

To  
Dr. Andrew Mitchell  
PeerJ, Academic Editor

Dear Editor,

We are grateful for the reviews we received, which undoubtedly will contribute to enhancing our work. The manuscript was modified according to the comments of the reviewers, and all featured comments are listed and answered below.

#### REVIEWER 1

**Line 155:**

Comments: Maybe better to say "with apex ...." and "Maybe better "not bifurcated"

✓ We have changed the text accordingly.

**Line 158:**

Comment: Does M. painensis also have teeth on paramere? If not, it would be important to mention it here as well.

✓ We have changed the text to clarify the sentence.

**Line 168:**

Comment: It should be "ommatidia" if you mean there is more than one.

✓ We have changed the text accordingly.

**Line 171:** I am not sure what this refers to? It looks like it should be in another place.

✓ To clarify the sentence, the text was changed, which also covering the comments made by the Reviewer #3.

**Line 191:**

Comment: This should be reworded or moved, e.g. "...carinate and open at base mesial face"

✓ Done.

**Line 192:**

Comment: How to distinguish "very short" from "short"?

✓ We deleted the qualifier "very" in the sentence.

**Line 205:**

Comment: In the diagnosis it was said there is only one paramere. Please, clarify or change the wording in diagnosis.

✓ We modified the text accordingly.

**Line 209:**

Comment: But the specimens were collected in different sites, right? Please, clarify what you mean by the single type locality here.

- ✓ We modified the text to cover the total sampling area of the new species.

**Figure 4:**

Comment: Should be Paederinae

- ✓ The name was corrected in the modified figure file.
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**REVIEWER 2**

**Line 22:**

Comment: It is also worth specifying the year

- ✓ Done, we added the year the species were described.

**Line 24:** If there is only one author of the name, his surname should appear from the beginning: Asenjo sp. nov.

- ✓ Done.

**Line 26:**

Comment: Every time a new species is mentioned it should have "sp. nov." indications

- ✓ Done.

**Line 67:**

Comment: I highly recommend adding a script showing all the steps taken in all analyses. It will allow not only for repetition but will be helpful for beginners.

- ✓ We have added a file containing the scripts for the commands, as indicated in the text.

**Line 161:**

Comment: The description should not contain any articles

- ✓ Done, we verified the verified the manuscript and corrected accordingly.

**Lines 233 and 234:**

Comments: I suggest adding the obtained alignment to the supplemental material and It is good to give the full command or all parameters used in the analysis

- ✓ We have provided the alignment and the command for the RAxML analysis as Supplementary Data S3 and S4, respectively, as indicated in the text.

**Line 362:**

Comment: Figure 1C is not cited anywhere in the text

- ✓ We corrected the mention in the line 203 – it was: **Figs. 1A-B**, and now it is **Figs. 1A-C**.

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### REVIEWER 3

#### Line 56:

Comment: isn't litter sampling a litter-associated collecting method?

- ✓ We adjusted the text, indicating that it was "soil sampling by flotation".

#### Line 65:

Comment: Add a little more information on the library preparation. From what i can read each samples would be dual indexed, so they could be sequenced with other samples. If this correct? If yes, then add this information, otherwise write how you were able to obtain 3 mitogenomes from one sequencing run.

- ✓ We described in more detail the used methods, covering the points indicate by the reviewer.

#### Lines 68 and 69:

Comment: why is at least added here? Do you expect that there are even more reads. You should know the total number. If this refers to the lowest number of reads for each mitogenome, then i would report the number of reads for each mitogenome seperately.

- ✓ We added the information for all three mitogenomes in the text.

#### Line 80:

Comment: Why not do measurements on multiple specimen to show variation?

- ✓ We performed measurements for additional specimens, with the data being presented in the Supplementary Data S2.

#### Line 84:

Comment: in mm? Or what scale?

- ✓ We mentioned the used scale in the previous paragraph.

#### Line 124:

Comment: I would add as an explanator the decimal degrees of the coordinates. In this case: [-49.6435E]. Looks like the following converter can be used: [https://sigam.ambiente.sp.gov.br/sigam3/Controles/latlongutm.htm?latTxt=ct100\\_con](https://sigam.ambiente.sp.gov.br/sigam3/Controles/latlongutm.htm?latTxt=ct100_con)

- ✓ Done. We added the locations in decimal degrees.

#### Line 143:

Comment: Why are these specimen not part of the types series as paratypes?

- ✓ Due to the small size of the specimens, these samples were used (and therefore destroyed) in the DNA extraction procedures.

**Line 158:**

Comment: Perhaps it would be good with a short comment on how it is distinguished from other *Metopiellus* speices that are not *M. crypticus*.

✓ We modified the text to clarify the sentence.

**Line 162:**

Comment: No quite sure what is meant here.

✓ We modified the text to clarify the sentence.

**Lines 170 and 171:**

Comment: Move this explanation to methods section and reword. Now it is not quite clear, but my guess it would be: maximum length of antennomere without peduncle in mm.

✓ Done.

In addition to the corrections indicated by the reviewers, we also included a few other modifications, such as the requirements such as the technical changes required regarding the LSID for the new species and the authorship of the Figure 1, which are also highlighted in the text, aiming to improve the manuscript.

Thank you very much for your kind attention.

Sincerely yours,



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