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New record of anthiadine fish, *Plectranthias yamakawai* (Actinopterygii: Perciformes: Serranidae), from the Philippines

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Abstract

A single specimen of *Plectranthias yamakawai* Yoshino, 1972, 168.86 mm SL, obtained in a fish market in Zambales, Philippines, represents the first report in the country. Currently, the fish is only known to occur in Japan, Taiwan, and Samoa Islands. This anthiadine fish varies from other species of genus *Plectranthias* by having 30–33 lateral-line scales, a single red blotch below the lateral line, and numerous dark green blotches on the upper half of the body. The mitochondrial cytochrome oxidase subunit I (*COI*) is also described for the first time for this species in this article. The pairwise genetic distance computation reveals that *P. yamakawai* has a very low distance from the sequences of the other eight species of *Plectranthias* that have been submitted to GenBank. This is the sixth species of the genus *Plectranthias* to be reported from the western coast of Luzon, Philippines.

Keywords

Anthiadinae, *COI*, morphology, serranids, taxonomy, Zambales

Introduction

The genus *Plectranthias* Bleeker, 1873 was initially revised by Yoshino (1972), who also recognized the two species *Plectranthias anthioides* (Günther, 1872) and *Plectranthias yamakawai* Yoshino, 1972. Subsequently, Randall (1980) made a thorough revision of the genus, naming additional 13 species, and mentioning that *P. anthioides* identified by Yoshino (1972) was a synonym of *Plectranthias kamii* Randall, 1980. The revision made by Randall (1980) was later followed by the identification of 31 new species (Fricke et al. 2022). Fishes of the genus *Plectranthias* are members of the subfamily Anthiinae, which Anderson (2022) noted had been elevated to the familial level, and Dornburg and Near (2021) recognized them as belonging to the family Anthiadidae. However, the current paper recognizes this specimen as a member of the family Serranidae since no morphological evidence has been provided by Dornburg and Near (2021).

The genus *Plectranthias* is one of the 29 genera that make up the subfamily Anthiadinae (Anderson 2018). This group is widely distributed throughout the tropical to subtropical seas of the Indo–Pacific and the western Atlantic and can be found in shallow to deeper waters (2–400 m) (Allen and Walsh 2015; Tang et al. 2020; Fricke 2021). This genus is distinguishable from other genera by its 10 dorsal spines, which are connected to the 13–20 dorsal-fin soft rays; three anal spines with 6–8 anal-fin soft rays; 12–18 pectoral-fin rays; 8–46 lateral-line tubed scales; absence of auxiliary scales on head or body; presence of teeth on the vomer and palatine but not on the tongue; having a V- or U-shaped vomer tooth patch; 26 (rarely 27) total vertebrae count, and presence of 12–31 total gill rakers (Gill et al. 2021). These fishes are difficult to catch using hook and line or bottom trawling, and they are also challenging to approach while scuba diving, and this, apparently, accounts for their underrepresentation in museum collections (Chen and Shao 2002; Heemstra and Randall 2009). Currently, there are 65 valid species of the genus (Fricke et al. 2022; Koeda et al. 2022), and only five species have been documented in the Philippines: *Plectranthias foresti* Fourmanoir, 1977; *Plectranthias inermis* Randall, 1980; *Plectranthias japonicus* (Steindachner in Steindachner et Döderlein, 1883); *Plectranthias knappi* Randall, 1996; and *Plectranthias sagamiensis* (Katayama, 1964) (see Fricke et al. 2022). With this report, *P. yamakawai* will now be included in the short list of the genus known from the waters of the Philippines.

Plectranthias yamakawai was firstly described by Yoshino (1972) from the Okinawa and Amami Islands. Wada et al. (2020) documented additional specimens from different islands of the Ryukyu Archipelago, which include Osumi, Yaeyama, and Tokara Islands, at depths of 100–300 m while Motomura and Harazaki (2017) reported the largest specimen, measuring 230.7 mm SL from Yaku-shima Island, Osumi Islands at 100 m deep. It has also been reported in Taiwan (Chen and Shao 2002) and Samoa in the South Pacific (Wass 1984). To our knowledge, no publication has provided a DNA barcode sequence of *P. yamakawai*. Thus, this publication will not only be the first to report the occurrence of this species in Philippine waters but also its mitochondrial cytochrome oxidase subunit I gene (*COI*), which is important for the validation of species identification.

