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Relationships and description of a new catfish species from Chapada Diamantina, the northernmost record of *Trichomycterus s.s.* (Siluriformes, Trichomycteridae)

Wilson J. E. M. Costa¹, Caio R. M. Feltrin¹, José L. O. Mattos¹, Axel M. Katz¹

1 Laboratory of Systematics and Evolution of Teleost Fishes, Institute of Biology, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil https://zoobank.org/0E463E5B-8BE7-49F9-98E7-B170F18CDC6B

Corresponding author: Wilson J. E. M. Costa (wcosta@acd.ufrj.br)

Academic editor: Nicolas Hubert • Received 9 November 2023 • Accepted 7 February 2024 • Published 6 March 2024

Abstract

Psammocambeva exhibits the largest geographical distribution amongst the subgenera of *Trichomycterus s.s.*, with its present northernmost represented by *Trichomycterus tete*, endemic to the upper Rio de Contas Basin in the Chapada Diamantina Region, north-eastern Brazil. Herein, we describe a new species recently collected in the Chapada Diamantina Region, but in the Rio Paraguaçu Basin, about 100 km north of the area inhabited by *T. tete*. A molecular phylogeny using one nuclear and two mitochondrial genes (2430 bp) supported the new species as sister to *T. tete*; both species are distinguished by colour patterns, morphometric data, relative position of dorsal and anal fins and osteological character states. The clade comprising the new species and *T. tete*, endemic to the semi-arid Caatinga biogeographical province, is supported as sister to a clade comprising species from the Rio Doce and Rio Paraíba do Sul Basins, in the Atlantic Forest biogeographical province. This study corroborated the Chapada Diamantina Region, a well-known mountainous biodiversity centre, as an important centre of endemism for trichomycterid catfishes.

Key Words

Caatinga, molecular phylogeny, mountain biodiversity, osteology, Rio Paraguaçu

Introduction

The Trichomycterinae (hereafter trichomycterines) are the most common fish group in South American mountainous regions (Costa 2021). In eastern and north-eastern Brazilian highlands, trichomycterines are represented by the genus *Trichomycterus* Valenciennes, 1832, which in its strict sense (i.e. *Trichomycterus s.s.*) is a well-supported clade, which is sister to a clade containing the genera *Cambeva* Katz, Barbosa, Mattos & Costa, 2018 and *Scleronema* Eigenmann, 1917 (Katz et al. 2018). *Trichomycterus s.s.* includes the type species of the genus, *Trichomycterus s.s.* includes the type species of the genus, *Trichomycterus ni-gricans* Valenciennes, 1832 and others about 80 species, in six subgenera (Costa 2021). Amongst these subgenera, *Psammocambeva* Costa, 2021, presently including 35 nominal species, exhibits the largest geographical distribution and is the only one occurring in north-eastern

Brazil (Costa 2021; Vilardo et al. 2023). *Psammocambeva* is well-supported in molecular phylogenies, but it is not diagnosable by unique morphological character states, with species positioning being determined mainly by molecular phylogenies, besides the absence of synapomorphic osteological characteristics of other genera and, exceptionally, by the presence of derived osteological characteristics that are shared by groups of species within *Psammocambeva* (Costa 2021; Costa et al. 2022, 2023).

The present northernmost record for *Psammocambeva*, as well as for *Trichomycterus s.s.*, is *Trichomycterus tete* Barbosa & Costa, 2011, endemic to the Rio de Contas Basin, southern Chapada Diamantina, north-eastern Brazil (Barbosa and Costa 2011). Recently, one of us (CRMF) collected another species of *Psammocambeva* in the Chapada Diamantina, but in the Rio Paraguaçu Basin, about 100 km north of the area inhabited by *T. tete* in the Rio de

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Contas Basin. The objectives of the present study are to conduct a phylogenetic analysis to investigate the positioning of the new species and to present a formal description.

