9TH INTERNATIONAL BARCODE OF LIFE CONFERENCE

THE ROLE OF GLACIAL CYCLES ON THE DIVERSIFICATION AND SPECIATION OF THE BIRDS OF SOUTHERN SOUTH AMERICA

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Background

- Studies of evolutionary biology in the Neotropics have focused mainly in areas of low latitude (Amazonia, northwest of South America, and the Atlantic Forest).

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Southern South America, and specifically the southern Andes and Patagonia, have been much less studied (in particular in relation to its avifauna).

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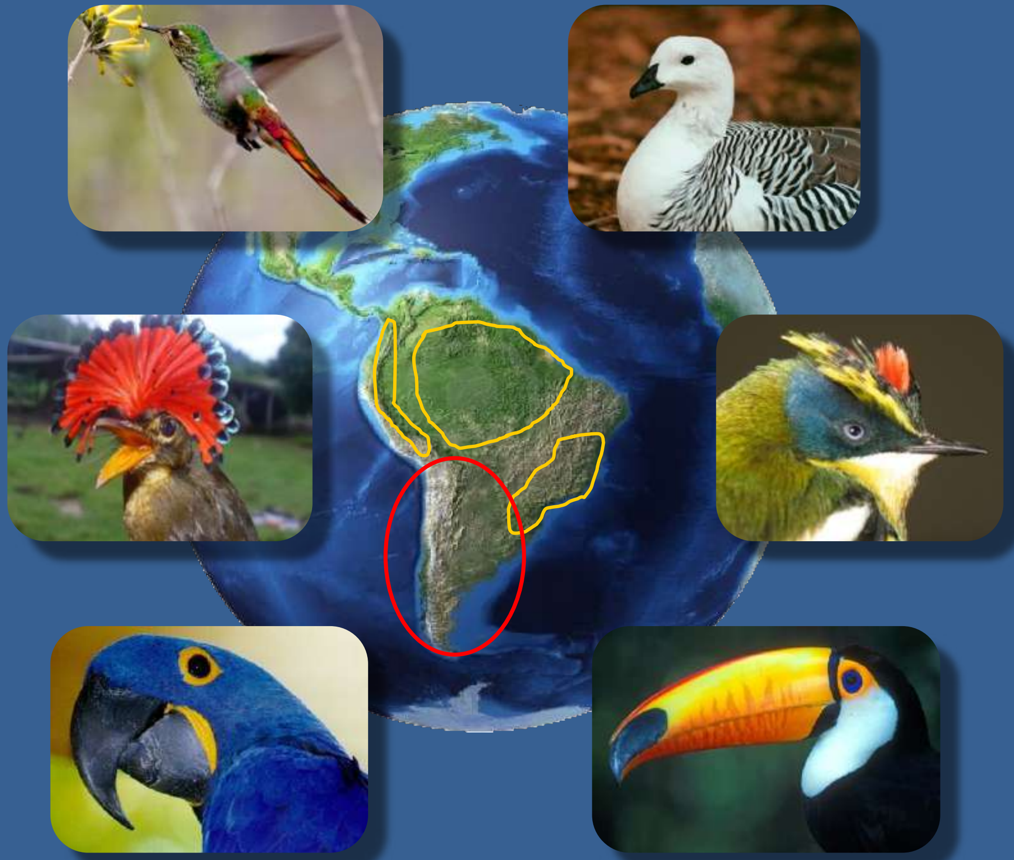

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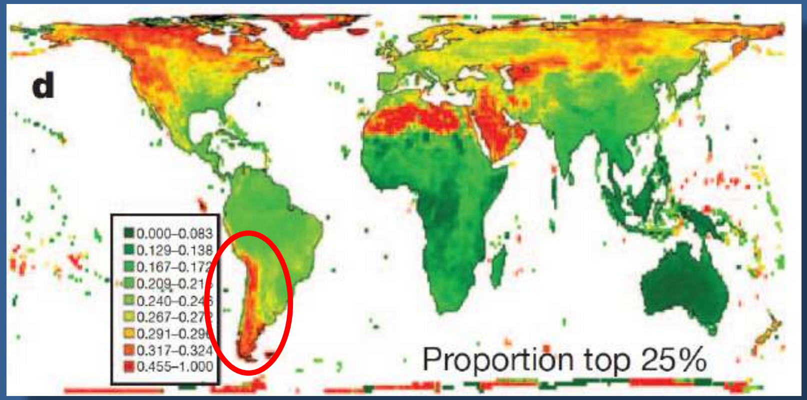
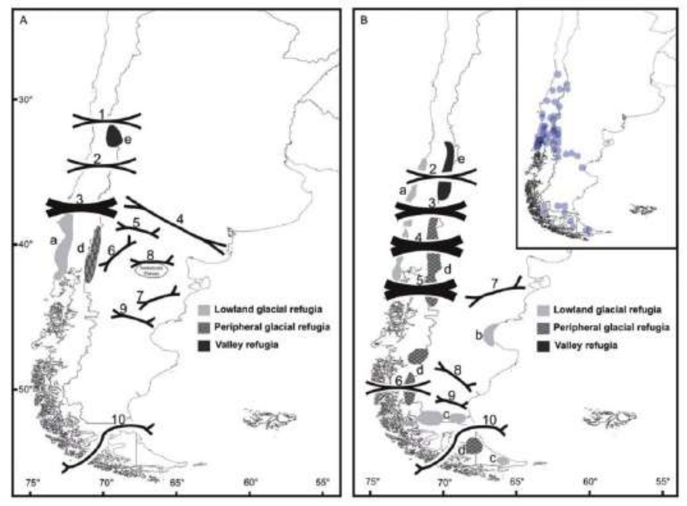
It is not clear whether the patterns described for the rest of the Neotropics hold for the southern extreme of the continent…



Jetz et al. 2012, Nature 491: 444 - 448.



Sérsic et al. 2011, BJLS 103: 475 - 494.

Two complementary approaches

We are studying the diversification and speciation of Neotropical birds with a focus on Patagonian populations at two different, complementary scales.

1. Large scale analysis with DNA barcodes.

2. Study of particular species with large distributions with a focus on Patagonia.

Southern Lapwing
(*Vanellus chilensis*)

House Wren
(*Troglodytes aedon*)

Rufous-collared Sparrow
(*Zonotrichia capensis*)

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1. Large scale analysis with DNA barcodes. → Results suggest a relevant role of glacial cycles in the southern Andes and Patagonia.
2. Study of particular species with large distributions with a focus on Patagonia.

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Study of particular species

Different approach: to study species with large distributions to analyze their evolutionary patterns with a focus on Patagonia