Methods

A single specimen of *Plectranthias yamakawai* was collected in a fish market in Zambales Province, Western Luzon, Philippines. The specimen was transported to the University of the Philippines Visayas (UPV), Miagao, Iloilo in an insulated ice cooler with crushed ice. Curatorial techniques followed Motomura et al. (2013). All measurements were taken using a digital caliper to the nearest 0.01 mm and followed Hubbs and Lagler (1947). For the proportional measurement, the standard length (SL) and head length (HL) were used, and the results were compared to the measurement of Yoshino (1972).

Muscle tissue was collected from the nape area on the right side of the fish and preserved in absolute ethanol. DNA extractions were carried out according to the instructions of the GF-1 Nucleic Acid Extraction Kit (Vivantis Technologies Sdn. Bhd, Malaysia). The combination of the forward and reverse primers below designed by Ward et al. (2005) was used to amplify the mitochondrial cytochrome c oxidase subunit I (*COI*) gene:

FishF1 – 5′TCAACCAACCACAAAGACATTGGCAC3′
FishR1 – 5′TAGACTTCTGGGTGGCCAAAGAATCA3′

The 25 µL PCR reaction was composed of 18.4 µL nuclease-free water, 2.25 µL 10× buffer, 1.25 µL $MgCl^2$ (25 mM), 0.5 µL dNTP mix (10 mM), 0.25 µL of each primer, 0.1 µL Taq DNA polymerase (Vivantis Technologies Sdn. Bhd, Malaysia), and 2 µL DNA template. The PCR thermocycling conditions used are as follows: initial step at 95°C for 2 min, 35 cycles of 94°C for 30 s (denaturation), 54°C for 30 s (annealing), and 72°C for 1 min (extension), with a final extension at 72°C for 10 min. The PCR products were visualized using 1% agarose gel with gel red. Purification of PCR products was carried out using GF-1 PCR Clean-up Kit. The genomic DNA was quantified using a MultiSkanTM Skyhigh Microplate Spectrophotometer (Thermo Fisher Scientific). The PCR products were sent to Macrogen Inc. (South Korea) for sequencing. Consensus sequences were formed, cleaned, and trimmed using Unipro EUGENE software (Okonechnikov et al. 2012). The generated sequence was checked against *COI* sequences in GenBank using the Basic Local Alignment Search TOOL (BLAST) of the National Center for Biotechnology Information (NCBI). Using the Mega X software (Kumar et al. 2018), the phylogenetic tree was constructed using the Neighbor-joining (NJ) method (Saitou and Nei 1987), computed using the Kimura 2-parameter (K2P) model (Kimura 1980), and a bootstrap test of 1000 replicates (Felsenstein 1985). The pairwise distance between the sequences was computed using the Kimura 2-parameter model (Kimura 1980), and standard error estimates were obtained by a bootstrap procedure (1000 replicates). A total of 15 nucleotide sequences from 8 different species of genus *Plectranthias* that were submitted to GenBank were included in the analysis.

Results

Family Serranidae Swainson, 1839
Plectranthias Bleeker, 1873

Plectranthias yamakawai Yoshino, 1972

(Figs 1 and 3; Tables 1 and 2)

Material examined. UPVMI-01360, 168.86 mm SL, Zambales fish market, the Philippines, 1 March 2022, leg. R.P. Babaran.

