A NEW GENUS OF Hemigobius GENERIC GROUP GOBY BASED ON MORPHOLOGICAL AND MOLECULAR EVIDENCE, WITH DESCRIPTION OF A NEW SPECIES

Shih-Pin Huang¹, Jaafar Zeehan², and I-Shiung Chen¹

Key words: new genus, new species, brackish water, mangrove.

ABSTRACT

Wahanlinigobius, a new genus of Hemigobius generic group would been established and assign from Mugilogobius polylepis Wu and Ni, 1985. Mugilogobius polylepis has been regarded as belong to genus Eugnathogobius based on lacking head pores and representing longitudinal sensory papillae in previous taxonomic study. However, we compared the osteological features of Mugilogobius polylepis Wu and Ni, 1985 and Eugnathogobius microps Smith, 1931 as well as the molecular phylogenetic analysis based on the mtDNA ND5, Cyt-b genes and D-loop region. The molecular phylogenetic tree including 9 related Hemigobius generic group reveal that this new genus represents an independent clade which is well separate from other related Hemigobius generic group. The papillae pattern, osteological features and molecular evidence strongly conclude that Eugnathogobius polylepis should be a new genus of Hemigobius generic group, on the other hand, an additional new species of Wahanlinigobius also will be described herein, and the diagnostic key of this new genus will be provided in this paper.

I. INTRODUCTION

Among the subfamily Gobionellinae of family Gobiidae, Hemigobius generic group defined herein consists of genera Brachygobius, Caecogobius, Calamiana, Eugnathogobius, Hemigobius, Mugilogobius, Pandaka, Pseudogobiopsis, Pseudogobius, Redigobius, Stigmatogobius, Tamankana and Weberogobius, which are related genera sharing the typical longitudinal papillar petterns. Among the taxonomic studies of Hemigobius generic group, thought Larson consider that genus Weberogobius Koumans, 1953 [15] is synonym of genus Mugilogobius Smith, 1900 [28], however, Miller consider genus Weberogobius is valid [20], in this study, we also consider that genus Weberogobius is a valid genus, genus Weberogobius can be easy distinguished from genus Mugilogobius by they have different vertebral count (11+15-16 vs. 10+16) as well as other their own features.

On the other hand, among the genus Eugnathogobius Smith, 1931, the genus Eugnathogobius was established based on Eugnathogobius microps Smith, 1931. According to mentions of Larson, genus Eugnathogobius consists of 9 nominal species [18], including E. illotus (Larson, 1999), E. indicus (Larson, 2009), E. kabilia (Herre, 1940), E. microps Smith, 1931, E. mindora (Herre, 1945), E. polylepis (Wu and Ni, 1985), E. siamensis (Fowler, 1934), E. stictos (Larson, 2009) and E. variegatus (Peters, 1868) [6, 8, 9, 16, 18, 24, 27, 32]. However, we consider the E. siamensis should belong to genus Pseudogobiopsis Koumans, 1935 [33], and E. mindora, E. illotus and E. variegatus should belong genus Calamiana Herre, 1945 [17] based on their different morphological features in head pores presented and medium size of mouth in adult male individual.

Mugilogobius polylepis Wu and Ni, 1985 was reported been a new species which is collected from southern China and has been considred that it should place to genus Eugnathogobius Smith, 1931 [18].

Eugnathogobius occurs in brackish water habitat of mangrove and estuary around the Indo-west Pacific, including southern China, Southeast Asia and Australia [18], the E. polylepis was distributed over in China and partial area of Southeast Asia [18, 33], furthermore, this species possess quite different exterior morphological features compare to type species, E. microps. Therefore, the further detailed comparison between the rather different species should be conducted to check the validity of their own generic status.

In this study, authors examine the E. polylepis specimens which are collected from Taiwan and southern China, and
compare to the *E. microps* and other related *Hemigobius* generic group based on exterior morphological features, osteological features and molecular evidence, the specific features and molecular phylogenetic result reveals the *E. polylepis* should be a distinct new genus, the detail morphological comparison and molecular phylogeny of this new genus and other related *Hemigobius* generic group will be provided herein.

