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Phylogenetic placement and description of a new species of *Leptorhamdia* (Siluriformes: Heptapteridae) from the Amazon basin

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Brachyglaniini is a recently described tribe of Heptapterinae, composed of four genera: *Brachyglanis*, *Gladioglanis*, *Leptorhamdia*, and *Myoglanis*. Expeditions to the Aripuanã and Tapajós River basins revealed an undescribed species of Brachyglaniini, characterized by a conspicuous light-colored band posterior to the head. Our phylogenetic results provide strong evidence that this new Brachyglaniini species belongs to the genus *Leptorhamdia* and is closely related to *L. marmorata* and *L. aspredinoides*. In addition to the color pattern, the new species can be distinguished from its congeners by having 19–22 anal-fin rays and 47 vertebrae.

Keywords: Brazilian shield, Catfish, Integrative taxonomy, Systematics.

Brachyglaniini é uma tribo recentemente descrita de Heptapterinae, composta por quatro gêneros: *Brachyglanis*, *Gladioglanis*, *Leptorhamdia* e *Myoglanis*. Expedições realizadas nas bacias dos rios Aripuanã e Tapajós revelaram uma espécie ainda não descrita de Brachyglaniini, caracterizada por uma faixa de cor clara e conspícua posterior à cabeça. Nossos resultados filogenéticos fornecem fortes evidências de que esta nova espécie de Brachyglaniini pertence ao gênero *Leptorhamdia* e está estreitamente relacionada a *L. marmorata* e *L. aspredinoides*. Além do padrão de coloração, a nova espécie pode ser distinguida de seus congêneres por possuir 19–22 raios na nadadeira anal e 47 vértebras.

Palavras-chave: Bagre, Escudo Brasileiro, Sistemática, Taxonomia integrativa.

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INTRODUCTION

Heptapteridae is a group of small Neotropical catfishes commonly known as bagrinhos, mandis, and mandizinhos, with 239 valid species classified into 23 genera (Fricke *et al.,* 2025a). Silva *et al.* (2021) recognized a monophyletic component of heptapterids composed of *Brachyglanis* Eigenmann, 1912, *Gladioglanis* Ferraris & Mago-Leccia, 1989, *Leptorhamdia* Eigenmann, 1918, and *Myoglanis* Eigenmann, 1912. This clade was classified as tribe Brachyglaniini, a group with 15 valid species whose diversity predominantly occurs in rivers of the Guyana Shield, such as Essequibo, Negro, Ventuari, Orinoco and Trombetas but which also includes a few species in rivers draining the Brazilian Shield, such as Madeira and Xingu. Besides being strongly supported by molecular data, Brachyglaniini is also supported by 10 morphological synapomorphies (Bockmann, 1998; Silva *et al*., 2021) and can be externally easily distinguished from other heptapterids by having the principal unbranched pectoral-fin ray forming an ossified, rigid spine (Faustino-Fuster *et al*., 2021).

After Silva *et al.* (2021) described the tribe Brachyglaniini, Faustino-Fuster *et al.* (2021) proposed a new phylogeny of Heptapteridae using a dense sampling of Brachyglaniini from the Guiana Shield in a multi-locus approach and recovered four main clades within the tribe: (1) *Brachyglanis*, (2) *Leptorhamdia* (with *Myoglanis koepckei* Chang, 1999, *M. aspredinoides* DoNascimiento & Lundberg, 2005, and *Brachyglanis nocturnus* Myers, 1928), (3) *Myoglanis*, and (4) *Gladioglanis*. Although these authors identified the main clades within Brachyglaniini, they did not diagnose the clades or its major subgroups from a morphological standpoint. Currently, *Leptorhamdia* is composed by five valid species: *L. aspredinoides* from the Venturari River; *L. essequibensis* (Eigenmann, 1912) from the Essequibo River; *L. marmorata* Myers, 1928, and *L. nocturna* from the Negro River and *L. schultzi* (Miranda Ribeiro, 1964) from the Xingu River (Fricke *et al*., 2025b). Herein, a new species of *Leptorhamdia* is described based on specimens collected in the tributaries of rio Arinos, and rio Aripuanã, in the Amazon basin.

