POPULATION STRUCTURE, DYNAMICS AND HISTORICAL DEMOGRAPHY OF THE GIANT ANTEATER *Myrmecophaga tridactyla* LINNAEUS, 1758 (PILOSA: MYRMECOPHAGIDAE)

Raphael Teodoro Franciscani Coimbra and Fabrício Rodrigues dos Santos*

Laboratório de Biodiversidade e Evolução Molecular, Departamento de Biologia Geral, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil. *Correspondence to fsantos@icb.ufmg.br

Tema/Meio de apresentação: Filogeografia/Oral

The giant anteater is a xenarthran species highly specialized for myrmecophagy that occupies various habitats, from grassland and floodplains to forests. Currently ranging from Honduras southwards to northern Argentina, it is constantly threatened by illegal hunt, habitat loss and fragmentation, wildfires and road kills. Although this iconic species holds a vulnerable conservation status, its populations are poorly studied. A recent work by Clozato *et al.* (2017) found an overall high genetic diversity for the species and signs of population expansion. Moreover, the authors detected a notable genetic divergence between populations from Cerrado (CE)+Pantanal (PT) and Amazonia (AM), and a possible past connection between AM and the Atlantic forest (AF). Thus, to test the robustness of the findings of Clozato *et al.* (2017) and further increase the knowledge on the population genetic structure, dynamics and ancestral demography of the giant anteater, we analyzed 2854 bp of mitochondrial (HVI, Cyt-b) and nuclear (RAG2, vWF exon 28, BDNF) sequences of 106 individuals, including the previous work's dataset. Despite nuclear amplification rate of only ≈ 60%, we were able to construct haplotype networks for each locus; to perform a spatial Bayesian clustering analysis with mitochondrial data on Geneland; and to recover a time-scaled multilocus Extended Bayesian Skyline Plot (EBSP). Geneland indicates two as the most likely number of genetic clusters, CE+PT+AF and AM, in agreement with patterns exhibited in the mitochondrial network. Signs of population expansion suggested by star-shaped mitochondrial and RAG2 networks were confirmed by the EBSP, which detected a ≈ 7.5-fold population growth starting between 60–40 kya.

The authors thank FAPEMIG, CNPq and Boticário Group Foundation for financial support. R.T.F.C. received a CAPES M.Sc. scholarship; F.R.S. holds a CNPq research fellowship.