European Journal of Taxonomy 1130: 1–18
https://doi.org/10.5852/ejt.2026.1130.3363
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europeanjournaloftaxonomy.eu
ISSN 2118-9773
2026 · Ho A.T. *et al.*

Received: 23 Sep. 2025 • *Accepted: 14 Oct. 2026* • *Published: 27 November 2026*

Topic editor: Tony Robillard • *Section editor: Felipe Ottoni* • *Desk editor: Eva-Maria Levermann*

Research article

urn:lsid:zoobank.org:pub:C860EEEE-B936-4ED0-8503-AF8CFC8D8DA8

Papuligobius quangi sp. nov., a new species of freshwater goby (Gobiiformes: Oxudercidae) from the Ngan Pho River basin, North Central region of Vietnam

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Abstract. Gobies (Gobiiformes) constitute an important component of the freshwater fish diversity of Vietnam. Here, we report a new species of freshwater gobiid in the genus *Papuligobius*, discovered in the Con River, a tributary of the Ngan Pho River basin in north-central Vietnam. Morphologically, the new species, *Papuligobius quangi* sp. nov. is readily distinguished from its congeners by a combination of characters, including 16–17 pectoral fin rays and 12–18 tiny papillae located below the eyes. In male specimens, the first dorsal fin comprises six spines, characterized by distal tips that extend into filamentous processes. These filaments are devoid of an interspinous membrane, with the third spine being the longest. Mitochondrial *COI* and *Cytb* data support the distinctiveness of *P. quangi*. Phylogenetic analyses recover the species as a well-supported monophyletic group sister to *P. uniporus*. Mean interspecific genetic distances between *P. quangi* and *P. uniporus* are 5.82% for *COI* and 5.30% for *Cytb,* while *Cytb* divergence from *P. ocellatus* reaches 8.95%. ASAP and bPTP analyses consistently delimit *P. quangi* as a separate molecular operational taxonomic unit (MOTU). These molecular results, together with the diagnostic morphological characters, support the recognition of *P. quangi* sp. nov. as a distinct species.

Keywords. *COI*, Con River, molecular phylogeny, morphological character.

Ho A.T., Hoang V.P., Hoang N.T., Huynh Q.T., Eljasik P. & Panicz R. 2026. *Papuligobius quangi* sp. nov., a new species of freshwater goby (Gobiiformes: Oxudercidae) from the Ngan Pho River basin, North Central region of Vietnam. *European Journal of Taxonomy* 1130: 1–18. https://doi.org/10.5852/ejt.2026.1130.3363

Introduction

The Ngan Pho River basin, located in Vietnam's North Central region, hosts a rich diversity of fish species, including a notable presence of gobies. A survey conducted between 2020 and 2022 documented 78 fish species in the basin, 39 of which were newly recorded in the area (Dinh *et al.* 2024). Gobies, especially those from the family Oxudercidae Günther, 1861, are notable for their abundance and ecological significance in both freshwater and estuarine ecosystems. A study in the Ka Long estuary identified 20 goby species, with Oxudercidae being the most dominant family (Ta *et al.* 2022). These findings suggest that a similar structure may be present in the Ngan Pho River basin. However, studies focused on ichthyofauna and genetic diversity are necessary to identify the composition and ecological roles of goby species in this region.

The genus *Papuligobius* Chen & Kottelat, 2003 is a distinct lineage of freshwater gobies endemic to Southeast Asia. Its designation was based on the type species *P. uniporus* Chen & Kottelat, 2003 collected in northern Laos. Members of this genus are distinguished by several morphological features, including the presence of minute cycloid scales on the prepectoral region, an additional terminal pore σ1 in the anterior oculoscapular canal positioned above the anterior nostril, tricuspid teeth in males, and a restricted gill opening that does not extend beyond the vertical through the middle of the opercle (Kottelat 2013).

Currently, two species are formally recognized within the genus: *Papuligobius uniporus* and *Papuligobius ocellatus* (Fowler, 1937), which are distributed in the Mekong River basin. *P. ocellatus* has been recorded in Southeast Asia (Laos, Thailand and Vietnam), whereas *P. uniporus* is known only from Vietnam and Laos (Kottelat 2013; Fricke *et al.* 2026). In Vietnam, *P. ocellatus* has been documented in the Hinh River (Hoang *et al.* 2024), while *P. uniporus* was reported in the Pu Mat National Park (Nguyen 2011).

During a survey of ichthyofaunal diversity in the main channel of the Con River, part of the Ngan Pho River basin in Son Hong Commune, Huong Son District, Ha Tinh Province, Vietnam, 27 specimens plausibly referable to the genus *Papuligobius* were collected. Therefore, the study aimed to characterise the collected specimens using a combination of morphological characteristics and molecular evidence, and propose a new species, *Papuligobius quangi* sp. nov. in this unique genus.

Material and methods

Sampling

Twenty-seven specimens (19 males and 8 females) were collected using a polyme net from the Con River, a tributary of the Ngan Pho River basin, located in Huong Son District, Ha Tinh Province, in the North Central Region of Vietnam (Fig. 1), in November 2024. Tissue samples for molecular analysis were collected individually using scissors from the lateral muscle of three specimens (two males and one female) and subsequently preserved in 90% ethanol until analysis. Whole individuals were fixed in 10% formaldehyde and later transferred in the laboratory to 4% formaldehyde for long-term storage. All specimens were deposited in the Biological Museum of Vinh University (BMVU), Nghe An, Vietnam.

Morphological analysis

All measurements and counts followed Chen and Kottelat (2003). Morphometric measurements were taken point-to-point using dial calipers to the nearest 0.01 mm. The following morphometric characters were recorded: standard length, head length, predorsal length (distance from the tip of the snout to the origin of the first dorsal fin), preanal length (distance from the tip of the snout to the origin of the anal fin); preanus length (distance from the tip of the snout to the anus); preventral length (distance from the tip of the snout to the origin of the pelvic fin); caudal peduncle depth (measured at the greatest depth, usually at the midpoint of the caudal peduncle); caudal peduncle length (distance from the posterior base of the anal fin to the base of the caudal fin); first dorsal-fin base length (distance from the base of the first to the last ray of the first dorsal fin); second dorsal-fin base length (distance from the base of the first to the last ray of the second dorsal fin); anal-fin base length (distance from the base of the first to the last ray of the anal fin); pectoral-fin length (distance from the fin base to the tip of the longest pectoral-fin ray); pelvic-fin length (distance from the fin base to the tip of the longest pelvic-fin ray); caudal-fin length (distance from the base of the caudal fin to the tip of the longest caudal-fin ray); body depth at pectoral-fin origin; body depth at anal-fin origin; body width at anal-fin origin; distance from pelvic-fin origin to anus; eye diameter (greatest diameter of the orbit); interorbital width (least distance between the upper margins of the two orbits); and snout length (distance from the tip of the snout to the anterior margin of the orbit).