MATERIAL AND METHODS

Morphological analysis. Measurements were taken from the left side of specimens and were made point to point to the nearest 0.1 mm with digital calipers. The nomenclature of osteology follows Bockmann, Castro (2010). Measurements and abbreviations follow Lundberg, McDade (1986). The nomenclature for lateral-line canals and branches follows Bockmann, Miquelarena (2008). Morphometrics are given as percentages of standard length (SL), except for subunits of head expressed as percentages of head length (HL). Specimens were cleared and stained (c&s) according to Taylor, Van Dyke (1985). Numbers of branchiostegal rays, gill rakers, vertebrae, ribs, and position of supporting elements of dorsal and anal fins were determined in cleared and stained specimens. Vertebral counts include those from the Weberian apparatus and the compound caudal centrum was counted as one. Morphological data for *L. marmorata*, *L. nocturna*, and *L. essequibensis* were obtained from images of type material, available at CAS Ichthyology Primary Types Imagebase website, and from ACSImageBase hosted at The Academy of Natural Sciences. *Leptorhamdia aspredinoides* data were obtained from their original descriptions (Do Nascimiento, Lundberg, 2005), and data for *L. schultzi* were obtained from ANSP image collections. Institutional abbreviations follow Sabaj (2020). Specimens were deposited at the Departamento de Ciências Biológicas da UNESP, São José do Rio Preto (DZSJRP), Laboratório de Biologia e Genética de Peixes, Universidade Estadual Paulista, Botucatu (LBP), and Museu de Zoologia, Universidade de São Paulo, São Paulo (MZUSP).

Molecular analysis. The extracted DNA of one sample of the new species of *Leptorhamdia*, which was used for the molecular analysis: LBP 20829 (tissue 81351; Genbank number: PX974334 (COI); PX984954 (Cytb); PX984955 (Rag2)). DNA extraction followed Ivanova *et al.* (2006). Partial sequences of the mitochondrial genes cytochrome oxidase c subunit I (COI) and cytochrome b (Cytb), as well as the nuclear gene recombination activating gene 2 (Rag2) were amplified by polymerase chain reaction (PCR) using primers FishF6/R7 (Jennings *et al*., 2019), L14841/H16460 (Oliveira *et al*., 2011) and 164F/176R (Oliveira *et al*., 2011), respectively. Reactions were carried out in a 12.5 µL reaction volume containing 1.25 µL of 10× PCR buffer, 0.40 µL $MgCl_2$ (50 mM), 0.30 µL dNTPs (2 mM), 0.25 µL of each primer (5 µM), 0.20 µL of PHT Taq DNA polymerase (Phoneutria), 2 µL DNA template (200 ng), and 7.85 µL of ddH2O. The PCR consisted of initial denaturation (5 min at 95°C) followed by 30 cycles with a chain denaturation (1 min at 95°C), primer hybridization (45 sec at 54°C), nucleotide extension (1 min at 72°C), and final extension (10 min at 72°C). All PCR products were checked using 1% agarose gel and purified with ExoSap-IT (USB Corporation) following the manufacturer's instructions. The purified PCR products were sequenced using the Big DyeTM Terminator v. 3.1 Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Austins, USA), purified through ethanol precipitation and loaded onto an ABI 3500 Genetic Analyzer (Applied Biosystems), in the Instituto de Biotecnologia (IBTEC), Universidade Estadual Paulista Júlio de Mesquita Filho, Botucatu, Brazil.

The sequences of two genes obtained in this study were assembled using the software GENEIOUS PRIME 2024.0.5 (Kearse *et al*., 2012). These sequences, along with available sequences from the phylogenetic study by Faustino-Fuster *et al.* (2021), which included three mitochondrial genes (COI, Cyt b, ND2) and two nuclear genes (RAG2 and Glyt) were aligned using muscle (Edgar, 2004) under default parameters to create a new dataset matrix comprising 40 specimens. Nucleotide variation and substitution patterns were examined using IQ-TREE v. 2.3.6 (Minh *et al*., 2020). To evaluate the occurrence of substitution of saturation in our data, we estimated the index of substitution saturation (Iss) using the method described by Xia *et al.* (2003) and Xia, Lemey (2009) using DAMBE v. 7.2.1 (Xia, 2018).

