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### CLIMATIC SUITABILITY, ISOLATION BY DISTANCE AND RIVER RESISTANCE EXPLAIN GENETIC VARIATION IN BRAZILIAN WHIPTAIL LIZARD

Eliana F. Oliveira<sup>1,8\*</sup>, Pablo A. Martinez<sup>2</sup>, Vinícius A. São-Pedro<sup>3</sup>, Marcelo Gehara<sup>4</sup>, Frank T. Burbrink<sup>4</sup>, Adrian A. Garda<sup>5</sup>, Guarino R. Colli<sup>6</sup> and Gabriel C. Costa<sup>7</sup>

1. Pós-Graduação em Ecologia, Centro de Biociências, Universidade Federal do Rio Grande do Norte, Natal, RN, Brazil; 2. Universidade Federal de Sergipe, Laboratório de Pesquisas Integrativas em Biodiversidade (PIBi Lab), Pós-Graduação em Ecologia e Conservação, São Cristóvão, SE, Brazil; 3. Universidade Federal de São Carlos, Campus Lagoa do Sino, Centro de Ciências da Natureza, Buri, SP, Brazil; 4. American Museum of Natural History, Department of Herpetology, New York, NY, USA; 5. Universidade Federal do Rio Grande do Norte, Centro de Biociências, Departamento de Botânica e Zoologia, Natal, RN, Brazil; 6. Universidade de Brasília, Departamento de Zoologia, Brasília, DF, Brazil; 7. Department of Biology, Auburn University at Montgomery, Montgomery, AL, USA; 8. Universidade Federal de Mato Grosso do Sul, Centro de Ciências Biológicas e da Saúde, Laboratório de Zoologia, Campo Grande, MS, Brazil. \*Correspondence to elianabio@gmail.com

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Spatial patterns of genetic variation can help understand how environmental factors either permit or restrict gene flow and create opportunities for regional adaptations. Organisms from harsh environments such as the Brazilian semi-arid Caatinga biome may reveal how severe climate conditions may affect patterns of genetic variation. Herein we combine information from mitochondrial DNA with physical and environmental features to study the association between different aspects of the Caatinga landscape and spatial genetic variation in the whiptail lizard *Ameivula ocellifera*. We tested five plausible hypotheses that may explain genetic diversity: (i) climatic suitability, (ii) climatic stability, (iii) water and energy availability, (iv) environmental heterogeneity, and (v) colonization history. We also tested six potential drivers of genetic differentiation: (i) geographical distance, (ii) connectivity through differences in the current climatic suitability, (iii) connectivity through differences in the past climatic suitability, (iv) resistance through differences in terrain slope, (v) resistance through differences in terrain roughness, and (vi) resistance of rivers. We found that genetic variation in *A. ocellifera* has been influenced mainly by temperature variability, which modulates connectivity among populations. Past climate conditions were important for shaping current genetic diversity, suggesting a time lag in genetic responses. Population structure in *A. ocellifera* was best explained by both isolation by distance and isolation by resistance (main rivers), although around 83.5% of the genetic differentiation was explained by Caatinga rivers. Our findings indicate that both physical and climatic features are important to explain the observed patterns of genetic variation across the xeric Caatinga biome.

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