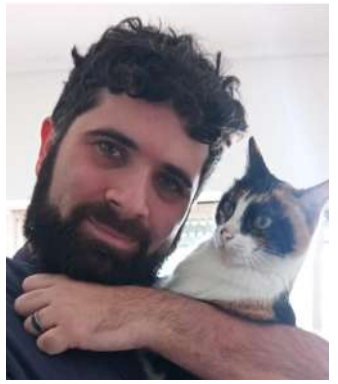
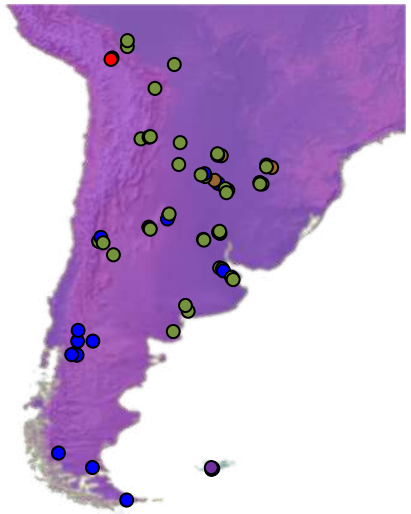
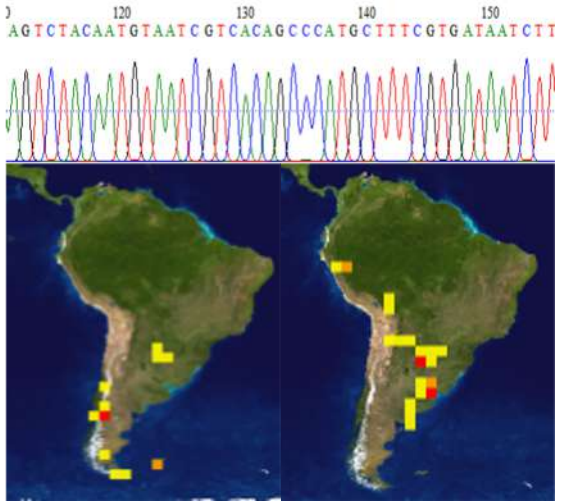
Divergent lineages meet: Does reproductive isolation exist in southern House Wrens?

Pablo A. Fracas, Ramiro S. Arrieta, Belén Bukowski, Leonardo Campagna, Pablo D. Lavinia, Paulo E. Llambías, Pablo L. Tubaro, Darío A. Lijtmaer



9TH INTERNATIONAL BARCODE OF LIFE CONFERENCE





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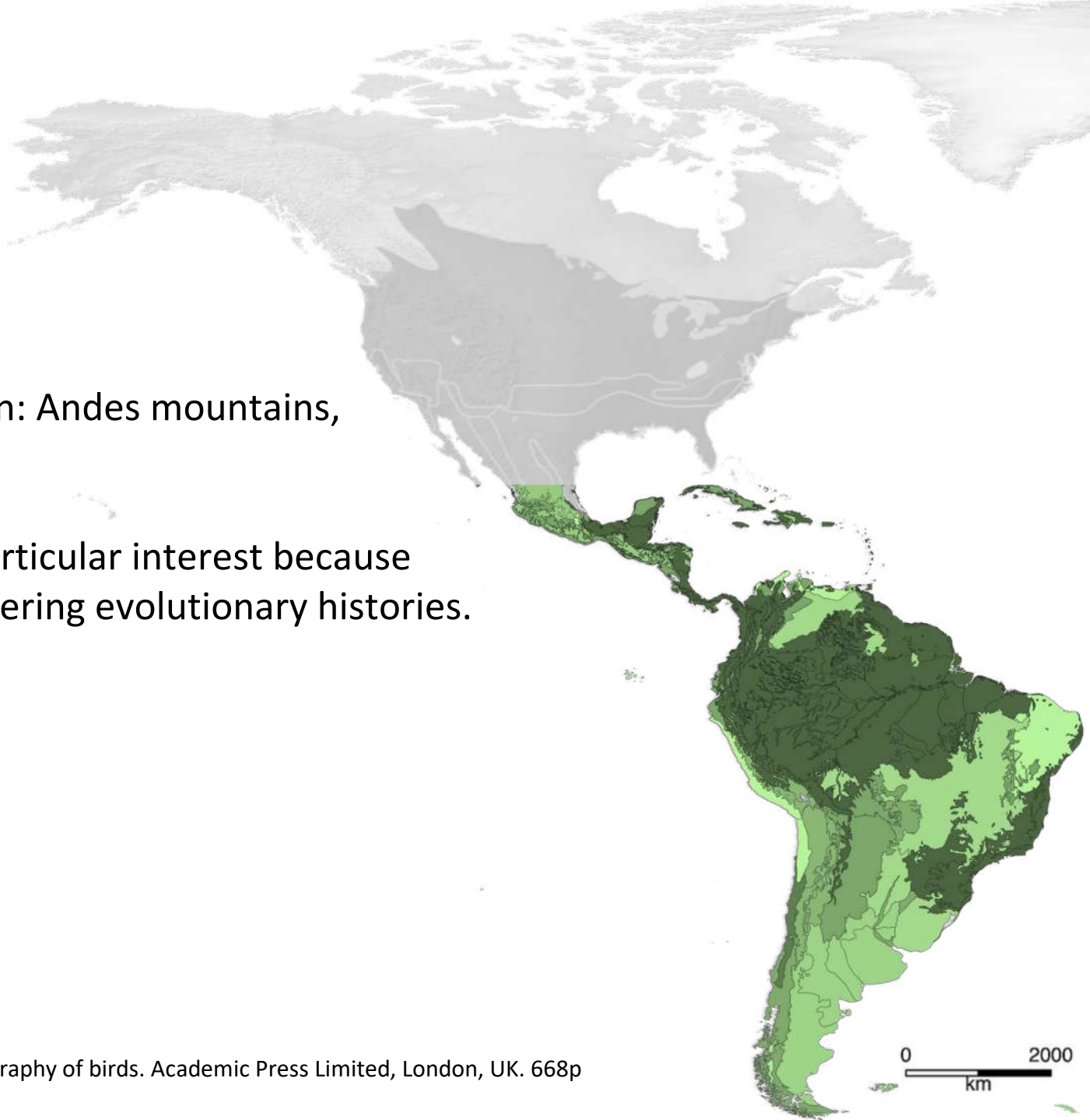
The Neotropical region

- Most biodiverse terrestrial region.
- > 3000 bird species (Newton 2003).
- Multiple factors promoting allopatric speciation: Andes mountains, wide rivers, etc.
- Species with large distribution ranges are of particular interest because they can include lineages/populations with differing evolutionary histories.



Newton, I. 2003. The speciation and biogeography of birds. Academic Press Limited, London, UK. 668p

The House wren (*Troglodytes aedon*)

- Continuous transcontinental distribution
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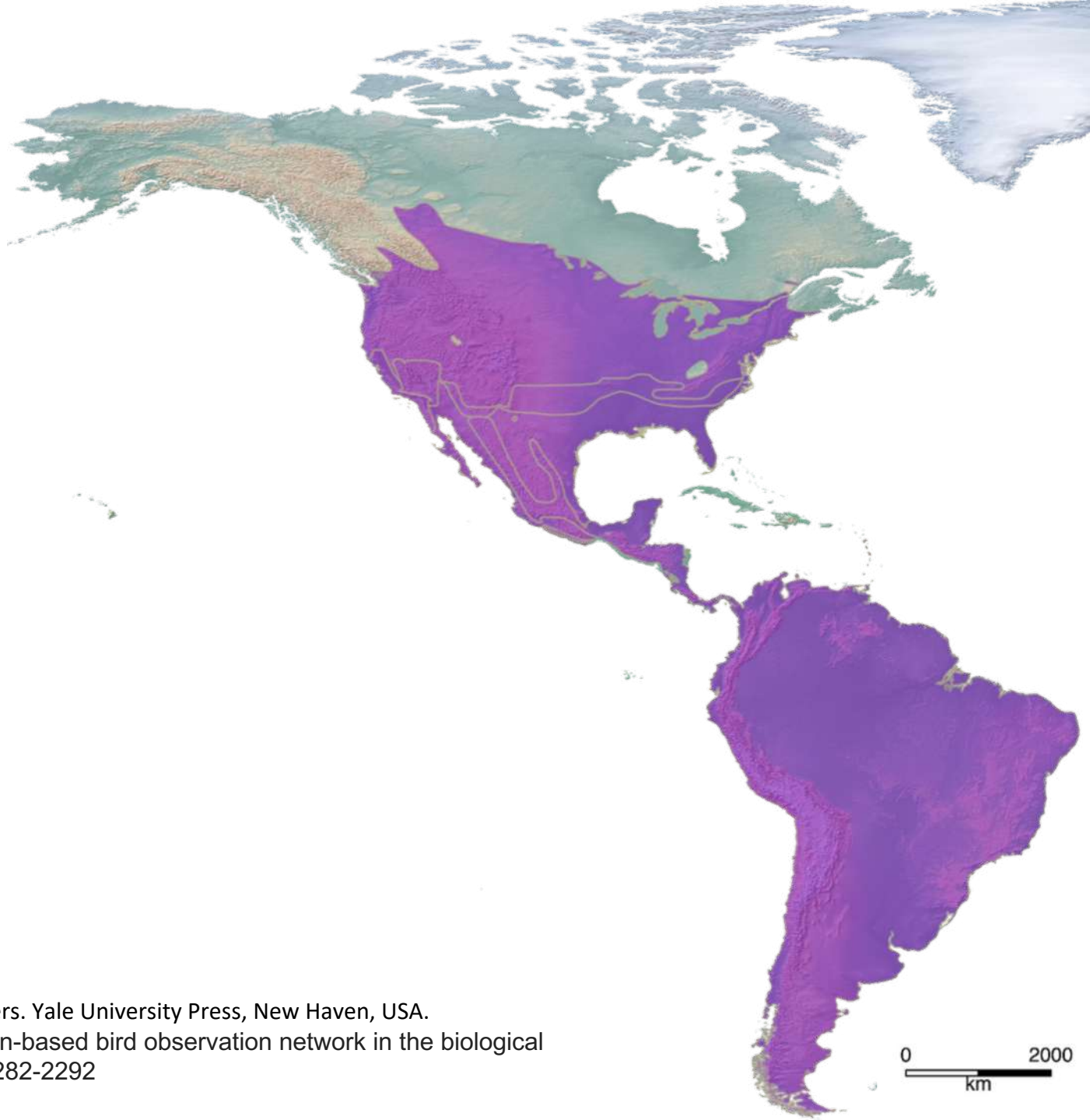

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- Sullivan, B.L., *et al*. 2009. eBird: a citizen-based bird observation network in the biological sciences. *Biological Conservation* 142: 2282-2292

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Kroodsma DE & D. Brewer. 2005. Family Troglodytidae (wrens). En: del Hoyo J, Elliott A, Christie DA, eds. Handbook of the birds of the world, Vol. 10. Cuckoo-shrikes to thrushes. Lynx Edicions, Barcelona, España.

