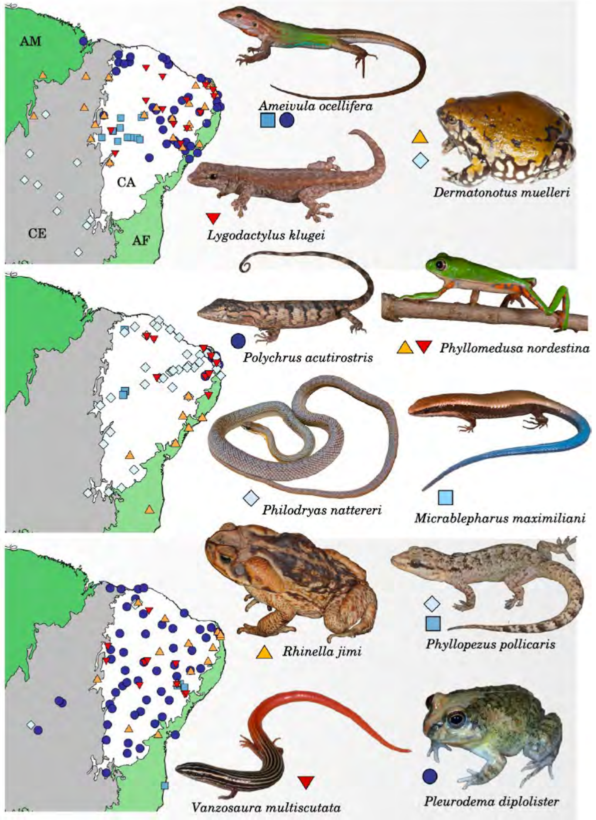
Filogeografía de Anfibios y Reptiles Neotropicales



Arley Camargo
CENUR Noreste & CENUR Este
Universidad de la República
arley.camargo@gmail.com

@bioevouy

Laboratorio Biogeografía & Evolución

CENUR NORESTE

UNIVERSIDAD DE LA REPÚBLICA URUGUAY

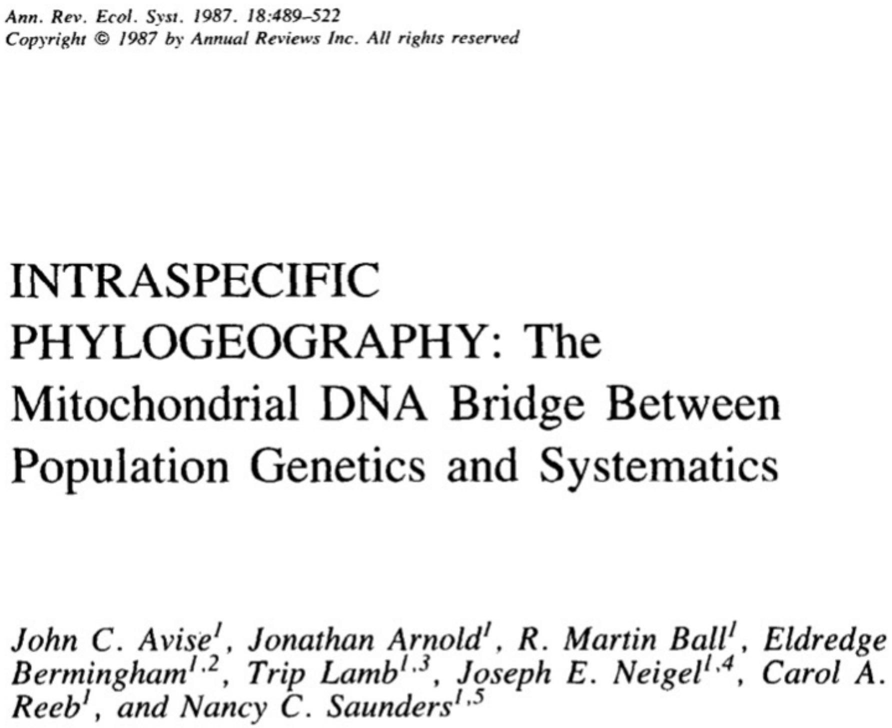
Esquema de la clase

- Filogeografía: conceptos y metodologías, controversias
- Filogeografía en la Región Neotropical: estudios en diferentes trans-biomas
- Casos de estudio: anfibios y reptiles

Filogeografía: conceptos y metodologías

- Definiciones
- Resumen histórico
- Enfoques descriptivos
- Análisis de clados anidados
- Controversias y enfoques alternativos
- Modelo coalescente

Filogeografía: el origen…



Ann. Rev. Ecol. Syst. 1987. 18:489–522
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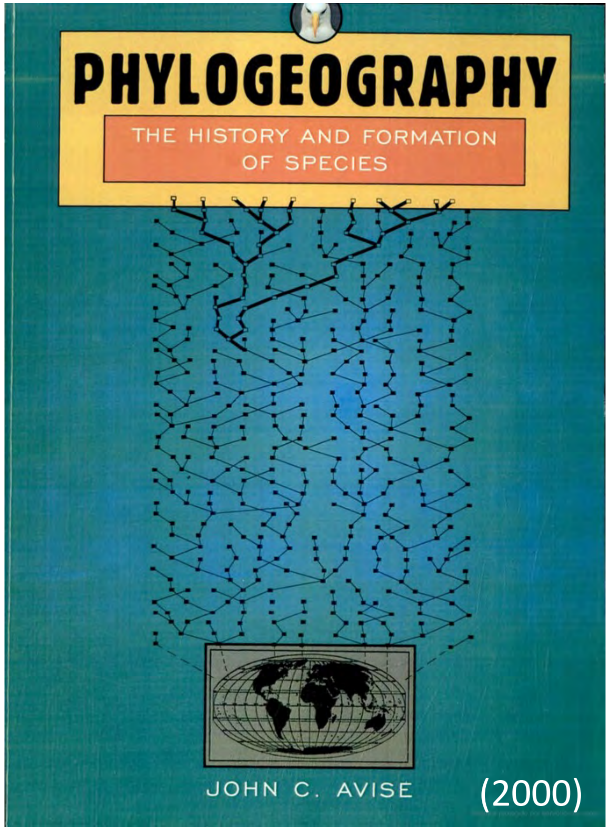
INTRASPECIFIC PHYLOGEOGRAPHY: The Mitochondrial DNA Bridge Between Population Genetics and Systematics

John C. Avise[1], Jonathan Arnold[1], R. Martin Ball[1], Eldredge Bermingham[1,2], Trip Lamb[1,3], Joseph E. Neigel[1,4], Carol A. Reeb[1], and Nancy C. Saunders[1,5]

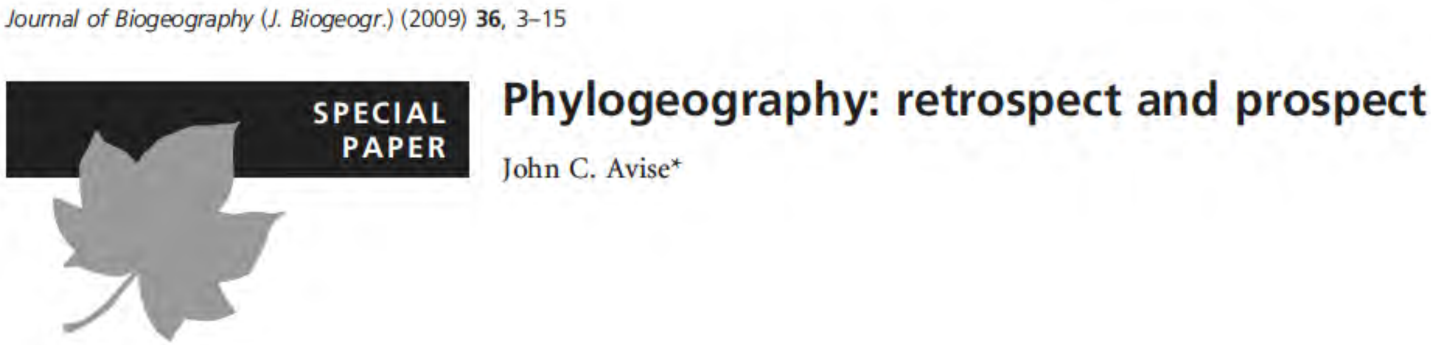


PHYLOGEOGRAPHY

THE HISTORY AND FORMATION OF SPECIES

JOHN C. AVISE

(2000)