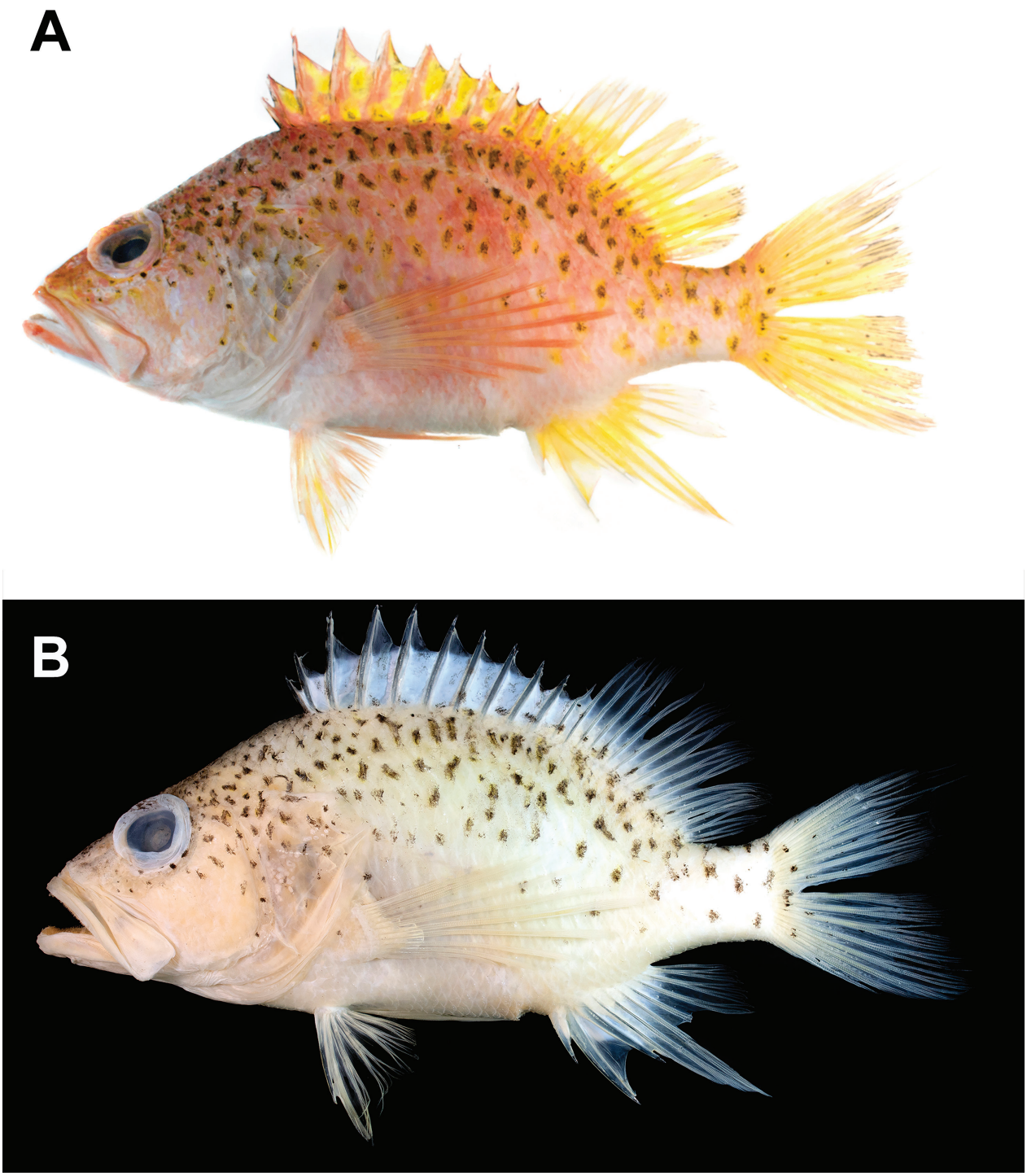

Figure 1. Images of fresh (**A**) and preserved (**B**) *Plectranthias yamakawai*, UPVMI-01360, 168.86 mm SL collected off Zambales, Western coast of Luzon, the Philippines.

Morphological diagnosis and description. Single specimen of *Plectranthias yamakawai* had following combination of characters: dorsal-fin spines X, dorsal-fin soft rays 18, anal-fin spines III, anal-fin soft rays 7, pectoral-fin rays 13, lateral-line scales 31, scales above lateral line 5, scales below lateral line 17, and gill rakers 6 + 10. Body compressed, moderately deep, depth 2.18 in SL; head large (length 2.19 in SL, depth 3.86 in SL), slightly convex dorsally. Mouth large, terminal; maxilla large, expanded easily, exposed when mouth closed; lower jaw significantly extending beyond upper jaw; opercle consisting of three spines (middle spine strongest and longest); preopercle serrated with three antrorse spines on lower margin of left side and two spines on right side; subopercle and interopercle margins not serrated. Teeth on both jaws minute; two enlarged conical teeth on right side and three on left side positioned anterior of upper

Table 1. A comparison of the counts and measurements of *Plectranthias yamakawai* from the Philippines (this study) with those of the Japanese holotype (Yoshino 1972).

Character	Holotype FAKU-44565	This study UPVMI-01360)	Difference [percentage point]
Meristics	X, 17	X, 18	
Anal fin	III, 7	III, 7	
Pectoral fin	13	13	
Gill rakers	6 + 10	6 + 10	
Lateral-line (LL) scales	33	31	
Scales above LL	—	5	
Scales below LL	—	17	
In %SL			
Head length	43.48	45.68	2.2
Head depth	—	25.92	
Body depth	37.17	45.86	2.4
Pectoral-fin length	35.34	39.84	4.5
Dorsal-fin base	—	57.79	
Anal-fin base	—	16.95	
Pectoral-fin base	—	8.24	
Pelvic-fin base	—	4.61	
In %HL			
Snout length	23.36	28.55	5.2
Maxillary length	44.44	45.02	0.6
Eye diameter	25.25	26.26	1.0
Interorbital width	13.81	10.40	–3.4
Pre-dorsal length	—	53.86	
Post orbital head length	56.18	50.29	–5.9
Caudal peduncle depth	31.25	28.31	–2.9
Caudal peduncle length	43.48	33.48	–10.0
Ventral fin length	47.17	49.97	2.8
Ventral spine length	27.86	31.13	3.3
3rd dorsal spine length	30.30	30.70	0.4
4th dorsal spine length	33.33	34.33	1.0
5th dorsal spine length	—	32.51	
Last dorsal spine length	17.54	20.34	2.8
Length of longest soft dorsal ray	41.49	Damaged	
1st anal spine length	15.27	18.27	3.0
2nd anal spine length	31.75	37.57	5.8
3rd anal spine length	28.57	35.84	7.3