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- Kaluthota C, et al. (2016). Transcontinental latitudinal variation in song performance and complexity in house wrens (Troglodytes aedon). Proceedings of the Royal Society B 283: 20152765.
- Ghani, B., Klinck, H., & Hallerberg, S. (2023). Classification of group-specific variations in songs within House Wren species using machine learning models. Ecological Informatics, 74, 101946.
- Arguedas, N., & Parker, P. G. (2000). Seasonal migration and genetic population structure in house wrens. The Condor, 102(3), 517-528.

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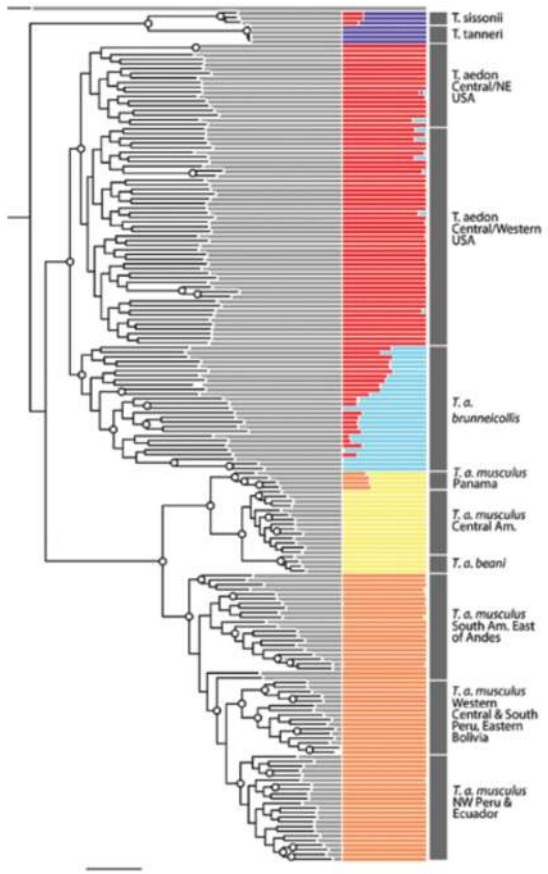

Edited from Klicka *et al*. 2023

Klicka, J., *et al*. (2023). Lineage diversity in a widely distributed New World passerine bird, the House Wren. Ornithology, ukad018.

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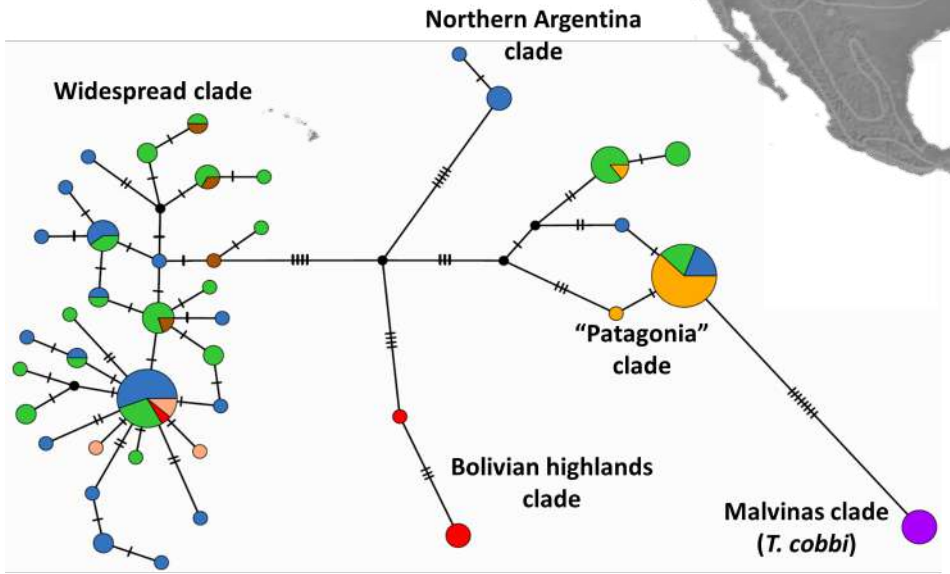
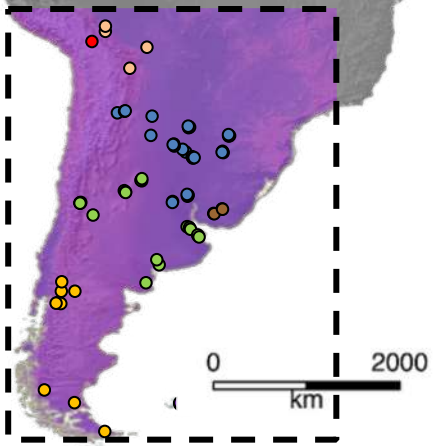
- Specifically in South America:

  Kerr *et al*. 2009, Campagna *et al.* 2012,

  Galen *et al*. 2015, Lijtmaer *et al.* in prep.





- Kerr et al. 2009. Probing evolutionary patterns in neotropical birds through DNA barcodes. PLoS ONE, 4(2).
- Campagna et al. 2012. Divergence between passerine populations from the Malvinas – Falkland Islands and their continental counterparts: a comparative phylogeographical study. Biological Journal of the Linnean Society 865–879.
- Galen et al. 2015. Contribution of a mutational hot spot to hemoglobin adaptation in high-altitude Andean house wrens. PNAS 112: 13958–13963.

The contact zone

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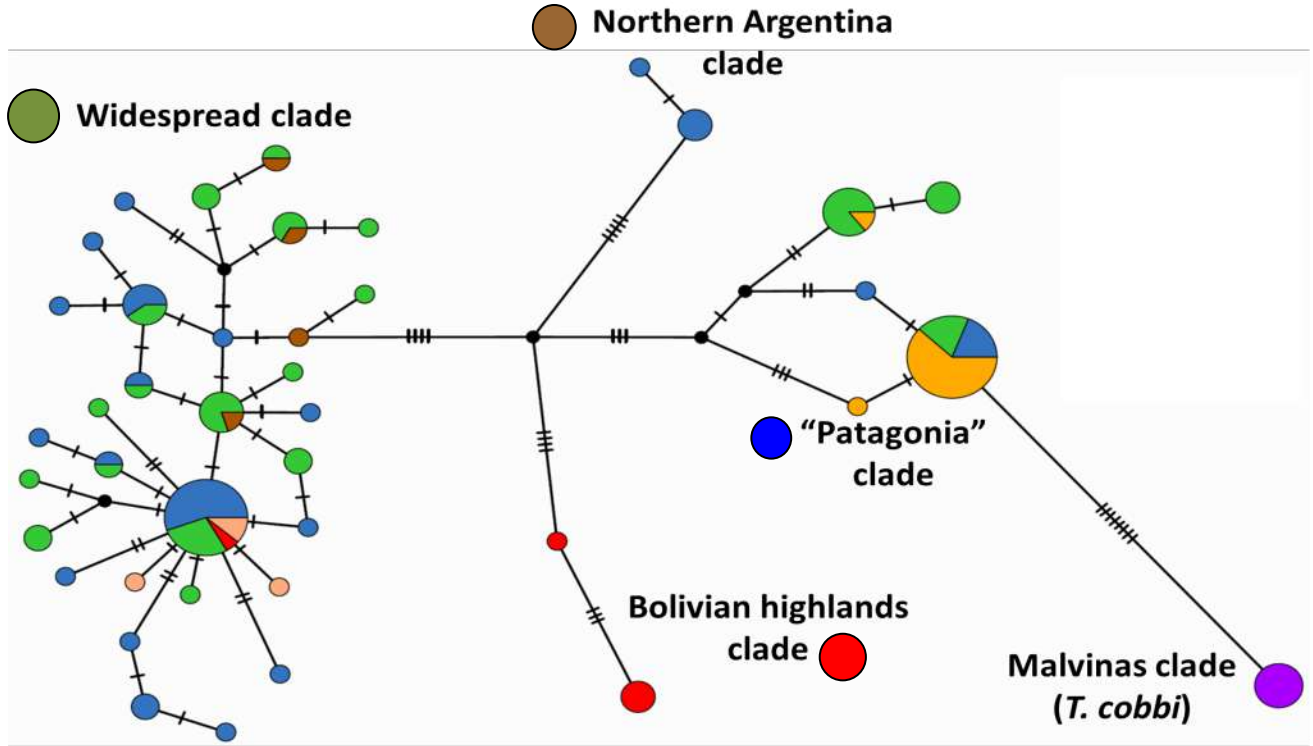