Abbreviations for morphological terms

A = anal fin
C = caudal fin

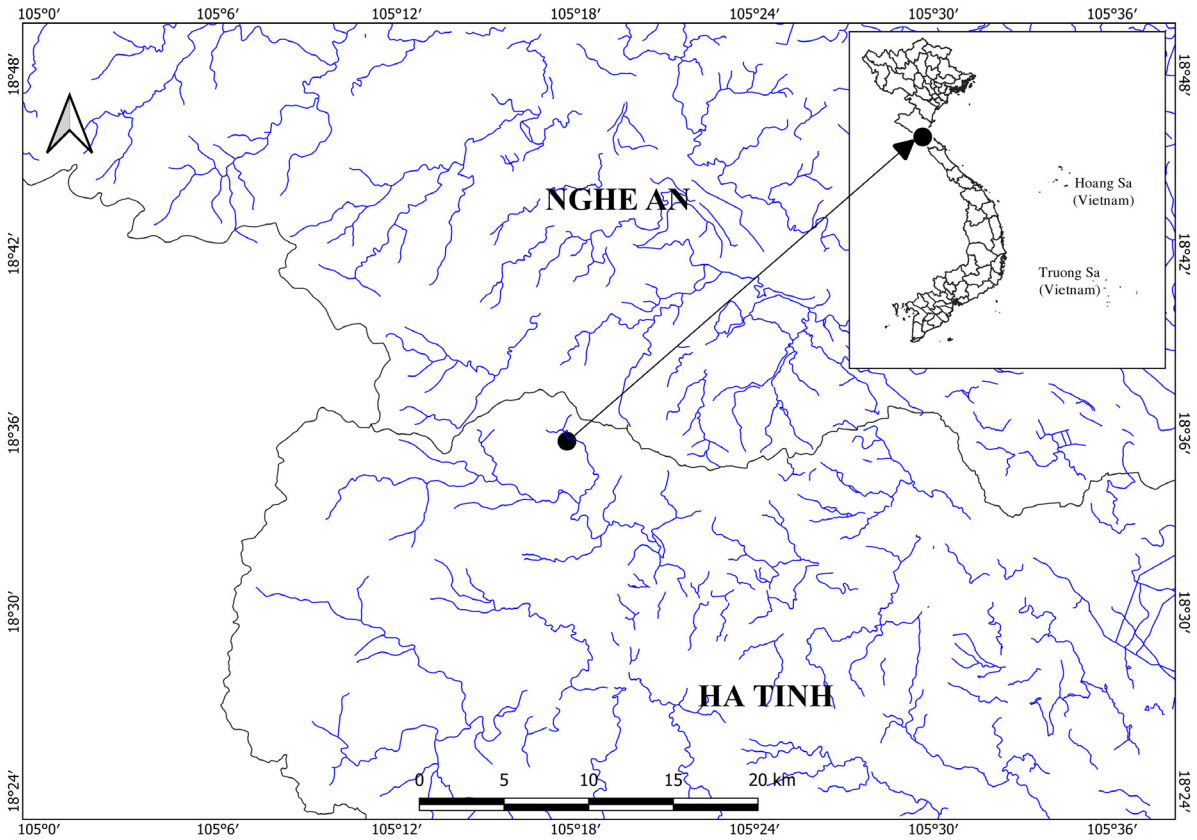


Fig. 1. Sampling location: Con River of the Ngan Pho River basin, North Central Vietnam.

D1 = first dorsal fin
D2 = second dorsal fin
HL = from the tip of the snout to the posterior margin of the operculum
LR = longitudinal scale series
P = pectoral fin
PreD = predorsal scales
SDP = scale series from origin of first dorsal fin to upper pectoral fin origin
SL = from the tip of the snout to the base of the caudal fin
TR = transverse scale series

Molecular analysis

Partial sequences of two mitochondrial genes, *COI* and *Cytb* were selected for genetic analysis. Genomic DNA was extracted from approximately 50 mg of lateral muscle tissue using the QIAamp DNA Mini Kit (QIAGEN, Germany). Qualitative and quantitative analyses of the DNA were performed by separation on 1% agarose gels and by spectrophotometric measurements using a NanoDrop 2000 spectrophotometer (Thermo Scientific, USA). Primer sets used for PCR amplification and sequencing are listed in Table 1.

The thermal profile began at 95ºC for 5 min, followed by 35 cycles of 95ºC (30 s), 52ºC (30 s), and 72ºC (90 s), with a final step of 7 min at 72ºC. PCR products were purified using the QIAquick Gel Extraction Kit (QIAGEN, Germany), and bidirectional sequencing was performed with the ABI BigDye Terminator Kit on an ABI PRISM 377-64 DNA Sequencer (Applied Biosystems) by SURAN Medical and Scientific Company (Vietnam).

Chromatograms were assembled and edited in Geneious ver. 8.0 (Kearse *et al.* 2012), and *COI* and *Cytb* sequences were compared to GenBank entries using BLAST (Altschul *et al.* 1990). Translation into amino acids was performed to verify sequence integrity and screen for potential nuclear pseudogenes, insertions, deletions, or premature stop codons. The obtained sequences were deposited in GenBank, and the details of the sequences used for genetic analyses are provided in Table 2.

Substitution saturation was assessed using Xia's test implemented in DAMBE7 (Xia 2018). Maximum-likelihood (ML) phylogenetic analyses were performed separately for *COI* and *Cytb* datasets using IQ-TREE ver. 3.1.1 (Wong *et al.* 2026). The best-fit substitution model was automatically selected using ModelFinder (Kalyaanamoorthy *et al.* 2017) implemented in IQ-TREE. Node support was assessed using 10 000 ultrafast bootstrap replicates (Hoang *et al.* 2018).

Luciogobius grandis Arai, 1970, a member of the subfamily Gobionellinae Bleeker, 1874 but outside the ingroup taxa, was selected as the outgroup for species delimitation analyses and ML tree rooting. Pairwise Kimura two-parameter distances were calculated in MEGA 12 (Kumar *et al.* 2024).

The species delimitation analyses were conducted using two complementary approaches: Assemble species by automatic partitioning (ASAP), and Bayesian poisson tree processes (bPTP). ASAP analysis was conducted using the ASAPy application with the following parameters: 1000 bootstrap replicates, Kimura two-parameter model, ts/tv: 2.0, and p-value threshold: 0.01 (Puillandre *et al.* 2021). bPTP analysis was performed on the ML tree using the bPTP application. The analysis ran for 10 0000 MCMC generations with a thinning of 100 and a burn-in of 0.25 (Zhang *et al.* 2013).

Fin-spines are in Roman numerals, fin-rays in Arabic.

Table 1. Primers used for PCR and sequencing reactions in this study.

Name	Sequence	Reference
*COI*_F	5'-TTCTCAACTAACCAYAAAGAYATYGG-3'	Kochzius *et al*. 2010
*COI*_R	5'-TAGACTTCTGGGTGGCCRAARAAYCA-3'	
*Cytb*_F	5'-TGACTTGAARAACCAYCGTTG-3'	Ryan & Esa 2006
*Cytb*_R	5'-CCCTCAGAATGATATTTGTCCTCA- 3'	

Table 2. List of sequences used for genetic analyses. Abbreviations: *COI* = *cytochrome c oxidase subunit I*; *Cytb* = *cytochrome b*; NA = not available.

