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Garra dengba, a new species of cyprinid fish (Pisces: Teleostei) from eastern Tibet, China

SHU-QING DENG[1,2], LIANG CAO[1,3] & E ZHANG[1]

[1]*Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, Hubei Province, China*
[2]*University of Chinese Academy of Sciences, Beijing 100049, China*
[3]*Corresponding author. E-mail: caoliang0205@ihb.ac.cn; Phone: +86-027-68780233*

Abstract

Garra dengba is here described from the Chayu-Qu, a tributary flowing into the Brahmaputra River, in Chayu County, eastern Tibet, China. It shares the presence of an incipient proboscis on the snout with *G. arupi*, *G. elongata*, *G. gravelyi*, *G. kalpangi*, and *G. rotundinasus*, but is distinguished from these five species in having, among other features, fewer branched dorsal- and anal-fin rays and more perforated lateral-line scales. Its validity was also confirmed by a molecular phylogenetic analysis based on the cytochrome *b* gene.

Key words: *Garra*, new species**,** morphology, cyt *b* gene, phylogenetic analysis

Introduction

The Chayu-Qu (= river) is one of largest rivers in eastern Tibet, China, rising in Kangri Garpo Range with the highest peak of 5475 m above sea level. The upper reach of this river is separated by this mountain range into two tributaries. The eastern one, also known as the Sang-Qu, has a total length of 178 km, a total fall of 4785 m in its course, and a catchment area of 6780 km^2. This tributary flows from northwest to southeast to Zhuwagen where it turns south, passing through the Chayu County seat and then heading towards Xiachayu to join the western tributary, Kangri Garpo-Qu. The western tributary, with its source in the southwestern side of Kangri Garpo, has a total length of 170 km, a total fall of 3000 m in its course, and a catchment area of 5376km^2. These two tributaries merge to form the Chayu-Qu (or Lohit River) that flows south into India and turns southwest into the Brahmaputra River basin.

The fish diversity of the Chayu-Qu is not well understood as the area drained by its lower reach is part of the disputed Himalayan ranges between China and India. Indian authors have done some research regarding the ichthyofaunal diversity of their claimed Arunachal Pradesh, which is referred to as Zangnan in China, whereas the lower reach of the Lohit River basin is inadequately sampled (Gurumayum *et al*. 2016). The fish species diversity of the Chayu-Qu was the subject of several Chinese authors (Wu *et al*. 1977; Wu *et al*. 1981; Wu &Wu 1992; Zhang *et al*. 1995). Eight valid species have been documented from this river (Zhu 1989; Chu 1999; Yue 2000). Among them are one loach (*Nemacheilus subfuscus*), three cyprinids (*Garra kempi*, *Schizothorax curvilabiatus*, and *Schizothorax molesworthi*), and four catfishes (*Exostoma labiatum*, *Glaridoglanis andersonii*, *Pareuchiloglanis kamengensis*, and *Pseudecheneis sulcata*). However, several species are poorly understood taxonomically. *Nemacheilus subfuscus* was synonymized with *Schistura scaturigina* McClelland 1839 (Kottelat 2012), and *Pareuchiloglanis kamengensis* was referred to a new genus *Creteuchiloglanis* Zhou, Li & Thomson (Zhou *et al*. 2011). It is also unveiled in the present investigation that specimens previously recognized by Chinese authors as *G. kempi* from the Chayu-Qu actually represent an undescribed species, here named as *G. dengba*.

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Materials and methods

Measurements were taken point-to-point with a dial caliper connected to a data recording computer and data recorded to the nearest 0.1 mm. Measurements and counts were made on the left side of individuals when possible following Zhang & Chen (2002), including counts of the lateral-line scales. Prepectoral, prepelvic, predorsal and preanal lengths were measured from the tip of snout to the pectoral-, pelvic-, dorsal-, and anal-fin origins, respectively. Disc width is the distance between the roots of two maxillary barbels; disc length is measured from the anterior mid-point of the anterior margin to the posterior mid-point of the posterior margin of the mental adhesive disc. Head width is the distance of the widest dimension with opercles closed; head depth is from the midline at the occiput vertically downwards to the ventral contour of the breast; pelvic-to-anal distance is from the pelvic-fin origin to the anal-fin origin. All morphometric data and meristic counts for specimens examined are summarized in Table1. The number of specimens with a specific meristic count is included in parentheses after the count. The anus-to-anal distance is given as a percentage of the pelvic-to-anal distance. Measurements of parts of the head are expressed as proportions of the head length (HL). The head length and measurements of other parts of the body are expressed as percentages of standard length (SL). The counts of dorsal- and anal-fin rays were taken from radiographs. Other fin rays were counted by utilizing a dissecting microscope. Vertebral counts including the Weberian apparatus were taken from radiographs following the method of Roberts (1989). The terms used in this study for description of the snout morphology and their definitions follow Reid (1985), Zhang & Chen (2002) and Nebeshwar & Vishwanath (2013).

Mitochondrial cytochrome *b* was selected for amplification and sequencing as it is the most widely used locus in fish phylogenetics (Zardoya & Meyer 1996). The genomic DNA was extracted from alcohol-stored fin tissues. The mitochondrial cyt *b* gene, around 1067bp (base pair), was amplified by the polymerase chain reaction in 25 μl reactions containing 1.5 μl dNTPs, 2.5 μl reaction buffer, 0.5 μl of each primer, 0.5 μl of Taq DNA Polymerase, 1 μl template DNA, and 18.5 μl H2O. The PCR reaction followed Yang *et al*. (2010): 94°C predenaturing (3min), 94°C denaturing (45s), 55°C annealing (45s), 72°C extension (1 min), for 35 cycles and a final 72°C final extension (7 min). Amplified products were subsequently purified and used for direct cycle sequencing by a commercial sequencing company. The primer pairs used for amplification and sequencing were LA-cyp ATGGCAAGCCTACGAA AAAC and HA-cyp TCGGATTACAAGACCGATGCTT (Tang *et al*. 2010).

The specimens used for molecular analysis and DNA sequences retrieved from GenBank are listed in Table 2. *Labeo stolizkae* and *Altigena lippa* were selected as outgroups following Zheng *et al*. (2010) and Wang *et al*. (2014); 22 congeners of *Garra* were used as ingroups for phylogenetic analysis. Multiple alignments were prepared for all sequences using MEGA 5.0 (Tamura 2011). Then DNASP v5 was used to filter the haplotype (Librado 2009). Phylogenetic analyses were performed using MrBayes 3.1.2 (Ronquist & Huelsenbeck 2003) with the following model: GTR + I + G. The model was selected by Akaike's information criterion (AIC), implemented in jModeltest (Darriba 2012). Bayesian analyses were initiated from random starting trees, and four Markov Chain Monte Carlo (MCMC) simulations were run simultaneously for 2,000,000 replicates, sampling one tree per 100 replicates for each run and the first quarter of the trees were discarded as burnin; the remaining trees from two independent runs were used to construct a 50% majority rule consensus tree.

