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Four new species of *Channa* from Myanmar (Teleostei, Labyrinthici, Channidae)

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Abstract. We describe four new species of *Channa* from Myanmar, all members of the Gachua group. *Channa rakhinica*, new species, is a species endemic to west-flowing streams on the western slope of the Rakhine Yoma in Rakhine State; *C. rubora*, new species, occurs in mountain streams south of Mogaung, Kachin State; *C. coccinea*, new species, co-occurs with *C. burmanica* in streams north of Putao, also Kachin State, at the foothills of the Himalayas; and *C. pyrophthalmus*, new species, is found in streams in Tanintharyi Region at the southernmost tip of Myanmar, bordering Thailand. All four species are readily diagnosed by their colour pattern from other Gachua group taxa. They show genetic distances of 3.5–19.9% in the COI barcoding gene to other Myanmar members of the Gachua group.

Key words. snakehead fishes, Channoidei, Indo-Burman ranges, Tenasserim ranges, Himalayan foothills

INTRODUCTION

Along with Anabantoidei, Badidae, Nandidae, and Pristolepididae, snakehead fishes or Channoidei are members of the teleostean acanthomorph order Labyrinthici (=Anabantiformes), a monophyletic group characterised by the shared derived possession of teeth on the parasphenoid (Britz et al., 2020). Channoidei is comprised of two families, the Aenigmachannidae and Channidae (Britz et al., 2020). While aenigmachannids are restricted to the southwestern corner of peninsular India, channids are known from Africa (three species) and Asia (53 species). The highest endemic species level diversity has been recorded from the mountain areas in Northeast India and western and northern Myanmar, an area previously referred to as the Eastern Himalaya biodiversity hotspot (Conte-Grand et al., 2017; Rüber et al., 2020). With over 20 described and several undescribed snakehead species, representing at least 40% of the species diversity of *Channa*, this hotspot has had a complex geological and biogeographical history (e.g., Gregory, 1925; Rüber et al., 2004, 2020; Zhang et al., 2019). Most of the species level diversity within *Channa* is in the Gachua group sensu Britz (2008), which includes a large number of narrow-range endemics with a preference for mountain streams (Rüber et al., 2020); their greatest diversity is concentrated in the Eastern Himalaya hotspot (see Fig. 1).

This Gachua group is also interesting behaviourally, as it includes not only egg float guarders, but also several mouthbrooding species (Rüber et al., 2020). Additionally, the unusual provisioning of offspring with trophic eggs has been recently described in a number of species of the Gachua group, in which the young are fed with infertile, yolk-rich eggs produced specifically for this purpose by the female (Weijola, 2022).

To date, Myanmar is known to be home to 11 species of snakehead fishes from five species groups: *Channa lucius* (Cuvier, 1831) from the Lucius group, *C. aurolineata* (Day, 1870) from the Marulius group, *C. striata* (Bloch, 1793) from the Striata group, *C. punctata* (Bloch, 1793) and *C. panaw* Musikasinthorn, 1998 from the Punctata group, and *C. limbata* (Cuvier, 1831), *C. stewartii* (Playfair, 1867), *C. harcourtbutleri* (Annandale, 1918), *C. burmanica* Chaudhuri, 1919, *C. ornatipinnis* Britz, 2008 and *C. pulchra* Britz, 2008 from the Gachua group.

Collections made in Myanmar during the last 15 years in the mountain areas of the Rakhine State, Kachin State, and Tanintharyi Region have revealed a further four new species of snakehead fishes from the Gachua group, and these are described in this paper.

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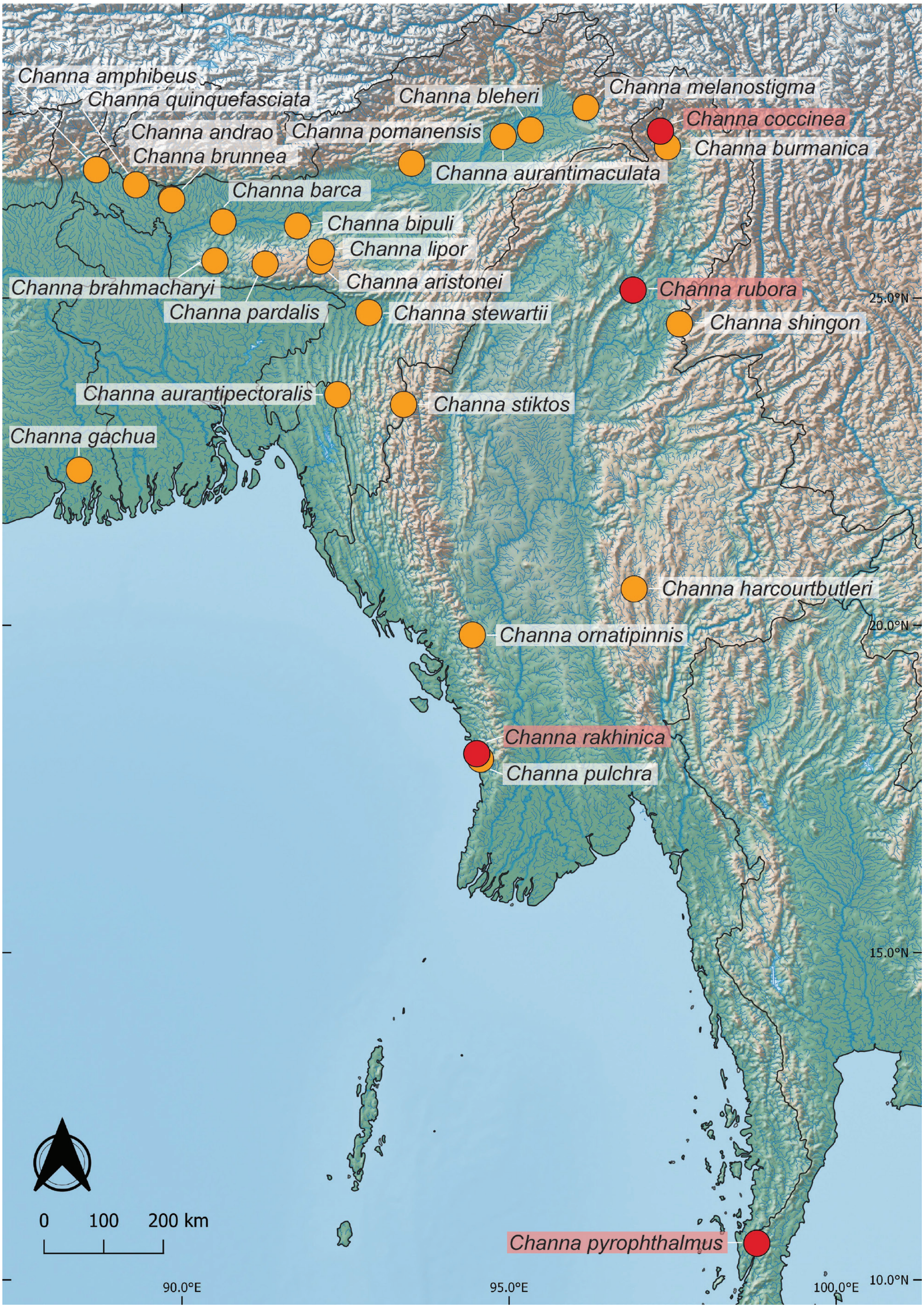

Fig. 1. Map of region of Eastern Himalaya and Indo-Burma biodiversity hotspots with type localities of snakehead species of the Gachua group. Type localities of the species described in this paper are highlighted in red. The type localities of the following species of the Gachua group lie outside of the map area: *Channa kelaartii* (Sri Lanka), *Channa limbata* (Java, Indonesia), *Channa orientalis* (Sri Lanka), *Channa rara* (Western Ghats, India). For type locality of *C. gachua* and other species described by Hamilton (1822), see Britz (2019).

MATERIAL AND METHODS

Morphology. Measurements follow Britz (2008) and were taken with digital calipers to the nearest 0.1 mm. Vertebrae were counted from radiographs. Fin-ray counts for unpaired fins were also obtained from radiographs, and those of pectoral fins under transmitted light. In the description, frequencies of counts are provided in parentheses after the count; fin ray and vertebral counts for holotypes are marked with an asterisk *.

One paratype of *Channa rakhinica* (MTD 40204, 113.0 mm SL), *C. rubora* (MTD 40207, 78.8 mm SL), *C. coccinea* (MTD 40202, 117.0 mm SL), and *C. pyrophthalmus* (MTD, 40203, 106.4 mm SL) were CT-scanned with a Zeiss XRadia Context at 80kV and 7W with an exposure of 1.5s, 3–4 frames, 4501 projections and a voxel size of 8–11 µm. Datasets were segmented and rendered with the software package Dragonfly and organised into figures in Adobe Photoshop.

Specimens are deposited in the collections of the Natural History Museum, London (BMNH), the Lee Kong Chian Natural History Museum, National University of Singapore, Singapore (ZRC), the Senckenberg Natural History Collections Dresden (MTD), the Museum of Natural History Vienna (NMW), and the Swedish Museum of Natural History, Stockholm (NRM).

Molecular data. In order to assess the genetic diversity among the Gachua group species, we assembled the most comprehensive cytochrome c oxidase subunit I (COI) nucleotide data set of snakeheads to date. The data set includes a total of 1092 Channidae sequences comprising: a) 772 individuals that were used in the analyses of Conte-Grand et al. (2017). From the 777 individuals used by Conte-Grand et al. (2017), we omitted five individuals (HM117177–HM117181) that showed unusual long branches in Conte-Grand et al. (2017); b) 281 individuals of members of the Gachua group published in GenBank after the DNA barcode study of Conte-Grand et al. 2017 (with accession numbers: KU667357–KU667361, KX399271–KX399275, KX946604, KX951877, KY214136–KY214143, KY356788–KY356799, KY562574–KY562579, KY563771–KY563773, KY863527–KY863530, KY863544–KY863546, LC189607–LC189638, LC190092–LC190132, LC190208–LC190214, LC190225–LC190234, LC190251, LC190327–LC190330, LC190338, LC645183, MF462267, MG736593–MG736595, MG825616–MG825618, MG976494, MG989241, MH156956, MH559819–MH559825, MH627036–MH627037, MH795975, MK191833–MK191834, MK216795, MK303761–MK303763, MK386958, MK424817–MK424818, MK431774, MK440660, MK440694, MK461185, MK471230, MK572105, MK599528–MK599531, MK610308, MK632315–MK632316, MK632318, MK913902, MN075125, MN504646–MN504650, MN685707, MN863381, MN863531–MN863534, MN900749–MN900752, MN902180, MN902181, MN910263, MT040625–MT040626, MT062517–MT062519, MT074045–MT074047, MT118102, MT158321–MT158324, MT160362–MT160365, MT299903–MT299913, MT439603–MT439616, MT720842–MT720847, MW002468, MW002470, MW002473–MW002475, MW002479, MW002494, MW454947–MW454966, MW485084, MW591026, MW967304, OK035705, OK035707, OK489448, OL343009, OP038555) and c) 39 sequences we newly generated specifically for this study (see Table 1 for details) and deposited in Genbank under accession numbers OR780450–OR780488. For the newly generated sequence data, we closely followed the protocol of Conte-Grand et al. (2017). Total genomic DNA was extracted from muscle tissue or fin clips preserved in 100% ethanol and stored at –80 °C using the DNeasy Blood and Tissue Kit on a QIAcube robotic workstation following manufacturer's instructions (Qiagen, Hilden, Germany). The universal COI barcoding region was amplified using the following primer combinations: FishF1 and FishR1 or FishF2 andFishR2 (Ward et al., 2005). PCR protocol and PCR conditions follow Conte-Grand et al. (2017). PCR products were cleaned and Sanger sequenced in both directions by LGC Genomics (Berlin, Germany), using the same primer pairs that were used for PCR amplification. Raw reads were edited and assembled into contigs using Geneious Prime v2022.0.2 (https://www.geneious.com) and individual consensus sequences together with sequences used by Conte-Grand et al. (2017) and those newly available from GenBank were aligned using MAFFT v7.017 (Katoh & Standley, 2013), as implemented in Geneious Prime. PAUP* v4.0a147 was used to generate a neighbour-joining (NJ) tree based on HKY distances and node support was evaluated with 1000 bootstrap pseudoreplicates. We used *Parachanna* as outgroup taxon. Genetic distances (p-distances) within and between species of interest were calculated in PAUP* v4.0a147 (Swofford, 2002).

