



Peer Community In Genomics

The Portuguese genomics community teams up with iconic species to understand the destruction of biodiversity

Fernando Racimo based on peer reviews by **Svein-Ole Mikalsen**  and 1
anonymous reviewer

João Pedro Marques, Paulo Célio Alves, Isabel R. Amorim, Ricardo J. Lopes, Mónica Moura, Gene Meyers, Manuela Sim-Sim, Carla Sousa-Santos, Maria Judite Alves, Paulo AV Borges, Thomas Brown, Miguel Carneiro, Carlos Carrapato, Luís Ceríaco, Claudio Ciofi, Luís da Silva, Genevieve Diedericks, Maria Angela Diroma, Liliana Farelo, Giulio Formenti, Fátima Gil, Miguel Grilo, Alessio Ianucci, Henrique Leitão, Cristina Máguas, Ann Mc Cartney, Sofia Mendes, João Moreno, Marco Morselli, Alice Mouton, Chiara Natali, Fernando Pereira, Rúben Rego, Roberto Resendes, Guilherme Roxo, Hannes Svardal, Helena Trindade, Sara Vicente, Sylke Winkler, Marcela Alvarenga, Andreia Amaral, Agostinho Antunes, Paula Campos, Adelino Canário, Rita Castilho, L. Filipe Castro, Angelica Crottini, Mónica Cunha, Gonçalo Themudo, Pedro Esteves, Rui Faria, Carlos Fernandes, Jean-Baptiste Ledoux, Bruno Louro, Sara Magalhães, Octávio Paulo, Gareth Pearson, João Pimenta, Francisco Pina-Martins, Teresa Santos, Ester Serrão, José Melo-Ferreira, Vítor Sousa (2023) Building a Portuguese Coalition for Biodiversity Genomics. EcoEvoRxiv, ver. 2, peer-reviewed and recommended by Peer Community in Genomics. <https://doi.org/10.32942/X20W3Q>

Submitted: 19 July 2023, Recommended: 20 November 2023

Cite this recommendation as:

Racimo, F. (2023) The Portuguese genomics community teams up with iconic species to understand the destruction of biodiversity. *Peer Community in Genomics*, 100257. [10.24072/pci.genomics.100257](https://doi.org/10.24072/pci.genomics.100257)

Published: 20 November 2023

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This manuscript describes the ongoing work and plans of Biogenome Portugal: a new network of researchers in the Portuguese biodiversity genomics community. The aims of this network are to jointly train scientists in ecology and evolution, generate new knowledge and understanding of Portuguese biodiversity, and better engage with the public and with international researchers, so as to advance conservation efforts in the region. In collaboration across disciplines and institutions, they are also contributing to the European Reference Genome Atlas (ERGA): a massive scientific effort, seeking to eventually produce reference-quality genomes for all species in the European continent (Mc Cartney et al. 2023).

The manuscript centers around six iconic and/or severely threatened species, whose range extends across parts of what is today considered Portuguese territory. Via the Portugal chapter of ERGA (ERGA-Portugal), the researchers will generate high-quality genome sequences from these species. The species are the Iberian hare, the Azores laurel, the Black wheatear, the Portuguese crowberry, the Cave ground beetle and the Iberian minnowcarp. In ignorance of human-made political borders, some of these species also occupy large parts of the rest of the Iberian peninsula, highlighting the importance of transnational collaboration in biodiversity efforts. The researchers extracted samples from members of each of these species, and are building reference genome sequences from them. In some cases, these sequences will also be co-analyzed with additional population genomic data from the same species or genetic data from cohabiting species. The researchers aim to answer a variety of ecological and evolutionary questions using this information, including how genetic diversity is being affected by the destruction of their habitat, and how they are being forced to adapt as a consequence of the climate emergency.

The authors did a very good job in providing a justification for the choice of pilot species, a thorough methodological overview of current work, and well thought-out plans for future analyses once the genome sequences are available for study. The authors also describe plans for networking and training activities to foster a well-connected Portuguese biodiversity genomics community.

Applying a genomic analysis lens is important for understanding the ever faster process of devastation of our natural world. Governments and corporations around the globe are destroying nature at ever larger scales (Diaz et al. 2019). They are also destabilizing the climatic conditions on which life has existed for thousands of years (Trisos et al. 2020). Thus, genetic diversity is decreasing faster than ever in human history, even when it comes to non-threatened species (Exposito-Alonso et al. 2022), and these decreases are disrupting ecological processes worldwide (Richardson et al. 2023). This, in turn, is threatening the conditions on which the stability of our societies rest (Gardner and Bullock 2021). The efforts of Biogenome Portal and ERGA-Portugal will go a long way in helping us understand in greater detail how this process is unfolding in Portuguese territories.