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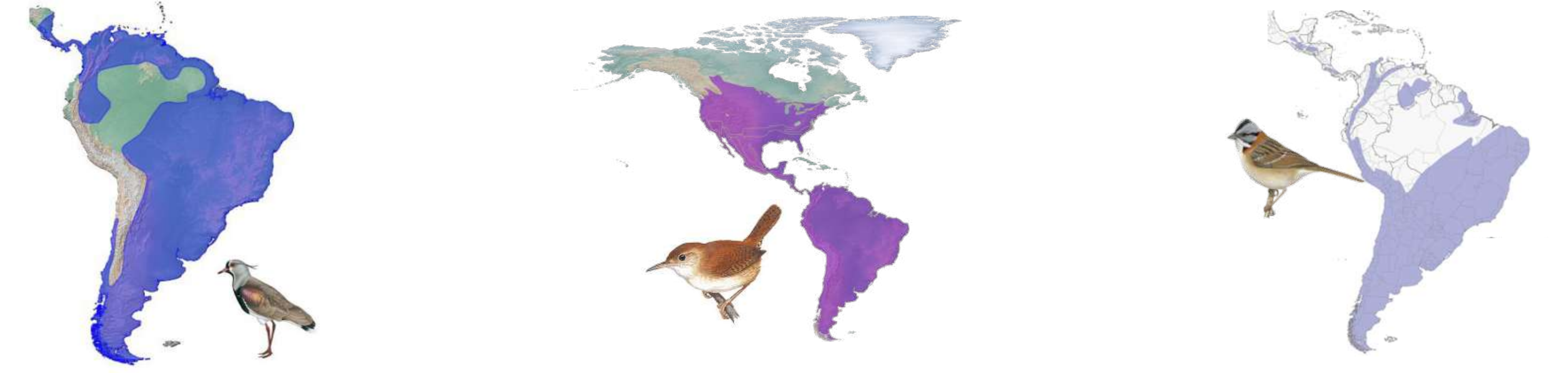
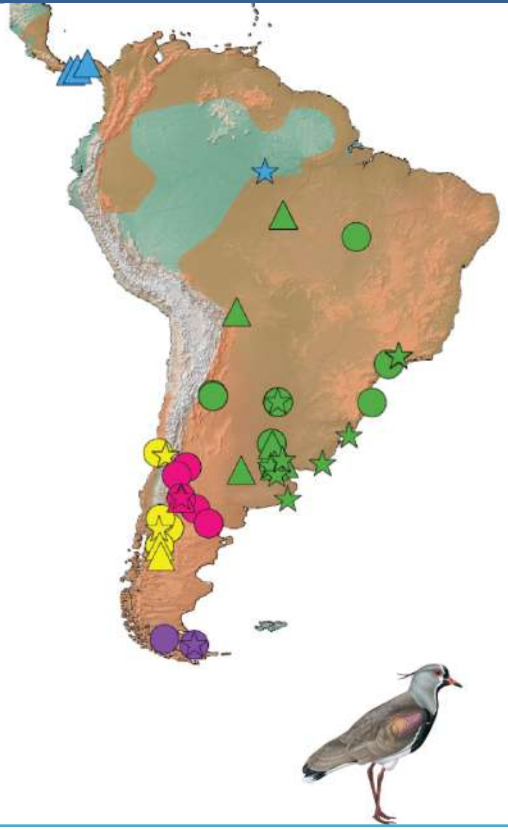
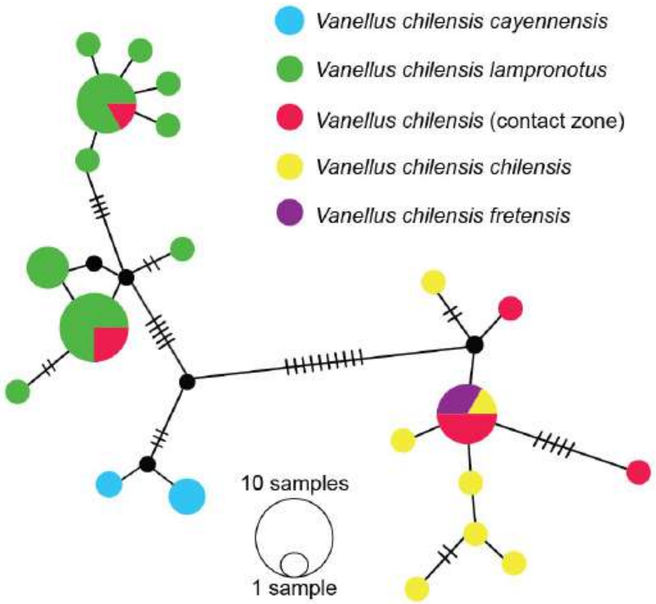
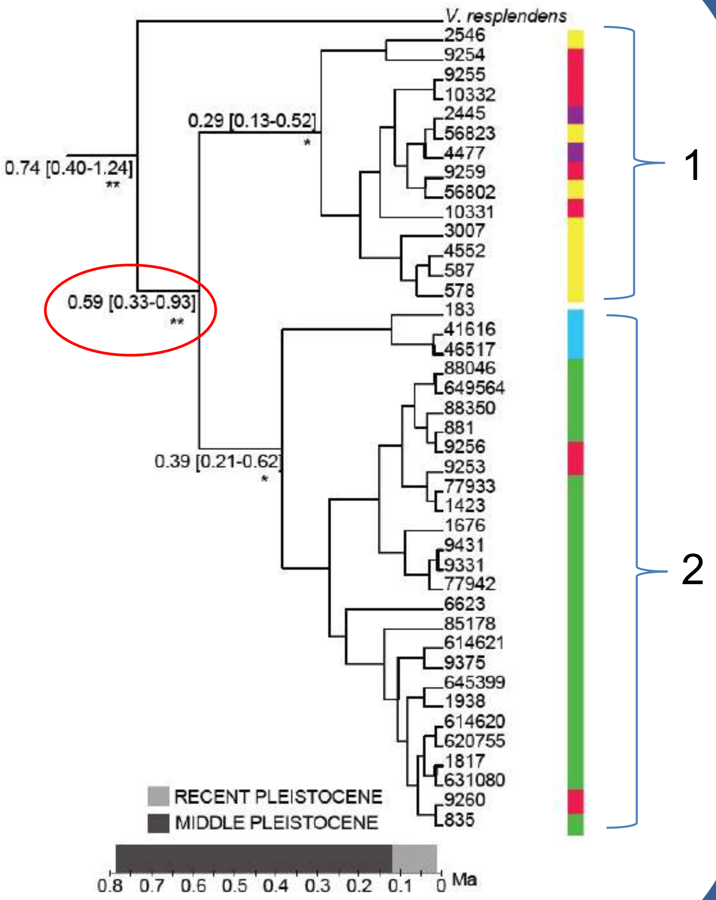


Southern Lapwing: Mitochondrial DNA (COI barcode fragment + cyt b)

