

DNA barcoding of South American mammals

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Applications of DNA Barcoding in Biodiversity Conservation

1. Gathering data on components of native biodiversity
 - 1.1. Baseline data
 - 1.2. Monitoring of biodiversity in impacted areas
2. Gathering data on threats to native biotas
 - e.g. invasive species, pathogens, wildlife trafficking
3. Helping to enforce actions aimed at curbing threats to biodiversity
 - e.g. wildlife forensic analyses

Neotropical mammals

How DNA barcodes can help the study and conservation of Neotropical mammals:

1. Improved reliability of surveys
 - Academic-oriented (e.g. geographic range refinements)
 - Environmental impact assessments
2. Ecological studies
 - Habitat association
 - Diet
 - Parasite interactions
 - Monitoring of species occurrence
3. Forensics and law enforcement applications

The effort towards Large-scale DNA barcoding of Neotropical mammals

History:

Precursor:

2005 – Beginning of the Brazilian DNA barcoding network

- Large-scale inventory of Brazilian biodiversity

- Multi-center project designed in 2005 to boost taxonomic research in Brazil using the DNA barcode concept as a catalyst to integrate field collections, museum-based biodiversity research, genome center networks and bioinformatics advances.

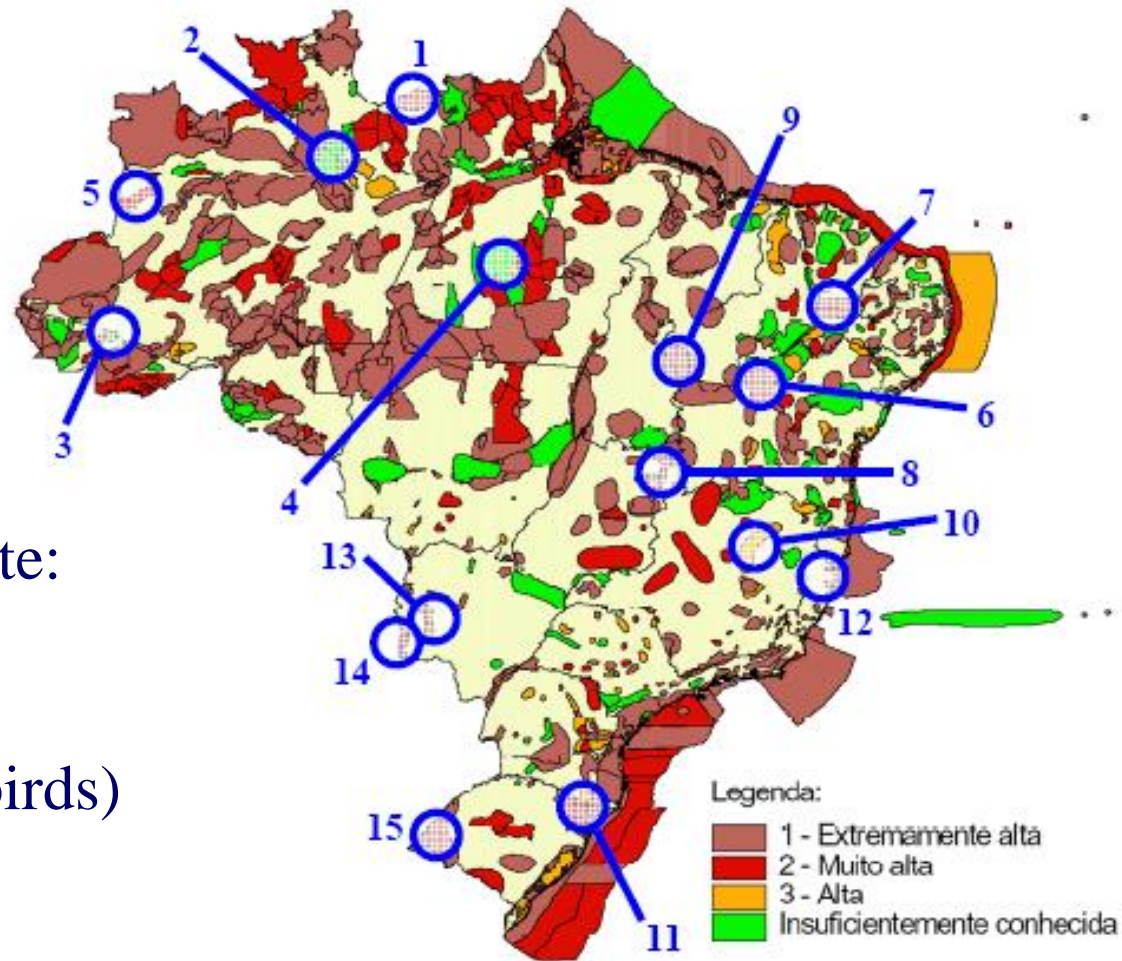
Large-scale inventorying of Brazilian biodiversity (2005)

Sampling strategy

15 sites:

-10,000 samples/site:

- fish
- amphibians
- reptiles (incl. birds)
- mammals
- spiders
- Leguminosae



Large-scale inventorying of Brazilian biodiversity

6 museums

- Involved in coordinating collection trips, curation of sampled specimens and their morphology-based analysis

14 Centers of Molecular Biodiversity:

- Network of genome centers and molecular biology laboratories performing high-throughput sequencing of DNA barcodes from 150,000 samples;

Bioinformatics tools: online management of data collection, analysis and integration (e.g. morphology, DNA barcodes, geography)

Training activities: courses, workshops.

The effort towards Large-scale DNA barcoding of Neotropical mammals

History:

2007 – Regional CBOL meeting in Campinas, Brazil

- Mammals emerge as a CBOL-endorsed regional priority for DNA barcoding.

- Several members of the 2005 network confirm participation, while additional partner institutions join.

The effort towards Large-scale DNA barcoding of Neotropical mammals

History:

2007 – present

Activities:

1. Talks, symposia and/or planning meetings during subsequent regional, national and international congresses:

- 2007, 2008 – Brazilian Congress of Genetics

- 2008 – Brazilian Congress of Zoology, Brazilian

Congress of Mammalogy, Regional Genetics Meeting (RS)

- 2009 – International Mammalogical Congress, Argentina

2. Funding proposals: CYTED (2007), PROSUL (2007, 2008).

PROSUL project proposal – 2008 (excerpt)

Goal:

To consolidate an international network whose aim is generate, analyze and apply an integrated data base of DNA barcodes for South American mammals.

Official participants: 21 research institutions from six countries (Brazil, Uruguay, Chile, Bolivia, Peru and Venezuela).

- museum-based groups working on mammal systematics
- molecular genetics laboratories

Proposed tasks:

- (i) Training of students from multiple countries in the use of molecular tools for biodiversity studies;
- (ii) Coordination meeting comprising group leaders;
- (iii) Reagent costs for the initial phase of data collection.

PROSUL 2008 participating institutions

Brazil

PUCRS - Pontifícia Universidade Católica do Rio Grande do Sul

UFMG - Universidade Federal de Minas Gerais

UFRGS - Universidade Federal do Rio Grande do Sul

UFES - Universidade Federal do Espírito Santo

FZB/RS - Fundação Zoobotânica do Rio Grande do Sul

URI – Universidade Regional Integrada

FURB – Universidade Regional de Blumenau

UFPR – Universidade Federal do Paraná

UFRJ - Museu Nacional

INCA - Instituto Nacional de Câncer

FIOCRUZ - Fundação Oswaldo Cruz

UERJ - Universidade do Estado do Rio de Janeiro

USP - Instituto de Biociências

USP/ESALQ - Escola Superior de Agricultura Luiz de Queiroz

INPA - Instituto Nacional de Pesquisas da Amazônia

UFMS - Universidade Federal de Mato Grosso do Sul

UCB-DF - Universidade Católica de Brasília

UFPA - Universidade Federal do Pará

UFAM - Universidade Federal do Amazonas

PROSUL 2008 participating institutions

Uruguay

FC - Facultad de Ciencias (Enrique Lessa)

Chile

UC - Universidad de Chile (Angel Spotorno)

Venezuela

USB - Universidad Simon Bolivar (Marisol Aguilera)

Peru

UPCH - Universidad Peruana Cayetano Heredia (Jose R. Espinosa)

Bolivia

MNHN - Museo Nacional de Historia Natural (Julieta Vargas)

South American Network for Mammalian DNA barcoding

Regional Nodes

Brazil

1. Rio Grande do Sul – PUCRS/UFRGS
2. Espírito Santo – UFES
3. Minas Gerais – UFMG
4. Rio de Janeiro – INCA/UERJ
5. São Paulo - USP
6. Pará - UFPA
7. Goiás/Brasília - UFG

Carnivora
Xenarthra
Rodentia
Chiroptera

Small mammals

Xenarthra
Chiroptera

Rodentia
Primates

Primates

Xenarthra
Chiroptera
Rodentia

Uruguay

1. Universidad de la Republica

Species sampled so far:

Porto Alegre (PUCRS/UFRGS)

Xenarthra – 5 spp.

