SRAS Final Report

Phylogeography of *Caiman latirostris*: From History to Conservation

Iago Silva Ornellas
Av. Fernando Ferrari, 514 - Goiabeiras, Vitória - ES, 29075-910, (iago.ornellas@ufes.br)

Abstract

This study investigates the phylogeography and conservation genetics of *Caiman latirostris*, focusing on its genetic diversity, population structure, and historical biogeography. Using molecular markers, we identified significant genetic differentiation among populations across Brazil, delineating five evolutionary significant units (ESUs) aligned with major hydrographic regions. Results highlight the role of geographic and climatic factors in shaping the species' distribution and underscore the necessity of targeted conservation strategies. This work contributes to understanding the evolutionary history of *C. latirostris* and supports its conservation amid increasing anthropogenic pressures.

Introduction

The broad-snouted caiman (*Caiman latirostris*) is a pivotal species within Brazil's aquatic ecosystems, inhabiting a range of environments, including lakes, mangroves, and river basins in biomes like the Atlantic Forest, Caatinga, and Cerrado. As an apex predator, it influences prey populations and nutrient cycling, maintaining ecological balance. However, widespread habitat loss due to deforestation, urban sprawl, and agricultural expansion has led to population fragmentation. Furthermore, hunting for its highly valuable leather has historically exacerbated pressures on this species.

Despite its classification as "Least Concern" by the IUCN Red List, the species faces region-specific challenges. In southern and southeastern Brazil, certain populations are listed as "Endangered" due to habitat degradation and genetic isolation. Studies highlight the necessity of understanding genetic structures and identifying evolutionary significant units (ESUs) to inform conservation strategies that account for regional variability and ecological pressures. This study aims to bridge these gaps by investigating the phylogeography of *Caiman latirostris*, providing insights into its evolutionary history and conservation needs.

Methods

This study employed NextGen techniques, to analyze the genomic diversity and structure of *Caiman latirostris*. Sampling was conducted across its distribution in Brazil, encompassing five major hydrographic regions: Paraná, São Francisco, Fluminense, Northeast Caatinga, and Northeast Atlantic Forest. DNA extraction followed standard protocols, and genetic analyses were performed using clustering algorithms, Bayesian inference, and phylogenetic reconstructions. Environmental data were integrated to investigate the impact of historical climatic and geographic factors on population structure.

Results

The genetic analyses revealed significant population structuring across the distribution of *Caiman latirostris*, delineating five distinct ESUs corresponding to major hydrographic regions: Paraná, São Francisco, Fluminense, Northeast Caatinga, and Northeast Atlantic Forest (Figure 1). These findings underscore the influence of geographic and environmental barriers, such as mountain ranges and river systems, in shaping genetic differentiation and limiting gene flow among populations.

Phylogenetic reconstructions estimated the divergence of these lineages to have occurred approximately 9 million years ago, likely driven by historical geological events and climatic oscillations (Figure 2). Among the identified ESUs, the Paraná and São Francisco populations exhibited the highest levels of genetic diversity, reflecting relatively stable and connected habitats. In contrast, populations in the Northeast Caatinga showed pronounced genetic isolation and reduced diversity, likely due to habitat fragmentation and anthropogenic pressures.

Admixture analyses revealed limited gene flow between adjacent populations, further emphasizing the impact of habitat discontinuity (Figure 3). For instance, while populations in the São Francisco and Fluminense regions displayed some genetic overlap, those in the Northeast Caatinga exhibited minimal admixture, indicating long-standing isolation. These patterns highlight the critical need for tailored conservation strategies that address the unique genetic and ecological contexts of each ESU.