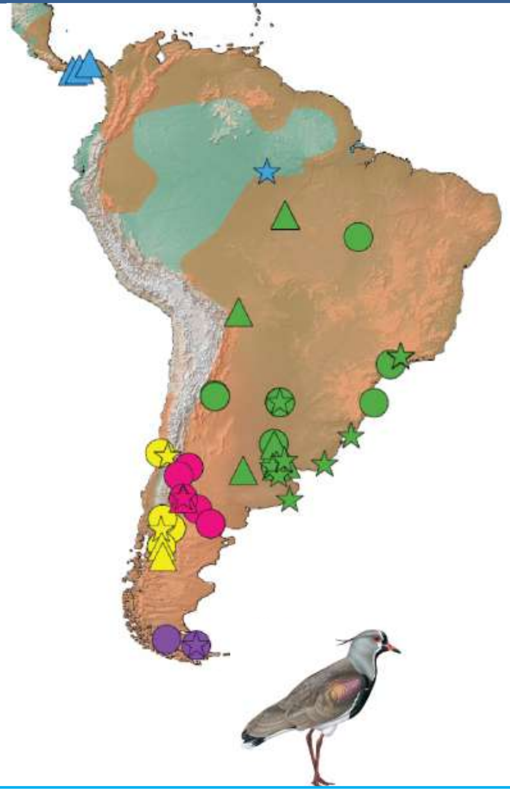




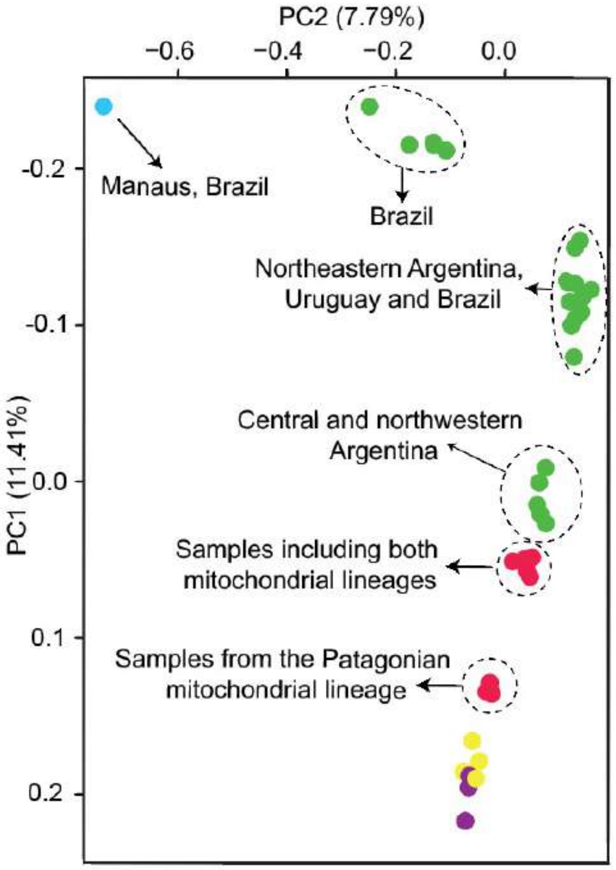


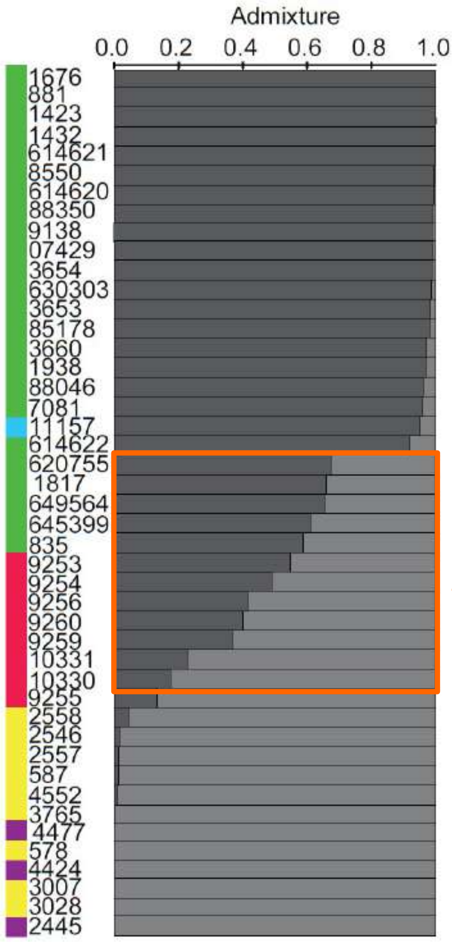
Two main mitochondrial lineages with 1.5% mean genetic distance that diverged around 600,000 years ago

Southern Lapwing: Nuclear genomic DNA



Extensive gene flow between the Patagonian lineage and the rest of the species distribution

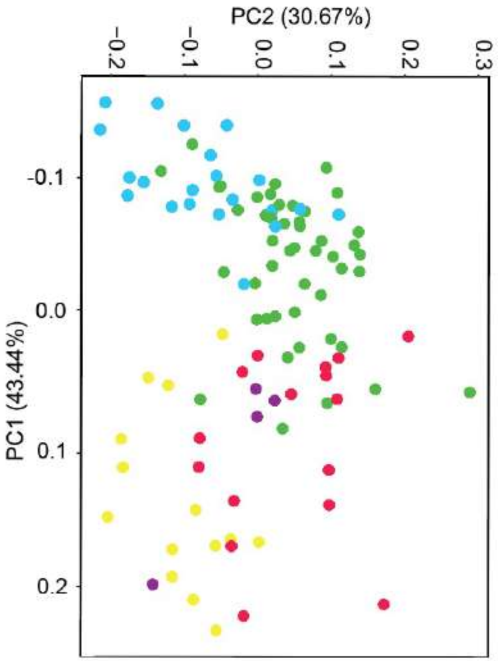


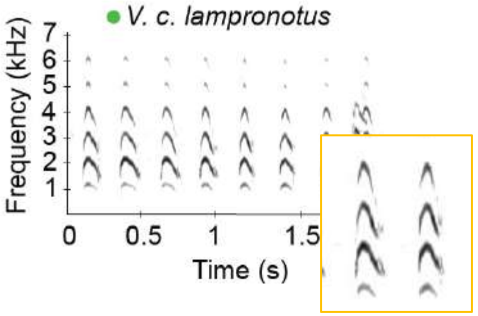


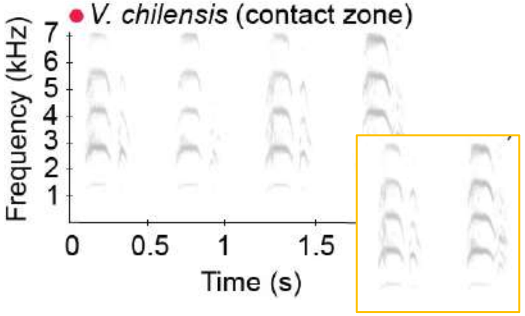
Genomic admixture

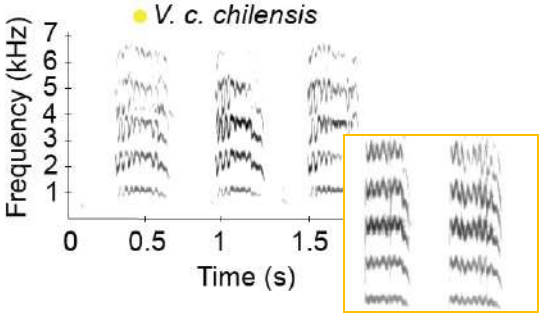
Southern Lapwing: Vocalizations

Vocalizations differ between the two main lineages and are intermediate in the contact zone