FAKU-44565, 173.2 mm SL; 75.3 mm HL. UPVMI-01360, 168.86 mm SL; 77.14 mm HL.

jaw; single, enlarged, conical tooth positioned in middle area on both sides of lower jaw. Both vomerine and palatine patches consisting of villiform teeth; vomerine tooth patch V-shaped while palatine tooth patches narrow band-shaped. Teeth on tongue absent; base of tongue broad becoming narrow at front end. Scales on body large, ctenoid in shape; head area covered with scales except for snout, lips, maxillary, and ventral area; operculum completely covered with large scales; nape area covered with smaller scales; dorsal-, anal-, and pectoral-fin bases with small scales. Dorsal-fin spines stiff and connected to dorsal-fin soft rays; 4th dorsal-fin spine longest (26.48 mm vs. 5th spine 25.08 mm and 3rd spine 23.68 mm). Anal-fin spines long and rigid; 2nd anal-fin spine as longest (28.98 mm vs. 1st spine 14.09 mm and 3rd spine 27.65 mm). Pectoral-fin rays long, longest fin ray reaching beyond posterior end of anal-fin base, 1st pectoral-fin ray unbranched; 2nd–13th pectoral-fin rays branched. Pelvic fin inserted anterior to pectoral-fin base; longest pelvic-fin ray not reaching anus. Caudal fin emarginate; 5th–7th upper lobe-fin rays filamentous.

Color in fresh sample. Body reddish-yellow (dorsal side) and white (ventral area) (Fig. 1A); yellow-fringed dark greenish blotches scattered on upper half of body and head; similar blotches present in entire caudal peduncle, dorsal- and caudal-fin bases; smaller blotches observed in pre-dorsal area; large red spot located just below lateral line and center of body; pectoral fin reddish; dorsal, anal, pelvic, and caudal fin reddish-yellow; posterior end of dorsal-fin soft rays and caudal-fin ray edges both black.

Color of preserved sample. Body light brown (Fig. 1B); dark green blotches still visible; red spot faded; fins colorless; posterior end of dorsal-fin soft rays and caudal-fin ray edges remain black.

Distribution. *Plectranthias yamakawai* is commonly collected from various fishing grounds in Ryukyu Islands, Japan (Yoshino 1972; Motomura and Harazaki 2017; Wada et al. 2020), and reports of it have also come from Taiwan (Chen and Shao 2002), and Samoan Islands (Wass 1984), as well as the western coast of Luzon Philippines (Fig. 2).

Table 2. Pairwise genetic distance calculated using the K2P model between the *COI* gene sequences of *Plectranthias yamakawai* from the Philippines (this study) and the 15 sequences of different species of *Plectranthia*s from GenBank. The number of base substitutions per site is given between the sequences. The standard error estimate(s) indicated above the diagonal were obtained using a bootstrap procedure (1000 replicates).