The concatenated matrix was partitioned by gene (Chernomor *et al*., 2016) and the best-fit model of nucleotide evolution was selected with ModelFinder (Kalyaanamoorthy *et al*., 2017) based on the Bayesian Information Criterion (BIC) and weighted BIC (w-BIC) scores. Phylogenetic relationships were inferred through the Maximum Likelihood (ML) analysis with 1000 ultrafast bootstrap replicates (Hoang *et al*., 2018). All analyses were conducted using IQ-TREE v. 2.3.6 (Minh *et al*., 2020). *Pimelodus ornatus* Kner, 1858 was used to root the phylogeny. Additionally, samples of Rhamdiini and Heptapterini were included in the analysis as additional related groups (Fig. **S1**). The final tree was visualized with the software FIGTREE v. 1.4.4 (Rambaut, 2014).

RESULTS

Leptorhamdia kamilai, new species

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(Figs. 1–2; Tab. 1)

Myoglanis sp. —Casatti *et al*., 2020:8, tab. 2 (inventory).

Myoglanis n. sp.1 Tapajós. —Silva *et al*., 2021:5, fig. 1 (phylogenomic of Heptapteridae).

Holotype. DZSJRP 16293, 92.4 mm SL, Brazil, Mato Grosso State, Campos de Júlio Municipality, rio Juruena, PCH Segredo, 13°13’27.6”S 59°01’34.4”W, Jun 2012, R. J. Ilario.

Paratypes. All from Brazil, Mato Grosso State. Rio Tapajós basin: DZSJRP 25393, 1, 71.5 mm SL, collected with holotype. DZSJRP 16302, 2, 53.8–91.0 mm SL, Campos de Júlio Municipality, rio Juruena, PCH Ilha Comprida, Jun 2012, R. J. Ilario. DZSJRP 21986, 2, 56.6–84.6 mm SL, Juina, rio Juruena, 11º31’49”S 58º49’33”W, 30 May 2018, G. Brejão. LBP 30639, 2, 31.4–66.3 mm SL, Nova Mutum Municipality, rio dos Patos, a tributary of rio Arinos, 13º48’4.79”S 56º1’37.4”W, 22 Aug 2021, C. S. Souza, E. V. Ywamoto, G. S. C. Silva, & L. Reia. LBP 20829, 4, 40.1–48.3 mm SL (1 c&s, 48.3 mm SL), Nova Mutum Municipality, rio dos Patos, a tributary of rio Arinos, 13º48’4.79”S 56º1’37.4”W, 29 Oct 2015, C. Araya, G. J. Costa-Silva, N. T. B. Mateussi, B. F. Melo & G. S. C. Silva. MZUSP 131552, 2, 32.9–47.8 mm SL, Nova Mutum Municipality, rio dos Patos, a tributary of rio Arinos, 13º48’4.79”S 56º1’37.4”W, 22 Aug 2021, C. S. Souza, E. V. Ywamoto, G. S. C. Silva, & L. Reia. Rio Aripuanã basin: DZSJRP 21470, 1, 30.8 mm SL, Aripuanã Municipality, 10°11’47.0”S 59°29’19.0”W, 27 Jul 2017. DZSJRP 21559, 1, 72.4 mm SL, Aripuanã Municipality, 10°11’26.0”S 59°24’34.0”W, 28 Jul 2017, G. Brejão. DZSJRP 21641, 1, 49.0 mm SL. Aripuanã Municipality, 10°08’15.0”S 59°24’57.0”W, 31 Jul 2017, G. Brejão. DZSJRP 21709, 2, 49.8–66.6 mm SL, Aripuanã Municipality, 10°15’38.0”S 59°17’06.0”W, 1 Aug, 2017, G. Brejão. DZSJRP 21755, 1, 33.2 mm SL, Aripuanã Municipality, 10°20’58.0”S 59°21’43.0”W, G. Brejão. DZSJRP 21778, 7, 24.973.9 mm SL (1 c&s 60.3 mm SL), Aripuanã Municipality, 10°21’52.0”S 59°21’38.0”W, 2, Aug 2017. G. Brejão. DZSJRP 21791, 1, 36.0 mm SL, Aripuanã Municipality, 10°25’59.0”S 59°21’41.0”W, 2 Aug 2017, G. Brejão. DZSJRP 21819, 2, 22.824.5 mm SL, Aripuanã Municipality, 10°46’49.0”S 59°13’37.0”W, 3 Aug 2017, G. Brejão. DZSJRP 21938, 1, 51.5 mm SL, Juína Municipality, 11°32’07.0”S 59°11’39.0”W, 9 Aug 2017, G. Brejão.