Samples of *G. dengba* were collected in fish investigations during 1973 and 2016 into a tributary flowing into the Brahmaputra River basin, Chayu-Qu in Chayu County, eastern Tibet, West China. Some of them were preserved in 10% formalin preservative for morphological examination and the others in 95% ethyl alcohol for DNA extraction. A total of 33 specimens were used for morphological measurements and 7 specimens for molecular analyses. All specimens were stored in the Freshwater Fish Museum at the Institute of Hydrobiology (IHB), Chinese Academy of Sciences, Wuhan City, Hubei Province, China.

***Garra dengba*, sp. nov.**

(Figs. 1–2)

Garra kempi: Wu *et al*., 1977: 378 (Chayu-Qu, eastern Tibet, West China); Wu & Wu, 1992: 293–294 (Chayu, eastern Tibet, West China); Yue, 2000: 244–245 (Chayu, eastern Tibet, West China).

TABLE 1. Morphometric measurements and meristic counts for *Garra dengba* **sp. nov.**

	G. dengba (n=33)			
	Holotype	Range	Mean	SD
Standard length (SL)	108.6	42.9–108.6	70.0	18.03
Morphometric measurements				
% SL				
Body depth	15.1	15.1–20.2	18.1	1.44
Head length	20.6	18.8–26.5	22.3	1.60
Head width	17.1	16.3–20.1	18.5	0.83
Head depth	11.6	11.6–16.2	13.8	1.12
Caudal-peduncle length	14.7	13.7–17.5	15.7	1.04
Caudal-peduncle depth	10.4	9.9–12.5	11.0	0.62
Dorsal-fin length	17.6	16.1–25.3	19.9	1.89
Pectoral-fin length	17.0	17.0–23.0	19.6	1.68
Ventral-fin length	16.0	15.4–20.9	17.6	1.14
Anal-fin length	15.1	14.1–19.9	16.2	1.43
Predorsal length	47.1	44.2–52.2	47.8	1.86
Prepectoral length	18.1	17.3–24.6	20.8	1.95
Preventral length	49.5	47.5–56.4	51.3	1.93
Preanal length	75.4	72.4–80.8	76.0	1.86
% HL				
Snout length	44.9	37.8–51.9	45.5	3.23
Eye diameter	15.2	13.3–28.4	19.7	3.50
Interorbital width	44.0	43.2–53.8	47.8	3.08
Disc length	49.1	38.2–51.0	43.9	2.79
Disc width	64.1	57.4–73.4	65.8	4.89
% caudal-peduncle length				
Width of caudal peduncle	70.5	63.1–79.0	70.5	4.65
% pelvic to anal distance				
Vent to anal distance	52.5	48.3–59.6	53.8	3.4
Meristic counts				
Dorsal-fin rays	iii, 6	iii, 6		
Anal-fin rays	iii, 4	iii, 4		
Pectoral-fin rays	i,13	i,11–13		
Pelvic-fin rays	i, 8	i, 8		
Lateral-line scales	44	42–44		
Scales above lateral line	4	3.5–4.5		
Scales below lateral line	3	2.5–3.0		
Predorsal scales	15	14–16		
Circumpeduncular scales	12	12–14		
Vertebrae	42	39–42		

Holotype. IHB 2016032616, 108.6 mm SL; West China: eastern Tibet: Chayu County: Chayu-Qu, a tributary flowing into Brahmaputra River; about 28°26'55"N 97°02'48"E, collected by Liang Cao, March 2016.

Paratypes. West China: eastern Tibet: Chayu County: IHB 2016032611–2615, 5 specimens, 80.6–97.1 mm SL, Chayu-Qu; about 28°26'55"N 97°02'48"E, other data same as holotype; IHB 2016032617–2622, 6 specimens, 44.9–86.0 mm SL, Chayu-Qu; approximately 28°17'59"N 97°01'3'E, other data same as holotype.

Non-type materials. West China: eastern Tibet: Chayu County: Chayu-Qu: IHB 73VII0063–0066, 73VII0147, 73VII0169–0171, 73VII0173–0175, 73VII 0224, 73VII 0284, 73VII0300, 14 specimens, 42.9–89.2 mm SL; about 28°36'22"N 96°54'44"E, collected by Wenxuan Cao, July 1973; IHB2016109150–9153, 4 specimens, 50.8–99.4 mm SL, about 28°22'41"N 97°02'20"E, collected by Liang Cao, October 2016; IHB2016109154–9156, 3 specimens, 61.6–98.2 mm SL, about 28°40'47" N 96°49'43"E, collected by Liang Cao, October 2016.

Diagnosis. *Garra dengba* is distinguishable from all other Asian species of the genus except *G. arupi*, *G. elongata*, *G. gravelyi*, *G. kalpangi*, and *G. rotundinasus* by possessing an incipient (vs. no or prominent) proboscis on the snout. It is distinct from these five species in having 6 (vs. 7 or 8) branched dorsal-fin rays, 4 (vs. 5) branched anal-fin rays, 42–44 (vs. 32–39) perforated lateral-line scales, no lateral black stripes on side of body (vs. present, except in *G. kalpangi*), body depth 15.1–20.2% of SL (vs. 21.1–25.8% in *G. arupi* and *G. gravelyi*), 12–14 (vs. 15–16 in *G. arupi* and *G. kalpangi*) circumpeduncular scales, 14–16 (vs. 8–13) predorsal scales, no mid-lateral black band on flank (vs. present in *G. gravelyi* and *G. rotundinasus*), no black spots along dorsal-fin base (vs. present in *G. gravelyi*), no black band across dorsal fin (vs. present in *G. arupi and G. elongata*), no longitudinal lateral black stripes on flank (vs. present, except in *G. kalpangi*), and scaled (vs. scaleless in *G. elongata*) breast.

Description. Morphometric data and meristic counts for type specimens are given in Table 1. Body elongate, anteriorly cylindrical and posteriorly slightly compressed laterally, with greatest depth at dorsal-fin origin and least caudal-peduncle depth slightly closer to caudal-fin base than to posterior end of anal-fin base. Dorsal profile of head somewhat convex; profile of predorsal body almost straight or slightly convex, nearly straight or slightly concave from dorsal-fin origin to origin of dorsal procurrent caudal-fin rays. Ventral profile of head straight to oblique; nearly straight and flattened or somewhat convex from pectoral-fin insertion to anal-fin origin; concave from there to origin of ventral procurrent caudal-fin rays.