Species/samples	GenBank/SRA	
	COI	***Cytb***
Papuligobius quangi sp. nov. holotype (BMVU202411001)	SRR34363242	SRR34362905
Papuligobius quangi paratype (BMVU202411017)	SRR34355893	SRR34362904
Papuligobius quangi paratype (BMVU202411020)	SRR34364156	SRR34362903
Papuligobius uniporus Chen & Kottelat, 2003	PQ331167.1	MT215242.1
Papuligobius ocellatus (Fowler, 1937)	NA	KF415628.1
Tridentiger bifasciatus Steindachner, 1881	OP498324.1	AB021254.1
Tridentiger trigonocephalus (Gill, 1859)	NC_029738.1	
Rhinogobius flumineus (Mizuno, 1960)	AB988823.1	LC633731.1
Rhinogobius leavelli (Herre, 1935)	NC_044964.1	
Luciogobius grandis Arai, 1970	NC_044715.1	

Results

Taxonomy

Class Actinopterygii Klein, 1885
Order Gobiiformes Bleeker, 1859
Family Oxudercidae Günther, 1861
Subfamily Gobionellinae Bleeker, 1874
Genus *Papuligobius* Chen & Kottelat, 2003

Papuligobius quangi sp. nov.
urn:lsid:zoobank.org:act:67687B12-31A8-44C9-A31C-D72A967382E5
Figs 2–7; Tables 2–5

Diagnosis

Papuligobius quangi sp. nov. exhibits all the diagnostic characteristics of the genus *Papuligobius* as described by Chen and Kottelat (2003): prepectoral area with minute cycloid scales; additional terminal pores σ1 on anterior oculoscapular canal above anterior nostril; distinct tricuspid teeth present in male; gill-opening restricted, never beyond vertical through midline of opercle; *cp* papilla single. Compared with species in the genus, *Papuligobius quangi* sp. nov. is distinguished from currently known species

of the genus *Papuligobius* by a combination of the following morphological characteristics: tiny papillae below the eyes 12–18; pectoral fin with 16–17 rays, vs 18–19 in *P. uniporus*, and 19–21 in *P. ocellatus*; scale series from origin of 1st dorsal fin to upper pectoral fin origin 10–11, higher than 8–9 in *P. uniporus* and 9–10 in *P. ocellatus*. In males, the first dorsal-fin spines prolonged distally into free filamentous extensions, a condition not known in other described species of *Papuligobius*.

Etymology

The specific epithet '*quangi*' honors Associate Professor Dr Hoang Xuan Quang for his significant contributions to vertebrate research at the Department of Zoology, Faculty of Biology, Vinh University, Vietnam. We recommend 'Cá bống quang' as the common name in Vietnamese for the new species.

Type material

Holotype

VIETNAM – **Ha Tinh Province** • ♂; Huong Son District, Con River of Ngan Pho River basin; 18°35′42″ N, 105°17′43″ E; 17 Nov. 2024; A.T. Ho and N.T. Hoang leg.; BMVU, BMVU.202411001.

Paratypes

VIETNAM – **Ha Tinh Province** • 18 ♂♂; same data as for holotype; BMVU, BMVU.202411002 to BMVU.20241119 • 8 ♀♀; same data as for holotype; BMVU, BMVU.2024111020 to BMVU.2024111027.

Description

Scale. First dorsal fin VI; second dorsal fin I/10½; anal fin I/9½; pectoral fin 16–17; pelvic fin I/5; longitudinal scale series 38–43; transverse scale series 14–17; predorsal scales 13–17; scale series from origin of first dorsal fin to upper pectoral origin 10–11.

Body. Elongate, subcylindrical; gradually tapering and compressed toward caudal peduncle. Body depth at pelvic-fin origin 5.73 (5.45–6.09) times in SL in males, 5.11 (4.64–5.53) in females; at anal-fin origin



Fig. 2. *Papuligobius quangi* sp. nov., holotype, ♂ (BMVU.202411001), 71.99 mm. Scale bar = 10 mm. Photograph: TAH.

5.87 (5.27–6.48) times in SL in males, 4.66 (4.20–5.09) in females. Body width at anal-fin origin 7.67 (7.18–8.54) times in SL in males, 7.54 (6.82–8.03) in females.

Head. Broad, slightly dorsoventrally flattened. Head length 3.19 (2.91–3.32) times in SL in males, 3.49 (3.25–3.67) in females; maximum head width 1.62 (1.50–1.75) times in HL in males, 1.45 (1.43–1.47) in females; minimum head width 1.44 (1.26–1.59) times in HL in males, 1.40 (1.26–1.53) in females.

Snout. Blunt, with a relatively short interorbital distance. Snout length 3.21 (2.92–3.48) times in HL in males, 3.08 (2.82–3.49) in females; eye diameter 5.58 (4.98–6.06) times in HL in males, 4.40 (4.17–4.65)