Journal of Biogeography (*J. Biogeogr.*) (2009) **36**, 3–15

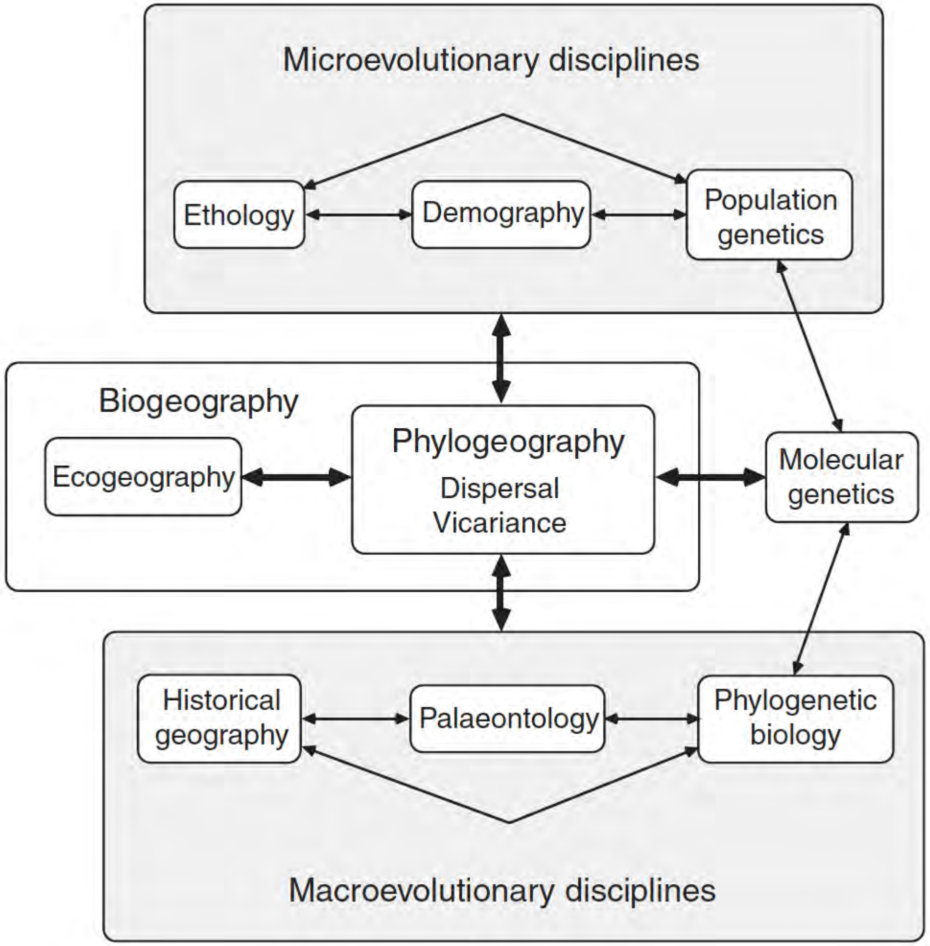
SPECIAL PAPER

Phylogeography: retrospect and prospect

John C. Avise*

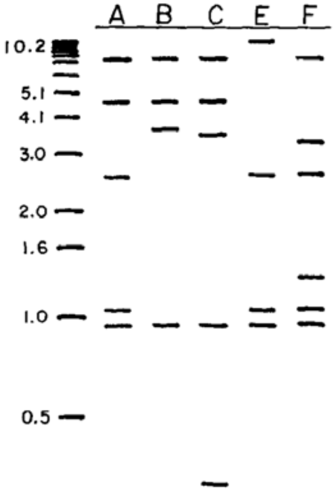
Filogeografía: definición

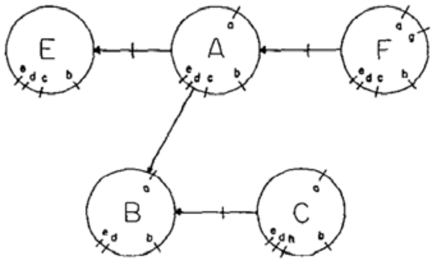
- Distribución espacial y temporal de linajes genéticos intraespecíficos y entre especies cercanamente emparentadas
- Inferencia de procesos históricos y demográficos a partir de patrones de diversidad genética
- Disciplina puente entre la sistemática filogenética y la genética de poblaciones



