DNA barcodes foster collaborative networking in Argentina: from evolutionary biology to invasive species and pathogen identification in food production

Lavinia, P.D.; Attiná, N.; Luszczak, P.; Núñez Bustos, E.; Canio, E.; Casale, A.; Bukowski, B.; Hünicken, L.; Moreno, P.; Campagna, L.; Lijtmaer, D.A. & Tubaro, P.L.

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CENTRO DE INVESTIGACIÓN APLICADA Y TRANSFERENCIA TECNOLÓGICA EN RECURSOS MARINOS ALMIRANTE STORNI • CIMAS •

Objective

Use the case of Argentina to illustrate how the DNA barcoding initiative promotes collaborative networking, contributing with new, meaningful insights in the fields of evolutionary biology, biological invasions and food production.

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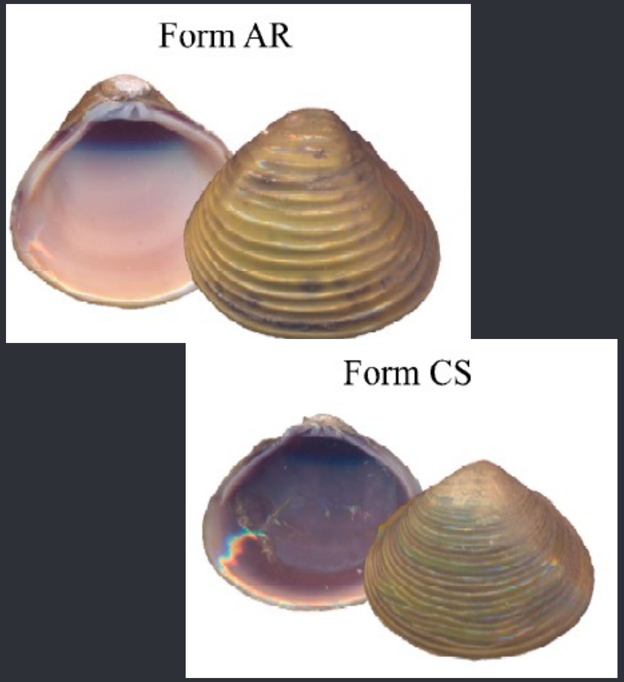

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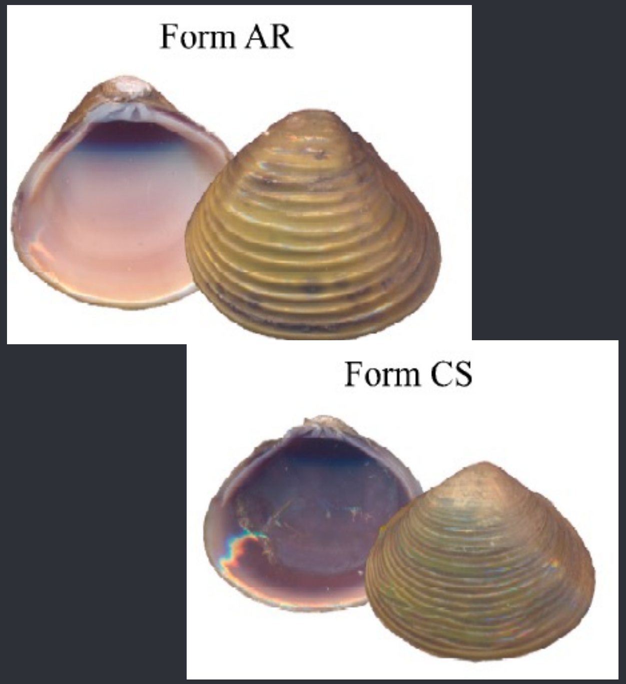

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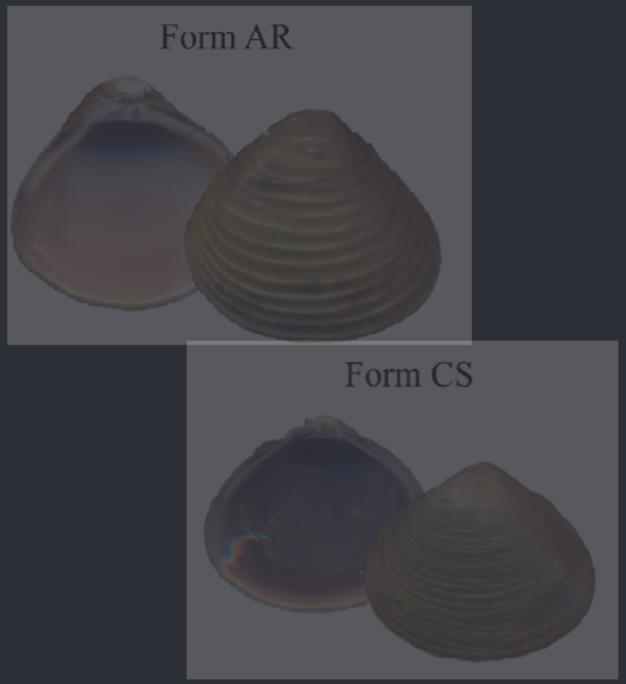
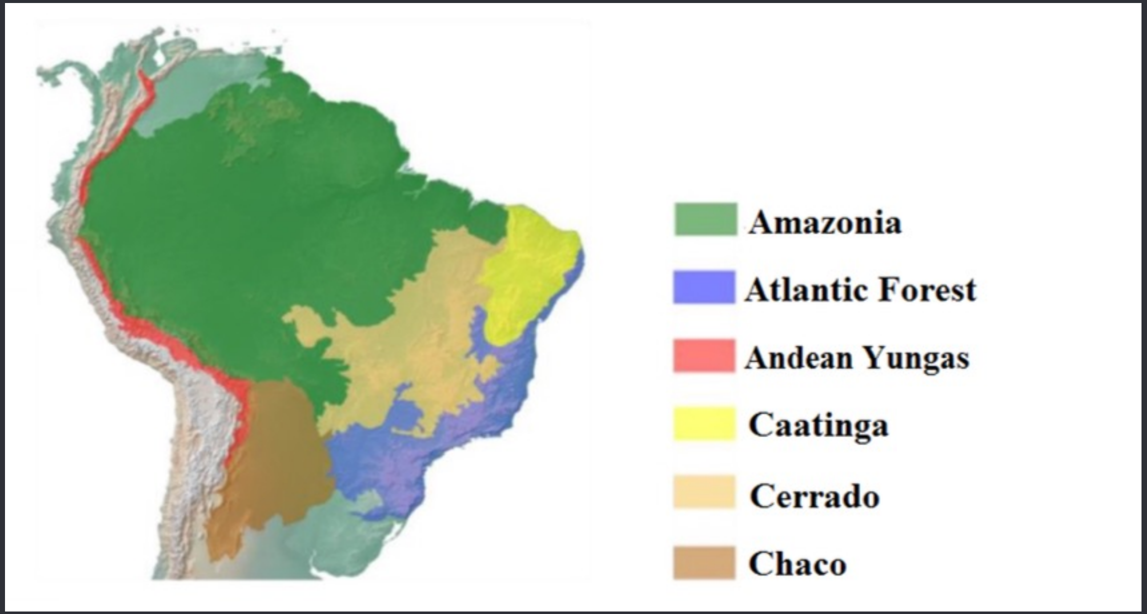


Large-scale analysis of intraspecific divergence among bird and butterfly populations of geographical isolated forests

The Atlantic Forest is currently isolated from Amazonia and the Andean forest by the more open and drier environments of the OVC.

