A new rare catfish species from southeastern Brazil provides insights into the origins of similar colour patterns in syntopic, distantly related mountain trichomycterines (Siluriformes, Trichomycteridae)

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https://zoobank.org/C3BED28C-2D3A-416F-BEBA-73DF1BECA132

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Abstract

Colour patterns are diverse in trichomycterine catfishes and are often used to diagnose species. Here, we analyse the first case of adults of two syntopic species of Trichomycterus sharing nearly identical colour patterns: a rare new species of the subgenus Paracambeva and Trichomycterus maculosus, a distantly related species of the subgenus Trichomycterus. Both species are endemic to the upper Rio Paraíba do Sul basin (RPSB), which had a different course until the Tertiary period and is situated within the Southeastern Brazilian Continental Rift, mostly active in the Eocene-Oligocene. A time-calibrated multigene analysis, 3144 bp, supported the new species as sister to Trichomycterus itatiayae, both comprising a lineage with Middle Miocene age, when that colour pattern would have first arisen. The new species is diagnosed by characters from the latero-sensory system and bone morphology. Our results, combined with available biogeographical data, indicated the colour pattern of T. maculosus arising in the Late Pliocene, following the dispersal of its group to the upper RPSB after river course changing. Two hypotheses for the independent origin of the same colour pattern are discussed. First, a case of evolutionary convergence for adaptation to live on a similarly coloured gravel substrate, giving some cryptic advantage against predators. Second, mimetic association through anti-predation features. In the latter case, although trichomycterids lack fin spines to inoculate venom as in other catfishes, the species here studied have a supposed axillary gland above the pectoral fin, just posterior to the opercular odontodes, but with properties and functions still unknown.

Key Words

Atlantic forest, molecular systematics, mountain biodiversity, Rio Paraíba do Sul basin, Serra da Mantiqueira

Introduction

Colouration has an important role in the biology of teleost fish species, involving attributes related to their behaviour and ecology (e.g., Price et al. 2008). Colour patterns are particularly diverse among the Trichomycteriinae (Eigenmann 1918), one of the most diverse groups of Neotropical catfishes, and as a consequence, they have been frequently used to diagnose species and groups since the 19th century (Valenciennes 1832). During field studies, colour patterns are often the primary tool to distinguish sympatric trichomycterine species, although chromatic polymorphism within species is not uncommon (Arratia et al. 1978; Sarmento-Soares et al. 2005; da Silva et al. 2010; Costa et al. 2023a; Vilardo et al. 2023). On the other hand, the occurrence of sympatric, non-closely related trichomycterine species exhibiting identical colour patterns is a rarely reported event (Costa et al. 2020a; Reis et al. 2020). The only report of two distantly related trichomycterines with the same colour pattern and found sharing the same habitat was made by Barbosa and Costa (2008) for Trichomycterus itatiayae Miranda Ribeiro, 1906, a species of the subgenus Paracambeva Costa, 2021, and Trichomycterus nigroauratus Barbosa & Costa, 2008, of the subgenus Trichomycterus (Costa 2021).
Herein we first report a rare new trichomycterine catfish species, with only four specimens found in the last two collections of six collecting trips between 1991 and 2023 to the upper Rio do Peixe drainage, Rio Paraíba do Sul basin (hereafter RPSB), southeastern Brazil. This species is morphologically similar to the syntopic Trichomycterus maculosus Barbosa & Costa, 2010, which is sister to T. nigroauratus. Specimens of this new species had a colour pattern approximately identical to that exhibited by larger adult specimens above 70 mm SL of T. maculosus (small spots on the dorsal part of the flank and a narrow dark grey longitudinal stripe along the flank midline; see description and included illustrations below), found in the same habitat (i.e., over gravel stream bottom). The two species are externally distinguishable by a few characters, comprising the relative position of the dorsal and anal fins, with the anal-fin origin positioned at a vertical line through the posterior-most portion of the dorsal-fin base in T. maculosus, vs. at a vertical line just posterior to the middle of the dorsal-fin base in the new species; number of pectoral-fin rays, eight in T. maculosus vs. seven in the new species; and body depth, with T. maculosus being more slender than the new species, reaching 12.8–13.8% of the standard length (SL) in T. maculosus, vs. 16.6–20.0% SL in the new species. Preliminary analysis in the laboratory revealed that the new species is sister to T. itatiayae, a member of Paracambeva, thus contrasting with the syntopic T. maculosus, a common species endemic to the upper Rio do Peixe drainage, belonging to the Trichomycterus nigroauratus group of the subgenus Trichomycterus (Barbosa and Costa 2010; Costa 2021). Paracambeva is diagnosed by an anterior infraorbital canal not attached to the lacrimal, a relatively short interopercle, and a relatively slender parapophysis of the second free vertebra (Costa 2021).

