

## *Psilorhynchus kamengensis*, a new species of fish (Teleostei: Psilorhynchidae) from northeast India

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### Abstract

*Psilorhynchus kamengensis*, new species, is described from a stream of the Kameng River, a northern tributary to the Brahmaputra drainage, Arunachal Pradesh, northeast India. The new species belongs to the *P. balitora* species group and can be distinguished from all other members of this group by the presence of a longer post-epiphyseal fontanelle, 3 unbranched anal-fin rays, 9+8 caudal-fin rays, 35 vertebrae and fin coloration. The validity of the species is also corroborated by molecular phylogenetic analysis based on the mitochondrial *cyt b* gene.

### Key words

Torrent minnow, Kameng, morphology, *cyt b*, phylogeny.

### Introduction

Cypriniform fishes of the genus *Psilorhynchus* McClelland, 1838 are characterized by having an arched dorsum with flattened ventral surface, horizontally-placed paired fins, a naked breast and an inferior mouth devoid of barbels (RAINBOTH, 1983). Currently, the genus has 30 valid species distributed throughout the torrential rivers and streams of Northeast and Peninsular India, Bangladesh, China, Nepal, Bhutan, Myanmar and Thailand (ARUNACHALAM & MURALIDHARAN, 2008; CONWAY & BRITZ, 2015; CONWAY & PINION, 2016; SHANGNINGAM & VISHWANATH, 2016; SHANGNINGAM *et al.*, 2019; DEY *et al.*, 2020). Six species, viz. *Psilorhynchus arunachalensis* (Nebeshwar *et al.*, 2007), *P. balitora* (Hamilton, 1822), *P. bichomensis* Shangningam *et al.*, 2019, *P. hamiltoni* Conway *et al.*, 2013, *P. nahlongthai* Dey *et al.*, 2020 and *P. sucatio* (Hamilton, 1822), are known from the Brahmaputra drainage in northeast India.

The Kameng River is the major drainage in East and West Kameng districts of Arunachal Pradesh, northeast India. The Kameng originates from the Greater Himalayas, at an elevation of more than 7000 m, and descends south through deep gorges and dense forests. During its initial course of approximately 183 km in Arunachal Pradesh, the river is joined by the Bichom from the west, and major streams, viz the Pachuk, Pachai, Pakke, Namiri and Mansari, and then enters Assam as the Jia Bhoroli and empties into the Brahmaputra as a major north bank tributary. A recent ichthyofaunal expedition to the Kameng included an unnamed species of *Psilorhynchus*, which is described herein as *Psilorhynchus kamengensis*, new species.

## Materials and methods

### Morphological measurements and analyses

Measurements were taken with a digital slide caliper to the nearest 0.1 mm. Methods for measurements follow CONWAY *et al.* (2013) and counts follow CONWAY & BRITZ (2010). Morphometric data are expressed in percent of standard length (SL) and head length (HL) respectively. Meristic counts were made under a Leica S8APO stereo-zoom microscope. A single specimen was cleared and stained following TAYLOR & VAN DYKE (1985) skipping staining for cartilage. Vertebral counts include the Weberian apparatus, counted as four, and the terminal compound centrum. Numbers in parentheses after a count represent the frequency of that count. Colour pattern and oromandibular descriptions follow CONWAY *et al.* (2013). Water parameters were analysed using an YSI Professional Plus (USA) digital water analysing kit. Type specimens are deposited at ZSI (Zoological Survey of India, Kolkata) and GUMF (Gauhati University Museum of Fishes, Assam).

### DNA analyses and phylogeny

Isolation of genomic DNA was carried out from fin-clips of specimens ( $n=2$ ; voucher no: GUAP: 0010/19; GUAP: 0011/19) preserved in 95% ethanol using the QIAamp® DNA Mini Kit (QIAGEN, Germany) following the manufacturer's protocol. PCR amplification was carried out for a total volume of 25  $\mu$ l reaction – 12.5  $\mu$ l ready-to-use PCR master mix [catalogue no: M7508B (PROMEGA, Madison, USA)], 7.5  $\mu$ l sterile water, 2.5  $\mu$ l genomic DNA, and 1.25  $\mu$ l of each primer. The mitochondrial cytochrome *b* (cyt *b*) gene was selected for amplification and sequencing as it is the most widely used locus in fish phylogenetics (ZARDOYA & MEYER, 1996). The partial cyt *b* gene was amplified and sequenced using LA-danio 5' GACTYGAARAACCACYGTTG 3' and HA-danio 5' CTCGATCTTCGGATTACAAG 3' (MAYDEN *et al.*, 2007). The PCR cycling conditions follow CONWAY *et al.* (2015). The annealing temperatures for the primers were standardized at 52°C. All amplified PCR products were outsourced for sequencing to AgriGenome Labs Pvt. Ltd. (Kerala, India) and sequenced in both directions using the same PCR primers as sequencing primers. Sequence ambiguities were edited by aligning forward and reverse reads using the computer program BIOEDIT sequence alignment editor 7.0.5.3 (HALL, 1999). All obtained sequences were deposited in the GenBank database; accession numbers are provided in Table 1.

The nucleotide sequences of the cyt *b* gene were aligned with available sequences of members of the genus *Psilorhynchus* obtained from GenBank ( $n=15$ , Table 1) using the default parameters in CLUSTAL W (THOMPSON *et al.*, 1994) built into MEGA7 software. From these aligned datasets, sequence divergences (uncorrected *p*-distances) were calculated using Molecular Evolutionary

**Table 1.** GenBank accession numbers of cyt *b* sequences used in the present study (\* indicate the accession numbers obtained for the new species).

