

Submission date. 22/10/2025

Associate editor's decision after peer review (27/03/2026).

Dear Dr. dos Reis:

Manuscript ID NI-2025-0183 entitled "Revealing hidden diversity through iterative approaches: eight new species of *Cambeva* (Siluriformes: Trichomycteridae) from the highly endemic Rio Iguaçu basin" which you submitted to the Neotropical Ichthyology, has been reviewed. The comments of the reviewer(s) are included at the bottom of this letter.

The reviewer(s) have recommended publication, but also suggest some minor revisions to your manuscript. Therefore, I invite you to respond to the reviewer(s)' comments and revise your manuscript.

To revise your manuscript, log into <https://mc04.manuscriptcentral.com/ni-scielo> and enter your Author Center, where you will find your manuscript title listed under "Manuscripts with Decisions." Under "Actions," click on "Create a Revision." Your manuscript number has been appended to denote a revision.

You may also click the below link to start the revision process (or continue the process if you have already started your revision) for your manuscript. If you use the below link you will not be required to login to ScholarOne Manuscripts.

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You will be unable to make your revisions on the originally submitted version of the manuscript. Instead, revise your manuscript using a word processing program and save it on your computer. Please also highlight the changes to your manuscript within the document by using the track changes mode in MS Word or by using bold or colored text.

Once the revised manuscript is prepared, you can upload it and submit it through your Author Center.

When submitting your revised manuscript, you will be able to respond to the comments made by the reviewer(s) in the space provided. You can use this space to document any changes you make to the original manuscript. In order to expedite the processing of the revised manuscript, please be as specific as possible in your response to the reviewer(s). **IMPORTANT:** Your original files are available to you when you upload your revised manuscript. Please delete any redundant files before completing the submission.

Because we are trying to facilitate timely publication of manuscripts submitted to the Neotropical Ichthyology, your revised manuscript should be submitted before 27-Apr-2026. If it is not possible for you to submit your revision by this date, we may have to consider your paper as a new submission.

Once again, thank you for submitting your manuscript to the Neotropical Ichthyology and I look forward to receiving your revision.

Sincerely,

Dr. Carlos DoNascimento

Associate Editor, Neotropical Ichthyology

repuglanis@hotmail.com

Anonymous reviewer #1**Recommendation.** Minor Revision

Comments. The manuscript entitled "Revealing hidden diversity through iterative approaches: eight new species of *Cambeva* (Siluriformes: Trichomycteridae) from the highly endemic Rio Iguaçu basin" presents the description of eight new species of the genus *Cambeva*. Overall, the work is well-written, with clear and concise descriptions, contributing significantly to the taxonomy of the group. The English is well-written and suitable for publication.

The diagnoses are presented clearly and objectively, with well-defined diagnostic characters that facilitate the distinction of the new species from their congeners. I would also like to highlight the quality of the illustrations and photographs of the specimens and localities, which are excellent and represent a valuable visual resource for the work. The phylogenetic approach follows the standards of the specialized literature, and the hypothesis is well-founded. The discussion is well-structured, but I feel it could be enriched with greater articulation with the existing literature on species delimitation for Trichomycteridae, deepening the contextualization of the results. The text requires careful revision of the layout in order to adapt some structural elements to the journal's standards. I am attaching a version of the manuscript with specific comments on these and other aspects that deserve attention.

In light of the above, I recommend publication of the manuscript after minor revisions, provided that the suggested adjustments are made, especially in the layout and in improving the discussion based on relevant literature.

Anonymous reviewer #2**Recommendation.** Minor Revision

Comments. The comments below are also provided as an attached file.

The manuscript represents a valuable and interesting contribution to the systematics and biogeography of *Cambeva*.

The sections addressing the morphological description (including osteology) of the eight new species, as well as the Discussion section, are well written and do not appear to require major revisions. Only minor commentaries: The diagnoses throughout the manuscript could perhaps be presented in a more concise manner (e.g., "(vs. stripe absent, or when present, narrow, continuous, and well defined)").