Head moderately large and depressed, longer than wide and wider than deep. Eye small, positioned dorso-laterally in upper half of head with slightly convex and broad interorbital space. Snout moderately rounded when ventrally viewed, and obtuse when laterally viewed; with weakly-developed proboscis pointed forward and reflected downward against snout in front of eyes; proboscis quadrate, delineated anteriorly from transverse rostral lobe and laterally from lachrymal field (or lateral lobe) by ethmoid furrow (or depressed rostral surface). Two pairs of barbels, shorter than eye diameter; rostral pair anterolaterally, maxillary ones hidden at corners of mouth, shorter than rostral ones. Rostral cap well-developed, pendulous and greatly crenulated with papillated distal margin, separated from upper jaw by deep groove, laterally continuous with lower lip around corners of mouth. Upper lip absent; upper jaw fully covered by rostral fold, with thin horny sheath on cutting edge. Lower lip modified to form mental adhesive disc. Disc elliptical, shorter than wide; anterior margin modified into transverse, fleshy and crescentic skin fold covered by numerous minute papillae, anteriorly separated from lower jaw by deep groove extending along entire length of lower jaw and posteriorly bordered in transverse deep groove with central callous pad; lateral and posterior margins surrounding central callous pad in shape of half circle, papillated and distally free; posterior margin reaching beyond vertical of posterior margin of eye.

Dorsal fin with 3 simple and 6 (33) branched rays, last one split to base; last simple ray slightly shorter than HL; origin slightly nearer to snout tip than to caudal-fin base; distal margin slightly concave. Pectoral fin with 1 simple and 11 (1), 12 (24), or 13 (8) branched rays, reaching about two-thirds distance to pelvic-fin insertion; shorter or equal to HL. Pelvic fin with 1 unbranched and 8 (33) branched rays, extending beyond midway to anal-fin origin and surpassing anus, somewhat shorter than HL; inserted closer to anal-fin origin than to anterior end of pectoral-fin base; positioned vertically at base of first or second branched dorsal-fin ray. Anal fin with 3 simple and 4 (33) branched rays, last one split to base; distal margin slightly concave; origin closer to pelvic-fin insertion than to caudal-fin base. Caudal fin deeply forked; upper and lower lobes equal in length and shape.

Body scaled; scales moderately sized; scales on chest and belly smaller than those on flank and embedded. Lateral line complete, horizontal, with 40 (20), 41 (8), or 42 (5) plus 2 scales on caudal-fin base; scale rows above lateral line 3 (1), 3.5 (9), or 4 (23) and below 2.5 (15) or 3 (18). Predorsal midline scales almost same size as flank scales and not embedded, regularly or irregularly arranged. Circumpeduncular scale rows 12 (32) or 14 (1). Axillary scales 2; first one present at base of pelvic fin, and last one reaching beyond base of last pelvic-fin ray. Anus positioned almost midway from pelvic- to anal-fin origin. Gas bladder bipartite, anterior chamber elliptical and posterior chamber stick-like, as long as anterior one. Intestine long, forming coils. Vertebrae 39 (3), 40 (16), 41 (12), or 42 (2).

FIGURE 1. *Garra dengba* **sp. nov.**, IHB 2016032616, holotype, 108.6 mm SL. Lateral (a), dorsal (b) and ventral (c) views of body. Scale bar = 1 cm.

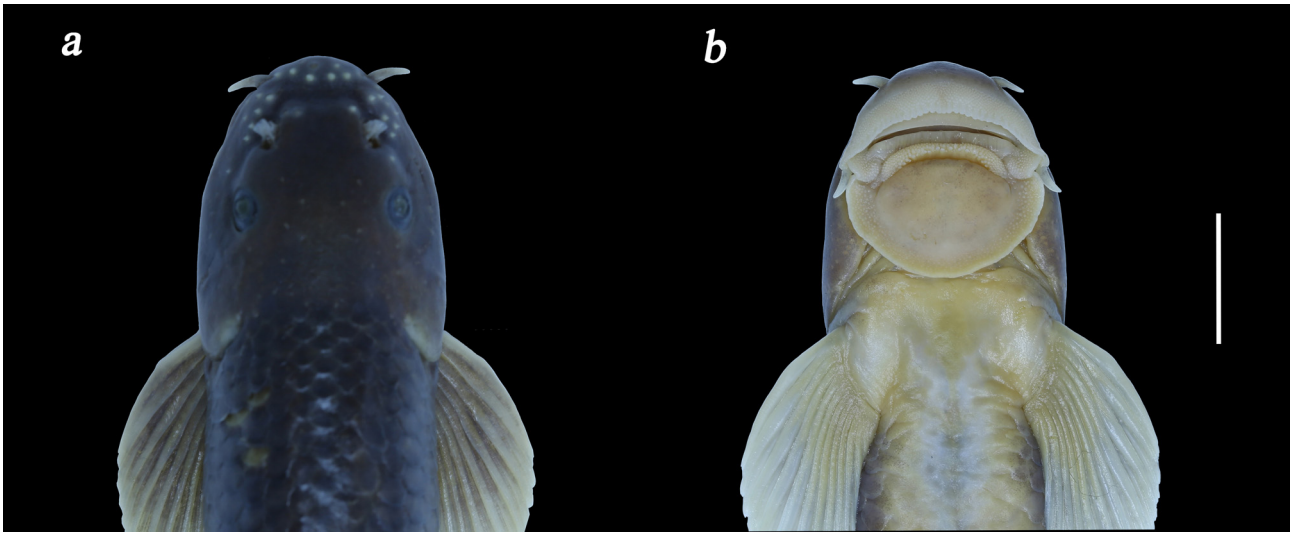

FIGURE 2. *Garra dengba* **sp. nov.**, IHB 2016032616, holotype,108.6 mm SL. (a) Dorsal view of head, and (b) ventral view of mental adhesive disc. Scale bar = 1 cm.

Coloration. In fresh specimens, head and body yellowish dorsally and laterally, grayish on ventral surface. In formalin-preserved specimens, head black or dark brown dorsally and laterally. Ground color of body dark or light

brown dorsally, becoming yellowish ventrally. Dorsal and caudal fins without dark chromatophores on distal interradial membranes constituting small black blotches. Dorsal, pectoral, pelvic, and anal fins grayish white with yellowish base.