Carnivora – 23 spp.  Next targets: Cetacea, Primates

Rodentia – 43 spp.

Cetartiodactyla – 4 spp.

Chiroptera – 15 spp.

Total: 90 spp (~ 600 specimens)

Belo Horizonte (UFMG)

Xenarthra – 7 spp.

Chiroptera – 35 spp. (> 200 specimens)

Espírito Santo (UFES)

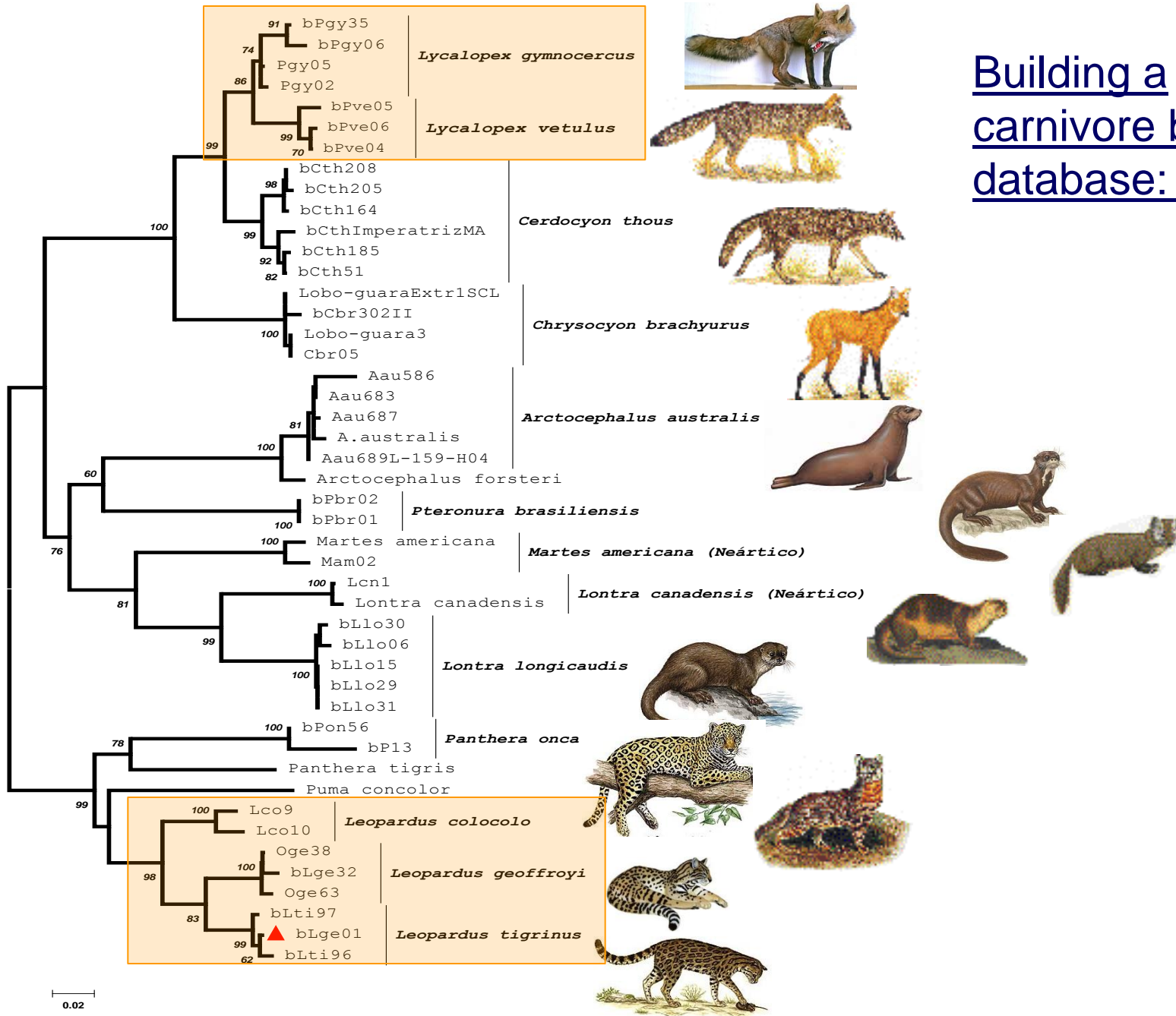
Rodentia, Didelphimorphia, Chiroptera – 85 spp. (259 specimens)

São Paulo (USP)

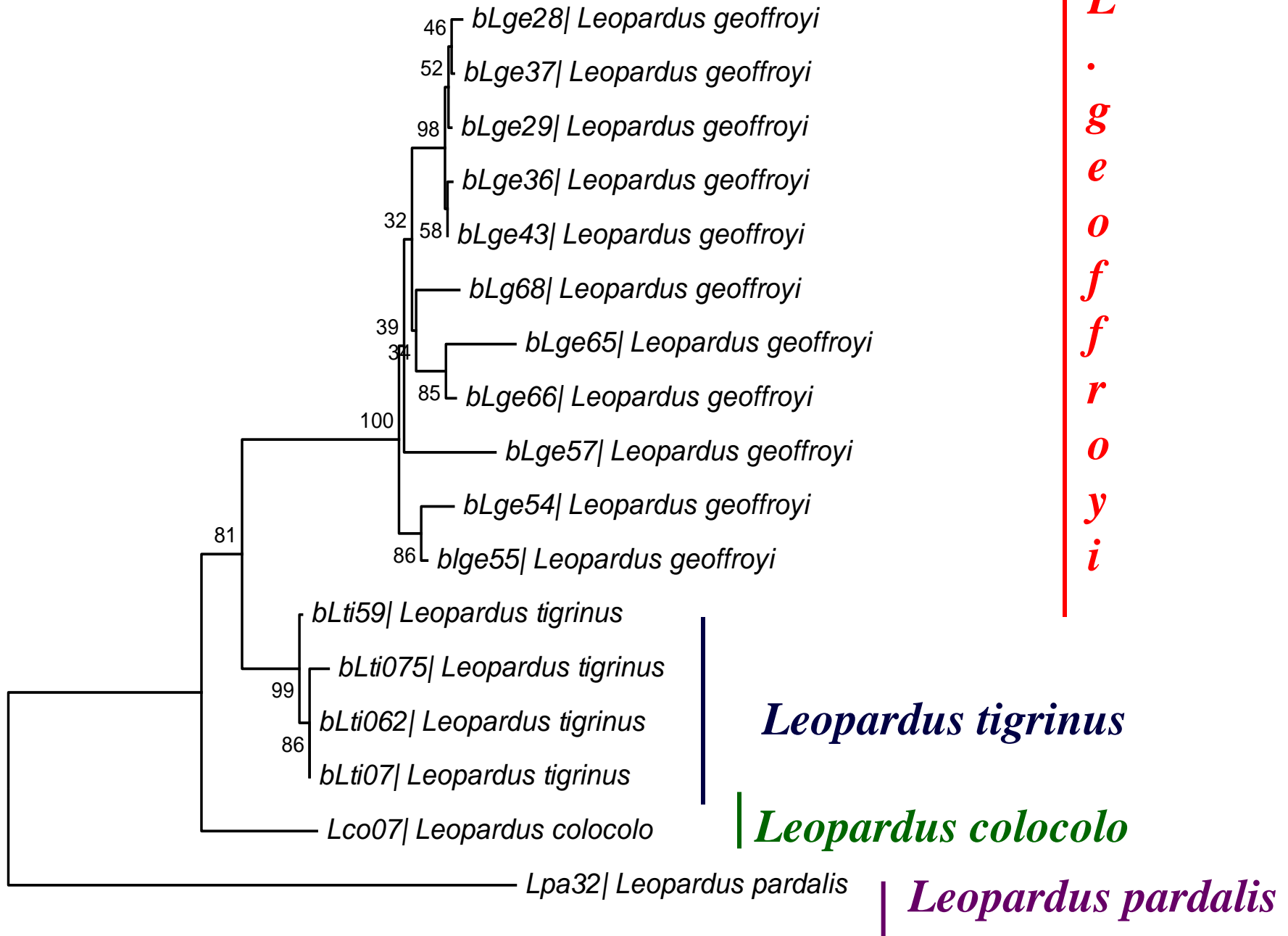
Xenarthra – 6 spp. (149 specimens) [N. Moraes-Barros]