The authors might also consider including a brief diagnosis for the genus *Cambeva* or for some of the clades recognized in the study. Although I acknowledge the difficulties in diagnosing some genera within Trichomycterinae, proposing potentially informative morphological characters could be useful, especially given that the precise phylogenetic placement of these eight species remains unresolved; such characters may also prove valuable for other genera within the subfamily Trichomycterinae.

The manuscript also raises relevant questions regarding the phylogenetic status and delimitation of molecular species of *Cambeva* from Rio Iguaçu drainage, particularly in relation to the possible synonymy of *C. papilliferus* and *C. ventropapillata*, and the discussion of the presence of *C. zonata*.

The illustrations (Figs. 1–22) and tables (1–10) are well presented and add value to the manuscript. I am not a native English speaker, so I prefer do not comment on potential grammatical issues.

Below are some specific points that should be addressed

P4 L15 Remove "W. J. E. M."

P5 L12 Please check "99% ethanol".

P5 L57 Verify the reference "dos Reis et al. 2025 in press".

P8 L10 Remove "&".

- P9 L29 The diagnosis might be simplified, for example “(vs. stripe absent, or when present, narrow, continuous, and well defined)” instead of “(vs. absence of longitudinal stripe in the mid-lateral surface of body or when present, formed by a narrow, continuous, and well-defined dark-brown longitudinal mid-lateral stripe in *C. naipi*”.
- P9 L35 Remove “e”.
- P11 L20 Please check “II+7*” by “II,7*”.
- P12 L45 Check using lowercase: “hypobranchial 2” and “hypobranchial 3”.
- P13 L55 Please change “Smaller specimens” to “Small specimens”.
- P16 L8–9 Is a short filament different from a rudimentary filament? Consider also adding Fig. 22.
- P16 L15 Consider “pelvic-fin rays (I,4 vs. I,3)” by “number of branched pelvic-fin rays (4 vs. 3)”.
- P16 L18 Perhaps “fold” instead of “skin crest”?
- P16 L22 Consider simplifying to “pelvic fin and girdle”.
- P16 L37 Perhaps “number of branched pectoral-fin rays (5 vs. 4)”.
- P18 L60 Lowercase “hypobranchial 2” and “hypobranchial 3”.
- P18 L9–10 Sentence “Vomer arrow-shaped with long posterior process extending to parasphenoid” appears twice.
- P18 L18–19 Please clarify whether teeth are conical, spatulate or both, for example outer row spatulate, inner row conical.
- P21 L41 Change “Cambeva tessellate” by “*C. tessellate*”.
- P21 L47 Change “*C. erivelti*” by “*Cambeva erivelti*”.
- P21 L56 Change to “pelvic fin and girdle”.
- P23 L43–44 Twice “Vomer arrow-shaped ...”.
- P24 L35 Lowercase “hypobranchial 2” and “hypobranchial 3”.
- P27 L41 Please replace “HL”.
- P28 L57 Check “pelvic-fin” instead of “pelvic fins”.
- P29 L27–28 Repeated text “Vomer arrow-shaped ...”.
- P29 L35 Please clarify tooth morphology (e.g., outer row spatulate, inner row conical).
- P30 L20 Change “H” by “h”.
- P31 L26 Remove “,,”.
- P34 L59–60 Repeated text “Vomer arrow-shaped ...”.
- P35 L53 Change “hypobranchial 2” and “hypobranchial 3”.
- P36 L54 Change “smallers” by “smaller rounded blotches”.
- P40 L27–28 Repeated text.
- P41 L18 Change “H” by “h”.
- P44 L38 Change “darkbrown” by “dark-brown”.
- P46 L31–32 Repeated text.
- P48 L35 Change “smallers specimens” by “smaller specimens”.
- P50 L7 Change “collor pattern” by “color pattern”.
- P51 L56 Check “... through anal fin aperture” or “through anal-fin base”.
- P52 L20–21 Repeated text.
- P52 L28–31 Please revise “... conical to spatulate teeth”; consider specifying rows (outer spatulate, inner conical).
- P53 L15 Change “H” by “h”.
- P54 L18 Change “Smaller” by “Smaller specimens”.
- P57 L7 Consider adding “... and short maxillary and rectal barbels”.
- P57 L17 Consider “... pectoral-fin rays, 5 branched” or “5 branched pectoral-fin rays”.
- P57 L26 Perhaps “Presence of I,6 or I,7 pectoral-fin rays” to “Pectoral fin rays, 5 or 6 branched” or “5 or 6 branched pectoral-fin rays” or “Pectoral fin rays I,6–7”.
- P59 L24 Authors might consider including a brief diagnosis of *Cambeva* based on morphological characters. I understand the inherent difficulties, so this is offered a suggestion only.