References:

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Reviews

Evaluation round #1

DOI or URL of the preprint: <https://doi.org/10.32942/X20W3Q>

Version of the preprint: 1

Authors' reply, 28 October 2023

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Decision by [Fernando Racimo](#), posted 31 August 2023, validated 31 August 2023

Few minor revisions needed

The manuscript by Marques et al. describe the Portuguese contribution to ERGA's pilot effort, involving the sequencing and annotation of genomes of six Portuguese species that are endemic, iconic or endangered. The manuscript also presents a new Portuguese network of researchers working on biodiversity genomics, aiming to jointly train scientists, generate new knowledge and engage with the public about biodiversity efforts in the region.

The manuscript is generally well written, and I believe it needs no major revisions. 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.

Once these minor concerns are addressed, I would be happy to recommend this manuscript in PCI Genomics.

Reviewed by [Svein-Ole Mikalsen](#) , 15 August 2023

Marques et al. describe the establishment of a Portuguese coalition for biodiversity genomics. Encompassing a part of continental Europe that have a high heterogeneity with regard to natural geography (coast, forests, mountains, large rivers, wetter and drier areas, etc.), and the far-flung Atlantic archipelagos Madeira and Azores (and Selvagens), and of course the corresponding marine environments, Portugal has a high and varied biodiversity. As elsewhere, the Portuguese biodiversity is under strain. The authors use well recognised references to build a case for this situation, including the IUCN Red List. The arguments follow what can be called classic reasoning in biodiversity conservation. The manuscript describes how Portuguese groups focusing on biodiversity genomics and other relevant topics have gone together to form the Portuguese branch of the European Reference Genome Atlas (ERGA) and their participation in the ERGA Pilot phase. Through a national inclusive process, they selected six species to be included in the pilot sequencing. The six species are described, including the reasons for inclusion in the pilot sequencing, and the rough outlines of the processes of sampling, sequencing and assembling the genomes.

In this reviewer's opinion, the efforts described here and those of the collected ERGA, Biodiversity Genomics Europe, Earth Biogenome Project, Darwin Tree of Life and other initiatives are highly justified considering the biodiversity situation. It is a good thing for the possibility of influencing practical national political decisions that papers describing national initiatives become available, especially from less resourceful countries (as Portugal is an EU "widening country"). There are plenty of examples of international agreements that are used

as “political garnish”, but are minimally put into practical political decisions at the national or local levels. I hope that the present paper can become a nudge in that direction for the Portuguese environment.

The manuscript is well written. It is easy to follow the arguments and explanations. For each of the six Portuguese pilot species, it is shortly mentioned how or what the genome assemblies can contribute to with regard to biological or evolutionary knowledge about the species, and/or its protection. Naturally, this kind of descriptive policy/perspective paper cannot go into all kinds of details, and I am looking forward to reading the species-related genome papers that will arise from these efforts. Hopefully, some years into the future, this and other ERGA efforts will also give rise to some papers that describe the practical consequences for conservation and protection of the sequenced species.

Reviewed by anonymous reviewer 1, 25 August 2023

The article Building a Portuguese Coalition for Biodiversity Genomics by Marques et al. aims at describing the engagement of researchers from Portuguese institutions in the use of genomics to inventory and characterize biodiversity to inform conservation policies and management and restoration practices. The diverse territories of Portugal's land and sea, from continental Europe to the Atlantic islands, makes Portugal an important reservoir of biodiversity. The participation of these researchers in the European Reference Genome Atlas (ERGA) initiative has strengthened the creation of the Biogenome Portugal.

The article outlines Portugal's contribution to ERGA's pilot project (<https://www.erga-biodiversity.eu/pilot-project>), which will produce high-quality reference genomes of more than 98 species. It details the current state of six endemic, iconic, and/or endangered species from Portugal, including plants, insects, and vertebrates (fish, birds, and mammals) from either the mainland of Portugal or the Azores islands. For each species, there is a thorough explanation of sample collection and processing as well as the current state of sequencing and assembly, however none of the species' data analysis are mentioned.

The article then goes on to detail the development of Biogenome Portugal, a national Portuguese network for biodiversity genomics. This network will link the nation's genomics research community, and aims to promote Portugal's active participation in global biodiversity genomics initiatives, facilitate the exchange of knowledge and infrastructure, organise advanced training programmes, and support knowledge dissemination and outreach initiatives. Members of the network will have a variety of specialties, including those in genomics, ecology, taxonomy, evolution, and other areas, and they will come from different taxonomic groups.

I only have two major comments:

1- 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- 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.

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