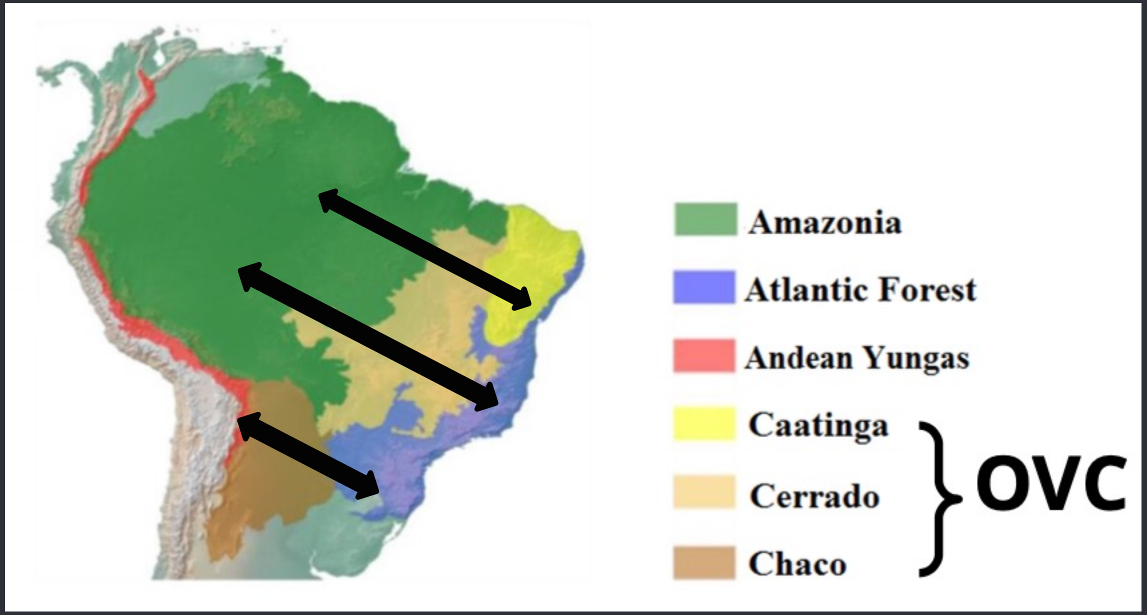


Large-scale analysis of intraspecific divergence among bird and butterfly populations of geographical isolated forests

The Atlantic Forest is currently isolated from Amazonia and the Andean forest by the more open and drier environments of the OVC.

Transiently and cyclically connected in the past, throughout the Neogene and Quaternary.

The OVC and the hystorical connections and disconnections between forest have affected their shared fauna.



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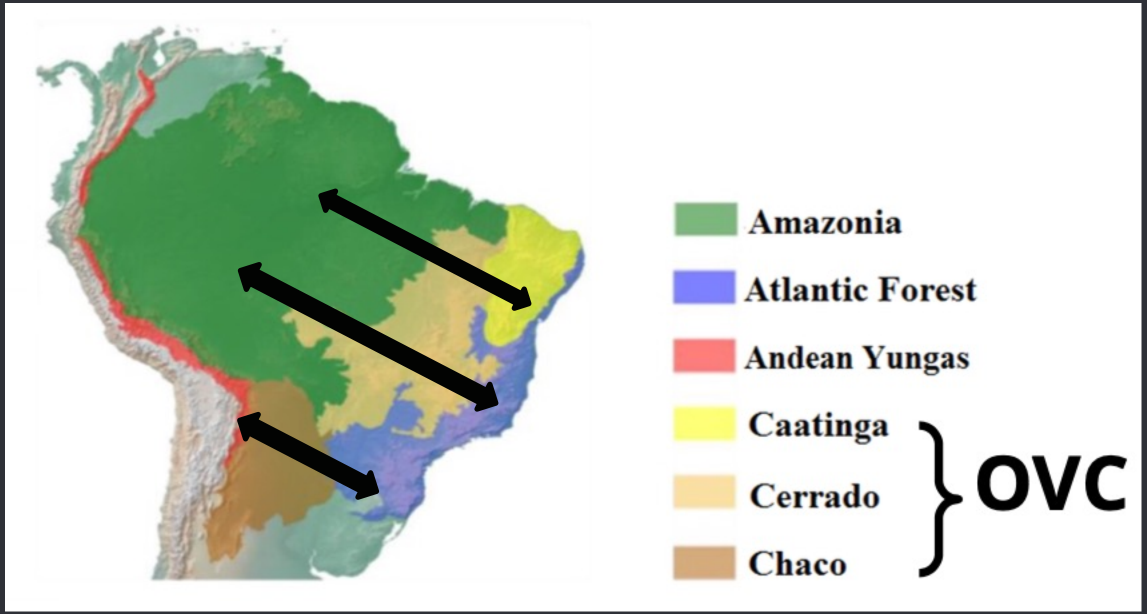


Are differences among species in the patterns of intraspecific variation across the OVC associated to their biological attributes?

Large-scale analysis of intraspecific divergence among bird and butterfly populations of geographical isolated forests

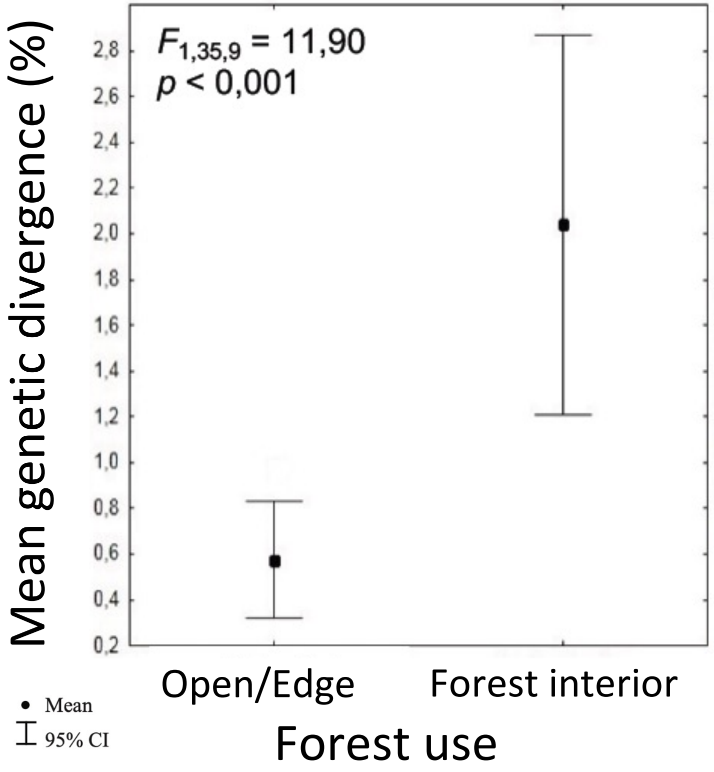
We estimated and compared instraspecific divergence at COI between populations east and west of the OVC.

Birds: 696 sequences representing 72 species

Butterflies: 887 sequences representing 85 species

We assessed whether species traits can predict the patterns of intraspecific divergence across the OVC.