P61 L3 Change “hostpot” by “hotspot”.
 P107 L15 Check “length” (in all Tables 1–8).
 P107 L26 Check “anal” (in all Tables 1–8).
 P107 L33 Change “length” (in all Tables 1–8).

Anonymous reviewer #3

Recommendation. Minor Revision

Comments. The manuscript “Revealing hidden diversity through iterative approaches: eight new species of *Cambeva* (Siluriformes: Trichomycteridae) from the highly endemic Rio Iguaçu basin” represents a highly informative taxonomic contribution, elucidating the diversity of *Cambeva* within a major Neotropical basin and highlighting the challenges of diagnosing recently diverged species using mitochondrial genes. The iterative approach, using morphological and molecular data, not only resolves taxonomic uncertainties regarding the diversity of *Cambeva* in the lower Rio Iguaçu but also provides a valuable example for addressing recently diverged groups. Moreover, the study contributes to a better understanding of the biogeography of this complex genus, thereby significantly advancing knowledge of its evolutionary history.

Despite the overall quality and relevance of this work, several points throughout the manuscript require revision before it is suitable for publication. Below, I outline the main issues that should be addressed, in addition to minor comments provided in the annotated PDF.

In the Introduction, the diversity of *Cambeva* species could be presented in a clearer and more structured manner. Given that the focus of the study is the description of eight new species from the lower Rio Iguaçu, it would be helpful to explicitly organize the known diversity across the upper, middle, and lower sections of the basin.

Regarding the molecular analyses, it is unclear why the same species delimitation methods were not applied to the CytB dataset. Also, considering that Trichomycterinae often exhibit high and complex evolutionary rates compared to most fishes, the use of a fixed threshold approach should be carefully justified. It is important to clarify whether this strategy is appropriate under such conditions.

The color pattern used as a diagnostic character for *C. kaingang* should be re-evaluated, as it appears to be inconsistent among specimens.

In the identification key, some steps rely on a single diagnostic character. These should be reinforced by adding additional characters, which would improve the robustness and usability of the key.

In the Discussion, there is an incomplete paragraph on page 61 (line 34) that needs to be corrected. Furthermore, this section could benefit from a more in-depth discussion of the points raised. As an example, the final subsection of the Discussion, “Insights about *Cambeva* species delimitation and future perspectives,” contains valuable information. However, its first two paragraphs seem more closely related to the preceding subsections. The organization of this section could be improved to enhance clarity and coherence. Alternatively, its content could be redistributed into the previous subsections, strengthening them and avoiding redundancy.

Finally, the appendices require substantial improvement. The tables are currently unformatted and lack clear identification. It is not possible to distinguish which sequences were generated in this study and which were obtained from GenBank. This information should be clearly indicated.

Author’s Rebuttal Letter (28/05/2026).

Dear Editor and Reviewers,

We are resubmitting the revised version of our manuscript NI-2025-0183. We appreciate your efforts in improving our manuscript. Furthermore, we have accepted all the suggestions and tried to be as specific as possible in our responses, which are detailed below.

If you need more information, we are available to provide any clarification.

Sincerely,

Renan B. dos Reis and Co-authors.

