75.7–335.0 mm SL): ASIZ P0807036, 186.42 mm SL – Keelung, Taiwan; ASIZ P0076118, 317.7 mm SL, P0076119, 288.2 mm SL – Chia-Yi, Taiwan; NTM S.16884-003, 335.0 mm SL – Hengchung market, Taiwan; NTUM 14370, 301.8 mm SL – Mimase fishing port, Tosa Bay, Japan; NTUM 14373, 75.7 mm SL – Iburi fishing port, Tosa Bay, Japan.

DISCUSSION

Inoue and Nakabo (2006), in a review of the *Saurida undosquamis* group, showed the name *S. undosquamis* (type locality: northwestern Australia) has been applied to a complex of species distributed widely throughout the Indo-West Pacific. They recognised three species from the Western Pacific in the group (*S. undosquamis* Richardson, 1848; *S. umeyoshii* Inoue and Nakabo, 2006; *S. macrolepis* Tanaka, 1917) and one

Table 2. Comparison of selected morphological characters of *Saurida weijeni* sp. nov. and other Western Pacific species of the “*S. undosquamis*” group: *S. umeyoshii*, *S. undosquamis*, *S. macrolepis* and *S. fortis*

	<i>S. weijeni</i> sp. nov.	<i>S. umeyoshii</i>	<i>S. undosquamis</i>	<i>S. macrolepis</i>	<i>S. fortis</i>
	South China Sea, Philippines <i>n</i> = 12	Japan, <i>n</i> = 11	NW Australia, <i>n</i> = 18	Japan, <i>n</i> = 10	Japan, Taiwan, Thailand <i>n</i> = 41
Pectoral-fin tip	Extending to or just beyond P–D line	Extending beyond P–D line	To or just short of P–D line	Just short of or extending slightly beyond P–D line	Just short of or extending slightly beyond P–D line
Body colour above lateral line	Dark brown	Dark brown	Light brown	Dark brown	Dark brown
Melanophores below lateral line (adults)	On 2–3 scale rows below lateral line	All scales	On 1–5 scale rows below lateral line	On 1–3 scale rows below lateral line	All scales, but more sparse ventrally
Black spots along caudal-fin upper margin	3–5 indistinct	7 distinct	4–12 distinct	3–8, sometimes indistinct	Indistinct
Colour of stomach	Dusky or black	Pale black	Whitish	Dusky or black	Whitish or greyish (pale black in young)
Colour of intestine	Black	Dense black	Whitish or pale grey	Black	Greyish or pale
Teeth rows on tongue	3–4	3–5	7–12	3–7	3–6
Vertebrae	47–49	47–51	50–54	45–47	51–54
Lat line scales	49–52	49–52	52–59	48–52	53–56

from the Western Indian Ocean (*S. longimanus* Norman, 1939). To this group may be added: *S. lessepsianus* Russell, Golani and Tikochinsky, 2015 from the Western Indian Ocean–Red Sea, and a now widely invasive species in the eastern Mediterranean Sea; *S. fortis* Furuhashi, Russell and Motomura, 2022 from Japan; and *S. weijeni* sp. nov. described here. It should be noted that *Saurida undosquamis* sensu Inoue and Nakabo (2006) may comprise more than one species (Furuhashi et al. 2022) and is the subject of ongoing study by BCR.

Saurida weijeni sp. nov. differs from other Western Pacific species of the *S. undosquamis* group (Table 2) as follows: lateral-line scales, 49–52 (versus 54–58 in *S. undosquamis* and 53–56 in *S. fortis*); fewer vertebrae, 47–49 (versus 50–54 in *S. undosquamis* and 51–54 in *S. fortis*); and has a black or dusky stomach and intestine (versus whitish pale grey in *S. undosquamis* and *S. fortis*). It differs from *S. umeyoshii* in having melanophores on the body extending only 2–3 scale rows below the lateral line (versus melanophores on all scales to ventral midline in *S. umeyoshii*) and having 3–5 indistinct black spots (versus 7 distinct spots in *S. umeyoshii*) on the upper margin of the caudal fin.

Morphologically, *Saurida weijeni* sp. nov. appears most closely related to *S. macrolepis* but differs from that species in having 47–49 vertebrae (versus 45–47 vertebrae in *S. macrolepis*) and is genetically distinct (K2P genetic difference 12.3% – Fig. 5).

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Authors' contributions: BCR and RAC-B performed

the morphometrics examinations. BCR, MCDM and RAC-B produced and analyzed the data and wrote and reviewed the manuscript. All authors read and approved the final version of the manuscript.

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Availability of data and materials: All mitochondrial COI DNA sequences in this study are available in GenBank. The metadata of the samples are attached in the Supplementary Materials.

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Supplementary materials

Table S1. Species name, museum ID, GenBank accession number, specimen voucher number locality, published source of all specimens used in the *COI* analysis in this study. (download)