FIGURE 1 | Left column: *Leptorhamdia kamilai*, holotype, DZSJRP 16293, 92.4 mm SL. Right column: paratypes, LBP 30639, from top to bottom: 66.3 mm SL; 47.8 mm SL; 31.4 mm SL.

TABLE 1 | Morphometric data for holotype (H) and paratypes of *Leptorhamdia kamilai*. N = number of specimens; SD = Standard deviation.

	H	Tapajós (N = 14)			Aripuanã (N = 9)		
		Range	Mean	SD	Range	Mean	SD
Standard length (mm)	92.4	31.4-92.4	-	-	22.5-73.9		-
Percentages of standard length							
Predorsal length	36.8	34.1-37.3	35.8	1.0	32.2-36.5	34.9	1.4
Dorsal-fin base	13.5	11.5-15.5	13.4	1.1	12.5-15.5	14.1	1.0
Dorsal fin to adipose fin	16.1	11.8-16.1	13.9	1.3	10.6-14.7	12.7	1.2
Preadipose length	62.1	57.4-64.5	61.5	1.8	58.3-61.3	59.9	1.2
Adipose-fin length	41.7	39.0-44.5	41.6	1.3	38.9-44.9	41.7	2.0
Prepelvic length	42.5	40.4-45.5	42.2	1.4	40.6-43.7	41.8	0.9
Preanal length	64.6	63.7-69.8	65.4	1.6	64.2-65.6	65.0	0.6
Anal-fin base	28.2	26.1-29.6	28.0	1.1	25.5-29.4	28.1	1.3
Caudal peduncle length	10.8	7.5-10.8	9.3	1.0	8.6-10.5	9.3	0.6
Caudal peduncle depth	8.7	7.2-11.4	9.0	1.2	7.9-9.5	8.7	0.5
Head length	23.2	22.3-26.2	24.1	1.2	21.7-24.3	23.0	0.9
Head width	20.1	16.2-20.4	18.2	1.0	16.3-17.6	17.0	0.5
Head depth	14.5	11.0-14,9	12.7	1.1	11.0-14.7	12.5	1.2
Maxillary-barbel length	34.7	31.4-38.7	34.5	2.0	36.2-40.9	37.7	1.4
Outer mental-barbel length	16.2	14.6-20.4	17.5	1.4	14.1-19.0	16.1	1.4
Inner mental-barbel length	8.4	8.4-12.9	9.8	1.2	7.5-11.0	9.1	1.4
Percentages of head length							
Snout length	32.9	28.3-32.9	31.1	1.8	30.4-34.0	32.9	1.2
Fleshy interorbital	29.1	24.0-29.5	26.8	1.7	21.8-27.6	25.5	2.0
Width between anterior nares	16.1	16.1-25.6	20.1	2.4	15.3-21.1	19.0	2.1
Width between posterior nares	20.2	18.5-23.4	21.8	1.4	19.4-24.9	22.3	2.1

Diagnosis. *Leptorhamdia kamilai* can be readily distinguished among its congeners by having a conspicuous light collar-band, yellowish in live specimens, posterior to the head (*vs*. coloration uniformly throughout body and head, lacking any distinctive bar). Additionally, *L. kamilai* differs from its congeners by having 19–22 anal-fin rays (*vs*. 17 in *L. essequibensis*; 15 in *L. marmorata*; 32–35 in *L. aspredinoides*; 12 in *L. nocturna*, 15–16 in *L. schultzi*) and by having 46–47 vertebrae (*vs*. 45 in *L. essequibensis*; 43 in *L.marmorata*; 38 in *L. nocturna*; 56–57 vertebrae in *L. aspredinoides* and 43 vertebrae in *L. schultzi*).

Description. Dorsal profile from snout tip to eyes convex, slightly concave in orbital region, convex from orbital region to collar-band, then straight to dorsal-fin origin, straight (descending) along dorsal-fin base, straight (ascending) from end of dorsal-fin base to origin of adipose fin, slightly concave along adipose-fin base and finishing slightly straight along caudal peduncle. Ventral profile straight from snout to posterior margin of branchiostegal membrane, then straight (ascending) to pelvic-fin origin, finishing gently concave to end of pelvic fin to caudal peduncle.