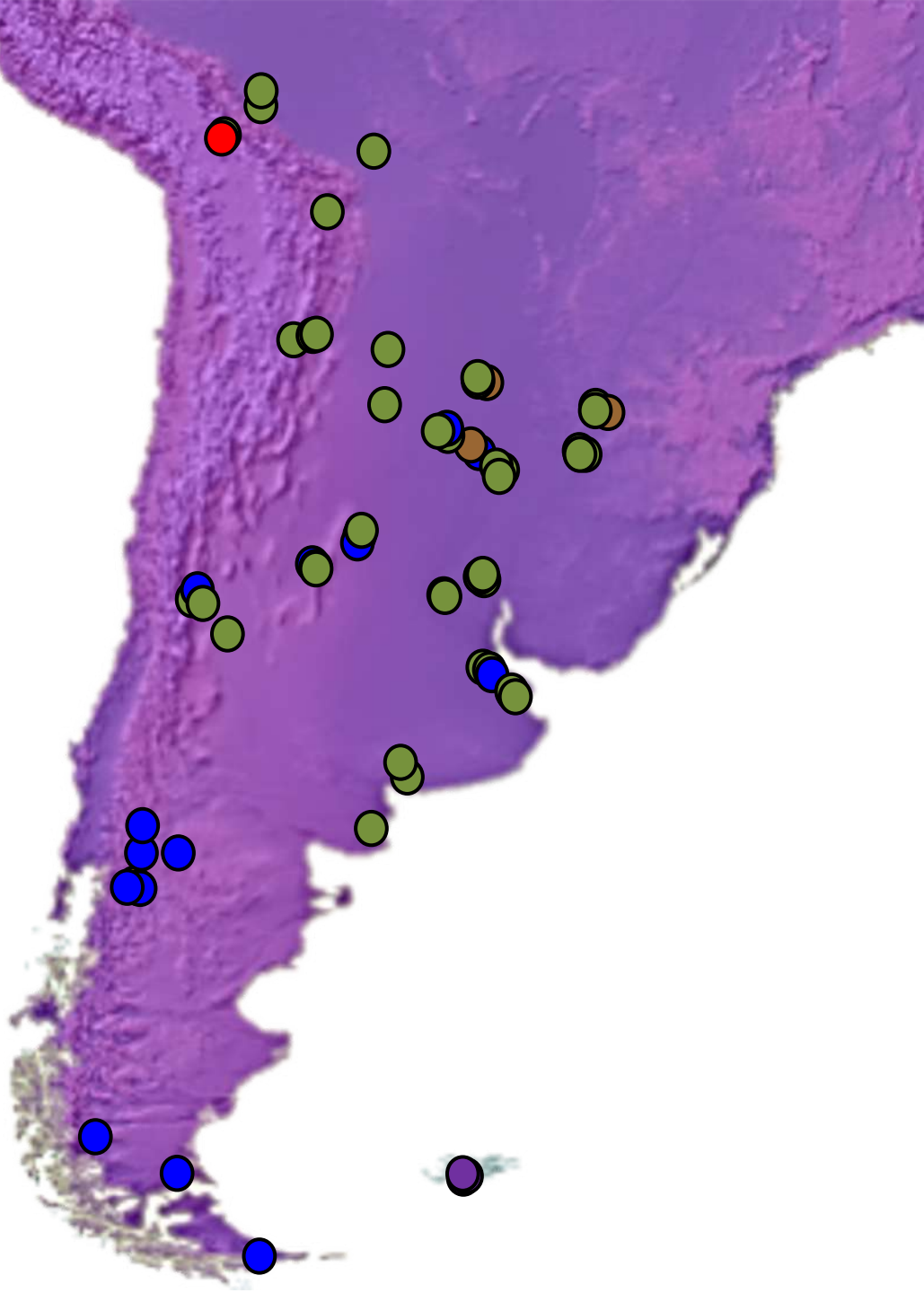

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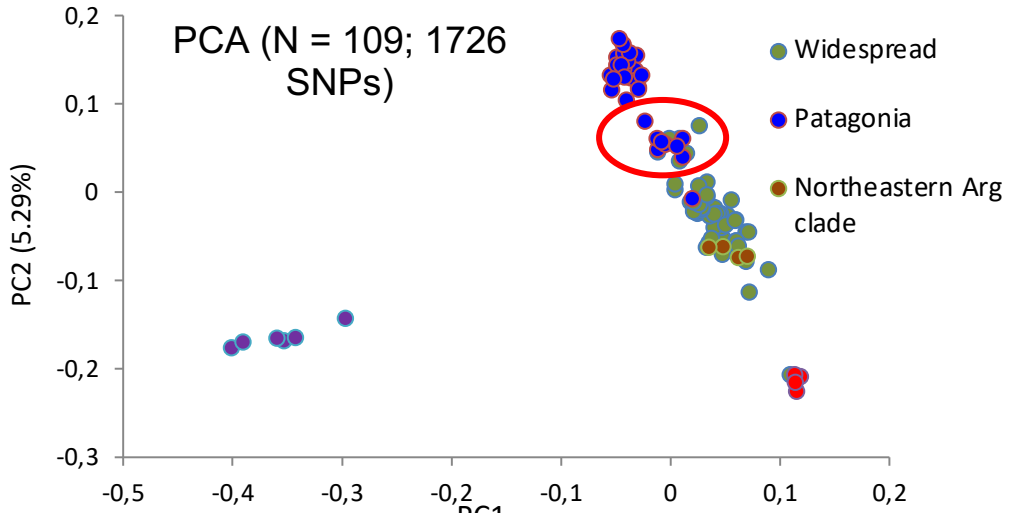