Distribution. Known only from the Chayu-Qu (or Lohit River), a tributary flowing into the Brahmaputra River basin, in Chayu County, eastern Tibet, West China (Fig 3).

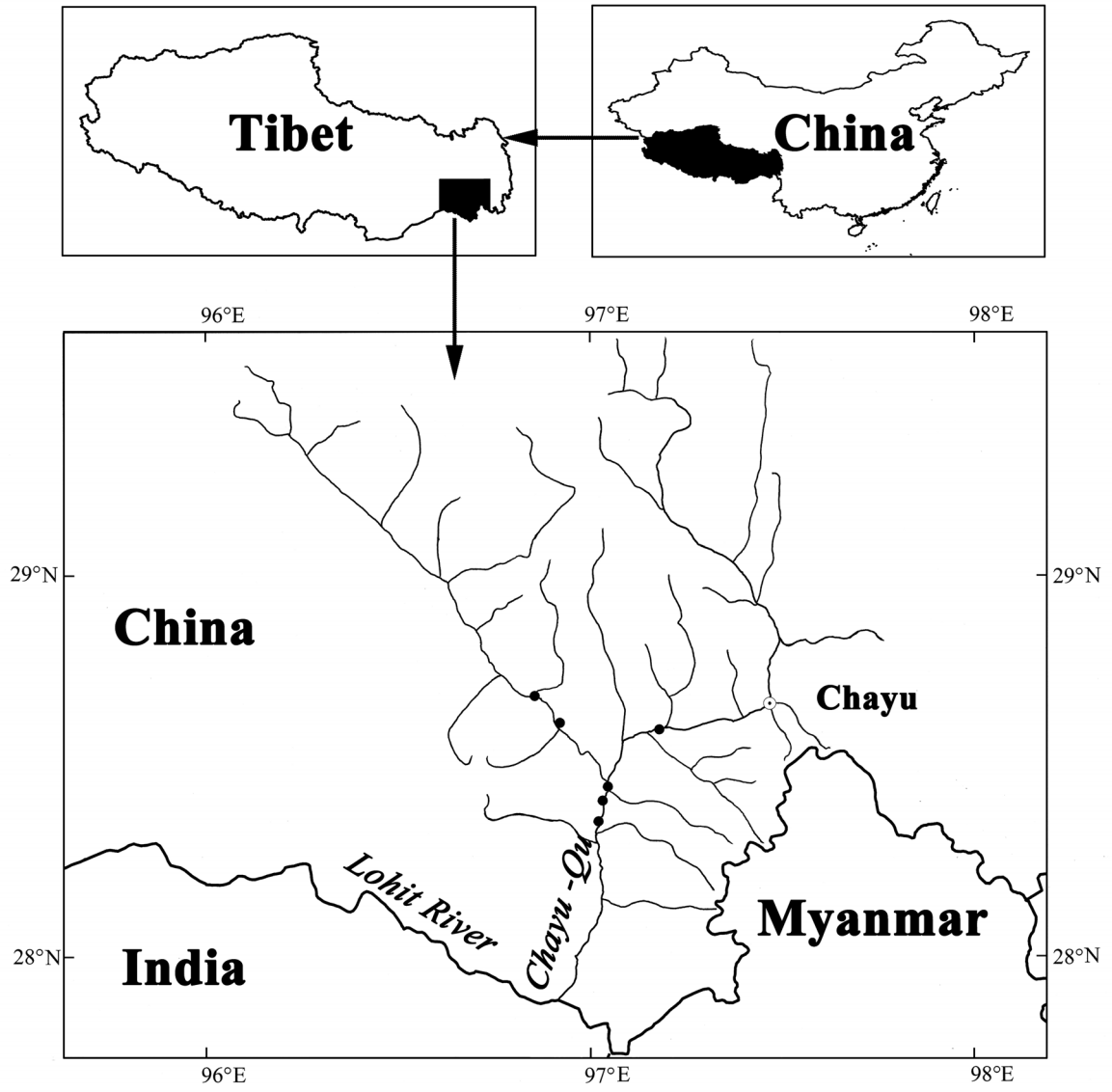

FIGURE 3. Collection localities of *Garra dengba* **sp. nov.**. Black dots indicate sampling sites.

Habitat and biology. This new species was caught in the mainstem and tributaries of the Chayu-Qu where it occurs in pebbly- and sandy-bottomed flowing water close to riverbanks (Fig. 4). Juveniles prefer shallow, slow-running water with pebbly sand substrate along the bank. Macroscopic visual examination of the gonads from some specimens caught in March showed the gonad maturation at the fourth stage, so indicating that this fish possibly spawns in spring. It mainly feeds on algae and organic debris as found in the gut content of several specimens examined.

Etymology. The specific epithet, herein utilized as a noun in apposition, is named after "Dengba", the Chinese name of Mishmi people who are not officially recognized as an ethnic group by the Chinese government. In China, Dengba people are now living in the area between the eastern Himalaya Mountains and western Hengduan Mountains at an altitude of 1000 meters above sea level. They have a concentrated distribution in Chayu County, eastern Tibet where the type material of the new species was collected.

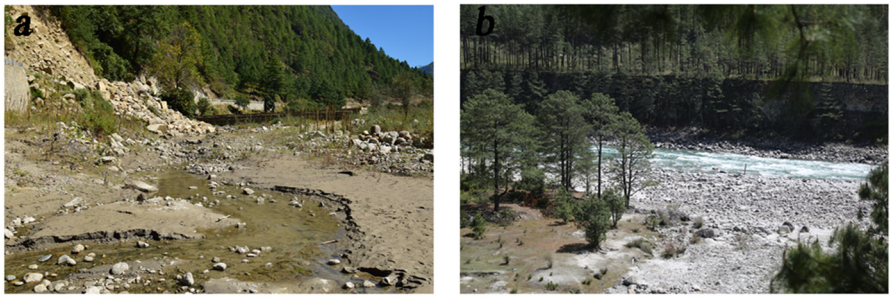

FIGURE 4. Habitat of *G. dengba*. (a) Hill stream with shallow, slowly running water with pebbly sand substrate along the river bank; (b) main stem with pebbly or sandy substrate, swiftly flowing water close to riverbanks.

TABLE 2. The mitochondrial cytochrome *b* sequences analyzed in this study.