The new species and T. maculosus are only known from streams belonging to the upper Rio do Peixe drainage, Rio Paraíba do Sul basin (hereafter RPSB), in the southern plateau of the Serra da Mantiqueira, a mountain range that is an important centre of biodiversity in the Atlantic Forest, with a great concentration of endemic trichomycterines of the genus Trichomycterus Valenciennes, 1832 (e.g., Costa and Katz 2021). The origin of the southern plateau of the Serra da Mantiqueira is related to an uplift during the Neo-Cretaceous as a result of the process of separation of the South American and African plates (Riccomini et al. 2004, 2010). The southern plateau of the Serra da Mantiqueira is presently a divisor between the Rio Paraná basin and the RPSB. Geological evidence indicates that the upper portion of the present RPSB, including all the area today inhabited by the new species T. itatiayae, T. maculosus, and T. nigroauratus between the Neo-Cretaceous and the Tertiary, had a different course, directed to the northwest and being connected to the Rio Tietê drainage, the Rio Paraná basin, instead of the middle and lower sections of the RPSB (King 1956; Riccomini et al. 2010). In addition, the Rio do Peixe drainage is situated in a core area of the region known as the South-eastern Brazilian Continental Rift, which had its greatest development in the Eocene-Oligocene, including the paleo-lake Tremembé formed during the Oligocene (e.g., Riccomini et al. 2004, 2010). The objectives of the present study are to describe the new species, perform a time-calibrated analysis to test the positioning of the new species, and infer the timing of the origin of derived colour patterns in both lineages using a biogeographical temporal context.

Materials and methods

Specimens

Field procedures were approved by CEUA-UFRJ (Ethics Committee for Animal Use of the Federal University of Rio de Janeiro; permit numbers: 065/18 and 084/23) and collecting permits were given by ICMBio (Instituto Chico Mendes de Conservação da Biodiversidade; permit number: 38553-11). For details about specimen euthanasia, fixation, and conservation, see Costa et al. (2023b). Specimens were deposited in the ichthyological collection of the Instituto de Biologia, Universidade Federal do Rio de Janeiro (UFRJ). Comparative material is listed in Barbosa and Costa (2008), Costa and Katz (2021), and Costa et al. (2023b). A complete list of specimens used in morphological comparisons, with their respective catalogue numbers and locality coordinates, appears in Suppl. material 1.

Morphological data

Methods for taking and describing morphological characters were according to recent studies on Paracambeva, including morphometric and meristic data following Costa (1992) and Costa et al. (2020b), osteological preparations following Taylor and Van Dyke’s (1985), latero-sensory system nomenclature following Arratia and Huacquin (1995) and Bockmann and Sazima (2004), bone terminology following Costa (2021) and Kubicek (2022), and fin ray formulae following Bockmann and Sazima (2004).