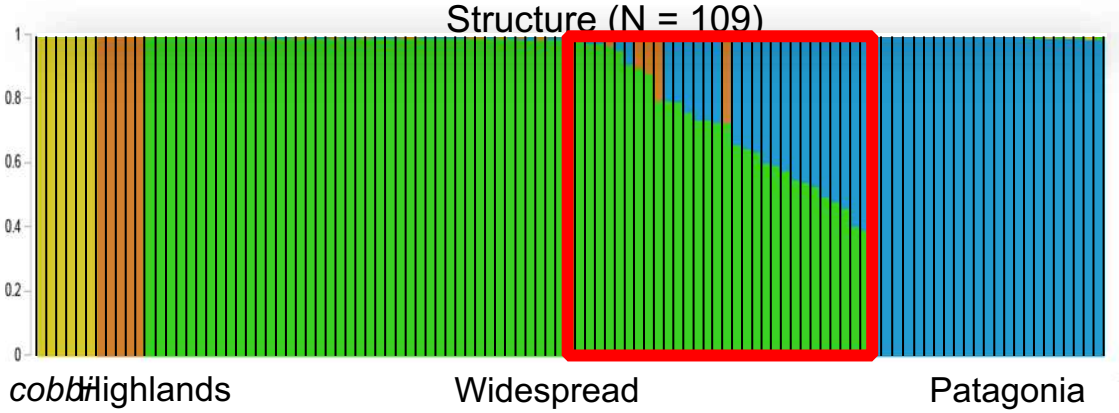

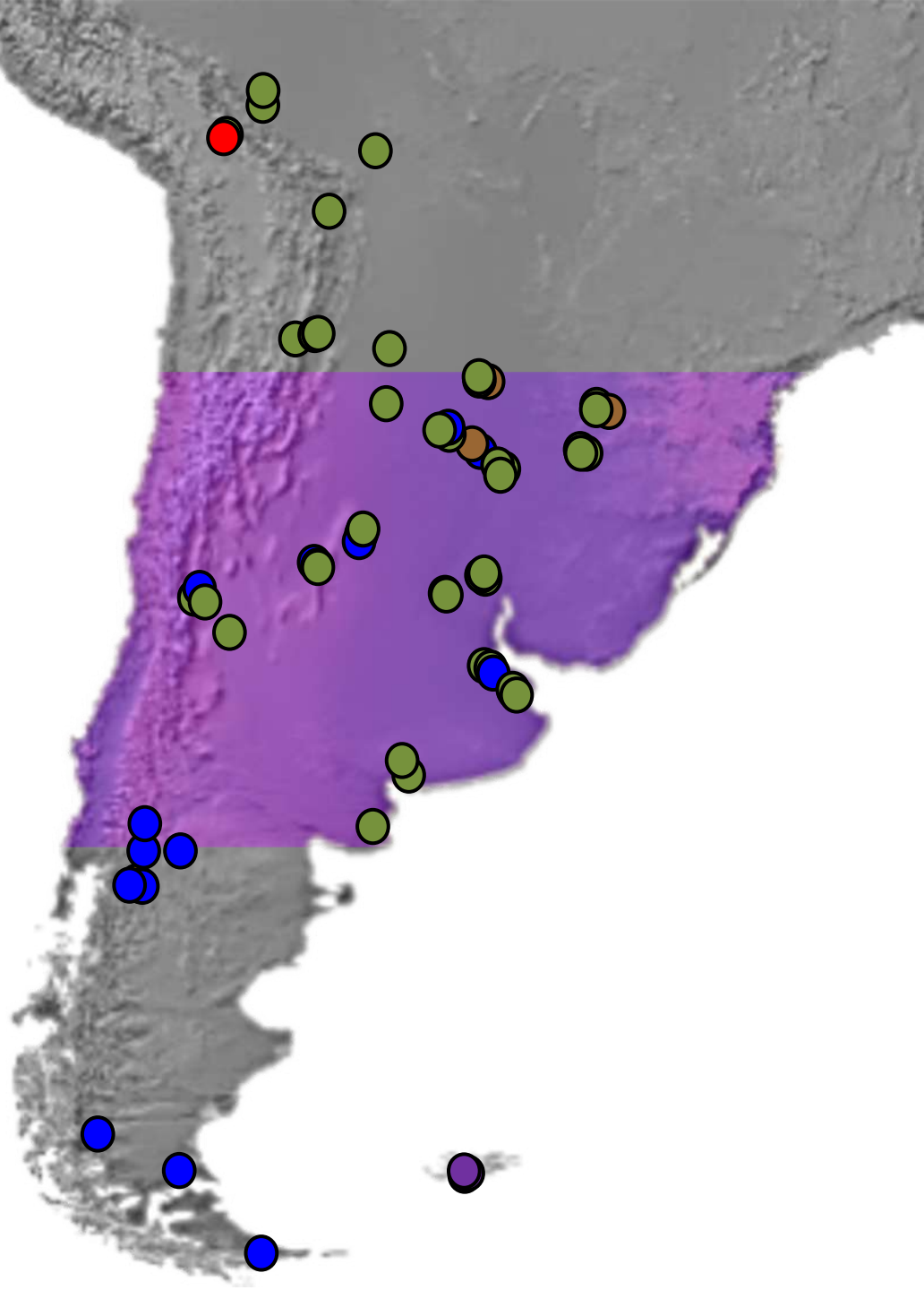

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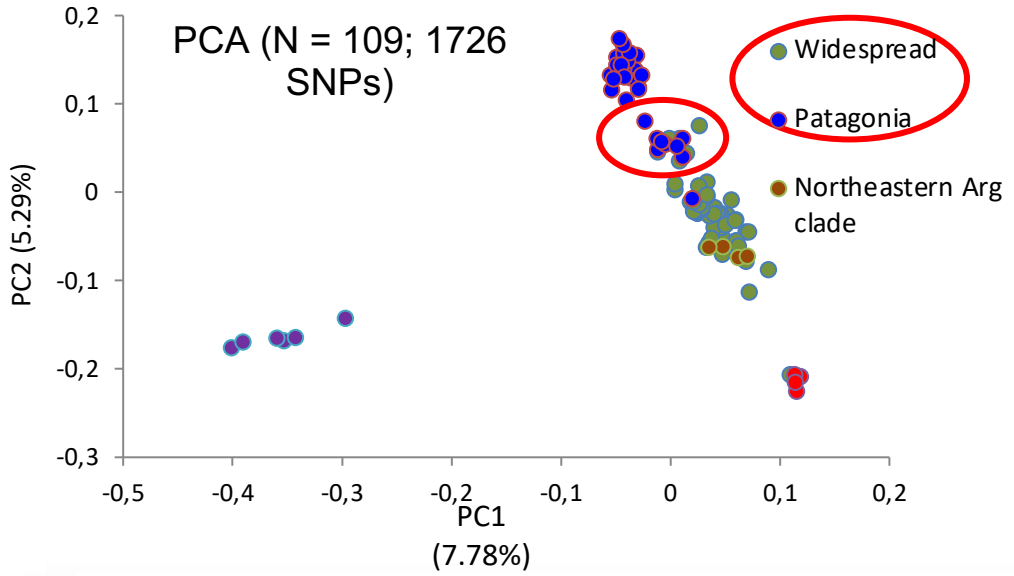
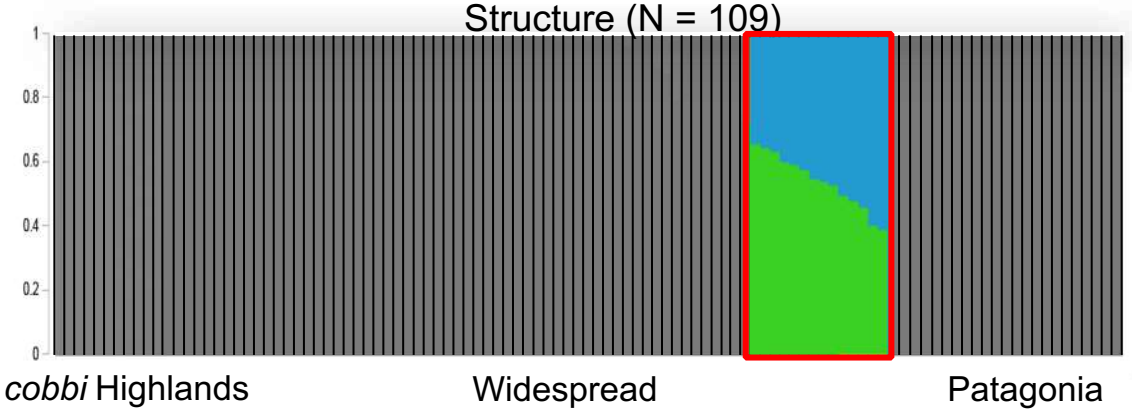
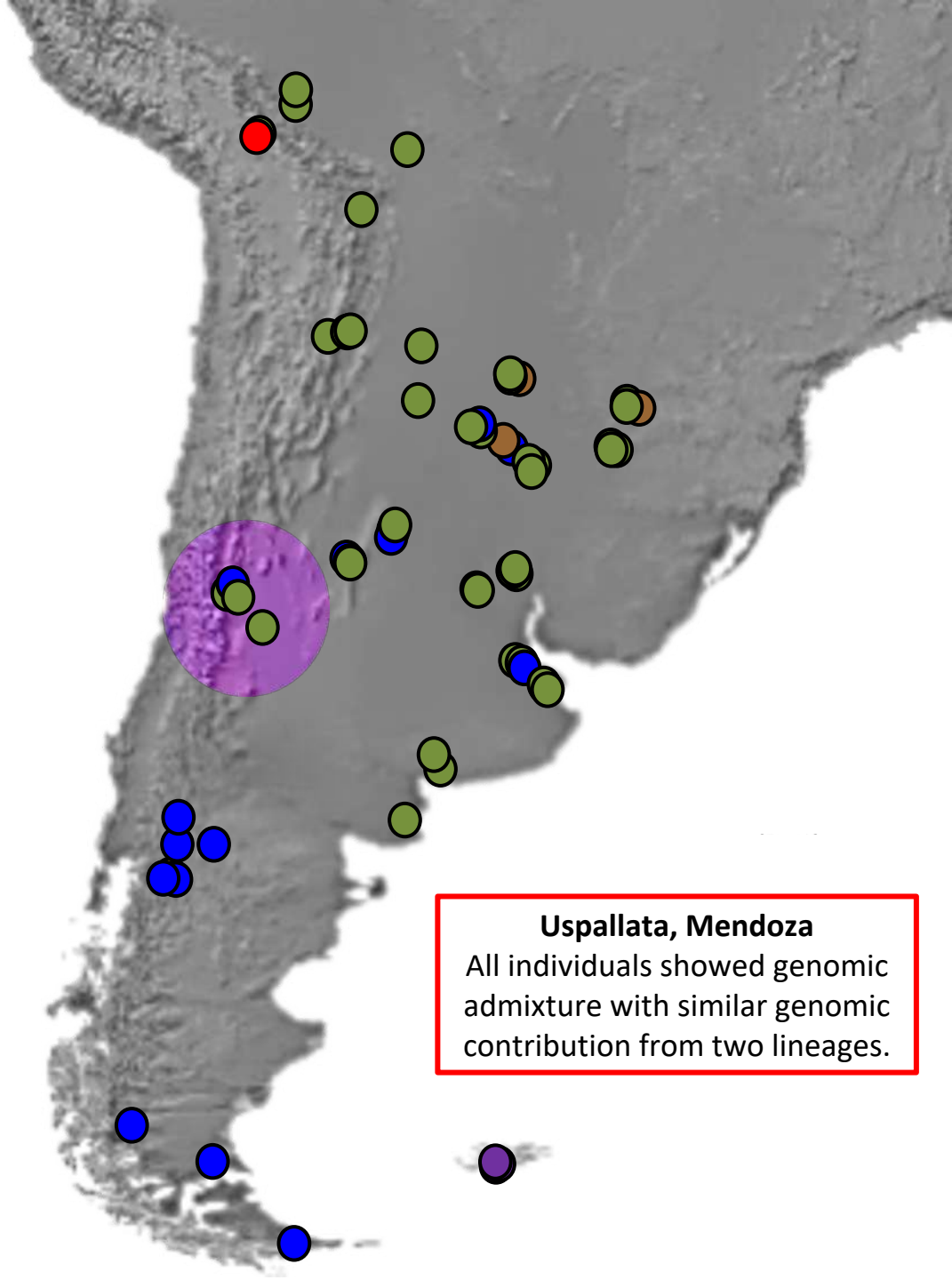






Uspallata, Mendoza
All individuals showed genomic admixture with similar genomic contribution from two lineages.

Objectives

1. Study whether there is assortative mating in the contact zone between lineages in Uspallata.

2. Study whether the divergence between parents affects offspring viability.

Methods - Study site:

- **Uspallata**, Mendoza, Argentina (32°34’00”S 69°19’00”W, alt: 2039).
- Forestation (400 x 400 m) of *Populus with* ≈50 nest boxes.

Photo: Paulo Llambías

Methods - Sampling

- 2 breeding seasons (2015 - 2016).
- Banding and blood sampling of all individuals.
- Number of laid eggs, nestlings & fledglings.
- Offspring viability variables:
  - **Hatching success** (nestlings / laid eggs).
  - **Fledging success** (fledglings / nestlings).
  - **Overall success** (fledglings / laid eggs).

Location of nest boxes

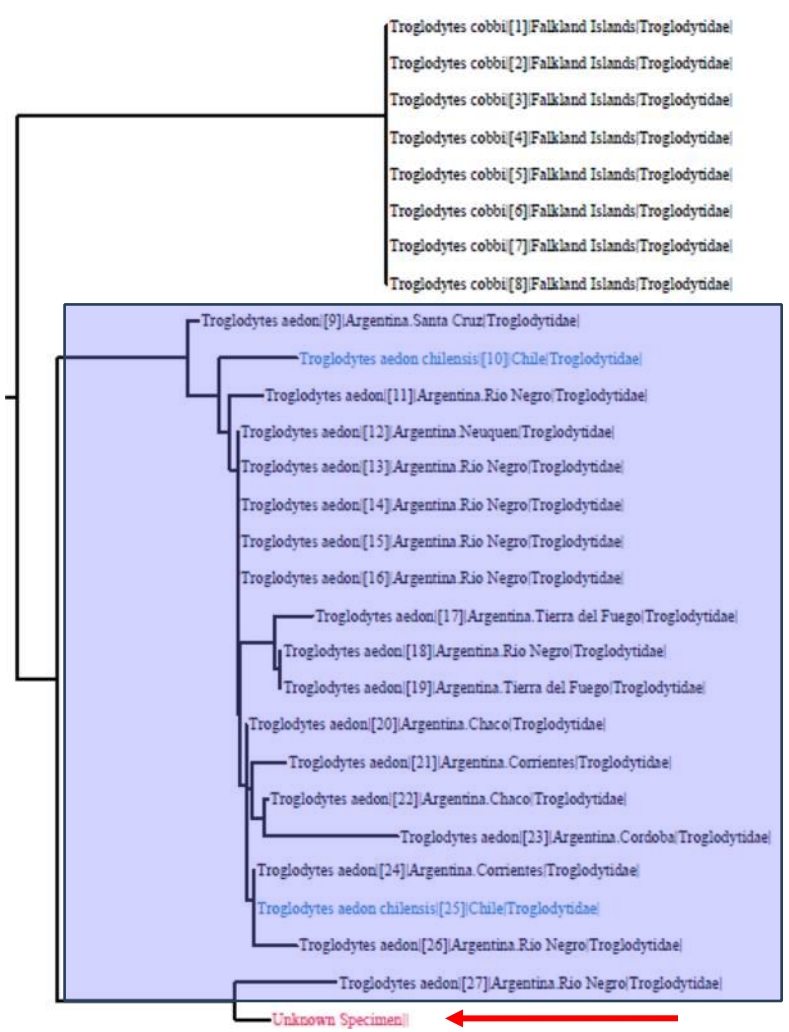
House wren guarding the nest box.

House wren nest inside nest box.

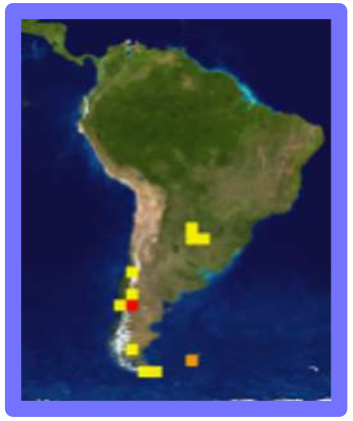
Photos: Paulo Llambías

Assigning parents to their mitochondrial lineage:

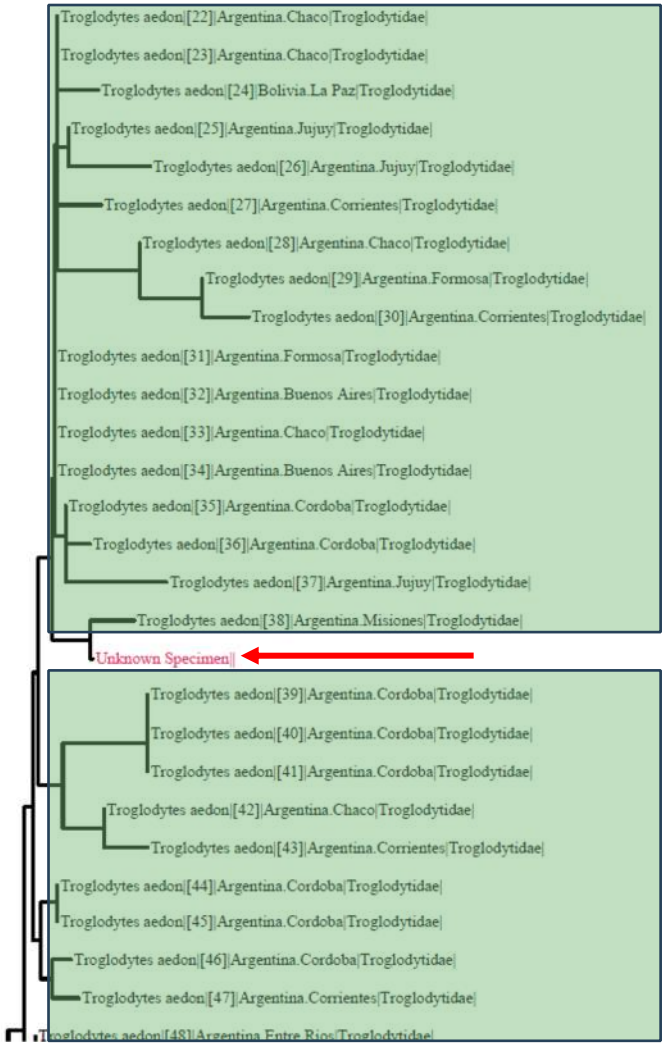
- Assignment by ID engine in BOLD (Barcode of Life Data systems).