Species	Accession No
<i>Psilorhynchus kamengensis</i>	MN180269*
<i>Psilorhynchus kamengensis</i>	MN180270*
<i>Psilorhynchus balitora</i>	KM207640
<i>Psilorhynchus balitora</i>	KM207641
<i>Psilorhynchus balitora</i>	KM207642
<i>Psilorhynchus balitora</i>	KM207643
<i>Psilorhynchus balitora</i>	KM207644
<i>Psilorhynchus balitora</i>	DQ026436
<i>Psilorhynchus balitora</i>	AP011224
<i>Psilorhynchus breviminor</i>	KM207645
<i>Psilorhynchus nepalensis</i>	KM207646
<i>Psilorhynchus nahlongthai</i>	MN017300
<i>Psilorhynchus nahlongthai</i>	MN045190
<i>Psilorhynchus rahmani</i>	KM207649
<i>Psilorhynchus gokkyi</i>	KM207651
<i>Psilorhynchus nudithoracicus</i>	KM207652
<i>Psilorhynchus nudithoracicus</i>	KM207653

Genetic Analysis 7 (MEGA7 Ver 7.0.26) (KUMAR *et al.*, 2016) with pairwise-deletion based on 1000 bootstrap replications. Phylogenetic analyses were performed on the cyt *b* gene data set under Maximum Likelihood (ML), Maximum Parsimony (MP) and Neighbour Joining (NJ) statistical methods. The best-fit nucleotide substitution model for the ML analysis was determined based on the lowest Bayesian Information Criterion (BIC=8270.641), corrected Akaike Information criterion (AICc=7992.377) and Maximum Likelihood ( $\ln L = -3960.109$ ) values in MEGA 7. Phylogenetic tree was constructed using HKY + G (Hasegawa-Kishino-Yano + Gamma distribution). For MP analysis, heuristic searches utilizing the tree-bisection and reconnection (TBR) branch swapping with starting trees obtained by random stepwise addition were used. The maximum number of trees saved during each run was allowed to automatically increase by 100. Phylogeny reconstruction for NJ method was based on *p*-distance and 1000 bootstrap replications.

## Results

### *Psilorhynchus kamengensis*, sp. nov.

LSID urn:lsid:zoobank.org:act:0F15CE6A-93BC-4C17-8D35-C9E8D76515CE

(Fig. 1, Table 2)

**Holotype.** ZSI FF 8422, 49.6 mm SL; India: Arunachal Pradesh: District: West Kameng: Kameng River (Brahmaputra drainage): Tippi Naala (stream) at Tippi; 27°01'40" N 92°36'44" E; 159 m asl; coll. A. Dey & party 16<sup>th</sup> May, 2019.

**Paratypes.** GUMF 516/9, 6 specimens, 31.8–47.5 mm SL; data same as Holotype. GUMF 516/9, 3 specimens, 36.1–40.1 mm SL;



**Fig. 1.** *Psilorhynchus kamengensis*, new species, holotype, ZSI FF 8422, 49.6 mm SL; India: Arunachal Pradesh: West Kameng district: stream near Tippri: Kameng River. Dorsal (top), lateral (middle) and ventral (bottom) views.

India: Arunachal Pradesh: West Kameng district: unnamed stream of Kameng River near Bhalukpong: 27°00'38"N 92°39'19"E; coll. A. Dey & party 18<sup>th</sup> May, 2019. GUMF 516/9, 45.2 mm SL, cleared and stained for osteology; data same as holotype.

**Diagnosis.** A member of the *Psilorhynchus balitora* species group which is distinguished from all its congeners by the combination of the following characters: absence of scales mid-ventrally post isthmus up to the region about three scale rows ahead of pelvic-fin origin; post-epiphyseal fontanelle longer than pre-epiphyseal and separated by wide strut of frontal; deeply arched dorsal

profile anterior to dorsal-fin origin; short caudal peduncle (9.1–10.3 % SL); 5–6 unbranched pectoral-fin rays; 3 unbranched anal-fin rays; 9+8 principal caudal-fin rays; 11–13 pre-dorsal scales; 32–33+2 lateral-line scales; 3 branchiostegal rays; 35 vertebrae; and a colour pattern comprising of six dorsal saddles, three black bars on caudal fin, and 5–6 indistinct dark brown lateral blotches superimposed on a distinct mid-lateral stripe.

**Description.** Body elongate, dorsal profile strongly arched, rising gradually to dorsal-fin origin, sloping steeply towards caudal-fin base. Body depth greatest

**Table 2.** Morphometric data of holotype (ZSI FF 8422) and eight paratypes (GUMF 516/9) of *Psilorhynchus kamengensis*, new species (\*data of holotype included in range; SD, standard deviation).

Measurements	Holotype	Range*	Mean	SD
Standard length (in mm)	49.6	31.8–49.6	—	—
<b>In % SL</b>				
Body depth	22.4	19.5–24.8	21.6	1.7
Head length	21.0	19.4–22.5	21.5	1.0
Pre-dorsal length	50.6	47.5–50.6	49.4	1.0
Pre-pectoral length	18.8	17.3–20.5	18.8	1.0
Pre-pelvic length	52.8	45.5–52.8	50.0	2.8
Pre-anal length	79.2	75.9–79.9	77.8	1.4
Snout to anus length	62.5	57.6–62.5	60.1	1.9
Anus to anal fin length	18.3	13.0–19.3	17.8	2.0
Caudal peduncle length	9.7	9.1–10.3	9.7	0.4
Caudal peduncle depth	7.7	7.6–8.3	8.1	0.3
Caudal peduncle width	6.0	4.5–6.1	5.5	0.5
Pectoral-fin length	22.0	22.0–24.1	23.2	0.8
Pelvic-fin length	16.9	16.9–18.9	18.1	0.7
Length of last unbranched anal-fin ray	14.7	13.8–18.0	15.6	1.3
Length of last unbranched dorsal-fin ray	22.2	20.2–23.6	21.8	1.2
<b>In % HL</b>				
Head width at orbit	75.0	67.5–78.9	74.1	3.7
Head depth at orbit	55.8	49.4–58.0	54.7	2.6
Eye diameter	26.0	23.4–34.7	27.9	3.4
Snout length	59.6	50.0–59.6	54.5	3.2
Inter-orbital width	41.3	38.2–51.1	42.9	4.3
Mouth width	36.5	30.1–36.5	33.2	2.2

at dorsal-fin origin and least at hypural flexure. Ventral profile straight from lower jaw to anal-fin origin, slightly inclined dorsally to caudal-fin base.