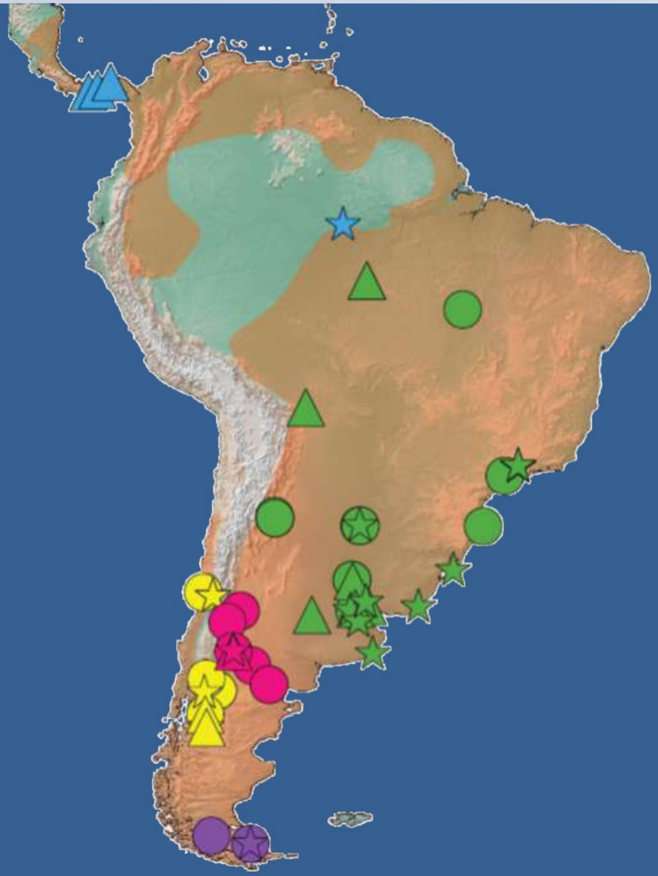








Southern Lapwing: Evolutionary scenario

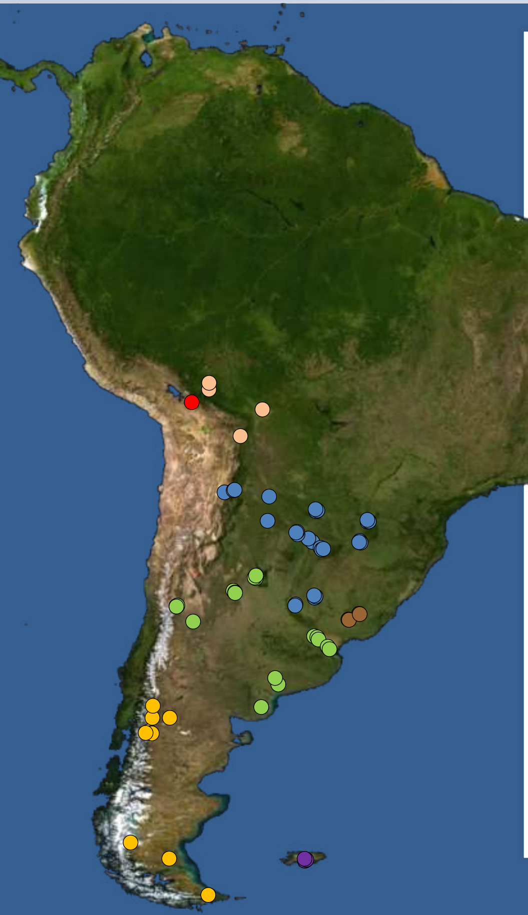


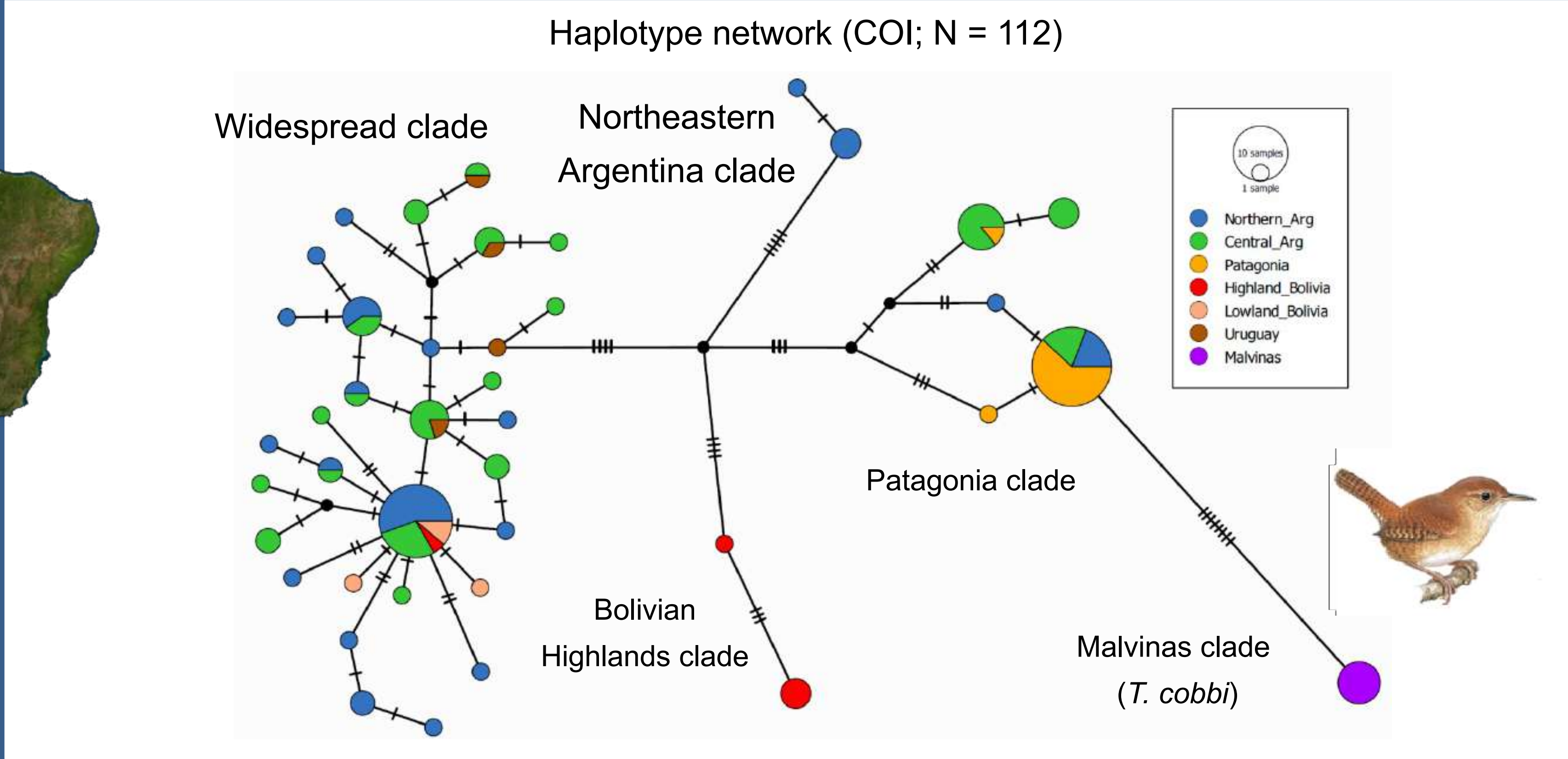
- Glacial periods isolated the Patagonian populations around 600,000 years ago.

- After the glacial cycles these populations expanded northwards and entered into secondary contact with the other lineage in northern Patagonia.

- There is extensive gene flow among lineages in the area, as well as intermediate vocalizations.

House wren species complex: COI barcode data



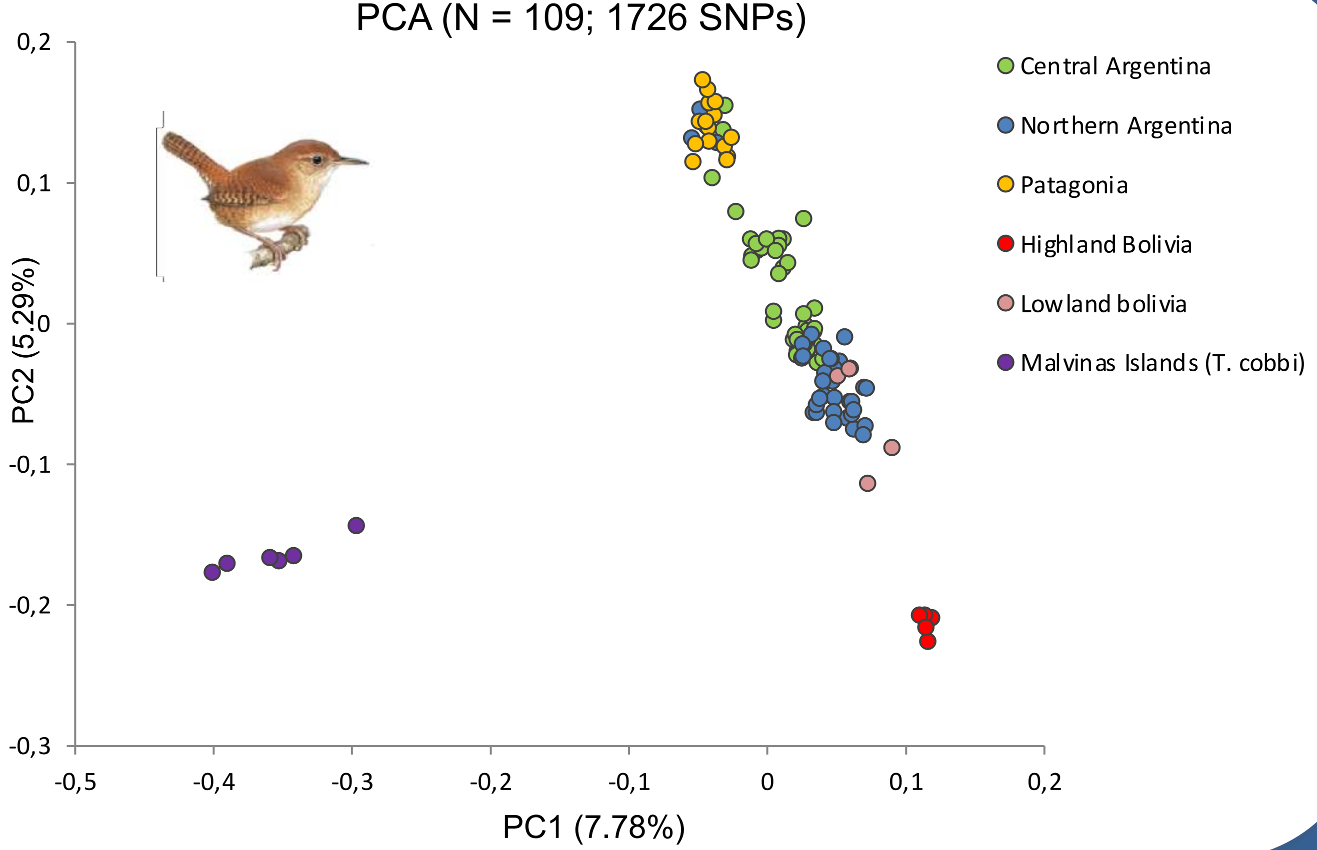


Haplotype network (COI; N = 112)

There are 5 mitochondrial clades, with sequence divergences as high as 5%.