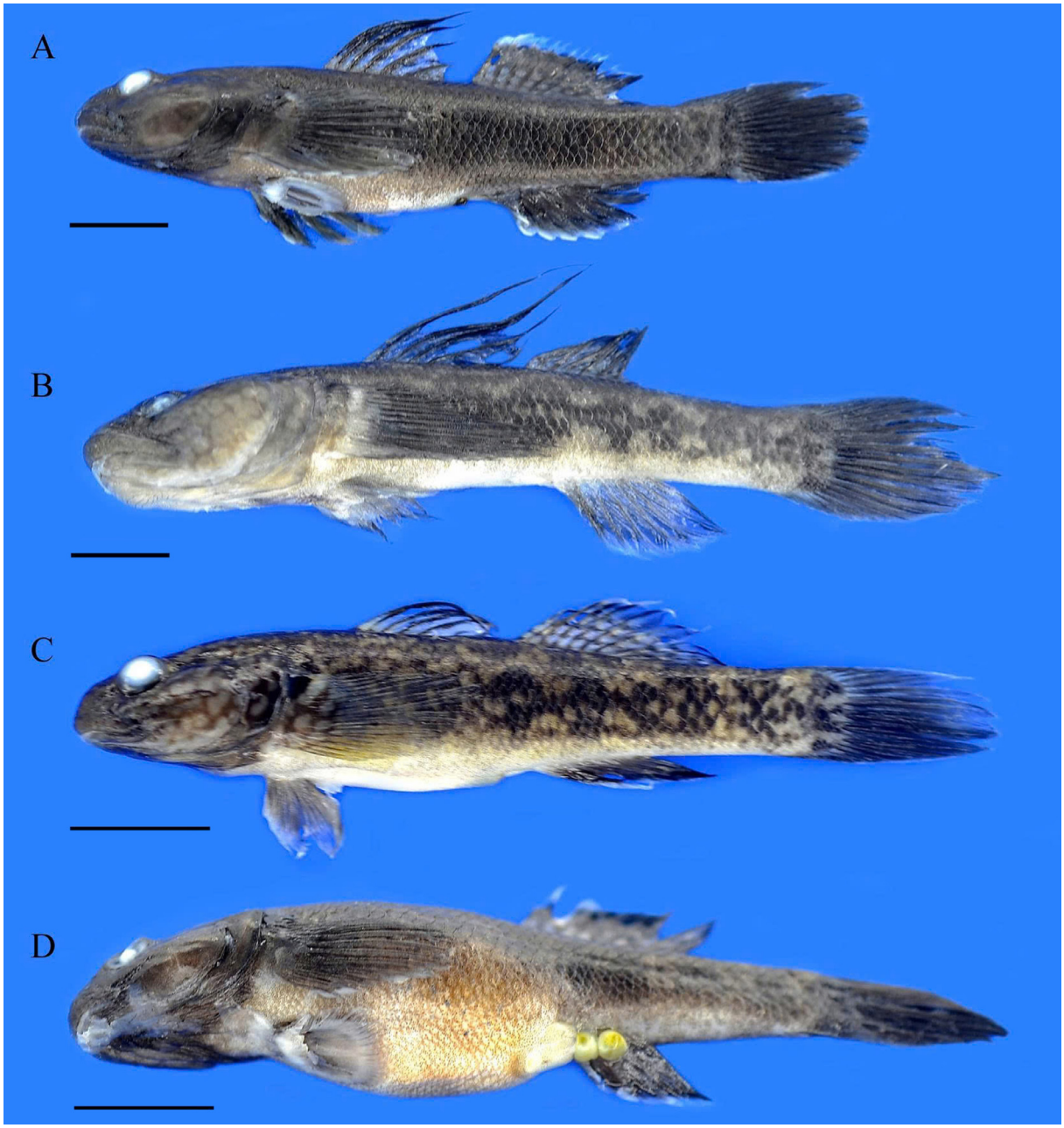


Fig. 3. *Papuligobius quangi* sp. nov. **A**. Paratype, ♂ (BMVU.202411018), lateral view. **B**. Paratype, ♂ (BMVU.202411019), lateral view. **C**. Paratype, ♀ (BMVU.202411020), lateral view. **D**. Paratype, ♀

in females; fleshy interorbital width 4.16 (3.39–4.75) times in HL in males, 3.35 (3.02–3.78) in females. The percentages of body parts relative to SL and HL of *Papuligobius quangi* sp. nov are shown in Table 3.

Mouth region. Cheek well developed, obliquely oriented, with a relatively wide gape. A distinctive feature is the chin area, which exhibits a complex texture of intersecting longitudinal and transverse grooves, giving the underside of the head a wrinkled appearance. Mouth terminal to slightly subterminal, with thick lips. Both jaws bear 2–3 rows of conical teeth, with the outer row comprising tricuspid teeth. Vomerine teeth absent.

Eyes. Rather large, positioned dorso-laterally on head.

Fins. First dorsal fin VI; in males, all spines prolonged distally into slender filamentous extensions projecting beyond the fin membrane most developed in the anterior spines. In females, first dorsal fin is lower, lacking pronounced filamentous extensions. Second dorsal fin I,10½, its origin approximately opposite to anal-fin origin. Anal fin I,9½, situated directly opposite to second dorsal fin, similar in shape but slightly shorter. Pectoral fins 16–17, posterior margin slightly rounded. Pelvic fins I,5, fused medially

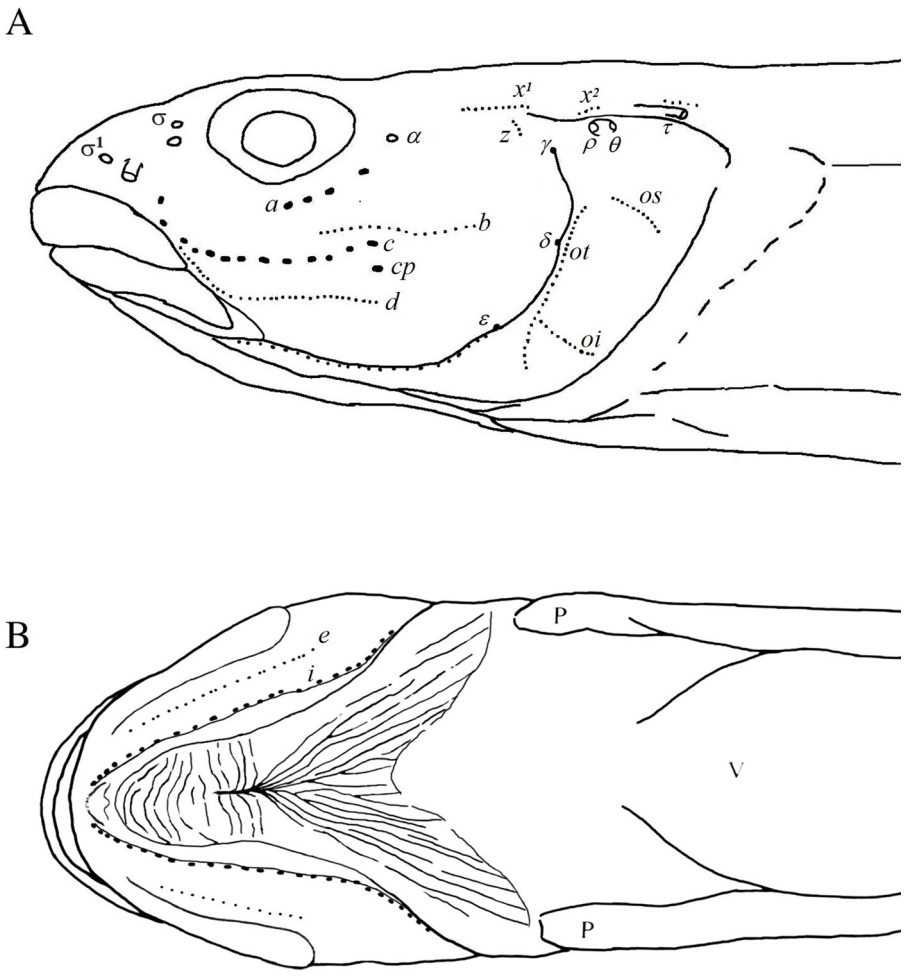


Fig. 4. Head lateral-line system in *P. quangi* sp. nov., paratype, ♂ (BMVU.202411016). **A**. Lateral view. **B**. Ventral view. Illustrator: HNT.

to form a broad, rounded suction disc. Caudal fin 13–15 rays, moderately wide, truncate to slightly rounded.

Head lateral-line system and sensory papillae. The cephalic lateral-line canal system (Fig. 4) is generally consistent with that of other species of *Papuligobius*, apart from row *b*, which contains fewer papillae (12–18 vs 23–26). The nasal extension of the anterior oculoscapular canal with pores *σ*1 slightly in front of the anterior nostril; pore *σ* above the posterior nostril; pore *a* in postocular; pores *r* and *q* are separated open into a single large pit; the preopercular canal contains pores *γ, δ*, and *ε*. Row *a* extends vertically to the middle of the orbit; row *b* is relatively long, with 12–18 tiny papillae densely set; rows *c* and *d* are long and reach the vertical through pore *σ*; papillae in rows *a* and *c* are larger than those in rows *b* and *d*; a single *cp* papilla; in the opercular, rows *ot* and *os* are distinct and separate, while *ot* and *oi* are slightly connected.

Coloration. In life, the body exhibits a generally dark brown to grey colouration, with the dorsal region appearing slightly darker than the ventral side. Scattered irregularly across the body are lighter-colored spots, which contrast subtly with the darker scales. These pale spots are not arranged in any consistent or predictable pattern, giving the fish a mottled appearance. In preserved specimens, the body coloration becomes paler and less contrasting, though the dorsal region remains darker than the ventral side (Fig. 3).