UPVMI-01360 *P. yamakawai* (E510)	—	0.00	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.02	0.02	0.02
KT601636_1 *P. bennetti* Australia	0.17	—	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
MF123989_1 *P. winniensis* Israel	0.19	0.20	—	0.00	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02
MF123988_1 *P. winniensis* Israel	0.19	0.20	0.00	—	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02
KC565480_1 *P. flammeus* Marquesas	0.21	0.20	0.22	0.22	—	0.00	0.00	0.00	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
KC565479_1 *P. flammeus* Marquesas	0.21	0.20	0.22	0.22	0.00	—	0.00	0.00	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
KC565478_1 *P. flammeus* Marquesas	0.21	0.20	0.22	0.22	0.00	0.00	—	0.00	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
KC565477_1 *P. flammeus* Marquesas	0.21	0.20	0.22	0.22	0.00	0.00	0.00	—	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
KC567663_1 *P. fourmanoiri* Marquesas	0.19	0.17	0.18	0.18	0.21	0.21	0.21	0.21	—	0.00	0.02	0.02	0.02	0.02	0.02	0.02
KC567662_1 *P. fourmanoiri* Marquesas	0.19	0.17	0.18	0.18	0.21	0.21	0.21	0.21	0.00	—	0.02	0.02	0.02	0.00	0.02	0.02
JQ432004_1 *P. longimanus* French polynesia	0.20	0.23	0.22	0.22	0.16	0.16	0.16	0.16	0.23	0.23	—	0.02	0.03	0.00	0.02	0.00
KU943548_1 *P. kamii* Taiwan	0.09	0.21	0.21	0.21	0.22	0.22	0.22	0.22	0.22	0.22	0.22	—	0.02	0.00	0.02	0.02
KU943449_1 *P. japonicus* Taiwan	0.18	0.17	0.20	0.20	0.20	0.20	0.20	0.20	0.15	0.15	0.25	0.18	—	0.00	0.02	0.03
KU943448_1 *P. japonicus* Taiwan	0.18	0.17	0.20	0.20	0.20	0.20	0.20	0.20	0.15	0.15	0.25	0.18	0.00	—	0.02	0.03
KC565483_1 *P. winniensis* Marquesas	0.19	0.21	0.10	0.10	0.20	0.20	0.20	0.20	0.18	0.18	0.21	0.22	0.20	0.20	—	0.02
KC565481_1 *P. nanus* Marquesas	0.20	0.23	0.22	0.22	0.16	0.16	0.16	0.16	0.22	0.22	0.00	0.22	0.25	0.25	0.21	—

