

Dear Fernando Racimo,

We would like to express our sincere gratitude to you and the reviewers for taking the time to review my manuscript titled "**Building a Portuguese Coalition for Biodiversity Genomics**" submitted to PCI Genomics. Your constructive feedback has been invaluable in improving the quality of the manuscript, and we are pleased to provide responses to the reviewers' comments and suggestions.

We have addressed each of the reviewers' comments in detail below:

1. Fernando Racimo:

1.1 Comment: Both reviewers agreed the text provides an extensive explanation behind the choice of species and methodological efforts underway. They both felt there was a bit of a need for enriching the manuscript with a brief statement about ongoing discoveries or concrete results that are emerging from the efforts described in the paper. I agree with them. I don't think this would have to go beyond one paragraph providing a taste of what is emerging from some of these sequencing studies, as I understand various manuscripts are also probably being prepared for each of the species. I also agree with anonymous reviewer 1 regarding the modification of Figure 2. A map detailing the locations of sampling (and perhaps species ranges?) would be a helpful addition.

1.1 Response: We agree that adding a brief description of the ongoing relevant biological discoveries for each species would be great. However, since we are still working on the genome assembly and/or annotation for all six species, there are no relevant results yet that are worth mentioning. The aim of this manuscript was to describe how we established this network, and how ERGA pilot project fostered interactions and collaboration among researchers and institutions working on biodiversity genomics in Portugal. For instance, we are using the data produced in the pilot project to strengthen our network of experts in genome assembly and annotation, as well as to use and test the available national computational resources. Several of the co-authors of this manuscript are involved in the assembly, annotation and data analysis efforts, and we are eager and looking forward for the relevant results for each species to emerge. Moreover, at the moment, the different projects are at different stages and reporting assembly statistics to compare the different species is thus outside the scope of this manuscript, and will be reported elsewhere. Yet, since we agree it is important to highlight how the reference genomes will be used, in the new version of the manuscript we highlight how we expect reference genomes will foster new discoveries and answer relevant biological questions for each species (adding a section "Expected results" for each species), as well as providing a short description of the state of the reference genome assembly and annotation for each species in the section "Sequencing and assembly". Finally, we have added a new figure with species distributions and sampling locations to the current version as suggested by the anonymous reviewer.

2. Anonymous reviewer:

2.1 Comment: The article doesn't make any reference of the Earth Biogenome project (EBP). The EBP, set up as an international confederated network of networks with numerous linked global or taxon-specific projects, intends to sequence, catalogue, and characterise the genome of all of Earth's eukaryotic species. Launched in 2018, it is one of the most important efforts taking place in biology right now. In fact, ERGA is an outstanding initiative and one of the most important EBP affiliated projects. Thus, the EBP must be mentioned and referred in the manuscript.

2.1 Response: We absolutely agree with the reviewer and indeed we were missing the fundamental mention of EBP as the international umbrella initiative under which ERGA is developed. We now mention this explicitly in the manuscript (Lines 206-212). We thank the reviewer for this important remark.

2.2 Comment: *If possible, a brief statement on what has been discovered about at least one species should be included to give the reader a taste of science. I understand that the genome of the two first species described has already been assembled and, ideally, annotated. Even though further papers with scientific material will presumably follow with this one, perhaps the authors can briefly indicate if anything interesting or novel has already been discovered from the sequence.*

2.2 Response: Issue addressed in the response to the editor's comment.

2.3 Comment: *Minor issue: It could be great to list or show the locations where the samples were taken from in Figure 2.*

2.3 Response: We added a new figure with species distributions and sampling locations to the current version.

We would like to emphasize that we have carefully considered all of the reviewers' suggestions and have made appropriate changes to the manuscript to address their concerns. In particular, we have added information about EBP, clarified the expected impacts of the ongoing work and updated Fig.2, as suggested by the reviewers.

We believe that the revisions made in response to the reviewers' comments have significantly improved the quality and clarity of the manuscript. We have enclosed a revised version of the manuscript with this letter for your review.

We would like to once again express our appreciation for the thorough review and constructive feedback provided by the reviewers. We are confident that the revised manuscript is now suitable for recommendation. Please do not hesitate to contact us if you or the reviewers have any further questions or require additional information.

Thank you for your consideration, and I look forward to your decision regarding the recommendation of our manuscript.

Sincerely,

João Pedro Marques, José Melo-Ferreira and Vítor Sousa