Sexual dimorphism. *Papuligobius quangi* sp. nov. exhibits marked sexual dimorphism. In males, the spines of the first dorsal fin are prolonged distally into filamentous extensions where the interspinous membrane is absent (Fig. 3). Males are also larger than females of the same age class. The urogenital papilla is sexually distinct: in females, it is tubular with a flattened tip, while in males it is pointed (Fig. 5).

Key to the species of *Papuligobius* Chen & Kottelat, 2003

1. Pectoral fin rays modally 16–17; sensory papillae below the eyes 12–18 (Ngan Pho River) ..... ***P. quangi*** sp. nov
– Pectoral fin rays more than 17; sensory papillae below the eyes 23–26 2

2. Scales in longitudinal series 34–37; pectoral fin rays modally 18–19 (Nam Mat basin) ..... ***P. uniporus*** Chen & Kottelat, 2003
– Scales in longitudinal series 40–43; pectoral fin rays modally 19–21 (Mekong basin) ..... ***P. ocellatus*** (Fowler, 1937)

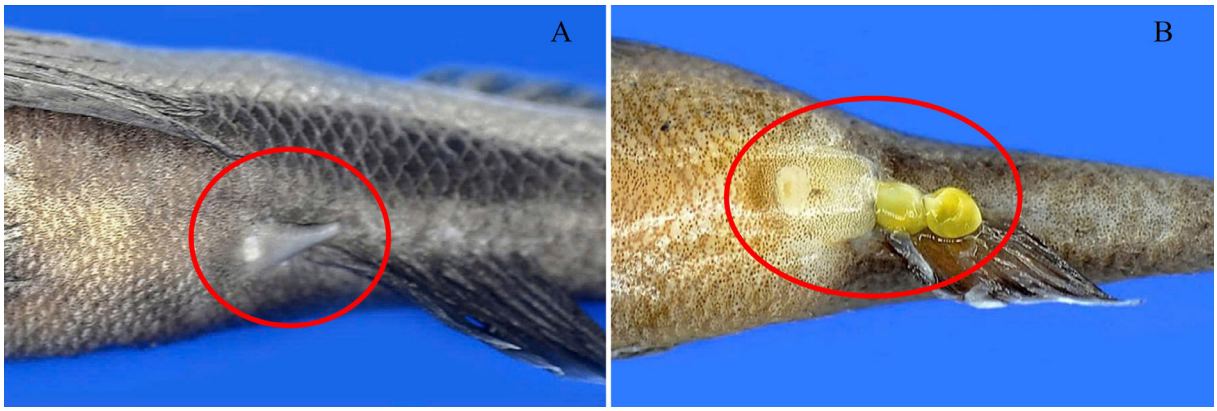


Fig. 5. The anus and urogenital papilla in *Papuligobius quangi* sp. nov. **A**. Holotype, ♂ (BMVU.202411001). **B**. Paratype, ♀ (BMVU.202411022). Photographs: HAT.

Table 3. Morphometrics of *P. quangi* sp. nov. from Ha Tinh Province, Vietnam.

	holotype (male)	**holo- + paratypes** (males: n = 19)			**paratypes** (females: n = 8)		
		mean	min	max	mean	min	max
standard length (mm)	71.99	70.66	63.49	78.35	56.10	53.22	59.60
in percents of SL							
head length	34.35	31.38	30.08	34.35	28.70	27.27	30.74
predorsal length	41.51	38.72	36.65	41.51	37.56	35.77	39.20
snout to 2nd dorsal fin origin	60.37	60.36	58.75	62.27	59.82	57.87	61.12
snout to anus	59.04	58.88	56.51	61.22	60.35	56.85	62.77
snout to anal fin origin	63.20	64.18	63.01	66.84	64.42	62.30	66.88
snout to pelvic fin origin	31.95	31.85	30.11	33.55	29.74	28.43	31.90
depth of caudal peduncle	10.77	11.24	10.77	11.55	11.43	10.56	12.06
length of caudal peduncle	23.41	23.24	21.00	24.25	22.14	20.77	23.69
first dorsal fin base	20.64	19.11	17.08	21.30	20.50	18.50	21.80
second dorsal fin base	18.77	18.08	16.98	19.60	18.97	17.59	20.24
anal fin base	13.29	13.21	12.61	13.60	14.13	12.42	14.72
pectoral fin length	30.56	27.65	24.07	32.49	25.95	25.24	26.80
caudal fin length	26.70	25.12	22.76	29.36	25.82	24.16	27.70
pelvic fin length	16.29	15.59	13.45	17.85	16.44	15.74	16.88
body depth at pelvic fin origin	16.97	17.47	16.43	18.33	19.62	18.09	21.53
body depth at anal fin origin	16.95	17.07	15.43	18.97	21.53	19.65	23.83
body width at anal fin origin	11.71	13.06	11.71	13.93	13.29	12.45	14.66
pelvic fin origin to anus	29.46	28.98	27.10	31.30	30.85	26.70	35.14
in percentage of HL							
snout length	29.76	31.20	28.71	34.23	32.68	28.66	35.43
eye diameter	17.71	17.98	16.49	20.09	22.72	21.51	23.96
postorbital length	59.60	58.23	54.81	60.60	52.49	50.13	55.39
cheek depth	39.47	38.54	35.74	42.17	35.25	32.68	37.80
maximal head width	67.12	69.87	62.87	79.60	71.53	65.36	79.17
minimal head width	58.07	61.89	57.03	66.82	68.76	67.93	70.01
fleshy interorbital width	23.78	24.13	21.04	29.53	29.93	26.45	33.08
lower jaw length	36.68	38.79	35.88	42.31	35.06	33.05	36.63
caudal peduncle depth/length	45.99	48.46	44.93	54.89	46.38	46.01	46.52
pelvic fin length/pelvic fin origin to anus	55.30	53.87	42.97	62.42	50.67	49.94	51.00

Comparison

Morphologically, *P. quangi* shares many meristic traits with *P. uniporus* and *P. ocellatus*, including similar counts of dorsal, anal, and pelvic fin rays, transverse scale series, predorsal scales, and vertebrae (Table 4).

Table 4. Meristics of the species of *Papuligobius* Chen & Kottelat, 2003.

	***P. quangi* sp. nov.**	***P. uniporus* Chen & Kottelat, 2003**	***P. ocellatus* (Fowler, 1937)**
first dorsal fin	VI	VI	VI
second dorsal fin	I/10½	I/9–10	I/9–11
anal fin	I/9½	I/8–9	I/8–9
pectoral fin	16–17	18–19	19–21
pelvic fin	I/5	I/5+I/5	I/5
longitudinal scale series	38–43	34–37	40–43*
transverse scale series	14–17	14–17	14–17*
predorsal scales	13–17	14–17	10–20
scale series from origin of first dorsal fin to upper pectoral origin	10–11	8–9	9–10
vertebrae	26	26	26

*According to Rainboth (1996), the longitudinal scale series ranges from 47 to 50, and the transverse scale series ranges from 15 to 17. Data of *P. uniporus* and *P. ocellatus* obtained from Chen & Kottelat (2003).