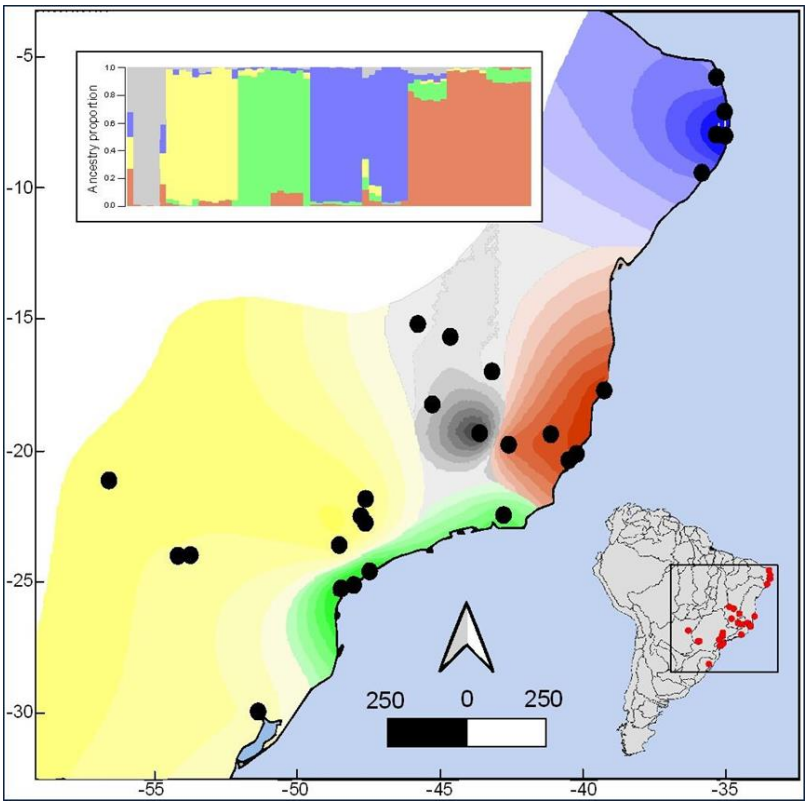


Figure 1: Tess3r Analysis Results The figure presents the results of the Tess3r analysis, which corroborate the five clusters identified in the DAPC analysis and the distance tree. The geographical representation of genetic variation within and among these groups, plotted with ancestry coefficients, aligns with the freshwater ecoregions. The results demonstrate high genetic differentiation in samples located closely, such as FLUMI-PARAN and SAOFR-NORMA. The ancestral matrix reveals a high level of admixture in two samples from the São Francisco group, while the other groups exhibit strong genetic structure with limited admixture among populations. São Francisco (SAOFR - Gray), Paraná (PARAN - yellow), Northeast Caatinga (NOCAA - blue), Northeast Mata Atlântica (NORMA - Red), and Fluminense (FLUMI - green).