II. MATERIALS AND METHODS

1. Sample Collection

All the examined *Hemigobius* generic group species specimens collected from Taiwan, Palau, Malay Peninsula and China were collected by hand-net. Specimens tissues used for molecular analysis were preserved in 95% ethanol; specimens used for morphological studies were fixed in 10% formalin before being transferred into 70% ethanol for long-term preservation.

2. Morphological Studies

Morphometric methods follow Miller [21]; meristic methods follow Chen and Shao, Chen and Kottelat, Chen and Miller and Huang and Chen [3-5, 10]; osteological methods follow Murdy and Birdsong et al. [1, 22]. Terminology of cephalic sensory canals and free neuromast organs (sensory papillae) is from Wongrat and Miller [31], based on Sanzo [26]. All examined materials are deposited at the Institute of Marine Biology, National Taiwan Ocean University, Keelung, Taiwan (NTOU).

Meristic abbreviations are as follows: A, anal fin; C, caudal fin; D1 and D2, first and second dorsal fins, respectively; LR, longitudinal scale series; P, pectoral fin; PreD, predorsal scales; SDP, scale series from origin of first dorsal fin to upper pectoral origin; TR, transverse scale series from second dorsal to anal fin; VC, vertebral count. All fish lengths are standard length (SL).

3. Molecular Phylogenetic Analysis

The phylogenetic relationships are employed the mtDNA sequence of full length of Cytochrom b (Cyt b), D-loop and partial mitochondrial NADH dehydrogenase subunit 5 (ND5) in this study. All DNA extractions of the samples were using a kit (Roche, High Pure Product Preparation kit). Cyt b region were amplified by polymerase chain reaction (PCR) using following two primers: (GGluF: 5’-TAACCCAGGACTARTG RCTTG-3’; GproR: 5’-GTARAAATCTCYYTTTGTGA-3’); D-loop region were amplified by polymerase chain reaction (PCR) using following two primers: (GTHR: 5’-TCAGCGCCGCYTVTTGTAA-3’; GproR: 5’-GTTARAATCTCYYTTCTTTGA -3’); ND5 region were amplified by PCR using following two primers: (PgleuD1: 5’-AAAGGAT AACAGCTCATCCTTTCTGCT-3’; ND5MR: 5’-CTAATTT TCGGAGTCTGYTG-3’).

PCR was done in a MODEL 2700 or 9700 thermal cycler (Perkin-Elmer) and 30-40 cycles were carried out. The 50 µL reaction volume contained 33.5 µL of sterile distilled water, 5 µL of 10X PCR buffer (Takara), 4 µL of dNTP (2.5 mM each), 3 µL of Mgcl2 (2.5 mM each), 1 µL of each primer, 0.5 µL of 0.5 unit Ex Taq (Takara) and 2 µL of template. The thermal cycler profile was as follows: denaturation at 94°C for 60 seconds, annealing at 52-58°C for 60 seconds and extension at 72°C for 120 seconds. A negative control without template was carried out for each run of PCR. The PCR products were run on a 1.0% L 03 agarose gel (Takara) and stained with ethidium bromide for band characterization under ultraviolet trans-illumination.

Double-stranded PCR products were purified using a kit (Roche, High Pure Product Purification kit), before undergoing direct cycle sequencing with dye-labeled terminators (ABI Big-Dye kit). The sequencing primers used were same as PCR using primers. All sequencing reactions were performed according to the manufacturer’s instructions. Labeled fragments were analyzed using as ABI PRISM Model 377-64 DNA Automated sequencer (ABI).

Nucleotide sequence alignment was verified manually after running through BIOEDIT version 5.9 [7]. The analysis of aligned mutation sites were conducted using Molecular Evolutionary Genetics Analysis (MEGA) version 5.05 [18] for aligned mutation sites analysis.

The parsimony (MP) analysis was carried out using PAUP* version 4.0b10 [29] using heuristic search. Branch support was established via bootstrap analysis (2000 replications). For the Bayesian (BI) analysis, the best-fitting model for sequence evolution was determined for mtDNA D-loop and ND5 sequences using MrMODELTEST version 2.2 [23]. The BI analyses were performed using MrBayes 3.0 [25]. The posterior probabilities of each node were computed from remaining 75% of all sampled trees.