Head large, wider than deep. Eye large, mouth inferior, relatively wide; snout short, rounded anteriorly, its ventral surface bordered by a deep longitudinal groove on each side. Rostral cap fused with upper lip, separated by shallow groove; posterior margin of rostral cap smooth. Upper lip covered with rows of unculi. Lower lip smooth, not continuous with upper lip around corner of mouth. Lower jaw covered by thick squarish soft tissue, densely papillated, continuous with skin of isthmus and connected with rostral cap by posterolateral skin fold around corner of mouth (Fig. 2a). Snout, lateral surface of head, rostral cap and papilliferous skin folds covered with small conical tubercles. Dorsal surface of head with large, irregular, (often) reticulated tubercles. Gill membranes joined to isthmus.

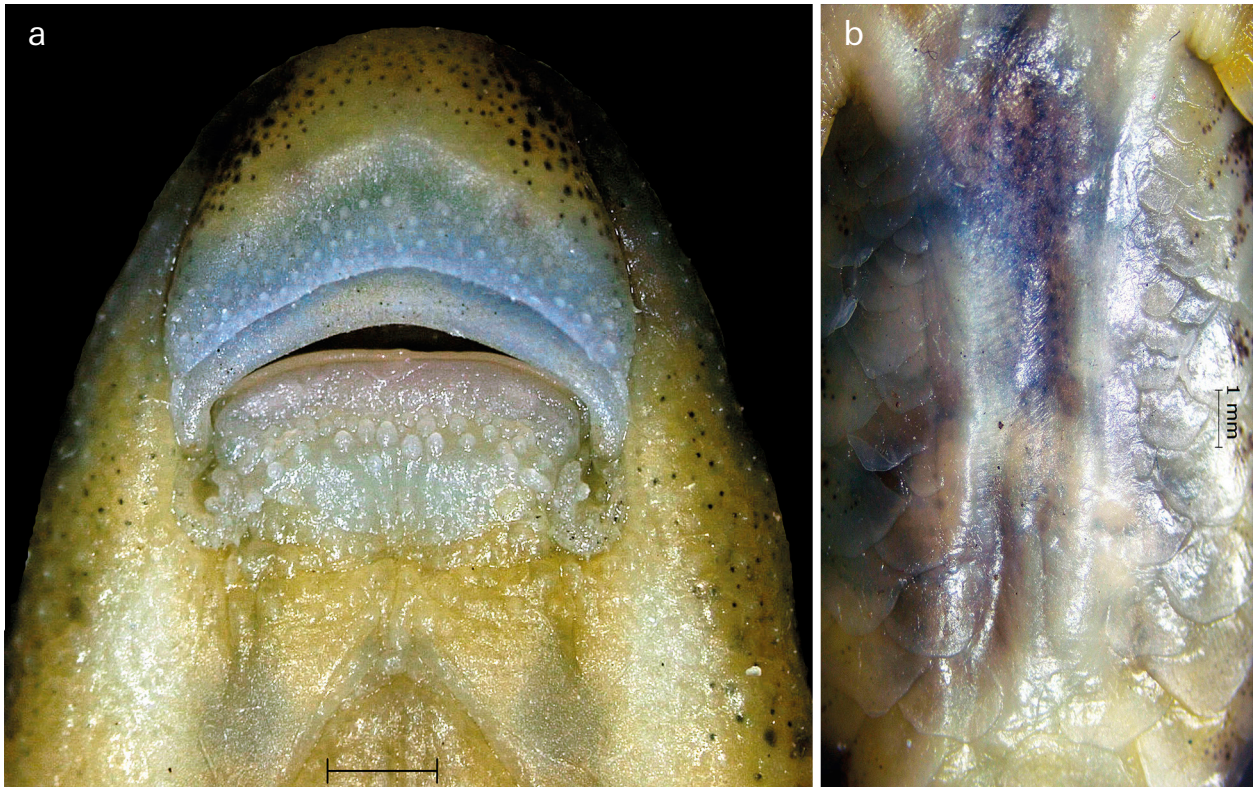
Dorsal-fin rays iii, 7 (1)–9 (8\*, including holotype [\*]); anal-fin rays iii, 6 (9\*). Principal caudal-fin rays 9 + 8 (9\*); dorsal procurrent rays 6 (9\*), ventral procurrent rays 5 (9\*). Pelvic-fin rays ii, 6, i (9\*); pectoral-fin rays v, 10 (2) or vi, 10 (7\*). Paired fins horizontally placed, pectoral fin larger than pelvic, not reaching vertical through dorsal-fin origin when appressed. Pelvic-fin origin opposite third branched ray of dorsal fin. Unculiferous pads present along ventral surface of unbranched pectoral and pelvic-fin rays. Dorsal fin moderately-high, tip rounded; its posterior margin slightly concave. Anal fin small, not reaching caudal-fin base, its posterior edge concave.

Caudal fin weakly-forked, tip of both lobes rounded, upper lobe slightly longer than lower.