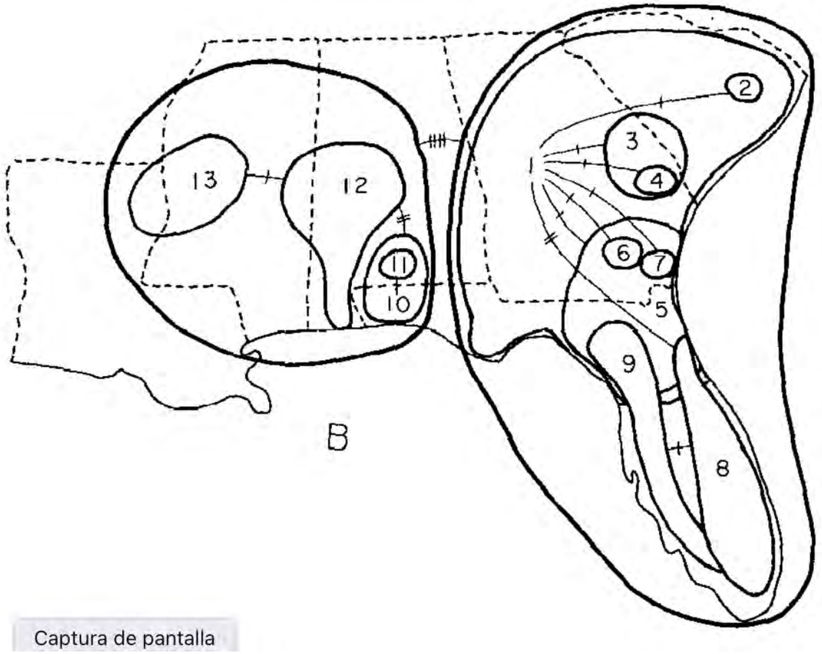
Filogeografía descriptiva

Datos

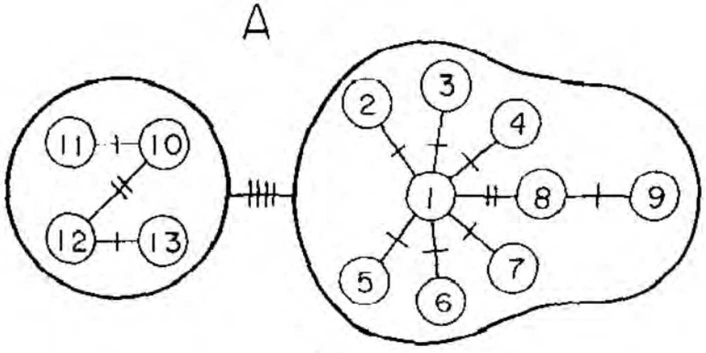




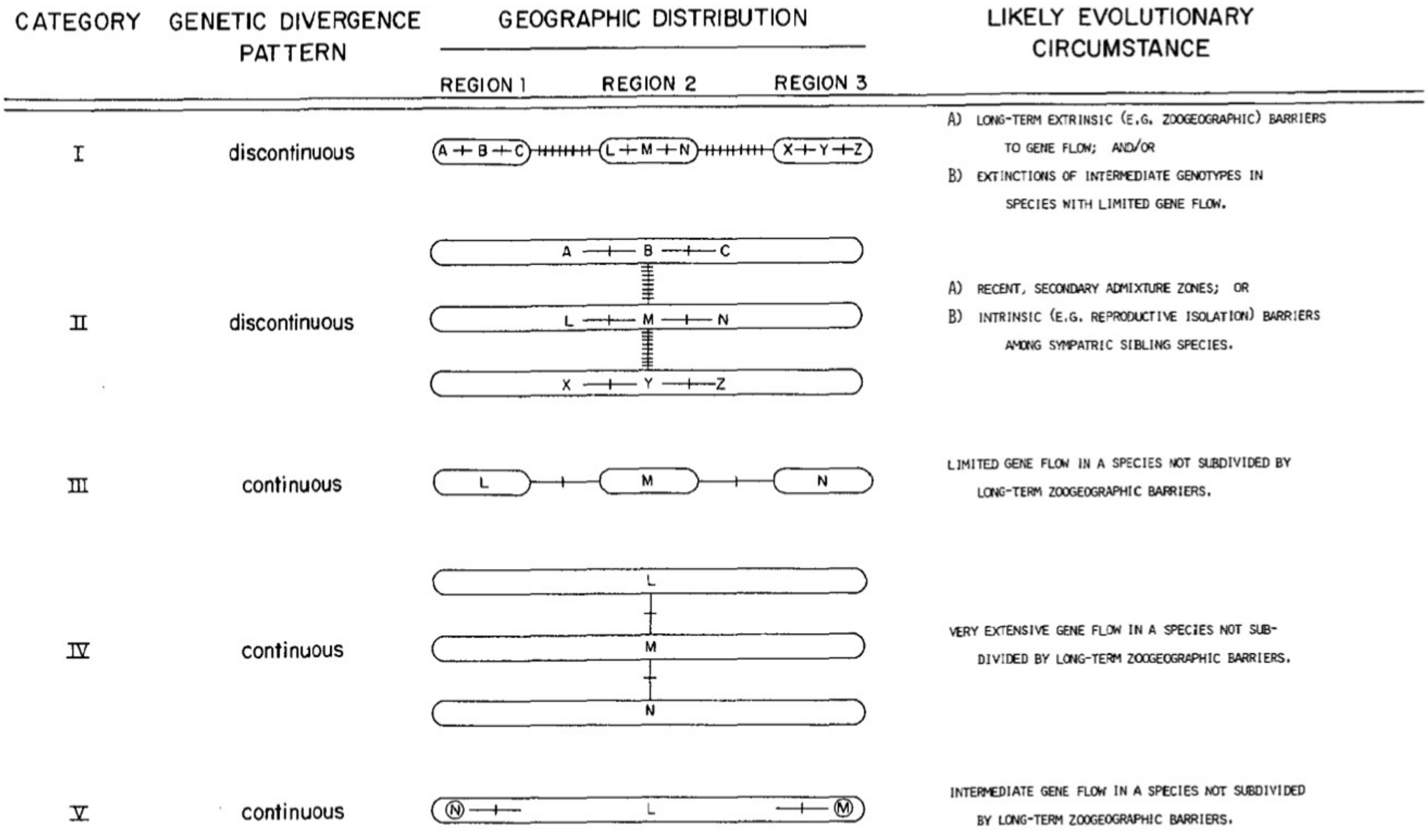
Distribución espacial



Árbol/red



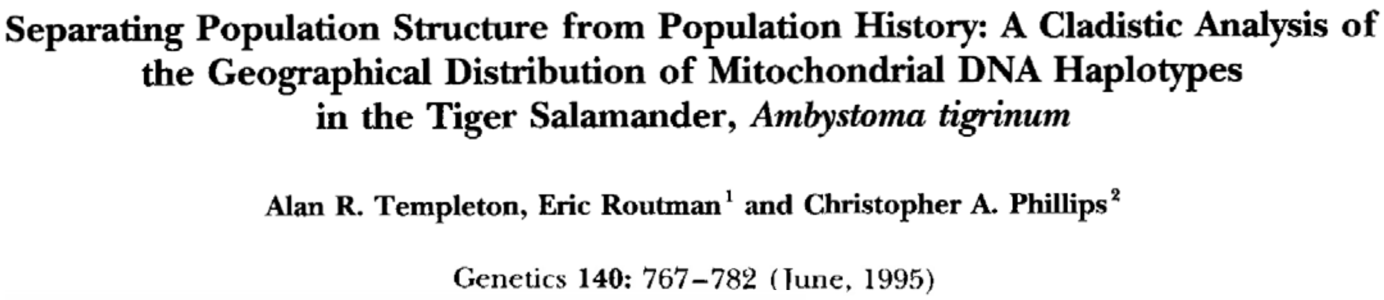
Filogeografía descriptiva



CATEGORY	GENETIC DIVERGENCE PATTERN	LIKELY EVOLUTIONARY CIRCUMSTANCE
I	discontinuous	A) LONG-TERM EXTRINSIC (E.G. ZOOGEOGRAPHIC) BARRIERS TO GENE FLOW; AND/OR B) EXTINCTIONS OF INTERMEDIATE GENOTYPES IN SPECIES WITH LIMITED GENE FLOW.
II	discontinuous	A) RECENT, SECONDARY ADMIXTURE ZONES; OR B) INTRINSIC (E.G. REPRODUCTIVE ISOLATION) BARRIERS AMONG SYMPATRIC SIBLING SPECIES.
III	continuous	LIMITED GENE FLOW IN A SPECIES NOT SUBDIVIDED BY LONG-TERM ZOOGEOGRAPHIC BARRIERS.
IV	continuous	VERY EXTENSIVE GENE FLOW IN A SPECIES NOT SUBDIVIDED BY LONG-TERM ZOOGEOGRAPHIC BARRIERS.
V	continuous	INTERMEDIATE GENE FLOW IN A SPECIES NOT SUBDIVIDED BY LONG-TERM ZOOGEOGRAPHIC BARRIERS.

Figure 4 General phylogeographic patterns (relationships between phylogeny and geography) theoretically observable in mtDNA surveys (see text).

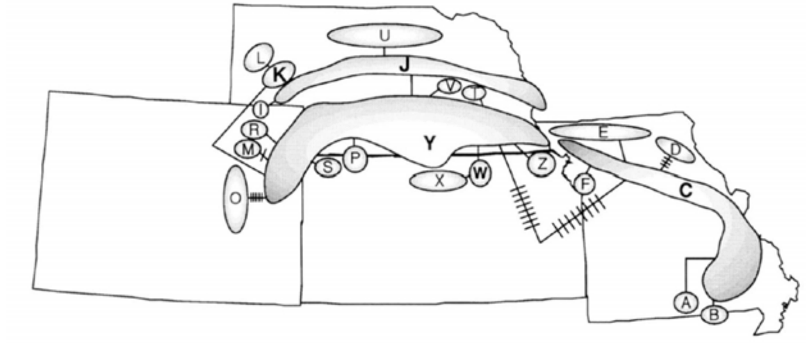
Filogeografía interpretativa

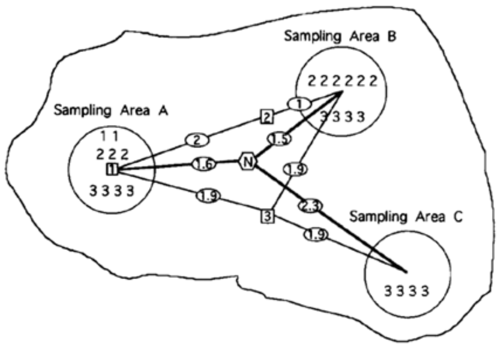


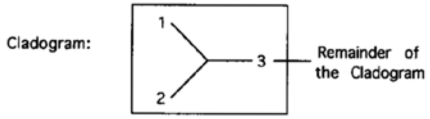
Separating Population Structure from Population History: A Cladistic Analysis of the Geographical Distribution of Mitochondrial DNA Haplotypes in the Tiger Salamander, *Ambystoma tigrinum*

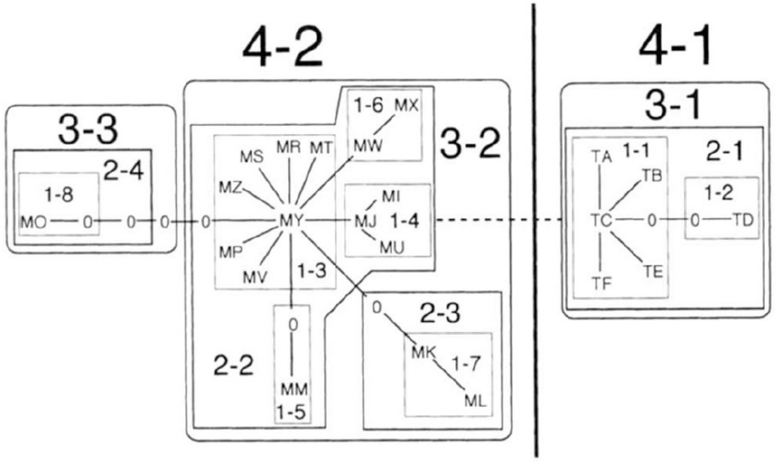
Alan R. Templeton, Eric Routman[1] and Christopher A. Phillips[2]