General comments:

We added the unique haplotype in a Suppl. Table itself, to avoid problems with table formatting, changing the suppl. table numbers. Note that *C. ventropapillata* and *C. papillifera* share one haplotype, and we added it in the discussion, providing more robust evidence for the possible synonymy between the species. Despite this, we didn't have access to specimen vouchers of *C. ventropapillata*, therefore, we didn't request a synonymization of the species.

Reviewer #1

1- Given the scope of this study, I suggest segregating the described species from the Rio Iguaçu basin into lower, middle, and upper sections. This approach will facilitate a clearer understanding of the genus diversity within the basin and highlight the taxonomic significance of the work.

Answer: Thank you for your suggestion. We rewrote the sentence to match the distribution of species described.

2- The way you wrote this paragraph makes me think that there is no *Cambeva* species in the lower section of the Iguaçu river. Let the current *Cambeva* diversity of the lower section of this river explicitly here.

Answer: Thank you for your suggestion. We rewrote the entire sentence to be specific about the distribution of the species.

3- I was unable to locate it; the table is quite disorganized in the PDF file.

Answer: Thank you for your observations. We apologize for the table being formatted incorrectly. It's an XLS file, which makes downloading it easy to access the numbers after publication. We've tried to fix it in this version of the revision.

4- Why not perform a Bayesian analysis, as was done for COI? Neighbor-Joining is a distance-based approach and does not adequately reflect evolutionary relationships.

5- Why not also CytB?

5.1- Why were the same species delimitation tests not applied to this gene?

5.2- Why did you not present the s and mGMYC using CytB?

Answer: We had some problems in species delimitation utilizing CytB. We agree that it is correct to use the same analyses for different genes, so we redid the analyses. However, sGMYC and mGMYC tends to group several species from different *Cambeva* groups, even after testing different outgroups and quantities of species, and different priors in the Bayesian analysis. This is probably due to the fact that there are not many CytB sequences, but we chose to demonstrate it in the same way.

6- Explicitly state that both sGMYC and mGMYC were applied, and briefly justify the rationale for using both approaches.

Answer: Thank you for the suggestion. We added in the text to explicitly indicate that we did both methods.

7- Additionally, the evolutionary rate in *Trichomycterinae* is relatively high and more complex than in most fishes. In this context, do you consider it appropriate to deliberately adopt a fixed threshold? I did a discussion about it in Reis & de Pinna (2022) *Trichos* from Rio Doce, maybe it may help you.

Answer: Thank you for your suggestion. We agree that a fixed distance threshold could lead to misinterpretation of our results. We did the same analysis for CytB when comparing to the COX1, using the species delimitation methods adopted.

8- Comparing your illustrations, *C. kaingang* is also close to *C. longistriata*, no?

Answer: Thank you for the valuable suggestion. Although these species are closely related in the gene tree, the shape of the longitudinal stripe differs between them. In my interpretation (R.B. dos Reis), *Cambeva kaingang* presents a stripe formed by coalescent rounded spots, whereas *C. longistriata* exhibits a continuous band, similar to the pattern observed in *Cambeva perkosi*, *C. piraquara*, species of the *Trichomycterus reinhardtii*

group, and *T. illuvies*. Based on these differences, we chose to maintain this character in the species diagnosis.

9- It is not present in all specimens of *C. kaingang*, as shown in the species illustration. Therefore, I suggest revising this diagnostic character.

Answer: Thank you for the valuable suggestion. Although smaller specimens show interruptions in the longitudinal stripe and are not entirely similar to larger individuals, they still exhibit a midlateral row formed by a sequence of rounded blotches of the size of the opercular patch of *Odontobutis*. Based on this observation, we have incorporated this character into the diagnosis.

“or in smaller specimens (< 40.0 mm SL), with midlateral row of dark-brown rounded blotches, with same size as opercular *odontobutid* patch, sometimes coalescing forming small interrupted stripes (Fig. 1B)”.

10- I understand your intention. However, as currently written, this character for *C. kaingang* overlaps with that of species exhibiting a continuous stripe

Answer: Thank you for your suggestion and observation. Please consider answer 8 for this question.