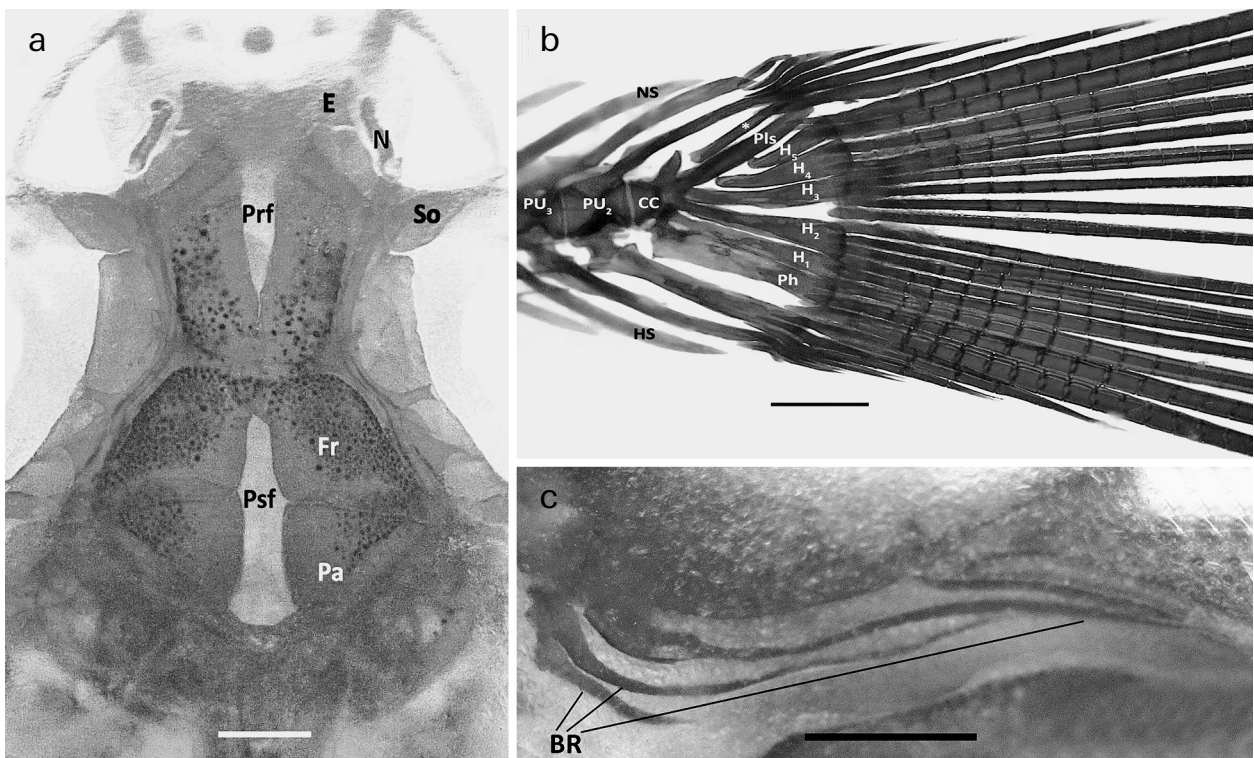
Scales cycloid, large, with well-developed radii directed posteriorly. Scales along lateral line 32 (7\*)–33 (2)+2 (9\*). Transverse scale rows from dorsal-fin origin to pelvic-fin origin  $3\frac{1}{2}/1/2$  (9\*); circumpeduncular scales 10 (9\*); pre-dorsal scales 11 (8\*)–13 (1). Anus located three scales behind pelvic-fin origin. Scales between anus and anal-fin origin 9 (7\*)–10 (2). Mid-ventral region between pectoral-fin origin and two scale rows ahead of pelvic-fin origin without scales (Fig. 2b).

**Osteology.** Pre-epiphyseal fontanelle long and dagger-shaped extending posteriorly to the middle of orbit. Post-epiphyseal fontanelle longer than pre-epiphyseal, broader and irregularly-shaped, arising from occiput and extending up to one-fourth of neurocranium. Pre- and post-epiphyseal fontanelles separated by narrow strut of frontal (Fig. 3a). Total vertebrae 35 (1), comprising 25 abdominal and 10 caudal vertebrae, respectively. Caudal-fin rays supported by neural and haemal spines of second and third preural caudal centra, pleurostyle, epural, five hypural elements and parhypural. Anteriormost tips of parhypural and first hypural fused, and firmly attached to compound centrum via cartilaginous head; epural is separated from compound centrum by short hiatus (Fig. 3b). Branchiostegal rays 3, anteriormost ray slightly reduced extending to one-third the length of second ray (Fig. 3c). Five infraorbitals (IO1–5): IO1 largest, IO1–3 plate-like, IO4–5 narrow tube-like bones composed of sensory ca-





**Fig. 2.** Ventral view of *Psilorhynchus kamengensis*, holotype, ZSI FF 8422, 49.6 mm SL, showing – (a) oromandibular structures and (b) scaleless patch on chest and abdomen between paired fins. Scale bar 1 mm.



**Fig. 3.** Osteology of *Psilorhynchus kamengensis*, GUMF 516/9, paratype, 45.2 mm SL – (a) Dorsal neurocranium [E: ethmoid, Fr: frontal, N: nasal, Pa: parietal, Prf: Pre-epiphyseal fontanelle, Psf: Post-epiphyseal fontanelle, So: supraorbital], (b) caudal skeleton [CC: caudal centrum, H1–H5: hypurals, HS: haemal spine, NS: neural spine, Ph: parhypural, Pls: pleurostyle, PU2 & PU3: preural centrum, \*: epural], and (c) branchiostegal rays [BR]. Scale bars 1 mm.