Materials and methods

Field studies were approved by ICMBio (Instituto Chico Mendes de Conservação da Biodiversidade; permit number: 38553-13) and field methods by the Ethics Committee for Animal Use of Federal University of Rio de Janeiro (permit number: 065/18). Euthanasia, fixation, preparation for morphological studies and conservation followed methods of our previous studies on trichomycterine systematics (e.g. Costa et al. (2023)). In lists of specimens, C&S indicates cleared and stained specimens for osteological analyses and DNA indicates specimens directly fixed and preserved in absolute ethanol. Geographical names followed Portuguese terms used in the region. Specimens were deposited in the Instituto de Biologia, Universidade Federal do Rio de Janeiro (UFRJ). Comparative material is listed in Costa et al. (2022, 2023). Methods to take and express morphometric and meristic data, morphological terminology, selection of described and illustrated osteological structures and sequence of morphological characters used in the species description are according to our previous studies on Psammocambeva (Costa et al. 2022, 2023).

Proceedings for DNA extraction, amplification and sequencing, reading and interpretation of sequencing chromatograms and sequences annotation were according to our previous studies on systematics of *Psammocambeva* (e.g. Costa et al. (2023)).

Primers for PCR reactions for the three genes used in the analysis, the mitochondrial genes cytochrome b (CYTB) and cytochrome c oxidase I (COX1) and the nuclear encoded gene recombination activating 2 (RAG2), were the same used in other studies on *Psammocambeva* (e.g. Costa et al. (2023)). The concatenated molecular data matrix comprised 2430 bp (COX1 521 bp, CYTB 1088 bp, RAG2 821 bp). Parameters for PCR reactions and thermal profile of PCR protocol were the same used in Costa et al. (2023). The sequencing reaction thermal profile was 35 cycles of 30 s at 95 °C, 30 s at 55 °C and 1.5 min at 73 °C. GenBank accession numbers are provided in Table 1.

Terminal taxa for the phylogenetic analyses comprised the new species and 22 species of *Psammocambeva* representing all included lineages. Outgroups were four congeners representing other subgenera of *Trichomycterus s.s.*, two species of the clade *Cambeva* plus *Scleronema*, the sister group of *Trichomycterus s.s.*, one species of a distantly related trichomycterine genus, two species representing other Trichomycteridae subfamilies and one species of the Nematogenyidae, the sister group of Trichomycteridae. Alignment of individual gene datasets was made with the Clustal W algorithm (Chenna et al. 2003) implemented in MEGA 11 (Tamura et al. 2021). The optimal partition scheme and the best-fit evolutive models (Table 2) were calculated using the Partition-Finder 2.1.1 (Lanfear et al. 2016) software, based on the
 Table 1. Species used in the phylogenetic analyses and respective GenBank accession numbers.

	COX1	CYTB	RAG2
Nematogenys inermis	KY857952	-	KY858182
Trichogenes longipinnis	MK123682	MK123704	MF431117
Microcambeva ribeirae	MN385807	OK334290	MN385832
Ituglanis boitata	MK123684	MK123706	MK123758
Scleronema minutum	MK123685	MK123707	MK123759
Cambeva barbosae	MK123689	MK123713	MN385820
Trichomycterus itatiayae	MW671552	MW679291	0L779233
Trichomycterus nigricans	MN813005	MK123723	MK123765
Trichomycterus albinotatus	MN813007	MK123716	MN812990
Trichomycterus brasiliensis	MK123691	MK123717	MK123763
Trichomycterus travassosi	MK123701	MK123730	OL752425
Trichomycterus alterrnatus	OQ357886	0Q355710	0Q400957
Trichomycterus pantherinus	MK123697	MK123725	MN812989
Trichomycterus goeldii	MT435136	MT436453	MT446427
Trichomycterus jacupiranga	OL764372	0L779234	0L779232
Trichomycterus pradensis	MN813003	MK123726	MN812988
Trichomycterus melanopygius	OQ357896	0Q355720	0Q400967
Trichomycterus auroguttatus	MT435135	MT436452	OP699434
Trichomycterus saquarema	OP698258	OP688464	OP688470
Trichomycterus macrophthalmus	OL741727	0L752426	0L752421
Trichomycterus astromycterus	ON036881	OK652453	OK652448
Trichomycterus altipombensis	OP698260	OP688466	OP688472
Trichomycterus puriventris	OP698259	OP688465	OP688471
Trichomycterus mimosensis	OQ357893	OQ355719	0Q400966
Trichomycterus longibarbatus	OQ357895	0Q355718	0Q400965
Trichomycterus gasparinii	OR354437	OR356032	0Q400962
Trichomycterus vinnulus	ON036819.1	OK652452	OK652449
Trichomycterus barrocus	OQ357889	0Q355713	0Q400959
Trichomycterus ipatinga	0Q357892	OQ355716	0Q400963
Trichomycterus illuvies	0Q357894	OQ355717	0Q400964
Trichomycterus tete	OL741729	MH620966	-
Trichomycterus diamantinensis	OR435278	OR438925	OR438926
Trichomycterus caudofasciatus	-	MK123719	MK123764