T. Cobbi appears as the sister lineage to the Patagonian clade.

House wren species complex: Nuclear genomic data



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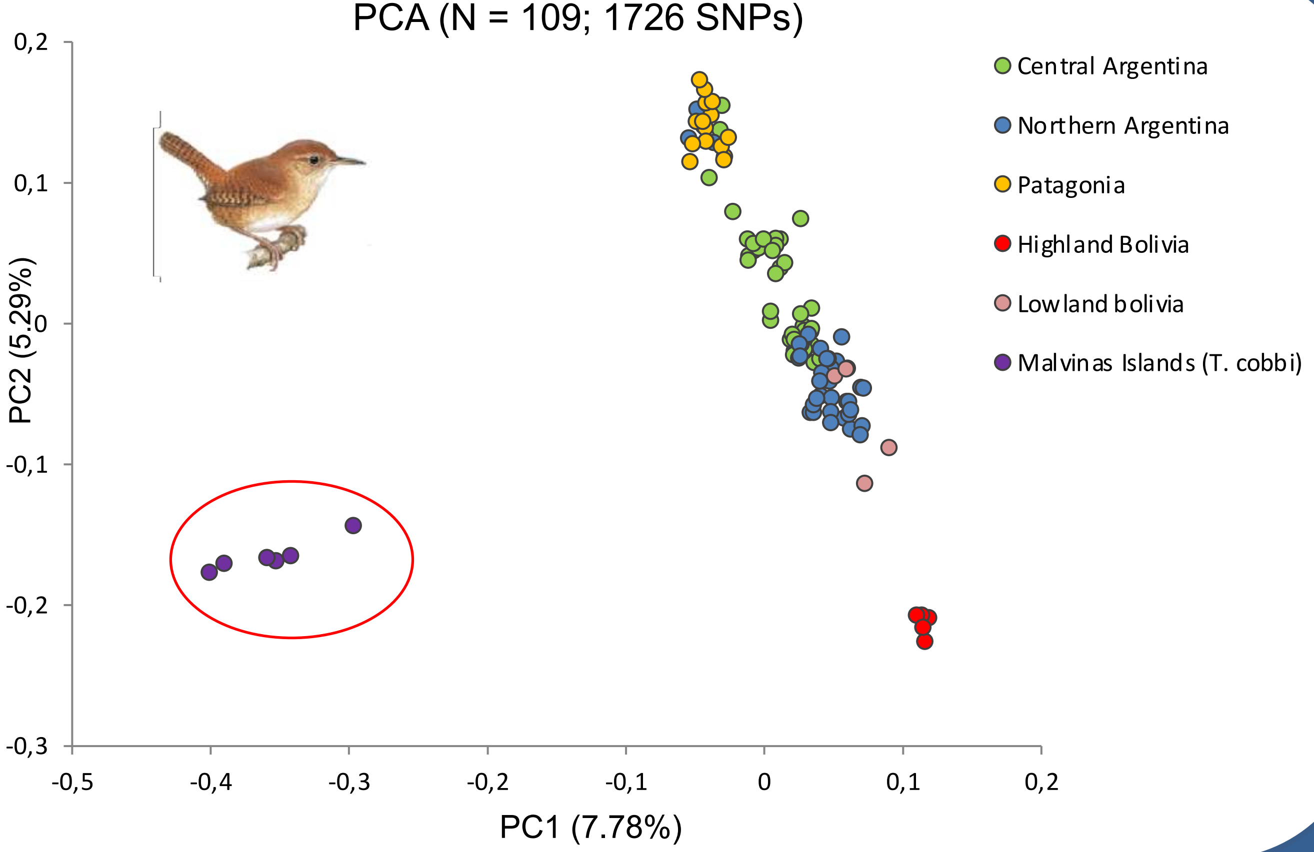
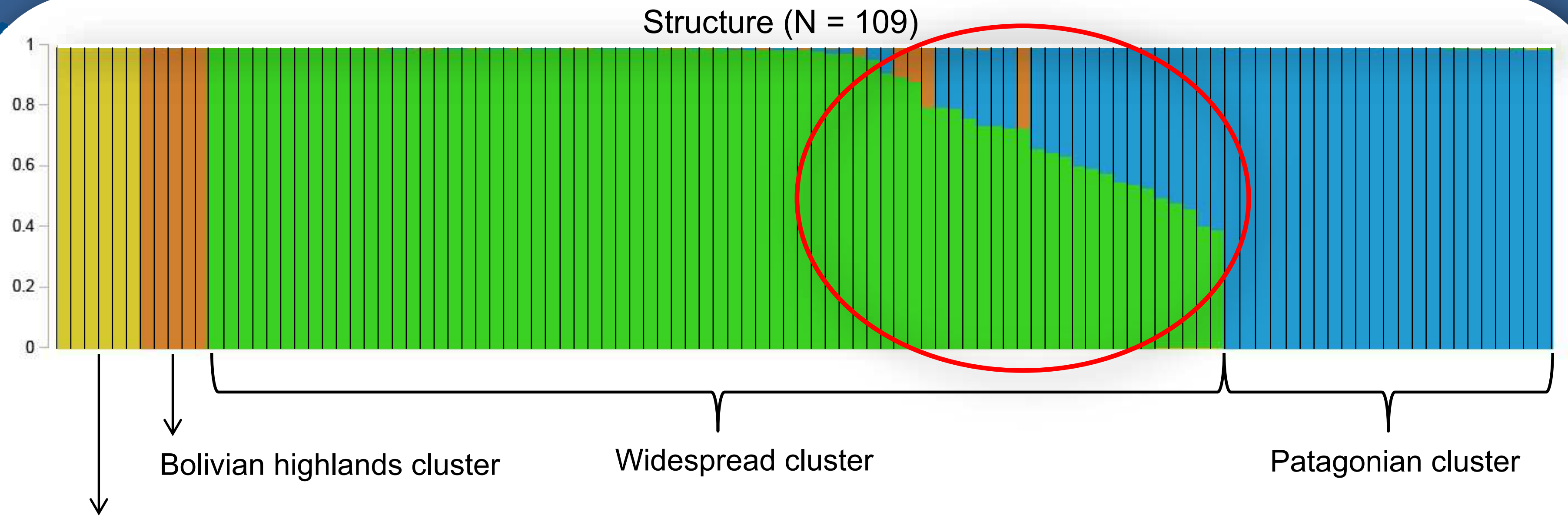


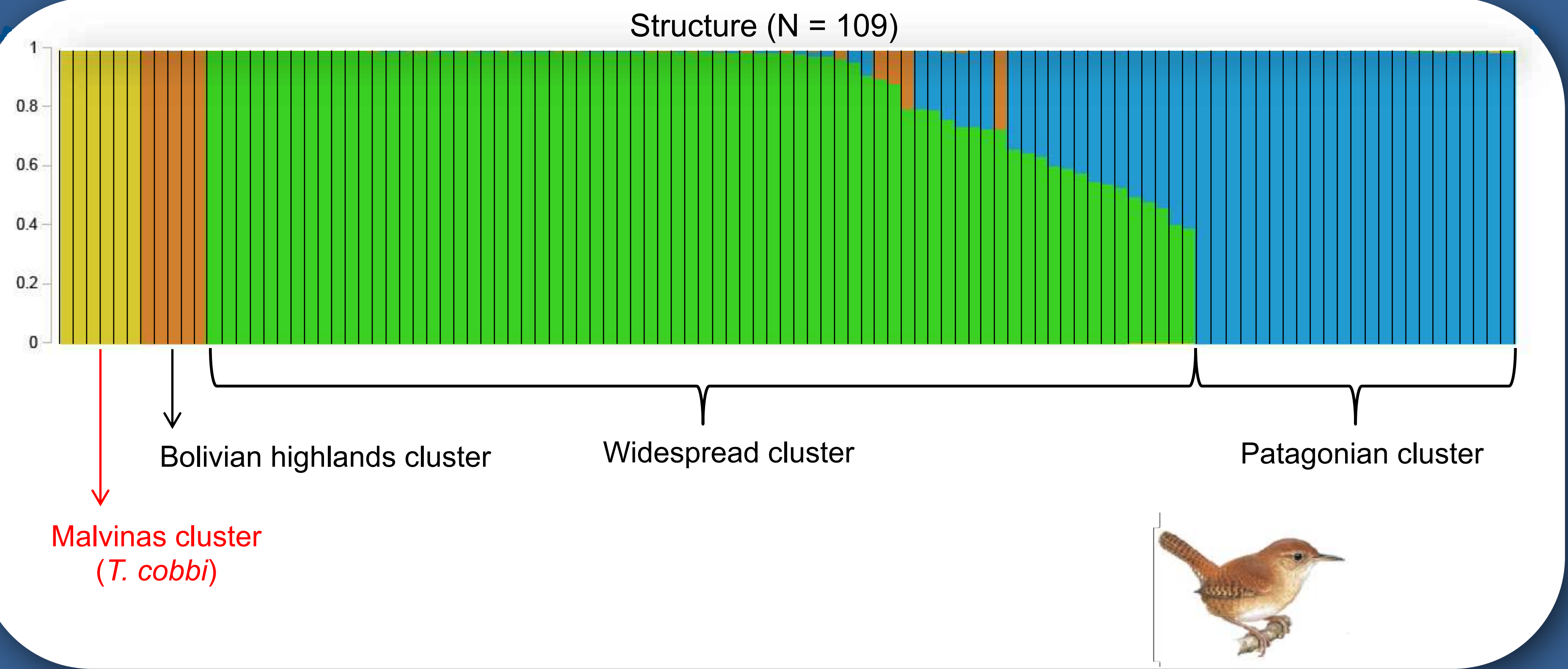
- *T. cobbi* from the Malvinas Islands is clearly differentiated.
- The continental clusters shows differentiation (mainly in PC2), but with a lot of individuals showing intermediate genomic content that suggest the presence of gene flow (particularly in Central Argentina between the Patagonian and widespread clusters).