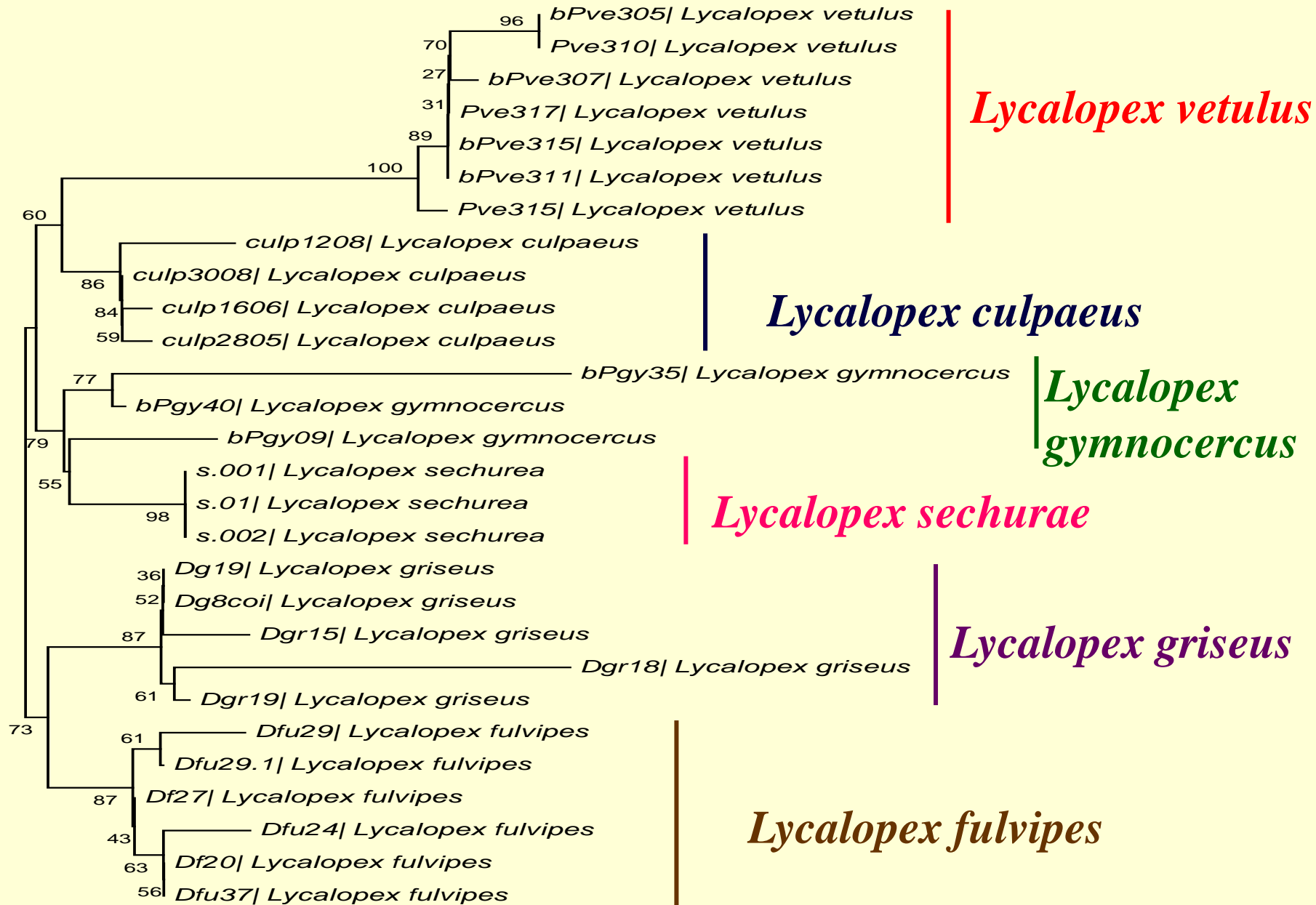
 Next targets: Chiroptera, Rodentia [F. Martins]