11- You previously stated that *C. balios* and *C. botuvera* share the same color pattern; however, you now indicate that they differ. This renders the diagnosis confusing.

Answer: Thank you for your suggestion and observation. We rewrote the text to fix possible ambiguous sentences. We would like to emphasize that our focus is on the overall distribution pattern of the blotches along the lateral surface of the body, rather than on the shape of the midlateral blotches or stripes themselves. For this reason, we chose to retain this character in the diagnosis.

12- Why did you not include the number of specimens examined next to the other pores?

Answer: Thank you for the suggestion. Usually, the variation in the pore presence/absence of some is lower than the counts of the lateral line pores. Probably, it has created a vicious cycle in species description. We re-wrote and added the counts of specimens in all pores.

13- If these highlighted lots are all from the same location and belong to the same collection/institution, why are the specimens divided into three lots?

Answer: Thank you for your observations. We did it because one lot is for morphology (the origin that was dismembered for donation to MZUSP), one is of c&s specimens (that needed to be dismembered in NUP collection), and one is for molecular study. The same occurs for all other species descriptions.

14- small compared with what? please say it.

Answer: Thank you for your observation. We rewrote the text and added the proportion of the filament's size.

15- *C. kaingang*, in some specimens as illustrated, has a long wide longitudinal stripe.

Answer: Thank you for your observation. Please consider answer 8 for this question.

16- 226 sequences from whom? Only the ingroup (new species), or from all *Cambevas*, or *Cambevas* and the outgroup?

Answer: Thank you for your suggestion.

It's for all specimens utilized in the analysis. We rewrote the text.

17- Highlight this section in some way, as it appears to belong to the description of *C. ytepapo*.

Answer: Thank you for your suggestions. Unfortunately, NI's author guidelines don't allow subtitles with other formatting.

18- Interesting to use iterative instead of integrative!!

Answer: Thank you very much. Still a lot of debate to standardize this concept, and some of the reviewers suggested another use of words. However, we maintained our criterion of using an iterative approach, in accordance with other studies.

19- Your results are not saying that. S and M GMYC do not segregate both species.

Answer: Thank you for your observation. Indeed, we rewrote the sentence.

20- Same situation with COI

Answer: Thank you. We rewrote the sentence.

21- Add additional diagnostic characters to the steps that currently include only one character, as this will strengthen the key. To assist readers, include the corresponding figure number next to each species.

Answer: Thank you for your suggestion. We rewrote the key to match your suggestions.

22- You could explore this topic further by discussing why some mitochondrial genes exhibit in some species low divergence. Additionally, address the occurrence of crypticism in Trichomycterinae species, particularly within *Cambeva*.

Answer: Thank you for your suggestion. We added some examples of crypticism in trichomycterids and there are some other example within *Cambeva* in the topic Insights about *Cambeva* species delimitation and future perspective.

23- ??? Incomplete paragraph

Answer: We deleted the sentence. We apologize for the incomplete text.

24- If this is well documented in *Cambeva*, where are the references?

Answer: Thank you for the suggestion. We added reference documenting all the low genetic distance between some species of *Cambeva* and other trichomycterids.

25- This first paragraph is more related to the first topic : Iterative methodologies.

Answer: Thank you for your suggestion. The paragraphs are indeed related to the previous topic; however, to preserve the flow and coherence of the ideas presented in this section, we chose to keep them as they are.

26- These are morphological characters, so you may say "such as osteological features like the..."

Answer: Thank you for your suggestion. We rewrote the text.

27- Is this paragraph more related to the Biogeographic topic?

Answer: Thank you for your suggestion. Please, consider answer n° 25.

28- A similar pattern occurs in *Trichomycterus*. *T. alternatus*, *T. astromycterus*, and *T. vinnulus* are morphologically distinct, yet appear as a single entity based on COI data in Reis & de Pinna 2022 *Trichomycterus* study. Conversely, the opposite pattern is also observed: species that are morphologically very similar (cryptic), such as *T. melanopygius* and *T. immaculatus*, are clearly distinct at the molecular level, as shown in Reis et al. 2020.