TAXONOMY

Channa rakhinica, new species

(Figs. 2–5)

Holotype. BMNH 2019.10.16.190, 124.5 mm SL; Myanmar: Rakhine State, Kyeinthali township, Kyauk Tan village, South Stream, 18.0380°N 94.5072°E, coll. Britz et al., 1 December 2009.

Paratypes. BMNH 2019.10.16.191–193, 3 ex., 80.0–92.5 mm SL; same information as holotype. MTD 40204, 1 ex., 113.0 mm SL; same information as holotype. —BMNH 2019.10.16.276–282, 7 ex., 64.5–86.5 mm SL; Myanmar, Kyeinthali, coll. Tin Win et al., October 2008. —BMNH 2022.6.23.1004–1006, 3 ex., 83.3–97.1 mm SL; Myanmar, Rakhine State, Kyeinthali township, Kyauk Tan village, North Stream, 18.0455°N 94.4942°E, coll. Britz et al., 1 December 2009. —BMNH 2019.10.16.259, 1 ex, 94.2 mm SL; Myanmar, Rakhine State, Kyeinthali township, Kyeinthali Chaung, coll. Tin Win et al., October 2008. —BMNH 2019.10.16.269–275, 7 ex., 95.7–125.3 mm SL; Myanmar, Rakhine State, Kyeinthali township, Kyeinthali Chaung, coll. Tin Win et al., October 2008. —BMNH

Table 1. List of novel sequences generated specifically for this study with LR numbers and GenBank accession numbers.

Species	Sample ID	GenBank	Collector	Locality
Channa aristonei	LR15516	OR780450	D. Niemeier	India; aquarium trade
Channa aristonei	LR15517	OR780451	D. Niemeier	India; aquarium trade
Channa barca	LR09004	OR780452	P. Antler	India; aquarium trade
Channa barca	LR14764	OR780453	D. Niemeier	India; aquarium trade
Channa barca	LR14765	OR780454	D. Niemeier	India; aquarium trade
Channa barca	LR14766	OR780455	D. Niemeier	India; aquarium trade
Channa barca	LR14767	OR780456	D. Niemeier	India; aquarium trade
Channa barca	LR14768	OR780457	D. Niemeier	India; aquarium trade
Channa burmanica	LR09386	OR780458	R. Britz	Myanmar, Putao, fish market
Channa cf. *pulchra*	LR15520	OR780459	D. Niemeier	Myanmar; aquarium trade
Channa cf. *rakhinica*	LR15543	OR780460	H.H. Tan	Myanmar; aquarium trade
Channa coccinea	LR15522	OR780461	D. Niemeier	Myanmar, Putao; aquarium trade
Channa coccinea	LR15553	OR780462	H.H. Tan	Myanmar; aquarium trade
Channa coccinea	LR15554	OR780463	H.H. Tan	Myanmar; aquarium trade
Channa coccinea	LR15555	OR780464	H.H. Tan	Myanmar; aquarium trade
Channa coccinea	LR15556	OR780465	H.H. Tan	Myanmar; aquarium trade
Channa melanostigma	LR15515	OR780466	D. Niemeier	India; aquarium trade
Channa pulchra	LR06620	OR780467	R. Britz	Myanmar, Taung Chaung, near Kyeintali
Channa pulchra	LR06626	OR780468	R. Britz	Myanmar, Comepyo Chaung near Gwa
Channa pulchra	LR06629	OR780469	R. Britz	Myanmar, Comepyo Chaung near Gwa
Channa pyrophthalmus	LR15549	OR780470	H.H. Tan	Myanmar; aquarium trade
Channa pyrophthalmus	LR15550	OR780471	H.H. Tan	Myanmar; aquarium trade
Channa rakhinica	LR08991	OR780472	P. Antler	Myanmar; aquarium trade
Channa rakhinica	LR02204	OR780473	R. Britz	Myanmar, Seik Chaung
Channa rakhinica	LR02261	OR780474	R. Britz	Myanmar, Seik Chaung
Channa rakhinica	LR02655	OR780475	T. Win	Myanmar, Kyeintali Chaung
Channa rakhinica	LR06615	OR780476	R. Britz	Myanmar, Comepyo Chaung near Gwa
Channa rakhinica	LR06619	OR780477	R. Britz	Myanmar, Taung Chaung, near Kyeintali
Channa rubora	LR06634	OR780478	R. Britz	Myanmar, Mogaung, preserved at Tin Win‘s farm
Channa rubora	LR06635	OR780479	R. Britz	Myanmar, Mogaung, preserved at Tin Win‘s farm
Channa rubora	LR15523	OR780480	H.H. Tan	Myanmar; aquarium trade
Channa rubora	LR15524	OR780481	H.H. Tan	Myanmar; aquarium trade
Channa rubora	LR15525	OR780482	H.H. Tan	Myanmar; aquarium trade
Channa rubora	LR15526	OR780483	H.H. Tan	Myanmar; aquarium trade
Channa rubora	LR15528	OR780484	H.H. Tan	Myanmar; aquarium trade
Channa shingon	LR15514	OR780485	D. Niemeier	China, Yunnan; aquarium trade
Channa stewartii	LR15539	OR780486	H.H. Tan	Myanmar; aquarium trade
Channa stewartii	LR12650	OR780487	R. Britz	India; aquarium trade
Channa torsaensis	LR15580	OR780488	D. Niemeier	India; aquarium trade

Fig. 2. *Channa rakhinica*, BMNH 2019.10.16.190, 124.5 mm SL, holotype, in dorsal (top), lateral (middle), and ventral (bottom) view; Myanmar: Rakhine State, South Stream.

2019.10.16.261–264, 4 ex., 95.1–126.0mm SL; Myanmar, Rakhine State, Kyeinthali township, Kyeinthali Chaung, coll. Tin Win et al., 5 December 2004. —BMNH 2007.8.17.1–10, 10 ex., 57.7–105,7 mm SL; Myanmar, Rakhine State, Ann township, Kazukaing villlage, remnant pools of Myaung Gyi Chaung, a tributary of Dalet Chaung, 19.9247°N 93.7933°E, coll. Britz et al., 5 April 2007. — BMNH 2019.10.16.207–258, 48 ex., 42.0–121.2 mm SL; Myanmar, Rakhine State, Ann township, Kazukaing villlage, remnant pools of Myaung Gyi Chaung, a tributary of Dalet Chaung, 19.9247°N 93.7933°E, coll. Britz et al., 5 April 2007. — MTD 40205, 5 ex., 55.4–110.9 mm SL; Myanmar, Rakhine State, Ann township, Kazukaing villlage, remnant pools of Myaung Gyi Chaung, a tributary of Dalet Chaung, 19.9247°N 93.7933°E, coll. Britz et al., 5 April 2007. — MTD 40206, 121.8 mm SL; Myanmar, Rakhine State, Kyauktaw township, Sinkae villlage, remnant pools of tributary stream of Laymyo (Lemro) River, 20.7554°N 93.2713°E, coll. Britz et al., 4 April 2007. —BMNH 2007.8.17.12–20, 9 ex., 56.5–114.7 mm SL; Myanmar, Rakhine State, Kyauktaw township, Sinkae villlage, remnant pools of tributary stream of Laymyo (Lemro) River, 20.7554°N 93.2713°E, coll. Britz et al., 4 April 2007.

Diagnosis. A member of the Gachua group readily distinguished from other Myanmar members by its colour pattern in life including reddish cheek, series of up to 5 semicircular concentric maroon pectoral bands wider than interbands, series of 6–7 saddle-like blotches, orange subdistal and white distal rim on dorsal- and caudal fins (vs. different colour pattern). It is further distinguished from *C. stewartii* by fewer dorsal-fin rays (34–38 vs. 39–41), and generally fewer anal-fin rays (23–25, rarely 22 or 26 vs. 26–27) and from *C. burmanica* by presence of pelvic fins (vs. absence). It also differs substantially from all Myanmar Gachua group snakeheads by a genetic distance of 12.9–18.5% in the COI gene.

Table 2. Selected morphometric information for *Channa rakhinica* (n=10), data for holotype in parentheses following range.

	Range (holotype)	**mean ± standard deviation**
Standard length (SL in mm)	80–125.3 (124.5)	
In % SL		
Head length	28.8–30.8 (28.8)	29.5±0.7
Body depth	15.8–17.9 (17.2)	16.7±0.7
Body width	11.3–13.7 (13.5)	12.5±0.9
Predorsal length	35.9–39.6 (36.9)	37.2±1.1
Preanal length	49.9–54.9 (53.4)	52.6±1.7
Prepelvic length	34.9–38.5 (34.9)	36.5±1.2
Dorsal-fin base length	54.0–60.5 (58.2)	58.5±1.9
Anal fin-base length	34.2–40.3 (37.3)	36.8±2.2
Pectoral-fin length	19.0–22.2 (19.8)	20.8±1.2
Pelvic-fin length	7.1–8.6 (8.3)	7.7±0.5
In % HL		
Eye diameter	14.7–16.2 (15.6)	15.4±1.7
Head depth	45.3–50.7 (50.7)	47.9±3.6
Head width	62.9–67.9 (66.9)	66.4±1.5

Fig. 3. *Channa rakhinica*, paratypes in lateral view, BMNH 2019.10.16.207-258, 111.7 mm, Myanmar, Rakhine State, Dalet Chaung (top), MTD 40206, 121.8 mm SL, Myanmar, Rakhine State, Laymyo Chaung (bottom).

Description. See Figs. 2–3, 5 for general appearance and Table 2 for morphometric information and Table 6 for select meristic characters. Body elongate, round in cross section anteriorly, laterally compressed at caudal peduncle, body depth 5.6–6.3 times in SL. Head large, length 3.2–3.5 times in SL. Head widest halfway between posterior margin of eye and that of opercle. Mouth large, maxilla extending posteriorly beyond jaw angle, lips fleshy. Premaxilla with multiple rows of small sharp, pointed teeth (Fig. 4a). Dentary also with several series of small teeth anteriorly, a single series of small teeth along most of the lateral margin and an internal series of larger canines (Fig. 4b). Vomer with a few very large teeth in the middle and smaller teeth at lateral corner (Fig. 4a). Palatine with external series of smaller teeth and an internal row of up to 7 much larger canines (Fig. 4a). Parasphenoid posteriorly with several medium sized teeth (Fig. 4d). Hypobranchial 3 with a patch of tiny teeth (Fig. 4c). Ceratobranchial 5 with series of large teeth with anteriorly directed tips along posterior and medial margin and smaller teeth in middle and along anterior margin (Fig. 4c). Pharyngobranchial 2 elongate with several series of tiny teeth (Fig. 4d). Pharyngobranchial 3 with prominent teeth with recurved tips (Fig. 4d). Upper pharyngeal toothplate 4 with larger recurved teeth anteromedially and smaller teeth posterolaterally (Fig. 4d).