Table 2. Best-fitting partition schemes and evolutive models.

Partition	Base pairs	Evolutive Model
COX1 1st	174	GTR+I
COX1 2 nd	174	F81
COX1 3 rd	173	GTR+G
CYTB 1 st	363	K80+I+G
CYTB 2 nd	363	HKY+I
CYTB 3rd	362	GTR+G
RAG2 1 st	455	K80+I+G
RAG2 2 nd	274	GTR+G
RAG2 3rd	273	K80+G

Corrected Akaike Information Criterion. Bayesian Inference was performed with MrBayes 3.2.7a (Ronquist et al. 2012), using two independent Markov Chain Monte Carlo (MCMC) runs with 5×107 generations; sampling frequency of every 1000 generations; Tracer 1.7.2 (Rambaut et al. 2018) for evaluation of convergence of the MCMC chains, attainment of the stationary phase, effective sample size adequacy and determination of the burn-in percentage; and 25% burn-in to calculate Bayesian posterior probabilities. Maximum Likelihood (ML) was performed using IQ-TREE 2.2.0 (Minh et al. 2020), with node support estimated through both ultrafast bootstrap (Hoang et al. 2018) and traditional bootstrap (Felsenstein 1985), with 1000 replicates for each one.

Results

Phylogenetic analyses

The phylogenetic analyses generated identical trees (Fig. 1), in which the new species is highly supported as sister to *T. tete*, the only other species of *Trichomycterus* endemic to the Chapada Diamantina.

Taxonomic accounts

Trichomycterus (Psammocambeva) diamantinensis sp. nov.

https://zoobank.org/2E7E0C0D-2FC6-452B-95EF-8931787C2D73 Figs 2, 3, 4A–C, Table 3

Type material. *Holotype.* BRAZIL • 1 ex., 82.2 mm SL; Bahia State: Palmeiras Municipality: Vale do Capão District: Rio da Bomba, tributary of Rio Preto, Rio Santo Antônio drainage, Rio Paraguaçu Basin; 12°39'35"S, 41°29'14"W; about 980 m a.s.l.; 15 May 2023; C. R. M. Feltrin, R. dos Santos-Junior, and G. L. Canella, leg; UFRJ 13688.

Paratypes. BRAZIL • 3 ex. (DNA), 39.7–60.5 mm SL; collected with holotype; UFRJ 13686; • 3 ex. (C&S), 49.4–70.0 mm SL; collected with holotype; UFRJ 13689; • 2 ex., 27.1 and 79.6 mm SL; collected with holotype; UFRJ 13690.