III. RESULTS

Molecular phylogenetic analysis

The aligned Cytb, D-loop and ND5 sequence consists of 56 haplotypes and from all 9 related genera of *Hemigobius* generic group as 21 species with 47 individuals, we choose *Rhino gobius changtinensis* Huang and Chen, 2007 [10] as outgroup. The length of combined sequence of Cytb, ND5 and D-loop sequence is 2994-3137 in total (1141 bp in Cytb, 818-961 bp in D-loop, and 1035 bp in ND5). This alignment contain 2508 total number of mutations, and 1501 number of polymorphic (segregating) sites. The phylogenetic analysis using neighbour-joining (NJ), parsimony (MP) analysis and Bayesian analysis (BI) method provided. The phylogenetic tree was reconstructed by NJ analysis based on Kimura 2-parameter model. The phylogenetic tree reconstructed by BI analysis based on HKY 85+G model.

The result of MP analysis by heuristic search only one tree, and tree length 6589; the Consistency index (CI) being 0.4117, Retention index (RI) being 0.7449 and Homoplasy index (HI) being 0.5883.
The phylogenetic trees reconstructed by NJ, MP and BI methods shows that same grouping result. The phylogenetic trees congruently reveal that this new genus is an independent clade, and the node with high bootstrap value reach to 95 in MP tree, 76 in NJ tree and posterior probabilities as high as 100 in BI tree, the specific level of node between this new genus and other related genera are strongly supported.

In comparison with mitogenetic divergence of all examined Hemigobius generic group genera, the range of mitogenetic divergence of this new genus and other 8 genera are 18.1-24.0% for Cytb sequences; 22.6-37.5% for ND5 sequences; and 21.7-39.3% for D-loop sequences; and 22.5-32.2% for combined Cytb, ND5 and D-loop sequences based on K2P model.

Compare to other related Hemigobius generic group, previous studies reveal the genetic divergence between Mugilogobius abei (Jordan and Snyder, 1901) [13] (KF 128984) and Pseudogobius javanicus (Bleeker, 1856) [2] (KF 193873) are 23.6 % for combined Cytb, ND5 and D-loop sequences [11, 12], compare to our study (22.5-32.2%), the genetic divergence between this new genus and other 8 genera are almost higher, so the molecular evidence strongly support that Eugnathogobius polylepis should be a independent genus based on their differentiation of mtDNA sequence from this new genus and other related genera.

IV. SYSTEMATICS

Wuhanlinigobius new genus

Diagnosis

This new genus can be well distinguished from other related genus by the unique combination of following features: (1) fin rays: D2 I/7-8; A/8-9; P 16-19; First dorsal fin low and rounded, spines never filamentous. (2) squamation: LR 47-59; TR 15-17; Pred 0-29 : Body covered with small sized ctenoid scales; cheek, operculum, prepelvic region and pectoral base region naked. (3) specific coloration: Adult individual with thin red lines at their upper and lower lip in both sexes. Caudal fin membrane with distinct black margin, upper caudal fin base with a circle black spot. (4) Head lateral-line system: Head pores absent; cheek with typical longitudinal papilla pattern; Sensory papillae row c merely with single papilla and located on under the starting point of row b; row s with two row papillae; row p complete. (5) Generally description: Body elongate and lowed; mouth medium sized in both sexes.

Type species

Mugilogobius polylepis Wu and Ni, 1985

Osteology of type species

In jaws and suspensorium, the maxilla stout and short. The ectopterygoid stout and short, and triangle shaped. The palaetine stout and short, and anterior tip with cartage. The metapterygoid rectangular form shaped. The posterior portion of premaxilla stout and short, upper portion elongated. The posterior portion of dentary tall and tip squared. The anguloarticular with two tips and upper tip longer than lower one. The quadrate joins anguloarticular and ectopterygoid in anterior margin, joins symplectic in posterior margin, joins metapterygoid in upper margin, and joins preopercle in lower margin. The hyomandibula joins metapterygoid in anterior margin, and joins preopercle in posterior margin. The preopercle L shaped, anterior tip elongated and sharped. The interopercle elongated and anterior tip sharped.