**Fig. 4.** Tippi Naala (stream) at Tippi, West Kameng district, Arunachal Pradesh, the type locality of *Psilorhynchus kamengensis*.

nal ossification. Anguloarticular portion of preoperculo-mandibular canal absent. Fifth ceratobranchial with four needle-like pharyngeal teeth arranged in a single row.

**Coloration.** In preservative: background light cream. Occiput greyish black. Dorsal surface between occiput and dorsal fin with two dark brown saddles: first, often indistinct, situated at one-third the distance between occiput and dorsal-fin origin, second, situated at dorsal-fin origin. Saddles posterior to dorsal-fin origin distinct, numbering four; positions variable except for first, situated below posterior half of dorsal fin (sometimes in contact with preceding one at dorsal-fin origin to form a single, large saddle, as in Fig. 1a), and last, situated at base of caudal fin. Saddles continuous with lateral blotches or lateral stripe, extending 2–3 scale rows on body sides. Flank bearing 5–6 indistinct dark brown lateral blotches; superimposed with distinct lateral stripe. Posterior margin of scales bordered with dark brown pigment. Scales in lateral-line scale row (L1) with dark brown blotch except along posteriormost rim. L+1 row indiscernible, except when distinct, reaching ventral through midway of dorsal-fin base; L+2 row usually absent, except when present (rarely), short and restricted to 4–5 anteriormost scales; L-1 row comprising sharply-contrasted brownish blotches covering complete surface of scales, and extending entire length of body, with interruptions at 1–3 scales in conjunct, or alternate, post anal-fin origin; L-2 row comprising of scattered brownish melanophores on posterior half of scales, originating from pectoral-fin base insertion, extending up to vertical through 5–6 scales beyond anus, and superimposing with pre-pelvic spot.

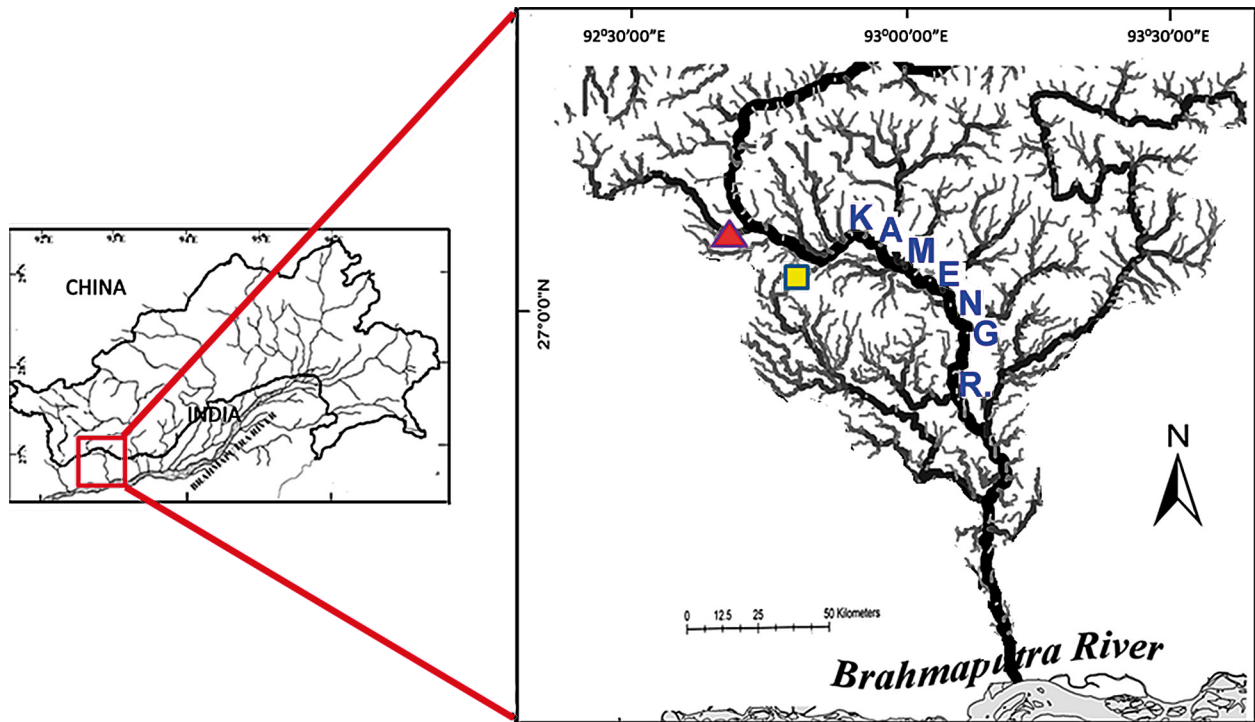
Scale-less base of pectoral-fin and scales adjacent to pelvic-fin origin peppered with dark brown melanophores, forming pectoral-base and pre-pelvic spots, respectively. Lateral surface of snout, region rimming ventral margin of orbit, and skin over opercle densely scattered with dark brown melanophores; nasal flap light cream. Ventral surface pale cream, devoid of any pigmentation, except for patches of dark brown melanophores on anterior tips of rostral cap groove. Dorsal surface of anterior pectoral- and pelvic-fin rays marked with small melanophores; dorsal fin with 1–3 rows of dark brown to black spots on undivided and branched rays; anal fin hyaline, except for row of pale brownish often indiscernible spots along branching points of fin rays. Caudal fin with three black bars: one at base of each lobe, giving appearance of a dumbbell-shaped bar constricted at centre; a second V-shaped bar across centre of fin, formed by small aggregated melanophores around first branching points of branched rays; and a third, highly-variable distal bar across tips of upper and lower lobes formed by aggregated melanophores, often indistinct on lower lobe.

