Phylogenetic diversity in space: A tool to evaluate the effect of paleoclimate on terrestrial biota

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Dr. Matias C. Baranzelli from Argentina, travelled to the Universidad Nacional Autónoma de Mexico as a PAGES-IAI International Mobility Research Fellow, from 18 May-19 August 2022. He studied the response to climate change over the last three million years on flowering plants, mammals, birds and amphibians, considering three levels of biodiversity: genetic diversity, species richness, and phylogenetic diversity. This is an integrating and novel approach to decipher the role of past climate change on current patterns of biodiversity.

Understanding how paleoclimatic changes have shaped global biodiversity has long been a challenge for biogeographers. In recent years, this has become an urgent goal to improve our ability to predict biodiversity response to global change. Uncovering the relationships between biodiversity and past climate change can provide testable hypotheses about the current and future impacts of ongoing anthropogenic climate change on biodiversity distribution. The impact of different anthropogenic activities on ecosystems is the main cause of the biodiversity crisis (Urban 2015); hence, there is a need for conservation biology to combine taxonomic, evolutionary, and phylogenetic research with ecological research (Eguiarte et al. 1999). In particular, phylogenetic diversity (PD) emerges as a fundamental conservation tool that combines information on species richness and phylogenetic relationships for any given region. In essence, PD is the total branch length of a phylogenetic tree that connects all species in a given group (Faith 1992). An ensemble with more distantly related species will be phylogenetically more diverse than one with species more closely related.

Different aspects of biodiversity are integrated into the PD and provide clues about ecosystem responses to climate change. Species that share a common evolutionary history are expected to have specific ecological traits that may enable them to persist, either in areas with historical climatic instability, or in areas with stable climates (Santos et al. 2022). In either case, species distributions may be significantly altered with each climate cycle, resulting in distribution patterns that are consistent with ecological features and shared phylogenetic signals (Santos et al. 2022). For example, communities within areas that underwent profound past climate change will tend to show species that are more phylogenetically clustered; that is, communities composed of more closely related species than expected by chance. Given this expectation, determining the relationship between phylogenetic diversity and past climate change can prove key to understanding how communities might respond to ongoing climate change. This can help identify priority regions for conservation.



Figure 1: Estimation of global (A) and regional (Patagonian Steppe) (B) phylogenetic diversity (PD) from phylogenetic data and georeferenced records of angiosperm species. Future studies will evaluate PD relationships with past climate change (C).

During the PAGES-Inter American Institute for Global Change Research Fellowship program (2021) at the UNAM, we estimated the phylogenetic diversity of flowering plants across the globe (Fig. 1a) and across the Patagonian Steppe in South America (Fig. 1b). For this, we used geographic data from Ramírez-Barahona et al. (2020) and Baranzelli et al. (2022), and combined them with the phylogenetic tree developed by Smith and Brown (2018). Our main goal was to evaluate the relationship between phylogenetic diversity and past climate change at different temporal and spatial scales (Fig. 1c). We also estimated phylogenetic diversity for three groups of terrestrial vertebrates across the globe (mammals, birds, and amphibians). The main results of this study were reported at the VII Mexican Congress of Ecology, which took place over the course of the PAGES-IAI Fellowship.

The experience at the UNAM also served to create new research collaboration experiences between different Latin American institutions to evaluate the role of past climate change on biodiversity. By combining the bioinformatic and conceptual capabilities of host and home institutions, it is expected that relevant models will be obtained to understand the effect of past climate change on current patterns of global biodiversity, considering all its dimensions (i.e. genetic diversity, species richness and phylogenetic diversity). We expect to submit the main results to a peer-reviewed journal in the following months.

AFFILIATIONS

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REFERENCES

Baranzelli MC et al. (2022) Biol Conserv 268: 109492

Eguiarte LE et al. (1999) Rev Chil Hist Nat 72: 475-492

Faith DP (1992) Cladistics 8: 361-373

Ramírez-Barahona SA et al. (2020) Nat Ecol Evol 4: 1232-1238

Santos AMC et al. (2022) Glob Ecol Biogeogr 29: 1758-1769

Smith A, Brown JW (2018) Am J Bot 105: 302-314 Urban MC (2015) Science 348: 571-573