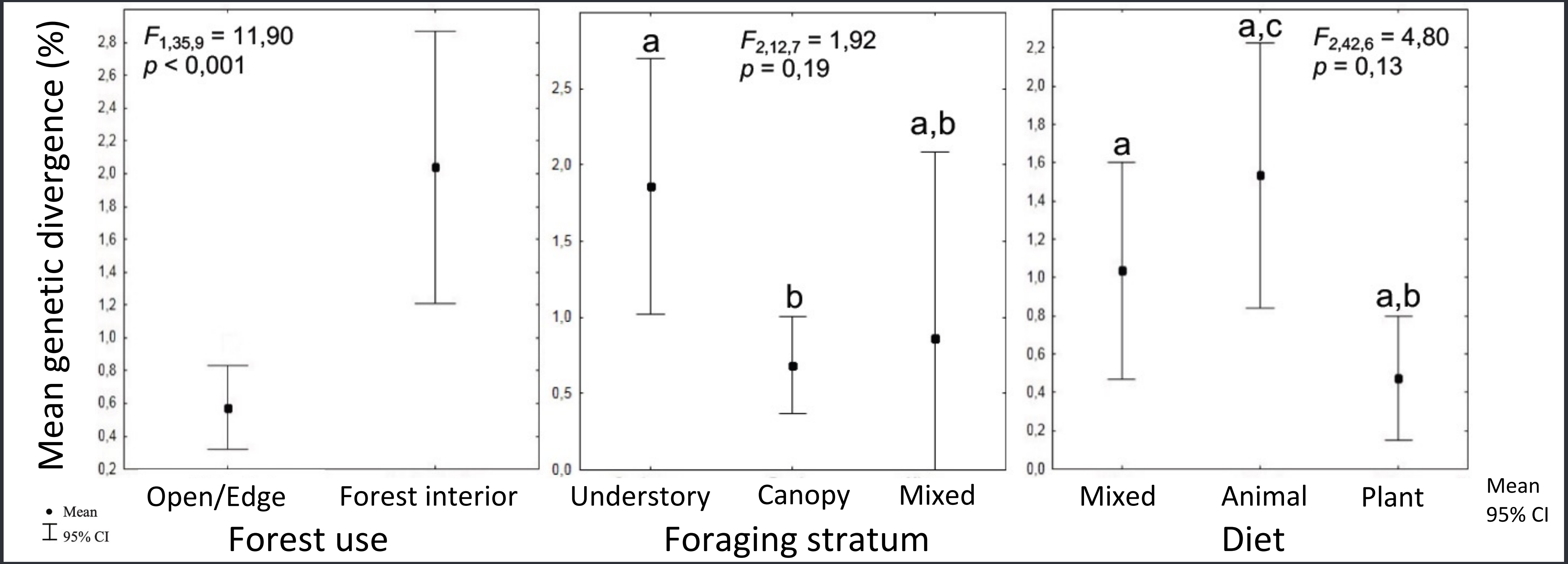
Birds



- Habitat dependence: intraspecific genetic distance across the OVC was significantly higher among forest specialists than among species that are also capable of inhabiting more open environments.

Undergrad thesis
(Spanish)

Birds



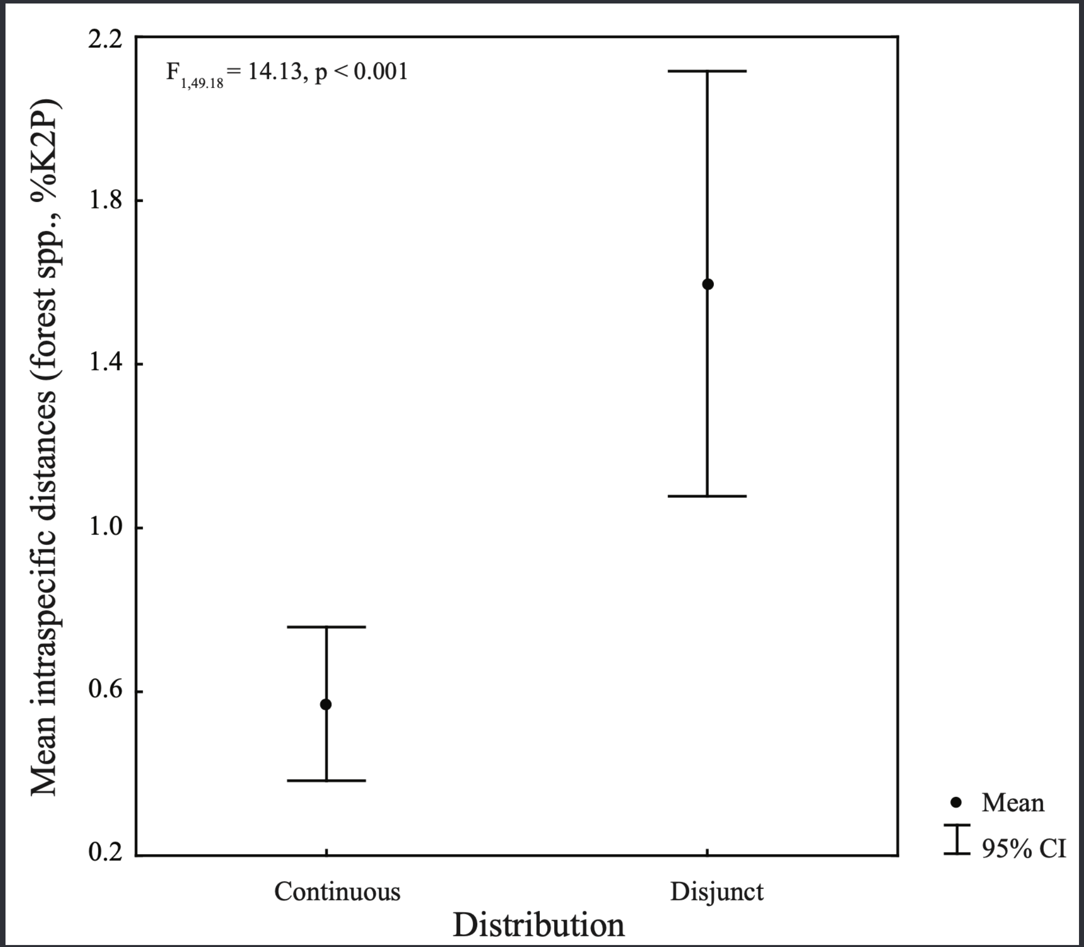
Undergrad thesis (Spanish)

- Habitat dependence: intraspecific genetic distance across the OVC was significantly higher among forest specialists than among species that are also capable of inhabiting more open environments.

- Foraging stratum and diet: understory species that feed on animals had a significantly higher intraspecific genetic distance across the OVC than those that feed on plant products and forage in the canopy.

Butterflies

Genetic distance across the OVC was significantly higher for the species with disjunct distributions between isolated forests than among those with a continuous range.



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RESOURCE ARTICLE

MOLECULAR ECOLOGY RESOURCES WILEY

Genetic variation in neotropical butterflies is associated with sampling scale, species distributions, and historical forest dynamics

Natalí Attiná[1] | Ezequiel O. Núñez Bustos[1] | Darío A. Lijtmaer[1] | Paul D. N. Hebert[2] | Pablo L. Tubaro[1] | Pablo D. Lavinia[1,3]

Butterflies

Genetic distance across the OVC was significantly higher for the species with disjunct distributions between isolated forests than among those with a continuous range.

Distribution as an ecological prior: species with disjunct ranges represent forest specialists for which the OVC constitutes a more critical barrier to dispersal and gene flow.