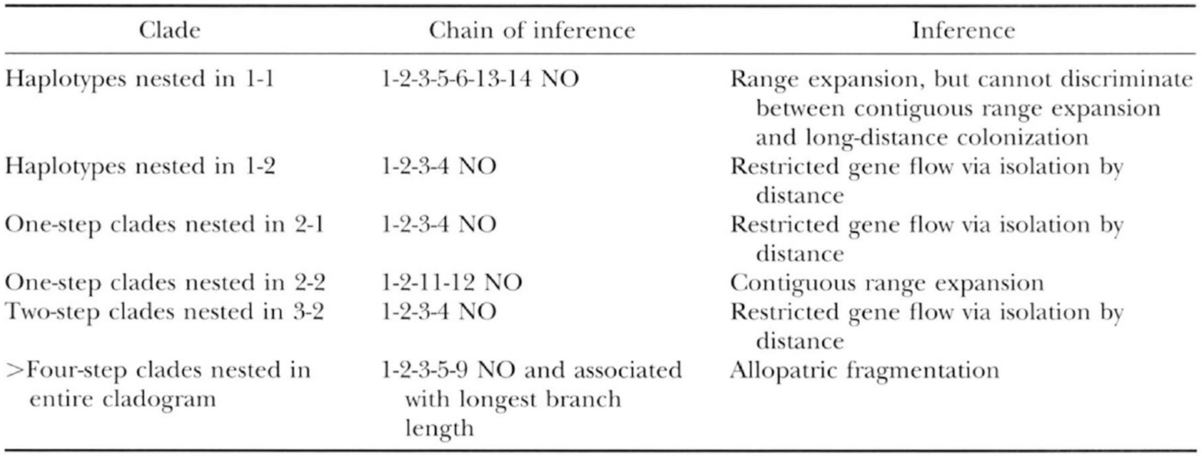
Genetics **140:** 767–782 (June, 1995)











Clade	Chain of inference	Inference
Haplotypes nested in 1-1	1-2-3-5-6-13-14 NO	Range expansion, but cannot discriminate between contiguous range expansion and long-distance colonization
Haplotypes nested in 1-2	1-2-3-4 NO	Restricted gene flow via isolation by distance
One-step clades nested in 2-1	1-2-3-4 NO	Restricted gene flow via isolation by distance
One-step clades nested in 2-2	1-2-11-12 NO	Contiguous range expansion
Two-step clades nested in 3-2	1-2-3-4 NO	Restricted gene flow via isolation by distance
>Four-step clades nested in entire cladogram	1-2-3-5-9 NO and associated with longest branch length	Allopatric fragmentation

APPENDIX

Start with haplotypes nested within a 1-step clade:

1. Are there any significant values for D_c, D_n, or *I-T* within the clade?
    - NO: the null hypothesis of no geographical association of haplotypes cannot be rejected (either panmixia in sexual populations, extensive dispersal in nonsexual populations, small sample size, or inadequate geographical sampling). Move on to another clade at the same or higher level.
    - YES: go to step 2.
2. Are the D_c values for tip or some (but not all) interior clades significantly small or is the *I-T* D_c distances significantly large?
    - NO: go to step 11.
    - YES: go to step 3.
    - Tip/interior status cannot be determined—Inconclusive Outcome.
3. Are any D_n and/or *I-T* D_n values significantly reversed from the D_c values, and/or do one or more tip clades show significantly large D_ns or interior clades significantly small D_ns or *I-T* significantly small D_n with the corresponding D_c values being nonsignificant?
    - NO: go to step 4.
    - YES: go to step 5.
4. Do the clades (or 2 or more subsets of them) with restricted geographical distributions have ranges that are completely or mostly nonoverlapping with the other clades in the nested group (particularly interiors), and does the pattern of restricted ranges represent a break or reversal from lower level trends within the nested series (applicable to higher-level clades only)?
    - NO: restricted gene flow with isolation by distance (restricted dispersal by distance in nonsexual species). This inference is strengthened if the clades with restricted distributions are found in diverse locations, if the union of their ranges roughly corresponds to the range of one or more clades (usually interiors) within the same nested group (applicable only to nesting clades with many clade members or to the highest-level clades regardless of number), and if the D_c values increase and become more geographically widespread with increasing clade level within a nested series (applicable to lower level clades only).
    - YES: go to step 9.
5. Do the clades (or 2 or more subsets of them) with restricted geographical distributions have ranges that are completely or mostly nonoverlapping with the other clades in the nested group (particularly interiors), and does the pattern of restricted ranges represent a break or reversal from lower-level trends within the nested series (applicable to higher-level clades only)?
    - NO: go to step 6.
    - YES: go to step 15.
6. Do clades (or haplotypes within them) with significant reversals or significant D_n values without significant D_c values define geographically concordant subsets, or are they geographically concordant with other haplotypes/clades showing similar distance patterns?
    - NO: go to step 7.
    - YES: go to step 13.
    - Too few clades (<2) to determine concordance—Insufficient genetic resolution to discriminate between range expansion/colinization and restricted dispersal/gene flow: proceed to step 7 to determine if the geographical sampling is sufficient to discriminate between short *vs.* long distance movement.
7. Are the clades with significantly large D_ns (or tip clades in general when D_n for *I-T* is significantly small) separated from the other clades by intermediate geographical areas that were sampled?
    - NO: go to step 8.
    - YES: restricted gene flow/dispersal but with some long-distance dispersal.
8. Is the species absent in the nonsampled areas?
    - NO: sampling design inadequate to discriminate between isolation by distance (short distance movements) *vs.* long distance dispersal
    - YES: restricted gene flow/dispersal but with some long-distance dispersal over intermediate areas not occupied by the species.
9. Are the different geographically concordant clade ranges separated by areas that have not been sampled?
    - NO: past fragmentation. (If inferred at a high clade level, additional confirmation occurs if the clades displaying restricted but at least partially nonoverlapping geographical distributions are mutationally connected to one another by a larger than average number of steps.)
    - YES: go to step 10.
10. Is the species absent in the nonsampled areas?
    - NO: geographical sampling scheme inadequate to discriminate between fragmentation and isolation by distance.
    - YES: allopatric fragmentation. (If inferred at a high clade level, additional confirmation occurs if the clades displaying restricted but at least partially nonoverlapping geographical distributions are mutationally connected to one another by a larger than average number of steps.)
11. Are the D_c values for some tip clades significantly large, and/or the D_cs for all interiors significantly small, and/or the *I-T* D_c significantly small?
    - NO: go to step 17
    - YES: range expansion, go to step 12.
12. Are the D_n and/or *I-T* D_n values significantly reversed from the D_c values?
    - NO: contiguous range expansion.
    - YES: go to step 13.
13. Are the clades with significantly large D_ns (or tip clades in general when D_n for *I-T* is significantly small) separated from the other clades by intermediate geographical areas that were sampled?
    - NO: go to step 14.
    - YES: long distance colonization.
14. Is the species absent in the non-sampled areas?
    - NO: sampling design inadequate to discriminate between contiguous range expansion and long-distance colonization.
    - YES: long-distance colonization.
15. Are the different geographically concordant areas separated by areas that have not been sampled?
    - NO: past fragmentation. (If inferred at a high-clade level, additional confirmation occurs if the clades displaying restricted but at least partially nonoverlapping geographical distributions are mutationally connected to one another by a larger than average number of steps.)
    - YES: go to step 16.
16. Is the species absent in the nonsampled areas?
    - NO: go to step 18.
    - YES: allopatric fragmentation. (If inferred at a high-clade level, additional confirmation occurs if the clades displaying restricted but at least partially nonoverlapping geographical distributions are mutationally connected to one another by a larger than average number of steps.)
17. Are the D_n values for tip or some (but not all) interior clades significantly small, or the D_n for one or more interior clades significantly large, or is the *I-T* D_n value significantly large.
    - NO: inconclusive outcome.
    - YES: go to step 4.
18. Are the clades found in the different geographical locations separated by a branch length with a larger than average number of mutational steps.
    - NO: geographical sampling scheme inadequate to discriminate between fragmentation, range expansion, and isolation by distance.
    - YES: geographical sampling scheme inadequate to discriminate between fragmentation and isolation by distance.