Pectoral-fin rays 14*–15. Dorsal-fin rays 34(4), 35(11), 36*(46), 37(23), 38(5). Anal-fin rays 22(2), 23*(20), 24(46), 25(18), 26(3). Caudal fin with 6(55) or 7*(39) +

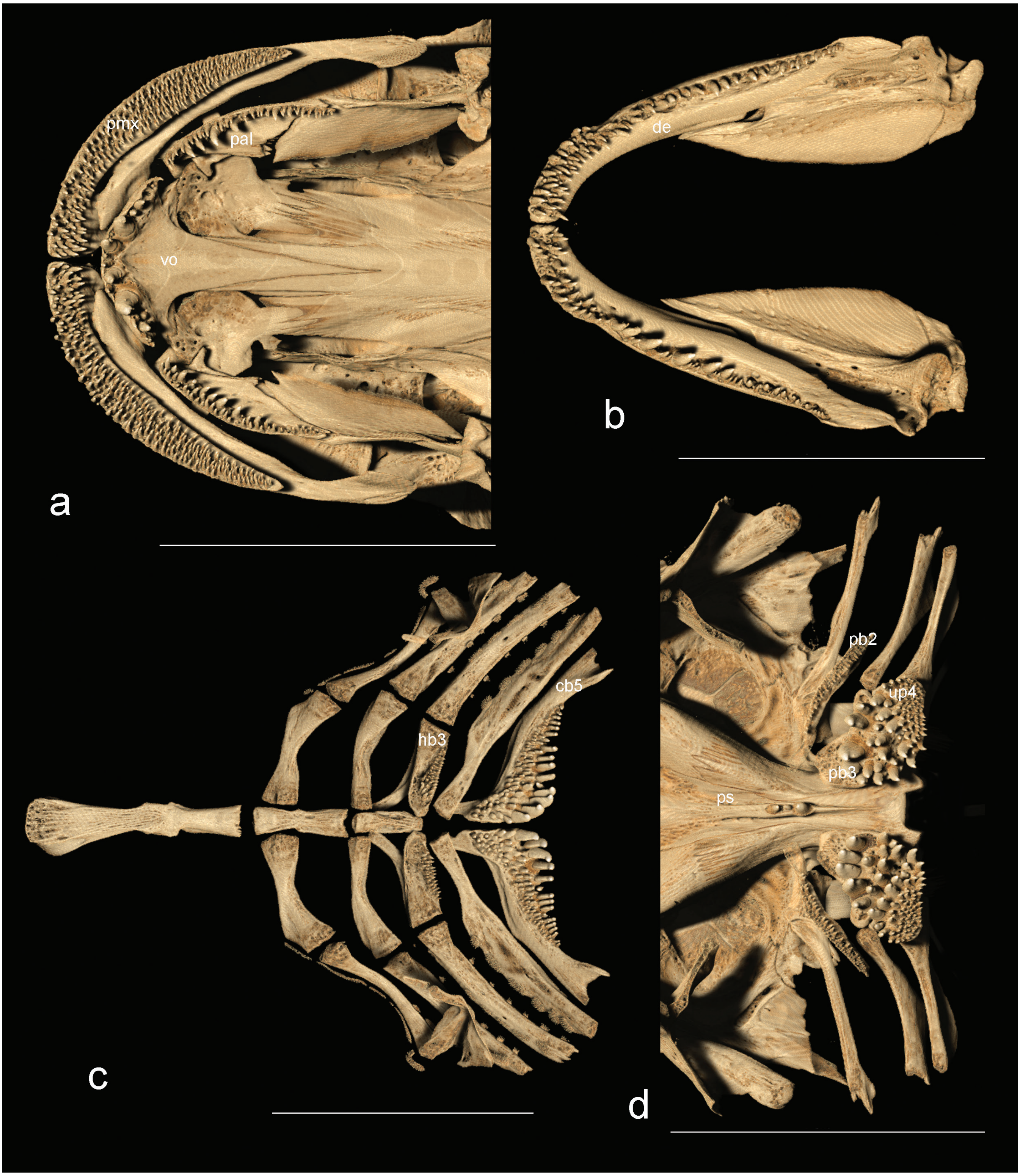

Fig. 4. *Channa rakhinica*, MTD 40204, paratype, 113.0 mm SL. Volume rendered 3D models illustrating dentition on premaxilla, vomer and palatine, in ventral view (a), lower jaw (b) in dorsal view, ventral branchial arches (c) in dorsal view, and upper pharyngeal jaws and parasphenoid patch (d) in ventral view. Note presence of caniniform teeth on palatine and dentary. Abbreviations: cb 5, ceratobranchial 5; de, dentary; hb3, hypobranchial 3; pal, palatine; pb2, pharyngobranchial; pb3, pharyngobranchial 3; pmx, premaxilla; ps, parasphenoid up4, upper pharyngeal toothplate 4. Scale bars 1 cm.

7(17), 8*(75) or 9 (1) principal rays and 2(30), 3*(57) or 4(7) dorsal and 2 (53), 3*(31) or 4 (4) ventral procurrent rays. 44(9), 45*(25), 46(50) or 47(12) vertebrae with 38(2), 39(16), 40*(38), 41(38) 42(1) abdominal and 4(3), 5*(51) or 6 (44) caudal vertebrae.

Predorsal scales 7–9. Lateral line with 45–47 scales extending from shoulder girdle in horizontal line, but dropping one scale row at scale 13–17, then continuing horizontally to end of caudal peduncle. Scales above lateral line 3.5 and below 6.5–7.5 at level of anal-fin origin. Postorbital scales

Fig. 5. *Channa rakhinica*, paratypes, examples of colouration in life, BMNH 2022.6.23.1004–1006 (top and middle), not measured, ca. 90 mm SL; BMNH 2019.10.16.269–275 (bottom), not measured, ca. 110 mm SL.

7 or 8. Circumpeduncular scales 28, with 8 larger scales on each side and 6 smaller to tiny scales along dorsal and ventral midline. Prepelvic scales 10–13. Single scale on ventral aspect of anguloarticular.

Colouration in preservative. See Figs. 2–3. Body and fins dark maroon, slightly lighter ventrally. Dorsal, anal, and caudal fins with narrow white rim. Pectoral fins with dark brown base and alternating dark wide and light narrow bands, bands regularly arranged in semiconcentric fashion in specimens from the south of distribution range, but in more northern populations dark bands wider and light bands sometimes incomplete, not reaching distal margin of fin.

Colouration in life. See Fig. 5. Colour of body a light maroon with light grey marbling especially in ventral area, light grey ventrally on jaw, gular area and abdominal preanal area and a series of 6–7 darker brown saddle-like blotches

Fig. 6. South stream near Kyeinthali, type locality of *Channa rakhinica*.

Fig. 7. Remnant pools under large boulders in dry stream beds, habitat from which *Channa rakhinica* paratypes were collected at Seik Chaung, a small tributary of Laymyo river and Myaung Gyi Chaung, a tributary of Dalet Chaung.

running from dorsal-fin base anteroventrally to upper third of side of body. Sides of head especially opercular region often with reddish brown cheek blotch. Dorsal fin with dark oblique markings separated by light oblique lines, sometimes forming black blotch in posteriormost area. Dorsal and caudal fins with submarginal orange rim and narrow white distal margin. Caudal fin with irregular semiconcentric dark narrow bands separated by lighter areas. Anal fin with dark brown subdistal rim and white distal margin. Pectoral fins with series of semicircular concentric maroon bands alternating with narrower cream bands. Pelvic fins light grey, like ventral abdomen.

Distribution and habitat. The new species was collected from small mountain streams near Kyeinthali in the southern Rakhine Yoma (Fig. 6) and from small remnant puddles beneath large boulders in the otherwise dry bed of a small tributary stream of Dalet Chaung in the middle Rakhine Yoma, and Laymyo River in the northern Rakhine Yoma, respectively (Fig. 7).

Etymology. The species name is derived from the name of the area where it occurs, the Rakhine Yoma in western Myanmar, an adjective.

Remarks. This species has been traded as an ornamental fish since at least 2012 under the name "*Channa* sp. mimetic pulchra" and has been referred to as *Channa* sp. Rakhine Yoma in Conte-Grand et al. (2017) and Rüber et al. (2020). Aquarium reports suggest that this is a mouthbrooding species.

Channa rubora, new species

(Figs. 8–10)

Holotype. BMNH 2019.10.16.194, 84.4mm SL mm SL; Myanmar, Kachin State, unnamed stream south of Mogaung, coll. Aung Myint, 23 February 2011.

Paratypes. BMNH 2019.10.16.195–206, 10 ex., 69.1–98.2 mm SL; same information as holotype. BMNH 2019.10.16.260, 1 ex., 95.5 mm SL; same information as holotype. MTD 40207, 78.8 mm SL; same information as holotype. —BMNH 2023.4.12.11–15, 5 ex., 65.4–127.5mm SL; same information as holotype.

Diagnosis. A member of the Gachua group distinguished from all other Myanmar members except *C. ornatipinnis*, *C. pulchra*, and *C. stewartii* by the presence of numerous black spots on the head and body (vs absence). It differs from the latter by the size of the spots (tiny, a quarter of pupil size vs. almost pupil size or larger) and by its unique fin colouration in life, consisting of a pectoral fin with orange fin rays, a bluish proximal blotch and 3–6 brown distal semicircular concentric bands, of dorsal-, anal- and caudal-fins with a blue middle section of the fin membranes margined by a proximal dark brown and distal bright orange rim in the dorsal and caudal fins and white rim in the anal fin (vs different colour pattern). It also differs substantially from all Myanmar Gachua group snakeheads by a genetic distance of 11.6–19.3% in the COI gene.

Description. See Figs. 8, 10 for general appearance and Table 3 for morphometric information and Table 6 for select meristic characters. Body elongate, round in cross section anteriorly, laterally compressed at caudal peduncle, body depth 5.7–6.4 times in SL. Head large, length 3.2–3.5 times in SL. Head widest halfway between posterior margin of eye and that of opercle. Mouth large, maxilla extending posteriorly beyond jaw angle, lips fleshy. Premaxilla with multiple rows of small sharp, pointed teeth (Fig. 9a). Dentary also with several series of small teeth and an internal series of slightly larger teeth, but no canines (Fig. 9b). Vomer with an external series of small teeth and an internal series of a few large teeth (Fig. 9a). Palatine with several series of smaller teeth but no canines (Fig. 9a). Parasphenoid posteriorly at level of pharyngobracnhial 3 with two teeth (Fig. 9d). Hypobranchial 3 with a patch of tiny teeth (Fig. 9c). Ceratobranchial 5 with series of large teeth with anteriorly directed tips along posterior and medial margin and smaller teeth in middle and along anterior margin (Fig. 9c). Pharyngobranchial 2 elongate with several series of tiny

Table 3. Selected morphometric information for *Channa rubora* (n=10), data for holotype in parentheses following range.

	Range (holotype)	**mean ± standard deviation**
Standard length (SL in mm)	71.4–95.5 (84.4)	
In % SL		
Head length	28.5–31.2 (30.2)	29.7±0.8
Body depth	15.7–17.7(16.5)	16.6±0.7
Body width	11.9–13.3 (12.7)	12.6±0.6
Predorsal length	35.8–38.9 (36.9)	36.7±0.9
Preanal length	50.5–53.8 (53.2)	52.2±1.3
Prepelvic length	34.7–36.8 (36.7)	35.9±0.7
Dorsal-fin base length	55.6–61.8 (57.2)	59.3±2.3
Anal fin-base length	38.9–42.4 (39.7)	40.8±1.3
Pectoral-fin length	18.4–21.7 (20.5)	19.5±1.2
Pelvic-fin length	5.9–7.9 (7.3)	7.0±0.7
In % HL		
Eye diameter	16.1–17.5 (16.1)	17.0±0.5
Head depth	46.7–51.2 (49.0)	48.8±1.3
Head width	61.7–68.0 (65.5)	65.2±2.1

Fig. 8. *Channa rubora*, BMNH 2019.10.16.194, 84.4mm SL; holotype, in dorsal (top), lateral (middle), and ventral (bottom) view; Myanmar, Kachin State, unnamed stream south of Mogaung.