However, it is distinguishable by several key biometric features. The pectoral fin of *P. quangi* sp. nov. bears 16–17 rays, fewer than in *P. uniporus* (18–19) and *P. ocellatus* (19–21). Its longitudinal scale series count (38–43) overlaps with that of *P. ocellatus* (40–43) but exceeds that of *P. uniporus* (34–37). Additionally, the scale series extending from the origin of the first dorsal fin to the upper origin of the pectoral fin (SDP) in *P. quangi* (10–11) is higher than in *P. uniporus* (8–9) and *P. ocellatus* (9–10) (Fig. 6).

Morphological evidence provided above supports the recognition of *P. quangi* sp. nov. as a valid and previously undescribed species. Furthermore, based on the description by Rainboth (1996), the longitudinal scale series of *P. ocellatus* (referred to therein as *Rhinogobius ocellatus*) is notably higher than that of *P. quangi* (47–50 vs 38–43), and it possesses an anal-fin ray count of I/10 compared to I/9½ in *P. quangi*.

In terms of morphometrics, *Papuligobius quangi* sp. nov. differs from *P. uniporus* in several characters, with consistent differences observed in both males and females. Expressed as percentages of standard length (SL), *P. quangi* generally exhibits lower values than *P. uniporus* in the following measurements: head length (♂: 31.38 vs 32.90; ♀: 28.70 vs 31.50), predorsal length (♂: 38.72 vs 41.30; ♀: 37.56 vs 39.70), snout to pelvic-fin origin (♂: 31.84 vs 34.70; ♀: 29.74 vs 34.20), anal-fin base length (♂: 13.21 vs 15.00; ♀: 14.13 vs 14.30), pelvic-fin length (♂: 15.59 vs 18.70; ♀: 16.44 vs 19.60), and body depth at pelvic-fin origin (♂: 17.47 vs 21.60; ♀: 19.62 vs 20.00).

In contrast, *P. quangi* sp. nov. shows higher values for pectoral-fin length (♂: 27.65 vs 25.30; ♀: 25.95 vs 25.20), caudal-fin length (♂: 25.12 vs 23.80; ♀: 25.82 vs 23.40), and first dorsal-fin base length (♂: 19.11 vs 14.30; ♀: 20.50 vs 16.40). The most pronounced differences between the two species are observed in the following proportions: distance from pelvic-fin origin to anus (♂: 28.98 vs 23.40; ♀: 30.85 vs 23.20), depth of the caudal peduncle (♂: 11.24 vs 30.20; ♀: 11.43 vs 25.50), and length of the caudal peduncle (♂: 23.24 vs 11.90; ♀: 22.14 vs 10.70).

Further distinct differences are observed between the two species: *P. quangi* sp. nov. exhibits higher values than *P. uniporus* in the following ratios: snout length in HL (♂: 31.20 vs 28.50; ♀: 32.68 vs

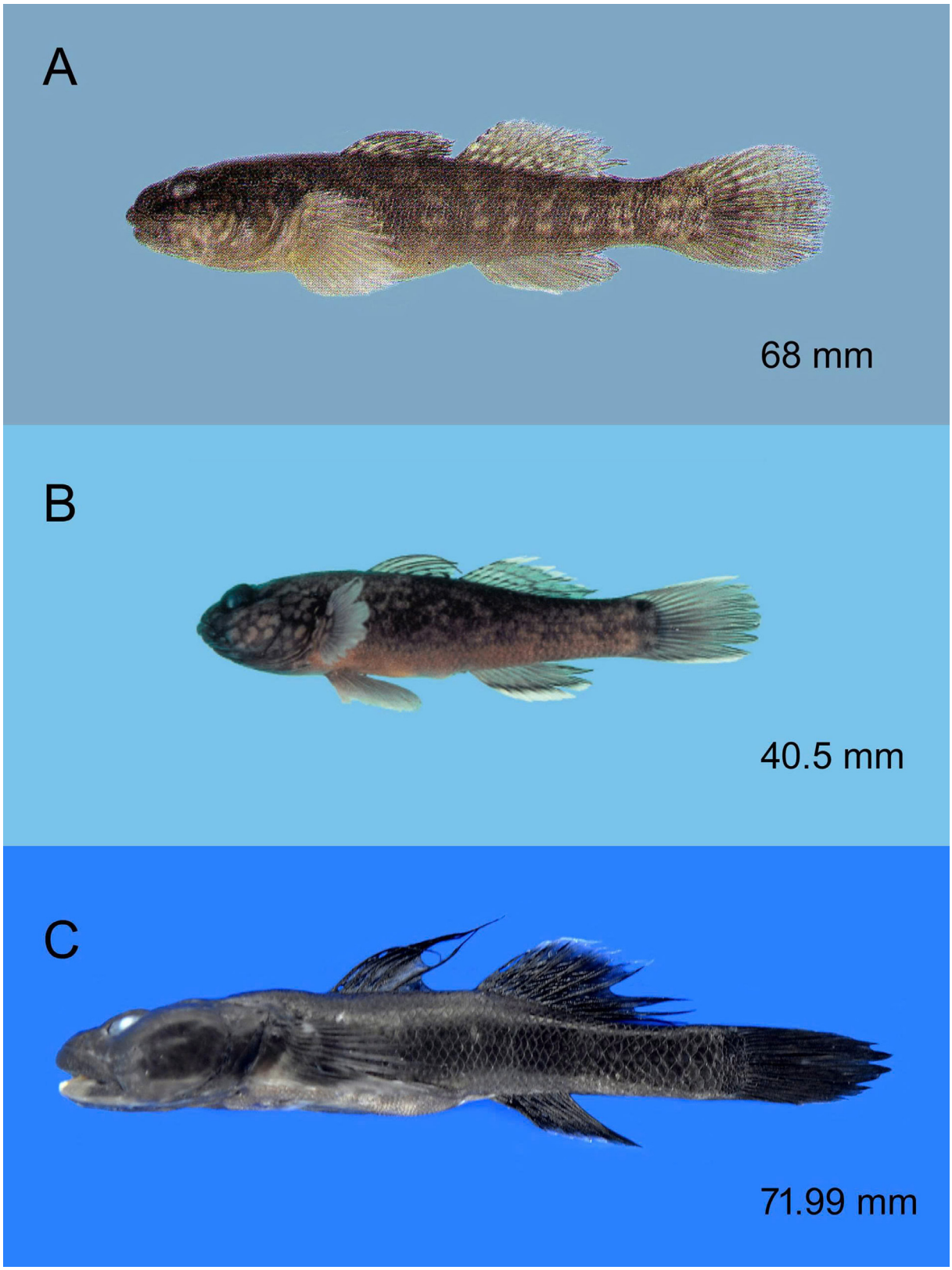


Fig. 6. Lateral views of species of *Papuligobius* Chen & Kottelat, 2003. **A**. *P. ocellatus* (Fowler, 1937), reproduced from Kottelat (2001: fig. 444). **B**. *P. uniporus* Chen & Kottelat, 2003, reproduced from Kottelat (2001: fig. 445). **C**. *P. quangi* sp. nov., holotype, ♂ (BMVU.202411001).