Patagonia (P)



Widespread (W)



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Assigning offspring to genetic father (incorporating extra-pair patternity):

- Ddrad Sequencing + assignement by *Cervus* (Kalinowski *et al*. 2007).
- **73%** assigned with confidence to social or extrapair sire (n = 150).
- **27%** assigned to a non sampled extrapair sire (n = 56).

Pablo Fracas working at the lab

Kalinowski, S. T., Taper, M. L., & Marshall, T. C. (2007). Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. Molecular ecology, 16(5), 1099-1106.

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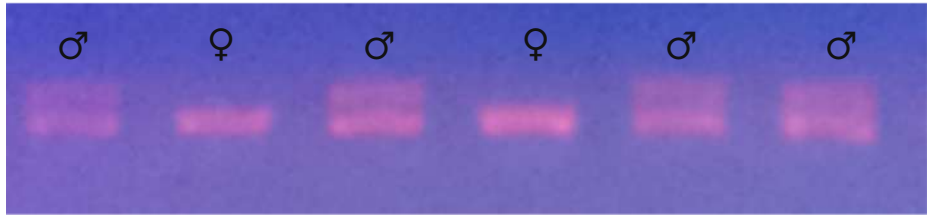
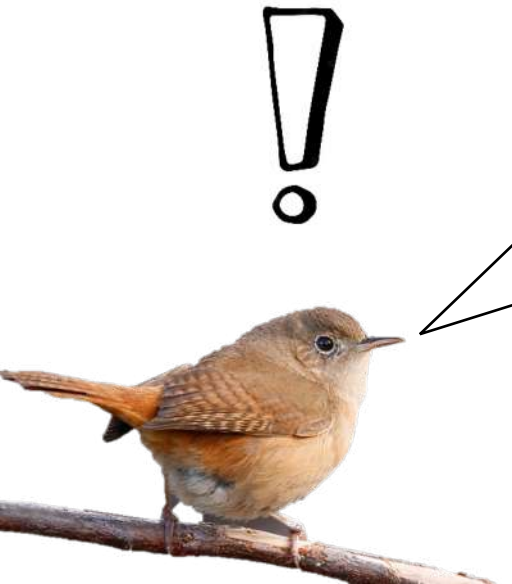
Determining offspring sex:

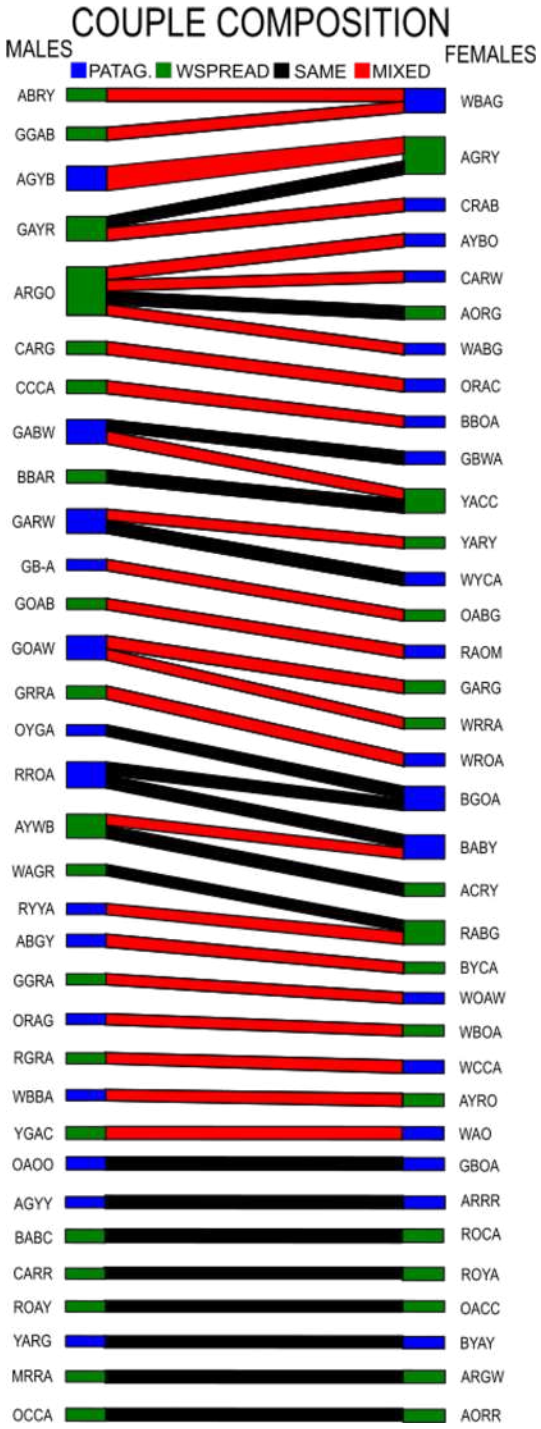
- Molecular sex determination.



PCR amplification of sex-specific fragmets

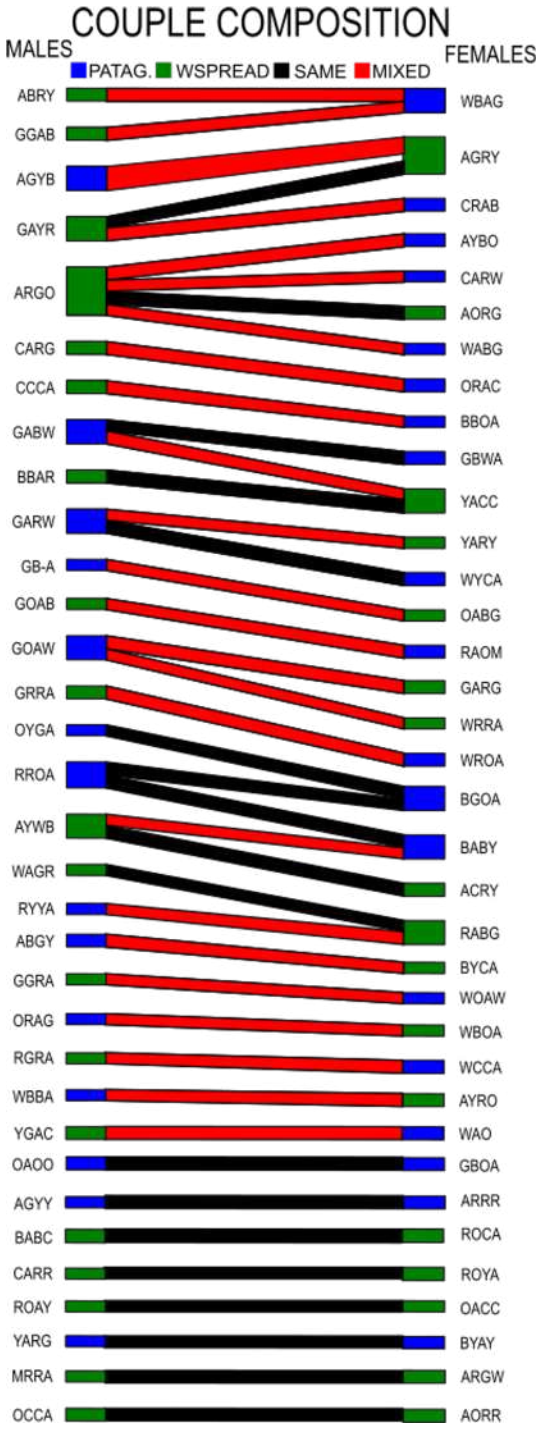
RESULTS





Assortative mating?

- n = 43 couples



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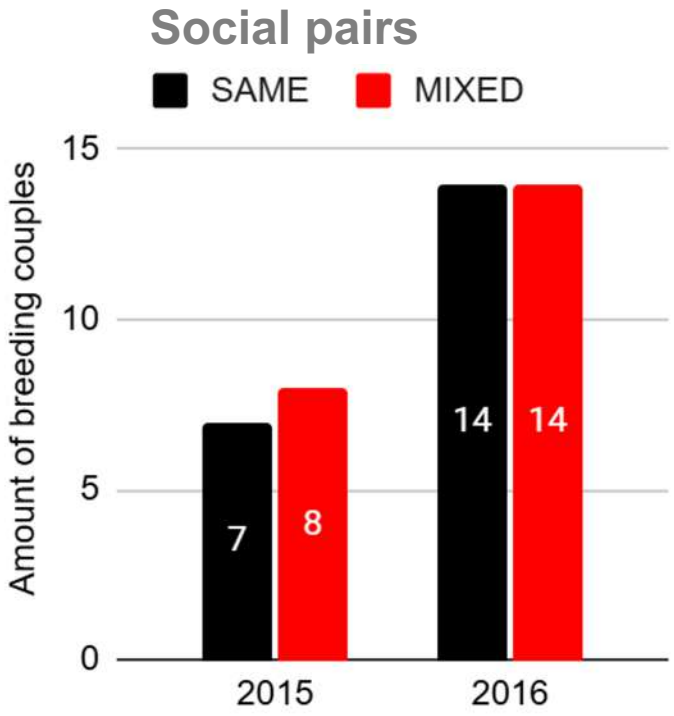