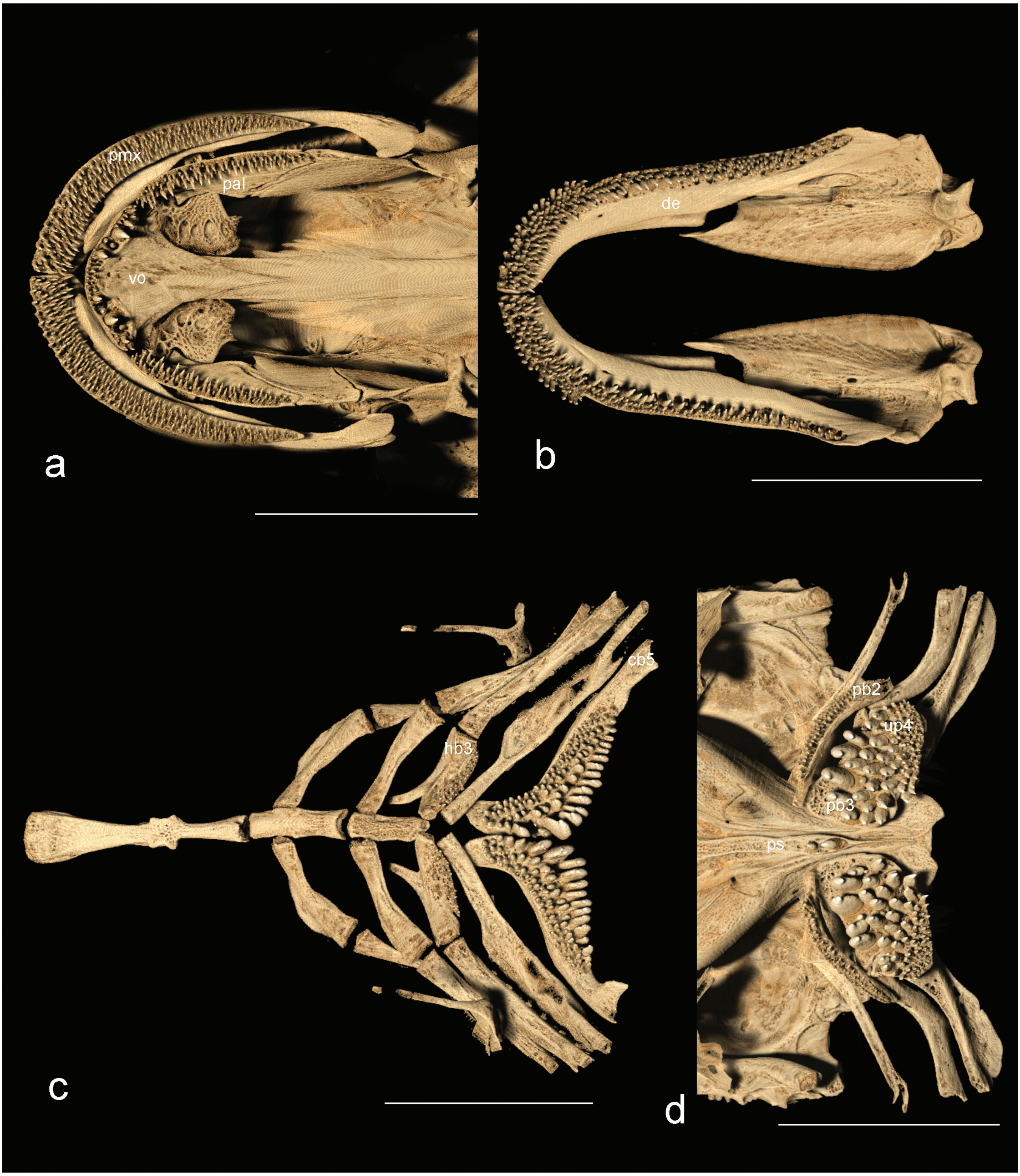

Fig. 9. *Channa rubora*, MTD 40207, paratype, 78.8 mm SL. Volume rendered 3D models illustrating dentition on premaxilla, vomer and palatine, in ventral view (a), lower jaw (b) in dorsal view, ventral branchial arches (c) in dorsal view, and upper pharyngeal jaws and parasphenoid patch (d) in ventral view. Note absence of caniniform teeth on palatine and dentary. Abbreviations: cb 5, ceratobranchial 5; de, dentary; hb3, hypobranchial 3; pal, palatine; pb2, pharyngobranchial; pb3, pharyngobranchial 3; pmx, premaxilla; ps, parasphenoid up4, upper pharyngeal toothplate 4. Scale bars 0.5 cm.

teeth (Fig. 9d). Pharyngobranchial 3 with prominent teeth with recurved tips (Fig. 9d). Upper pharyngeal toothplate 4 with larger recurved teeth anteromedially and smaller teeth posterolaterally (Fig. 9d).

Pectoral–fin rays 13–15*. Dorsal-fin rays 34(1), 35(2), 36*(8), 37(6), or 39(1). Anal-fin rays 23(1), 24*(4), 25(7), 26(4) or 27(2). Caudal fin with 6+6*(12*), 6+7(2) or 7+6(1) principal rays and 2(2) or 3*(16) dorsal and 3*(15) or 4(3) ventral procurrent rays. 43(3), 44(9), 45*(3) or 46(2) vertebrae with

Fig. 10. *Channa rubora*, paratypes, colouration in life, Myanmar, Kachin State, unnamed stream south of Mogaung, BMNH 2019.10.16.260 (top), 95.5 mm SL; BMNH 2019.10.16.195–206 (bottom), not measured, ca. 90 mm SL.

38 (2), 39(7), 40(5), 41*(3) or 42(1) abdominal and 4*(9) or 5(9) caudal vertebrae.

Predorsal scales 7–8. Lateral line with 44–47 scales extending from shoulder girdle in a horizontal line, but dropping one scale row at scale 13–17, then continuing horizontally to end of caudal peduncle. Scales above lateral line 3.5 and below 5.5–6.5 at level of anal–fin origin. Postorbital scales 7–8. Circumpeduncular scales 24, including 9 larger scales on each side and 3 tiny scales along dorsal and ventral midline. Prepelvic scales 10–12. A single scale on ventral aspect of anguloarticular.

Colouration in preservative. See Fig. 8. Head grey, rest of body maroon with series of 7–8 darker saddle-like blotches between base of dorsal fin and lateral line. Numerous small black spots on lateral and ventral sides of head and laterally on rest of body. Dorsal- and anal-fin rays light grey, intermittent membrane darker grey, with distal tips of dorsal- and anal-fin rays white. Pectoral fin with dark brown base and 3–4 dark semicircular concentric bands alternating with 3 lighter bands. Pelvic fins light beige.

Colouration in life. See Fig. 10. Colour a light brown in dorsal third of head and body with light grey to blueish grey lips, lateral and ventral sides of head and ventral abdominal area. A series of 6–7 darker brown saddle like blotches running from dorsal-fin base anteroventrally to lateral midline of body. Head and body with tiny black spots of varying number. Dorsal fin with light brown base, blue middle, narrow dark submarginal band and bright orange rim with distalmost tips of rays sometimes white. Caudal fin with irregular dark markings on fin rays arranged in a ladder-like fashion, blue fin membrane, narrow submarginal dark band and bright orange rim. Anal fin with brown proximal and blue middle area, a darker submarginal band and a white or orange rim. Pectoral fin with dark brown base and 3–4 dark semicircular concentric bands alternating with 3 lighter bands. Pelvic fins light grey.

Distribution. The new species is known from streams in the mountain area south of Mogaung.

Etymology. The species name, *rubora*, a noun in apposition, is derived from the Latin nouns 'rubor' for redness, and 'ora' for rim. The name was inspired by the orange-red rim of the dorsal and caudal fins.

Remarks. This species has been traded as an ornamental fish since at least 2012 under the name "*Channa* sp. red fin" and has been referred to as *Channa* sp. Mogaung in Conte-Grand et al. (2017) and Rüber et al. (2020). Aquarium reports suggest that this is a mouthbrooding species, in which larvae and small juveniles are of a yellow colour. Among the Gachua group species in Myanmar, *C. rubora* is readily distinguished from all other species by its colour pattern, specifically the numerous tiny spots on the head and flanks. It is also clearly distinguished from *C. burmanica* by presence of pelvic fins (vs. absence). From the other three species described in this paper, *C. coccinea*, *C. pyrophthalmus*, and *C. rakhinica*, *C. rubora* also differs in lacking caniniform teeth on the palatine and dentary.

Channa coccinea, new species
(Figs. 11–13)

Holotype. ZRC 64931, 125.4 mm SL; Myanmar, Kachin State, unnamed streams north of Putao, coll. Min Htet Kyaw, February 2022.

Table 4. Selected morphometric information for *Channa coccinea* (n=10), data for holotype in parentheses following range.

	Range (holotype)	**mean ± standard deviation**
Standard length (SL in mm)	98.6–132.7 (125.4)	
In % SL		
Head length	28.4–30.6 (28.5)	29.5±0.8
Body depth	12.7–14.9 (13.2)	13.9±0.8
Body width	10.3–12.2 (10.9)	11.3±0.6
Predorsal length	35.2–38.0 (35.7)	36.4±0.8
Preanal length	49.0–52.2 (49.0)	50.7±1.0
Prepelvic length	32.7–35.6 (33.8)	34.3±0.9
Dorsal-fin base length	55.7–61.2 (61.2)	58.7±1.6
Anal fin-base length	39.7–43.5 (41.8)	40.7±1.2
Pectoral-fin length	17.2–20.3 (20.3)	18.5±0.8
Pelvic-fin length		
In % HL		
Eye diameter	12.7–14.4 (13.2)	13.7±0.6
Head depth	40.3–47.6 (47.6)	42.7±2.1
Head width	60.0–66.6 (63.6)	63.2±2.0

Fig. 11. *Channa coccinea*, ZRC 64931, 125.4 mm SL; holotype, in dorsal (top), lateral (middle), and ventral (bottom) view; Myanmar, Kachin State, unnamed stream near Putao.

