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DIMENSIONS US-BIOTA SÃO PAULO: A MULTIDISCIPLINARY FRAMEWORK FOR BIODIVERSITY PREDICTION IN THE BRAZILIAN ATLANTIC FOREST HOTSPOT

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View of Serra do Caraça, MG. Picture by Claydson Pinto de Assis Bezerra.

We are applying a hypothesis-testing framework to predict spatial patterns of biodiversity in the megadiverse and threatened Atlantic Forest (AF) of Brazil. To describe the current spatial patterns of diversity, we are synthesizing the distribution of producers, consumers, parasites, and symbionts. We are expanding on phylogenetic and phylogeographic analyses and summarizing patterns of endemism and turnover. To advance diversity prediction, we are integrating data on the ecological mechanisms acting on the flora and fauna with climatic models of the last glacial-interglacial cycles. We are using genetic and genomic data to test the fit of the aggregate population histories to the inferred time-calibrated landscape shifts and demographic processes. We are describing the dissimilarity of communities as a function of geographical and environmental turnover in space and time. Based on population histories of co-

distributed taxa, we are inferring community-level macro-ecological processes of community assembly, detecting forces behind regional biodiversity patterns, and understanding how historical changes in environmental features affected species distributions. The remote sensing analyses are providing data relevant to studies of carbon cycling, productivity, and biomass. We are generating a long-term paleorecord to describe the spatial heterogeneity of forest response to climate change over time. This is permitting us to construct a framework for biodiversity prediction and promote cross-fertilization among the fields. Finally, this project has significant impacts in conservation, synergy with existing research, and training. The reconstruction of population histories is revealing regions of high stability and genetic diversity and areas of historical connectivity between the AF and other South American forests. We are determining areas and groups under greater extinction threats and predicting AF responses to future climatic shifts. Numerous postdocs, doctoral, masters and undergraduate students are being trained in a collaborative environment to advance the documentation and conservation of biodiversity.

SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

We compiled phylogenetic, phylogeographic, taxonomic, and locality data for hundreds of vertebrate, butterfly and plant species in a single, comparative analysis of the patterns of geographic distribution of taxonomic and phylogenetic diversities, endemism and turnover along the Atlantic Forest (AF). The preliminary analyses show that taxonomic and phylogenetic diversity have similar distributions and the highest diversity occurs in an area that includes the Serra do Mar.

Two of our multi taxa studies of AF organisms (summarized below) indicate that geological landmarks are not the only drivers of biotic diversification, but climate changes have also been important.

Two climatic domains (northern [above 2005] lowland and mid-elevation forests vs. southern and southeastern Brazilian cooler and higher elevation forests) with high turnover around the Rio Doce were revealed by an analysis of the genetic diversity of 25 vertebrates (Carnaval et al. 2014). Endemism patterns observed after independent modeling of these domains indicate different climatic drivers. This result is congruent with studies of cave deposits and fossil pollen, suggesting that the northern and the southern AF were differently affected by climatic variability during the last 250 kyr.



Tangara cyanocephala (red-necked tanager), Guarujá, SP. Picture by Andressa Nuss.

Population genetic structures and models of present and past distributions of 15 birds showed that geographic ranges changed in concert with Pleistocene glacial cycles, but ranges during glacial maxima were slightly larger, equally fragmented and displaced from the interglacial ranges (Cabanne et al. 2016). Population genetic structure was increased by the combined effect of temporal fragmentation variation, small current range size, and range stability. However, genetic diversity was not affected by fragmentation and range stability. In sum, there is a high variance in evolutionary responses of birds to Pleistocene range shifts.

MAIN PUBLICATIONS

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