Answer: Thank you for your observation and suggestion. We added these examples in the text and the reference.

29- from the... cause you are talkig about origin.

Answer: Thank you for your correction. We rewrote all the basins of origin for the specimens.

30- So why did u mentioned them here in the figure caption? I suggest to remove the abbreviations not used in the figure.

Answer: Thank you for your suggestion. We rewrote the figure captions and added a legend to the figures of i1 and i3, and edited the figure.

31- Why cf? have you not analyzed this voucher?

Answer: Thank you for your observation. The specimen was examined; however, it lacked clear diagnostic features. Only two small individuals were available, with molecular data generated by other authors and originating from a distant locality. The use of the name cf. *longistriata* could therefore lead to ambiguity. For this reason, in the revised version we retained the previous identification but adopted the designation aff. (*Cambeva* aff. *davisi*), as the specimens exhibit spots distributed across the body.

32- You did not have the CYTb of *C. aff. davisi* neither the *C. cf. longistriata* from the bayesian tree? was there some problem with the amplification?

Answer: Thank you for your observation. Unfortunately the specimens were not amplified in our analysis.

33- To make it easier to read, enumerate the species column.

Answer: Thank you for the suggestion. We rewrite the table to make it easier to read.

34- What is this? Table without identification, format and legend. Which sequences are from this study, and which ones are from the GenBank?

Answer: Thank you for the observation. We write the captions of the suppl. tab. 1, and added an asterisk in the sequences generated in this study.

35- Costa-Silva et al. 2015 (*Rineloricaria*); Reis et al. (2020), and Reis & de Pinna, 2022 (*Trichomycterus*) have argued the same point and are worth citing.

Answer: Thank you for your suggestion. Indeed, they are very good references. We added in the text.

Reviewer #2

1- padronizar

Answer: Padronizamos o texto.

2- Sugiro começar uma outra frase.

Iniciando com o número total de espécies alocadas ao gênero, originalmente, por Katz et al. (2018).

E então demonstrar a quantidade de espécies descritas desde a descrição do gênero. E então, indicar que mais metade ou pouco menos da metade (por um valor de porcentagem) das espécies foram descritas num período de sete anos.

Answer: Obrigado pela sugestão. Indicamos a quantidade de espécies realocadas por Katz et al. (2018).

3- suggestion: integration of multiple lines of evidence

Answer: Obrigado pela sugestão. Adicionamos a frase no texto, porém mantivemos a linha de abordagens iterativas em todo o texto. Sabemos da discussão em relação ao termo, porém optamos por manter dessa forma, em vista que toda discussão e título utilizam essa terminologia.

4- Suggestion: american zoologist John Diederich Haseman in the first decade of the XX century that.

Answer: Obrigado pela sugestão. Adicionamos no texto,

5- Consigo compreender isto. No entanto está um pouco confuso devido as palavras indicativas das posições das localidades dos rios estão próximas e repetitivas. O que facilmente pode fazer um leitor se confundir ao longo da leitura do manuscrito. Faço uma sugestão abaixo para facilitar a fluidez da frase. Sugestão: taxonomic efforts have been predominantly concentrated in the upper and middle sections of the Rio Iguaçu. In contrast, the lower Iguaçu tributaries, including Rio Jordão and the adjacent basins, have received comparatively less attention and have not yet been systematically explored with regard to alpha taxonomy of the genus.

Answer: Obrigado pela sugestão. Modificamos o texto.

6- Os resultados vão além da descrição das espécies, mas a proposição das suas posições filogenéticas, delimitação molecular e dos status de conservação das espécies.

Recomendo incorporar esses outros resultados.

Answer: Obrigado pela sugestão. Adicionamos no texto.

7- Diversos pesquisadores são críticos a essa expressão. Tentando maximizar a leitura e críticas ao manuscrito, recomendo a utilização de 'multiple lines of evidence'.