Filogeografía estadística

Molecular Ecology (2002) **11**, 2623–2635

Statistical phylogeography

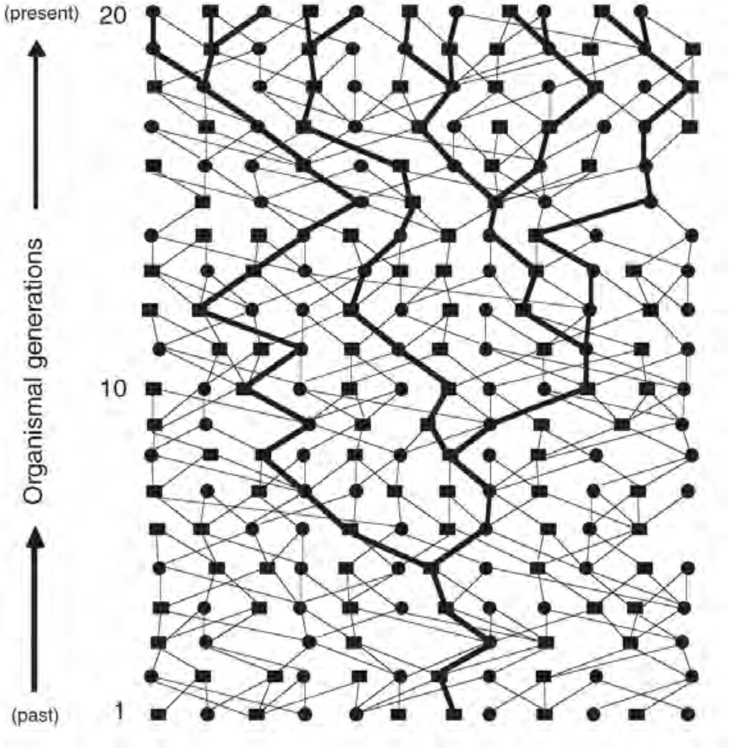
L. LACEY KNOWLES and WAYNE P. MADDISON
Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, Arizona 85721–0088, USA

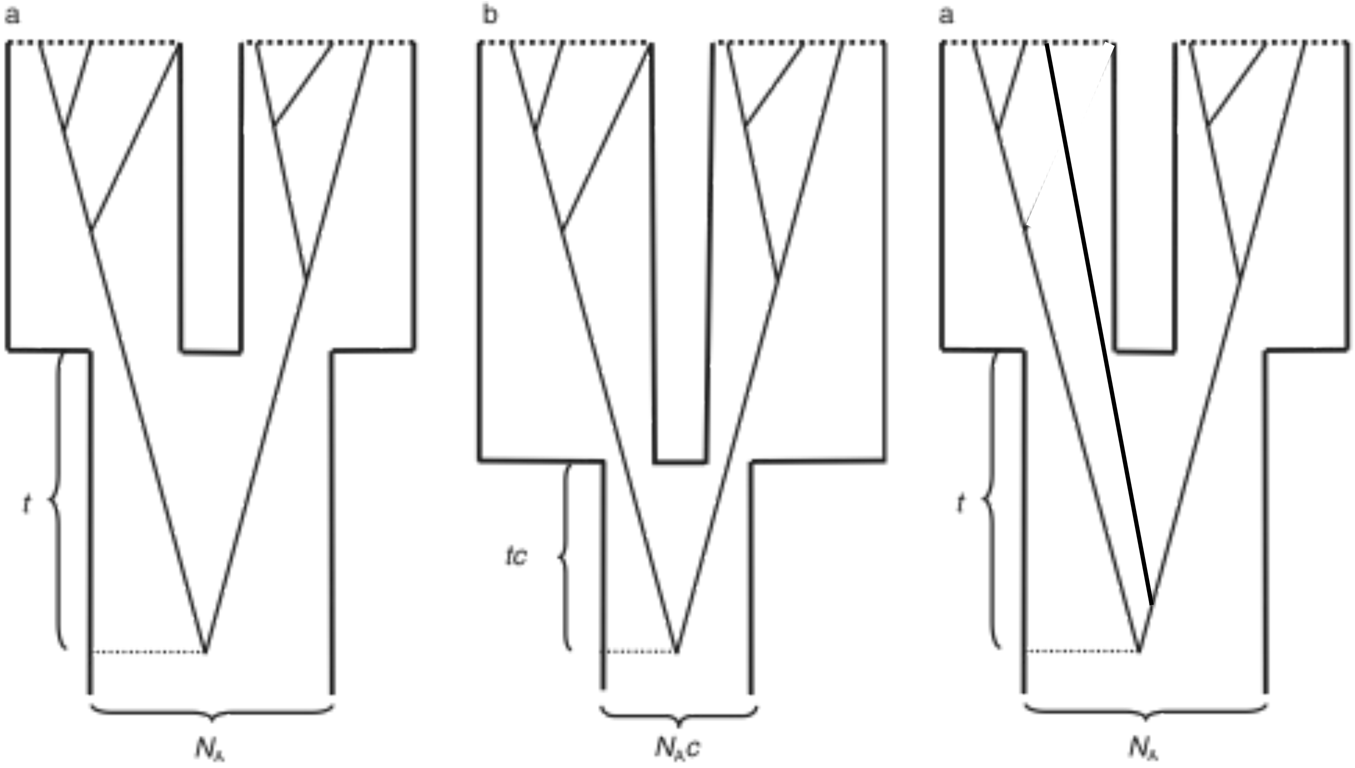
Molecular Ecology (2009) **18**, 1034–1047