Building a carnivore barcode database: COI



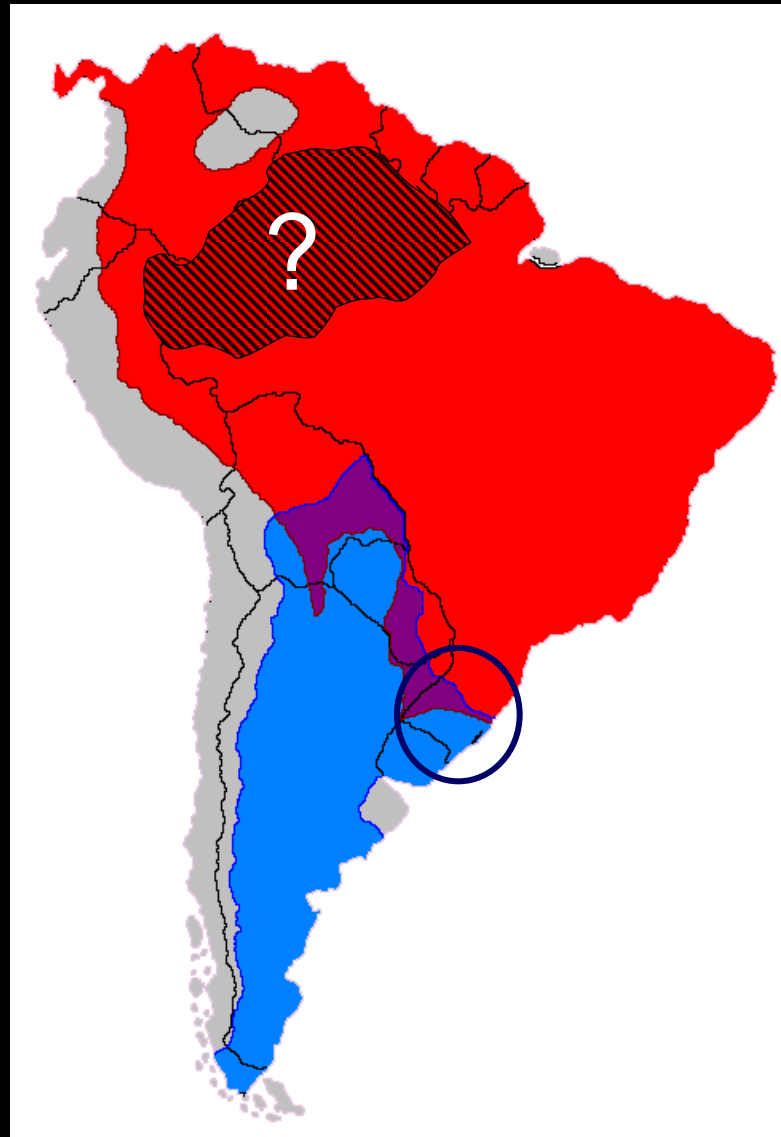
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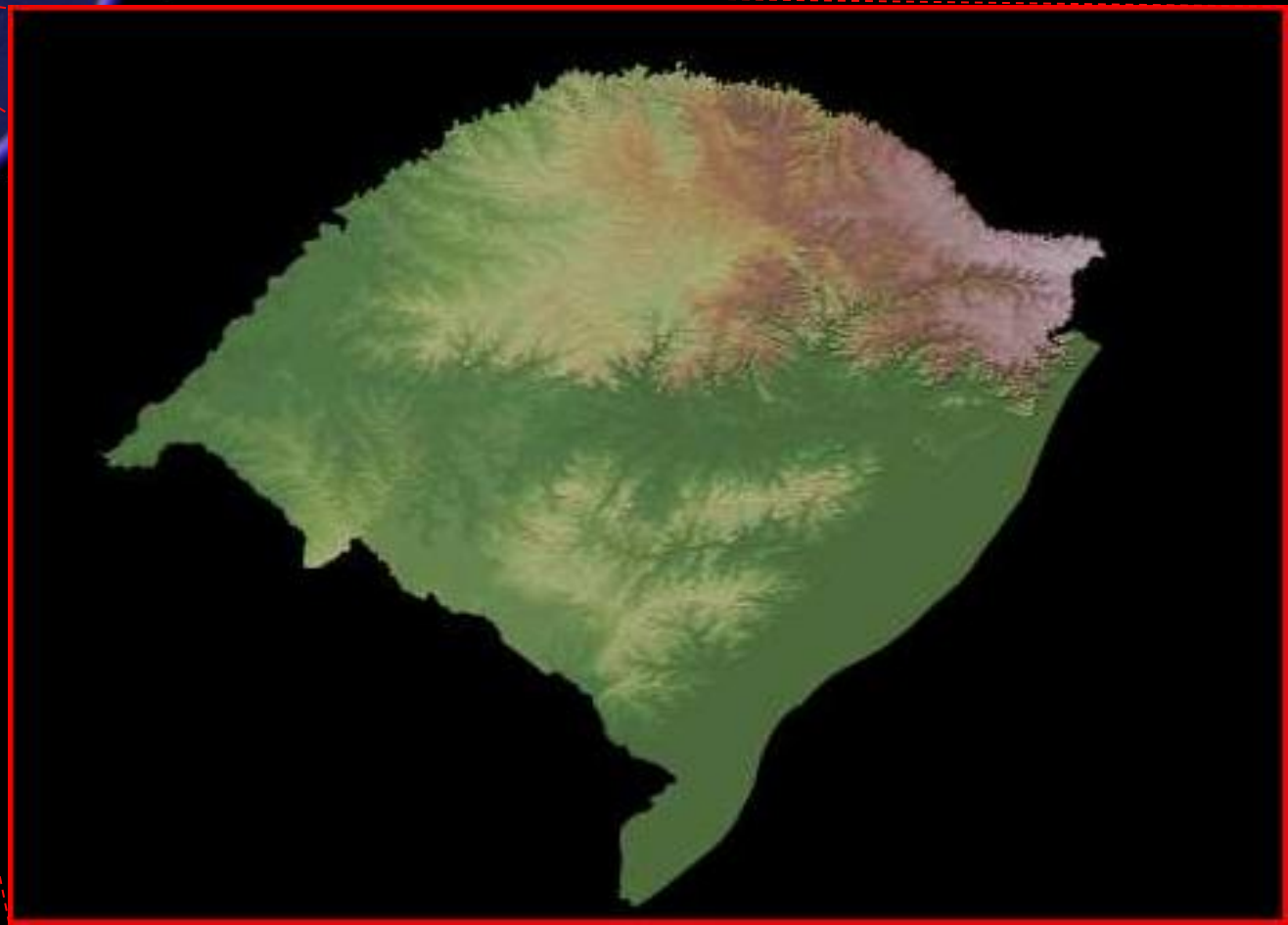
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Evolutionary ecology of *L. tigrinus* and *L. geoffroyi*