House wren species complex: Nuclear genomic data



There is a clear evidence of admixture between continental lineages at the genomic level, indicating the presence of high levels of gene flow in central Argentina.

House wren species complex: Nuclear genomic data



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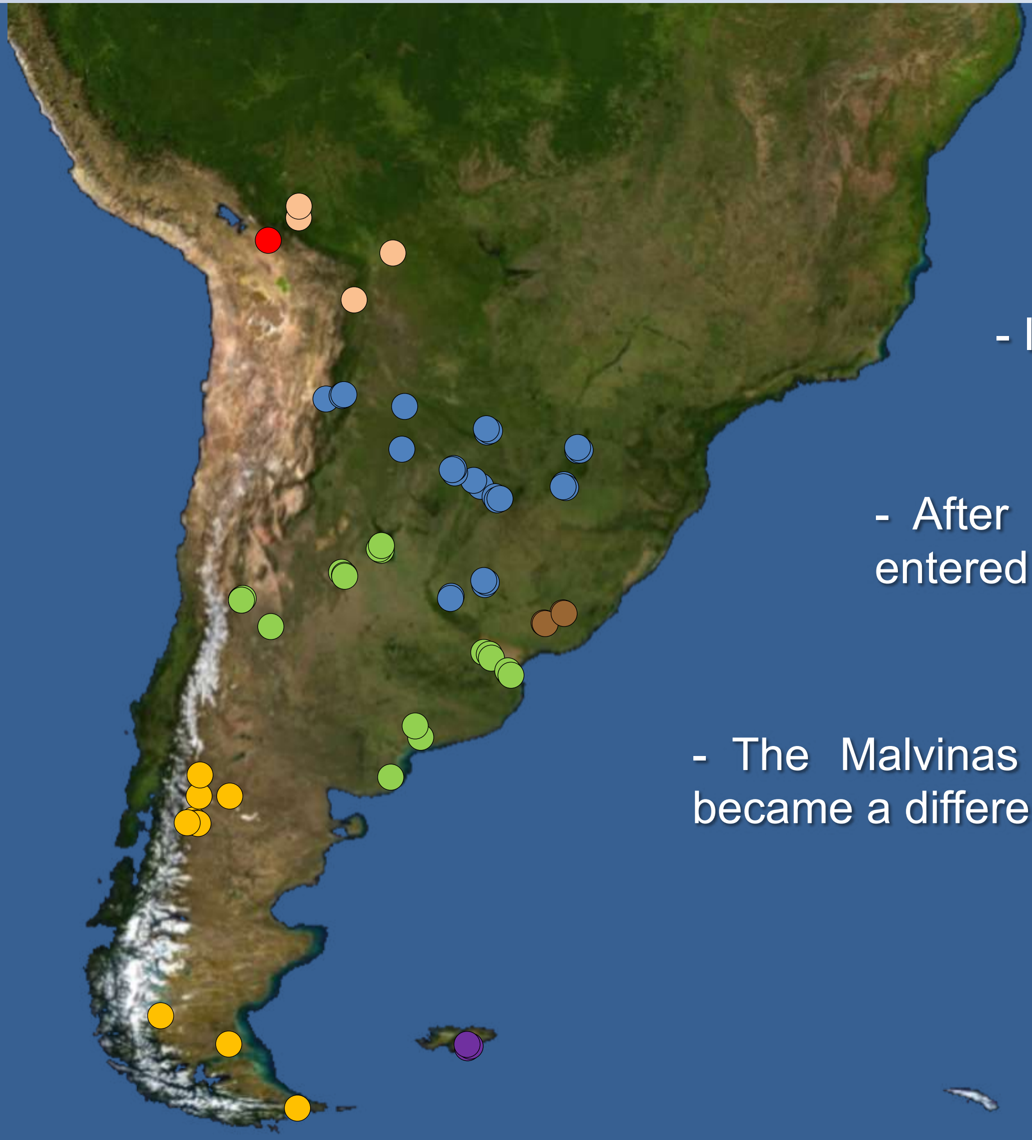
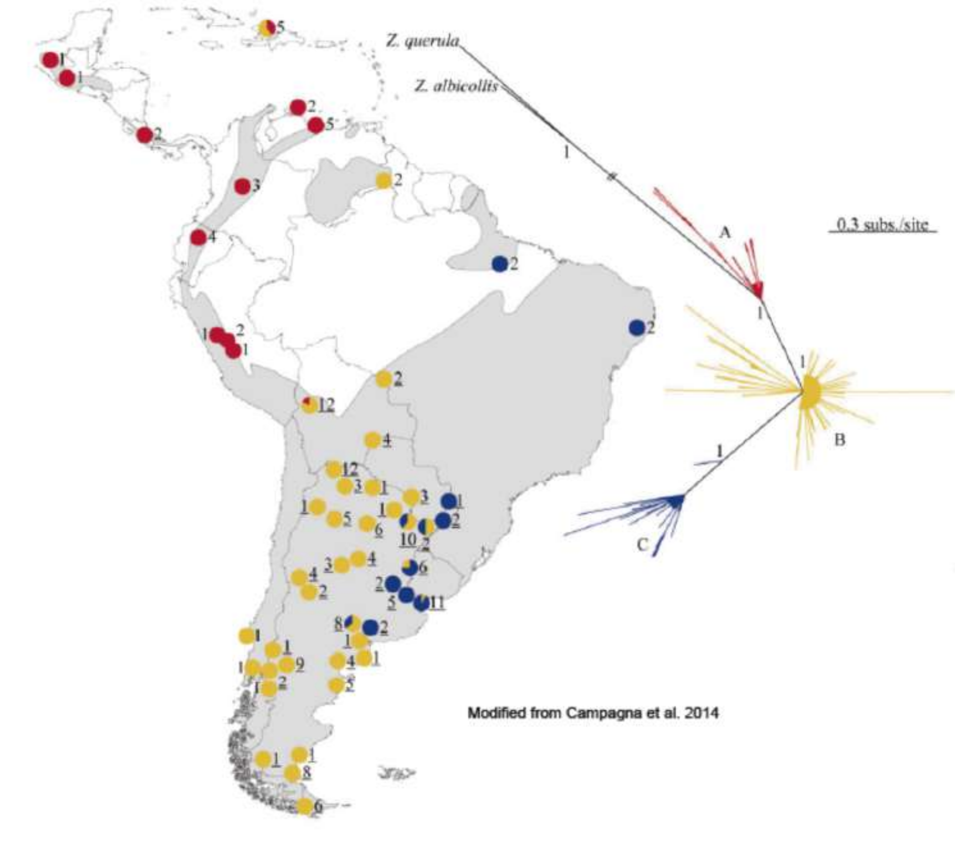
The only isolated cluster is that of *T.cobbi* from the Malvinas Islands.

House wren species complex: Evolutionary scenario



- During glaciations (around 2 million years ago) both Patagonian and Andean populations became isolated.
- In this period, the Malvinas Islands were colonized from Patagonia.
- After glacial cycles ended, the continental populations of *T. aedon* entered into secondary contact with extensive gene flow among lineages.
- The Malvinas population, on the contrary, remained isolated and eventually became a different species.