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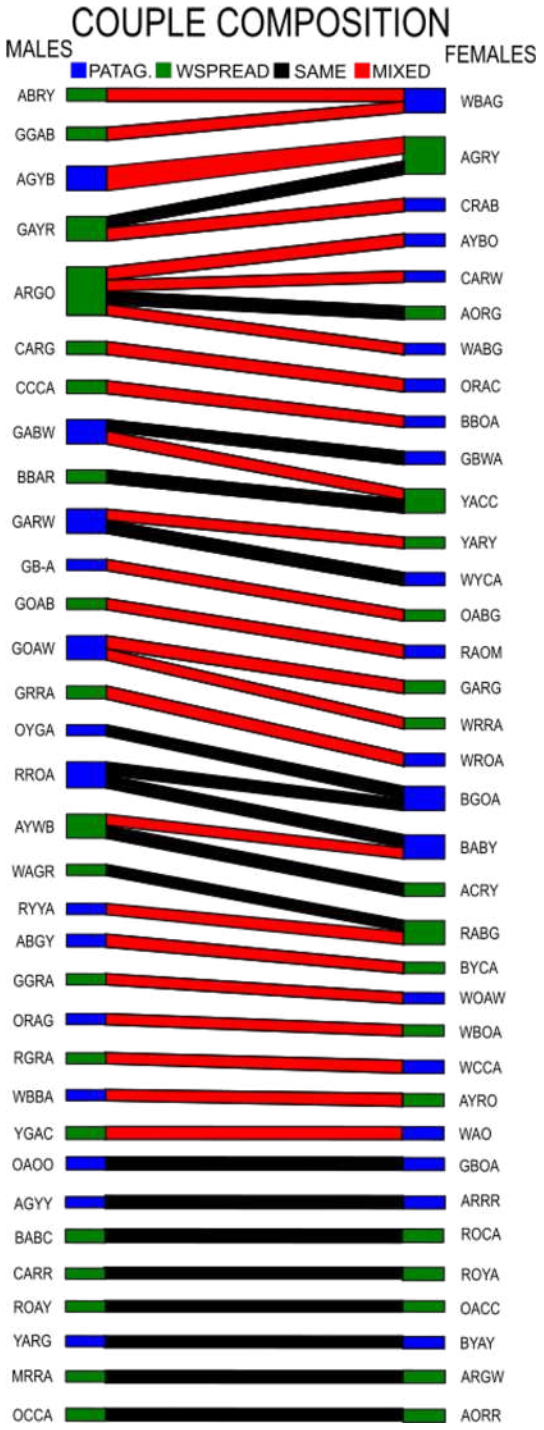

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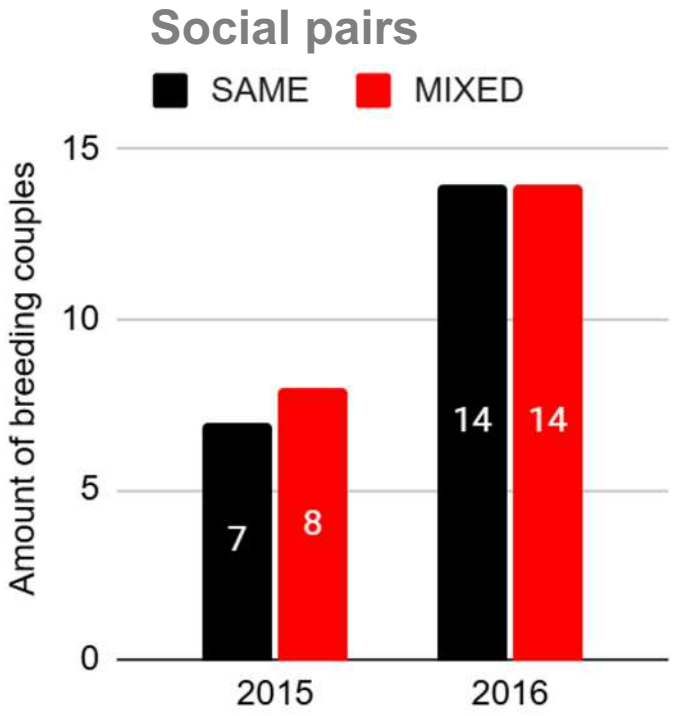
  2) 37% of offspring overall



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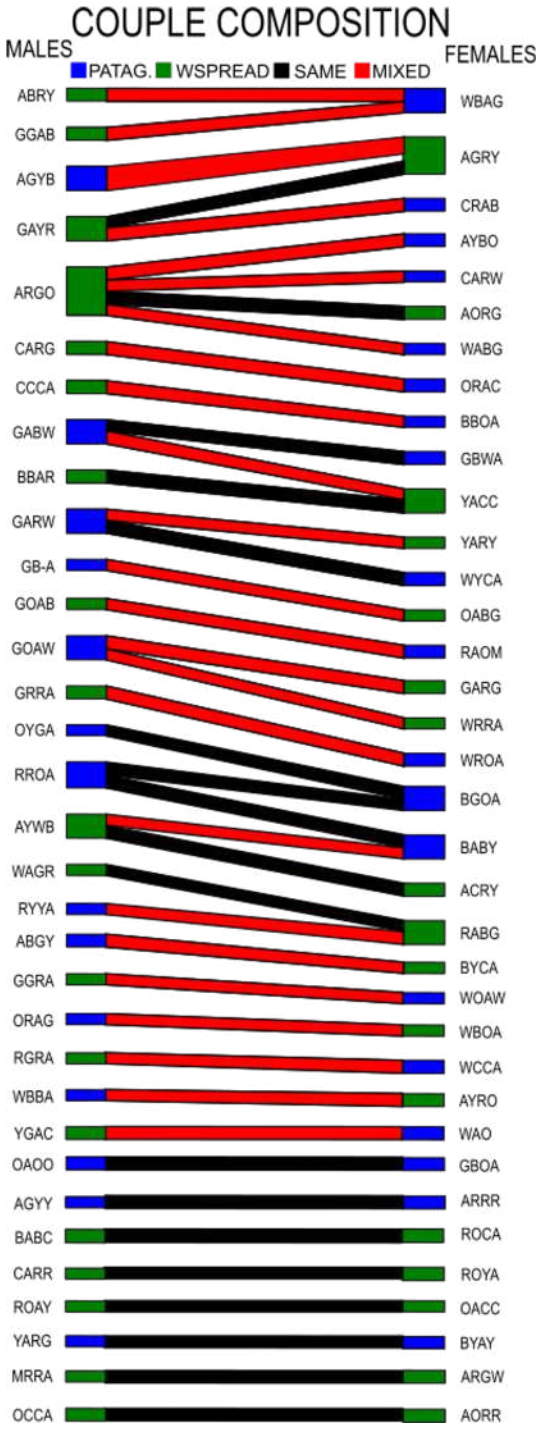

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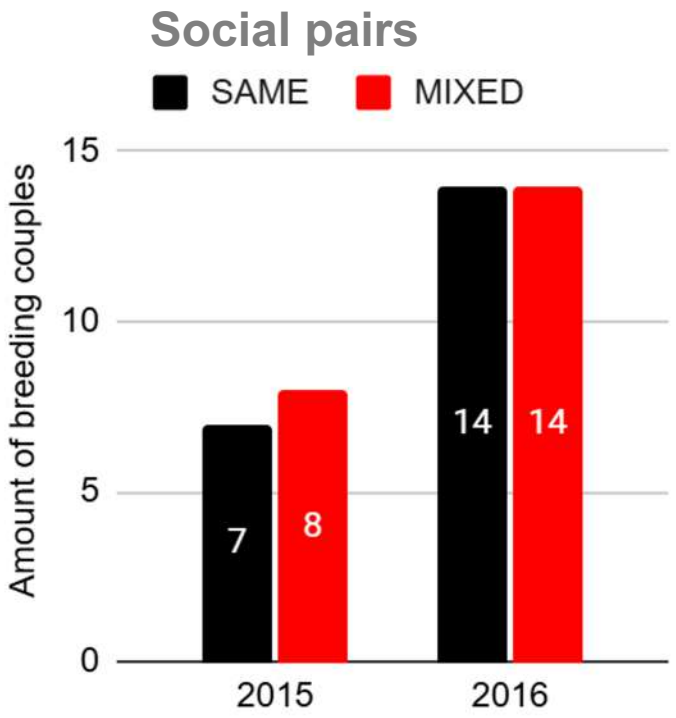

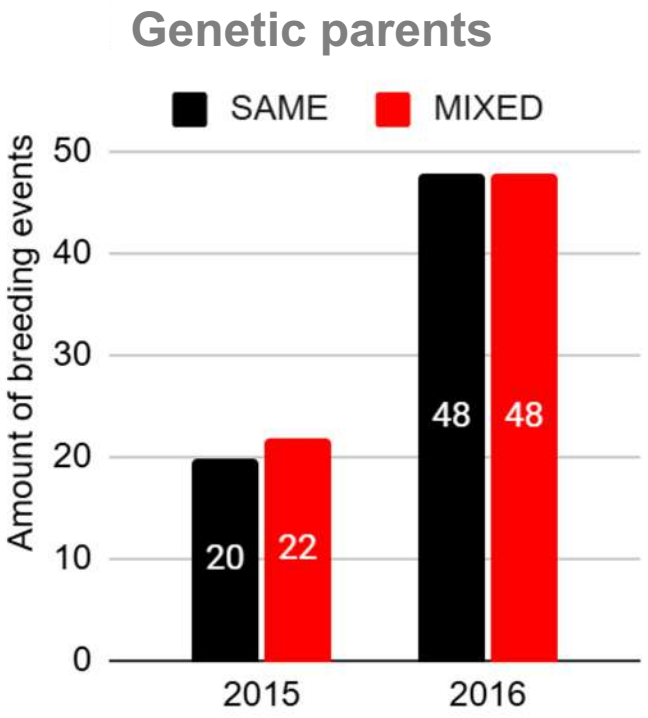

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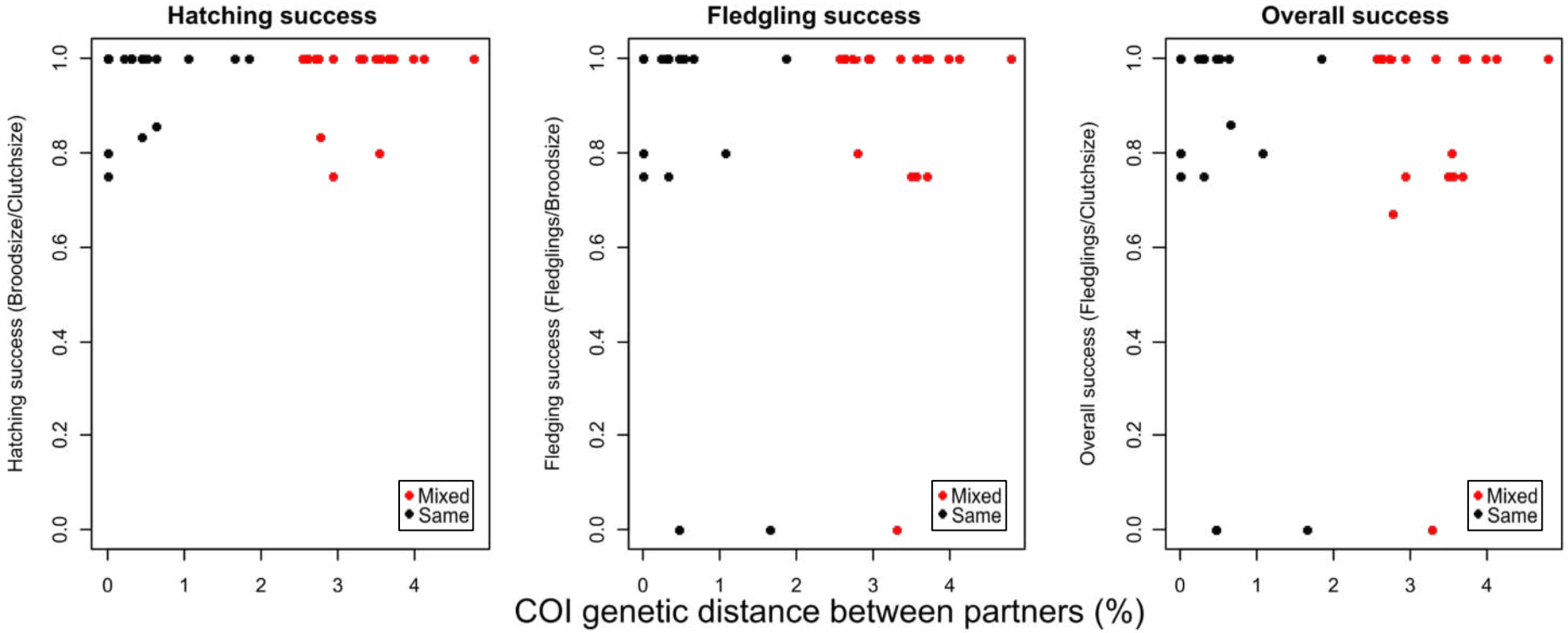