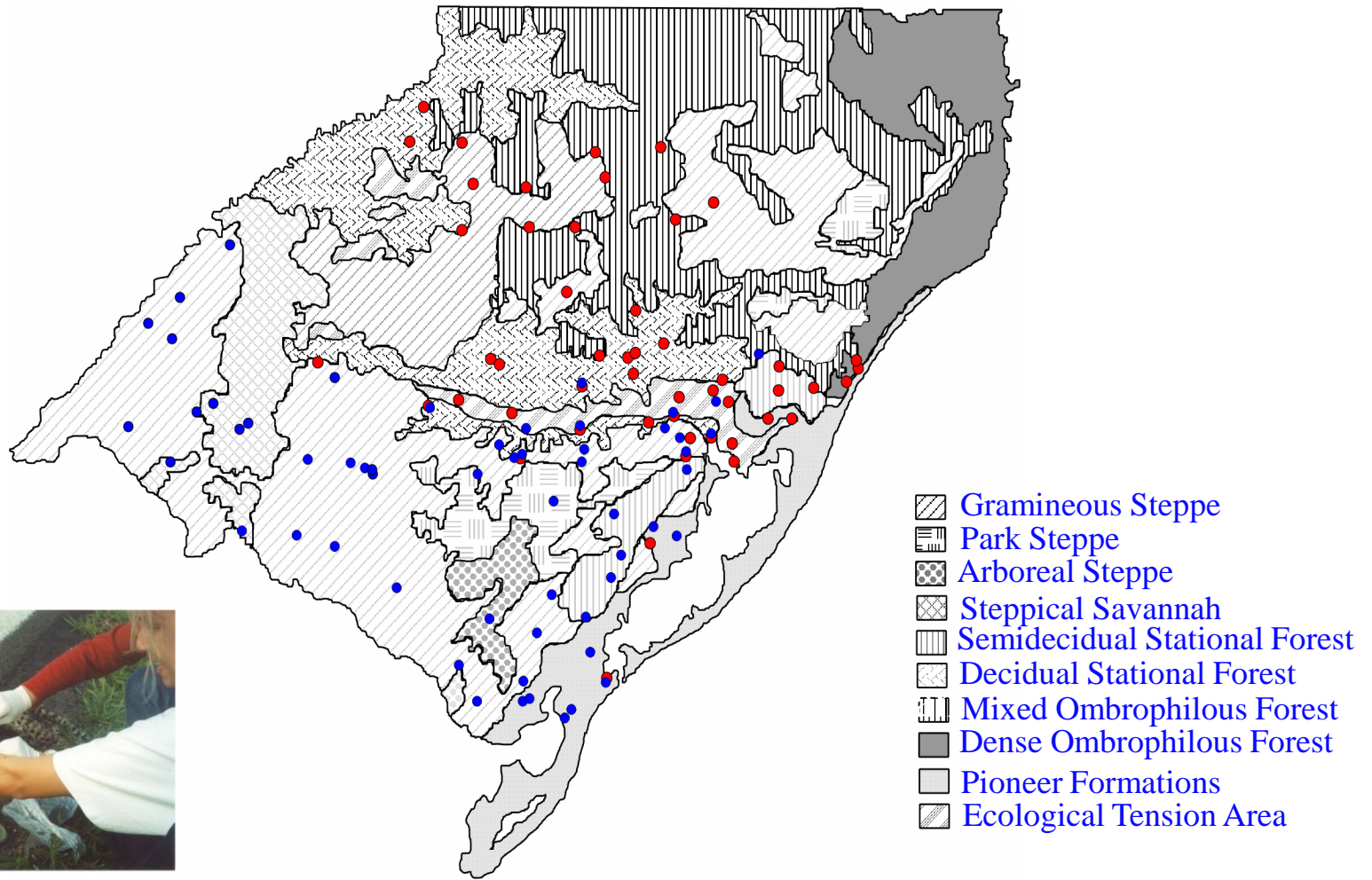




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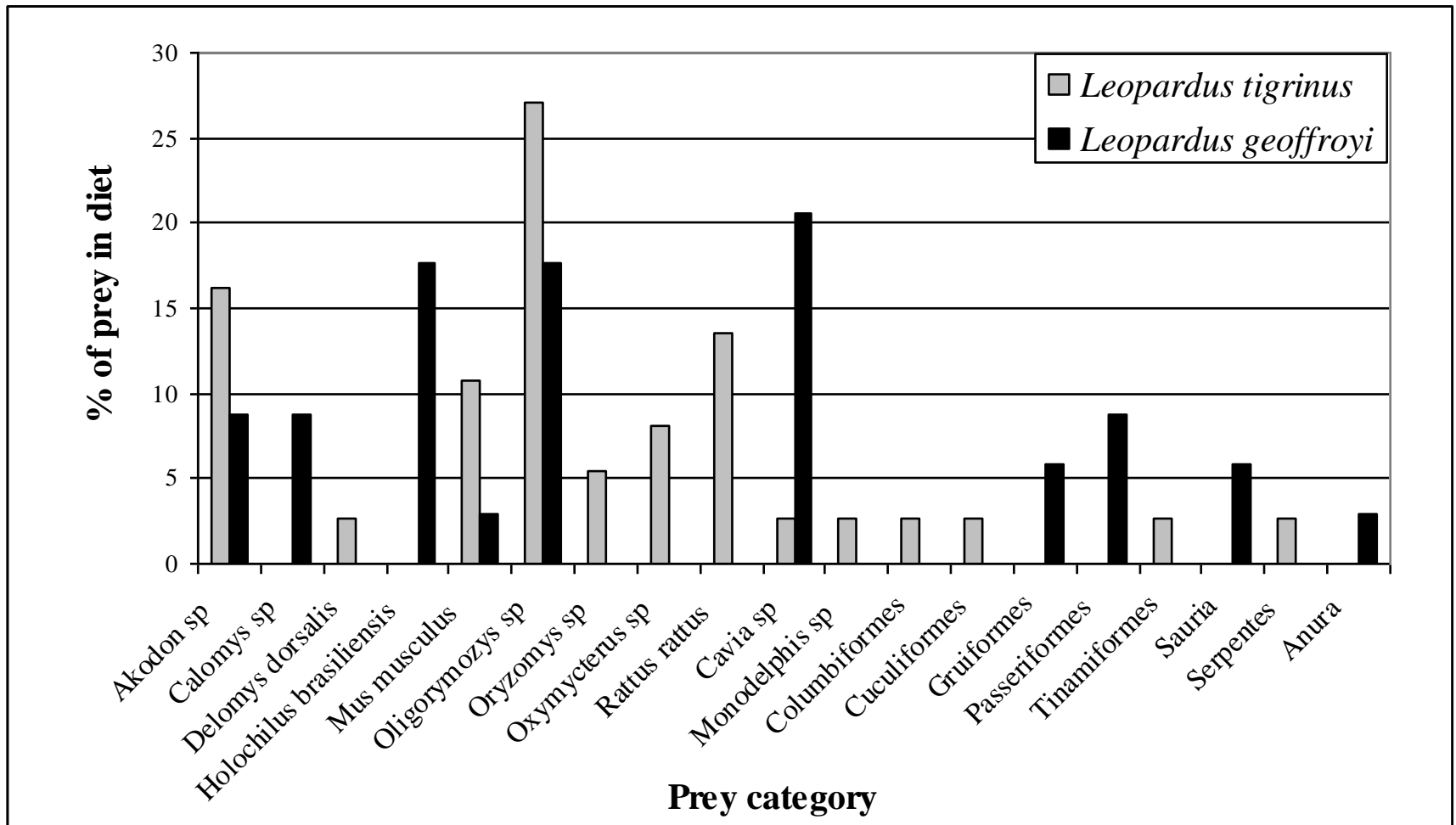
Habitat use of *L. tigrinus* and *L. geoffroyi* in RS state



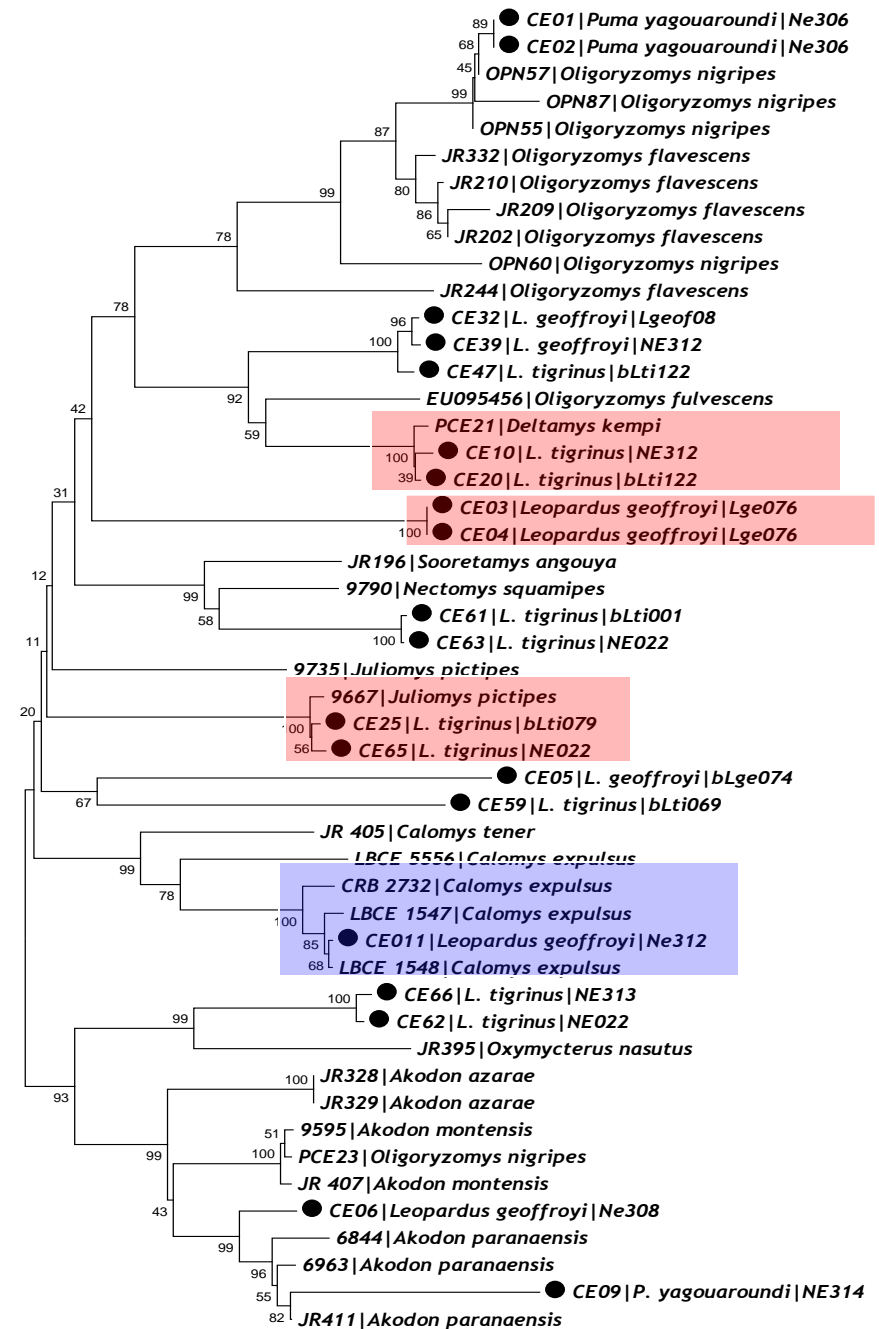
100 miles



Dietary analysis of *L. tigrinus* e *L. geoffroyi* using stomach contents of roadkilled animals