In anterior vertebrae skeleton, the anterior vertebrae and associated pterygiophore formula is 3-12210. In the caudal skeleton, the hypurals 1&2, 3&4 close up each other respectively, caudal skeleton consists of hypurals 1&2, hypurals 3&4, hypurals 5, single epural and parhypural, the epural rectangular form shaped, the parhypural elongated and sharped.

Etymology

The generic name, Wuhanlinigobius, is referred to the Chinese ichthyologist, “Prof. Wu, Han-lin” for recognizing his great contribution for the ichthyological research in China especially for gobioid fishes.

Remarks

Among the subfamily Gobionellinae of family Gobiidae, Hemigobius generic group consists of genera Brachygobius, Caecogobius, Calamiana, Eugnathogobius, Hemigobius, Mugilogobius, Pandaka, Pseudogobiopsis, Pseudogobius, Redigobius, Stigmatogobius, Tamanka, Weberogobius and this new genus.

Wuhanlinigobius polylepis can be well distinguished from Eugnathogobius microps and other Hemigobius generic group genera based on following morphological features:

Wuhanlinigobius can be well distinguished from genera Calamiana, Hemigobius, Pseudogobius, Pseudogobiopsis, Redigobius and Stigmatogobius by lacking head pores; and distinguished from Caecogobius by Caecogobius having greatly reduced eye; and genus Wuhanlinigobius can be distinguished from genera Mugilogobius, Pandaka and Tamanka by different sensory papillae row c (genus Wuhanlinigobius with single papillae c; genera Mugilogobius and Tamanka with papillae row c and cl; genus Pandaka with a row of papillae row c). Wuhanlinigobius can be well distinguished from genus Brachygobius by Brachygobius having distinctive dark banded color pattern and scale present on upper operculum region. Wuhanlinigobius can be well distinguished from genus Weberogobius by genus Weberogobius with vertebral count 11+15-16, and restricted in freshwater lake of Sulawesi, Indonesia; Wuhanlinigobius with vertebral count 10+16, and live in brackish water of mangrove habitat.

Further more, in comparaion of Eugnathogobius microps, which is type species of genus Eugnathogobius, Wuhanlinigobius can be well distinguished based on following morphological features:

In exterior morphological features, this new species snout slightly prominent than the lower lip; mouth medium sized,
Table 1. Sampling localities, OTU codes and accession number of molecular sequence analysis of Wuhanlinigobius species and other Hemigobius generic group species and outgroup from Taiwan, Palau, China, Tailand and Malay Peninsula.

<table>
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<th>Locality</th>
<th>Accession number</th>
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<td>Calamiana variepatia</td>
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<td>KF929307</td>
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<tr>
<td>CVAML2</td>
<td>Calamiana variepatia</td>
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<td>Magilogobius abei</td>
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</table>

maxillary extending to the vertical of anterior margin of pupil in male; body covered with small sized ctenoid scales and with more longitudinal scale series 47-50. The E. microps mouth medium sized, maxillary beyond the posterior margin of orbit and extending to preoperculum region in adult male; body covered with big sized ctenoid scales and with fewer longitudinal scale series 23-27 (original description see Larson, 2009).

In osteological features, compare to E. microps (original drawing see Fig. 11 in Larson, 2009), this new genus can be well distinguished from E. microps based on jaws and suspensorium system. In this new genus, the maxilla and pala- line stout and short. The ectopterygoid stout and short, and triangle shaped. The metapterygoid rectangular form shaped.
Table 2. Morphometric measurements of two Wuhanlinigobius species from Taiwan, China and Malay Peninsula.