Taxon	Location	Drainage	Accession number
Garra dengba1	Chayu, Tibet, China	Brahmaputra River	MH243429
Garra dengba2	Chayu, Tibet, China	Brahmaputra River	MH243435
Garra dengba3	Chayu, Tibet, China	Brahmaputra River	MH243431
Garra dengba4	Chayu, Tibet, China	Brahmaputra River	MH243434
Garra dengba5	Chayu, Tibet, China	Brahmaputra River	MH243430
Garra dengba6	Chayu, Tibet, China	Brahmaputra River	MH243432
Garra dengba7	Chayu, Tibet, China	Brahmaputra River	MH243433
Garra imberba	Xinping, Yunnan, China	Red River	KC119047
Garra nujiangensis	Cangyuan, Yunnan, China	Salween River	KC119055
Garra findolabium	Jinping, Yunnan, China	Red River	JQ864598
Garra fasciacauda	Puer, Yunnan, China	Lancang-Jiang	JQ864597
Garra tengchongensis	Tengchong, Yunnan, China	Irrawaddy River	JQ864586
Garra dulongensis	Dulongjiang,Yunnan, China	Irrawaddy River	JQ864590
Garra qiaojiensis	Yingjiang, Yunnan, China	Irrawaddy River	JQ864583
Garra salweenica	Dehong, Yunnan, China	Salween River	JQ864593
Garra orientalis	Longlin, Guangxi, China	Red River	JQ864581
Garra mirofrontis	Yunxian, Yunnan, China	Lancang-Jiang	JQ864584
Garra bicornuta	Peninsular India	Thunga River	JX074238
Garra ceylonensis	Sri Lanka		X074252
Garra cf annandalei	Nepal	Ganges River	JX074253
Garra flavatra	Myanmar	Sea tributary	AP011410
Garra fuliginosa	Thailand	Chao Phraya River	JX074255
Garra gotyla	Unknown	Brahmaputra River	JX074256
Garra kempi	India	Brahmaputra River	JX074243
Garra lamta	Nepal	Ganges River	JX074241
Garra lissorhynchus	India	Brahmaputra River	JX074242
Garra mullya	Peninsular India		JX074237
Garra nasuta	India	Brahmaputra River	JX074295
Garra spilota	Myanmar	Irrawaddy River	AP011327
Labeo stolizkae	Ruili, Yunnan, China	Irrawaddy River	GU086536
Altigena lippa	Mengna, Yunnan, China	Lancang-Jiang	JX074198

Sequence variation and molecular phylogeny

A total of seven sequences of cyt *b* (1067 bp) gene of *G. dengba* were successfully amplified; 22 sequences of *Garra* congeners retrieved from GenBank, along with these seven sequences, were used as ingroups for phylogenetic analysis. For the 1067 bp cyt *b* sequences, there were 628 conserved sites, 439 variable sites, 345 parsimony informative sites, and 94 singleton sites. The average frequency of four nucleotides of this new species was A=29.4%, T=29.8%, C=27.0%, and G= 13.8%; the base composition was A-T rich (59.2%). The seven sequences of *G. dengba* had 0.1–0.6% sequence divergence, with an overall intraspecific distance value 0.3%. Interspecific genetic distance values among sampled species pairs of *Garra* were 6.4–21.3% (overall mean distance 13.3%). The species under description had the minimum sequence divergence of 10.3% with *G. dulongensis,* and the maximum one of 17.2% with *G. lissorhynchys* and *G. imberba*; the mean genetic distance values between it and other sampled congeneric species was 14.1 %.

The Bayesian 50% majority consensus tree based on cyt *b* gene for this new species and 22 congeneric species is shown in Fig. 5. From the tree topologies, *G. dengba* was distantly related to *G. kempi*. It clustered with *G. dulongensis* and *G. tengchongensis*, both from a tributary flowing into the Irrawaddy River basin, to form an independent lineage with 100% posterior probability. *Garra kempi* was sister to *G. spilota* from the Irrawaddy River basin in Myanmar; this pair grouped with *G. flavatra* and *G. lissorhynchys* to represent a lineage poorly supported with < 50% posterior probability. The sister group of this lineage included two lineages: the one including *G. dulongensis*, *G. tengchongensis*, and *G. dengba* and the other whose basal group was occupied by the species pair *G. gotyla* and *G. qiaojiensis*.

TABLE 3. Main diagnostic characters for *Garra dengba* and five closely associated congeners with an incipient proboscis on the snout.

Characters	*G. dengba*	*G. arupi*	*G. elongata*	*G. gravelyi*	*G. kalpangi*	*G. rotundinasus*
Body depth in % SL	15.1–20.2	21.8–23.6[a]	17.4–19.2[b]	21.1–25.8[b]	18.9–23.8[f]	18.5–21.0[e]
Branched dorsal-fin rays	6	7[a]	7[c]	7[d]	8[f]	8[e]
Branched anal-fin rays	4	5[a]	5[b]	5[d]	5[f]	5[e]
Lateral-line scales	42–44	35–36[a]	41–42[b]	34–36[b]	32–33[f]	36–37[e]
Circumpeduncular scales	12–14	15–16[a]	12[a]	12[c]	16[f]	12[e]
Predorsal scales	14–16	11–12[a]	13[b]	8–9[b]	10–11[f]	10–11[e]
Mid-lateral black band on flank	absent	absent[a]	absent[b]	present[d]	absent[f]	absent[e]
Black spots at dorsal-fin base	absent	absent[a]	absent[b]	present[d]	absent[f]	absent[e]
Black band across dorsal fin	absent	present[a]	present[b]	absent[b]	absent[f]	absent[e]
Lateral stripes on side of body	absent	present[a]	present[b]	present[d]	absent[f]	present[e]
Scales on chest	present	present[a]	absent[b]	present[d]	present[f]	present[e]

Data from: a—Nebeshwar *et al* (2009); b—Vishwanath & Kosygin (2000); c—Kullander & Fang (2004); d—Menon (1964); e—Zhang (2006); f—Nebeshwar *et al* (2012).