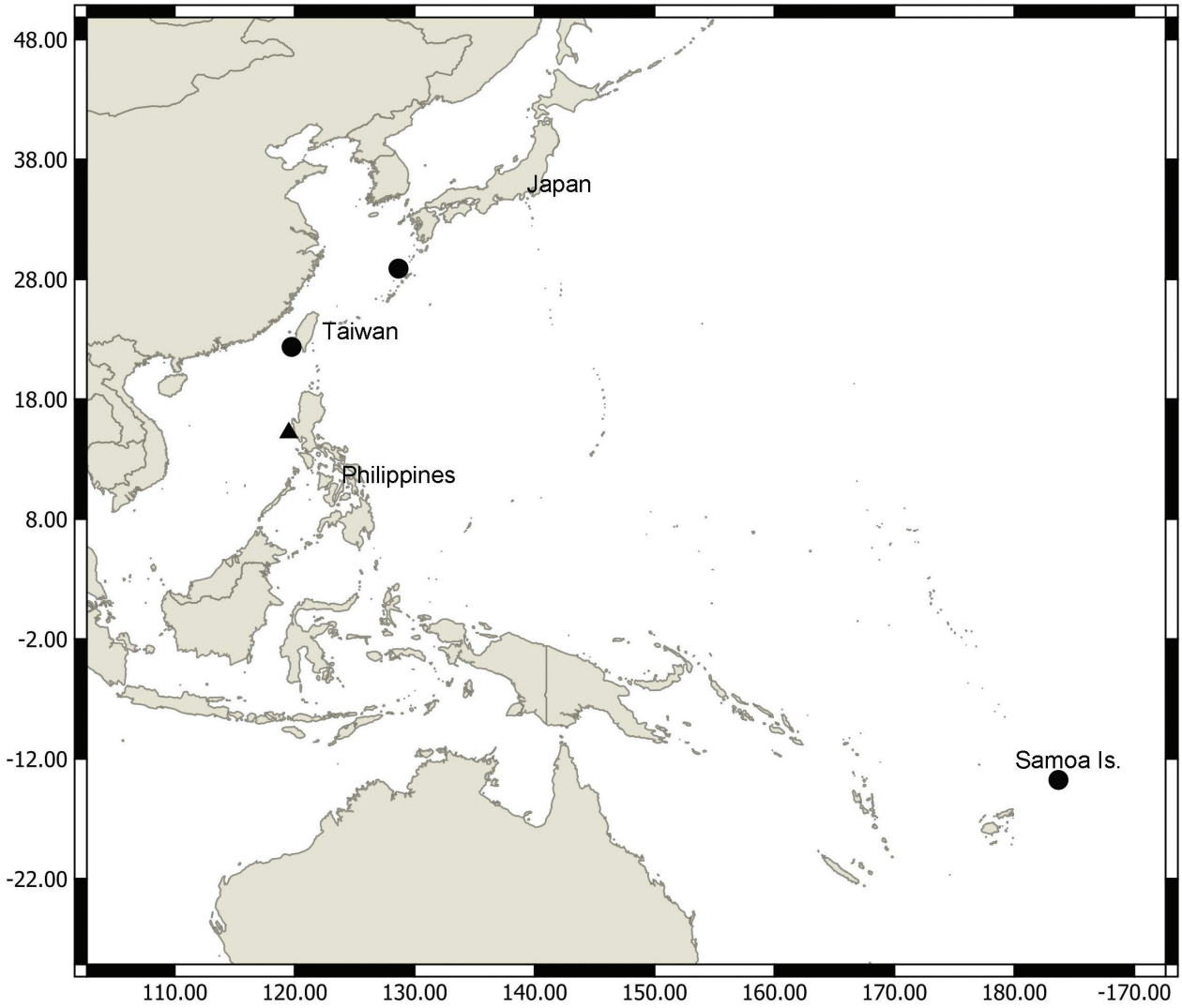

Figure 2. Distribution of *Plectranthias yamakawai*, based on published records and the presently reported study.

Previous Philippine records. Three of the five species of *Plectranthias* previously documented in the Philippines have been described as new species based on the Philippine specimens, *P. foresti*, *P. inermis*, and *P. knappi*, while the other two are documented as new records (*P. japonicus* and *P. sagamiensis*). *Plectranthias foresti* was described based on four specimens trawled at depths of 183–185 m off southwestern Luzon (Fourmanoir 1977; Randall 1980). *Plectranthias knappi*, was discovered in the Visayan Sea from a single specimen obtained at 90 m deep (Randall 1996). Similarly, the holotype of *P. inermis* was collected from Batangas, Southern Luzon Region, Philippines at 30 m deep, with later reports of the species from Mauritius, Christmas Island, Fiji, and Papua New Guinea (Randall 1980; Fricke et al. 2022). *Plectranthias sagamiensis*, originally described in Japan (Katayama 1964) was later collected off southwest Luzon at depths of 82–86 m and served as the first report of the species in the Philippines (Iwamoto and McCosker 2014). *Plectranthias japonicus* was originally described in Japan (Steindachner and Döderlein 1883) and first reported by Randall (1980) taken from 185–200 m off Manila Bay, Philippines.

Discussion

The presently reported specimen was identified as *Plectranthias yamakawai* based on the following characteristics: a single large red spot located just below the lateral line, yellow-fringed dark greenish spots scattered on the upper half of the body and head, 4th and 5th dorsal spine longer than the 3rd dorsal spine, and 30–33 lateral-line scales (Yoshino 1972; Randall 1980, 1996; Chen and Shao 2002; Wu et al. 2011; Wada et al. 2020). The specimen also matches the colored photograph provided by Motomura et al. (2019). According to Yoshino (1972), *P. yamakawai* and *P. anthioides*, which were later regarded as synonyms of *P. kamii* by Randall (1980), resemble each other in general appearance, but the former varies from the latter by having fewer lateral-line scale count (30–33 vs. 35–36), 4th dorsal spine is the longest instead of the 3rd spine. Moreover, *P. yamakawai* reported by Hobbs et al. (2014) from Christmas Island was a misidentified specimen of *P. kamii*. However, *P. yamakawai* can further be distinguished from *P. kamii* based on body coloration; *P. yamakawai* has numerous evenly distributed