**Habitat.** The new species was collected from swift, moderately-turbid water. The river bed consisted of gravel, cobbles or larger boulders, mostly covered with green algae, and stretches of sand. The river bank consisted of dense tropical deciduous vegetation (Fig. 4). The water parameters recorded during the month of May, 2019 were temperature 20.6 °C, pH 7.84, dissolved oxygen 5.3 mg/l and conductivity 183.2  $\mu\text{Scm}^{-1}$ . The associated fish species included *Barilius bendelisis*, *Mustura dikrongensis*, *Devario aequipinnatus*, *Garra* sp. and *Mastacembelus armatus*.

**Distribution.** *Psilorhynchus kamengensis* is presently known from its type locality – Tippi Naala (a stream at Tippi), and adjacent streams of the Kameng River in Arunachal Pradesh, India (Fig. 5).

**Etymology.** The new species is named after the Kameng River.

**Genetic distance and phylogeny.** The two *cyt b* sequences obtained from two specimens of *Psilorhynchus kamengensis* (GenBank accession numbers: MN180269 and MN180270), both 1107 bp long, have an intra-specific genetic distance (uncorrected pairwise *p*-distance) of 0.7 %. A nucleotide BLAST search at GenBank (NCBI) non-redundant database (*nr*) found no exact matches. However, the closest values belong to *P. balitora*, *P. nepalensis* and *P. nahlongthai*, with pairwise *p*-distances of 4.2 %, 8.5 % and 9.0 %, respectively. Genetic distance with *P. breviminor*, *P. gokkyi* and *P. rahmani* (all members of the *P. balitora* species group) are 15.5 %, 16.5 % and 16.3 %, respectively. Moreover, the genetic distance between *P. kamengensis* and *P. nudithoracicus* (from two available *cyt b* sequences) is 21.2 % and 21.5 %, respectively (Table S1). In the phylogram (Fig. 6) resulting from Maximum Likelihood (ML) analysis, reproduced



**Fig. 5.** Basin map of Kameng River (Brahmaputra drainage) showing the distribution and collection localities of *Psilorhynchus kamengensis* (Filled triangle: holotype; filled square: paratypes).

from the *cyt b* data set (including two *cyt b* sequences of *P. kamengensis* and 15 sequences of nearest congeners retrieved from GenBank), *P. kamengensis* is recovered as a member of the *P. balitora* species group, showing a sister group relationship with *P. balitora*. However, all other members of the *P. balitora* species group are placed in a separate clade as supported by the robust bootstrap values. An identical grouping was also obtained in the results for MP and NJ analyses (not shown herein).

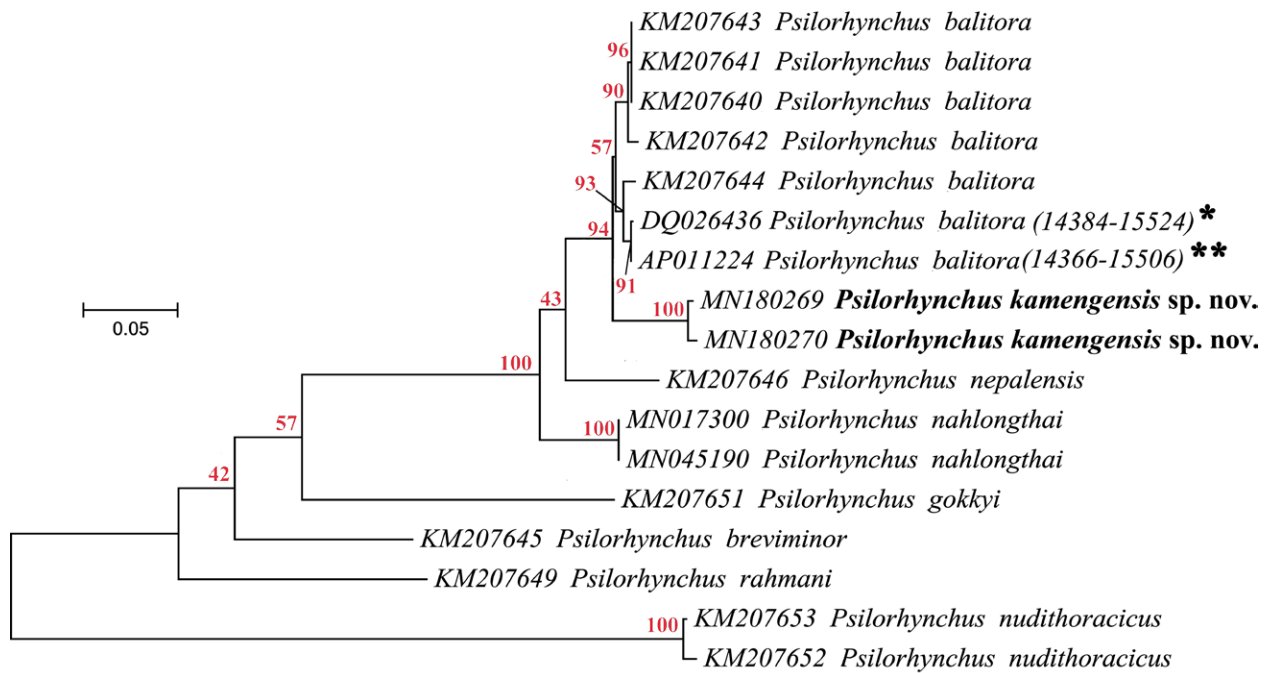
## Discussion

Members of the *Psilorhynchus balitora* species group are characterized by having a reduced anteriormost branchiostegal ray; a weakly-forked caudal fin, the upper and lower lobes with rounded tips; and absence of the articular portion of the preoperculo-mandibular sensory canal (CONWAY *et al.*, 2013). *Psilorhynchus kamengensis*, too, is placed in the *P. balitora* species group as it shares the aforementioned characters with other members of this group.