DNA extraction, amplification, and sequencing

Methods for DNA extraction, amplification, and sequencing followed the most recent phylogenetic analysis of Paracambeva (Costa et al. 2023b), with PCR reactions performed in 45 μl with the following reagent concentrations: 5× GreenGoTag Reaction Buffer (Promega), 1.0 mM MgCl₂, 1 μM of each primer, 0.2 mM of each dNTP, 1 μ of Promega GoTaq Hot Start polymerase, and 50 ng of total genomic DNA; thermal profile: 95 °C for 5 min; 35 cycles of 94 °C for 1 min; 50–60 °C for 1–1.5 min;
and 73 °C for 7 min; sequencing reactions performed in 20 μL reaction volumes containing 4 μL BigDye, 2 μL sequencing buffer 5× (Applied Biosystems), 2 μL of the PCR products (30–40 ng), 2 μL primer, and 10 μL ultrapure water; and the thermal profile was 35 cycles of 30 s at 95 °C, 30 s at 55 °C, and 1.5 min at 73 °C. Primers used for mitochondrially encoded genes were: Cytb Siluri F and Cytb Siluri R (Villa-Verde et al. 2012) for cytochrome b (CYTB); FISHF1 and FISHR1 (Ward et al. 2005) for cytochrome c oxidase I (COX1). Primers for the nuclear encoded genes were: MYH6 TRICHO F and MYH6 TRICHO R (Costa et al. 2020c) for myosin heavy chain 6 (MYH6), and RAG2 TRICHO F and RAG2 TRICHO R (Costa et al. 2020c) for recombination activating 2 (RAG2). MEGA 11 (Tamura et al. 2021) was used to read and interpret sequencing chromatograms, to perform the sequence annotation, and to translate DNA sequences into amino acid residues to verify the absence of premature stop codons or indels. GenBank accession numbers are in Table 1.

Phylogenetic analyses

The terminal taxa for the phylogenetic analyses include all species of Paracambeva, including the new species herein described, and all species of the subgenus Trichomycterus. The remaining species of Trichomycterus and outgroups included in the analysis are the same as those used in Costa et al. (2023b). See Costa et al. (2023b) for justification for outgroup selection. Each gene dataset was aligned using the Clustal W algorithm (Chenna et al. 2003) implemented in MEGA 11 and analysed for determination of the optimal partitioning and evolutionary models (Table 2) using the Corrected Akaike Information (AICc) in PartitionFinder 2.1.1 (Lanfear et al. 2016). Phylogenetic analyses followed the methods described in Costa et al. 2023b), comprising Bayesian Inference performed with Beast 1.10.4 (Suchard et al. 2018), using the Yule process as the tree prior (Gernhard, 2008), two independent Markov chain Monte Carlo (MCMC) runs with 9 × 10^7 generations with a

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**Table 1.** Terminal taxa and GenBank accession numbers by gene used in molecular analyses.

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Table 2. Best-fitting partition schemes with the respective number of base pairs and the best-suited evolutionary models.

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<td>TRN+I+G</td>
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<td>CYTB 1st</td>
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Divergence-time estimation

The divergence time analysis was conducted in Beast 1.10.4 using the same dataset, partitions, evolution models, and parameters as described above. Additionally, the analysis incorporated a lognormal uncorrelated relaxed clock model and a Yule speciation process as the tree prior (Gernhard 2008). Calibration points were established as follows: the origin of the Trichomycteridae with a normal prior distribution (mean = 106 MA, SD = 5.0), following the estimative of Betancur-R et al. (2015), which is often used as an indirect calibration strategy in other studies on trichomycteriids (e.g., Ochoa et al. 2017; Vilardo et al. 2023); and the origin of the genus Corydoras with a lognormal prior distribution (mean = 55 MA, SD = 1), based on the dating of Corydoras revelatus Cockerell, 1925, the oldest known fossil of callichthyid catfishes. MCMC chains were assessed to verify convergence by evaluating the effective sample size of the runs in Tracer 1.7.1. The time-scaled tree was obtained using Tree Annotator version 1.10.4 to generate the consensus tree.

Results

Taxonomic accounts

Trichomycterus (Paracambeva) antiquus sp. nov.

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Figs 1–3, Table 3

Type material. Holotype. BRAZIL • 1 ex., 72.2 mm SL; Estado de São Paulo: Município de São José dos Campos: small stream tributary of the Rio Santa Bárbara, Rio do Peixe drainage, Rio Paraíba do Sul basin, São Francisco Xavier, Serra dos Poncianos, part of the Serra da Mantiqueira; 22°5'47"S, 45°54'60"W; about 980 m asl; 21 April 2023; C.R.M. Feltrin, leg.; UFRJ 13674.