INVITED REVIEW

Statistical inferences in phylogeography

RASMUS NIELSEN*† and MARK A. BEAUMONT‡

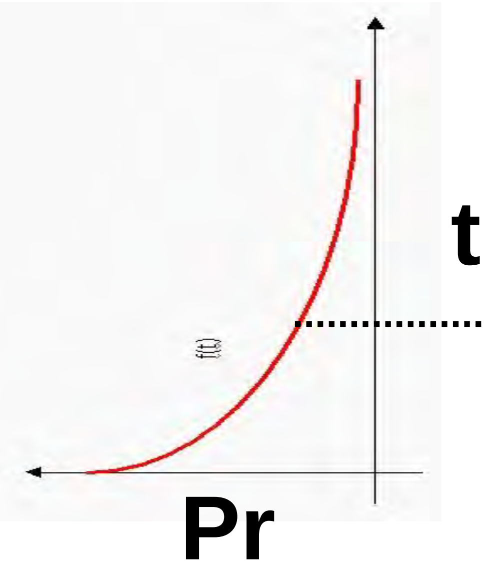


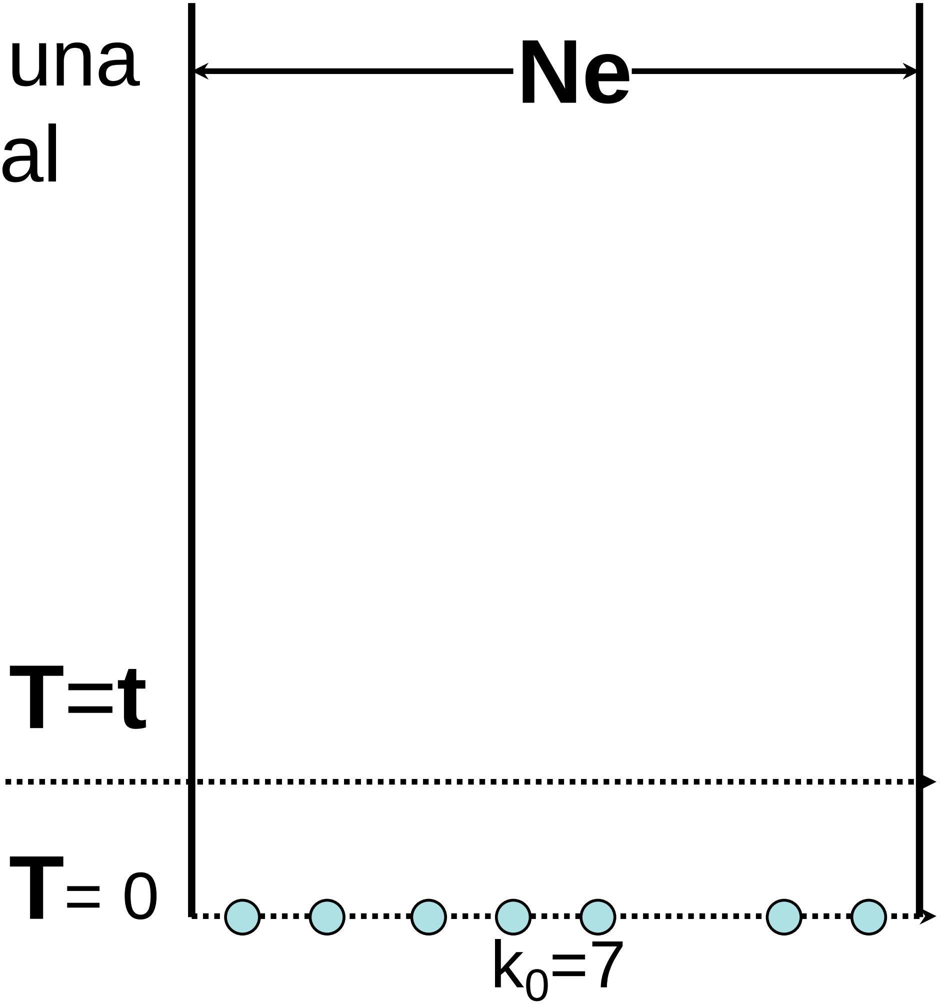


El Modelo Coalescente

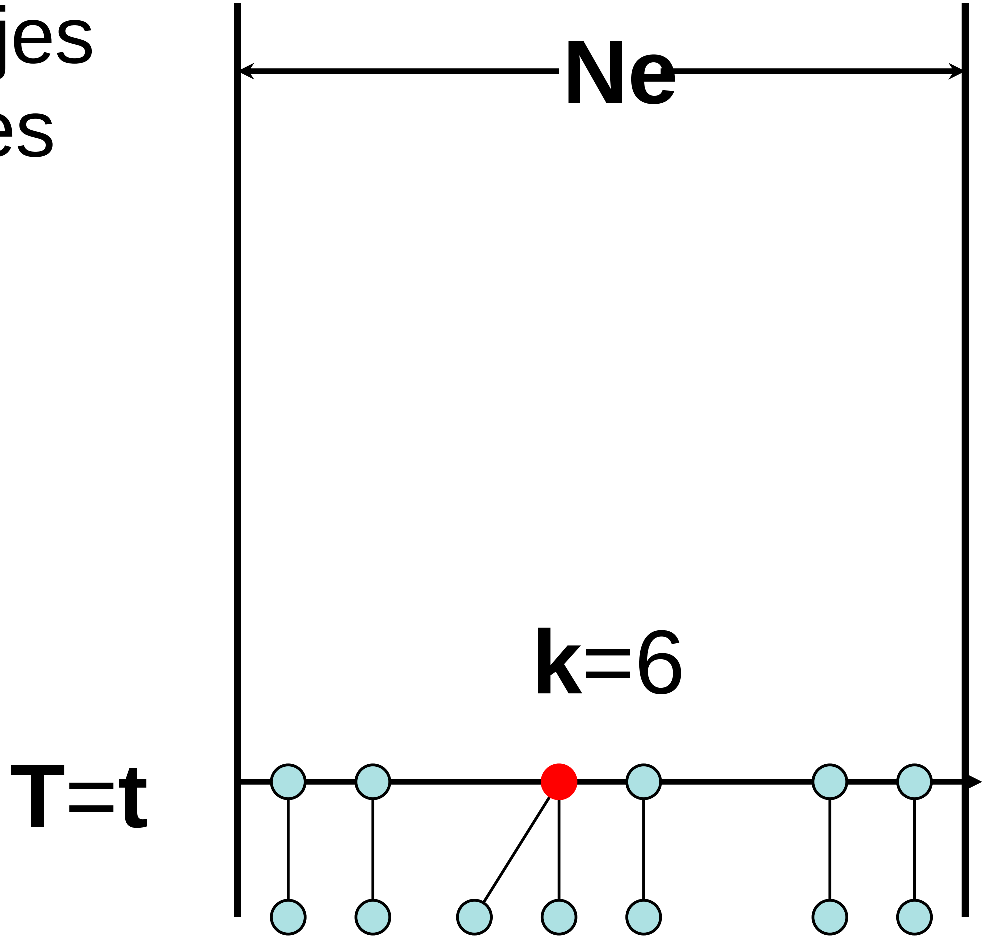
1) Sortear **t** al azar de una distribución exponencial