<table>
<thead>
<tr>
<th>Characters</th>
<th>Wuhanlinigobius polyplepis</th>
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<td>Female</td>
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<td>Percent standard length (%)</td>
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<td>Head length</td>
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<td>28.1</td>
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<td>Predorsal length</td>
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<td>Snout to 2nd dorsal origin</td>
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<td>Snout to anus</td>
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<td>Snout to anal fin origin</td>
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<td>Prepelvic length</td>
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<td>Percent head length (%)</td>
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<td>Head width in upper gill</td>
<td>41.8</td>
<td>49.1</td>
</tr>
<tr>
<td>Bony interorbital width</td>
<td>19.5</td>
<td>19.7</td>
</tr>
<tr>
<td>Fleshy interorbital width</td>
<td>35.5</td>
<td>38.7</td>
</tr>
<tr>
<td>Lower jaw length</td>
<td>47.9</td>
<td>51.4</td>
</tr>
</tbody>
</table>

The posterior portion of premaxilla stout and short, upper portion elongated. The posterior portion of dentary tall and tip squared. The preopercle L shaped, anterior tip elongated and sharpened. The interopercle elongated and anterior tip sharpened. In *E. microps*, the maxilla and palatine slender and long. The ectopterygoid long. The metapterygoid triangular form shaped. The posterior portion of premaxilla slender and very long, the tip sharpened, upper portion short. The posterior portion of dentary low and tip sharpened. The preopercle L shaped, anterior tip short and truncated.

In head lateral-line system, compare to *E. microps* (original drawing see Fig. 12 in Larson, 2009), this new genus can be well distinguished from *E. microps* based on following features: this new genus *c* located on under the starting point of row *b*, and *E. microps* *c* located on under the center of row *b*. This new genus with row *d* elongate and forming a straight line on upper lip margin; *E. microps* with row *d* forming a Y-shaped on upper lip margin.

**Wuhanlinigobius polyplepis** (Wu and Ni, 1985)

*(Tables 2, 3, Figs. 1a, 2a, 3a, 3b)*

**Mugilogobius polyplepis** Wu and Ni, 1985: 95 (Zhonggang, Fengejian, Shanghai, China); Wu and Zhong, 2008: 500 [32, 33].

**Calamiana** sp. nov: Larson, 2001: 61 [17].

**Calamiana polyplepis**: Larson et al., 2008: 141 [19].

**Eugnathogobius** Larson, 2009: 143 [18].

**Material examined**


**Other material**

Table 3. Frequency distribution of meristic features of the two Wuhanlinigobius species from Taiwan, China and Malay Peninsula.

<table>
<thead>
<tr>
<th></th>
<th>D1</th>
<th>D2</th>
<th>A</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>VI</td>
<td>I/7</td>
<td>I/8</td>
<td>x/9</td>
</tr>
<tr>
<td>W. polylepis</td>
<td>20</td>
<td>6.8</td>
<td>8.0</td>
<td>9.8</td>
</tr>
<tr>
<td>W. malayensis n. sp.</td>
<td>15</td>
<td>6.0</td>
<td>2.5</td>
<td>13.0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>LR</th>
<th>TR</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>47</td>
<td>50</td>
</tr>
<tr>
<td>W. polylepis</td>
<td>4</td>
<td>18</td>
</tr>
<tr>
<td>W. malayensis n. sp.</td>
<td>2</td>
<td></td>
</tr>
</tbody>
</table>

Fig. 1. The specimen photographs of two Wuhanlinigobius species, a, Wuhanlinigobius polylepis, NTOP 2012-04-130, male, 31.0 mm SL; b, Wuhanlinigobius malayensis n. sp., NTOP 2012-05-151, holotype, male, 31.3 mm SL.

Fig. 2. Head lateral-line system of two Wuhanlinigobius species, a, Wuhanlinigobius polylepis, NTOP 2012-04-133, male, 22.7 mm SL; b, Wuhanlinigobius malayensis n. sp., NTOP 2012-05-151, male, 31.3 mm SL. Bar = 1 mm. Drawing by Shih-Pin Huang.