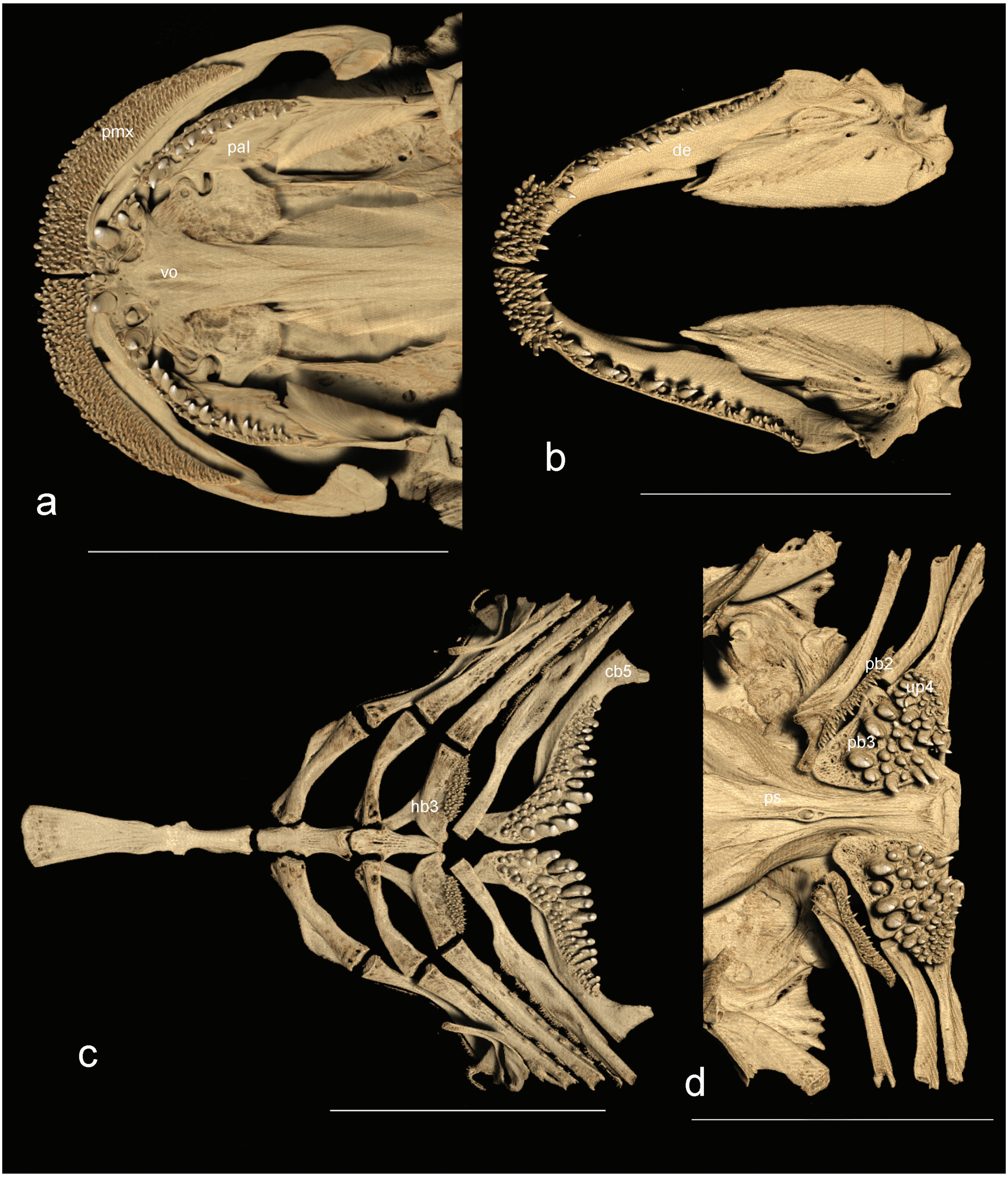

Fig. 12. *Channa coccinea*, MTD 40203, paratype, 117.0 mm SL. Volume rendered 3D models illustrating dentition on premaxilla, vomer and palatine, in ventral view (a), lower jaw (b) in dorsal view, ventral branchial arches (c) in dorsal view, and upper pharyngeal jaws and parasphenoid patch (d) in ventral view. Note presence of caniniform teeth on palatine and dentary. Abbreviations: cb 5, ceratobranchial 5; de, dentary; hb3, hypobranchial 3; pal, palatine; pb2, pharyngobranchial; pb3, pharyngobranchial 3; pmx, premaxilla; ps, parasphenoid up4, upper pharyngeal toothplate 4. Scale bars 1 cm.

Paratypes. ZRC 64932, 7 ex., 98.6–132.7 mm SL; same data as holotype. —MTD 40203, 2 ex., both 106.4 mm SL, same data as holotype.

Diagnosis. *Channa coccinea* can be distinguished from all other Myanmar species of the Gachua group by its colour pattern consisting of oblique reddish saddle-like markings and lines (vs. different colour pattern). It can be distinguished

Fig. 13. *Channa coccinea,* colouration in life, ZRC 64932, 120.5 mm SL; Myanmar, Kachin State, unnamed stream near Putao.

from *C. burmanica*, which occurs in the same area, by presence of pelvic fins (vs absence). It also differs from all Myanmar Gachua group snakeheads by a genetic distance of 3.5–19.9% in the COI gene.

Description. See Figs. 11, 13 for general appearance and Table 4 for morphometric information and Table 6 for select meristic characters. Body elongate, round in cross section anteriorly, laterally compressed at caudal peduncle, body depth 6.7–7.9 times in SL. Head large, length 3.3–3.5 times in SL. Head widest halfway between posterior margin of eye and that of opercle. Mouth large, maxilla extending posteriorly beyond jaw angle, lips fleshy. Premaxilla with multiple rows of small sharp, pointed teeth (Fig. 12a). Dentary also with several series of small teeth and an internal series of larger canines (Fig. 12b). Vomer with a number of smaller teeth at anterior margin and only a few very large teeth internally (Fig. 12a). Palatine with an external series of smaller teeth and an internal row of prominent large canines (Fig. 12a). Parasphenoid with a tooth at level of pharyngobranchial 3 (Fig. 12d). Hypobranchial 3 with a patch of tiny teeth (Fig. 12c). Ceratobranchial 5 with series of large teeth with anteriorly directed tips along posterior and medial margin and smaller teeth in middle and along anterior margin (Fig. 12c). Pharyngobranchial 2 elongate with several series of tiny teeth (Fig. 12d). Pharyngobranchial 3 with prominent teeth with recurved tips (Fig. 12d). Upper pharyngeal toothplate 4 with larger recurved teeth anteromedially and smaller teeth posterolaterally (Fig. 12d).

Pectoral-fin rays 15*–16. Dorsal-fin rays 36(4), 37 (5) or 38*(1). Anal-fin rays 24(1), 25(1), 26(6) or 27*(2). Caudal fin with 6*(10) + 6*(8) or 7 (2) principal rays and 3*(10) dorsal and 2(2)–3*(8) ventral procurrent rays. 44 (1), 45(1), 46(6), or 47*(3) vertebrae with 40(2), 41(6) or 42*(3) abdominal and 4(2), 5*(8) or 6(1) caudal vertebrae.

Predorsal scales 7–8. Lateral line with 43–47 scales extending from shoulder girdle in a horizontal line, but dropping one scale row at scale 13–14, then continuing horizontally to end of caudal peduncle. Scales above lateral line 4.5 and below 6.5 at level of anal-fin origin. Circumpeduncular scales 24, including 9 larger scales on each side and 3 tiny scales along dorsal and ventral midline Postorbital scales 8–9. Prepelvic scales 9–10. One or two scales on ventral aspect of anguloarticular.

Colouration in preservative. See Fig. 11. Body dark brown-grey, slightly lighter ventrally. Series of 6–8 darker, saddle-like blotches along base of dorsal fin and caudal peduncle, extending to lateral midline. Dorsal, anal, and caudal fins brown-grey with white rim. Caudal fin also with darker vertical marbling arranged in ladder-like fashion. Pectoral fins dark brown base with narrow cream bands, the latter not reaching fin margins laterally. Pelvic fin dark grey with light distal rim.

Colouration in life. See Fig. 13. Body of cream background colour, light beige ventrally. Series of oblique saddle-like reddish markings, extending as irregular lines beyond lateral midline in abdominal and reaching anal-fin base in caudal area. Lips, gular area, and side of head light grey. Postorbital head and opercular area often with irregularly arranged reddish spots. Bases of dorsal, caudal, and anal fins with similarly reddish irregular markings. Dorsal fin with greyish-blue middle band, darker grey subdistal band, and whitish rim. Caudal with with reddish marbling and cream intermarbling, dark grey subdistal area, and whitish rim. Pectoral fin with dark grey base, and reddish-brown bands alternating with cream to yellowish interbands. Pelvic fin grey with white margin.

Distribution. The new species was found in streams near Putao, Kachin State, northern Myanmar.

Etymology. The species name is derived from the Latin adjective ‘coccineus’, -a , -um, red, alluding to the reddish markings on the head and sides of the body.

Table 5. Selected morphometric information for *Channa pyrophthalmus* (n=10), data for holotype in parentheses following range.

	Range (holotype)	**mean ± standard deviation**
Standard length (SL in mm)	91.5–126.6 (95.6)	
In % SL		
Head length	31.2–34.4 (33.2)	32.2±1.4
Body depth	14.7–16.0 (15.2)	15.0±0.2
Body width	11.6–13.3 (13.3)	12.5±1.2
Predorsal length	37.8–40.1 (38.7)	38.2±0.7
Preanal length	53.3–57.2 (55.5)	54.4±1.6
Prepelvic length	36.7–38.9 (38.1)	36.9±1.7
Dorsal-fin base length	55.0–58.0 (57.3)	57.6±0.4
Anal fin-base length	36.5–39.4 (37.3)	37.6±0.4
Pectoral-fin length	19.8–22.8 (20.0)	20.0±0.1
Pelvic-fin length	8.7–10.7 (8.9)	8.8±0.1
In % HL		
Eye diameter	13.3–16.7 (16.7)	15.5±1.7
Head depth	40.7–43.8 (43.8)	42.8±1.5
Head width	59.6–64.1 (61.8)	63.0±1.6

Remarks. This species has been traded as an ornamental fish since early 2022 under the name "*Channa* sp. ignis". Its reproductive mode is still unknown, but it is likely a mouthbrooder.

Channa pyrophthalmus, new species

(Figs. 14–16)

Holotype. ZRC 64933, 97.1 mm SL, Myanmar, Taninthary Region, Lon Phaw, Kra Buri River drainage, coll. Ko Phyo Wei Latt, February 2022.

Paratypes. ZRC 64934, 7 ex., 91.5–121.3 mm SL, same data as holotype. —MTD 40202, 2 ex., 117.0–125.4 mm SL, same data as holotype.

Diagnosis. *Channa pyrophthalmus* is distinguished from other Myanmar species of the Gachua group by the colour pattern of its head consisting of a bright orange suborbital patch combined with steel blue lips. It is further distinguished from them by generally having fewer dorsal- (32–34 vs. 34–40) and anal-fin rays (20–22 vs. 22–27) and vertebrae (40–41 vs. 41–48). It also differs substantially from all Myanmar Gachua group snakeheads by a genetic distance of 10.1–18.8% in the COI gene.

Description. See Figs. 14, 16 for general appearance and Table 5 for morphometric information and Table 6 for select meristic characters. Body elongate, round in cross section anteriorly, laterally compressed at caudal peduncle, body depth 6.1–6.7 times in SL. Head large, length 2.9–3.2 times in SL. Head widest halfway between posterior margin of eye and that of opercle. Mouth large, maxilla extending posteriorly beyond jaw angle, lips fleshy. Premaxilla with multiple rows of small sharp, pointed teeth (Fig. 15a). Dentary also with several series of small teeth and an internal series of larger canines (Fig. 15b). Vomer with a few smaller teeth at external margin and a series of larger teeth internal to them (Fig. 15a). Palatine with an external series of smaller teeth and a few larger teeth internally (Fig. 15a). Parasphenoid with a tooth at level of pharyngobranchial 3 (Fig. 15d). Hypobranchial 3 with a patch of tiny teeth (Fig. 15c). Ceratobranchial 5 with series of large teeth with anteriorly directed tips along posterior and medial margin and smaller teeth in middle and along anterior margin (Fig. 15c). Pharyngobranchial 2 elongate with several series of tiny teeth (Fig. 15d). Pharyngobranchial 3 with prominent teeth with recurved tips (Fig. 15d). Upper pharyngeal toothplate 4 with larger recurved teeth anteromedially and smaller teeth posterolaterally (Fig. 15d).

Pectoral-fin rays 14–15. Dorsal-fin rays 32*(6), 33(3) or 34(1). Anal-fin rays 20(2), 21(3) or 22*(5). Caudal fin with 6*(8) or 7(2) + 6*(6) or 7(4) principal rays and 2(2) or 3*(8) dorsal and 2(4) or 3*(6) ventral procurrent rays. 40*(6) or 41(4) vertebrae with 35*(1), 36(6) or 37(3) abdominal and 4(8) or 5*(2) caudal vertebrae.

Predorsal scales 6–7. Lateral line with 39–41 scales extending from shoulder girdle in a horizontal line, but dropping one scale row at scale 13–15, then continuing horizontally to end of caudal peduncle. Scales above lateral line 3.5 and below 5.5–6.5 at level of anal-fin origin. Postorbital scales 6–8. Circumpeduncular scales 24, including 9 larger scales on each side and 3 tiny scales along dorsal and ventral midline. Prepelvic scales 8. One or two single scales on ventral aspect of anguloarticular.

Colouration in preservative. See Fig. 14. Body and fins dark dark greyish-brown, slightly lighter ventrally. Dorsal, anal, and caudal fins with narrow light rim. Pelvic fins dark grey with lighter rim. Pectoral fin with dark grey base followed distally by narrow light cream band, narrow dark grey band, slightly wider second cream band and more distal area with darker grey fin rays and translucent light cream membrane.