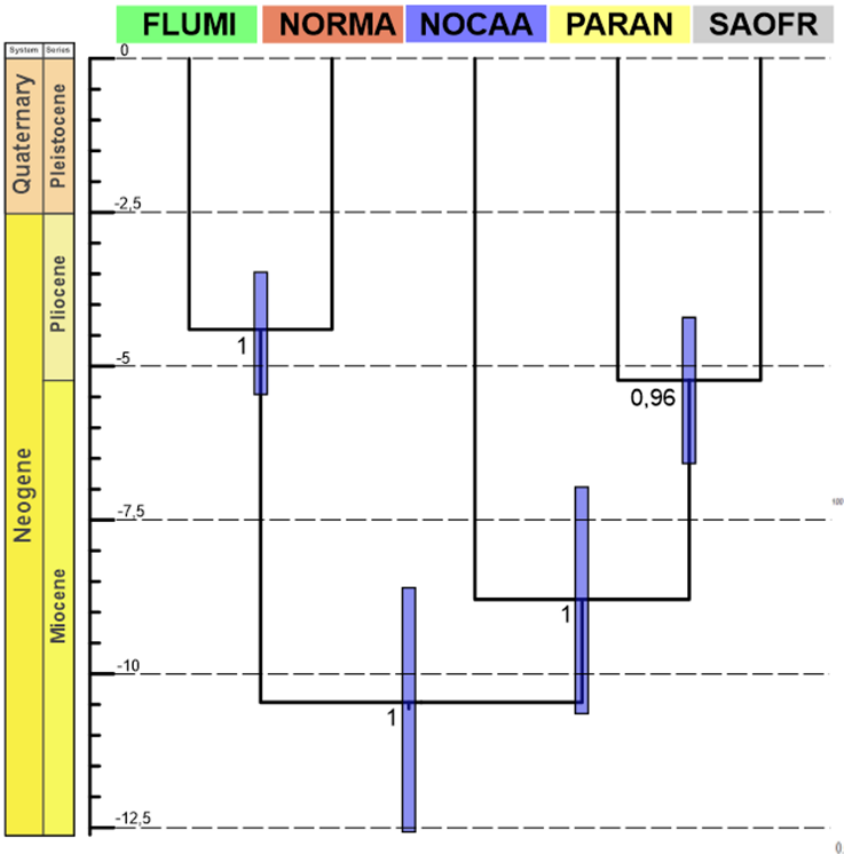


Figure 2: Phylogenetic analysis and divergence time estimation of *C. latirostris*. Description: The figure shows the results of two phylogenetic methods, ASTRAL and SNAPP on BEAST, both yielding the same supported topology. The gene tree inferred by ASTRAL and the species tree inferred by SNAPP recovered five monophyletic groups with high posterior support (>0.95). These groups align with the clusters identified in the population genetic analysis.

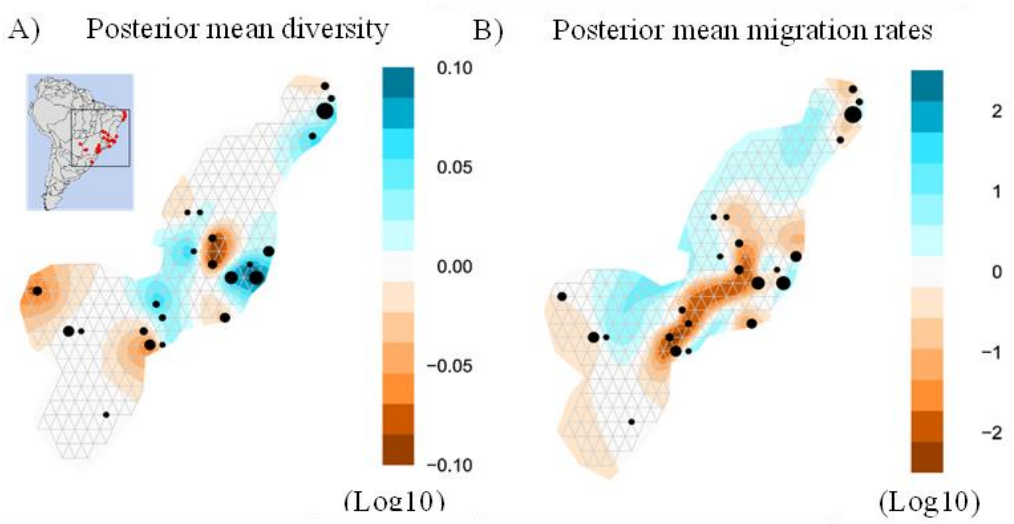


Figure 3: (A)Effective diversity surface and (B)Effective Migration Mapping of *Caiman latirostris* in Brazil using EEMS: this map delineates the Diversity rates and Effective Migration Surfaces (EEMS) specific to *Caiman latirostris* across its Brazilian habitat. (A)Diversity rates and Migration rates (m) are displayed on a logarithmic scale, with a log10 indicating a tenfold increase relative to the species' average, color-coded from regions of minimal migration or low diversity (brown) to heightened migration or high diversity(blue). Data point sizes correlate with the number of sampled *Caiman latirostris* individuals, ranging from 1 to 10.

Discussion

The genetic structure of *Caiman latirostris* reflects the influence of historical biogeographic processes and recent anthropogenic pressures. The identification of five ESUs highlights the necessity of region-specific conservation strategies. For example, the high genetic diversity in Paraná and São Francisco populations presents opportunities for in situ conservation, while the isolated populations in Northeast Caatinga require immediate measures to prevent further genetic erosion. Habitat restoration, protection of hydrographic corridors, and community engagement are critical to ensuring the long-term survival of these populations. Additionally, the presence of cryptic diversity within the species warrants further taxonomic and ecological investigations.

Conclusions

This study underscores the importance of integrating genetic data into conservation planning for *Caiman latirostris*. The identification of five ESUs provides a foundation for region-specific strategies, addressing unique ecological and genetic contexts. Effective conservation will require collaborative efforts, including habitat restoration, mitigation of anthropogenic pressures, and public education. Future studies should explore cryptic diversity within the species and assess the feasibility of translocation or captive breeding programs to bolster vulnerable populations.