Diagnosis

Wuhanlinigobius polylepis can be well distinguished by the unique combination of following features: (1) fin rays: D2 I/8; A I/8-9 (modally 8); P 16-19 (modally 18); First dorsal fin low and rounded, spines never filamentous. (2) squamation: LR 47-50 (modally 48); TR 15-16 (modally 16); PreD 0-19 (modally 0); Body covered with small sized ctenoid scales. Predorsal region covered with cycloid scales in female, and usually naked in male. Cheek, Operculum, prepelvic region...
Osteological features of *Wuhanlinigobius polylepis*, a, lateral view of jaws and suspensorium; b, caudal skeleton, NTOUP 2012-04-131, male, 23.6 mm SL. Bar = 1 mm. Drawing by Shih-Pin Huang.

and pectoral base region naked. (3) Specific coloration: Cheek and preoperculum region with three horizontal blackish brown stripes. Adult individual with thin red lines at their upper and lower lip in both sexes. Caudal fin membrane yellow and with distinct black margin in adult male, caudal fin membrane with 3-5 vertical black line in both sexes.

**Description**

Body elongate and lowed, subcylindrical anteriorly and compressed posteriorly. Head medium sized. Snout slightly prominent than the lower lip. Eye rather large. Mouth medium sized, male slightly bigger than female, maxillary extending to the vertical of anterior margin of pupil in male, but maxillary reach the vertical of anterior margin of orbit in female. Anterior nasal as short tube, posterior nasal as round hole. Gill-opening extending ventrally forward the middle vertical line of operculum. VC 10 + 16 = 26 (in 7).

**Fins**

D1 VI; D2 I/8; A I/8-9 (modally 8); P 16-19 (modally 18). First dorsal fin low and rounded, spines never filamentous; second to fourth spines always longest, the spine is slightly longer in male than female, and can not extending to anterior edge of second dorsal when pressed in both sexes. Anal fin inserted below first branched rays of second dorsal fin. Pelvic fin medium sized and rounded. Caudal fin rounded.

**Scales**

LR 47-50 (modally 48); TR 15-16 (modally 16); PreD 0-19 (modally 0); SDP 11-13 (modally 12). Body covered with small sized ctenoid scales. Predorsal region covered with cycloid scales in female, and usually naked in male. Belly covered with smaller cycloid scales. Cheek, operculum, pre-pelvic region and pectoral base region naked.

**Head lateral-line system**

**Head canals** - Head pores absent.

**Sensory papillae** - Cheek with typical longitudinal papilla pattern. Row a short, about half of orbit diameter. Row b with densely-set papillae, and equal to orbit diameter. Row c merely with single papilla and located on under the starting point of Row b. Row cp short, about half of orbit diameter. Row d long, about equal to orbit diameter. Row s with two row papillae. Row p complete. Opercular rows with rows os, oi and ot. Rows oi and ot slightly closed. Rows f with a pair of single papillae.

**Coloration in life**

Head and trunk with pale yellowish brown or pale yellow background. Body side and neck with many irregular brown bars. Belly pale yellowish white. Cheek and preoperculum region with three horizontal blackish brown stripes. Adult with thin red lines at their upper and lower lips in both sexes. Pectoral fin base with a horizontal brown bar. Upper caudal fin base with a big sized circle black spot, and merely smaller spot in female. First and second dorsal fin membranes gray and with yellow margin. Anal fin membrane gray and with white margin. Pectoral and pelvic fin membranes grayish white. Caudal fin membrane yellow and with distinct black margin in adult male, and caudal fin membrane grayish white and with indistinct black margin in female, caudal fin membrane with 3-5 vertical black line in both sexes.

**Distribution.** This species originally found from Shanghai, and it also found from Fujian, Guangdong Province in China and also Kinmen, Charyi counties in Taiwan.

**Wuhanlinigobius malayensis** new species
(Tables 2, 3, Figs. 1b, 2b)

**Material examined:**

**Holotype.** -NTOUP 2012-05-151, 31.3 mm SL, male, Matang mangrove, Malaysia, coll. I-S. Chen and S. P. Huang, 20 April, 2011.