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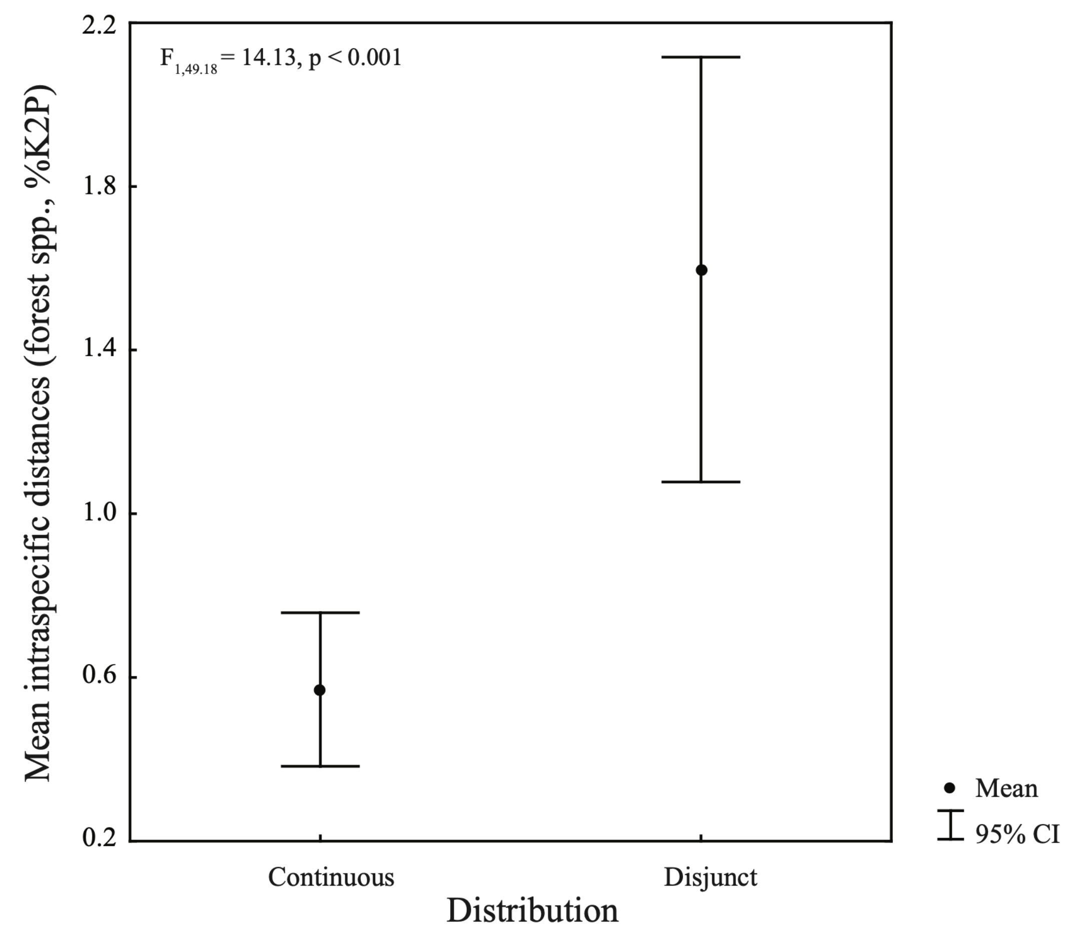

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Large-scale analysis of intraspecific divergence among bird and butterfly populations of geographical isolated forests

Main conclusions

1. Biological atributes do play a key role in the diversification history of neotropical fauna.

2. The OVC differentially affects the species depending on their attributes, being a more important barrier to dispersal for forest specialists, understory species and those that feed on animals.

Diversity screenings of DNA barcodes highlight the effect of Pleistocene glaciations in the Andean-Patagonian avifauna

The avifauna of Patagonia has been much less studied

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Patagonia is arguably one of the regions most heavily impacted by widely recognized diversification drivers.

Pleistocene glaciations: alternating series of glacial (cold and dry) and interglacial (hot and warm) periods during the last ~2.5 My.

Retreat and expansion vs *in situ* divergence models

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Diversity screenings of DNA barcodes highlight the effect of Pleistocene glaciations in the Andean-Patagonian avifauna

Rufous-collared Sparrow
(*Zonotrichia capensis*)

Southern Lapwing
(*Vanellus chilensis*)

House Wren
(*Troglodytes aedon*)

Plain-mantled Tit-Spinetail
(*Leptasthenura aegithaloides*)

Diuca finch
(*Diuca diuca*)

Blog post (preliminary, outdated results)

Published paper

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Pleistocene glaciations seem to have played a major role in isolating southern populations and promoting diversification within Patagonia during the last two million years.

Populations resumed gene flow after glacial retreat through the northward expansion of southern populations, homogenizing nuclear but not mtDNA.

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The Diuca finch shows a contrasting pattern: two mtDNA lineages that seemed to have diverged elsewhere and colonized Patagonia from two different routes, without resuming gene flow.

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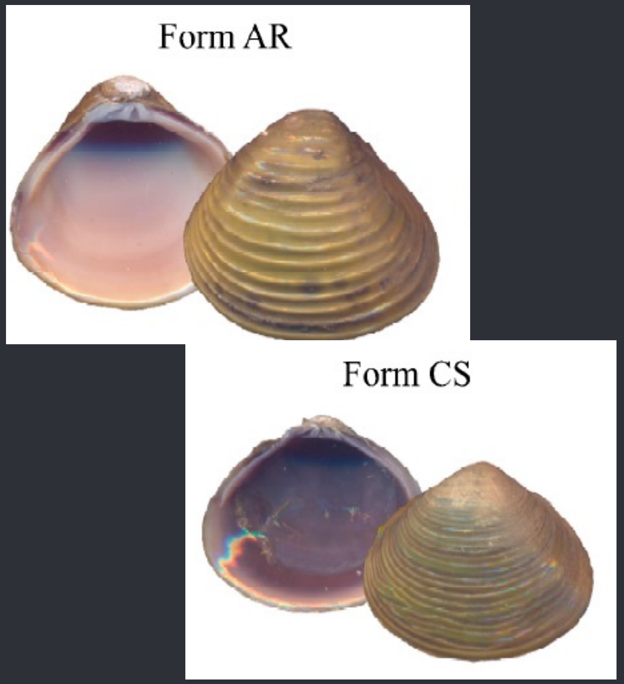
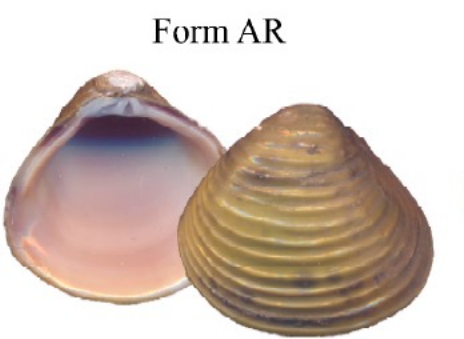
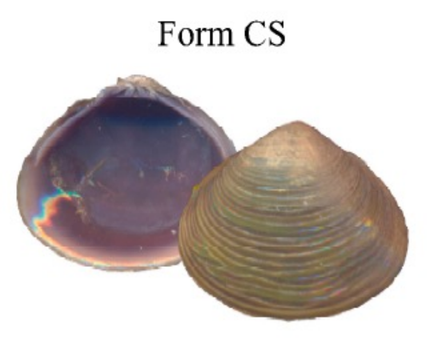


DNA barcodes provide new insights into the expansion of the invasive *Corbicula* clams in Argentina and reveal individuals of hybrids origin

Freshwaters clams native to Africa, Asia, Australia and the Middle east. Invasive in Europe and America.