Head trapezoid in dorsal view. Adductor mandibulae muscles prominent on cheeks and extending dorsally over skull roof posterior to eyes. Eyes rounded and small, dorsally positioned, close to snout tip. Skin covering eye thin. Mouth subterminal, with upper jaw slightly longer than lower. Premaxilla and dentary with four to five irregular rows of conical teeth. Maxillary barbel surpassing vertical through dorsal-fin origin. Outer mental longer than inner mental barbel, reaching posterior margin of branchiostegal membrane. Branchiostegal membranes supported by seven rays and joined to isthmus only at anterior point. Five gill rakers along anterior border of first ceratobranchial. Total vertebrae 46–47 with 15 precaudal (including eight or nine supporting pleural ribs) and 31–32 caudal.

Laterosensory canal of the head with simple tubes ending in single pores. Supraorbital sensory canal usually with four branches and pores: s1, s2, s3, and s4. Supraorbital pore 1 medially adjacent to anterior nares. Supraorbital s2 at midway between anterior and posterior nares, s3 inside posterior nares, at the notch of the cutaneous membrane. Pores s4 paired, close together near midline, posterior at level of orbit. Infraorbital laterosensory canal with five branches and pores: i1, i2, i3, i4, and i5. Infraorbital pore i1 adjacent to anterior naris, between anterior naris and maxillary barbel; i2 laterally positioned at the midway between anterior and posterior naris. Pore i3 at vertical through anterior margin of orbit; i4 at vertical through posterior margin of orbit. Pore i5 posterior to eye. Preoperculomandibular laterosensory canal with 11 branches and pores: pm1 in the medial portion of dentary; pm2, pm3, and pm4 aligned anteriorly to inner and outer mental barbel; pm5 dorsal to outer mental barbel base; pm6 and pm7 at vertical through the anterior and posterior margin of orbit respectively. Four pores in preopercle region: pm8, pm9, pm10 and pm11.

Pectoral fin with seven branched rays preceded by a short and strong spine, with retrorse dentitions along both margins; serrae of posterior margin of spine more developed than the anterior margin. Pelvic fin i,5; first ray shorter than the posterior rays. Dorsal-fin i,6; first basal radial inserted on sixth or seventh vertebra and last basal radial anterior to neural spine of twelfth vertebra. Adipose fin elongate (40.0–44.5% of SL) with it posterior margin united to dorsal margin of caudal fin. Anal fin elongated with 19 to 22 rays, first three or four rays simple. Anal fin supported by 20–22 basal radials (2 c&s). Ventral caudal plate formed by parhypural free from hypurals 1 and 2. Dorsal caudal plate formed by uroneural, hypurals 3 and 4 fused and 5 free. Caudal fin lanceolate with i,7,8,i principal rays. Dorsal and ventral caudal-fin lobes with 5 and 9 procurrent rays, respectively.

Coloration in alcohol. Overall coloration uniform dark, mostly unpigmented on ventral half of head and trunk (Fig. 2). A conspicuous band of pale coloration, yellowish in live specimens, extending dorsally from slight posterior to supraoccipital, along the sides, to the ventral midline on branchiostegal membrane. In small specimens (< 30 mm SL) light collar band separated by a narrow-pigmented stripe at its midline portion. Adipose-, dorsal-, and anal-fin bases dark. Fin rays and interradial membranes hyaline.

Geographical distribution. The new species *Leptorhamdia kamilai* is known from tributaries of the upper rio Arinos and Juruena in the rio Tapajós basin and from tributaries of the rio Aripuanã in the rio Madeira basin, Mato Grosso State, central Brazil (Fig. 3). The new species was collected about 1.5 m deep, hidden beneath a leaf layer and muddy bottom (Fig. 4).

Conservation status. *Leptorhamdia kamilai* was collected at several sampling sites in the Upper Tapajós and Aripuanã river basins, with no imminent threats to the species detected. Therefore, we recommend that *L. kamilai* be categorized as Least Concern (LC) under IUCN's criteria (IUCN, 2024).

Etymology. The specific name, *kamilai*, honors our dear friend Dr. Kamila Mayumi Duarte Kuabara, an entomologist and lab manager of the Ornithology Department at The Academy of Natural Sciences of Drexel University. A noun in a genitive case.