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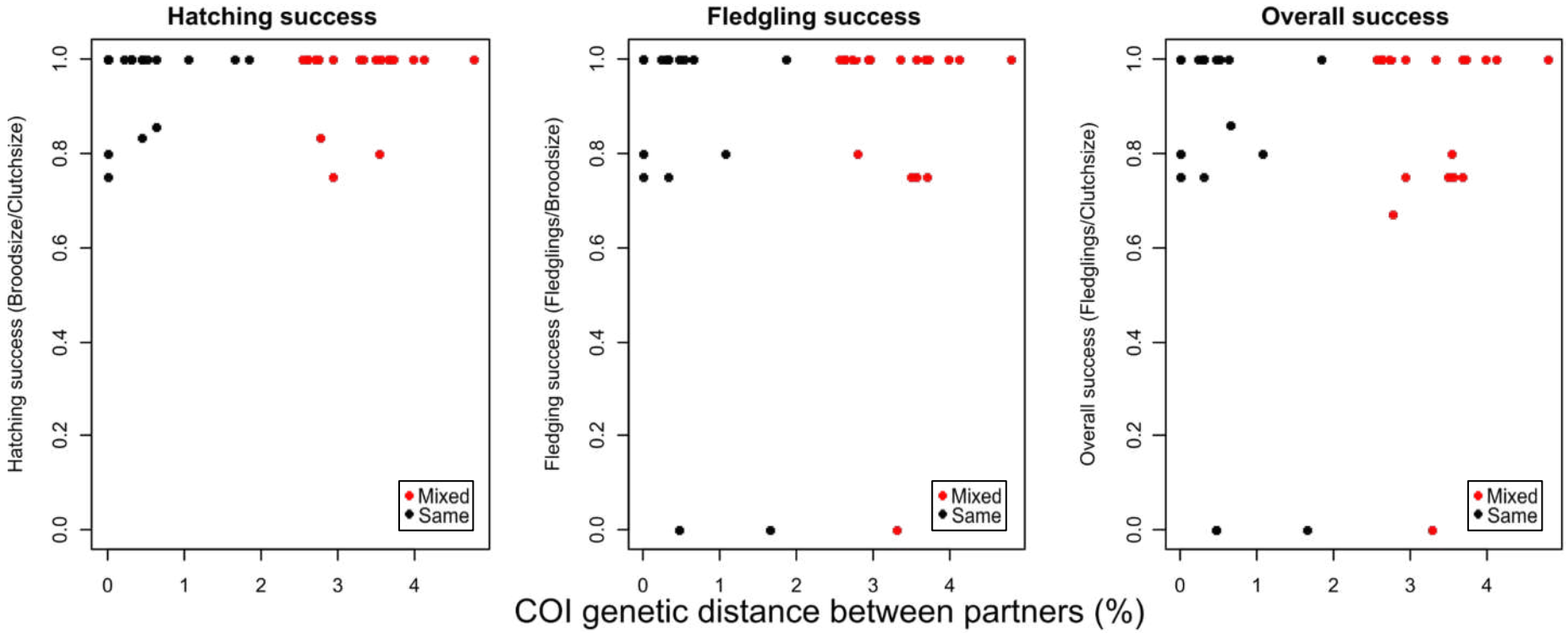

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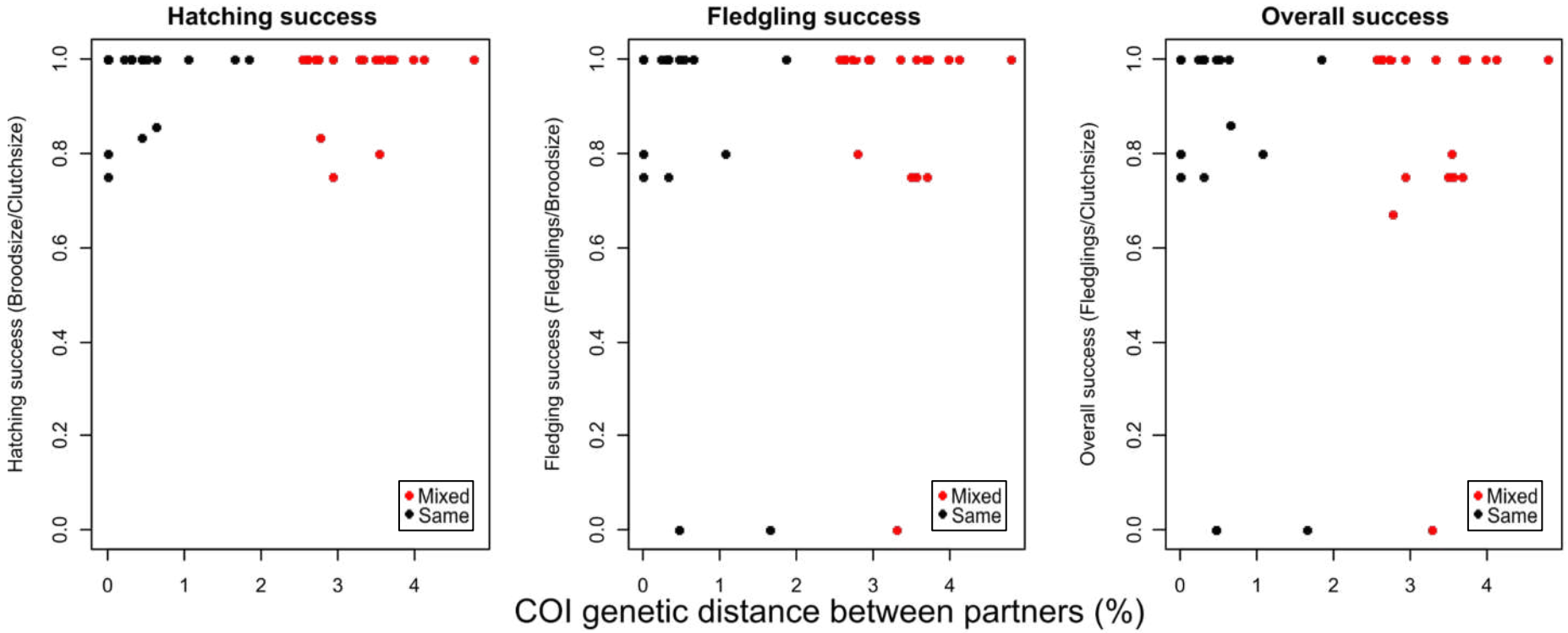

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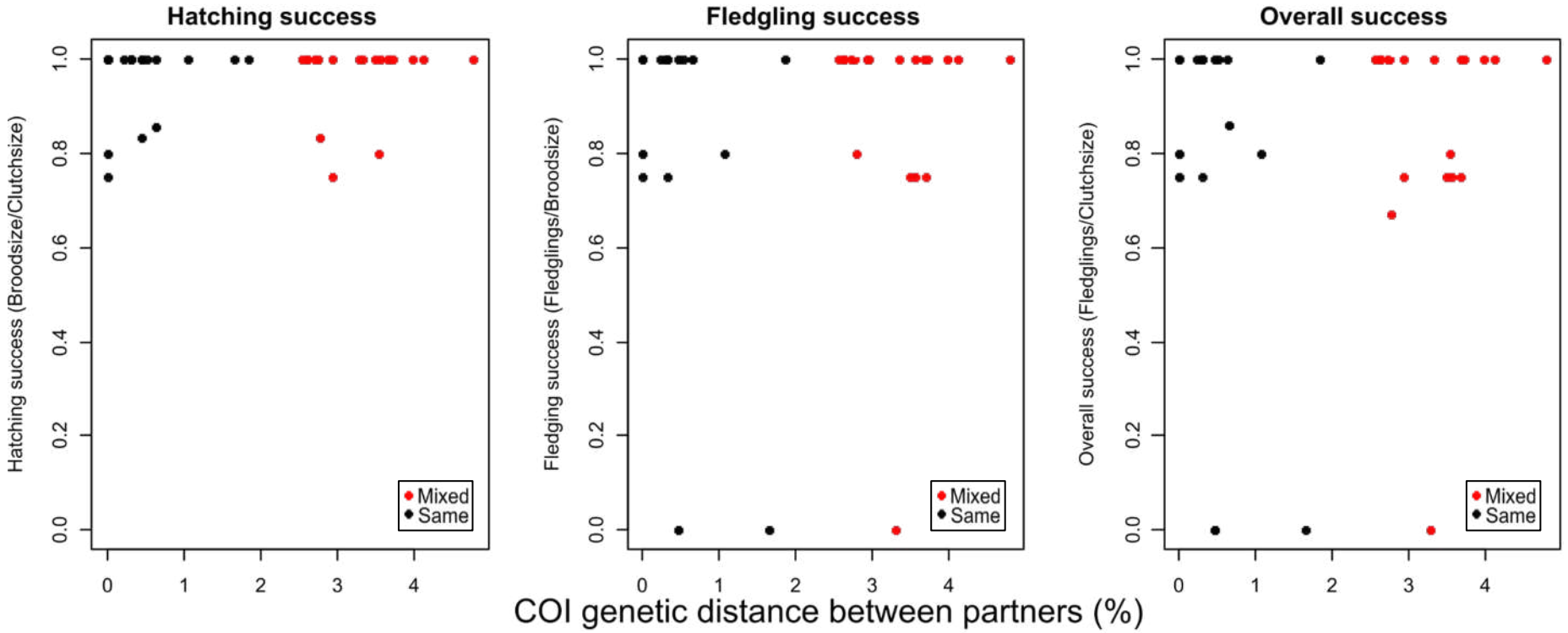