Para mais informações sobre essa expressão que estou propondo, sugiro dos artigos:

The barcode trap—Description of a new species of *Microglanis*, with a review of the status of *Microglanis cibellae* (Siluriformes: Pseudopimelodidae) – Alborno et al. (2024) & Hidden or unnoticed? Multiple lines of evidence support the recognition of a new species of *Pseudocorynopoma* (Characidae: Corynopomini) – Malabarba et al. (2020)

Answer: Obrigado pela sugestão. Adicionamos no texto, porém também mantivemos o termo “iterative”. Sabemos da crescente discussão em relação ao termo, porém como toda a ideia e o título do trabalho são voltados ao termo iterative, decidimos por manter.

8-Institutional abbreviations follow Sabaj (2022).

Recomendo translocar essa frase para essa seção do texto.

Uma vez que vocês descrevem as instituições aqui, enquanto a referência para a padronização dos nomes das instituições está mais abaixo.

Answer: Obrigado pela sugestão. Modificamos o texto.

9- Particularmente tendo a não traduzir nomes de instituições brasileiras. Assim como vocês não traduziram nomes das instituições brasileiras, recomendo manter o mesmo padrão..

Answer: Modificamos o texto. Obrigado.

10- Agora que o manuscrito foi publicado, colocar a citação correta do artigo adicionar virgula após o et al.

Answer: Obrigado pela observação. Modificamos o texto.

11- a informação do número de acesso do genbank já consta na tabela

Answer: Obrigado pela sugestão. Optamos por manter aqui também para facilitar para o leitor. Não adicionamos as novas sequências por ter muitas e não estarem em ordem.

12- De qual gene? Adicionar qual foi. Se foi para os dois genes COXI e CYTB, recomendo a tabela gerada seja incorporada no manuscrito, com as diagonais correspondendo a cada um dos genes. Pode ser tanto a tabela numérica, quanto um heatmap para uma visualização mais dinâmica dos resultados.

Answer: Obrigado pela observação. Foi dos dois genes, porém como há vários espécimes, optamos por manter apenas as espécies da bacia do rio iguaçu no texto. Nas tabelas suplementares temos todos os espécimes analisados.

13- Primeira menção da espécie. Adicionar descritores e ano.

Answer: Revisamos todas as espécies e descrições e modificamos o texto.

14- Padronizar ao longo do manuscrito a forma que revista solicita ao mencionar uma espécie nova, que vocês estão descrevendo neste manuscrito. Lendo rapidamente, percebi que não há uma padronização, ora está desta forma, ora não.

Answer: Obrigado pela sugestão. Revisamos e modificamos o texto, retirando o new species quando inserido na diagnose, padronizando da maneira como a revista pede.

15- Padronizar ao longo do texto. Na introdução e em outra parte do texto, é utilizado o termo traduzido. Aqui, o termo traduzido é seguido em parenteses do nome em português. Como mencionei anteriormente, tendo a não traduzir nomes das instituições. Nesse caso, fica ao critério dos autores. Mas, que seja padronizado ao longo do texto.

Answer: Obrigado pela observação. Padronizamos o texto mantendo o nome traduzido, porém citando na primeira vez o nome em português.

16- Aqui eu faria uma breve discussão e um apanhado geral das descrições de espécies descritas de Trichomycteridae que também utilizaram essa evidência para propor táxons novos. Por exemplo, Reis & de Pinna 2019 na descrição de diversas espécies de Trichomycterus também observaram valores baixos de divergência. Medeiros et al. 2024 e Villa-Verde et al. 2013, também observaram baixos valores de distância genética para o gênero Listrura. Além de outros trabalhos conduzido pelo grupo de pesquisa aqui.

A ideia se matém a mesma, não existe um número mágico que defina e delimite os táxons, mas deixar claro que embora os valores apresentados das divergências genéticas serem baixos, utilizar outras abordagens como a morfologia e testes de delimitação de espécies, quando em conjunto demonstram não só a proposição de uma linhagem distinta. Mas também que, potencialmente, estamos lidando com eventos recentes de especiação.