Paratypes. (all from Estado de São Paulo: Município de São José do Campos: Rio do Peixe drainage, Rio Paraíba do Sul basin, São Francisco Xavier, Serra dos Poncianos, part of the Serra da Mantiqueira): BRAZIL • 1 ex., 75.6 mm SL (stained with alizarin and partially dissected); collected with holotype; UFRJ 13673; 1 ex., 79.1 mm SL; stream tributary of Rio Santa Bárbara; 22°53'45"S, 45°56'34"W; about 765 m asl; same collector and date as holotype; UFRJ 13681; 1 ex., 44.5 mm SL (cleared and stained for osteological analysis); same locality and collector as holotype; 29 October 2023; UFRJ 14201.

Diagnosis. Trichomycterus antiquus is distinguished from all other species of Paracambeva, except T. itatiayae, by having a relatively large head, its length 20.4–22.8% SL (vs. 11.4–18.1% SL), the presence of a deep concavity on the postero-ventral margin of the metapterygoid, accommodating a pronounced expansion of the postero-dorsal quadrate outgrown (Fig. 3B, see also Costa 2021: fig. 3B for similar condition in T. itatiayae; vs. metapterygoid concavity, when present, never deep and quadrate expansion, when present, never pronounced in other species of Paracambeva, e.g. Costa et al. 2023b: figs. 6G, H) and the presence of a deep U-shaped concavity on the dorsal margin of the anterior hyomandibular anterior outgrown (Fig. 3B, see also Costa 2021: fig. 3B for similar condition in T. itatiayae; vs. concavity, when present, never U-shaped, e.g. Costa et al. 2023b: figs. 6G, H). Trichomycterus antiquus differs from T. itatiayae by the presence of the anterior infraorbital canal (vs. absence), jaw teeth sharply pointed (vs. incisiform), a wider body and head (body width 11.9–15.0 vs. 6.2–8.8% SL; head width 51.8–58.4 vs. 68.7–75.7% SL), a longer pre-dorsal length (66.0–65.2 vs. 59.2 – 64.0% SL), a longer pre-pelvic length (66.0–65.2 vs. 60.0–65.9% SL), a deeper head (head depth 51.5–58.4 vs. 39.0–50.8% SL), a large eye (eye diameter 8.8–11.3 vs. 7.4–8.2% of the head length), a short sesamoid supraorbital, about twice longer than the lacrimal (Fig. 3A; vs. long, about four times longer, Costa 2021: fig. 2B); a well-developed postero-lateral process of the autopalatine (Fig. 3A; vs. rudimentary, Costa 2021: fig. 2B); and a slender and long maxilla, longer than premaxilla (Fig. 3A; vs. relatively deep, shorter than premaxilla, Costa 2021: fig. 2B).
Description. General morphology. Morphometric data appear in Table 3. Body relatively deep (Fig. 1A), greatest body depth at vertical through midway between pectoral and pelvic-fin bases. Trunk subcylindrical to compressed on caudal peduncle, dorsal and ventral lateral profiles weakly convex to almost straight. Whole body, except venter, covered with minute papillae. Small putative axillary gland above pectoral fin, below lateral line, with small orifice just posterior to opercular patch of odontodes (Fig. 2A). Lateral line of trunk consisting of anterior minute canal with two pores obliquely arranged, posterior followed by almost imperceptible line between humeral region and caudal-fin base with minute superficial neuromasts. Anterior-most pore of lateral line more ventrally positioned than posterior one. Urogenital opening consisting of transverse aperture situated in shallow depression. Anus positioned immediately in front of urogenital opening, at vertical just posterior to dorsal-fin origin.

Head sub-trapezoidal in dorsal view, dorsal surface flat (Fig. 1B). Eye small, positioned on dorsal head surface, nearer snout tip than posterior margin of opercle. Distance between anterior and posterior nostrils approximately

![Figure 1. *Trichomycterus (Paracambeva) antiquus* sp. nov., UFRJ 13674, holotype, 72.2 mm SL. A. Left lateral view; B. Dorsal view; C. Ventral view.](image-url)