Rufous-collared Sparrow



Modified from Campagna et al. 2014

Typical *Z. capensis* coloration

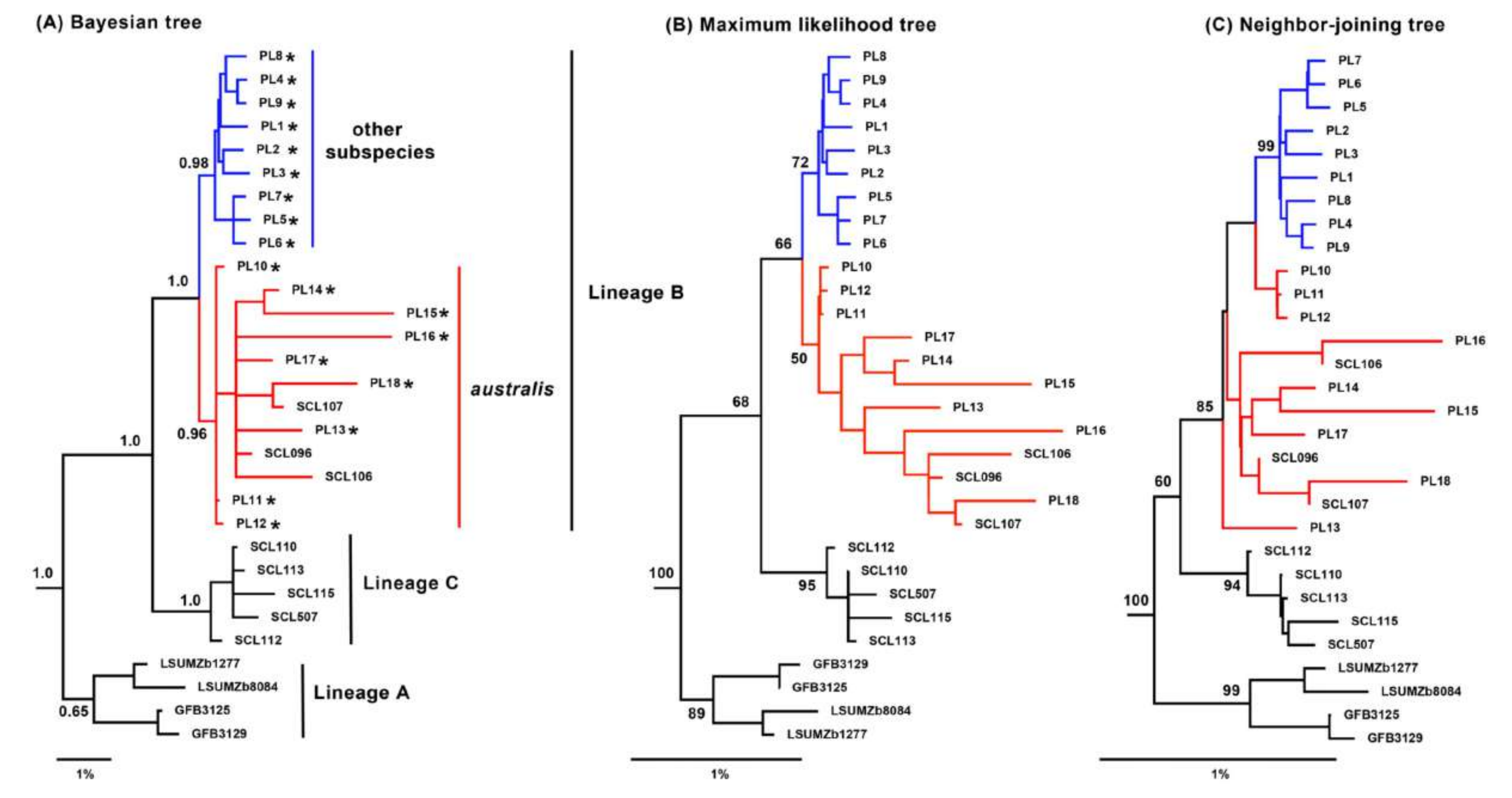
Z. Capensis australis coloration

Patagonian populations are not particularly differentiated from a mitochondrial perspective but the Patagonian subspecies is the most differentiated in morphology and song of its entire distribution.

We performed whole-genome resequencing (18 specimens) to study evolutionary history and the genomic basis of the colour differentiation of *Z. c. australis*.

Rufous-collared Sparrow: Mitochondrial data

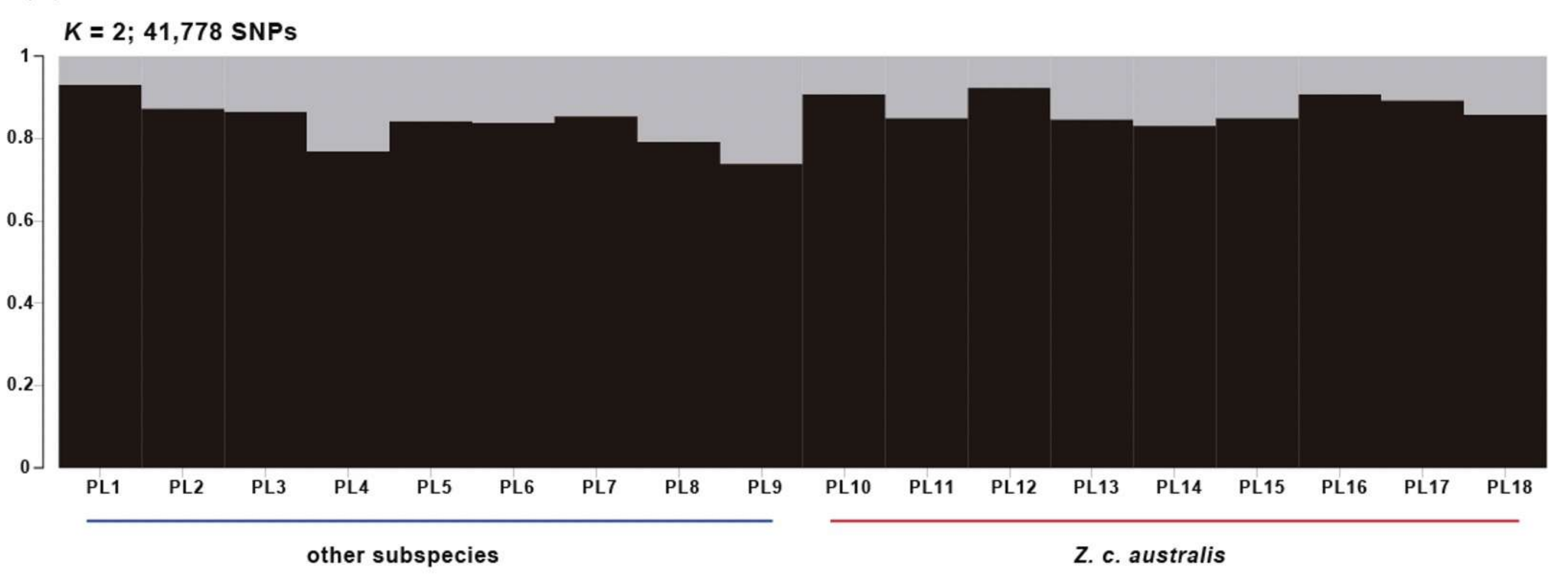
Phylogenetic analysis based on complete mitochondrial sequences (17 Kb)



