

## Reviewer Report

**Title: The state of Medusozoa genomics: current evidence and future challenges**

**Version: Original Submission**    **Date: 1/9/2022**

**Reviewer name: David A. Gold**

### Reviewer Comments to Author:

In this paper, Santander et al. review the field of medusozoan genomics, which has burgeoned in the last three or so years. Overall, I found this a clear, interesting read. The manuscript is well-written, the figures are valuable, and the authors nicely describe the history of the research as well as the state of the field. The findings are not monumental, but it is a worthwhile exercise to survey the rapidly-increasing dataset of genomes in a systematic way, and this review will be a useful start for further work in medusozoan comparative genomics. I rarely suggest a paper should be accepted during the first round of review, and I usually try to provide more constructive feedback than I do here, but I really don't have much too much to quibble with. A couple thoughts are provided below:

- 1) The set of suggestions for future work near the end of the document are fine, but they could apply broadly to any genome project. I encourage the authors to consider whether there are specific problems related to medusozoan evolution that are hampered by inconsistencies between studies, and discuss how their recommendations (or additional ones) could help resolve them.
- 2) I would encourage the authors to practice what they preach in terms of transparency, and make the code they used in their methods public (e.g. statswrapper.sh, AGAT, BUSCO, ETE Toolkit, Matplotlib, Seaborn). The code does not need to be executable, but a supplemental text and/or repository with as much of the starting data and commands executed as possible would make it easier for others to replicate this work and apply it to future comparative genomics projects.

Other than that, I found a couple minor issues:

- 3) Line 236: "...ploidy level, heterochromatin contente." This should be changed to "...ploidy level, and heterochromatin content."
- 4) Line 253-254: "...evolution of genome size is a long-standing question that is included in the so-called C-value Enigma [40]." The authors provide a citation, but I think this sentence would be stronger with a brief explanation of what the C-value Enigma is. Medusozoans are a great example of this "enigma", so it's worth reinforcing.

Congratulations to Santander et al. for a wonderful review!

## Methods

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