

Submission date. 19/08/2025

Associate editor's decision after peer review (02/02/2026).

Dear Dr. CORTÉS HERNÁNDEZ:

Manuscript ID NI-2025-0147 entitled "A common but poorly named species of the genus *Pimelodella* (Siluriformes: Heptapteridae) from southeastern South America" 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 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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When submitting your revised manuscript, you will be able to respond to the comments 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 reply POINT TO POINT all the suggestions of the reviewers and be as specific as possible in your response to the comments.

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 04-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,

Marcelo Britto

Associate Editor, Neotropical Ichthyology

mrbritto2002@yahoo.com.br

Anonymous reviewer #1

Recommendation. Minor Revision

Comments. The article provides an important contribution to the taxonomy of *Pimelodella*, particularly those occurring in the southern portion of South America. In addition, it is very well written and clear.

However, some points need clarification:

Major comments

- Justification for the phylogenetic analysis: What is the rationale for including a

phylogenetic analysis? These relationships are not presented in the results nor discussed in the text.

- Issues with the phylogeny: There are several problems with the phylogenetic analysis, such as weakly supported nodes and the inclusion of a very limited number of terminal taxa.
 - Use of parsimony analysis: What is the rationale for performing a parsimony analysis? The stated objective was to assess genetic distances among *Pimelodella* samples from southern South America. For that purpose, phylogenetic methods based on statistical models that provide branch lengths (NJ, ML, BI) are much more appropriate. A parsimony analysis does not provide this type of information. Furthermore, it is well established in the literature that parsimony should not be used for molecular data.
 - Missing results: The Results section is incomplete. It should include (1) a table with the genetic distances and (2) a description of the relationships recovered among the species.
- Minor comments
- Figure 7: The phylogeny needs to be properly arranged (e.g., using FigTree: Trees - Order Nodes - Increasing or Decreasing).
 - Page 9, third paragraph, second line: The expression "...both forming a monophyletic clade with..." is redundant, since a monophyletic group is, by definition, a clade.

Anonymous reviewer #2

Recommendation. Major Revision

Comments. Dear authors, the work presents important results for the systematics and taxonomy of *Pimelodella*, correcting an error in the identification of a species widely distributed in southern Brazil and adjacent countries. However, the title presents an imprecision in the term "poorly named", which, in my view, should be "poorly described", since subsequent authors were unable to identify it in the analyzed samples, which led to the creation of synonyms. The Introduction also lacks information on the identification problem and a synonymy hypothesis. The integrative use of analytical methods is a positive point, but it fails to account for body proportions in PCA, as these data violate several principles of this type of analysis. The diagnosis can be improved by including comparisons with other species. The last paragraph of the discussion is very similar to the diagnosis and is better written. Therefore, I suggest that this paragraph be transferred and readjusted as Diagnosis. The writing is good, but it can still be improved; I have made several suggestions throughout the manuscript. In the morphometric data table (Table 1), replace the commas with periods. I noted additional corrections in the manuscript. I believe that, with these corrections, the manuscript will become suitable for publication.

Author's Rebuttal Letter (18/03/2026).

Dear Marcelo Britto

We thank the reviewers for their constructive comments on the manuscript and have edited the manuscript to address their concerns.

We attached a letter with a table where responding to the comments and critical suggestions made by the reviewers and editors.

Sincerely,

Reviewer: 1

Comments: Justification for the phylogenetic analysis: What is the rationale for including a phylogenetic analysis? These relationships are not presented in the results nor discussed in the text.

Reply: Systematic interpretations can only be understood in a phylogenetic (evolutionary) context. Even if not absolutely necessary, including a phylogenetic analysis would never be out of context, if it can be included. Nevertheless, we included the relationships in the results and discussed them.

Comments: Issues with the phylogeny: There are several problems with the phylogenetic analysis, such as weakly supported nodes and the inclusion of a very limited number of terminal taxa.

Reply: The weakly supported nodes are not a problem with the analysis but a problem with the volume of data. And the inclusion of more or less data (which is ultimately which determines the nodal supports) wasn't our decision, but it simply was determined with the available information for these fishes. We're always very careful with the conclusions we got, because, as systematists we're also completely aware that our phylogenetic hypothesis is not conclusive, but an approach with the available data. The issues regarding the sampling and node values are discussed in the text.

Comments: Use of parsimony analysis: What is the rationale for performing a parsimony analysis? The stated objective was to assess genetic distances among *Pimelodella* samples from southern South America. For that purpose, phylogenetic methods based on statistical models that provide branch lengths (NJ, ML, BI) are much more appropriate. A parsimony analysis does not provide this type of information. Furthermore, it is well established in the literature that parsimony should not be used for molecular data.