Discussion

This new species has until now been misidentified as *G. kempi* by Chinese authors (Wu *et al*. 1977; Wu & Wu 1992; Yue, 2000; Zhang & Chen 2002). The type locality of *G. kempi* is in the Siyom River below Dema, Abor Hills in the Brahmaputra River basin (Hora 1921). It was documented by Menon (1964) and Talwar & Jhingran (1992) from the Siyom River, and by Vishwanath (1993) from the Leimarkhong stream and tributaries of the Tuival River of the Chindwin River basin in Manipur, India. Wu *et al*. (1977) were the first to record this species from the Chayu-Qu in Chayu County, eastern Tibet, China. Their identification was followed by Wu &Wu (1992) to document *G. kempi* from the river and by Zhang *et al*. (1995) from the Yarlung Zangbo-Jiang (the main Brahmaputra River in China before it enters into India) in Motuo County. The historical distribution of the species

also included the Daying-Jiang and Longchuan-Jiang, two tributaries discharging into the upper Irrawaddy River basin in Yunnan, China (Chu & Cui 1989; Chen 1998). Actually, the species under the name of *G. kempi* from this river basin was the misidentification of *G. tengchongensis* (Zhang & Chen 2002). Despite the recognition of the specimens from the Yarlung Zangbo-Jiang basin in eastern Tibet, China as *G. kempi* by Chinese researchers, they had no access to the type specimens of this species. The data utilized by Zhang & Chen (2002) for *G. kempi* was from Menon (1964). The updated information about this species is available in both Nebeshwar *et al*. (2009) and Nebeshwar & Vishwanath (2017). According to this information, *G. kempi* is a deep-bodied species (depth 20.7–23.1% of SL) which develops a weakly developed transverse lobe delineated posteriorly by a shallow transverse groove and no proboscis on the snout; 7–8 and 5 branched dorsal- and anal-fin rays, respectively; and 40–42 perforated lateral-line scales. By contrast, *G. dengba* has a slender body (depth 15.1–20.2 vs. 20.7–23.1% SL) with a weakly developed or incipient proboscis on the snout, 6 branched dorsal-fin rays, 4 branched anal-fin rays, and 42–44 perforated lateral-line scales (see Table 1).

Garra dengba is characterized by having a weakly developed or incipient proboscis on the snout. This character is shared with four congeners: *G. elongata*, *G. gravelyi*, *G. kalpangi*, and *G. rotundinasus* (Nebeshwar *et al*. 2012). It is also present in *G. arupi*, a new species first described by Nebeshwar *et al*. (2009) from the upper Brahmaputra River basin. In its original description, the species was referred to as a species without a proboscis on the snout, but the accompanying image 3 (page 199) clearly illustrated an incipient proboscis with several tubercles along the anterior margin before the nostrils, forwarded-pointed and reflected downward against the snout, separated anteriorly from the tuberculated rostral field or transverse lobe and laterally from the infraorbital field by a shallow ethmoid furrow (Reid 1985). Undoubtedly, *G. arupi* has an incipient proboscis in common with *G. dengba*, *G. elongata*, *G. gravelyi*, *G. kalpangi*, and *G. rotundinasus*. A prominent proboscis on the snout can be found in *G. bispinosa*, *G. qiaojiensis*, and *G. orientalis* (Zhang 2005: fig. 2) and also in *G. arunachalensis*, *G. birostris*, *G. cornigera*, *G. gotyla, G. koladynensis*, *G. quadratirostris*, and *G. trilobata* (Nebeshwar & Vishwanath 2017: fig. 4). The proboscis of this kind is distinct, heavily tuberculated and more or less anteriorly free. See the diagnosis and Table 3 for morphological differences among *G. dengba* and other five congeneric species with a weakly-developed proboscis on the snout.

Garra rupecula was originally described by McClelland (1838) from the Mishmi Hills in the Brahmaputra River basin. Menon (1964) designated it to the species group having a dark band across the dorsal fin, a W-shaped band in the caudal fin, and naked chest and belly. Other species that can be put under this group are *G. lissorhynchus*, *G. ahboyai*, *G. nambulica*, and *G. paralissorhynchus* (Vishwananth & Joyshree 2005) and *G. dampaensis* (Lalronunga *et al*. 2013). It appears that *G. rupecula*, like all these species, possesses 4 branched anal-fin rays. However, the description of the species by Menon (1964) was based on specimens collected from Manipur valley (in the Chindwin River basin) and its distribution in this basin has been ruled out (Vishwanath & Linthoingambi 2008). *Garra rupecula* is currently known only by McClelland's (1838) very brief statement (Lalronunga *et al*. 2013). According to its original description, it has 16 circumpeduncular scales, 35 perforated lateral-line scales, and no scales on the chest, thus differing from the species under description.

Garra dengba has 4 branched anal-fin rays instead of 5 in most currently recognized species of *Garra*, or even genera of the Labeonini. This character was found in other eight species: *G. manipurensis* by Vishwanath & Sarojnalini (1988), *G. nambulica* by Vishwanath & Joyshree (2005), *G. abhoyai*, *G. paralissorhynchus*, and *G. lissorhynchus* by Nebeshwar *et al*. (2012), *G. dampaensis* by Lalronunga *et al*. (2013), *G. tyao* by Arunachalam *et al*. (2014) and *G. namyaensis* by Shangningam & Vishwanath (2012) (see Table 4). This new species differs from these eight species in having an incipient proboscis on the snout (vs. absent), and 42–44 (vs. 31–37) lateral-line perforated scales; from all of them except *G. namyaensis* in having 12–14 (vs. 15–16) circumpeduncular scales; from all of them except *G. lissorhynchus* in having 14–16 (vs. 18–29 in *G. abhoyai* or 8–12 in *G. manipurensis*, *G. paralissorhynchus* and *G. tyao*) predorsal scales; from all of them except *G. abhoyai* and *G. nambulica* in having rostral lobes (vs. absent); and from all of them except *G. manipurensis* in the absence (vs. presence) of a W-shaped band on the caudal fin. It further differs from *G. tyao* in having a shallower (vs. deeper) body (depth 15.1–20.2 vs. 21.2–29.6 % of SL), six (vs. seven) branched dorsal-fin rays; further from *G. paralissorhynchus* in having a shallower (vs. deeper) body (depth 15.1–20.2 vs. 23.7–26.7 % of SL) and an anteriorly moved anus (vent-anal distance 48.3–59.6 vs. 31.7–35.2 % of ventral-anal distance); further from *G. manipurensis* in possessing six (vs. seven) branched dorsal-fin rays and a scaled (vs. scaleless) chest; further from *G. lissorhynchus* in lacking W-shaped band on the caudal fin.

