

## ASSESSING THE PHYLOGEOGRAPHIC STRUCTURE OF THE SOUTHERN-THREE BANDED ARMADILLO (*TOLYPEUTES MATACUS*) IN ARGENTINA

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### RESUMO

The southern three-banded armadillo (*Tolypeutes matacus*) is currently distributed in xeric areas of the Chacoan Region (Eastern Bolivia, Argentina, and Paraguay) and it extends its distribution to the Pantanal Region (South-western Brazil). To date, no study has focused on trying to understand how the populations of this species evolved to reach the distributional range that we are seeing nowadays. To contribute with knowledge that helps recognize conservation priorities for the species, here we share preliminary results from a phylogeographic study aimed to better understand the patterns and processes that ruled the evolutionary history of this species' populations. We obtained 44 tissue samples from 18 localities throughout Argentina during field trips and collected by colleagues. We obtained DNA sequences for the control region of the mitochondrial genome and generated a haplotype network and a haplotype frequency map using PopArt v 1.7. We estimated the number of genetic clusters and their limits using Geneland v. 4.9.2, and calculated several genetic diversity indices for each cluster and population differentiation indices using Arlequin v. 3.5. The haplotype network for the 44 sequences obtained showed a complex pattern with most of the haplotypes being connected to their neighbors by only one mutational step. The exceptions were two haplotypes from northern Argentina that were connected with their neighboring haplotypes by four to six mutational steps. The most frequent haplotype was present in southern localities, being almost the only haplotype found in this region. Geneland analysis detected two genetic clusters ( $K=2$ ): a northern cluster including localities from Salta, Formosa, Chaco, Tucuman, Santiago del Estero, and northern of Cordoba provinces, whereas the southern cluster included localities from western Cordoba, La Rioja, San Juan, and San Luis. Both clusters showed significant genetic differentiation ( $F_{CT} = 0.153$ ,  $P = 0.006$ ). Diversity indices were in general higher for northern group ( $H=0.942 \pm 0.033$ ;  $\pi=0.172 \pm 0.100$ ) than those found for southern cluster ( $H=0.649 \pm 0.110$ ;  $\pi=0.096 \pm 0.061$ ). The haplotype network suggests low population genetic structure for *T. matacus* in Argentina. However, our data support the existence of two genetic groups, with geographical coherence. Lower genetic variability in the southern cluster may be associated with their proximity to glaciers and expansion of the Patagonian steppe during Pleistocene glacial periods. Also, the northern region, where we found the highest genetic diversity, are in agreement with climatic refugia proposed for a chacoan tree. These are preliminary

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results and a further step to a better understanding of the evolutionary patterns of the species would be to include localities in the most northern regions of its range from Bolivia, Paraguay, and Brazil. The information generated from this phylogeographic study contributes to increase the knowledge on the species and will enable establishing better conservation strategies.

**PALAVRAS-CHAVE:** Chaco forest, Population structure, Control region, *Tolypeutes matacus*, Phylogeography

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