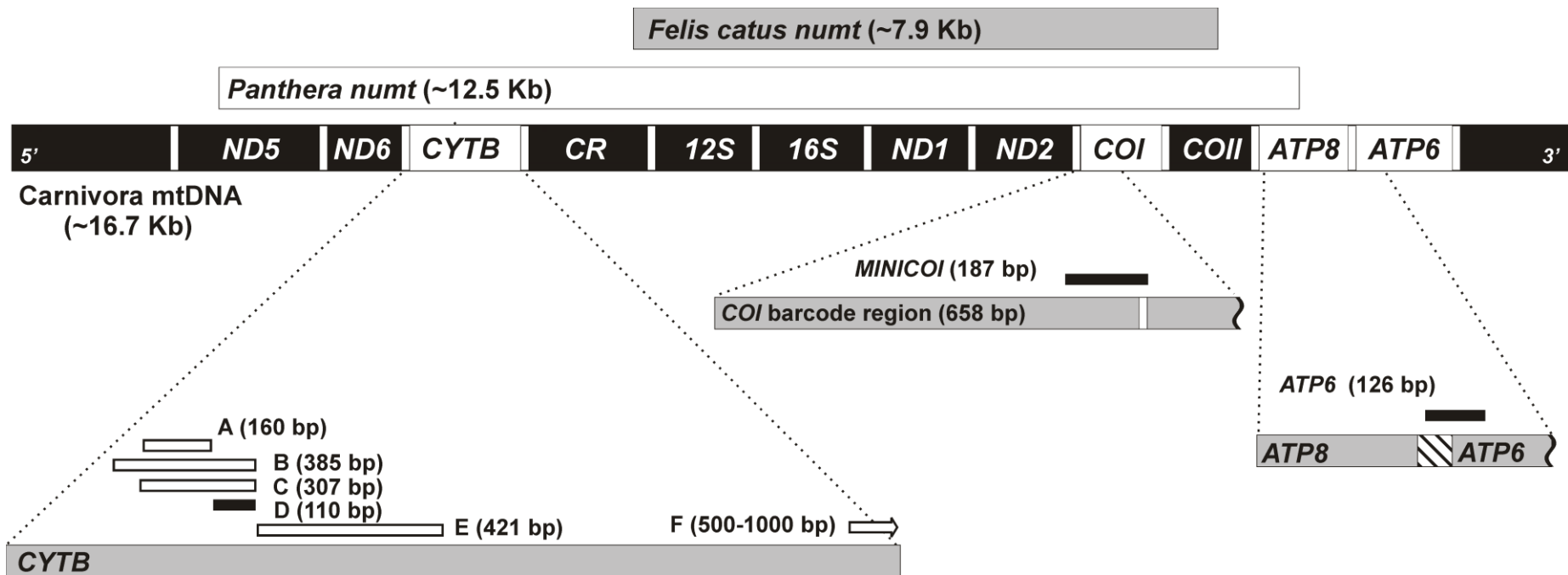


Dietary analysis of *L. tigrinus* e *L. geoffroyi* using stomach contents of roadkilled animals: DNA barcoding of prey items



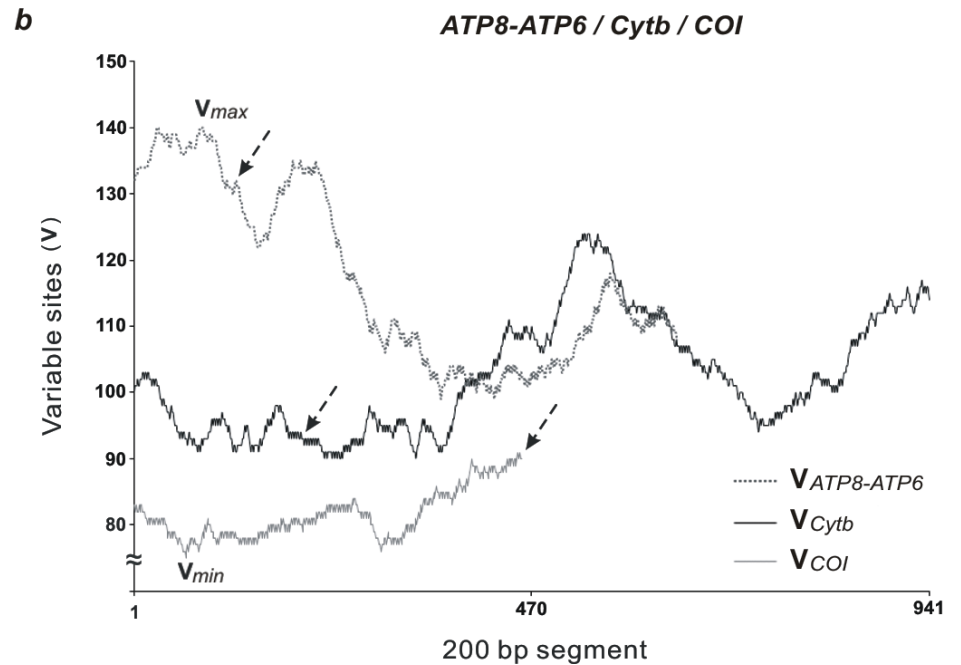
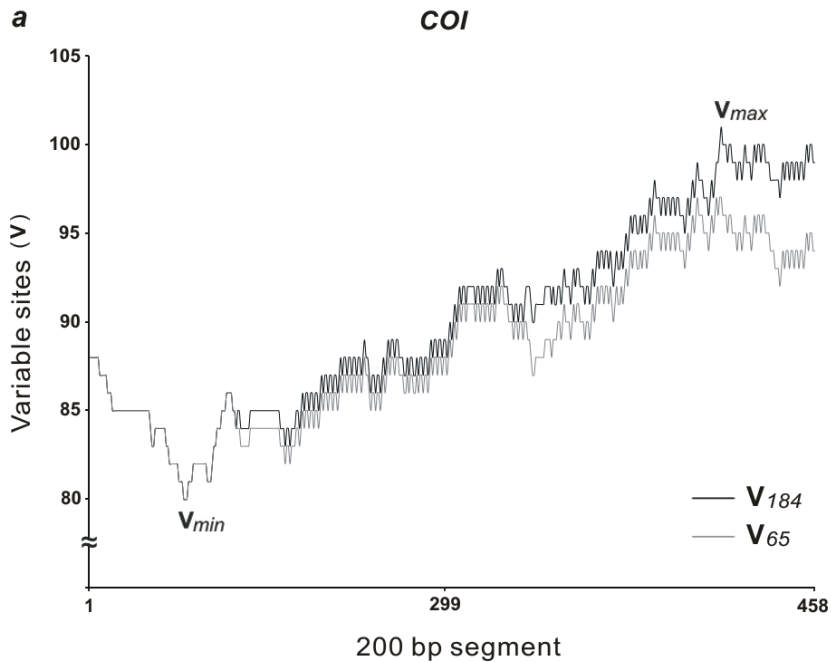
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Development of molecular tools for carnivore species identification from faecal DNA



“Molecular scatology meets DNA barcoding”

Assessment of variability in mtDNA segments

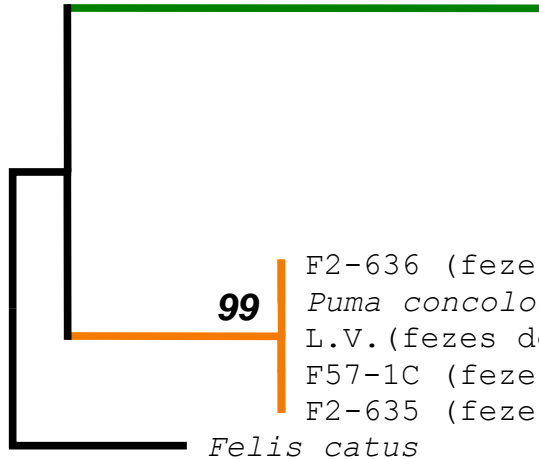


➔ Generation of large data bases of carnivore sequences

Development of molecular tools for carnivore species identification from faecal DNA