Novamente, recomendo a leitura do manuscrito anteriormente mencionando de Albornoz et al. 2024 sobre o "barcode trap", onde uma belíssima discussão sobre essa temática é abordada. E Nesta seção, faria uma discussão mais robusta mostrando os valores abaixo dos valores limites (threshold 2%), tanto para as espécies novas aqui descritas, quanto das espécies já descritas. para pumbla e igobi também é 0.2%, adicionar esses valores também. Pois corrobora com seus achados das espécies novas e das espécies já descritas

Answer: Obrigado pela sugestão. Realmente discutir esses valores e o potencial que existe na utilização dos delimitadores moleculares na delimitação de trichomycterids é bem interessante. Dessa forma, adicionamos alguns trabalhos sugeridos por você e por

outro revisor. Em relação as espécies que possuem baixa distancia genética, inserimos o exemplo das espécies do grupo *C. stawianski* (*C. igobi*, *C. cauim*, *C. melanoptera*, *C. plumbea*, essas duas potencialmente fazendo parte do grupo.). Porém, para não ficar redundante com a seção da discussão: Insights about *Cambeva* species delimitation and future perspective; não colocamos todo o texto nessa parte, e sim no final. Decidimos por manter assim, em vista de que nossos resultados são mais voltados para as espécies novas, e ficando para essa outra seção às espécies já descritas são citadas nessa seção, posteriormente.

Para manter uma sequência lógica, modificamos a ordem dos subtópicos na discussão, deixando a parte de biogeografia no final do texto.

Associate editor's decision after peer review (06/06/2026).

Dear Dr. dos Reis:

It is a pleasure to accept your manuscript entitled "Revealing hidden diversity through iterative approaches: eight new species of *Cambeva* (Siluriformes: Trichomycteridae) from the highly endemic Rio Iguaçu basin" in its current form for publication in the Neotropical Ichthyology.

Congratulations for the acceptance of your article, and be aware on the following topics:

1. Publication Fee

NI will charge a publication fee if none of the co-authors is an active SBI member. This measure is essential to strengthen SBI and thus ensure the continuity of our journal, scientific society, and biannual meetings. SBI is not limited to Brazilians but is open to anyone interested in freshwater and marine Neotropical fishes. More details on SBI are available at <https://www.sbi.bio.br/>. Please email tesouraria.sbi@gmail.com to confirm whether any of your co-authors is a current SBI member and to activate your SBI membership if needed. Otherwise, if you will cover the publication fee of R\$1.000, please inform us at the same email. For authors outside Brazil, the fee will be converted to US dollars based on the official exchange rate on the date of payment. The only exceptions to this fee are invited articles.

2. Science Communication and Social Media

NI actively promotes published articles to both academic colleagues and the general public, including science journalists. To support this, we create social media posts and require images and/or videos of fish related to your work. If your article does not include such images, please send a photo of a representative fish species, preferably alive in its natural habitat. If you do not have your own photo, you may provide a link to an online image, along with the source, author, and, if applicable, authorization for its use. We also publish video summaries of articles in Portuguese on our Instagram (@neoichth). We ask you to designate one author to record a short video using a mobile phone, following the attached instructions. The video should include visual materials (photos, graphics) and a script for subtitles to enhance accessibility. Please email the completed material to our Social Media Editor, Igor Souto-Santos, at icass.ufjf@gmail.com within 30 days.

Additionally, if your article is taxonomic in nature and has been submitted to Zoobank, it is your responsibility to update the manuscript's status on Zoobank once it has been published.

All of the above information and materials are mandatory for the publication of your article, including the scientific dissemination component, which is crucial in the current climate of science denial and misinformation. If you have any questions, please feel free to contact us at neoichth@nupelia.uem.br.

Please send an e-mail to neoichth@nupelia.uem.br within five working days to let us know you are aware of all the important points mentioned above.

Thank you for your fine contribution. On behalf of the Editors of the Neotropical Ichthyology, we look forward to your continued contributions to the Journal.

Sincerely,

Dr. Carlos DoNascimento

Associate Editor, Neotropical Ichthyology

tepuglanis@hotmail.com

Neotropical Ichthyology



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