$$P_c(t) = \frac{1}{2N_e} e^{-\frac{t-1}{2N_e}}$$

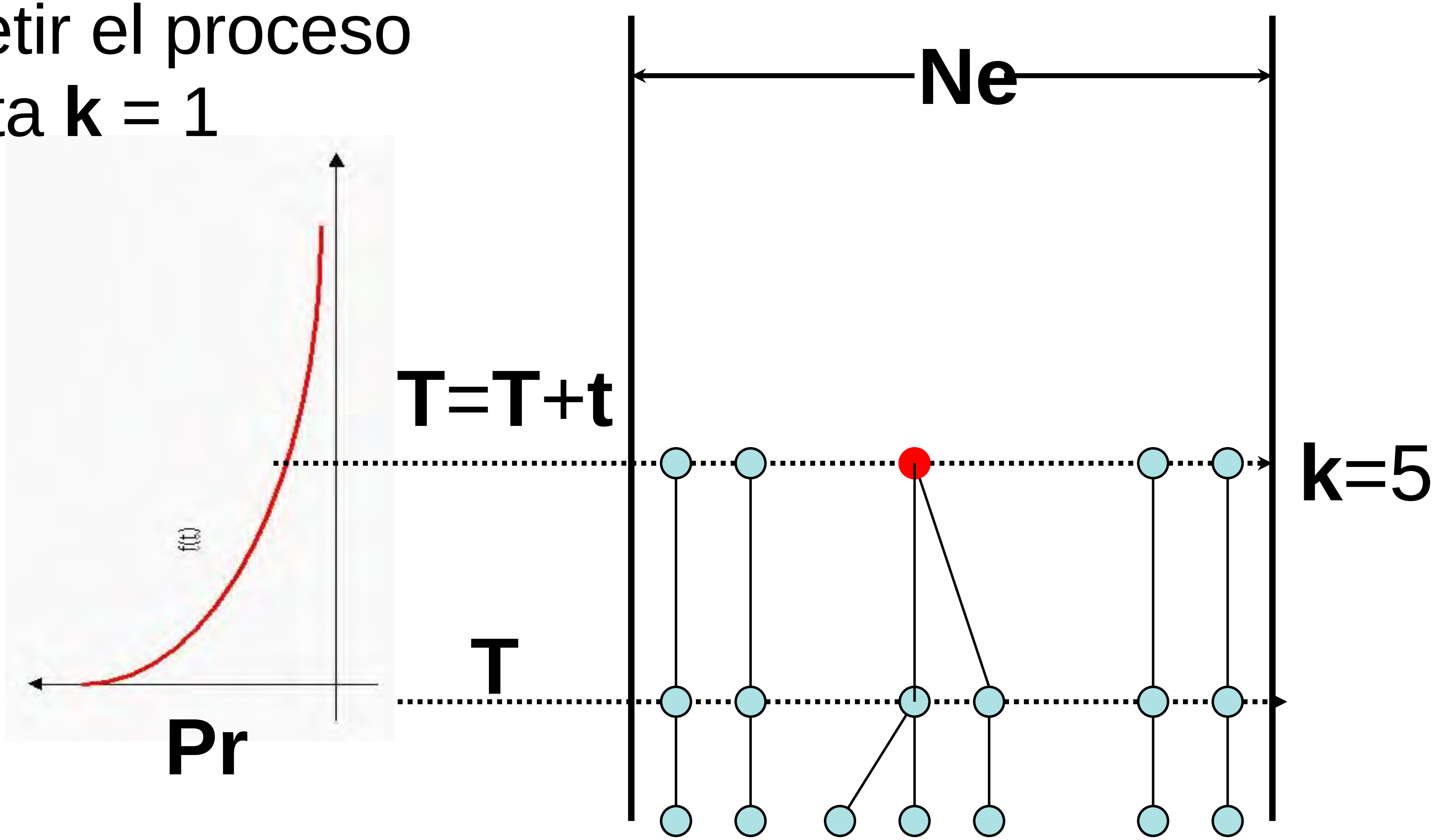


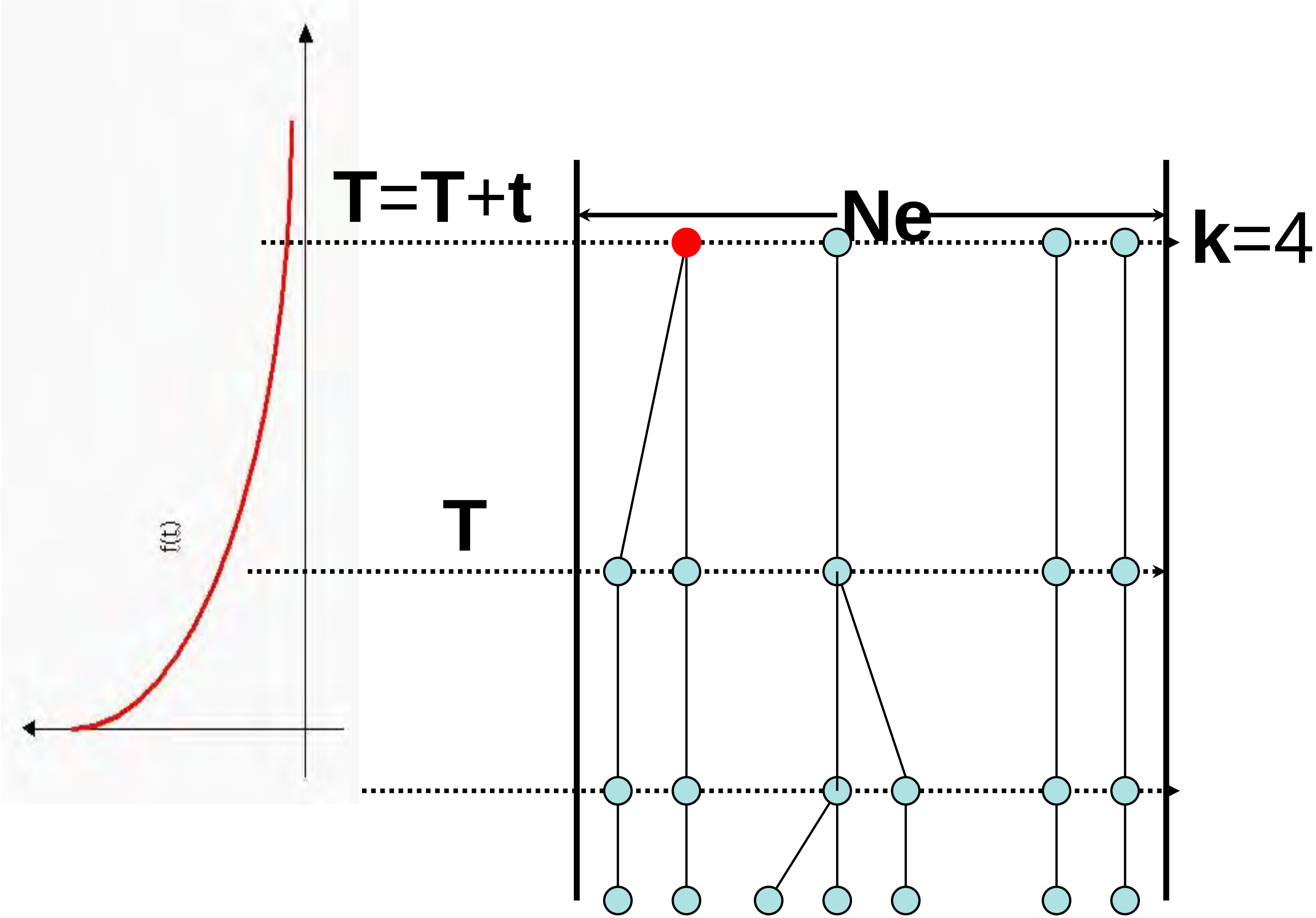


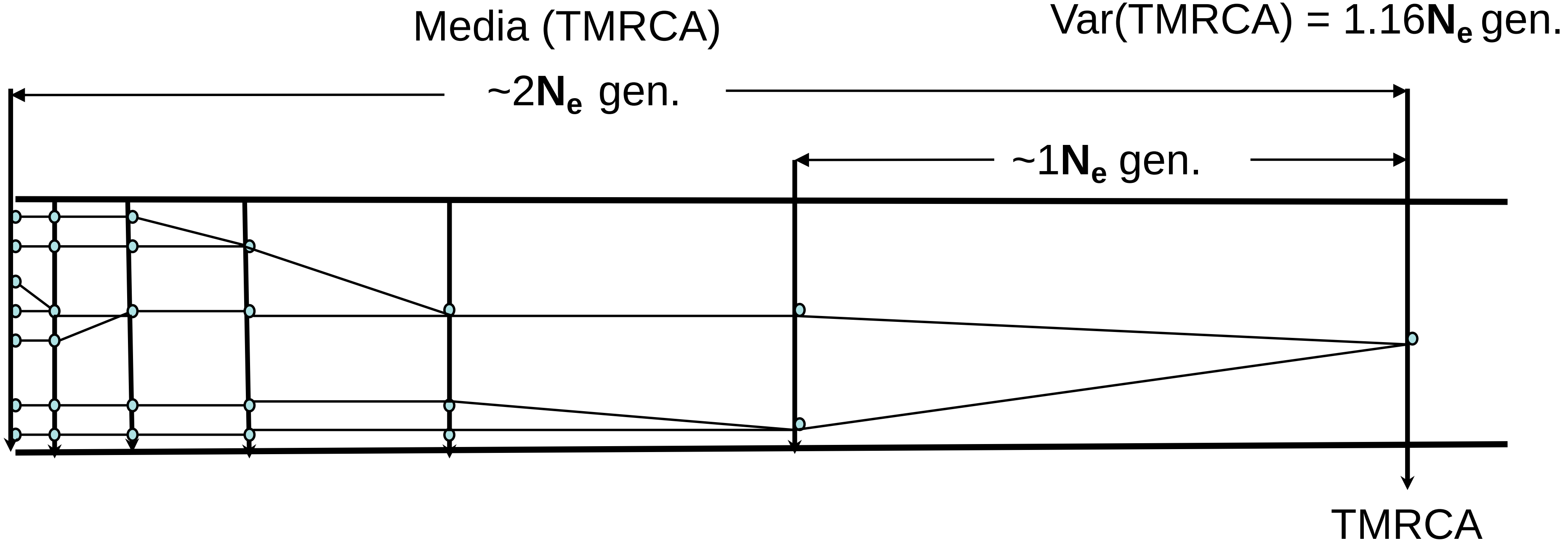
2) Coalescen al azar
2 copias de **k** linajes
para dar **k**-1 linajes
en **T=t**



3) Cambiar **T=t** y repetir el proceso hasta **k** = 1




T=T+t
Ne
k=4
T
f(t)



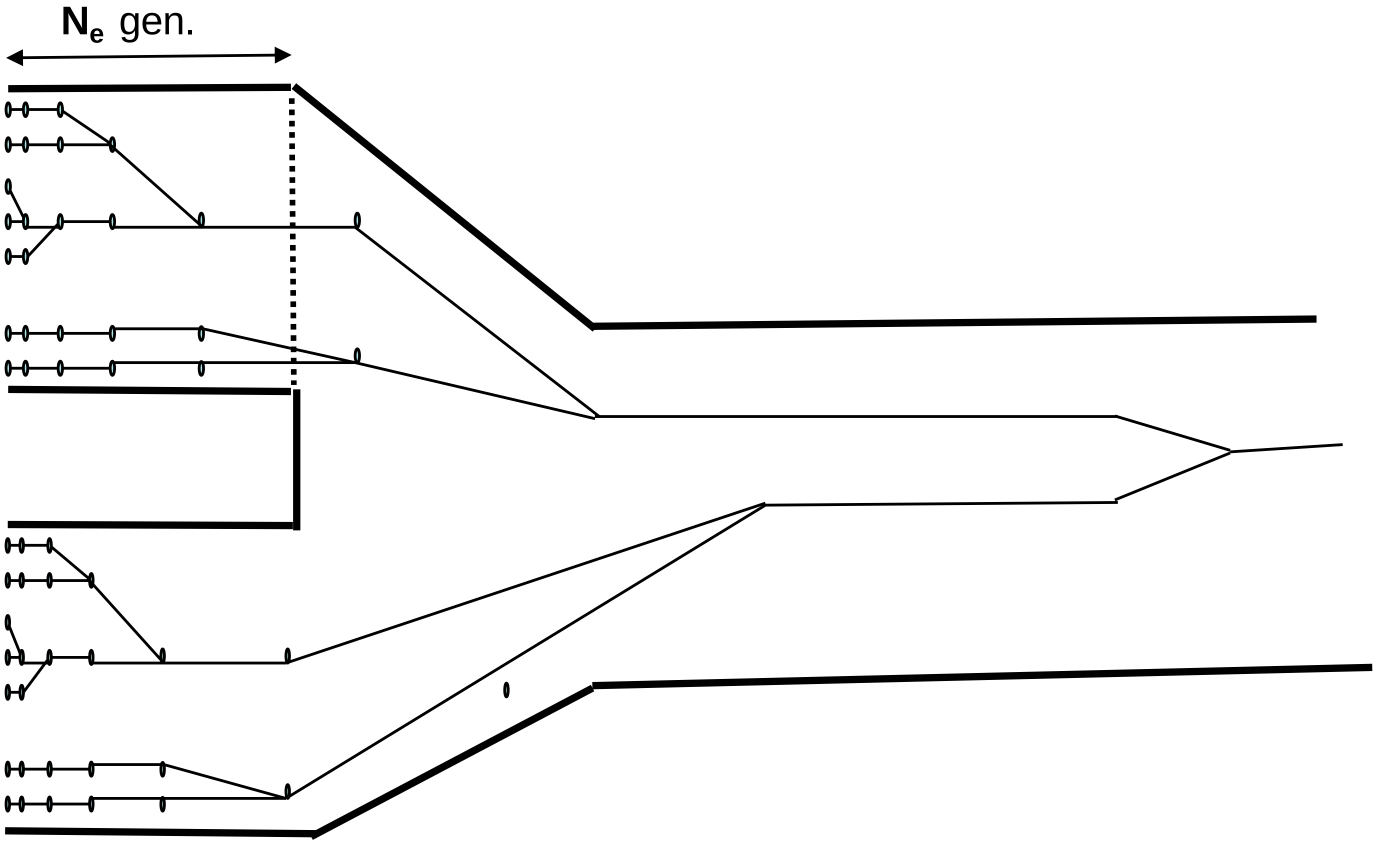
Media (TMRCA)