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

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<th>Paratypes (n=3)</th>
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<td>Standard length (SL)</td>
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<table>
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<th>Percentage of head length</th>
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<td>Eye diameter</td>
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72.2 mm SL; p. 72

terus 1–2, lateral line pores 1–2; PO, preopercular patch of odontodes. UFRJ 13676, 97.6 mm SL. AO, supposed axillary organ; LL toral-fin length. Pelvic posteriorly overlapping anus and terminating in short filament, its length about 20% of pectoral-fin length. Pelvic posteriorly overlapping anus and bone, sub-incisiform in larger odontodes of larger specimens, about straight, irregularly arranged, 14 or 15 on opercle and 44 or 45 on interopercle. Cephalic latero-sensory system comprising long canal interconnecting supraorbital, posterior section of infraorbital, and postorbital canals, and isolated anterior infraorbital canal. Supraorbital sensory canal with three pores, s1, s3, and s6; anterior section of infraorbital canal with two pores, i1 and i3; posterior section of infraorbital canal with two pores, i10 and i11; and postorbital canal with two pores, pol and po2. All pores paired. Pore s6 about equidistant from orbit than its homologous pore. Fins thin with thick bases and convex free margins (Fig. 1A). Anal-fin origin at vertical, immediately posterior to middle of dorsal-fin base, at vertical through base of 4th bifid dorsal-fin ray. First pectoral-fin ray terminating in short filament, its length about 20% of pectoral-fin length. Pelvic posteriorly overlapping anus and bone. Posterior extremity of pelvic fin at vertical through area just anterior to middle of dorsal-fin base. Pelvic-fin bases medially separated by minute interspace. Caudal fin subtruncate. Total dorsal-fin rays 11 (ii + II + 7), total anal-fin rays 9 (ii + II + 5), total pectoral-fin rays 7 (I + 6), total pelvic-fin rays 5 (I + 4), total principal caudal-fin rays 13 (I + 11 + I), total caudal dorsal procurent rays 15 (xiv + I), total caudal ventral procurent rays 13 (xii + I).

**Osteology (Fig. 3).** Mesethmoid slender, T-shaped, anterior margin about straight, cornu narrow, longitudinal main axis gently laterally widening close anterior margin of lateral ethmoid. Lateral ethmoid without lateral projections. Lacrimal thin, not associated to infraorbital canal, separated from sesamoid supraorbital by long interspace. Sesamoid supraorbital short and slender, its length about twice lacrimal length, its width about equal lacrimal width. Premaxilla sub-trapezoidal in dorsal view, slightly tapering laterally. Maxilla slender, boomerang-shaped, slightly longer than premaxilla.


Parurohyal lateral process relatively short, with blunt extremity, slightly curved posteriorly. Parurohyal head well-developed, with pronounced anterolateral paired process. Middle parurohyal foramen large, longitudinally elongate. Posterior process of parurohyal long, its length about four fifths distance between anterior margin of parurohyal and anterior insertion of posterior process. Branchiostegal rays 8.

corresponding to hypurals 3 + 4 + 5; single ventral hypural plate corresponding to hypurals 1 + 2 + parhypural.

**Colouration in alcohol.** Flank pale yellow to yellowish white ventrally, with diffuse dark grey stripe along longitudinal midline, widening and breaking into small spots posteriorly. Great concentration of small dark grey spots on dorsal portion of flank, no or few similar spots on ventral portion. Dorsal surface of trunk and head pale brown, with small, faint grey spots, ventral surface white. Nasal and maxillary barbels pale brown, rictal barbel white. Fins hyaline, with whitish bases. In specimen UFRJ 13681, longitudinal stripe broader and darker, brown spots on dorsum, dorsal, and ventral portions of flank.

**Etymology.** From the Latin *antiquus* (old), referring to the relatively old estimated age of the species lineage in the Miocene (see below), when compared with the major species diversification of *Paracambeva* in the Pliocene.

**Distribution.** *Trichomycterus antiquus* is only known from the upper Rio do Peixe drainage, Rio Paraíba do Sul basin, south-eastern Brazil, at altitudes between about 765 and 980 m asl (Fig. 4).