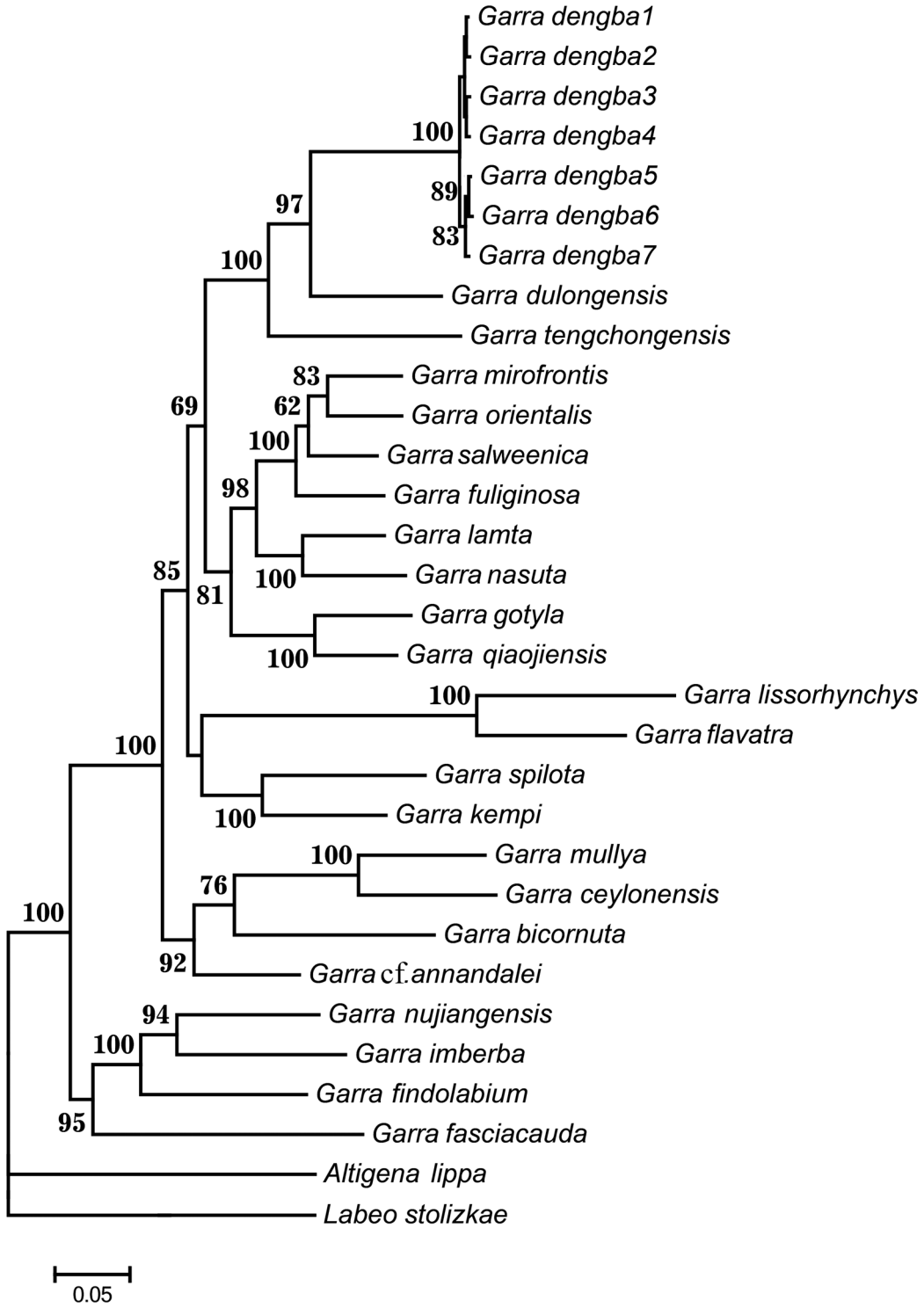

FIGURE 5. Bayesian inference tree derived from cyt *b* gene for 23 species of *Garra*. Nodal numbers are posterior probability values larger than 50%.

Kullander & Fang (2004) also found that five species of *Garra* from the Rakhine Yoma, southern Myanmar possessed three or four branched anal-fin rays: *G. propulvinus*, *G. vittatula*, *G. rakhinica*, *G. flavatra*, and *G. poecilura*. *Garra dengba* is distinct from these five species in having, among other features, no rostral lobe (vs. present), a weakly developed proboscis (vs. absent), a shallower (vs. deeper) body (depth 15.1–20.2 vs 21.9–30.0% of SL), more perforated lateral-line scales (42–44 vs. less than 35), more predorsal scales (14–16 vs. no more than 12), and fewer circumpeducular scales (12–14 vs. 16).

TABLE 4. Main diagnostic characters for *Garra dengba* and other congeners with four branched anal-fin rays.

	G. dengba	*G. abhoyai*	*G. dampaensis*	*G. lissorhynchus*	*G. manipurensis*	*G. nambulica*	*G. namyaensis*	*G. paralissorhynchus*	*G. tyao*
Body depth **(% SL)**	15.1–20.2	17.6–18.7[a]	20.1–22.7[c]	18.1–20.0[d]	20–21.2[f]	16.4–19.5[g]	19.0–21.0[h]	23.7–26.7[b]	21.2–29.6[j]
Vent-anal distance % pelvic-anal distance	48.3–59.6	38.2–46.5[a]	15.9–19.6[c]	37.3–40.2[d]	24–26.4[f]	34.0–43.4[g]	28.0–33.3[h]	31.7–35.2[b]	about 30%[j]
Dorsal-fin rays	iii, 6	iii, 6[a]	ii,6[c]	iii, 6[d]	ii, 7[f]	ii,6[g]	ii,6.5[h]	iii, 6[b]	ii–iii, 7[j]
Anal-fin rays	iii, 4	iii, 4[a]	iii, 4[c]	iii, 4[d]	ii, 4[f]	ii,4[g]	ii,4–4.5[h]	iii, 4[b]	ii–ii, 3–4[j]
Lateral line scales	42–44	34–36[b]	27–29[c]	34–35[d]	34–35[b]	36–37[g]	31[h]	32–33[d]	31[j]
Predorsal scales	14–16	18–29[b]	10–11[c]	14–15[d]	10–11[f]	16–29[g]	13[h]	11–12[i]	8–10[j]
Circumpeduncular scales	12–14	16[a]	16[c]	16[d]	16[f]	16[g]	14[h]	16[c]	15–16[j]
Rostral lobe	absent	absent[a]	present[c]	present[d]	present[b]	absent[g]	present[h]	present[b]	present[j]
W-shaped black band on caudal fin	absent	present[a]	present[c]	present[d]	absent[b]	present[g]	present[h]	present[i]	present[j]
Dark band across dorsal fin	absent	present[a]	present[c]	present[d]	absent[f]	present[g]	present[h]	present[i]	present[j]
A dark spot at upper extremity gill-opening	absent	absent[a]	present[c]	present[e]	absent[k]	present[g]	present[h]	present[i]	present[j]
Proboscis	present	absent[a]	absent[c]	absent[e]	absent[f]	absent[g]	absent[h]	absent[i]	absent[j]
Scales on chest and belly	present;	absent[a]	present[c]	absent[e]	absent on chest present on belly[f]	absent[g]	present[h]	absent[i]	present[j]