Diagnosis. Trichomycterus diamantinensis is distinguished from all other species of Psammocambeva by having a unique colour pattern of adult specimens consisting of a faint brown stripe along the lateral mid-line of trunk, overlapped by a great concentration of rounded light brown spots in a more superficial layer of skin (vs. never a similar colour pattern). Trichomycterus diamantinensis also differs from its hypothesised sister species and the only other species of the CD-clade, T. tete, by having the anal-fin origin at a vertical posterior to the dorsal-fin base (vs. through the posterior portion of the dorsal-fin base), a longer nasal barbel, its tip posteriorly reaching the opercular patch of odontodes (vs. reaching area between the orbit and the opercular patch of odontodes), 39 or 40 vertebrae (vs. 36 or 37), a deeper body (body depth 14.0-17.3% SL vs. 12.5-13.2%), a deeper caudal peduncle (caudal peduncle depth 11.5-12.9% SL vs. 9.7-10.8%), a wider body (body width 11.2-12.3%) SL vs. 7.3-9.0%), a wider head (head width 83.1-89.3%) of head length vs. 68.7-77.5%), the anal-fin origin at a vertical through the centrum of the 25th vertebra (vs. 22nd or 23rd vertebra), the sesamoid supraorbital slender, without a lateral process (Fig. 4A; vs. with a lateral expansion, often forming a distinctive process, Fig. 4D), a relatively wider metapterygoid and quadrate (Fig. 4B vs. Fig. 4E) and a minute ventral middle foramen of the parurohyal (Fig. 4C; vs. broad, Fig. 4F).

Description. *General morphology.* Morphometric data are in Table 3. Body moderately slender, head and trunk excluding caudal peduncle with dorsal profiles

Table 3. Morphometric data of *Trichomycterus diamantinensis*sp. nov.

	Holotype	Paratypes (n=4)
Standard length (SL)	70.0	49.4–79.6
Percentage of standard length		
Body depth	14.0	14.9–17.3
Caudal peduncle depth	11.5	11.6-12.9
Body width	11.2	11.5-12.3
Caudal peduncle width	5.1	4.1-5.5
Pre-dorsal length	63.7	62.6-64.3
Pre-pelvic length	59.3	58.3-61.0
Dorsal-fin base length	10.0	10.6-11.6
Anal-fin base length	8.1	8.0-10.3
Caudal-fin length	17.0	14.6-16.5
Pectoral-fin length	14.1	12.8-13.3
Pelvic-fin length	8.9	9.4–9.6
Head length	19.7	18.5-20.8
Percentage of head length		
Head depth	48.8	51.4-55.3
Head width	84.0	83.1-89.3
Snout length	42.7	39.7-44.0
Interorbital width	26.0	26.4-29.9
Pre-orbital length	12.2	14.2-15.6
Eye diameter	13.1	12.2-16.9

slightly convex, and ventral profile nearly straight, dorsal and ventral profiles of caudal peduncle approximately straight. Greatest body depth at vertical just anterior to pelvic-fin base. Trunk subcylindrical anteriorly, compressed posteriorly. Anus and urogenital papilla at vertical through dorsal-fin origin or just posterior to it. Head subtrapezoidal in dorsal view, snout profile slightly convex. Eye relatively small, dorsally positioned in head, nearer snout margin than opercle. Posterior nostril located nearer anterior nostril than orbital rim. Tip of maxillary barbel posteriorly reaching between posterior limit of interopercular patch of odontodes and pectoral-fin base, rictal barbel reaching posterior portion of interopercular patch of odontodes and tip of nasal barbel reaching opercular patch of odontodes. Mouth subterminal. Jaw teeth pointed, slightly curved, arranged in irregular rows. Premaxillary teeth 45-50, dentary teeth 44-50. Odontodes conical, elongate; opercular odontodes arranged in irregular transverse rows, interopercular odontodes arranged in irregular longitudinal rows. Opercular odontodes 17-19, interopercular odontodes 38-42. Branchiostegal rays 7.