31.90); fleshy interorbital width in HL (♂: 24.13 vs 22.80; ♀: 29.93 vs 22.50), and lower jaw length in HL (♂: 38.79 vs 34.70; ♀: 35.06 vs 32.80). In contrast, *P. quangi* shows markedly lower values than *P. uniporus* in eye diameter in HL (♂: 17.98 vs 27.90; ♀: 22.72 vs 26.20), and maximum head width in HL (♂: 69.87 vs 82.20; ♀: 71.53 vs 77.70). The most pronounced differences between the two species are found in cheek depth in HL (♂: 38.54 vs 19.30; ♀: 35.25 vs 17.70), and minimum head width in HL (♂: 61.89 vs 50.5; ♀: 68.76 vs 48.7). Several additional ratios further distinguish the two species. The ratio of caudal peduncle depth to length is higher in *P. quangi* (♂: 48.46, ♀: 46.38) than in *P. uniporus* (♂: 42.0, ♀: 41.9). Conversely, the ratio of pelvic-fin length to the distance from pelvic-fin origin to anus is markedly lower in *P. quangi* (♂: 53.87, ♀: 50.67) than in *P. uniporus* (♂: 80.7, ♀: 84.6).

Papuligobius ocellatus was originally described by Fowler (1937) as *Tukagobius ocellatus*. In the original description, morphometric data were provided collectively for all five specimens (one holotype and four paratypes), without separating males and females. Nevertheless, several proportional differences can be identified between *P. quangi* sp. nov. and *P. ocellatus*. In *P. ocellatus*, the ratio of SL to head length ranges from 3.0 to 3.17, whereas in *P. quangi* it is 3.19 (2.91–3.32) in males and 3.49 (3.25–3.67) in females. The ratio of HL to eye diameter in *P. ocellatus* ranges from 5.33 to 5.75, and snout length to eye diameter from 2.6 to 2.75. In comparison, *P. quangi* shows HL/eye diameter values of 5.58 (4.98–6.06) in males and 4.40 (4.17–4.65) in females, and snout length/eye diameter values of 1.74 (1.58–2.07) in males and 1.44 (1.25–1.60) in females.

The ratio of HL to interorbital width in *P. ocellatus* ranges from 6.0 to 7.25, whereas in *P. quangi* sp. nov. it is lower, at 4.16 (3.39–4.75) in males and 3.35 (3.02–3.78) in females. Taki (1974) subsequently redescribed *P. ocellatus* as *Ctenogobius ocellatus*; based on that account, the ratio of SL to body depth in *P. ocellatus* is 4.9–5.8, compared with 5.73 (5.45–6.09) in males and 5.11 (4.64–5.53) in females of *P. quangi*.

Distribution

Papuligobius quangi sp. nov. is currently known only from the main channel of the Con River, within the Ngan Pho River basin, Son Hong commune, Huong Son district, Ha Tinh Province, North Central Vietnam.

Maximum Likelihood phylogenetic tree

Maximum Likelihood (ML) phylogenetic analyses based on the mitochondrial *Cytb* and *COI* datasets consistently recovered the three examined specimens of *P. quangi* sp. nov. (BMVU.202411001, BMVU.202411017, and BMVU.202411020) as a well-supported monophyletic group (Fig. 7). In both gene trees, the *P. quangi* clade was positioned as sister to *Papuligobius uniporus*, highlighting their close phylogenetic relationship within the genus. Additional codon-partitioned analyses yielded congruent topologies and therefore only the main ML tree is presented.

Pairwise genetic distance matrices further supported the status of *P. quangi* sp. nov. as an independent evolutionary lineage, demonstrating a pronounced and well-defined barcoding gap between intra- and interspecific variations (Table 5). Within *P. quangi*, intraspecific distances ranged from 0.0% to 1.26% for *Cytb* (with zero sequence divergence between BMVU.202411001 and BMVU.202411017) and from 0.62% to 1.68% for *COI*. In contrast, interspecific genetic differentiation from its closest congeners was remarkably high. For the *Cytb* marker, *P. quangi* differed by an average of 5.3 % from *P. uniporus* and 8.95 % from *P. ocellatus*. For the *COI* marker, divergence between the new species and *P. uniporus* ranged from 5.76% to 5.95%, while its divergence from the remaining outgroup gobioid taxa exceeded 18.0%.

Table 5. Pairwise genetic distances between specimens of *Papuligobius quangi* sp. nov. and its closest congeners based on *Cytb* and *COI* sequences using the Kimura two-parameter model in MEGA 12. Values are presented as ranges and mean percentages.

Gene	Comparison	Range (%)	Mean (%)
Cytb	within *P. quangi* sp. nov.	0.00–1.26	0.84
	P. quangi vs *P. uniporus* Chen & Kottelat, 2003	4.88–5.84	5.30
	P. quangi vs *P. ocellatus* (Fowler, 1937)	8.46–9.68	8.95
COI	within *P. quangi*	0.62–1.68	1.08
	P. quangi vs *P. uniporus*	5.76–5.95	5.82

The *P. quangi* lineage was recovered as sister to *P. uniporus* and *P. ocellatus*, indicating a close phylogenetic relationship between the two taxa (Fig. 7). Phylogenetic relationships inferred from *Cytb* and *COI* sequences were largely congruent and consistently recovered *P. quangi* sp. nov. as a distinct monophyletic group.

Species delimitation analyses

Species delimitation analyses based on both *Cytb* and *COI* datasets utilizing ASAP and bPTP approaches yielded highly congruent results, consistently validating *P. quangi* sp. nov. as a distinct, independent species-level lineage. For both genetic markers, the ASAP analyses successfully separated the new species from its closest congeners, including *Papuligobius uniporus* and *Papuligobius ocellatus*. Under the best-scoring *COI* partition (ASAP score: 2.00; probability: 0.495), all three specimens of *P. quangi* were assigned to a single Molecular Operational Taxonomic Unit (MOTU). Similarly, the second-ranked *Cytb* partition (ASAP score: 3.0) recovered all three specimens as a single cohesive MOTU. Although the top-ranked *Cytb* partition (ASAP score: 1.5) further separated the slightly divergent specimen BMVU.202411020 from the remaining two, these minor internal discrepancies affected only the intraspecific structure of the new species and did not influence its robust interspecific separation from other examined taxa.

