

PhD Dissertation
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Title: Evolutionary History of Procyonidae (Mammalia, Carnivora): Integrating Genomics, Morphology and Biogeographic Modeling

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ABSTRACT

Procyonids are among the most well-known mammals across their range. Conversely, only recently this group has been subject to studies aiming to understand even basic aspects of its biology and diversity. Currently, there is much debate in the scientific community regarding the timing of the Great American Biotic Interchange (GABI), a major event that connected the faunal assemblages of North and South America via the closure of the Panamanian Isthmus, putting an end to millions of years of isolation of South America. Geological evidence and fossil records have suggested that the closure of the isthmus occurred ca. 3 million years ago (mya), but recent studies suggest a much older age for the formation of a landbridge between North and South America, ca. 15 mya. Among mammals, the family Procyonidae has one of the longest histories in South America. The fossil record shows that an extinct member of this group was the first North American mammal to immigrate to South America, around 7-9 mya, but recent estimates based on DNA analyses revealed that this family has a much older history in South America. We adopted an integrative approach based on museomics (genomic analyses of museum specimens), traditional morphometrics, biogeographic modeling and whole genome sequencing. Our first goal was to generate intrageneric phylogenies to unveil hidden diversity and understand the evolutionary history of *Nasua* and *Nasuella* (coatis), and *Potos* (kinkajous) using mitogenomes and genome-wide nuclear markers from museum specimens. We also collected morphometric and morphological data for the genera *Nasua* and *Nasuella*, which was

analyzed separately and in conjunction with comparative genomic data to test hypotheses regarding procyonid evolution. Second, we created a new biogeographical and evolutionary model to reassess the tempo and geographic pattern of diversification of procyonids associated with the Great American Biotic Interchange (GABI) that accommodates the most recent DNA and geological evidence to be tested against the traditional fossil-based hypothesis. Finally, building on our studies of the evolutionary history and taxonomy of procyonids, and filling the gap in an underrepresented branch of the tree of life, we sequenced the whole genomes of two genera of this family (*Potos* and *Procyon*), the first procyonid genomes to be sequenced. Our results challenge the current assumptions regarding the taxonomy and the evolutionary history of procyonids in the Neotropics and provide a more complete picture of the complexity of mammalian evolution in that region.