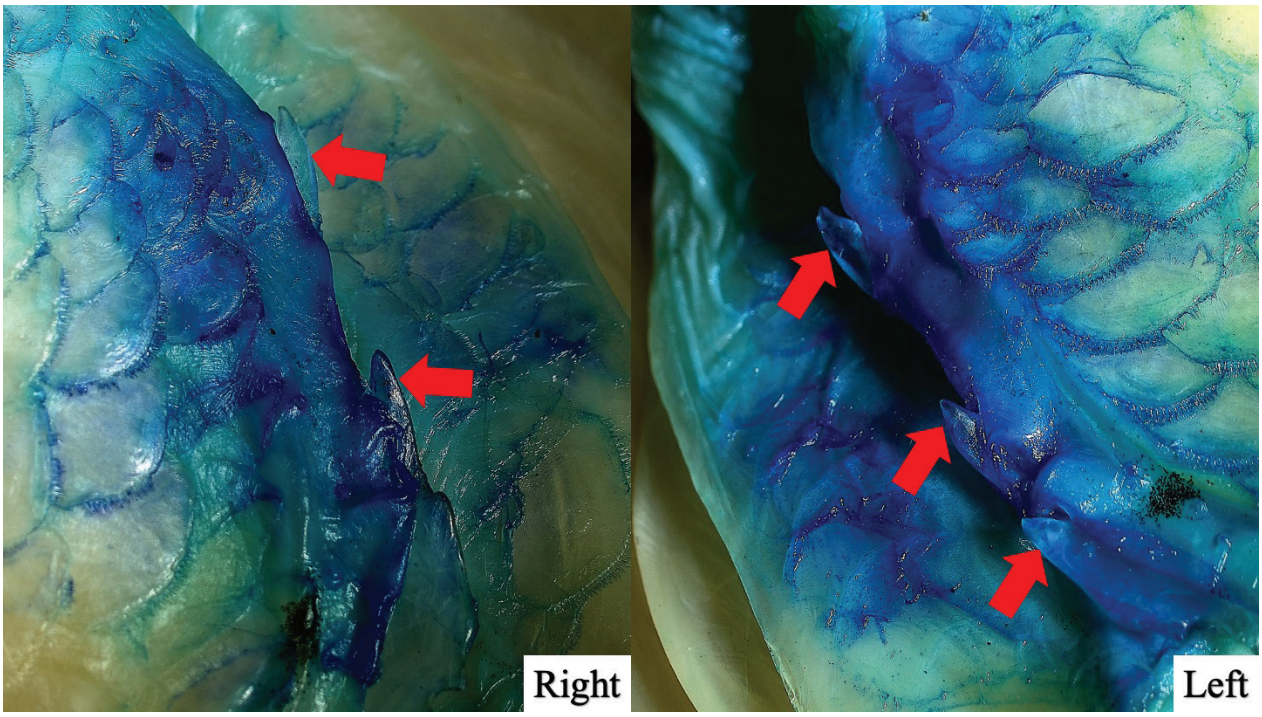

Figure 3. Antrorse spines observed on both sides of the *Plectranthias yamakawai* from the Philippines.

dark greenish spots on the upper half of the body while *P. kamii* has several orange patches on top of the head and upper half of the body, as well as similar coloration along the dorsal base and irregular longitudinal patches along the mid-side of the body. In addition, *P. kamii* lacks the single large red spot located just below the lateral line which was observed in the previous *P. yamakawai* specimens (Yoshino 1972; Gill et al. 2021) and in the presently reported study.

Plectranthias yamakawai has a lateral-line scale count similar to *Plectranthias whiteheadi* Randall, 1980 and *Plectranthias sheni* Chen et Shao, 2002; however, *P. yamakawai* differs from these two species due to distinct colored spots on the body as compared to the yellowish pink with a series of golden blotches on the body of *P. sheni* and the presence of two rows of large dark red blotches located dorsally on the body of *P. whiteheadi* (Chen and Shao 2002). Moreover, *P. yamakawai* varies from *P. sheni* by having the 4th dorsal spine as the longest instead of the 3rd spine.

Yoshino (1972) reported that there are two antrorse spines located on the lower margin of the preopercle, but our specimen shows three spines on the left side and only two on the right (Fig. 3). This apparent abnormality needs further verification and may be clarified through future specimen collections of this species.

A comparison of the measurements of the Philippine specimen and the holotype of this species is presented by recalculating Yoshino's (1972) proportional measurements as a percentage of the standard length and head length (Table 1). The majority of the morphological characters (12 of 18 or 67%) varied within 3 percentage points, indicating that the measurement taken from the Philippine specimen is close to the holotype. The result also indicates that all other morphological parameters, excluding interorbital width, post-orbital length, depth of caudal peduncle, and length of caudal peduncle, are greater in the specimen from the Philippines compared to the holotype. Some of the characters varied by as much as 10 percentage points, but this result is not unusual as some characters of paratypes of Yoshino (1972) also had similar variations.

The mitochondrial DNA sequence obtained from this study was submitted to GenBank under accession number OP614925 and serves as the first report on the cytochrome c oxidase subunit I gene (*COI*) of *Plectranthias yamakawai*. The BLAST analysis shows that there are no close matches of the Philippine sequence with the submitted sequences in GenBank. Pairwise genetic distances are shown in Table 2 and indicate that the Philippine sequence of *P. yamakawai* is closest to the *P. kamii* from Taiwan (KU943548) with a K2P distance of 9 percentage points. Moreover, the neighbor-joining tree (Fig. 4) constructed using the sequences of the nine different species of *Plectranthias*, shows that *P. yamakawai* is closest to *P. kamii*. The Philippine specimen, however, cannot be *P. kamii* since it has 36 lateral-line scales (Randall 1980; Peristiwady et al. 2018) whereas the Philippine specimen has only 31.

Conclusion

Reporting *Plectranthias yamakawai* as a new record from the Philippines is very important to update the information on the distribution of the organism as well as the current information on fishes occurring in the country.