100

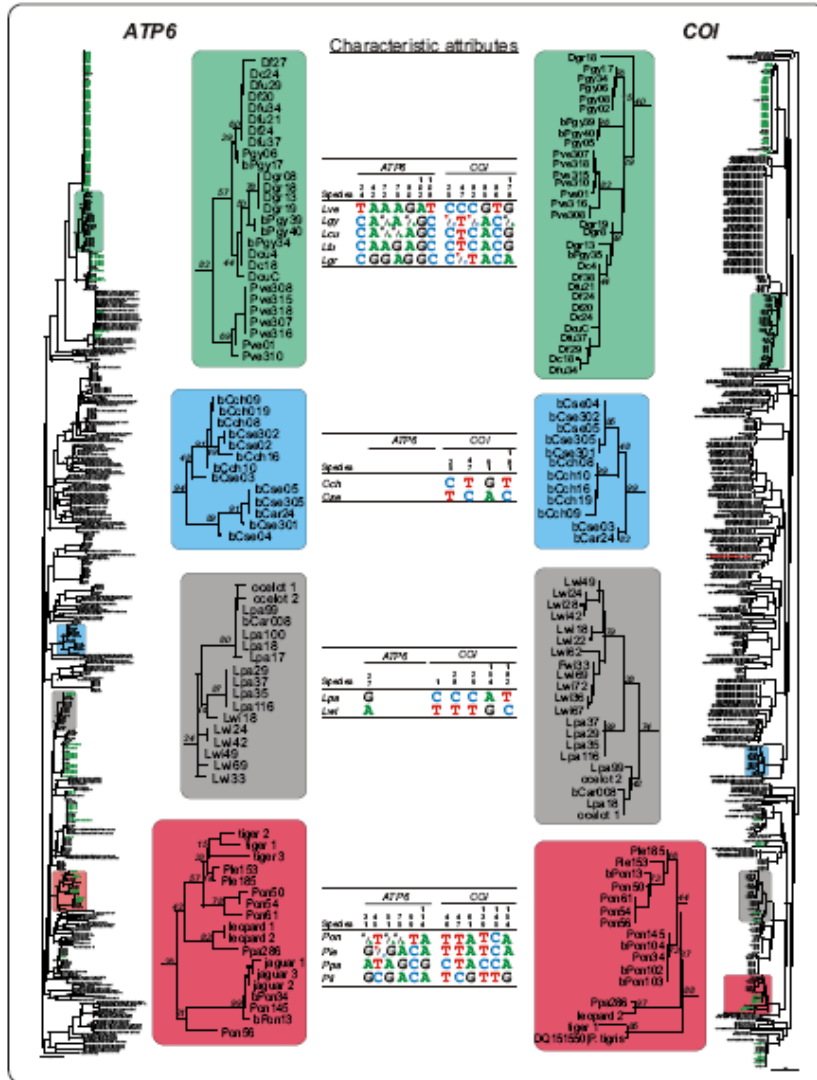


- bPon56 (fezes *Panthera onca* em álcool)
- bPon55 (fezes de *Panthera onca* em DET)
- bPon306 (fezes de *Panthera onca*)
- bPon307 (fezes de *Panthera onca*)
- bPon56 (fezes *Panthera onca* - 98 mg)
- bPon32 (sangue de *Panthera onca*)
- bPon56 (fezes de *Panthera onca* em DET)
- P3-16 (pele de *Panthera onca*)
- bPon305 (fezes de *Panthera onca*)
- P3-2 (pêlos de *Panthera onca*)
- bPon56 (fezes de *Panthera onca* - 48 mg)
- bPon24 (sangue de *Panthera onca*)
- P31-1 (pêlos de *Panthera onca*)

- F2-636 (fezes de felino grande)
- Puma concolor* (sangue)
- L.V. (fezes de felino grande)
- F57-1C (fezes de felino grande)
- F2-635 (fezes de felino grande)



Identification of carnivores using short DNA segments



Goal: global standardized system for carnivore identification.

Application in ecological, biogeographic and forensic studies.

Ongoing tests in multiple field sites in South America
Brazil (RS, ES, MS, MT, TO, MG,DF), Argentina.

Identification of carnivores using short DNA segments



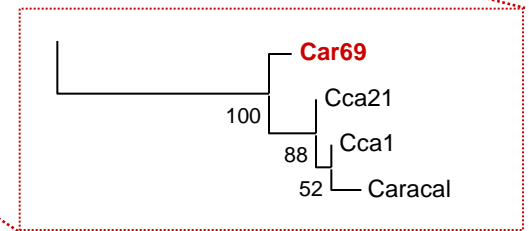
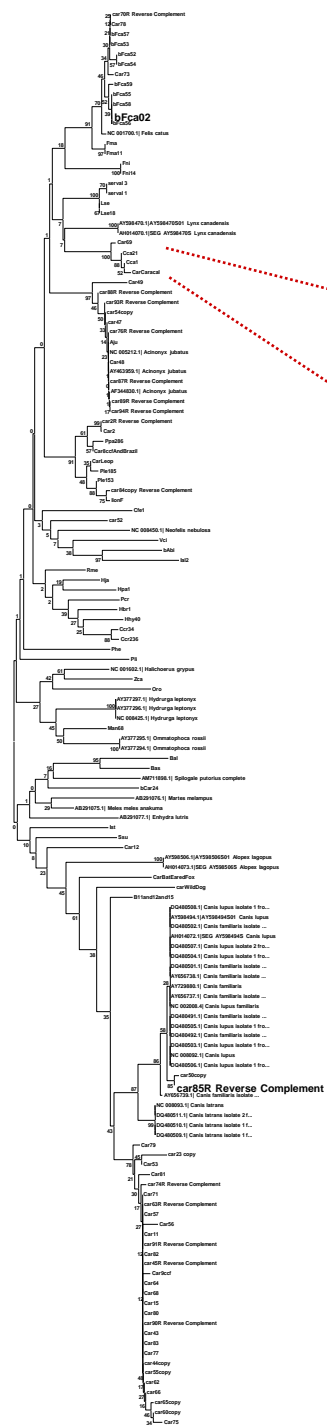
Ongoing surveys and ecological studies

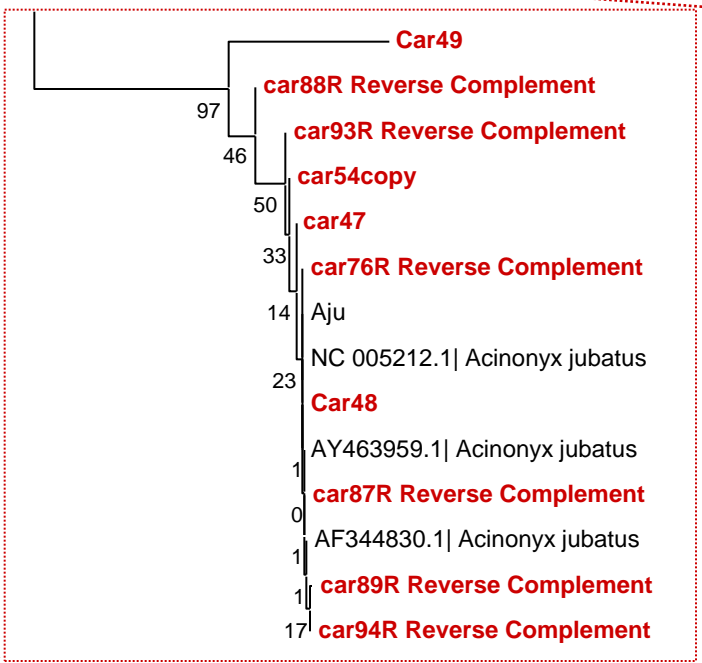
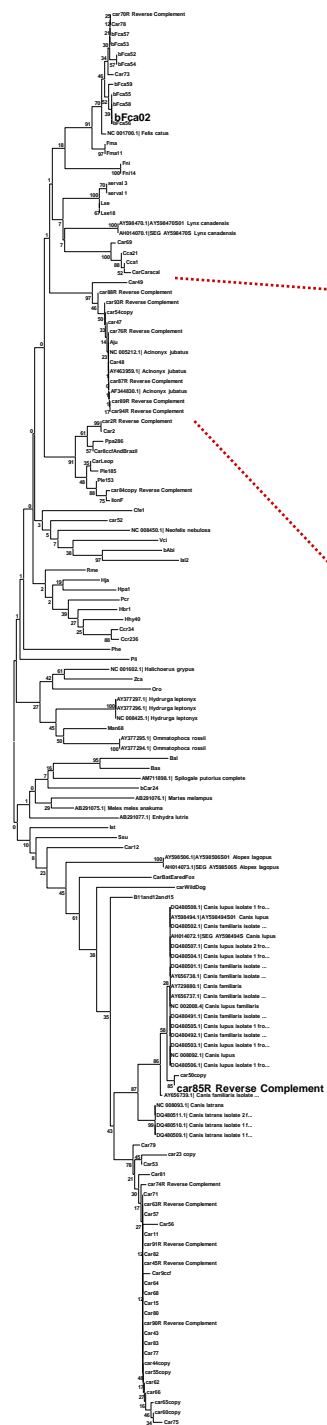