Form AR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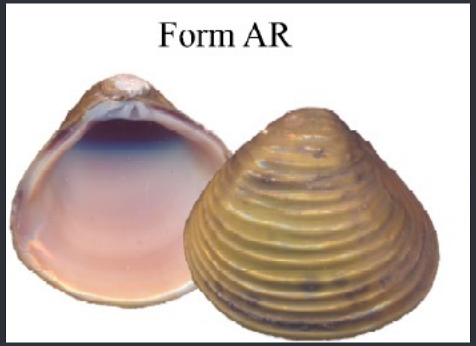
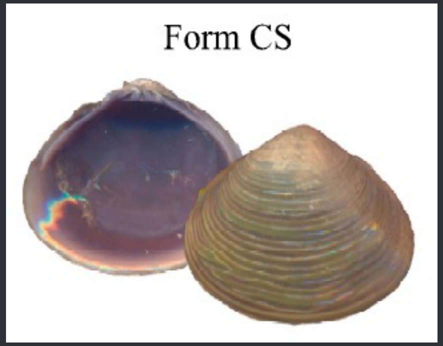
Intrincate taxonomy: consensus to use ”forms” and lineages or haplogroups to describe the different “species”



FW5



FW17

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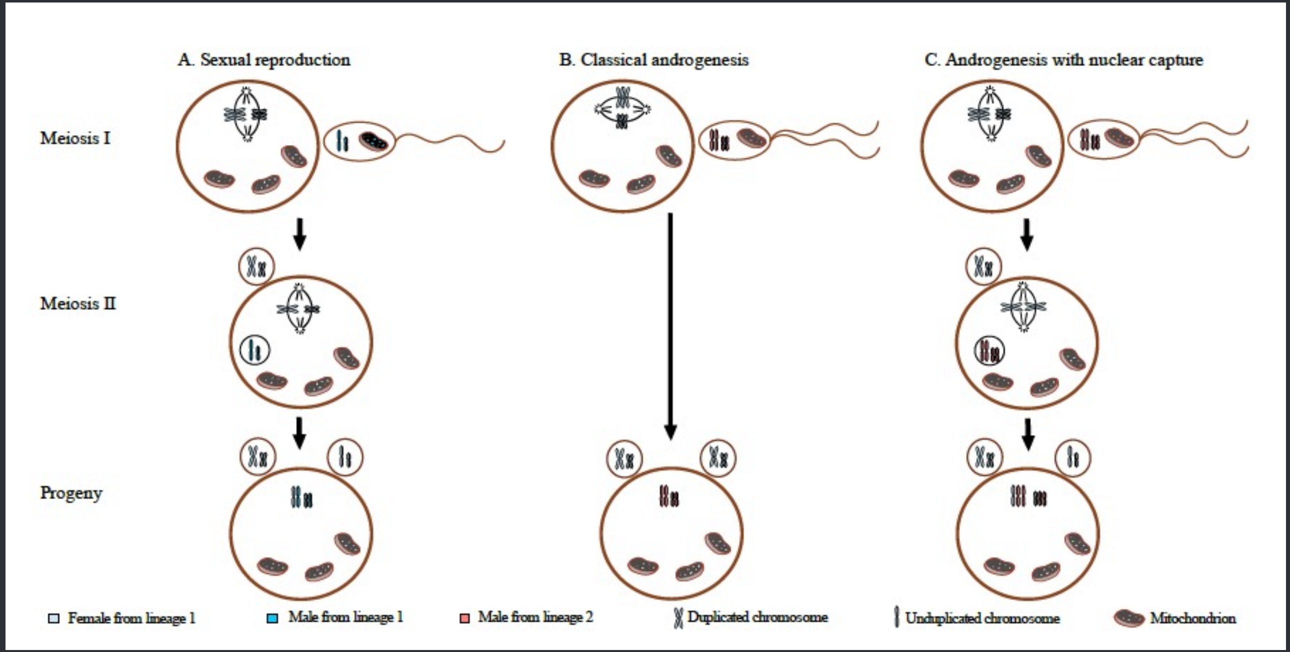
Native range: dioecious sexual and hermaphroditic androgenetic “species” coexist.

Invasive range: exclusively hermaphroditic androgenetic “species”



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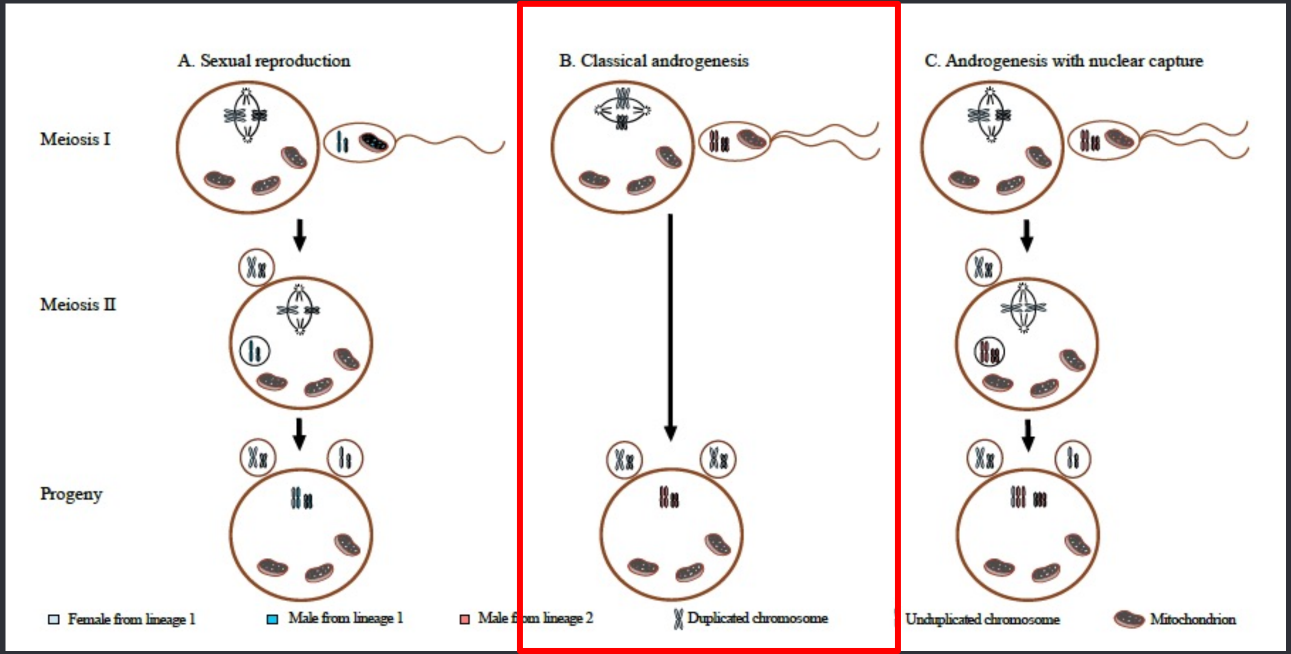

Androgenesis: maternal nuclear DNA is extruded after fertilization and the progeny is diploid from paternal nuclear DNA, but retains maternal mtDNA.

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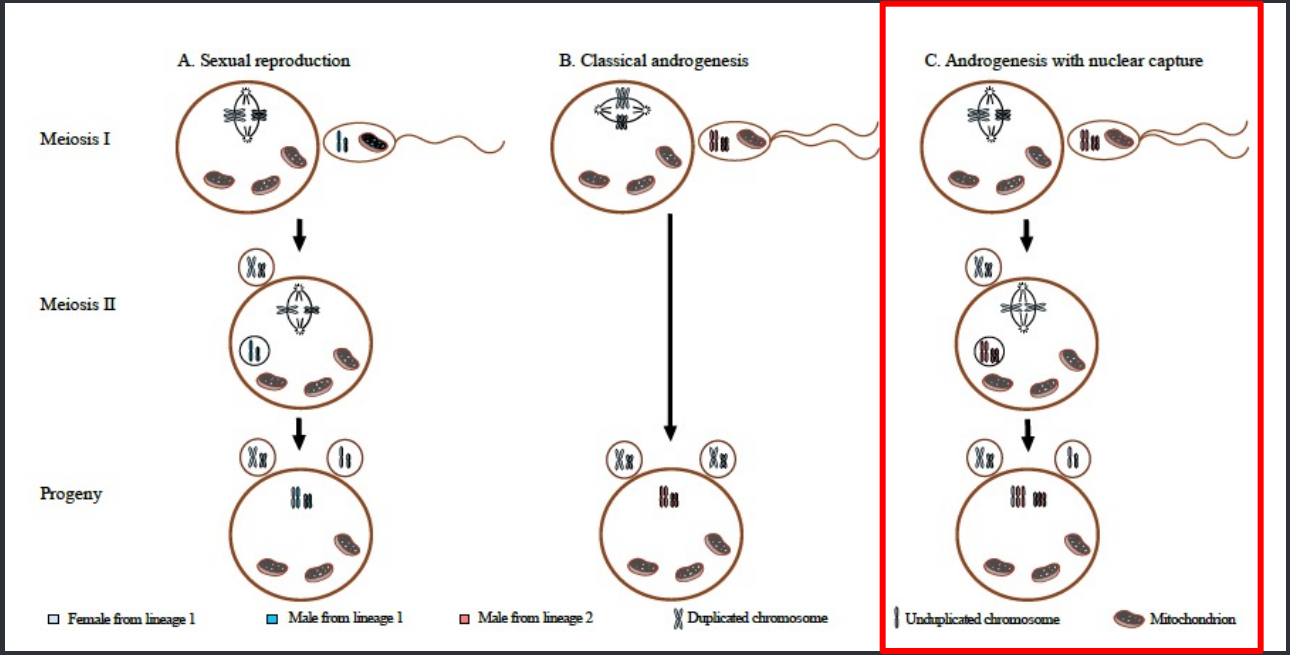