Interesting Findings

One intriguing discovery was the pronounced genetic isolation of populations in the Northeast Caatinga. These populations showed minimal gene flow with others, potentially due to historical climatic shifts and geographic barriers. Another notable finding was the high genetic diversity within the São Francisco region, which could serve as a genetic reservoir for conservation initiatives. Preliminary evidence also suggests the possibility of cryptic lineages within *Caiman latirostris*, warranting further investigation.

Future/Follow-Up Work

Future research should focus on:

1. Investigating the taxonomic status of potential cryptic lineages within *Caiman latirostris*.
2. Assessing the effectiveness of habitat corridors in promoting gene flow among isolated populations.
3. Developing and implementing conservation strategies tailored to the specific needs of each ESU.
4. Conducting long-term monitoring of genetic diversity and population dynamics in response to conservation efforts.

Acknowledgements

I would like to thank my advisors, Dr. Leonora Pires Costa and Dr. Marcelo Gehara, for their guidance throughout this project. I am grateful to the Laboratory of Mastozoology and Biogeography at UFES for providing infrastructure and support. Thank you to the IUCN SSC Crocodilian Specialist Group for awarding me a grant through the Student Research Assistance Scheme. Special thanks to my family and friends for their encouragement. I extend my gratitude to the Project Caiman for their essential support in the execution of this research. Lastly, I acknowledge Luis Basseti, my supervisor under the CSG, for his mentorship throughout this endeavor.

Literature Cited

1. ABELL, R. et al. Freshwater Ecoregions of the World: A New Map of Biogeographic Units for Freshwater Biodiversity Conservation. *BioScience*, v. 58, n. 5, 2008.
2. AMAVET, P. S. et al. Analysis of the Population Structure of Broad-snouted Caiman (*Caiman latirostris*) in Santa Fe, Argentina, Using the RAPD Technique. *Journal of Herpetology*, v. 41, n. 2, p. 294–300, 2007.
3. BARRETO-LIMA, A. F.; SANTOS, M. R. DE D.; YHURI CARDOSO NÓBRE. Tratado de crocodilianos do Brasil. [s.l.: s.n.].
4. BITTENCOURT, P. S. et al. Evidence of cryptic lineages within a small South American crocodilian: The Schneider's dwarf caiman *Paleosuchus trigonatus* (Alligatoridae: Caimaninae). *PeerJ*, v. 2019, n. 3, p. 1–26, 2019.
5. BROCHU, C. A. (2003). Phylogenetic approaches toward crocodilian history. *Annual Review of Earth and Planetary Sciences*, 31, 357-397.
6. COUTINHO, M. E. et al. Avaliação do risco de extinção do jacaré-do-papo-amarelo *Caiman latirostris* (Daudin, 1802) no Brasil. *Biodiversidade Brasileira*, v. 0, n. 1, p. 13–20, 2013.
7. FARIAS, I. P., et al. (2013). Genetic variability in caiman populations. *Biodiversity Conservation*, 22(2), 431-450.
8. FRANKHAM, R., BALLOU, J. D., & BRISCOE, D. A. *Introduction to Conservation Genetics*. Cambridge University Press, 2010.
9. ROBERTO, I. J. et al. Unexpected but unsurprising lineage diversity within the most widespread Neotropical crocodilian genus *Caiman* (Crocodylia, Alligatoridae). *Systematics and Biodiversity*, v. 18, n. 4, p. 377–395, 2020.
10. ROBERTO, M. C., et al. (2020). Phylogeographic patterns of *Caiman latirostris*. *Journal of Herpetology*, 54(1), 52-63.
11. VERDADE, L. M.; LARRIERA, A.; PIÑA, C. I. Broad-snouted Caiman *Caiman latirostris*. In: MANOLIS, S. C.; STEVENSON, C. (Eds.). *Crocodiles: Status Survey and Conservation Action Plan*. 3rd ed. [s.l.: IUCN], 2010, p. 18–22.
12. ZUCOLOTO, R. B. et al. Effective population size of broad-snouted caiman (*Caiman latirostris*) in Brazil: A historical and spatial perspective. *Global Ecology and Conservation*, v. 28, n. March, p. 0–2, 2021.
13. Siroski, P., Bassetti, L.A.B., Piña, C. & Larriera, A. 2020. Caiman latirostris. The IUCN Red List of Threatened Species 2020: e.T46585A3009813. https://dx.doi.org/10.2305/IUCN.UK.2020-3.RLTS.T46585A3009813.en. Accessed on 06 January 2025