Data from: a-Vishwanath & Linthoingambi (2008); b-Nebeshwar *et al* (2012); c-Lalronunga *et al* (2013); d-Nebeshwar *et al* (2009); e-Menon (1964); f-Vishwanath & Sarojnalini (1988); g-Vishwanath & Joyshree (2005); h-Shangningam & Vishwanath (2012); i-Vishwanath & Shanta (2005); j-Arunachalam *et al* (2014); k-Nebeshwar, & Vishwanath (2017)

TABLE 5. Genetic distances of cyt *b* computed by MEGA among 23 species.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1. *G. dengba*																						
2. *G. bicornuta*	0.142																					
3. *G. ceylonensis*	0.165	0.126																				
4. *G.* cf. *annandalei*	0.131	0.103	0.130																			
5. *G. dulongensis*	0.103	0.140	0.157	0.114																		
6. *G. findolabium*	0.159	0.169	0.165	0.128	0.148																	
7. *G. flavatra*	0.169	0.171	0.182	0.158	0.173	0.183																
8. *G. fuliginosa*	0.119	0.133	0.143	0.108	0.132	0.156	0.168															
9. *G. gotyla*	0.156	0.140	0.139	0.129	0.131	0.144	0.155	0.111														
10. *G. imberba*	0.172	0.174	0.189	0.147	0.164	0.129	0.194	0.149	0.158													
11. *G. kempi*	0.126	0.139	0.157	0.112	0.124	0.131	0.167	0.115	0.129	0.129												
12. *G. lamta*	0.128	0.136	0.148	0.098	0.124	0.144	0.163	0.092	0.119	0.156	0.107											
13. *G. lissorhynchys*	0.172	0.159	0.184	0.166	0.159	0.187	0.116	0.161	0.157	0.213	0.183	0.173										
14. *G. mirofrontis*	0.120	0.139	0.127	0.114	0.123	0.142	0.155	0.075	0.111	0.148	0.131	0.096	0.171									
15. *G. mullya*	0.147	0.133	0.094	0.134	0.137	0.159	0.160	0.138	0.140	0.162	0.150	0.142	0.166	0.130								
16. *G. nasuta*	0.136	0.147	0.147	0.115	0.120	0.155	0.170	0.101	0.118	0.158	0.126	0.077	0.176	0.105	0.142							
17. *G. nujiangensis*	0.170	0.170	0.168	0.140	0.161	0.111	0.196	0.159	0.168	0.111	0.154	0.157	0.212	0.149	0.165	0.167						
18. *G. orientalis*	0.114	0.134	0.126	0.101	0.122	0.146	0.160	0.073	0.104	0.143	0.120	0.089	0.165	0.065	0.129	0.109	0.145					
19. *G. qiaojiensis*	0.144	0.148	0.147	0.129	0.128	0.142	0.153	0.116	0.075	0.166	0.122	0.112	0.169	0.104	0.127	0.113	0.159	0.104				
20. *G. salweenica*	0.118	0.127	0.124	0.109	0.112	0.146	0.161	0.068	0.110	0.158	0.118	0.093	0.165	0.064	0.139	0.094	0.154	0.070	0.109			
21. *G. spilota*	0.133	0.150	0.151	0.128	0.137	0.143	0.176	0.133	0.126	0.151	0.102	0.130	0.181	0.122	0.145	0.126	0.151	0.128	0.124	0.120		
22. *G. tengchongensis*	0.119	0.158	0.153	0.116	0.122	0.151	0.180	0.128	0.133	0.181	0.154	0.121	0.187	0.128	0.142	0.123	0.155	0.121	0.138	0.125	0.143	
23. *G. fasciacauda*	0.160	0.166	0.176	0.136	0.153	0.147	0.198	0.138	0.158	0.147	0.154	0.144	0.191	0.146	0.167	0.142	0.149	0.139	0.152	0.145	0.159	0.152

Garra dengba is so far known only from the Chayu-Qu, a tributary discharging into the Brahmaputra River basin where a total of 15 species from *Garra* have been identified as valid (Nebeshwar & Vishwanath 2017). Among them, seven species have a snout with a proboscis and a transverse lobe in common with *G. dengba*, namely *G. arunachalensis*, *G. birostris*, *G. gotyla*, *G. kalpangii*, *G. nasuta*, *G. quadratirostris*, and *G. tamangi*. The new species is distinct from *G. arunachalensis*, *G. birostris*, *G. gotyla*, and *G. quadratirostris*, in terms of Nebeshwar & Vishwanath (2013), in possessing more lateral scales (42–44 vs. 33–37), a more anteriorly positioned anus (vent to anal distance 48.3–59.6 % of pelvic to anal distance vs. 19.0–44.0%), and a shallower (vs. deeper) body (depth 15.1–20.2% of SL vs. 20.3–28.2%). *Garra nasuta* is a poorly understood species which is known only by its original description (Nebeshwar & Vishwanath 2013). It is a pit between the nares and also likely a proboscis with an anteriorly truncate margin and a transverse lobe. The first character can easily distinguish *G. nasuta* from *G. dengba*. Judged from the illustration of McClelland (1838), reproduced as fig. 9 in Nebeshwar & Vishwanath (2013), *G. nasuta* has a prominent proboscis on the snout instead of an incipient one in *G. dengba*. The new species is distinguished from *G. tamangi*, according to Gurumayum *et al*. (2016), by having more perforated lateral-line scales (42–44 vs. 33–34), fewer branched dorsal-fin rays (6 vs. 8–9), more predorsal scales (14–16 vs. 10–11) and a shallower (vs. deeper) body (depth 15.1–20.2 vs. 20.7–22.3% SL).

The recognition of *G. dengba* as a valid species is corroborated by its marked sequence divergence from sampled congeners (Table 5), and its monophyletic nature recovered in the phylogenetic trees inferred from cyt *b* (Fig. 5). This new species had a significant sequence divergence from sampled congeners (10.3–17.2%). The BI trees produced in this study clearly showed that *G. dengba* grouped with *G. tengchongensis*, *G. dulongensis* into a monophyletic lineage where *G. dengba* and *G. dulongensis* were paired species sister to *G. tengchongensis*, and its monophyly was well supported with 100% posterior probability. Given *G. dulongensis* and *G. tengchongensis* are regarded as valid, the species status of *G. dengba* is warranted.

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