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Nuclear capture: triploid progeny due to partial retention of maternal nuDNA; if occurs between lineages = hybridization (leads to intermediate forms)

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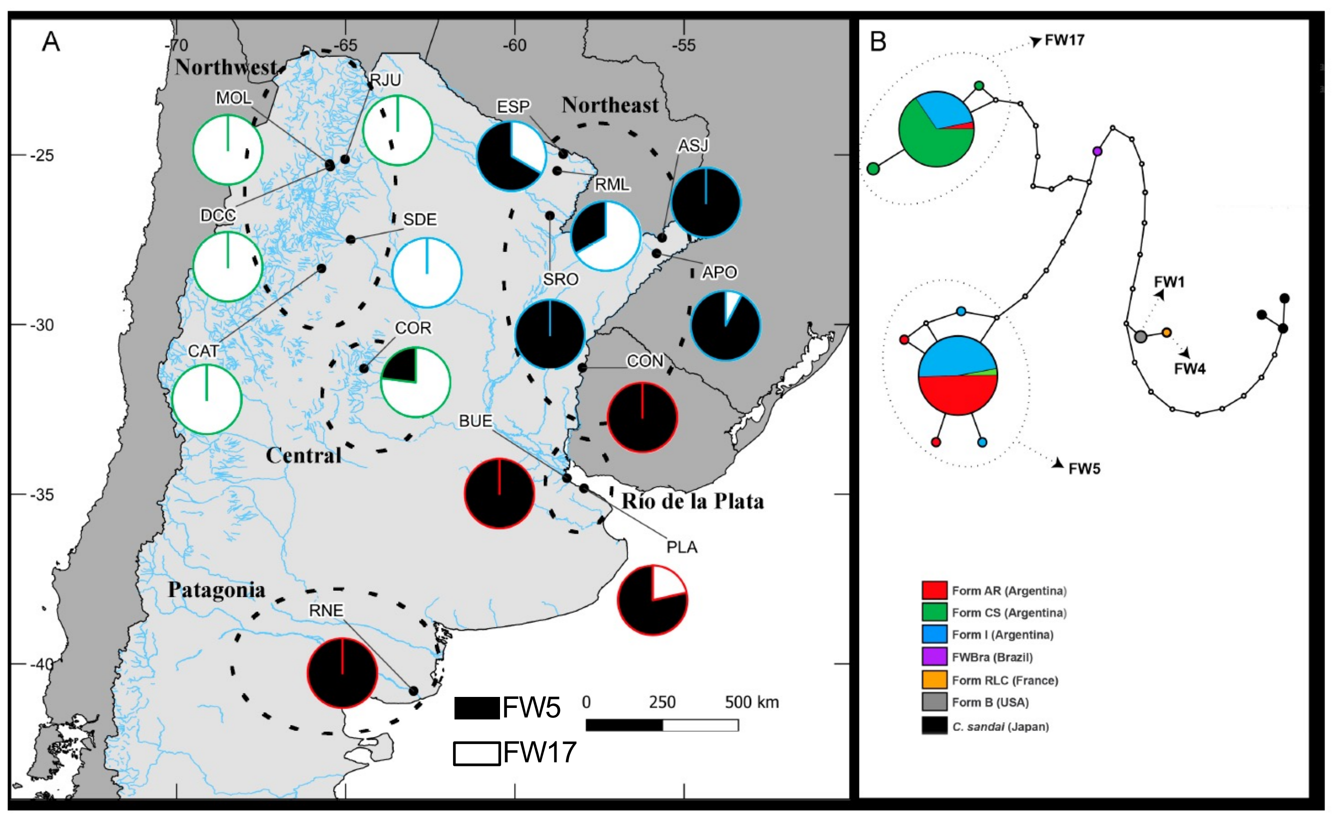

Article

Morphological and Genetic Assessment of Invasive *Corbicula* Lineages in Southern South America: A Case Study in Argentina

Leandro A. Hünicken [1,2,3,*,†], Esteban M. Paolucci [1,2], Pablo D. Lavinia [1,4,5] and Francisco Sylvester [1,3,6]

210 specimens sampled across 15 localities

All samples clustered within two of the four major invasive FW mitochondrial lineages: FW5 and FW17

FW5 and FW17 were virtually segregated, except in northeastern ARG were they were found in sympatry

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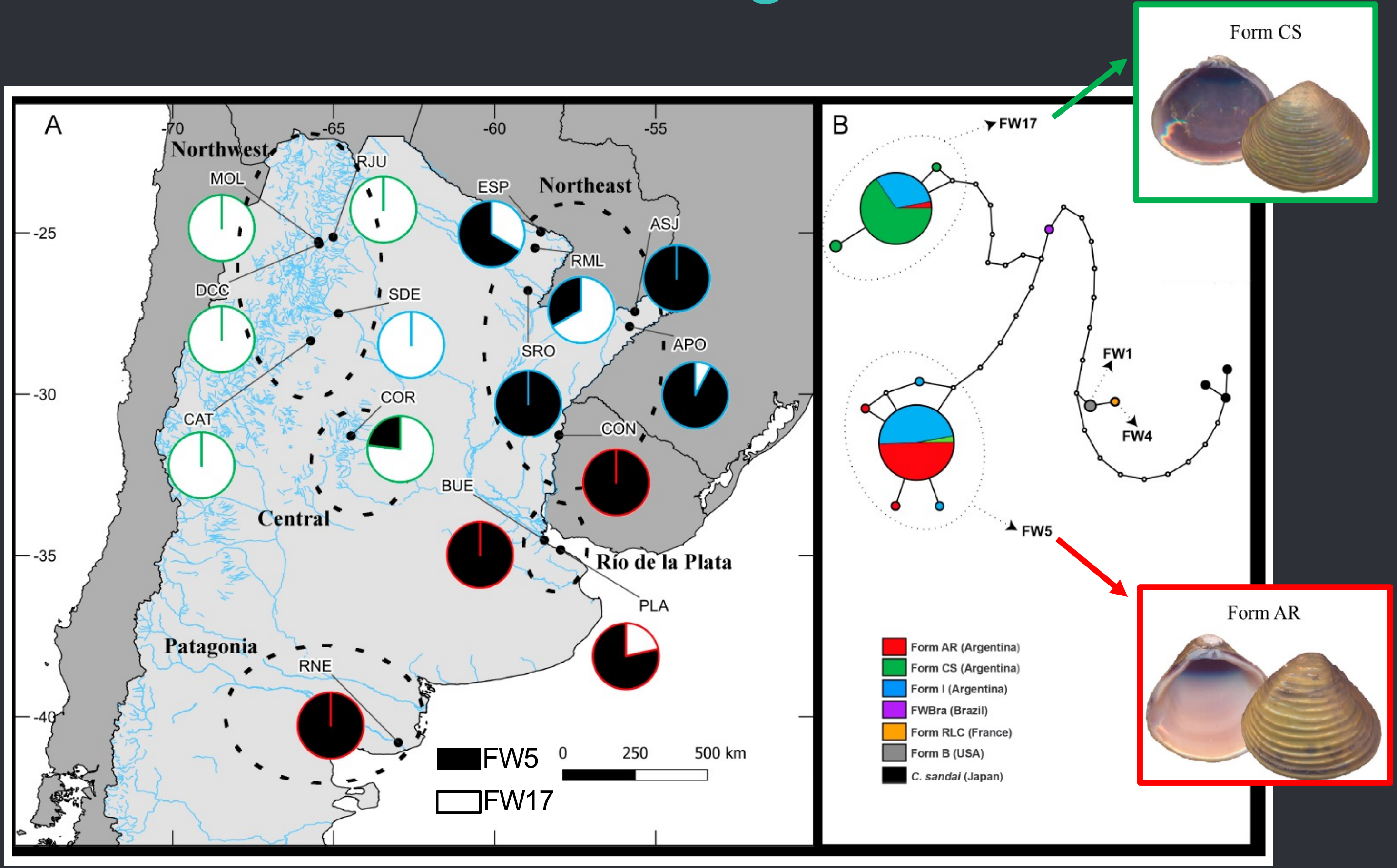