Currently, 16 species belong to the *Psilorhynchus balitora* species group – *P. balitora*, *P. hamiltoni*, *P. nahlongthai* and *P. nepalensis* from the Ganga-Brahmaputra drainage; *P. amplicephalus* from the Barak-Surma-Meghna drainage; *P. chakpiensis*, *P. maculatus* and *P. ngathanu* from the Chindwin drainage; *P. brachyrhynchus*, *P. breviminor*, *P. gokkyi*, *P. olliei* and *P. piperatus* from the Irrawaddy drainage; *P. kaladanensis* from the Kaladan drainage; *P. rahmani* from the Karnaphuli drainage; and *P. pavimentatus* from the Ann Chaung drainage.

*Psilorhynchus kamengensis* differs from all other members of the *P. balitora* species group in having a longer post-epiphyseal fontanelle, except *P. hamiltoni* [compare Fig. 3a with Fig. 13F–L in CONWAY *et al.* (2013)] and *P. nahlongthai*. However, it can be differentiated from *P. hamiltoni* in having a greater body depth (19.5–24.8 % SL vs. 14.4–17.1), shorter caudal peduncle (9.1–10.3 % SL vs. 12.9–16.7), wider head (67.5–78.9 % HL vs. 63.9–66.6), fewer lateral-line scales (32–33 vs. 34–35), more unbranched anal-fin rays (iii vs. ii), more branchiostegal rays (3 vs. 2), fewer dorsal procurrent rays (6 vs. 9), and fewer caudal vertebrae (10 vs. 18); and from *P. nahlongthai* in having more unbranched anal-fin rays (iii vs. ii), fewer branched anal-fin rays (6 vs. 8), pectoral fin not reaching (vs. reaching) vertical through dorsal-fin origin, more vertebrae (35 vs. 34), anteriormost branchiostegal ray extending one-third the length of second ray (vs. greatly reduced), and saddles continuous (vs. not continuous) with lateral blotches.

*Psilorhynchus kamengensis* differs from *P. balitora* in the absence (vs. presence) of scales in the mid-ventral region between the pectoral fins (see Fig. 2b), anteriormost branchiostegal ray extending one-third the length of second ray (vs. greatly reduced) [see Fig. 3c], and fewer caudal vertebrae (10 vs. 15–16); from *P. nepalensis* in having a shorter pectoral fin (not reaching vs. reaching vertical through dorsal-fin origin), adpressed anal fin not reaching (vs. reaching) the caudal-fin base, fewer rows of pre-anal scales in the mid-ventral region (3–4 vs. 7–8) [see Fig. 12H in CONWAY *et al.* (2013)], and the presence (vs. absence) of a prominent V-shaped bar in the middle of the caudal fin.



**Fig. 6.** Phylogram of Maximum Likelihood (ML) analyses ( $\ln L = -3960.109$ ) of *Psilorhynchus kamengensis*, based on *cyt b* gene sequences [\**cyt b* sequence retrieved from the whole mitochondrial genome of a specimen identified as *P. homaloptera* (NCBI Accession number: DQ026436: 14384–15524), following a BLAST search, reidentified as *P. balitora* by CONWAY *et al.* (2015); \*\**cyt b* sequence retrieved from the whole mitochondrial genome of a specimen labelled as *P. homaloptera* (NCBI Accession number: AP011224: 14366–15506), following a BLAST search, having 99.9 % similarity with the *P. balitora* sequence DQ026436].

ARUNACHALAM *et al.* (2007) reported the presence of 35–36 lateral-line scales in their original description of *Psilorhynchus amplicephalus*. However, cross examination of the type material by SHANGNINGAM & VISHWANATH (2013b) revealed the actual presence of 32+2 lateral-line scales. Although this lateral-line scale count falls within the range of *P. kamengensis* (i.e. 32–33+2), this species can be easily distinguished from *P. amplicephalus* in having fewer branched pectoral-fin rays (10 vs. 11–12), lesser head depth (49.4–58.0 % HL vs. 72.3–77.4), shorter caudal peduncle (41.0–48.9 % HL vs. 63.9–73.4), longer pectoral fin (22.0–24.1 % SL vs. 17.5–19.6) and in the presence (vs. absence) of transverse rows of unculi on the rostral cap.

Further, *Psilorhynchus kamengensis* can be distinguished from *P. brachyrhynchus* in having more branchiostegal rays (3 vs. 2), more unbranched anal-fin rays (iii vs. ii), a longer snout (50.0–59.6 % HL vs. 43.1–48.4), and fewer caudal vertebrae (10 vs. 17–18); from *P. breviminor* in having more vertebrae (35 vs. 32), fewer caudal vertebrae (10 vs. 15), and fewer principal caudal-fin rays (9+8 vs. 10+9); from *P. chakpiensis* in having more unbranched anal-fin rays (iii vs. ii), more lateral-line scales (32–33 vs. 30–31), a shorter caudal peduncle (9.1–10.3 % SL vs. 17.8–20.5), and fewer principal caudal-fin rays (9+8 vs. 10+9); from *P. gokkyi* in the absence (vs. presence) of a deep notch situated at the level of the ethmoid region, more unbranched anal-fin rays (iii vs. ii), fewer principal caudal-fin rays (9+8 vs. 10+9), a shorter caudal peduncle (9.1–10.3 % SL vs. 12.4–13.3) and more abdominal vertebrae (25