Colouration in life. See Fig. 16. Body light brown with bluish-grey postorbital and opercular area and bluish-grey

Table 6. Counts of dorsal- and anal-fin rays, and vertebrae in species of the Gachua group in Myanmar. Counts for *C. harcourtbutleri* based on Ng et al. (1999), for *C. ornatipinnis* and *C. pulchra* based on Britz (2008), for Myanmar *C. limbata* based on NRM 40696 (n=7) and NRM 40808 (n=21), for *C. burmanica* on ZRC 47206 (n=2), NRM 47192 (n=4) and BMNH 2023.4.12.22–42 (n=21), for Myanmar *C. stewartii* on BMNH 1867.2.14.19 (n=1) and BMNH 2023.4.12.1–4 (n=4). New species highlighted in grey.

	Dorsal-fin rays	**Anal-fin rays**	**Vertebrae**
Channa harcourtbutleri	34–38	23–26	42–44
C. limbata	34–37	22–26	41–45
C. ornatipinnis	34–37	23–24	44–45
C. pulchra	34–36	23–25	44–45
C. stewartii	39–40	26–27	46–48
C. burmanica	34–37	22–25	45–47
C. rakhinica	34–38	22–26	43–48
C. rubora	34–39	23–27	43–46
C. coccinea	36–38	24–27	44–47
C. pyrophthalmus	32–34	20–22	40–41

Fig. 14. *Channa pyrophthalmus*, ZRC 64933, 95.6 mm SL; holotype, in dorsal (top), lateral (middle) and ventral (bottom) view; Myanmar, Taninthary Region, Lon Phaw, tributary of Kra Buri.

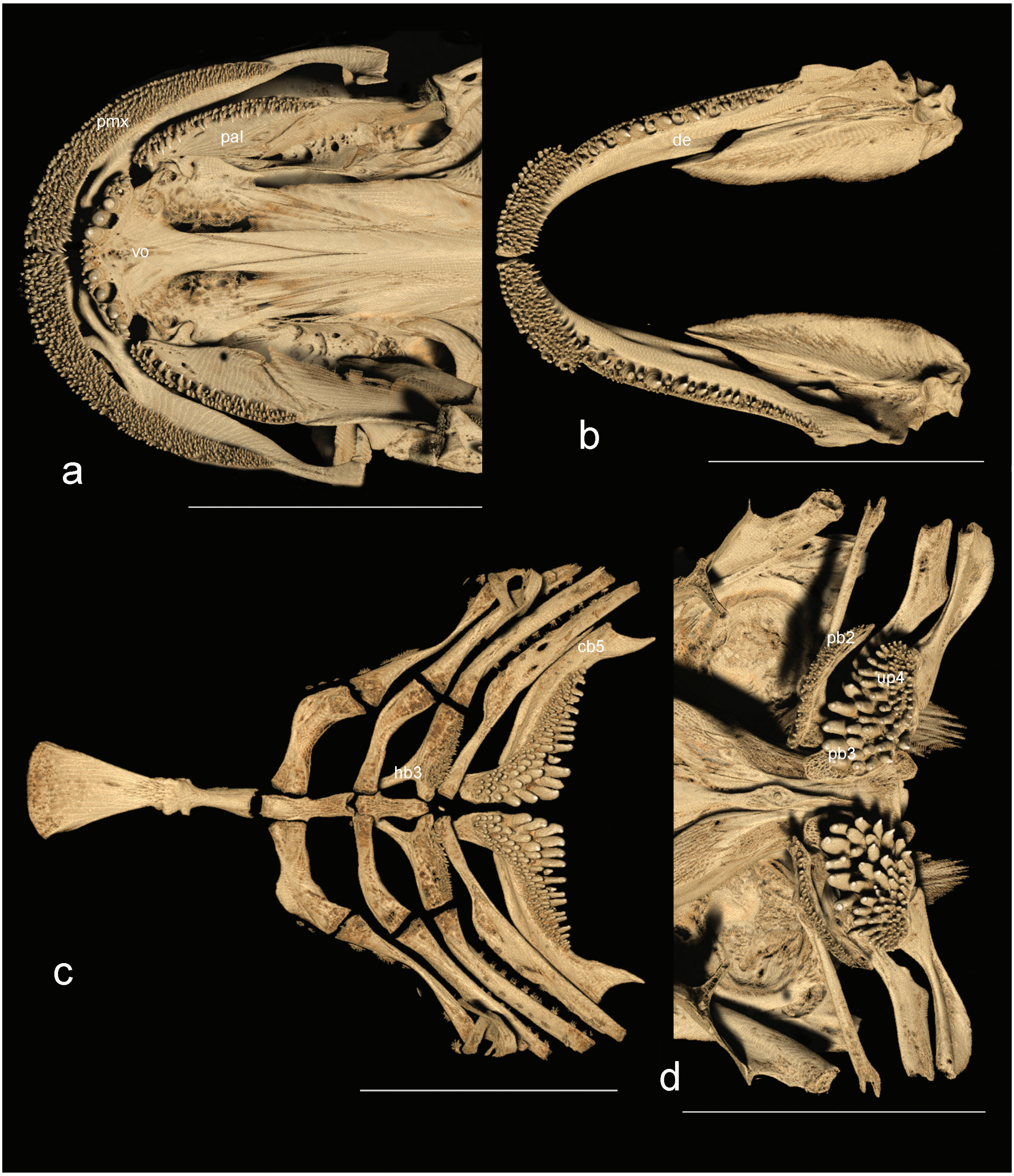

Fig. 15. *Channa pyrophthalmus*, MTD 40202 paratype, 106.4 mm SL. Volume rendered 3D models illustrating dentition on premaxilla, vomer and palatine, in ventral view (a), lower jaw (b) in dorsal view, ventral branchial arches (c) in dorsal view, and upper pharyngeal jaws and parasphenoid patch (d) in ventral view. Note presence of caniniform teeth on palatine and dentary. Abbreviations: cb 5, ceratobranchial 5; de, dentary; hb3, hypobranchial 3; pal, palatine; pb2, pharyngobranchial; pb3, pharyngobranchial 3; pmx, premaxilla; ps, parasphenoid up4, upper pharyngeal toothplate 4. Scale bars 1 cm.

marbling on side above anal-fin base. Lips and lachrymal margin steel blue, area anterior of eye, below eye, and posterior to eye a bright orange. Jaws and gular area light blue-grey. Dorsal fin with light brown base, blue middle, narrow dark grey subdistal band, and bright orange margin, with individual fin rays sometimes with white distalmost tips. Caudal fin with light grey fin rays showing darker markings arranged in a ladder-like fashion, with iridescent bluish interradial membrane and distal orange rim. Pectoral fin with dark blue-grey base, orange-red fin rays, and translucent

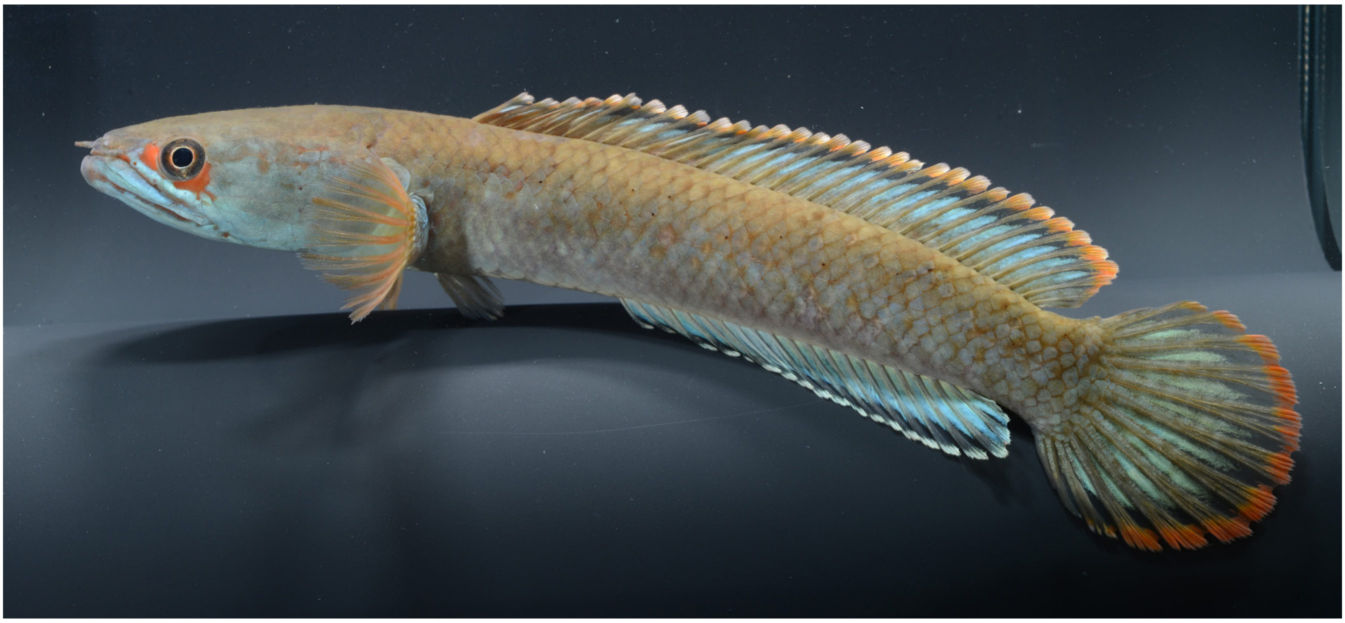

Figure 16. *Channa pyrophthalmus*, colouration in life, ZRC 64934, 121.3 mm SL; Myanmar, Tanintharyi Region, Lon Phaw, tributary of Kra Buri.