**Positioning of Trichomycterus antiquus and time-calibrated analysis**

All phylogenetic analyses resulted in identical tree topologies (Fig. 5), in which *T. antiquus* is supported as sister to *T. itatiayae*, a species endemic to another region of the RPSB, with broad occurrence in streams draining the Maciço de Itatiaia, and the adjacent Serra da Bocaina (Fig. 4). The clade comprising *T. antiquus* and *T. itatiayae*, hereafter the *Trichomycterus itatiayae* group, is supported as sister to a clade comprising all other species of *Paracambeva* known as the *T. reinhardtii* species group (Costa 2021; Costa and Katz 2021). The independent analysis of individual gene trees indicated that all loci collaborated for this topology, since all gene trees corroborated monophyly of *Paracambeva* and both the RAG2 tree and the mitochondrial locus tree corroborated monophyly of the clade comprising *T. antiquus* and *T. itatiayae*, which is supported in both trees as sister to a clade comprising the remaining species of *Paracambeva* (Suppl. material 2). The age of the *Paracambeva* lineage was estimated at about 24.5 Ma, Late Oligocene (95% HPD age interval 15.68–36.01), whereas according to the analysis, the divergence between the *T. itatiayae* group and the *T. reinhardtii* group occurred at about 14.9 Ma, Middle Miocene (95% HPD age interval 7.16–24.84), and between *T. antiquus* and *T. itatiayae* at about 9.8 Ma, Late Miocene (95% HPD age interval 4.74–16.87).

**Temporal origin of similar colour patterns**

The presence of a broad black longitudinal stripe along the midline of the flank in juveniles, which often gradually becomes diffuse and fragmented into small spots in adults, combined with dark spots on the dorsum, occurs in most species of *Paracambeva* (Costa 2021; Costa and Katz 2021; Costa et al. 2023b), as well as in most species of the *T. nigroauratus* group of the subgenus *Trichomycterus* (e.g., Barbosa and Costa 2008; Costa et al. 2022). However, the specific colour pattern described here for *T. antiquus* and *T. maculosus* above about 70 mm SL, including a narrow stripe that posteriorly breaks into small spots, combined with the scarcity or absence of dark spots on the ventral part of the flank, occurs only in these two species and in *T. itatiayae* (Barbosa and Costa 2008: fig. 5). According to our analysis, this specific pattern would have first appeared in the ancestor of the clade comprising *T. antiquus* and *T. itatiayae*, around 14.9 Ma (95% HPD age interval 8.87–23.64), and a second time in the exclusive ancestor of *T. maculosus*, around 2.3 Ma (95% HPD age interval 0.85–4.56) (Fig. 5; Suppl. material 3).
Discussion

Temporal diversification and biogeographical context

According to a recent biogeographical analysis, the most recent common ancestor of *Paracambeva* lived in an area presently occupied by the upper Rio Paraná, upper Rio São Francisco, and Rio Paraíba do Sul basins (Vilardo et al. 2023). Presently, *Paracambeva* occupies a large region encompassing these three basins, with the *T. itatiayae* group occurring in a portion of the RPSB between the Rio do Peixe and the area close to the Serra da Bocaina and the *T. reinhardti* group occurring in a broad area of the upper Rio Paraná and upper Rio São Francisco basins (Fig. 4). Timing estimates support a Late Oligocene origin for the *Paracambeva* lineage and a Middle Miocene age for the split between the *T. itatiayae* and *T. reinhardti* groups (Fig. 5). Despite conclusive hypotheses about the time of origin of the present configuration of these basins that are not yet available, geological data point to a past connection between the upper section of the Rio Paraiba
do Sul, above the area close to the Serra da Bocaina, and the Rio Paraná basin (King 1956; Riccomini et al. 2010), and between the upper section of the latter basin and the upper section of the Rio São Francisco basin (Rezende et al. 2018). Therefore, the present distribution of Paracambeva and our estimates for the time of origin of this subgenus fit into this model of river basin evolution, with the rupture between the upper Paraíba do Sul and the Paraná-São Francisco basin that would have occurred in the Paleogene (Riccomini et al. 2010) corresponding to the divergence between the T. itatiayae and T. reinhardti groups, which preceded the rupture of the connection between the upper Rio Paraná and upper Rio São Francisco basins during the Middle Miocene (Rezende et al. 2018), corresponding to the wide distribution of the T. reinhardti group in these basins (Fig. 4; Costa and Katz 2021).