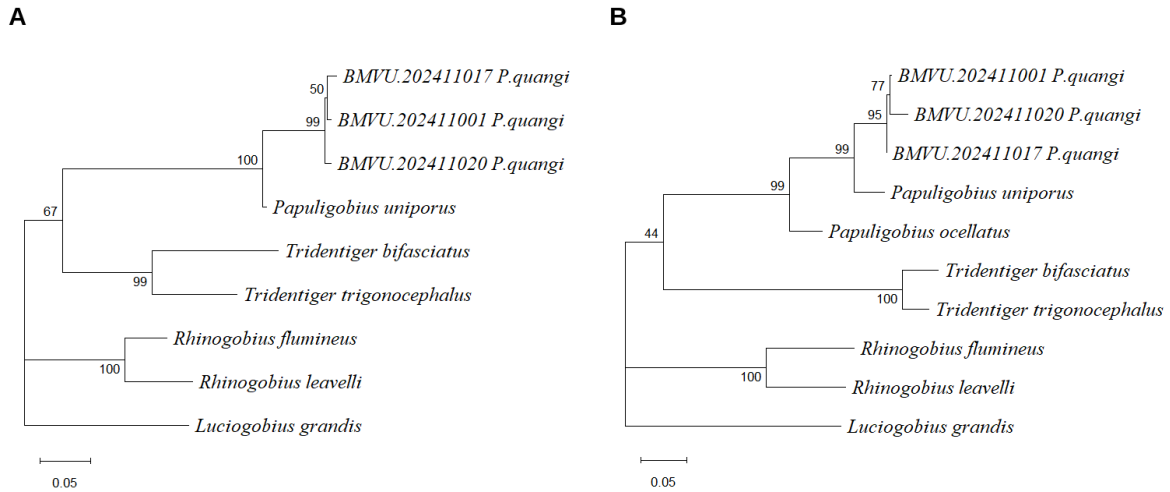


Fig. 7. Maximum Likelihood (ML) phylogenetic trees of the genus *Papuligobius* Chen & Kottelat, 2003. **A**. Tree topology derived from the mitochondrial *COI* dataset (1572 bp). **B**. Tree topology derived from the mitochondrial *Cytb* dataset (1122 bp). Numbers at nodes represent ML bootstrap support values.

The Bayesian poisson tree processes (bPTP) analyses further consolidated these findings across both datasets with identical support values. In both the *COI* and *Cytb* bPTP models, all three specimens of *P. quangi* sp. nov. were delimited as a single, unified species unit with an identical posterior probability support value of 0.769. While specimen BMVU.202411020 exhibited a slightly divergent position within the *Cytb* clade, statistical support for further subdivision was negligible, indicating insufficient evidence for internal lineage splitting. Furthermore, the bPTP analyses strongly rejected alternative lumping hypotheses; for instance, the *COI* model combining *P. quangi* and *P. uniporus* into a single species received remarkably low support (PP: 0.187), whereas *P. uniporus* was independently validated as a distinct entity with high confidence (PP: 0.802). Together with the congruent Maximum Likelihood (ML) topologies and pronounced pairwise genetic distances, these multi-locus species delimitation analyses provide robust, mutually reinforcing evidence for the recognition of *P. quangi* as an independently evolving lineage.

Discussion

The congruent results from both distance-based (ASAP) and coalescent–based (bPTP) delimitation models provide robust molecular evidence for the validity of *P. quangi* sp. nov. By collapsing the examined specimens into a single, statistically well-supported MOTU and explicitly rejecting a lumping hypothesis with its sister taxon, *P. uniporus*, these analyses confirm the existence of a distinct barcoding gap.

The single incongruence, the splitting of specimen BMVU.202411020 by the top *Cytb* ASAP partition, is best interpreted as an artifact of algorithmic over-splitting driven by localized haplotype variation or incomplete lineage sorting (Puillandre *et al.* 2021). Because a morphological re-examination proved this specimen is phenotypically identical to the other types in all diagnostic meristic and qualitative traits, the morphological uniformity effectively overrules the distance-based genetic split, framing this variation as intraspecific polymorphism rather than true evolutionary divergence.

This multi-locus genetic framework aligns seamlessly with morphological divergence, satisfying the rigorous criteria of integrative taxonomy (Dayrat 2005; Padial *et al.* 2010) and mitigating the risks of taxonomic inflation inherent to single-criterion diagnoses (De Queiroz 2007). The interspecific genetic distances separating *P. quangi* sp. nov. from *P. uniporus* and *P. ocellatus* substantially exceed the established intraspecific thresholds for gobioid fishes (Ward *et al.* 2005), matching clear-cut morphological boundaries.

While retaining the diagnostic synapomorphies of *Papuligobius*, the new species is easily diagnosed from *P. uniporus* and *P. ocellatus* by discrete differences in pectoral-fin ray counts, predorsal-pectoral scale rows, and suborbital papillae density. Most crucially, the prolonged, free filamentous dorsal spine extensions observed in adult males serve as an unmistakable, unique autapomorphy. Together, these congruent lines of genetic and morphological evidence establish *P. quangi* sp. nov. as a discrete, unambiguous evolutionary unit.

The genus *Papuligobius* was originally diagnosed based on a unique combination of cephalic sensory papillae patterns, pore arrangements, tricuspid teeth in males, and a restricted gill opening (Chen & Kottelat 2003). The molecular results obtained here provide additional support for the taxonomic distinctiveness of *Papuligobius* and offer new insights into its evolutionary position among East Asian freshwater gobies. The recovery of *Papuligobius* as a well-supported monophyletic group in both *COI* and *Cytb* analyses confirms that these morphological traits correspond to an independently evolving evolutionary unit rather than representing convergent adaptations.

Although Wei *et al.* (2025) recently suggested synonymizing *Papuligobius* with *Tridentiger*, the present results neither contradict the distinctiveness of the new species nor diminish the taxonomic significance of its diagnostic characters. Pending broader systematic revision of the group, we follow the current classification adopted by Eschmeyer's Catalog of Fishes and retain *P. quangi* sp. nov. Regardless of future generic assignment, the combined molecular and morphological evidence unequivocally supports the status of this taxon as a valid species.

Funding

This research received no external funding.

Data availability

Data supporting this manuscript will be available from the corresponding author upon reasonable request.

Author contribution

Conceptualization, Data curation: HAT, HVP. Methodology: all authors. Resources: HQT, HNT, PE. Investigation: HAT, HVP, HQT, HNT. Formal analysis: HAT, HVP, HNT, HQT, EP, PE. Writing – original draft: HAT, HVP, HQT. Supervision, visualization HNT, PE, RP. Validation: RP. Writing – review and editing: HAT, HVP, HNT, HQT, EP, PE.

Ethical approval

All samples in this study are not listed among endangered or rare aquatic species according to Decree No. 26/2019/ND-CP of the Government of Vietnam. Sampling was conducted using standard ichthyological procedures that did not involve harmful experimentation on live animals. No protected species were harmed.

Acknowledgments

We extend our sincere gratitude to Nguyen Thi Kim Chung (Centre for Experimental Practices, Vinh University) and Hoang Nghia Cong (Pu Mat National Park, Nghe An Province) for their instrumental support with map construction and laboratory analyses. We also thank Assoc. Prof. Dr Ngoc Yen Tran (Department of Foreign Languages, Vinh University) for English language editing. We express our sincere gratitude to Dr Maurice Kottelat for his monumental work "Fishes of Laos" (2001), which provided invaluable morphological data and comparative iconography (specifically figs 444–445) essential for diagnosing and establishing the boundaries of *P. quangi* sp. nov. against its congeners, *P. uniporus* and *P. ocellatus*.

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The members of the *EJT* consortium are: Muséum national d'Histoire naturelle, Paris, France; Royal Museum for Central Africa, Tervuren, Belgium; Royal Belgian Institute of Natural Sciences, Brussels, Belgium; Meise Botanic Garden, Meise, Belgium; Natural History Museum of Denmark, Copenhagen, Denmark; Naturalis Biodiversity Center, Leiden, the Netherlands; Museo Nacional de Ciencias Naturales-CSIC, Madrid, Spain; Leibniz Institute for the Analysis of Biodiversity Change, Bonn – Hamburg, Germany; National Museum of the Czech Republic, Prague, Czech Republic; The Steinhardt Museum of Natural History, Tel Aviv, Israel.