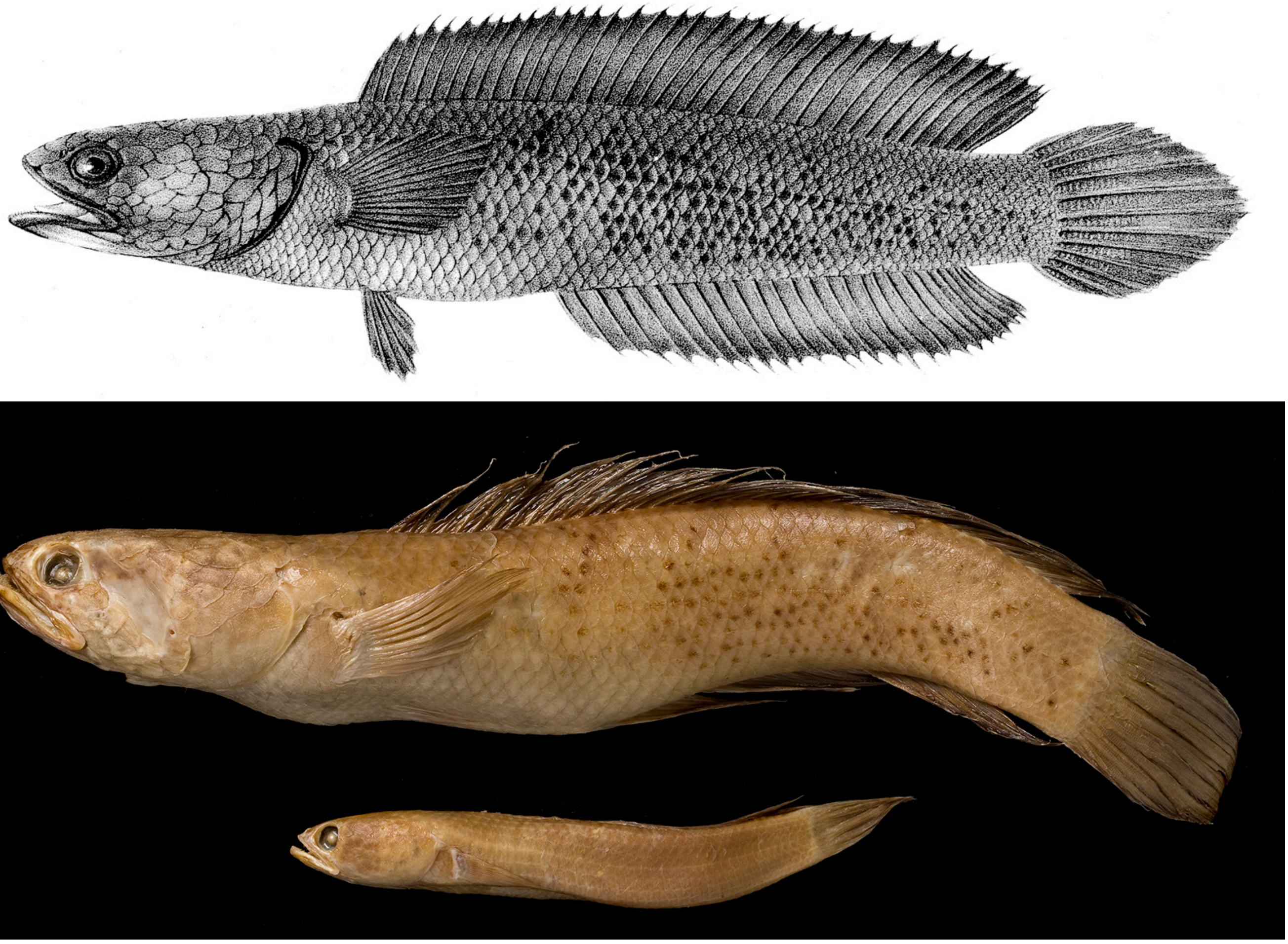

Fig. 17. Specimens of type series of *Channa stewartii*. Illustration of larger syntype (top) from Playfair (1867). BMNH 1867.2.14.19, 204 mm SL, larger syntype (middle), designated as lectotype here, and BMNH 1867.2.14.20, 90.4 mm SL, paralectotype (bottom), actually a specimen of *C. gachua*.

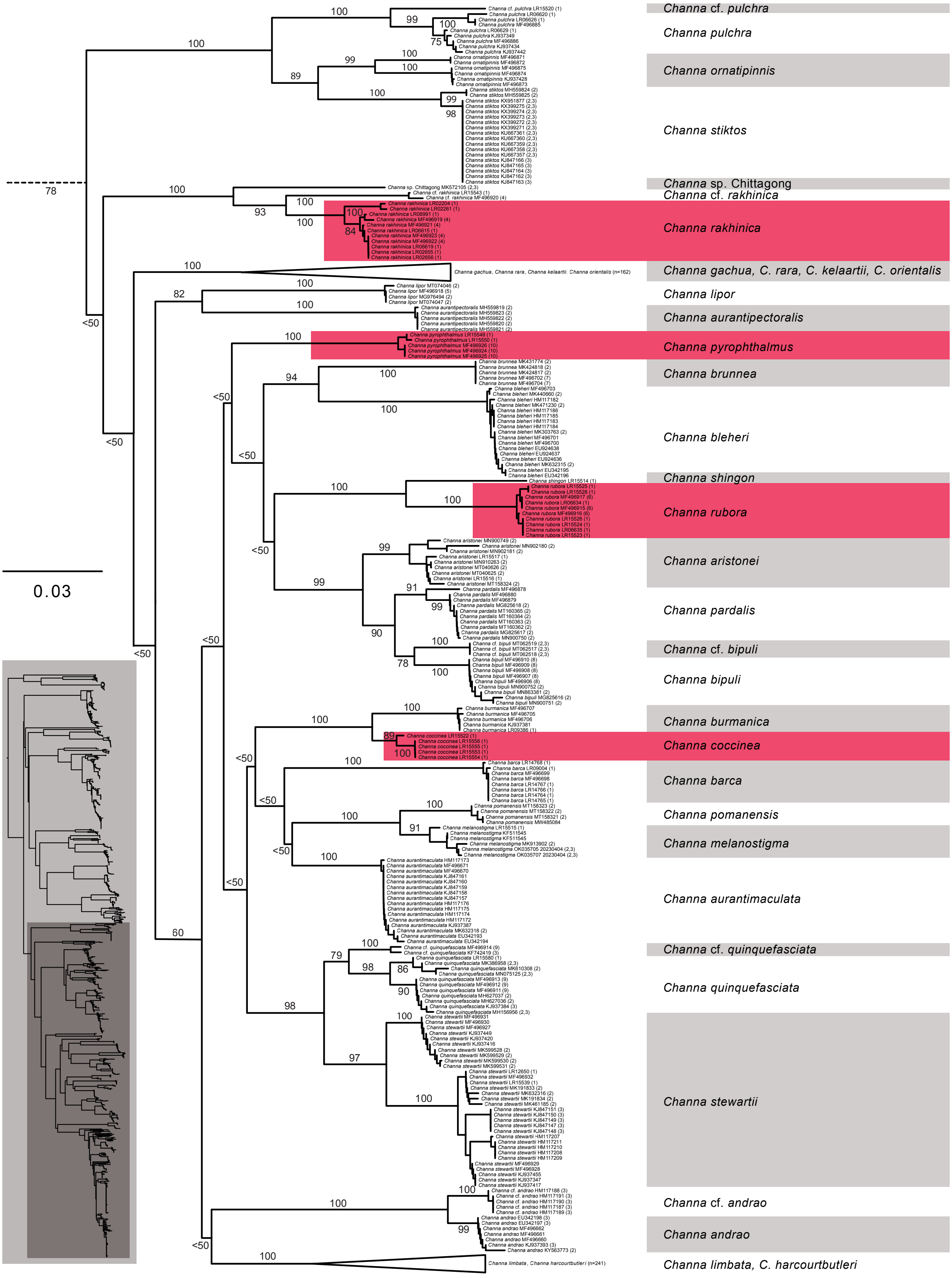

Fig. 18. Neighbour-joining phylogram, based on HKY distances of 1092 channid COI sequences. Inset on lower left highlighted in grey shows entire tree with Gachua group clade highlighted in dark grey, illustrated in detail in main figure. Four new species highlighted in red; clade comprising *C. gachua*, *C. rara*. *C. kelaartii*, *C. orientalis*, and clade comprising *C. limbata* and *C. harcourtbutleri* were collapsed. Bootstrap support values are shown above or below individual branches. Numbers in parentheses after sample name indicate: (1) sequences newly generated for this study, (2) new GenBank sequences added to Conte-Grand et al. (2017) data set, (3) species name given here differs from species name in GenBank, (4) as *Channa* sp. Rakine Yoma in Conte-Grand et al. (2017) and Rüber et al. (2020), (5) as *Channa* sp. Northeast India in Conte-Grand et al. (2017), (6) as *Channa* sp. Mogaung in Conte-Grand et al. (2017) and Rüber et al. (2020), (7) as *Channa bleheri* in Conte-Grand et al. (2017), (8) as *Channa* sp. Assam in Conte-Grand et al. (2017), (9) as *Channa* sp. Bhutan foothills in Conte-Grand et al. (2017).

Table 7. Pairwise genetic distances (p-distances) between the four newly described species and the Myanmar species of the Gachua group.

Channa rakhinica	*Channa rakhinica* (n=11)	0.0–2.0
	Channa burmanica (n=5)	12.9–13.5
	Channa harcourtbutleri (n=12)	15.8–16.7
	Channa limbata (n=35)	14.4–16.5
	Channa ornatipinnis (n=6)	17.1–18.4
	Channa pulchra (n=8)	16.7–18.5
	Channa stewartii (n=32)	14.1–16.5
Channa rubora	*Channa rubora* (n=10)	0.0–0.6
	Channa rakhinica (n=11)	14.7–16.2
	Channa burmanica (n=5)	14.7–15.1
	Channa harcourtbutleri (n=12)	14.8–15.4
	Channa limbata (n=35)	13.6–15.4
	Channa ornatipinnis (n=6)	17.1–18.3
	Channa pulchra (n=8)	18.2–19.3
	Channa stewartii (n=32)	11.6–13.8
Channa coccinea	*Channa coccinea* (n=5)	0.0–0.8
	Channa rubora (n=10)	13.9–14.5
	Channa rakhinica (n=11)	13.7–14.2
	Channa burmanica (n=5)	3.5–3.8
	Channa harcourtbutleri (n=12)	11.8–12.4
	Channa limbata (n=35)	10.9–12.7
	Channa ornatipinnis (n=6)	19.3–19.9
	Channa pulchra (n=8)	19.4–19.9
	Channa stewartii (n=32)	8.9–11.0
Channa pyrophthalmus	*Channa pyrophthalmus* (n=5)	0.0–0.6
	Channa coccinea (n=5)	10.1–10.3
	Channa rubora (n=10)	12.2–12.5
	Channa rakhinica (n=11)	14.5–15.0
	Channa burmanica (n=5)	11.0–11.5
	Channa harcourtbutleri (n=12)	11.6–11.9
	Channa limbata (n=35)	11.5–12.7
	Channa ornatipinnis (n=6)	16.5–17.4
	Channa pulchra (n=8)	18.2–18.8
	Channa stewartii (n=32)	10.5–11.9

interradial membranes. Anal fin bluish, with dark subdistal rim and white distal margin. Pelvic fins light grey.

Distribution. The new species is known from the area around Lon Phaw, Kra Buri River drainage, southern Tanintharyi Region, close to the border with Thailand.

Etymology. The species name is derived from the Greek words πῦρ (pyr), fire, and ὀφθαλμός (ophthalmos), eye. It was inspired by the bright orange area under the eye, a colour reminiscent of that of glowing embers. Used as a noun in apposition.

Remarks. This species has been traded as an ornamental fish since 2009 under the name "*Channa* sp. ice & fire" or "*Channa* sp. fire and ice" and has been referred to as *Channa* sp. Tenasserim in Conte-Grand et al. (2017) and Rüber et al. (2020). Aquarium reports suggest that this is a mouthbrooding species. Among the Gachua group species in Myanmar, *C. pyrophthalmus* is readily distinguished from all other species by its colour pattern which includes a bright orange are around the eye combined with light blue lips and throat and a light blue margin of the anterior infraorbitals. Among Myanmar Gachua group snakehead fishes, it has the lowest dorsal- (32–34) and anal-fin ray (20–22), as well as vertebral counts (40–41).

Lectotype designation for *Channa stewartii*: During our study, we checked the type material of *Channa stewartii*, which consists of two syntypes registered as BMNH 1867.2.14.19–20. The larger, 204 mm SL, syntype is the specimen illustrated on Plate III in Playfair (1867), reproduced here (Fig. 17). It has 40 dorsal-fin rays, 27 anal-fin rays, 47 (42+5) vertebrae, and 49 lateral line scales with 4.5 scales above and 8.5 below the row of lateral line scales. It also still shows the characteristic series of black spots on the body (Fig. 17), as in the illustration in Playfair (1867). The other, smaller, 90.4 mm SL specimen (Fig. 17) has only 35 dorsal-fin rays, 23 anal-fin rays and only 41 (37+4) vertebrae, 41 lateral line scales and 3.5 scaled above and 7.5

scales below the row of lateral line scales. It thus belongs to a different species with its characters matching those of *Channa gachua*, and we consider this smaller syntype to be a specimen of this latter species. For the sake of stability and to avoid any future nomenclatural confusion we fix the name *Channa stewartii* to the specimen illustrated on Plate III in Playfair (1867), following Recommendation 74b of the International Code of Zoological Nomenclature, by designating the 204 mm SL syntype as the lectotype of this species.

Molecular data and phylogenetic analysis. The final alignment of 1092 sequences of snakeheads was 654 bp long and the resulting NJ tree is shown in Figure 18. A summary of the intra- and interspecific p-distances for the Myanmar species of the Gachua group is provided in Table 7.