On the other hand, temporal estimates indicated the origin of the subgenus Trichomycterus lineage in the early Miocene. The biogeographical analysis performed by Vilardo et al. (2023) indicated that the MRCA of the subgenus Trichomycterus inhabited an ancestral area comprising only the Rio Paraíba do Sul, contrasting with its present distribution that includes both this basin and smaller coastal basins (Fig. 4; Costa 2021). However, geological data support a Cenozoic configuration of the RP SB different from the present one, in which its lower course corresponded to the present lower course of the Rio São João (Riccomini et al. 2010), which is now an isolated coastal basin. Thus, geological data are congruent with the hypothesised ancestral area of the subgenus in the Rio Paraiba do Sul alone, which in the past did not include the present upper course but included a present coastal basin in its lower course. The upper course of the RP SB probably was blocked for dispersion of trichomycterine catfishes that live in fast flowing streams by the great depression in its main channel responsible for the formation of the paleolake Tremembé during the Oligocene (Riccomini et al. 2004). Thus, it is possible that these two subgenera lineages, Paracambeva and Trichomycterus, were not in contact in the upper Rio Paraiba do Sul before the Middle Miocene. The origin of the specific colour pattern shared by the syntopic T. antiquus and T. maculosus is estimated to have occurred first in the T. itatiayae group during the Middle Miocene and much later in T. maculosus during the Late Pliocene in T. maculosus, which is compatible with the hypothesis of a more recent occupation of the upper RP SB by the subgenus Trichomycterus.

Interestingly, the other case involving similarly coloured syntopic species of trichomycterines from eastern South America involves T. itatiayae, the sister group of T. antiquus, and T. nigroauratus, the sister group of T. maculosus (Fig. 5). These two species are endemic to streams of the RP SB draining the Serra da Mantiqueira and the adjacent Serra da Bocaina (Barbosa and Costa 2008) and are commonly found associated with bottom leaf litter (Costa 2021). Juvenile specimens of these species share a colour pattern consisting of a broad black longitudinal stripe along the flank midline, whereas larger specimens assume a different colour pattern (Barbosa and Costa 2008). A broad black longitudinal stripe is present in all other species of Paracambeva (Costa and Katz 2021; Costa et al. 2023b), therefore already present in the
MRCA of this subgenus, whereas this colour pattern is present in part of the species of the *T. nigroauratus* group among species of the subgenus *Trichomycterus* (Costa et al. 2022), thus arising after the initial diversification of this group. Considering the estimated age of *Paracambeva* in the Late Oligocene and the initial diversification of the *T. nigroauratus* group in the Late Pliocene, over 20 million years later, the most plausible hypothesis is that the colour pattern in the *T. nigroauratus* group had arisen after this group was in contact with species of *Paracambeva* in RPSB.

Possible explanations for the occurrence of syntopic trichomycterines with similar colour patterns

The sympatric occurrence of distantly related species of Neotropical catfishes exhibiting similar derived colour patterns has been often aprioristically considered as primary evidence of mimetic association (Axenrot and Kullander 2003; Alexandrou et al. 2011; Slobodian and Bockmann 2013), but may also be a result of evolutionary convergence for adaptation to live in special habitats like those occurring among sympatric psammophilic species (Zuanon et al. 2006; Costa et al. 2020c). Therefore, the occurrence of two species of *Trichomycterus* in the same habitat sharing the same colour pattern (Figs 1A, 6) but belonging to two distantly related subgenera could suggest a case of mimic association or convergence for adaptation to live in a gravel bottom where both species were found, since their colour pattern is cryptic in this habitat. However, direct evidence to explain syntopic trichomycterines with similar colour patterns is not available for any of these hypotheses.