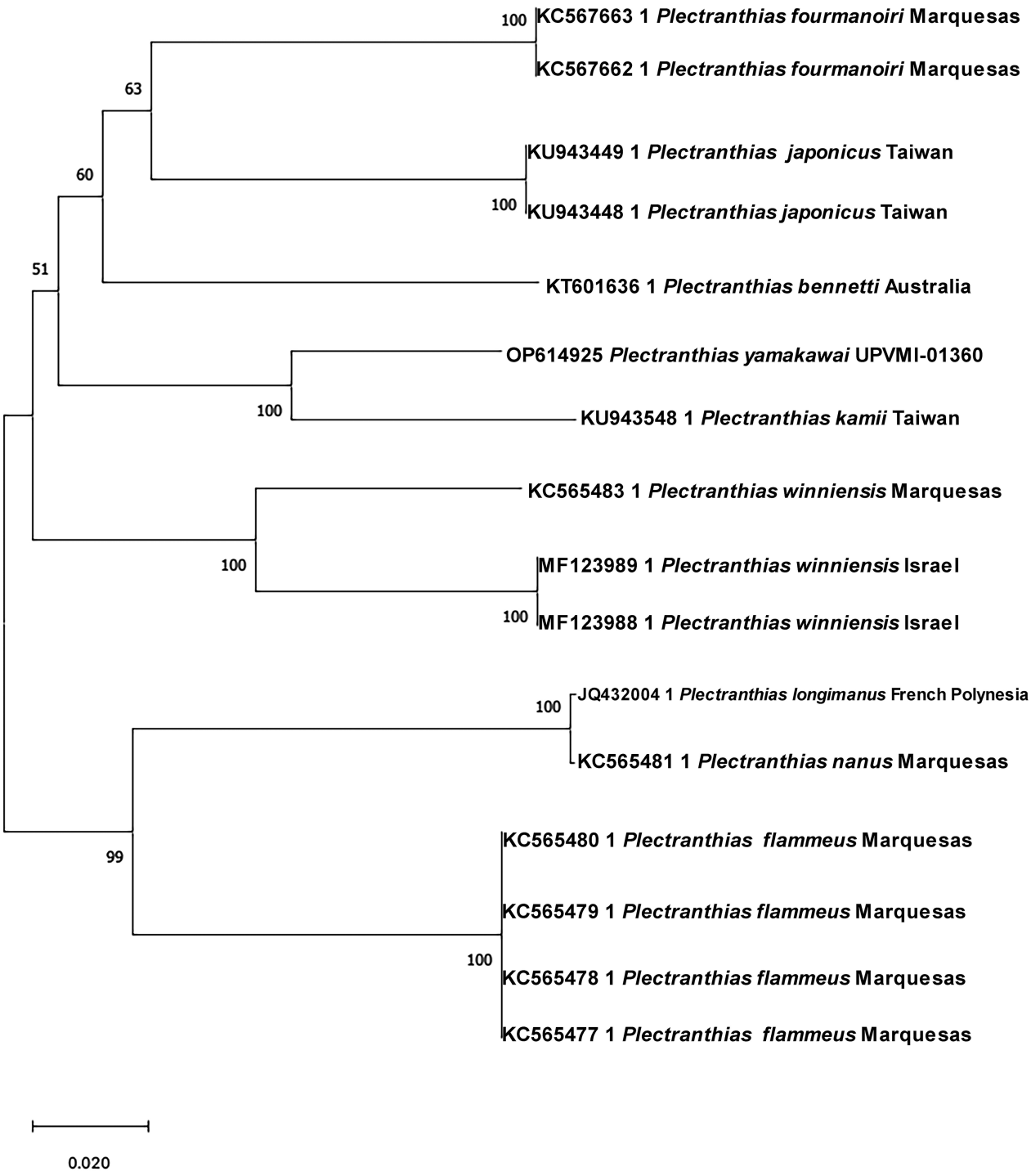

Figure 4. Phylogenetic tree constructed using the neighbor-joining tree method of only one *COI* sequence of *Plectranthias yamakawai* from the Philippines (this study) and the 15 sequences of eight different *Plectranthias* species from GenBank.

As a result of this study, six species of *Plectranthias* are now known to exist in the country. Furthermore, none of the five species of this genus previously reported in the Philippines presently have genetic information in GenBank. Since the majority of the species of *Plectranthias* were described using only one or two specimens and lacked genetic information, species identification is challenging. Therefore, studies such as this, and further documentation of other species in this group, will help in filling in data gaps.

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