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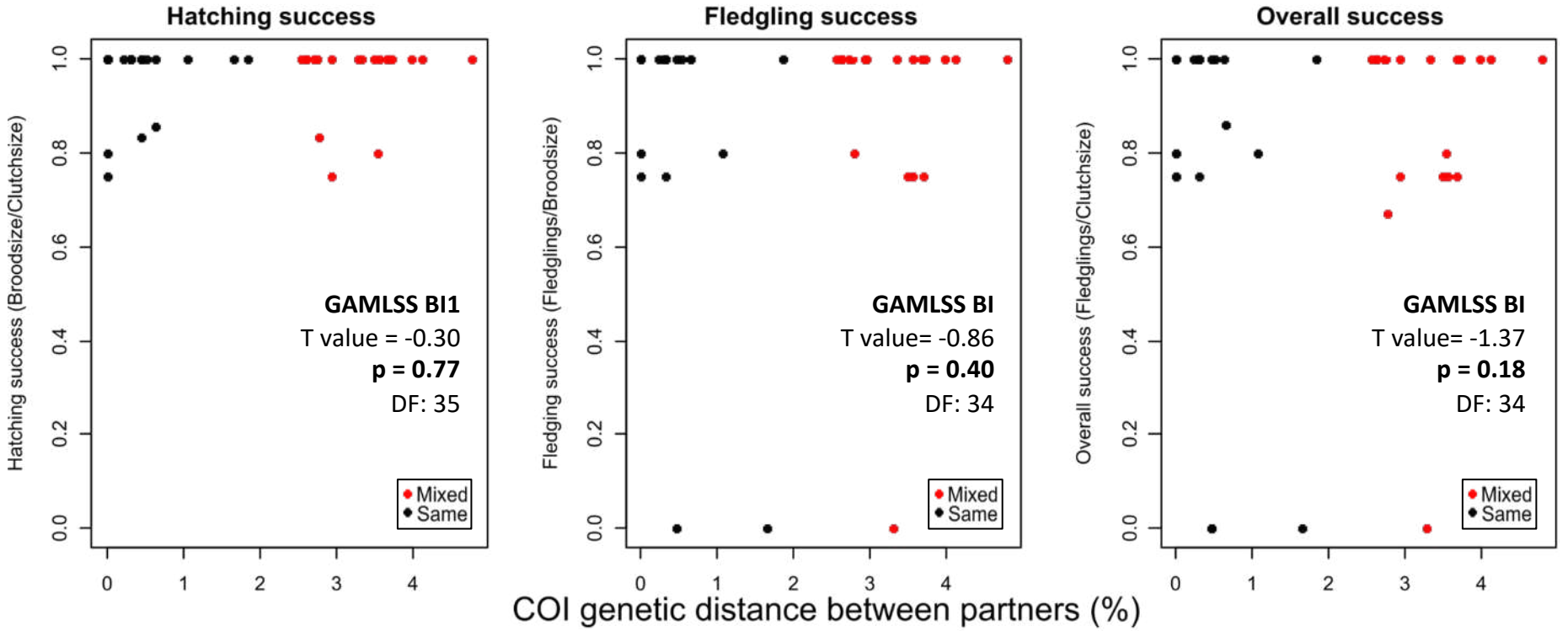

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No significant association between viability and COI distance between partners

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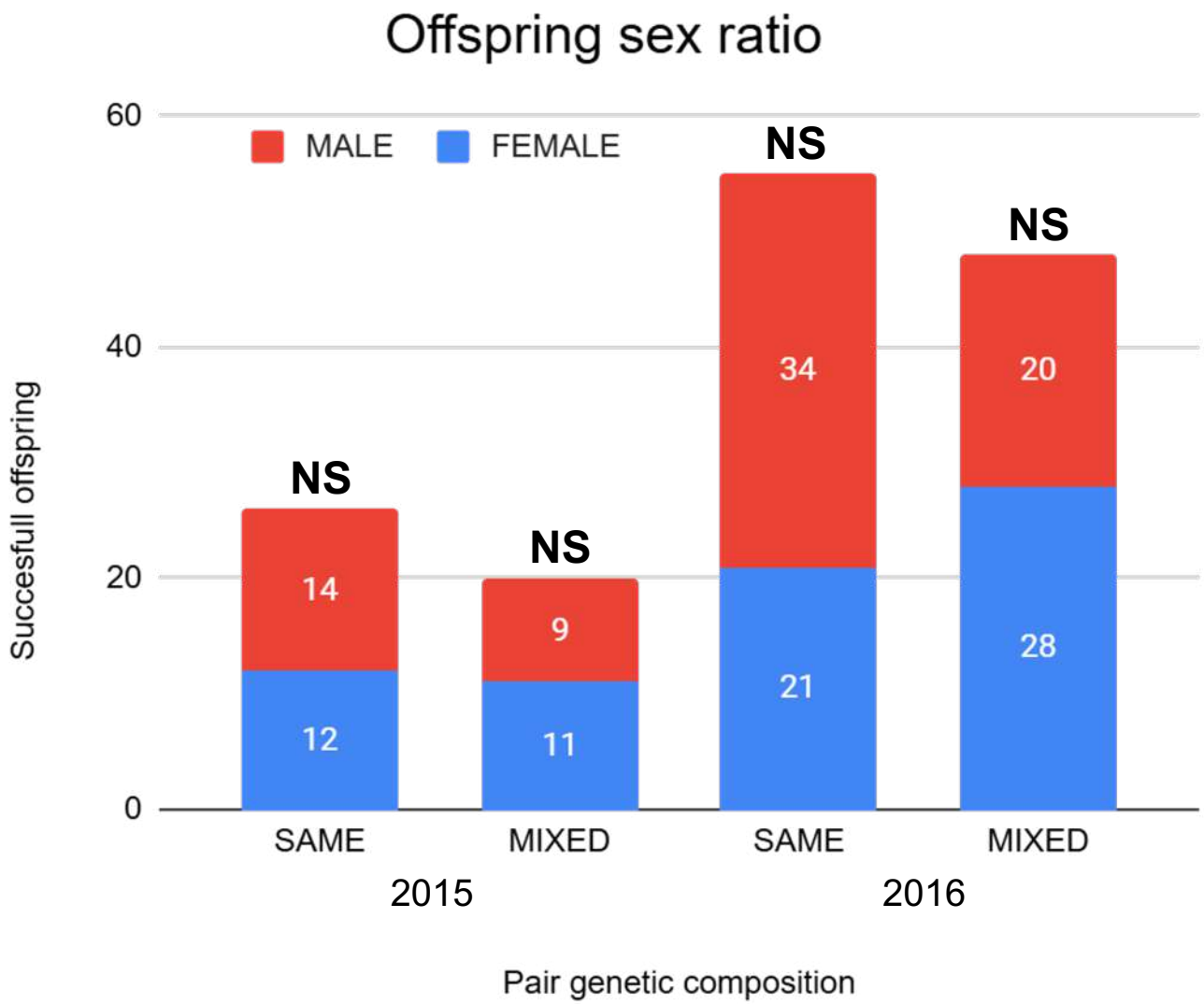
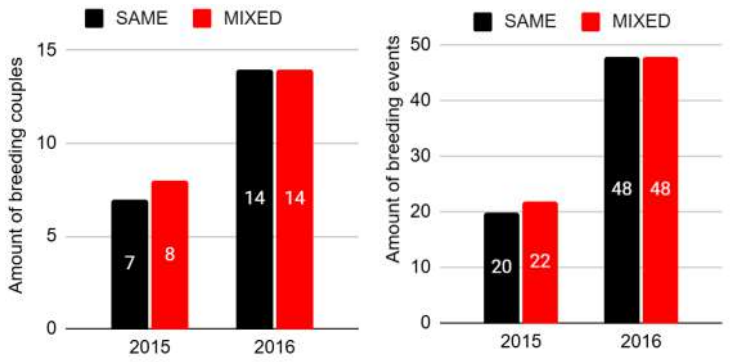


Discussion

Main conclusions

1. **No assortative mating:**
   - Even though lineages separated around 2 million years ago, there is no pattern of preference for mating with individuals of the same lineage.
   - Apparently there are no prezygotic reproductive isolation mechanisms in place, such as differences in song or colour.



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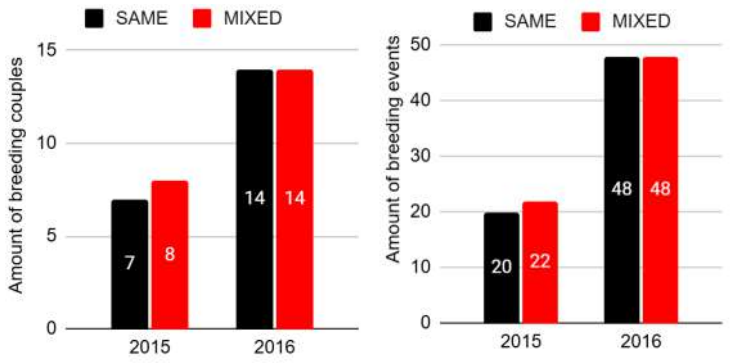
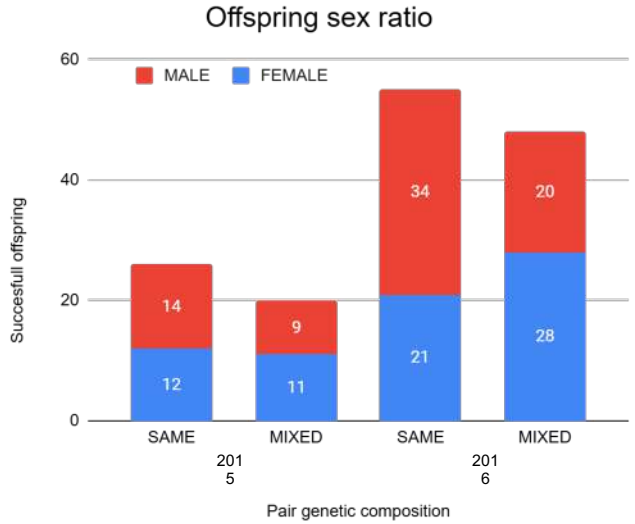


2. **No association between mitochondrial genetic distance of partners and offspring viability:**
   - Although there is around 5% COI sequence divergence between lineages, we did not find evidence of reduced viability (i.e., no evidence of postzygotic reproductive isolation mechanisms).



What’s next?

Analysis of songs in the contact zone vs. allopatric areas of each lineage to determine if there is vocal character displacement.

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Study how the **nuclear genes that interact with mitochondrial** products can do so successfully irrespective of the mitochondrial lineage of each individual.

Co-authors

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Laboratorio de Investigación y conservación de la Biodiversidad

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Agencia Nacional de Promoción de la Investigación, el Desarrollo Tecnológico y la Innovación

AVES ARGENTINAS
100 AÑOS JUNTO A VOS Y LA NATURALEZA

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¡Thank you!

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