Dorsal and anal fins subtriangular, anterior and posterior margins slightly convex. Total dorsal-fin rays 12 (iii + II + 7), total anal-fin rays 10 (iii + II + 5); anal-fin origin at vertical just posterior to dorsal-fin base end. Dorsal-fin origin at vertical through centrum of 20^{th} vertebra; anal-fin origin at vertical through centrum of 25^{th} vertebra. Pectoral fin subtriangular in dorsal view, posterior margin slightly convex, first pectoral-fin ray terminating in filament, its length about 25% of pectoral-fin length without filament. Total pectoral-fin rays 8 (I + 7). Pelvic fin subtruncate, its posterior extremity not reaching urogenital papilla, at vertical through dorsal-fin origin or immediately posterior to it. Pelvic-fin bases medially in close proximity. Total pelvic-fin rays 5 (I + 4). Caudal fin truncate. Total principal caudal-fin rays 13 (I + 11 + I),



Figure 1. Bayesian Inference topology calculated using MrBayes 3.2.7a for 33 taxa. The dataset comprised two mitochondrially encoded genes (COI, CYTB) and one nuclear gene (RAG2), with a total of 2430 bp. The numbers above branches indicate Bayesian posterior probabilities from the Bayesian Inference analysis and the ultrafast bootstrap and regular bootstrap values from the Maximum Likelihood analyses, respectively, separated by a bar. Asterisks (*) indicate maximum support values and dashes (-) indicate values below 50.

total dorsal procurrent rays 17 or 18 (xvi–xvii + I), total ventral procurrent rays 13 or 14 (xii–xiii + I).

Latero-sensory system. Supraorbital canal, posterior section of infraorbital canal and postorbital canal continuous. Supraorbital sensory canal with 3 paired pores: s1, adjacent to medial margin of anterior nostril; s3, adjacent and just posterior to medial margin of posterior nostril and s6, at transverse line through posterior half of orbit; s6 pore about equidistant from its symmetrical homologous s6 pore than orbit. Infraorbital sensory canal with 2 pores: i1, at

transverse line through anterior nostril and i3, at transverse line just anterior to posterior nostril. Posterior infraorbital canal with two pores: i10, adjacent to ventral margin of orbit and i11, posterior to orbit. Postorbital canal with 2 pores: po1, at vertical line above posterior portion of interopercular patch of odontodes, and po2, at vertical line above posterior portion of opercular patch of odontodes. Lateral line of trunk with 2 pores just posterior to head.

Osteology (Fig. 4A-C). Anterior margin of mesethmoid nearly straight, mesethmoid cornu rod-shaped,



Figure 2. *Trichomycterus (Psammocambeva) diamantinensis* sp. nov., UFRJ 13688, holotype, 82.2 mm SL: A. Left lateral view; B. Dorsal view; C. Ventral view.

tip rounded. Lacrimal oval, its largest length about one third of sesamoid supraorbital length. Sesamoid supraorbital narrow, rod-like, longer than premaxilla largest length. Premaxilla sub-rectangular in dorsal view, slightly tapering laterally. Maxilla boomerang-shaped, slender, slightly shorter than premaxilla, with minute posterior process. Autopalatine sub-rectangular in dorsal view when excluding posterolateral process, its shortest width about half autopalatine length, lateral and medial margins weakly concave. Latero-posterior process of autopalatine triangular, its length about two thirds of autopalatine length excluding anterior cartilage. Metapterygoid subtriangular, deeper than long, with distinctive posterior projection; anterior margin weakly bent, posterior margin slightly sinuous. Quadrate robust, dorsoposterior outgrowth in close proximity to hyomandibular outgrowth. Hyomandibula long, anterior outgrowth with small concavity on dorsal margin. Opercle moderately elongate, opercular odontode patch slender, its depth about half length of dorsal articular facet of hyomandibula; dorsal

process of opercle short and blunt. Interopercle long, its longitudinal length about three fourths of hyomandibula longitudinal length. Preopercle compact, without ventral expansion. Parurohyal robust, lateral process relatively elongate, sharply pointed. Parurohyal head well-developed, with minute anterolateral paired process. Middle parurohyal foramen small, its largest length about one fourth of distance between anterior margin of parurohyal and anterior insertion of posterior process. Posterior parurohyal process long, slightly longer than distance between anterior margin of parurohyal and anterior insertion of posterior process. Vertebrae 39 or 40. Ribs 13. Two dorsal hypural plates, corresponding to hypurals 4 + 5 and 3, respectively; single ventral hypural plate corresponding to hypurals 1 and 2 and parhypural.

