

REPLY TO RAPOSO DO AMARAL ET AL.:

# The "Atlantis Forest hypothesis" adds a new dimension to Atlantic Forest biogeography

Yuri L. R. Leite<sup>a,1</sup>, Leonora P. Costa<sup>a</sup>, Ana Carolina Loss<sup>a</sup>, Rita G. Rocha<sup>a,b</sup>, Henrique Batalha-Filho<sup>c</sup>, Alex C. Bastos<sup>d</sup>, Valéria S. Quaresma<sup>d</sup>, Valéria Fagundes<sup>a</sup>, Roberta Paresque<sup>e</sup>, Marcelo Passamani<sup>f</sup>, and Renata Pardini<sup>g</sup>

One or two diversification models alone cannot explain biodiversity evolution in the Atlantic Forest, or any other megadiverse biome, as we (1, 2) pointed out long before Raposo do Amaral et al. (3). In our recent paper (4), we present the Atlantis Forest hypothesis (AFH), which is an additional perspective to the Atlantic Forest evolution, beyond the forest refuge hypothesis (FRH). The AFH incorporates irrefutable Quaternary sea-level changes, which had been overlooked in the literature, and this is the main point of our paper. Support for the AFH came from small mammal distribution modeling and coalescent simulations based on mitochondrial DNA (mtDNA) sequences, which have been successfully used in thousands of biogeographical studies for over 30 y, forming the basis of the booming field of phylogeography (5) and providing support for the FRH (6). We agree that analyses based on a single locus might be subject to stochastic error, and a recent review found mito-nuclear discordance in 18% of biogeographical studies (7). This is not a negligible number, but most mtDNA results can be taken as reliable indicators of geographical population structure and phylogeographical patterns (8).

Species with different ecological requirements will show distinct responses to climatic changes. Under the same ecological constraints, some species ranges may contract, whereas others would expand or remain the same. Thus, it is not surprising that other studies found evidence for range contraction during glacial periods (9). We found evidence of range and population expansions during the last glacial period, which is in agreement with the AFH and several studies showing the persistence of humid forest under a cool climate during this time (4).

As clearly stated in our paper (4), we carefully selected five small mammal species based on a robust dataset on their ecology and distribution (10). These are all forest specialist species that respond negatively to recent forest reduction and fragmentation, and should have responded to historical events of this nature as well. Their similar habitat requirements and genetic signatures lead us to conclude that their demographic histories may have been shaped by the same historical event: forest expansion during the last glacial period. The distinct climatic history of the northern and southern Atlantic Forest has not been ignored in our paper, as suggested by Raposo do Amaral et al. (3). This is actually an important part of our discussion regarding latitudinal differentiation, including the role of the continental shelf.

The AFH resulted from discussions integrating research fields that are often apart: the evolution and biogeography of the terrestrial biota on the one hand, and the geomorphology of marine habitats and evolution of coastal environments on the other. Further tests of the AFH using large nuclear datasets from ecologically and taxonomically diverse species, as suggested by Raposo do Amaral et al. (3), are most welcome. The AFH adds a new dimension to the evolution of the Atlantic Forest biodiversity, but only time will tell whether this hypothesis is supported by additional data. That is how science marches on.

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<sup>a</sup>Departamento de Ciências Biológicas, Centro de Ciências Humanas e Naturais, Universidade Federal do Espírito Santo, 29075-910, Vitória, ES, Brazil; <sup>b</sup>Departamento de Biologia, Centro de Estudos do Ambiente e do Mar, Universidade de Aveiro, Campus Universitário de Santiago, 3810-193, Aveiro, Portugal; <sup>c</sup>Departamento de Zoologia, Instituto de Biologia, Universidade Federal da Bahia, 40170-115, Salvador, BA, Brazil; <sup>d</sup>Departamento de Oceanografia e Ecologia, Centro de Ciências Humanas e Naturais, Universidade Federal do Espírito Santo, 29075-910, Vitória, ES, Brazil; <sup>e</sup>Departamento de Ciências da Saúde, Centro Universitário Norte do Espírito Santo, Universidade Federal do Espírito Santo, 29932-540, São Mateus, ES, Brazil; <sup>f</sup>Departamento de Biologia, Universidade Federal de Lavras, 37200-000, Lavras, MG, Brazil; and <sup>g</sup>Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, 05508-090, São Paulo, SP, Brazil

Author contributions: Y.L.R.L., L.P.C., A.C.L., R.G.R., H.B.-F., A.C.B., V.S.Q., V.F., R. Paresque, M.P., and R. Pardini wrote the paper.

The authors declare no conflict of interest.

<sup>1</sup>To whom correspondence should be addressed. Email: yuri\_leite@yahoo.com.

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