Reply: We respectfully disagree with part of the reviewer opinion on the matters. Some of the authors are actively and consciously against the large set of assumptions needed for model-based phylogenetic analysis (e.g., Goloboff, 2003; Goloboff & Pol 2005; Goloboff et al. 2018). Actually we included a model-based analysis only because there are colleagues, as this anonymous reviewer, that are interested in this kind of results. However, it is false that model-based analyses are objectively better than parsimony in any circumstances or with some particular kind of data. There is a lot of papers since the decade of 1970's (See Goloboff 2003) about that issue and we very happily would discuss our position with this reviewer about it, but we think it's beyond a review for a paper in which the phylogenetic analysis is relatively tangential in importance. We know in detail the methods, how they evolved, their assumptions and the pros and cons of each one, and our decision to work in the Parsimony paradigm is the result of it, since the option between a probabilistical or parsimony analysis relies in the chosen paradigm to opt between different relationship hypothesis. In our case, we present both analyses, but opt to discuss the relationships recovered under the parsimony criterion. But addressing the concrete critiques of this anonymous reviewer regarding the chosen paradigm and its supposed caveats: (1) branch-lengths are not a result itself in the ML analysis, but a shortcut of the methods to concurrently assign the increase or decrease of the probabilities of mutations of each character along that particular branch. In an infinitesimally short branch, the probability of change of the descendants relative to the ancestor will be zero. Contrary, in very long branches, the probability of each base (in the case of nucleotids) will be 1/4 (i.e. as completely independent of how it was hypothesized to be in the ancestor). And this is, casually, one of the problems that model-based analyses have. Branch lengths increase or decrease the probabilities of all the characters. If they're associated with time (as usual), it would imply that only time affects the evolutionary rates for characters that are analyzed under the same model/partition. That in turns implies that model-based analyses are compatible only with exclusively neutral evolution, something we think there is a lot of evidence against. Parsimony analysis doesn't need branch lengths as a methodological requirement, because each character is analyzed according to its own distribution of states. Neither shortcuts or generalizations across characters nor some specific assumption of how evolution works are needed, which is an obvious advantage over model-based methods. Nevertheless, values of branch length can be recovered in parsimony analyses referring to the number of apomorphies. (2) It's true that model-based analyses are "well established", and that's the main reason for which we included them in the manuscript. The reasons by which these analyses are well established are unclear for us. We think it's rather associated with some communitary confidence of having obtained the "true" phylogeny provided

by usually high clade probabilities (that completely other discussion that's also beyond this review). Relative with it, we only can say that the reasons for the popularity of these methods are more a sociological issue than something strictly related with the pros and cons of the methods.

Comments: Missing results: The Results section is incomplete. It should include (1) a table with the genetic distances and (2) a description of the relationships recovered among the species. Minor comments

Reply: The genetic distance table is included. Also included a description of the relationships.

Comments: Figure 7: The phylogeny needs to be properly arranged (e.g., using FigTree: Trees – Order Nodes – Increasing or Decreasing).

Reply: The trees were built in Figtree, following the criteria mentioned.

Comments: Page 9, third paragraph, second line: The expression "...both forming a monophyletic clade with..." is redundant, since a monophyletic group is, by definition, a clade.

Reply: The expression was adjusted

Reviewer: 2

Comments: What does it mean? The species received the wrong name? Or did the authors mean that the species was poorly described?

Reply: The species whose name has the priority was poorly described and, in the absence of reviews for a long time, the name was not used. Only with the examination of several type materials and other comparative specimens we were able to comprehend that *Pimelodella straminea* has the priority over *Pimelodella laticeps*. But we agree that "poorly named" has a dubious connotation, and "poorly described" would fit better.

Comments: In the abstract, the species *P. australis* and *P. garbei* were cited as possible junior synonyms of *P. straminea*, along with *P. laticeps*. The latter was listed for Argentina, but the other two were not. Thus, I recommend that the authors present them in the introduction and hypothesize that they are synonymous with *P. straminea*, with appropriate justification.

Reply: We include a paragraph where we justify the problem and propose the hypothesis of synonymization.

Comments: You must explain why this species was poorly named.

Reply: See first comment

Comments: This procedure is not appropriate. Instead, you must use a "Shear analysis" (Humphries et al., 1981) on raw morphometric data. Body proportions violate several principles required by PCA, such as independence among variables, artificial correlations, possible loss of normality, and the creation of ambiguities that make interpretation difficult. If it is not possible to perform the "Shear analysis", it is still preferable to use the traditional PCA on the logarithm of the morphometric data, even if there is some residual size factor in the subsequent components. Also, it is common to plot PCA2 vs. PCA3 in a scatter plot.

Reply: We performed the shear analysis according to the reviewer's instructions.

Comments: Transfer the last paragraph of the discussion to the diagnosis, retrieving information that is not in that paragraph but is present in this diagnosis. In addition, rewrite the diagnosis in a comparative way.

Reply: The final paragraph of the discussion is transferred to the diagnosis section. We also clarified the comparative features in the diagnosis section. Nevertheless, we also opted to present a diagnosis by means of an exclusive character combination, complementary to the comparative diagnosis.

Associate editor's decision after peer review (25/03/2026).

Dear Dr. CORTÉS HERNÁNDEZ:

It is a pleasure to accept your manuscript entitled "A common but poorly described species of the genus *Pimelodella* (Siluriformes: Heptapteridae) from southeastern South

America" 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.

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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,

Marcelo Britto

Associate Editor, Neotropical Ichthyology

mrbritto2002@yahoo.com.br

Neotropical Ichthyology

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HOW TO CITE THIS ARTICLE

- Cortés-Hernández MA, Slobodian V, Márquez Fernández EJ, Aguilera G, Mirande JM. A common but poorly described species of the genus *Pimelodella* (Siluriformes: Heptapteridae) from southeastern South America. *Neotrop Ichthyol.* 2026; 24(3):e250147. <https://doi.org/10.1590/1982-0224-2025-0147>



Official Journal of the
Sociedade Brasileira de Ictiologia