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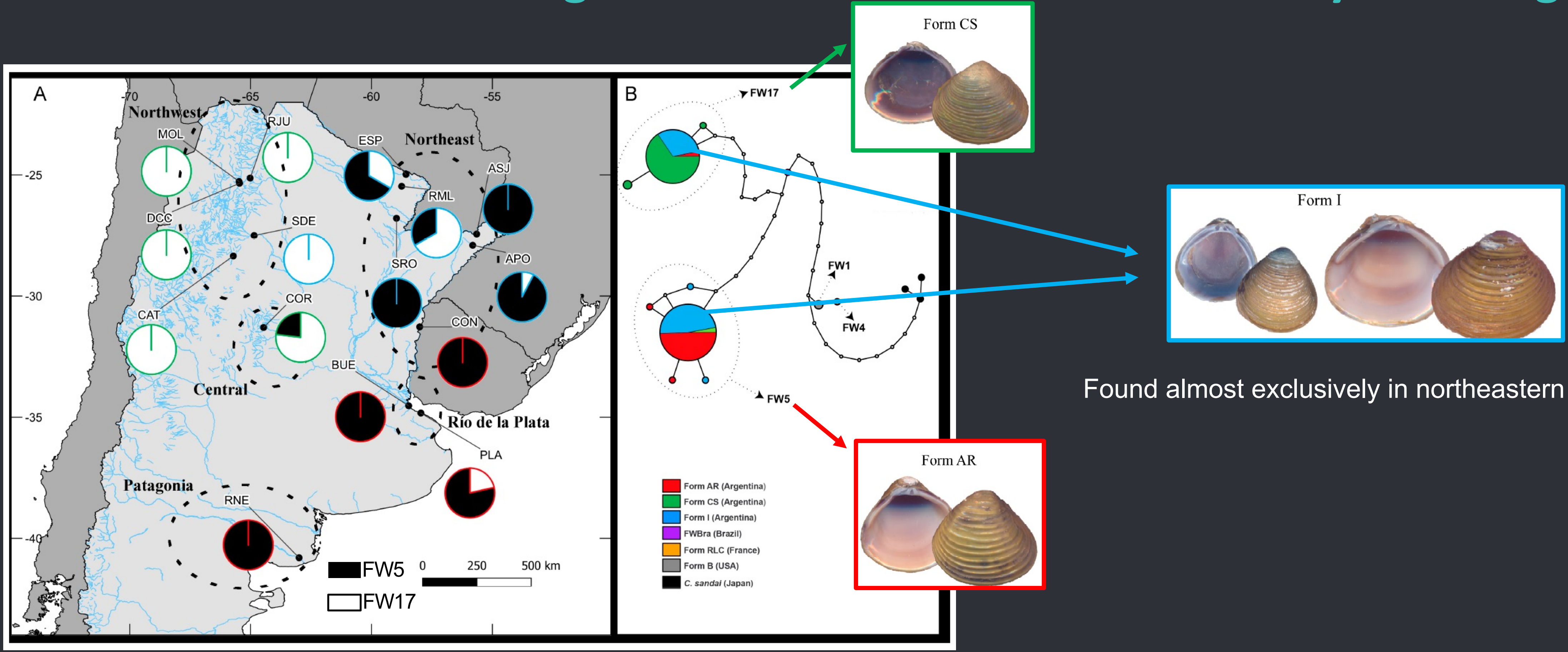

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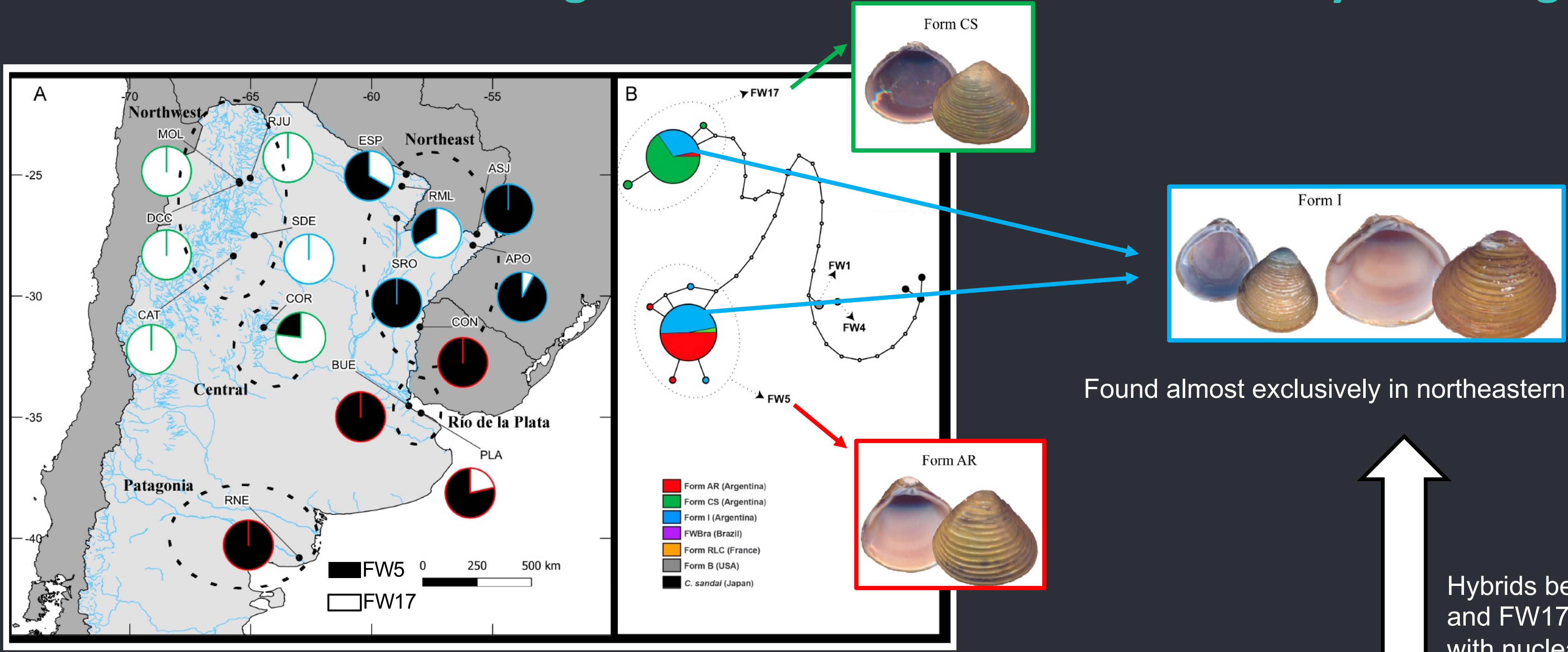

