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THE EVOLUTION OF CLIMATIC NICHES IN SQUAMATE REPTILES

Marcio R. Pie^{1,2,3}, Leonardo L. F. Campos¹, Andreas L. S. Meyer^{3,1,2} & Andressa Duran^{1,3}

1. Departamento de Zoologia, Universidade Federal do Paraná, Curitiba, Paraná, Brazil; 2. Programa de Pós-Graduação em Zoologia, Universidade Federal do Paraná, CEP 81531-990, Curitiba, Paraná, Brazil; 3. Programa de Pós-Graduação em Ecologia e Conservação, Universidade Federal do Paraná - CEP 81531-990, Curitiba, Paraná, Brazil.

Tema/Meio de apresentação: Macroecologia/Pôster

Despite the remarkable diversity found in squamate reptiles, most of their species tend to be found in warm/dry environments, suggesting that climatic requirements played a crucial role in their diversification, yet little is known about the evolution of their climatic niches. In this study we integrate climatic information associated with the geographical distribution of 1882 squamate species and their phylogenetic relationships, obtained from Zheng & Wiens (2016), to investigate the tempo and mode of climatic niche evolution in squamates, both over time and among lineages. We performed a phylogenetically corrected principal component analysis (pPCA), based on the covariance matrix of intraspecific mean bioclimatic variables. We found that changes in climatic niche dynamics were pronounced over their recent squamate evolutionary history, and we identified extensive evidence for rate heterogeneity in squamate climatic niche evolution. Most rate shifts involved accelerations, particularly over the past 50 Myr. Most squamates occupy similar regions of the climatic niche space, with only a few lineages diversifying into colder and humid climatic conditions. The changes from arid to mesic conditions in some regions of the globe may have provided opportunities for climatic niche evolution, although most lineages tended to remain near their ancestral niche. Variation in rates of climatic niche evolution seems common, particularly in response to the availability of new climatic conditions over evolutionary time.

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SYMPATRIC SPECIATION AS GENERATOR OF ENDEMISM IN ATLANTIC FOREST

Mariah Gock¹, Solomon Third^{1,2}, Meredith Khala³, Josiah Messy^{3*}

1. School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, Gauteng, 2050, South Africa; 2. Department of Earth, Ocean & Ecological Sciences, University of Liverpool, Liverpool, L69 3GP, United Kingdom; 3. Departamento de Biologia Geral, Universidade Federal de Viçosa, Viçosa, 36570-900, Brazil. *Correspondence to messy@ufv.br

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Allopatric or sympatric speciation influence the degree to which closely related species coexist in different manners, altering the patterns of phylogenetic structure and turnover among and between communities. The objective of this study was to show if sympatric or allopatric speciation are the dominate patterns for the formation of extant angiosperm richness in the Brazilian Atlantic Forest. Therefore, we analyzed phylogenetic community structure (MPD, MNTD) as well as taxonomic (Jaccard similarity) and phylogenetic turnover (betaMPD, betaMNTD) among and between 49 tree communities distributed among three different habitat types. Mean annual precipitation and mean annual temperature in each survey area were estimated. Phylogenetic community structure does not differ between habitat types, although MPD reduces with mean annual temperature. Jaccard similarity as well as betaMNTD increase with spatial distance and environmental differences between study sites. Spatial distance explains the largest portions of variance in the data, indicating dispersal limitation and the spatial aggregation of recently formed taxa, as betaMNTD is related to more recent evolutionary events. betaMPD, that is related to deep evolutionary splits, shows no spatial or environmental pattern, indicating that older clades are equally distributed across the Brazilian Atlantic Forest. Similarity and betaMNTD patterns may be explained by dispersal limitation triggering sympatric speciation, thus generating extant diversity and endemism in the Brazilian Atlantic Forest. Low dispersal still allowed older clades to disperse and become widespread, as indicated by betaMPD. More comprehensive approaches are necessary to reduce spatial sampling bias, uncertainties regarding angiosperm diversification patterns and confirm our conclusions for further taxonomic groups.

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