Phylogeny. The concatenation resulted in a matrix of Heptapteridae with five loci and 4150 pb. No saturation was observed in the matrix, since the values of Iss (Index of Substitution Saturation) were lower than Iss.c (Critical Index of Substitution Saturation). According to BIC the best model fitted each gene were TPM2u+F+I+G4 (LogL -6087.950) for COI; TVM+F+I+R3 (LogL -9138.688) for Cyt b; TPM3+G4 (LogL -3158.490) for Glyt; TPM2+G4 (LogL -3601.665) for RAG2; TPM2u+F+I+R3 (LogL -8437.546) for ND2. The ML tree (LogL -30419.782) and Consensus tree (LogL -30419.809) returned identical topology and values of bootstrap. Our results recovered the same major clades identified in a recent phylogenomic study of Heptapteridae (Faustino-Fuster *et al*., 2021; Silva *et al*., 2021). Additionally, our results found *Leptorhamdia kamilai* nested in the tribe Brachyglaniini and sister group to *L. marmorata*+*L. aspredinoides*, two species from Guyana Shield (Figs. 5, **S1**).

FIGURE 2 | Live specimens of *Leptorhamdia kamilai*, paratype, LBP 30639, 66.3 mm SL. Photographed by Eric V. Ywamoto.

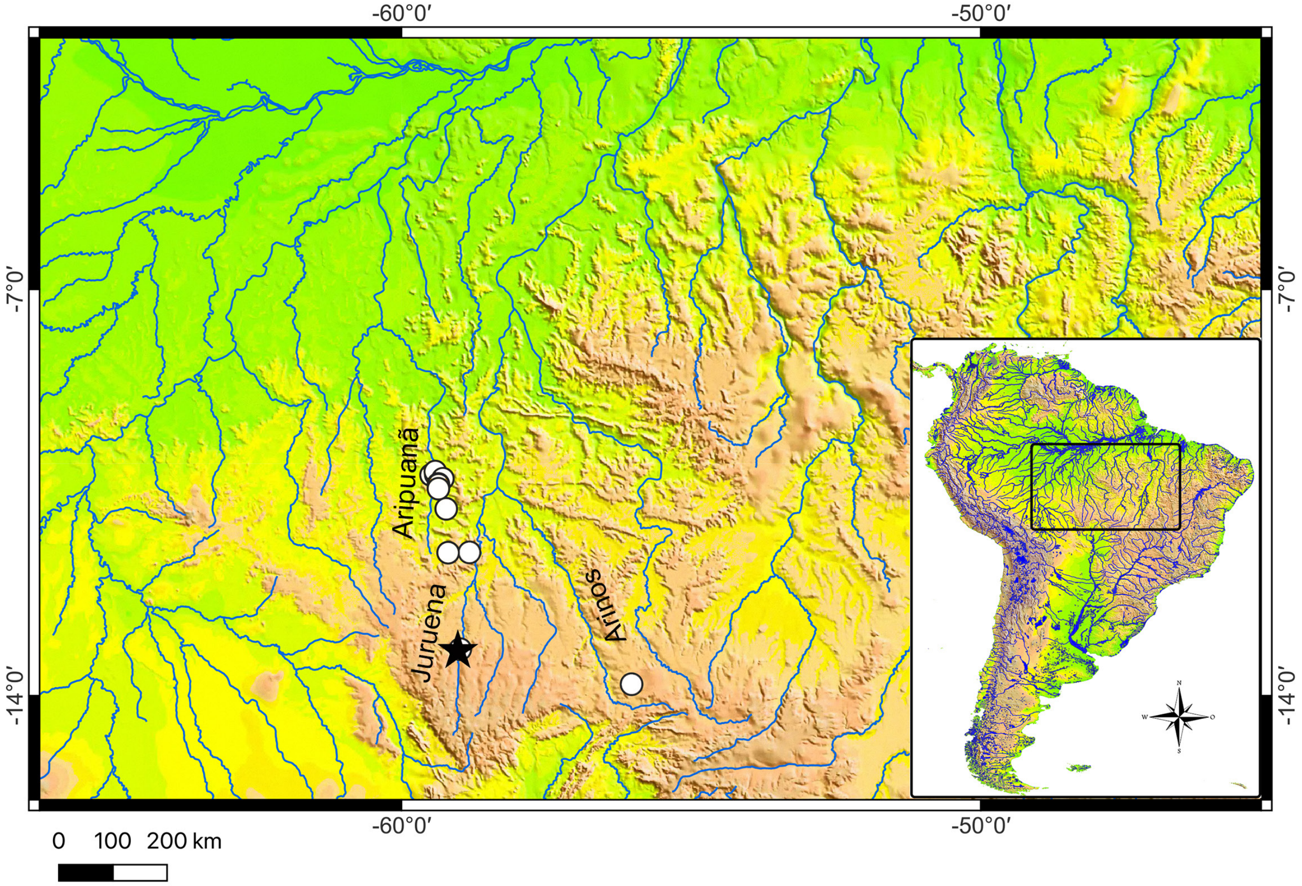

FIGURE 3 | Geographic distribution of *Leptorhamdia kamilai* in Brazilian Shield. Black star: holotype; white circles: paratypes.

FIGURE 4 | Habitat of *Leptorhamdia kamilai*, rio dos Patos, tributary of the upper Arinos River in Tapajós River basin.

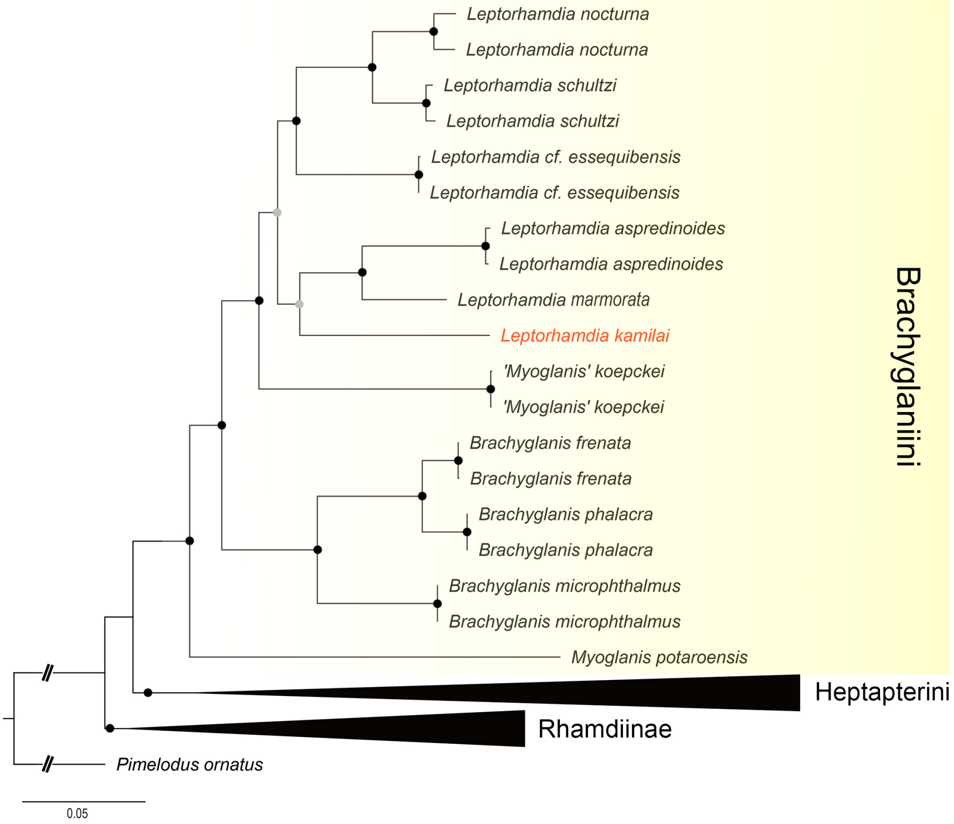

FIGURE 5 | Maximum likelihood tree of Heptapteridae showing the relationships among *Brachyglaniini* species. Black nodes indicate support between 90% and 100% bootstrap values; gray nodes indicate nodal support between 80% and 89%.