Colouration in alcohol (Figs 2, 3). Dorsum and flank brownish-grey, lighter ventrally, with faint brown stripe along lateral mid-line of trunk, overlapped by great concentration of rounded light brown spots extending over flank and dorsum in more superficial layer of skin. Dorsum



Figure 3. *Trichomycterus (Psammocambeva) diamantinensis* sp. nov., UFRJ 13690, paratype, 27.1 mm SL: A. Left lateral view; B. Dorsal view; C. Ventral view.

light brown with yellowish-grey with mid-dorsal row of small brown spots between nape and dorsal-fin origin. Dorsal and lateral portions of head brownish-grey with brown spots. Ventral surface of head and trunk white. Jaws and barbels brown. Fins hyaline, with faint brown spots on basal portion of unpaired and pectoral fins. Smallest specimen (27.1 mm SL) with flank pale yellow and narrow black stripe along lateral mid-line, which becomes paler and diffuse and overlapped by brown spots in larger specimens.

Distribution and habitat. *Trichomycterus diamantinensis* is presently known only from the type locality, the Rio da Bomba, a tributary of the Rio Preto, Rio Santo Antônio drainage, Rio Paraguaçu Basin (Fig. 5). Rio da Bomba at the type locality is a dark-coloured small river, about 15 m wide and about 1 m at deepest places, with dense riparian forest in the river banks (Fig. 6). Specimens of *T. diamantinensis* were found amongst small and medium-sized loose stones, with diameters ranging from 1 cm to 50 cm, approximately, in shallow (about between 5 and 50 cm) and fast-flowing places, with the

presence of mosses, algae and fallen leaves composing the microhabitats. They were collected both in shaded and fully sun-exposed places.

Etymology. The name *diamantinensis* is an allusion to the occurrence of the new species in the Chapada Diamantina, north-eastern Brazil.

Discussion

The present description of *T. diamantinensis* expands the distribution of *Trichomycterus s.s.* about 100 km to north, consisting of the first record of the genus for the Rio Paraguaçu Basin, an important fluvial system of north-eastern Brazil, with a surface area about 54,900 km2. A previous record of the occurrence of *Trichomycterus* further north in north-eastern Brazil by Sarmento-Soares et al. (2011), in the Rio Itapicuru Basin, was actually due to a misplacement of the species *Ituglanis payaya* (Sarmento-Soares, Zanata & Martins-Pinheiro, 2011), as discussed by Costa



Figure 4. Osteological structures of A–C. *Trichomycterus diamantinensis* sp. nov.; D–F. *T. tete.* A, D. Mesethmoidal region and adjacent structures, left and middle portions, dorsal view; B, E. Left jaw suspensorium and opercular series, lateral view; C, F. Parurohyal, ventral view. Larger stippling represents cartilaginous areas.



Figure 5. Map of geographical distribution of: 1. Trichomycterus diamantinensis sp. nov. and 2. T. tete.

et al. (2021). No species of *Trichomycterus s.s.* was found during our field studies in the Rio Itapicuru Basin.

This study supported a clade endemic to the Chapada Diamantina Region, in the semi-arid Caatinga biogeographical province (sensu Morrone (2006)), comprising *T. diamantinensis* from the Rio Paraguaçu Basin and *T. tete* from the Rio de Contas Basin (Fig. 1). No other species of *Trichomycterus s.s.* is known to occur in the Caatinga. The analysis indicated that the clade comprising *T. diamantinensis* and *T. tete* is sister to a well-supported clade including species endemic to the Rio Doce Basin, in the Atlantic Forest biogeographical province: *Trichomyc*-



Figure 6. Rio da Bomba at the type locality of *Trichomycterus diamantinensis* sp. nov.