DISCUSSION

With the description of the four new species, *Channa rakhinica*, *C. rubora*, *C. coccinea*, and *C. pyrophthalmus*, Myanmar harbours a total of 10 species of the Gachua group including *C. burmanica*, *C. harcourtbutleri*, *C. limbata*, *C. pulchra*, *C. ornatipinnis*, and *C. stewartii* (Britz, 2008, Conte-Grand et al., 2017, Rüber et al., 2020).

Adding further to the number of endemic channid species of the Gachua group from this part of Asia, *Channa rakhinica*, *C. rubora*, and *C. coccinea* come from what was previously termed the Eastern Himalaya biodiversity hotspot, an area which is now part of the Himalaya and Indo-Burma biodiversity hotspots (see Conservation International, 2023). Rüber et al. (2020) reported an uneven distribution of Gachua group endemics between the area west and east of the Indo-Burman ranges. They found that of the 18 endemic species, 15 species occurred west of the Indo-Burman ranges, whereas only two were found east of the mountain ranges and a single species inhabited areas on both sides of the mountain range. Since Rüber et al. (2020), three additional species of the Gachua group species of snakeheads have been described from the Himalaya and Indo-Burma biodiversity hotspots, all from the western side of the Indo-Burman ranges (Praveenraj et al., 2019, 2020; Chakraborty et al., 2020): *C. aristonei* Praveenraj, Thackeray, Singh, Uma, Moulitharan & Mukhim, 2020, *C. brahmacharyi* Chakraborty, Yardi & Mukherjee, 2020, and *C. brunnea* Praveenraj, Uma, Moulitharan & Kannan, 2019 with its junior synonym *C. amari* Dey, Chowdhury, Nur, Sarkar, Kosygin & Barat, 2019). The recently published online paper by Pathak et al. (2023) attempting to describe a new species of *Channa* of the Gachua group from Assam is another example of what Kullander et al. (2019) termed hipshot taxonomy, i.e., inadequate species descriptions often combined with many misidentifications or provisional identifications of published DNA sequences. The species name *Channa assamensis* is not available from the online publication because it was not registered with Zoobank and the information and photos provided in the paper suggest that even if it were made available by the printed version of the journal, it would be a junior synonym of *Channa quinquefasciata* Praveenraj, Uma, Knight, Moulitharan, Balasubramanian, Bineesh & Bleher, 2018. Unfortunately, it is the Indian region of the Himalaya hotspot which is especially plagued by such hipshot taxonomy and premature and invalid publication of species descriptions (see e.g. Kulabtong et al., 2012; Basumatary et al., 2016; Dey et al., 2019; Chakraborty et al., 2020).

Among the Myanmar Gachua group species, *Channa stewartii* is easily diagnosed by its higher fin-ray counts of 39–40 dorsal- and 26–27 anal-fin rays. Among the remaining Myanmar Gachua group taxa, *Channa burmanica*, *C. coccinea*, *C. harcourtbutleri*, *C. limbata*, *C. rakhinica*, and *C. rubora*, share lower counts of dorsal- and anal-fin rays with only 34–39 dorsal- and 22–26 anal-fin rays. *Channa pyrophthalmus*, however, is an exception here: it has the lowest counts among the Myanmar Gachua group taxa with only 32–34 dorsal- and 20–22 anal-fin rays. The easiest way to distinguish the new species of the Myanmar Gachua group from each other and from other group members is colour pattern, as detailed above.

Our CT study of the dentition among the four new species revealed several differences in tooth types. *Channa rubora* lacks the lingually situated row of larger caniniform teeth along the palatine and dentary, which are present in the other three species. Differences in the presence or absence of caniniform teeth in the palatine dentition have previously been reported only for a few snakehead species of the Gachua group (e.g. Praveenraj et al., 2018a, 2018b). Palatine dentition without caniniform teeth has been illustrated for *C. quinquefasciata*, *C. pardalis* Knight 2016, *C. bipuli* Praveenraj, Uma, Moulitharan & Bleher, 2018, *C. lipor* Praveenraj, Uma, Moulitharan & Singh, 2019, and *C. gachua* (Hamilton, 1822) (e.g., Praveenraj et al., 2018a, 2018b, 2019), but these species all have caniniform teeth in the dentary. Interestingly, the only other Gachua group snakehead in addition to *C. rubora* that has been reported to lack caniniform teeth in the dentary is *C. shingon* (Endruweit, 2017). In our molecular analysis, *C. shingon* is recovered as the sister species of *C. rubora* and the lack of caniniform dentary teeth is a shared derived character of the two species. We think that future comparative data on channid dentition may provide additional useful characters for taxonomic and phylogenetic studies.

While there is some variation in the dentition of the upper and lower jaws and palatine in the four new species described here, we found little differences in the dentition of their upper and lower pharyngeal jaws. The parasphenoid tooth patch was best developed in our specimen of *C. rakhinica* with three teeth, while *C. rubora* had two teeth, and *C. coccinea* and *C. pyrophthalmus* had just a single tooth. As we scanned just a single specimen of each species, we are uncertain whether these represent species-level differences.

All four new species also show significant genetic divergence in the barcoding gene from other Myanmar Gachua group members ranging from around 10–20%. *Channa coccinea* is an exception here with a divergence of 3.5–3.8% from its closest relative *C. burmanica*, a level of divergence common among closely related sister species of *Channa* (see Praveenraj et al., 2018b, 2020). *Channa coccinea* and *C. burmanica* are, however, readily distinguished by the presence of pelvic fins in the former and their absence in the latter. While the phylogram of our NJ analysis shown in Fig. 18 is based only on COI sequences, we are confident that the phylogenetic position of *C. coccinea* as the sister taxon to *C. burmanica* will not change even when more genes are included. Of the other three new species, only *Channa rakhinica* (as *C.* sp. Rakhine Yoma) has been included in the phylogenetic analysis of Rüber et al. (2020), in which it was recovered with a posterior probability of 1.0 as the sister group of the clade consisting of *Channa kelaartii* and *C. orientalis* from Sri Lanka, and *C. gachua* from India, a result consistent with that of the barcoding study of Conte-Grand et al. (2017), but with only poor support. In our barcoding tree, there are two clades of *C. rakhinica* representing the northern Rakhine Yoma locality of *C. rakhinica* (LR02204, LR02261) from the Lemyo River which is separated genetically from the more southern Rakhine Yoma localities with a genetic divergence of 1.7–2.0%. This *C. rakhinica* clade clusters with two snakehead clades with similar sequences, referred to here as *C.* sp. cf. *rakhinica* and *C.* sp. Chittagong. *Channa* sp. cf. *rakhinica* is from aquarium trade specimens reported to have come from Myanmar, and *C.* sp. Chittagong is a COI sequence on Genbank from a *Channa* from Bangladesh (*Channa*_sp_MK572105, Rahman et al., 2019).

Channa rubora and *C. pyrophthalmus* have also been included previously in Conte-Grand et al. (2017) as *C.* sp. Mogaung and *C.* sp. Tenasserim, respectively. Both taxa were recovered in their study within a clade containing a mixture of Northeast Indian species and the Myanmar *C. burmanica* and C. *harcourtbutleri*, as well as *C. limbata*, a species with a wide distribution east of the Indo-Burman ranges. This result is also repeated here, but the branches leading from the backbone to these lineages are very short, as they were in Conte-Grand et al. (2017), reflecting poor support and thus indicating uncertainty about their precise phylogenetic position.

Interestingly the new species, *C. rubora*, clusters in our analysis with a sample that we refer to as *C. shingon*. This was obtained through the aquarium trade and said to have come from the type locality of *C. shingon* in Yunnan, China. *Channa shingon* was described by Endruweit (2017) and its validity was questioned by Britz et al. (2019) who pointed out that Endruweit failed to diagnose it properly from *C. harcourtbutleri*. We have not studied any preserved specimens from which our DNA sample was taken, but our current analysis would lend additional support to Endruweit's (2017) idea that *C. shingon* is a valid species.

Another species, whose validity was questioned by Britz et al. (2019) is *Channa torsaensis*, described shortly after *C. quinquefasciata*, both from the Torsa River basin in West Bengal. Britz et al. (2019) suggested that the former is a junior synonym of the latter and our molecular analysis lends support to this hypothesis, as the genetic divergence of 1.38–1.7% between them is well within species level variation.

Our new analysis further demonstrates that the species-level diversity within the Gachua group of Asian snakeheads is still incompletely known. Our tree identifies several units that would likely deserve species-level status: *Channa* sp. cf. *rakhinica* and *C.* sp. Chittagong, showing a genetic divergence to *C. rhakinica* of 6.0–6.6% to the former and even 8.2–9.2% to the latter. Considerable divergence is also found between *Channa pulchra* and C. sp. cf. *pulchra*, with 4.59–5.20%. *Channa ornatipinnis* from the type locality and aquarium trade specimens reportedly from a more southern locality show a genetic divergence between each other of 4.43–4.46% warranting a closer examination. *Channa stewartii* samples in our analysis were also grouped into two clades with an unexpected genetic divergence of 3.2–4.1%, calling for a thorough revision of this group of snakehead fishes. And finally, *Channa* samples in GenBank from Uttar Pradesh are closest to *Channa andrao*, but with quite a substantial divergence of 1.98–2.99% asking for a closer morphological inspection of the Uttar Pradesh material.

We anticipate that future studies and new collections of snakeheads of the Gachua group from this biodiverse area will lead to a substantial increase in species-level diversity. One of the reasons for high species-level endemism of the Gachua group in this area of Asia is most likely that these mountain stream-adapted snakeheads had plenty of opportunity to speciate as a result of the highly complex and frequently changing biogeographical settings during the geological history of the Eastern Himalayas, the Indo-Burman Ranges, the Hengduan Mountains, and the Tenasserim Mountain Range (see e.g., Gregory, 1925; Rüber et al., 2004, 2020; Zhang et al., 2019). Coinciding with the high number of species of Gachua group snakeheads is also the high species-level diversity of other mountain stream-dwelling taxa in this region, as e.g., the cyprinid genera *Danio* (see Kullander, 2015; Kullander & Britz, 2015) and *Devario* (Kullander & Norén, 2022), the cyprinid genus *Garra* (Kullander & Fang, 2005), and the badid genus *Badis* (Kullander & Britz, 2002; Kullander et al., 2019).

To get a better idea about their precise phylogenetic relationships and the resulting biogeographic scenarios, it would be desirable to add these new Gachua group taxa to the dataset compiled by Rüber et al. (2020), as COI is only a relatively short DNA fragment, and is unsuitable for phylogenetic questions at this level.

Comparative Material

Channa gachua: BMNH 1867.2.14.20, 90.4 mm SL, paralectotype of *C. stewartii*. BMNH 2023.4.12.16–21, 6 ex., 94.2–116.1 mm SL. BMNH 2023.4.12.5–10, 6 ex., 99.2–109.1 mm SL. NRM 40539, 3 ex., 89.0–101.7 mm SL. NRM 71760, 1 ex., 88.7 mm SL. NRM 71761, 1 ex., 86.1 mm SL. NMW 73908, 3 ex., 64.9–99.4 mm SL. NMW 74001, 1 ex., 118.8 mm SL. NMW 73909, 64.1–75.9 mm SL. NMW 74002, 4 ex., 87.1–106.6 mm SL

Channa stewartii: BMNH 1867.2.14.19, lectotype, 204 mm

SL. BMNH 2023.4.12.1–4, 4 ex., 107.1–115.2 mm SL. NRM 40423, 1 ex., 120.0 mm SL. NRM 40501, 2 ex., 112.3–152.6 mm SL. NRM 40296, 1 ex., 160.0 mm SL.

Channa burmanica: BMNH 2023.4.12.22–42, 21 ex., 69.5–131.2 mm SL. ZRC 47206, 2 ex., 108.2–120.3 mm SL. ZRC 47192, 4 ex., 58.0–101.6 mm SL.

Channa limbata: MNHN 36, holotype, 115 mm SL. NRM 40808, 25 ex., 70.6 mm–185.4 mm SL. NRM 40696, 8 ex., 75.0–195.1 mm SL.

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