**Diagnosis**

*Wuhanlinigobius malayensis* n. sp. is well distinguished
from other congeners by the unique combinations of the following features: (1) fin rays: D2 I/7-8 (modally 8), A I/8-9 (modally 8), P 18-19 (modally 8), and first dorsal fin never filamentous; (2) squamation: lateral body with small ctenoid scales, longitudinal scale rows 56-59 (modally 57), predorsal scales 23-29 (modally 26); (3) specific coloration: Caudal fin creamy yellow or pale yellow, with broad black submarginal edge in male, upper caudal fin base with a large rounded black spot in male.

Description

Body elongate, subcylindrical anteriorly and compressed posteriorly. Head large. Upper lip more prominent than lower lip. Eyes rather large. Mouth small, maxillary extending to the vertical of center of pupil in male, and extending to the vertical of anterior margin of pupil in female. Anterior nasal as short tube, posterior nasal as round hole. Gill-opening restricted, ventrally extending to the two third of vertical line of operculum. VC 10 + 16 = 26 (in 10).

Fins

D1 VI; D2 I/7-8 (modally 8); A I/8-9 (modally 8); P 18-19 (modally 18). First dorsal fin spines never filamentous, second to fourth spines longest. Anal fin inserted below spine of second dorsal fin. Pelvic fin large and rounded. Rear margin of caudal fin rounded.

Scales

LR 56-59 (modally 57); TR 16-17 (modally 16); PreD 23-29 (modally 26); SDP 13-14 (modally 13). Body covered
with small ctenoid scales. Predorsal region with small cycloid scales. Belly with smaller cycloid scales, prepelvic fin region naked. Cheek and opercle naked.

**Head lateral-line system**

**Head canals-** Head pores absent.

**Sensory papillae-** Row a short, about half of eye diameter. Row b with densely-set papillae, and longer than eye diameter, starting from vertical of rear margin of pupil. Row c merely single papillae. Row cp about two-third orbit diameter, and starting from vertical of anterior margin of pupil, extending to rear margin of orbit. Row d longer than eye diameter. Row s with two row papillae. Row p completed. Opercular rows with rows oz, oi and ot. Rows oi and ot well separated. Rows f with a pair of single papillae.

**Coloration in life**

Head and body generally creamy yellow or pale yellowish brown, upper half of lateral trunk with many irregular vertical blackish brown short bars or spots. Lateral scales with blackish brown margin. Belly creamy white. Cheek and opercle with numerous black spots. Pectoral fin membrane pale gray or grayish white, base with some black spots. First dorsal fin and second dorsal fin grayish white, with pale yellow margin in adult male, but merely grayish white in female. Anal fin membrane gray, with white margin. Pelvic fin gray in male, pale gray in female. Caudal fin creamy yellow or pale yellow, with broad black submarginal edge in male, and with unapparent gray margin in female, upper caudal fin base with a large rounded black spot in male, and with an unapparent smaller gray spot in female.

**Habitat**

Wuhanlinigobius malayensis n. sp. can be found in the shallow tidal pools of the mangrove region of Malay Peninsula, a muddy intertidal habitat.

**Distribution.** This species found from Matang, and Sungai Haji Dorani, Malay peninsula and also found in Singapore.

**Etymology**

The Latin specific name, “malayensis” referring to this new species distributed in the brackish water habitat of Malay Peninsula region.

**Remarks**

Wuhanlinigobius malayensis n. sp. and Wuhanlinigobius polylepis with similar sensory papilla and small size of body scales, both species caudal fin with broad black submarginal edge, upper caudal fin base with a large rounded black spot in male. However, W. malayensis can be distinguished from W. polylepis by the following features: (1) more longitudinal scale series 56-59 vs. 47-50, (2) more predorsal scale series 23-29 vs. 0-19, and (3) W. malayensis with same predorsal scales distribution region in both sexes, the W. polylepis male usually naked in predorsal region.

**A diagnostic key to genus Wuhanlinigobius**

1a. longitudinal scale series 47-50; predorsal scales series 0-19; predorsal region covered with cycloid scales in female, and usually naked in male; caudal fin membrane with 3-5 vertical black line in both sexes

1b. longitudinal scale series 23-29; predorsal scales series 0-19; predorsal region covered with cycloid scales in both sexes; caudal fin membrane without vertical black line

**ACKNOWLEDGMENTS**

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