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Kenneth De Baets, Ph.D.
Academic Editor, *PeerJ*
Geozentrum Nordbayern
Friedrich-Alexander Universität Erlangen-Nürnberg
Erlangen, Germany

RE: MS #26838, "Phylogeny and divergence times of suckers (Cypriniformes: Catostomidae) inferred from Bayesian total-evidence analyses of molecules, morphology, and fossils"

Dear Editor:

Thank you for your recent news concerning our manuscript. We were pleased to learn that you consider the manuscript essentially accepted for publication at *PeerJ*, pending minor revisions that you outlined in your decision letter.

Please accept the corrected version of our manuscript, enclosed herein in files with tracked changes (with my edits highlighted in green, for ease of viewing) and without tracked changes. I was able to correct the manuscript as you indicated and fix all points raised, as illustrated by the brief itemized list below containing your suggestions followed by my responses highlighted in gray.

Thanks very much to you and to the reviewers for suggesting ways of clarifying/improving the manuscript, and helping us bring it to this point. We look forward to seeing the manuscript published in open access format in your fine journal.

Sincerely,

A handwritten signature in blue ink, appearing to read 'Justin C. Bagley', is written over a white background.

Justin C. Bagley, Ph.D.
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Editor's Decision and Recommendations:

MINOR REVISIONS

Thank you for addressing our suggestions, implementing most of them (when they made sense to you) and explaining your approach pertaining to ESS scores in greater detail. Your paper is as good as accepted.

Thank you very much for this good news. We were happy to revise the manuscript and also believe that the paper is highly suitable for publication in *PeerJ*. We hope our edits below meet all of your expectations.

Editor point 1: I just had some minor suggestions i would like to take care of before publication. I feel it would make it easier to follow your paper and discussion if you refer to Figure 2 in the text when discussing the datasets and referring the same abbreviations used to refer to them subsequently (A-G).

Thanks for these specific suggestions. We fixed this by going back and rewriting this section of the Methods of the manuscript so that it refers to Figure 2A-G (referring the reader to the Results section), as well as Table 3 (which contains additional details on each of the seven datasets). We felt it could also increase readability to briefly note that the datasets are discussed in this section (and given in Table 3) in the same order as in the results Fig. 2. Specifically, we change the first sentence of the “Dataset construction...” section to read, **“We collated seven datasets for our analyses that we describe here, and which correspond sequentially to datasets listed in Table 3 and trees shown in Figs. 2A–G (see Results),”** at **Lines 156 to 157** of the revised draft with tracked changes.

In addition to making these changes consistent with the Editor’s recommendations, we also noticed that one potential point of confusion might have been that dataset 4 was not outlined in this section, as you might expect. We fixed this by adding a brief description of this dataset to complete the list in this paragraph. This change occurs at **Lines 169 to 170** of the revised manuscript with tracked changes.

Editor point 2: More specifically, i would refer to "(see Fig. 2)" on line 154 after "analyses" and mention the particularly letter (A-G) pertaining to each particular dataset when they are discussed here (see annotated pdf). I would also mention here how these datasets were combined for completeness sake (e.g., morphology with mtDNA (D) and in the total evidence approach (E)).

As noted above, we now refer the reader to Fig. 2 at this point of the manuscript using letters A–G corresponding to the figure panels. We also followed your suggestion to state that the morphology data were analyzed in three different datasets (three separate analyses), which we felt was a good idea. Specifically, we appended to this section a brief sentence about morphology stating, **“Overall, the morphology dataset was analyzed alone (dataset 3; see Results Fig. 2C), in concert with mtDNA genes (dataset 4; see Results Fig. 2D), and combined with the full DNA sequence dataset in total-evidence analyses of dataset 5 (e.g. see Results Fig. 2E).”** We hope this completes this section and makes our description of the datasets used in the complex set of analyses we conducted more accessible to all readers.

Additional Changes to the Revised Manuscript

We realized that two areas of the manuscript referred to “section 2.2”, a carryover from a previous draft of the manuscript in which we had numbered the sections. We fixed this by replacing references to this



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section with references to the ensuing text “below”, at **Lines 116 and 153** of the revised manuscript with tracked changes.

Editor, thank you sincerely again for all of your help with this manuscript, and also please know that the annotated version of the manuscript that you provided was very helpful during this process.

Best regards,

JCB

Revised manuscript files enclosed