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Hybrids between FW5 and FW17 (androgenesis with nuclear capture of maternal DNA)

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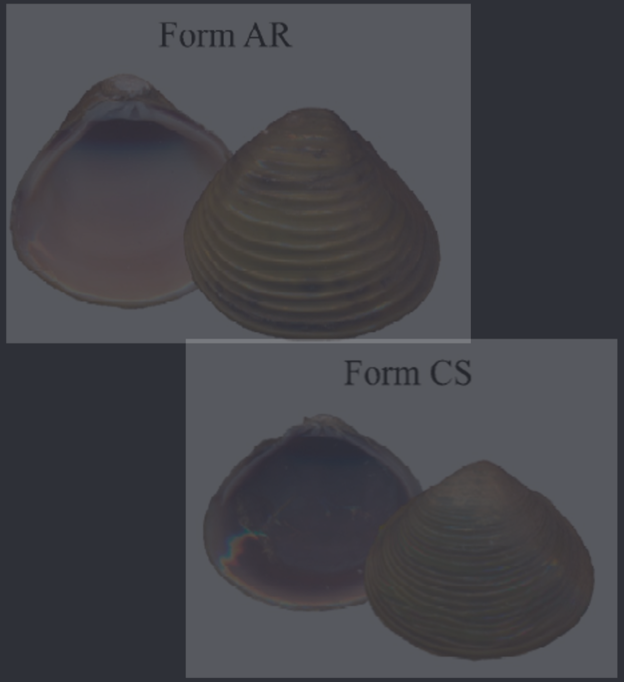

DNA barcodes aid pathogen identification in fish aquaculture

Ph.D. Thesis
(Spanish)

The CEAN fish farming station breeds differents species of salmonids, which are commonly infected by Oomycetes.

These are protists that affect fishes at all stages, causing mortality and economic losses.

DNA barcodes aid pathogen identification in fish aquaculture

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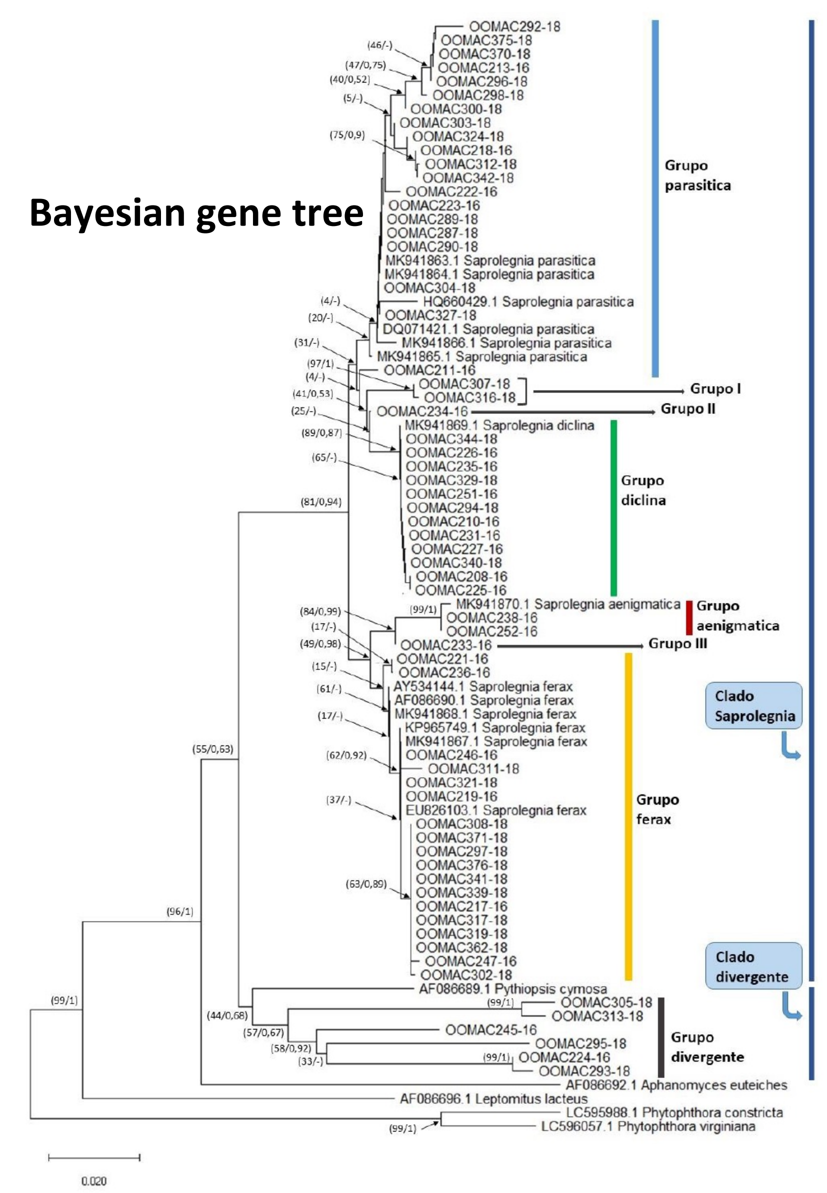
Bayesian gene tree

The CEAN fish farming station breeds differents species of salmonids, which are commonly infected by Oomycetes.

Oomycetes (order Saprolegniales) are protists pathogens that affect farmed (and wild) fishes at all stages, causing mortality.

To aid in the control of this pathogenes, we amplified CO2 from 62 isolated protists and assessed the efficiency of DNA barcodes for the spececies identification.

The majority of samples corresponded to four species of *Saprolegnia,* the most common genus of Oomycetes.

Six samples corresponded most likely to 3-4 undescribed species or genera.

General conclusions

DNA barcodes analyses contributes with new, meaningful insights in the fields of evolutionary biology, biological invasions and food production.

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In Argentina, the DNA barcoding initiative fosters collaborative, interdisciplinary networking among local researchers.

DNA barcodes have been key components of undergradute and Ph.D. thesis, contributing to the academic formation of new professionals.

Acknowledgements

Collaborators

Members of the “expanded” Ornithology research group (MACN–UNRN)

- International collaborators
- Field assistants and staff of the different Institutions involved


Pablo Tubaro


Darío Lijtmaer


Belén Bukowski


Elvira Canio

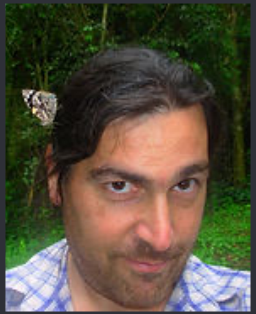

Leandro Hünicken


Priscila Luszczak


Agustín Casale


Leo Campagna


Natalí Attiná


Ezequiel Núñez Bustos


Pablo Moreno

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- Genome Canada
- IDRC
- Lounsbery Foundation
- UNRN
- Aves Argentinas

Thank you for your attention!

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ResearchGate

Youtube video (Spanish)