terus barrocus Reis & de Pinna, 2022, Trichomycterus illuvies Reis & de Pinna, 2022, Trichomycterus ipatinga Reis & de Pinna, 2022 and Trichomycterus melanopygius Reis, dos Santos, Britto, Volpi & de Pinna, 2020. Recent molecular data indicated that Trichomycterus brucutu Reis & de Pinna, 2022 from the Rio Doce Basin is also a member of this group (Vilardo et al. 2023), here named as the Psammocambeva beta-clade. Our molecular studies in progress and molecular data presented in Reis and de Pinna (2022) support Trichomycterus tantalus Reis & de Pinna, 2022 also from the Rio Doce Basin as closely related to T. ipatinga and T. melanopygius. Trichomycterus tantalus is distinguishable from Trichomycterus largoperculatus Costa & Katz, 2022, a species endemic to the Rio Paraíba do Sul Basin, south-eastern Brazil, not available for molecular analyses, only by minor morphological features (i.e. odontode counts) and both species share river migrating habits (Costa and Katz 2022; Reis and de Pinna 2022). Thus, available evidence indicates that T. largoperculatus and T. tantalus are also members of the Psammocambeva beta-clade. On the other hand, the present study supports Trichomycterus pradensis Sarmento-Soares, Martins-Pinheiro, Aranda & Chamon, 2005, a species occurring in coastal river basins of north-eastern Brazil (Sarmento-Soares et al. 2005), as distantly related to the Psammocambeva beta-clade. Relationships of other nominal species morphologically similar and occurring in areas close to the distribution area of T. pradensis (e.g. Trichomycterus bahianus Costa, 1992, Trichomycterus itacambirussu Triques & Vono, 2004, Trichomycterus jequitinhonhae Triques & Vono, 2004 and Trichomycterus landinga Triques & Vono, 2004) are still unknown.

The colour pattern of adult specimens of *T. diamantinen*sis, comprising dark pigmentation occurring in two layers of the skin, with a faint brown stripe along the lateral midline of the trunk at an internal layer, overlapped by a great concentration of rounded light brown spots at a more external layer (Fig. 2), immediately distinguishes this species from all other congeners of *Psammocambeva*. In *T. tete*, its hypothesised sister species, the colour pattern consists of dark pigmentation arranged in a single layer, forming round spots separated by broad interspaces (Barbosa and Costa 2011: fig. 1). However, juvenile specimens below about 30 mm SL of both species (Fig. 3), share an identical colour pattern, in which the flank is pale yellow with a narrow black stripe along the longitudinal mid-line, possibly corroborating sister group relationships, since no other species of *Psammocambeva* has a similar colour pattern in juvenile specimens. In the distantly-related *Trichomycterus saquarema* Costa, Katz, Vilardo & Amorim, 2022, in addition to a broad black stripe along the lateral mid-line, there is another stripe on the dorsal part of the flank (Costa et al. 2022: fig. 14C), thus considered a non-homologous condition.

The sources of the Rio Paraguaçu are located in the Chapada Diamantina, a well-known mountainous biodiversity centre with numerous endemic plants (Giulietti et al. 1997). The present study corroborates the Chapada Diamantina as an important centre of endemism for trichomycterid catfishes. In addition to *T. diamantinensis* and *T. tete*, endemic trichomycterids include the whole subfamily Copionodontinae (de Pinna 1992), two species of the trichomycterine genus *Ituglanis* Costa & Bockmann, 1993 (Campos-Paiva and Costa 2007; Costa et al. 2021) and one species of the sarcoglanidine genus *Ammoglanis* Costa, 1994 (Costa et al. 2020).

Acknowledgements

We are grateful to Ronaldo dos Santos-Junior and Gustavo L. Canella for assistance during field studies. Instituto Chico Mendes de Conservação da Biodiversidade provided collecting permits. Thanks are also due to Felipe Ottoni and Valter Azevedo-Santos for comments and suggestions. This work was partially supported by Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq; grant 304755/2020-6 to WJEMC) and Fundação Carlos Chagas Filho de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ; grant E-26/201.213/2021 to WJEMC, E-26/202.005/2020 to AMK and E-26/202.327/2018 to JLM). This study was also supported by CAPES (Finance Code 001) through Programa de Pós-Graduação em Biodiversidade e Biologia Evolutiva /UFRJ and Programa de Pós-Graduação em Genética/UFRJ.

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