Results compatible with a scenario of multiple glacial refugia in Patagonia

Rufous-collared Sparrow: Nuclear genomic data

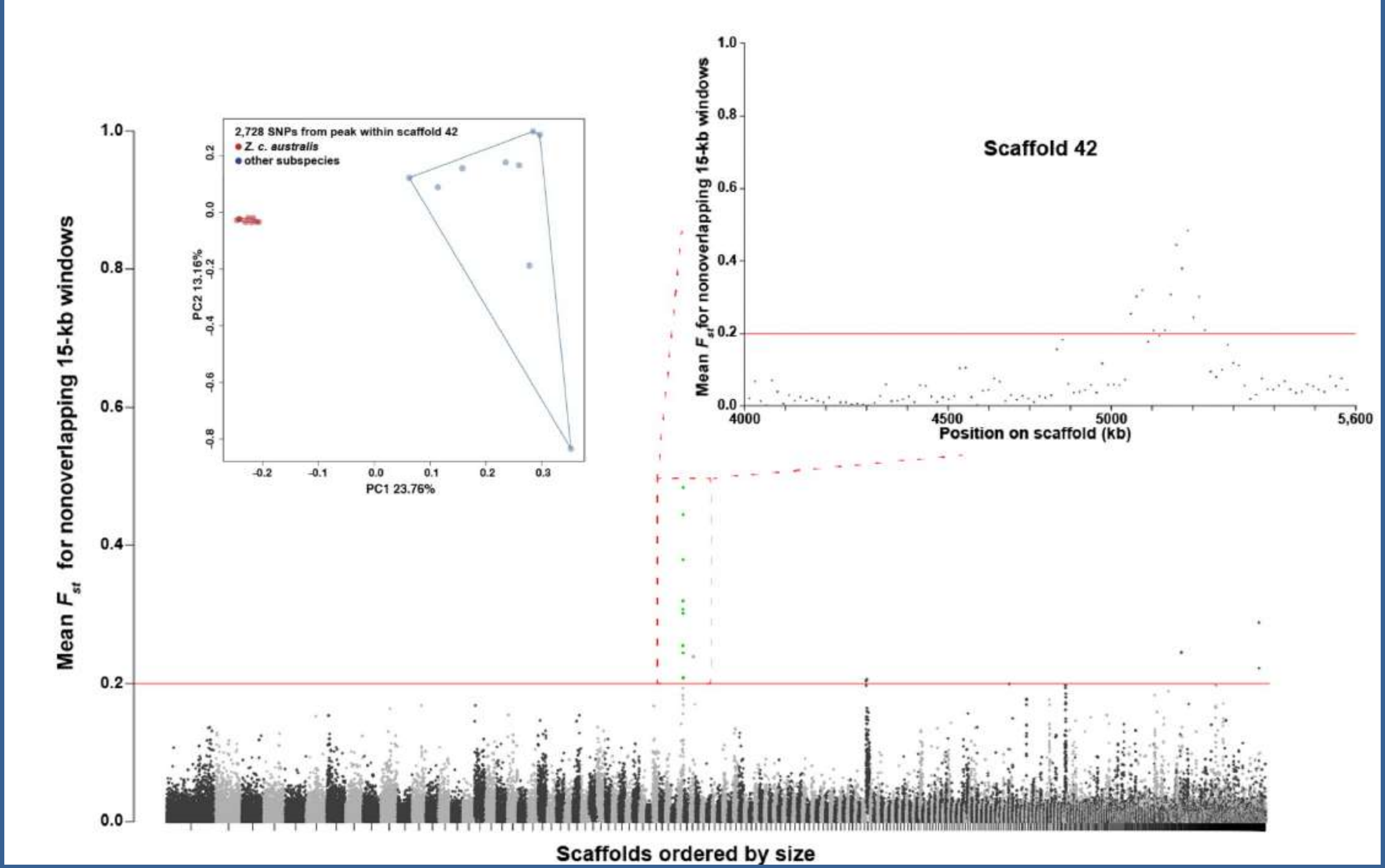
Structure analysis (41,778 SNPs)



- Results suggest that there is actually one population and gene flow is extensive between Patagonia and the rest of the distribution in the southern cone.

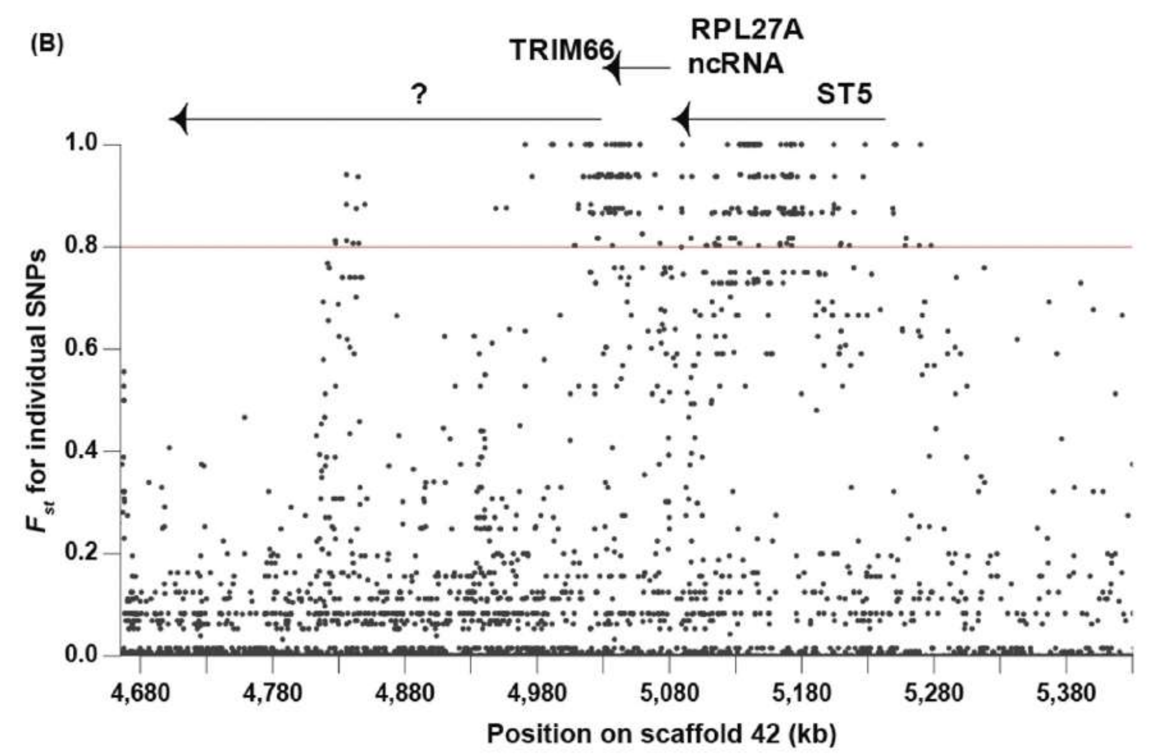
Rufous-collared Sparrow: Nuclear genomic data

Manhattan plot of the entire genome



There is one particularly evident peak of diverge in a general context of little differentiation.

Rufous-collared Sparrow: Nuclear genomic data



This region was mapped to chromosome 5, and differences were located mainly within and downstream ST5 gene. This gene regulates RAB9A, which is required for melanosome biogenesis and melanocyte pigmentation in mammals.

Rufous-collared Sparrow: Evolutionary scenario

Evolutionary scenario:

- Patagonian populations become isolated around 400,000 years ago and persisted and diverged in multiple refuges.

- After the retreat of the ice, these populations entered into contact and resumed gene flow between each other first and then with those from other regions of the southern cone, homogenizing their nuclear but not their mitochondrial DNA.

- Phenotypic differentiation evolved relatively rapidly and with low levels of overall genomic divergence. This is apparently due to differences in ST5 and its effect on melanogenesis.

General conclusions

- Both the large-scale analysis and our three models show the relevance of glacial periods in isolating southern populations and promoting diversification and speciation. This is the case of the Malvinas Cobb’s Wren (*Troglodytes cobbi*).

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- The species are quite consistent in their geographical pattern, but not that much in their temporal estimation of the separation, ranging between around 2 million years ago (House Wren) and 400,000 years ago (Rufous-collared Sparrow).

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- The species are quite consistent in their geographical pattern, but not that much in their temporal estimation of the separation, ranging between around 2 million years ago (House Wren) and 400,000 years ago (Rufous-collared Sparrow).

- In our three models, continental lineages/subspecies resumed intense gene flow after glacial retreated and southern populations expanded northwards, and nuclear genomes appear to be homogenizing again.

General conclusions

- In addition to genomic differentiation, in the case of the Rufous-collared Sparrow this isolation period generated phenotypic differences in Patagonia, and the same is true for vocalizations in the Southern Lapwing.

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- In the Rufous-collared Sparrow differences appear to have evolved fastly and based mainly on a single gene.

Many thanks to...

Collaborators and co-authors

- Members of our team at MACN and the Cornell Lab of Ornithology.
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Belén Bukowski


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Pablo Fracas

Leo Campagna


Pablo Tubaro

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- Genome Canada
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- Provincial fauna authorities
- National Parks Administration

Questions?