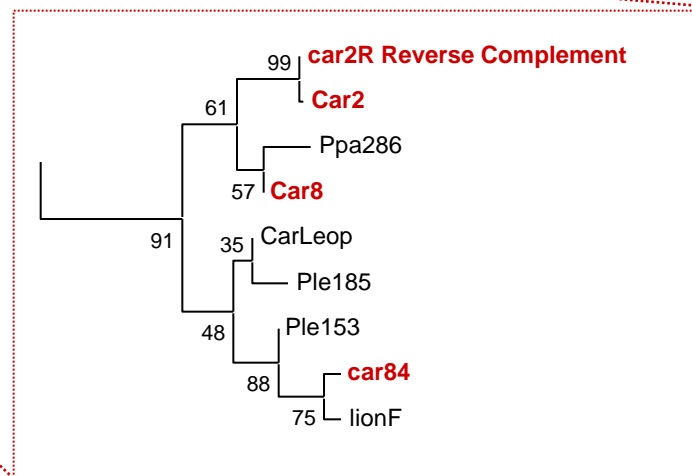
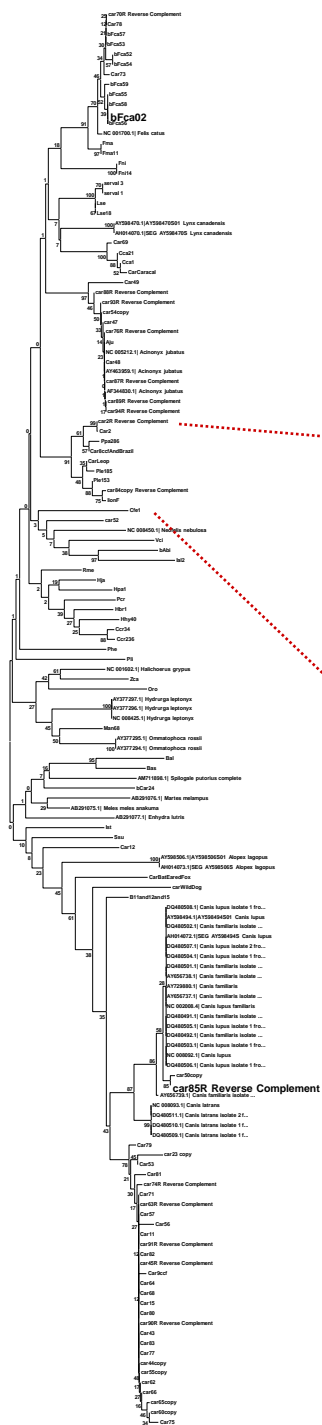
Identification of carnivores using short DNA segments

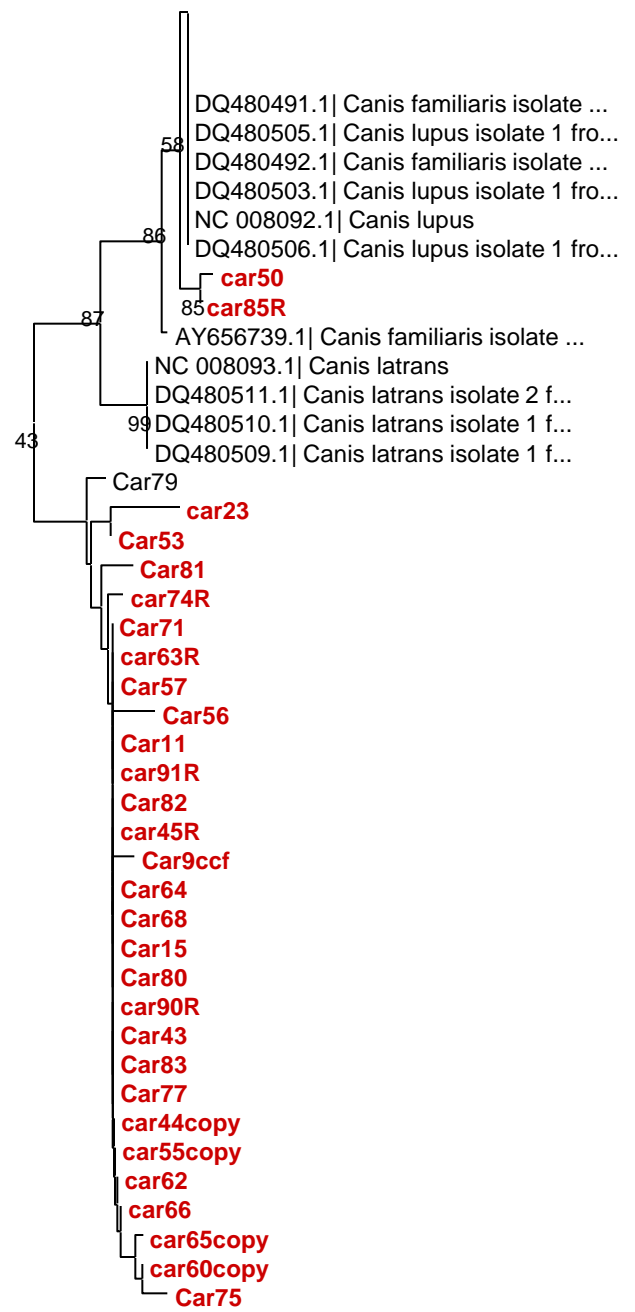
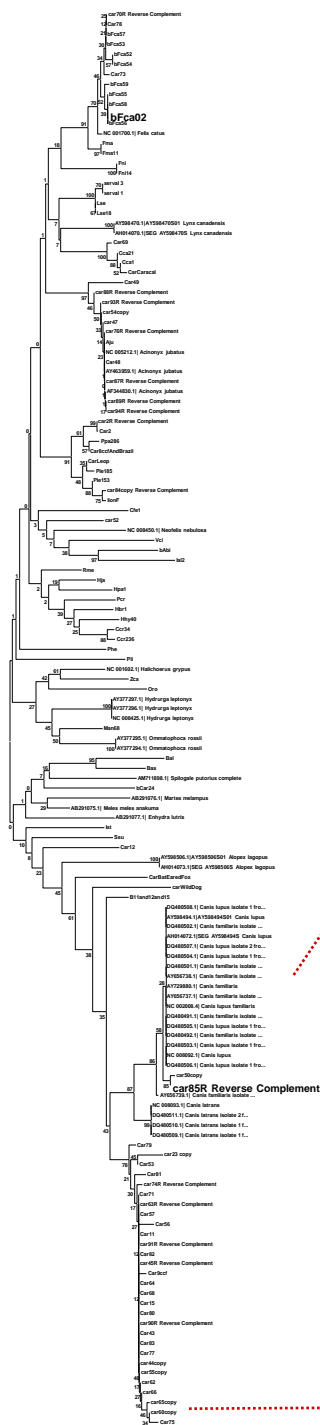
Testing and optimization of protocols for African carnivores:
Partnership with CCF, Namibia.











Current challenges for large-scale DNA barcoding of Neotropical mammals:

1. Samples with no vouchers (especially medium-sized and large species).
2. Museum vouchers with no tissue samples.
3. Unsampled species.
4. Poor geographic coverage for most species.
5. Taxonomically complex taxa (need for thorough revision).
6. Lack of manpower, lack of large-scale funding.

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