In the case of evolutionary convergence for adaptation to live in special habitats, a possible explanation is that the colour pattern gives these two species some cryptic advantage in their habitat against predators since the colours are similar to the gravel substrate where they live. In the case of mimic associations, including both Batesian and Müllerian mimicry, the model species (Batesian) or both species (Müllerian) have effective anti-predation features, which among catfishes usually comprise venom glands associated with fin spines (Wright 2009; Harris and Jenner 2019). For example, in mimetic associations involving siluroids with a well-developed pectoral-fin spine, the main anti-predation morpho-physiological attribute is the presence of an axillary venom gland associated with a pungent pectoral-fin spine (e.g., Greven et al. 2006; Wright 2011; Carvalho et al. 2021). The defence mechanism involves not only glands and the pectoral-fin spine but also special muscles and connective tissue (Wright 2015; Harris and Jenner 2019). However, mechanisms for anti-predation in trichomycterines are still unknown, and potential trichomycterine predators living in the Rio do Peixe drainage have not been presently recorded, although the Neotropical otter *Lutra longicaudis* (Ollers, 1818) and the catfish *Steindachneridion parahybae* (Steindachner, 1877) today rare or absent in the region, were until recently potential predators.

Although anti-predation features consisting of venom glands associated with fin spines occur in most catfish lineages (Wright 2009, 2015), they are unknown among trichomycterids. Unlike other catfishes, trichomycterids do not have pectoral and dorsal spines.

In a survey on the presence of venom axillary glands in catfish lineages, Wright (2009) did not detect them in *Trichomycterus* areolatus Valenciennes, 1846, concluding that these glands are not present in trichomycterids. However, a supposed axillary gland (e.g., Eigenmann 1918) or suprapectoral adipose organ according to Myers and Weitzman (1966) and axillary organ according to de Pinna (1989), situated at the same place as the venom axillary glands of other catfishes and having a similar orifice, have been superficially described for candiru and other trichomycterids (e.g., Eigenmann 1918). This supposed axillary gland, comprising a sack-like protuberance above the pectoral fin and just below the anterior pores of the lateral line of the flank, is also present in trichomycterines (Fig. 2), which is proportionally smaller than in other trichomycterids (e.g., sarcoglanidines, Myers and Weitzman 1966), with an orifice that is more conspicuous in juvenile specimens below about 40 mm SL, often having a great concentration of melanophores around its margin. Both *T. antiquus* and *T. maculosus* have a small axillary gland-like protuberance below the short lateral line canal and above the pectoral fin (Fig. 2). The absence of a pectoral spine in trichomycterids also imposes a limitation on the possibility of the axillary organ acting as a venom gland. Nonetheless, the stinging action of the opercular odontodes, which are located close to the ax-

Figure 6. *Trichomycterus (Trichomycterus) maculosus*, UFRJ 13676, 97.6 mm SL, left lateral view.
illary gland-like protuberance (Fig. 2) and may become bristly when the fish is molested, could be performed as the pectoral spine of other catfishes. However, a more detailed morphological study at the histological and biochemical level is necessary to investigate the presence of glandular tissue and toxic substances in T. antiquus and close relatives, which is not presently possible with the small sample of specimens currently available. Future studies are necessary to check what hypothesis best explains the unexpected syntopic occurrence of similarly coloured T. antiquus and T. maculosus.

Acknowledgements

Thanks are due to Léia C. Medeiros, Gustavo L. Canella, and Ronaldos dos Santos-Junior for field assistance. We are also grateful for the comments and criticisms provided by F. Langeani, H.H. Ng, F. Ottoni, and an anonymous reviewer, who contributed to improving the present version of the manuscript. The Instituto Chico Mendes de Conservação da Biodiversidade provided collecting permits. This work was partially supported by the 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-26/210.213/2021 to WJEMC, E-26/202.005/2020 to AMK, and E-26/203.524/2023 to JLM). This study was also supported by CAPES (Finance Code 001) through the Programa de Pós-Graduação em Biodiversidade e Biologia Evolutiva/UF RJ and the Programa de Pós-Graduação em Genética/UF RJ.

References


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Supplementary material 1

List of comparative material of the subgenus Paracambeva

Authors: Wilson J. E. M. Costa, Caio R. M. Feltrin, José Leonardo O. Mattos, Axel M. Katz
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Link: https://doi.org/10.3897/zse.100.118000.suppl1

Supplementary material 2

The independent analysis of individual gene trees

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Supplementary material 3

Beast divergence-time estimation

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