vs. 18–19); from *P. kaladanensis* in having fewer principal caudal-fin rays (9+8 vs. 10+9), more unbranched anal-fin rays (iii vs. ii), in the presence (vs. absence) of a prominent V-shaped band in the middle of the caudal-fin, and more vertebrae (35 vs. 32–33); from *P. maculatus* in having fewer lateral-line scales (32–33 vs. 35–36), more unbranched anal-fin rays (iii vs. ii), fewer principal caudal-fin rays (9+8 vs. 10+9), a shorter caudal peduncle (9.1–10.3 % SL vs. 11.3–12.7), and lesser head depth (49.4–58.0 % HL vs. 62.0–65.0); from *P. ngathanu* in having more unbranched anal-fin rays (iii vs. ii), fewer principal caudal-fin rays (9+8 vs. 10+9), and a shallower head (49.4–58.0 % HL vs. 63.3–73.1); from *P. olliei* in having fewer principal caudal-fin rays (9+8 vs. 10+9), more vertebrae (35 vs. 32–33), anteriormost branchiostegal ray extending one-third the length of second ray (vs. greatly reduced) and shorter caudal peduncle (9.1–10.3 % SL vs. 11.2–16.2); from *P. pavimentatus* in having fewer unbranched dorsal-fin rays (iii vs. ii), more unbranched anal-fin rays (iii vs. ii), fewer principal caudal-fin rays in the lower lobe (8 vs. 9), fewer caudal vertebrae (10 vs. 16), and the presence (vs. absence) of dark vertical bars across the caudal-fin; from *P. rahmani* by the presence (vs. absence) of dark bars across the dorsal and caudal fins, fewer principal caudal-fin rays (9+8 vs. 10+9 or 9+9), and more vertebrae (35 vs. 32); and from *P. piperatus* in having fewer branched rays in lower lobe of caudal fin (8 vs. 9), presence (vs. absence) of three regular vertical bars across the caudal-fin, shorter caudal peduncle (9.1–10.3 % SL vs. 11.3–13.4), and fewer caudal vertebrae (10 vs. 16).



Genetic distances have been used as a supporting aid in delimiting putative species in numerous taxonomic studies. Although the genetic divergence between *P. kamengensis* and *P. balitora* is not very high (= 4.2–4.8 %), it exceeds the threshold value of 4 % considered to be indicative of species level divergence in *cyt b* for fishes (ŘIČAN & KULLANDER, 2006 and WANG *et al.*, 2019). The phylogenetic analysis (Fig. 6), as inferred from the *cyt b* dataset, shows that *P. kamengensis* is grouped with *P. balitora* as a monophyletic lineage, where *P. kamengensis* is the sister species to *P. balitora*. Moreover, the molecular analyses support the view based on morphological characters to place the new species as a member of the *P. balitora* species group. This is evident from the well-supported clade for the new species with respect to *P. nudithoracicus*. Unavailability of *cyt b* sequences of *P. amplicephalus* and *P. hamiltoni* (also members of the *P. balitora* species group from Barak and Brahmaputra drainages) as of January 2020 in the GenBank database, restricted us to make further genetic comparisons in the present study. However, the two species can be easily separated from *P. kamengensis* based on morphological differences as discussed above.

Two *cyt b* sequences, labelled as *Psilorhynchus homaloptera* (GenBank Accession numbers: DQ026436: 14384–15524; AP011224: 14366–15506), revealed 98.95 % and 99.04 % similarities, respectively, with one sequence of *P. balitora* (GenBank Accession number: KM207644) and represent a misidentification; this is also evident in Figure 6 where they form a monophyletic group with other *P. balitora* sequences. The sequence DQ026436 (collection locality – India: Assam: aquarium trade, Brahmaputra drainage) was reidentified as belonging to *P. balitora* by CONWAY *et al.* (2015). The sequence AP011224 (collection locality – unknown), too, showed 99.9 % similarity with the *P. balitora* sample DQ026436, indicating an apparent misidentification.

## Comparative materials examined

*Psilorhynchus amplicephalus*: GUMF 520, 40.6 mm SL; India: Assam: Dima Hasao district: Unnamed stream of Jatinga River (Barak drainage) about 10 km downstream of Jatinga village. Additional data from ARUNACHALAM *et al.* (2007) and SHANGNINGAM & VISHWANATH (2013b).

*Psilorhynchus balitora*: GUMF 512/5, 5 specimens, 26.3–34.4 mm SL; India: West Bengal: Alipurduar District: Sankosh River at Barobisha. Additional data from RAINBOTH (1983) and CONWAY & MAYDEN (2008).

*P. breviminor*: Manipur University Museum of Fishes, Chanchipur, MUMF 12004, 47 mm SL; India: Manipur: Chandel District: Chakpi River at Ducho-Dujang.

*P. chakpiensis*: Manipur University Museum of Fishes, Chanchipur, MUMF 12071, holotype, 53.1 mm SL; India: Manipur: Chandel District, Chakpi River at Chakpikarong. Additional data from SHANGNINGAM & VISHWANATH (2013b).

*P. ngathanu*: Manipur University Museum of Fishes, Chanchipur, MUMF 12087–12091, 5 specimens, 52.3–60.0 mm SL; India: Manipur: Chandel District: Dutah River at Larong village. Additional data from SHANGNINGAM & VISHWANATH (2013c).

Published information used for comparison: CONWAY (2011) and CONWAY & KOTTELAT (2007) for *P. pavimentatus*; CONWAY & BRITZ (2010) for *P. brachyrhynchus*, *P. gokkyi*, *P. piperatus* and *P. rahmani*; CONWAY *et al.* (2013) for *P. hamiltoni*; SHANGNINGAM & VISHWANATH (2013a) for *P. maculatus*; CONWAY & MAYDEN (2008) and SHANGNINGAM & VISHWANATH (2013c) for *P. nepalensis*; LALRAMLIANA *et al.* (2015) for *P. kaladanensis*; CONWAY & BRITZ (2015) for *P. olliei*.

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