DISCUSSION

Our phylogenetic analysis revealed that the new species of Brachyglaniini described here is part of the clade composed of *Leptorhamdia* species, sister to *L. marmorata*+*L. aspredinoides*, justifying its allocation within this genus. Additionally, *L. kamilai* shares one of the three morphological characters proposed by Bockman, Slobodian (2018) to define *Leptorhamdia*: a premaxillary tooth plate formed as a compact triangular or rectangular structure, bearing a distinct posterolateral projection (*vs*. forming an arch, lacking a posterolateral projection in *Myoglanis* species). The other two diagnostic characters proposed by Bockman, Slobodian (2018) to distinguish *Leptorhamdia* from *Myoglanis* were not found in the new species: adipose fin very low, with the same depth along its entire length and adipose fin disconnected from caudal fin, with a distinct rounded posterior margin forming a lobe. These latter characters are absent in the new species, suggesting that they may not be suitable for defining the genus.

The new species described here, *L. kamilai*, is known from two distinct and adjacent drainages: the Juruena and Aripuanã river basins. Although representatives of this species occur in allopatry, specimens from both basins exhibit no morphological differences. Dagosta, de Pinna (2019) pointed out that the Aripuanã and Juruena Rivers share several ichthyofaunal elements, such as *Hemigrammus silimoni* Britski & Lima, 2008, *Moenkhausia levidorsa* Benine, 2002, and the genus *Utiaritichthys* Miranda Ribeiro, 1937, and argued that recent geomorphological events have caused biotic dispersal in the headwater of both rivers. Although the specimens of *L. kamilai* from the Juruena and Aripuanã are highly similar in morphological terms, genetic analyses of samples from the Aripuanã River are still pending, and it is not possible to assess potential genetic disparity between them.

During two expeditions to the rio dos Patos (the type locality), we were only able to collect eight specimens of *L. kamilai*. The difficulty in capturing this species is because these fish live buried in the leaf litter at the bottom of the river, at a depth of about 1.5 m. To collect specimens of *L. kamilai*, it was necessary to dive to the bottom of the riverbed and remove the layer of mud, where the species is associated with the leaf litter. Among the members of Brachyglaniini, only *L. kamilai* and *Myoglanis koepckei* have been reported to inhabit the leaf litter banks (Lima *et al*., 2005); all other members of the tribe are found in rapids, associated with rock-bottomed, fast-flowing rivers (Bockman, Slobodian, 2018).

Among members of Brachyglaniini, only *Leptorhamdia kamilai* exhibits a conspicuous light collar-band posterior to the head, which is regarded as an autapomorphy for this species. Similar pigmentation patterns are also observed in other heptapterid taxa, including species of *Pariolius* (*P. armillatus* and *P. maldonadoi*) and *Chasmocranus* stricto sensu (*C. brevior* and *C. longior*). According to recent phylogenetic hypotheses for Heptapteridae (Silva *et al*., 2021), *L. kamilai* (there named as *Myoglanis* n. sp. 1 Tapajós), *Pariolius* and *Chasmocranus* are phylogenetically distant, indicating that the light collar-band represents a homoplastic condition that evolved independently multiple times in the family. However, the selective pressures driving the convergent evolution of such pigmentation patterns within the group remain to be investigated.

Comparative material examined. Brazil. *Leptorhamdia shultzi*: ANSP 197846, 1, 88.1 mm SL; ANSP 200078, 1, 90.0 mm SL. **Peru.** *Myoglanis koepckei*: ANSP 167657, 6, 33.3–55.3 mm SL. **Venezuela.** *Leptorhamdia* sp.: ANSP 192588, 1, 65.6 mm SL.

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Gabriel de S. C. Silva: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Resources, Writing-original draft.

Lais Reia: Data curation, Formal analysis, Methodology, Software, Writing-review and editing.

Camila S. Souza: Data curation, Funding acquisition, Methodology, Writing-review and editing.

Eric V. Ywamoto: Data curation, Methodology, Writing-review and editing.

Claudio Oliveira: Data curation, Funding acquisition, Project administration, Supervision, Writing-review and editing.

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ETHICAL STATEMENT

Not applicable.

DATA AVAILABILITY STATEMENT

All molecular markers generated and analyzed in this study are deposited in GenBank. Accession numbers are provided in the manuscript.

AI STATEMENT

The authors declare that AI tools were used exclusively to perform minor English language corrections, without any influence on the scientific content, data analysis, or interpretation of the results.

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COMPETING INTERESTS

The authors declare no competing interests.

SUPPLEMENTARY MATERIAL

Supplementary material **S1**

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