
Metabarcoding analysis of endemic lizards' diet for guiding reserve management in the Macaronesian islands

Catarina Jesus Pinho^{1,2}, Vanessa Gil³, Bárbara Santos^{1,2}, Vanessa A. Mata^{1,2}, Carlos Aguiar³, Mariana Seguro¹, Carolina Jardim⁴, Maria Romeiras^{3,5}, Rui Rebelo³, Ricardo Jorge Lopes², and Raquel Vasconcelos^{*†2}

¹Departamento de Biologia, Faculdade de Ciências da Universidade do Porto (FCUP) – R. Campo Alegre, 4169-007 Porto, Portugal

²CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Universidade do Porto (CIBIO/InBIO) – Campus Agrário de Vairão, 4485-661 Vairão, Portugal

³Centre for Ecology, Evolution and Environmental Changes (cE3c) – Faculdade de Ciências Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal

⁴Instituto das Florestas e Conservação da Natureza (IFCN) – IP-RAM, Funchal, Madeira, Portugal

⁵LEAF, Linking Landscape, Environment, Agriculture and Food, ISA, Instituto Superior de Agronomia (LEAF-ISA) – Tapada da Ajuda, 1349-017 Lisboa, Portugal

Abstract

Islands are considered natural laboratories as they represent simplified models and hold a higher number of endemic and threatened species when compared with the mainland. Therefore, studying their ecological networks is of high importance for developing accurate conservation plans. Interesting study models for evolutionary and ecological studies are the reptiles of the Macaronesian Islands, especially the ones inhabiting remote areas. Some of them present uncommon ecological and evolutionary patterns, and most have simplified trophic webs that remain poorly studied. The diet of the most widespread continental *Tarentola* species is already widely studied using classical methods. However, only one known study was performed using next-generation sequencing (NGS) techniques for this genus and very few for reptiles in general. The main objective was to assess diet composition of two endemic geckos from Macaronesia, the emblematic giant wall gecko of Cabo Verde *Tarentola gigas*, and the Selvagens gecko *Tarentola (boettgeri) bischoffi* of those Portuguese islands, using DNA metabarcoding to provide valuable information to the conservation of these threatened species. Little was known on both their ecology and dietary habits. In the first study, we aimed to compare the diet of the two subspecies of *T. gigas* to discuss options regarding its reintroduction on an island where it went extinct. In the second, we compared morphological and DNA metabarcoding techniques associated to very different sampling efforts to check the impacts on the representation of the Selvagens gecko's diet and discussed advantages and limitations of both methods. Results have revealed that both species are generalists, feeding on plants, invertebrates and even vertebrates. Using metabarcoding, we were able to identify a higher diversity of dietary items, many that formerly went unnoticed, with generally

*Speaker

†Corresponding author: raquel.vasconcelos@cibio.up.pt

higher taxonomic resolution than using traditional methods, and to reveal that plants have a significant role in their diets. They also revealed the importance of expeditions to remote areas, such as Monaco Explorations, to decrease knowledge gaps. Overall, the information revealed by these ecological networks is important for the development of conservation plans on these protected areas and reinforce the important and commonly neglected role of reptiles on island system.

Keywords: conservation genetics, protected Areas, remote areas