Var(TMRCA) = 1.16$\mathbf{N_e}$ gen.

~2$\mathbf{N_e}$ gen.

~1$\mathbf{N_e}$ gen.

TMRCA


N_e gen.

Filogeografía: controversias

- Ambigüedades del NCPA: “loops” en red de haplotipos, anidamiento de clados, interpretación de la clave de inferencia (Nielsen & Beaumont 2009)
- Evaluación con simulaciones (Knowles & Maddison 2004, Panchal & Beaumont 2007): alta tasa de falsos positivos (50%) debido a testeo múltiple sin corrección

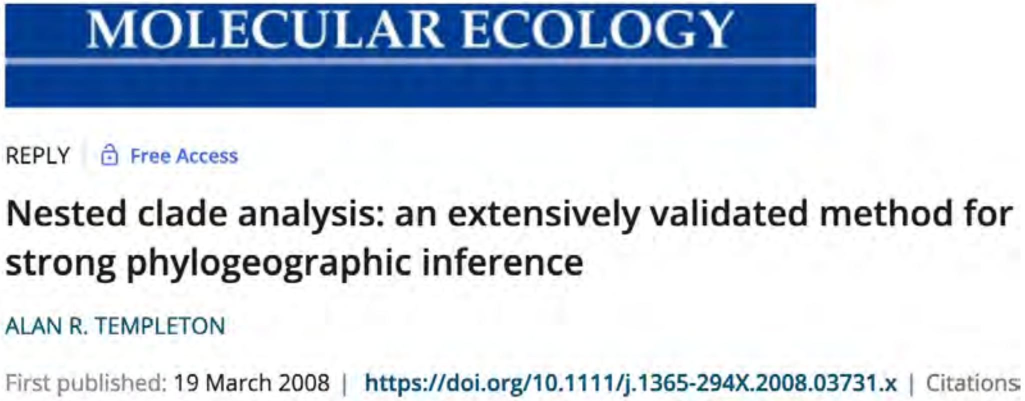
MOLECULAR ECOLOGY

Free Access

The coup de grâce for the nested clade phylogeographic analysis?

RÉMY J. PETIT

First published: 20 December 2007 | https://doi.org/10.1111/j.1365-294X.2007.03589.x |



MOLECULAR ECOLOGY

REPLY | Free Access

Nested clade analysis: an extensively validated method for strong phylogeographic inference

ALAN R. TEMPLETON

First published: 19 March 2008 | https://doi.org/10.1111/j.1365-294X.2008.03731.x | Citations

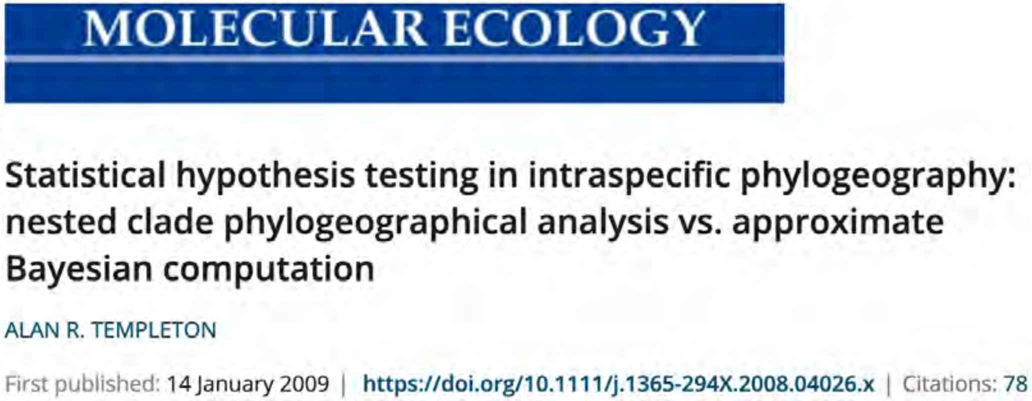
MOLECULAR ECOLOGY

COMMENT | Free Access

On the validity of nested clade phylogeographical analysis

MARK A. BEAUMONT, MAHESH PANCHAL

First published: 08 May 2008 | https://doi.org/10.1111/j.1365-294X.2008.03786.x | Citations:



MOLECULAR ECOLOGY

Statistical hypothesis testing in intraspecific phylogeography: nested clade phylogeographical analysis vs. approximate Bayesian computation

ALAN R. TEMPLETON

First published: 14 January 2009 | https://doi.org/10.1111/j.1365-294X.2008.04026.x | Citations: 78

Filogeografía: mas controversias…

Free Access

WHY DOES A METHOD THAT FAILS CONTINUE TO BE USED?

L. Lacey Knowles

First published: 24 October 2008 | https://doi.org/10.1111/j.1558-5646.2008.00481.x | Citations: 61

Free Access

WHY DOES A METHOD THAT FAILS CONTINUE TO BE USED? THE ANSWER

Alan R. Templeton

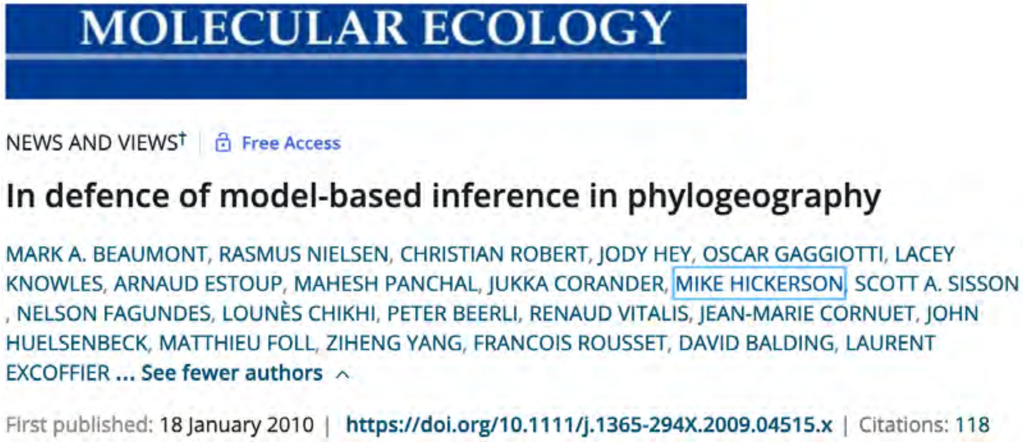
First published: 20 March 2009 | https://doi.org/10.1111/j.1558-5646.2008.00600.x | Citations: 42

NEWS AND VIEWS† | Free Access

Coalescent-based, maximum likelihood inference in phylogeography

ALAN R. TEMPLETON

First published: 18 January 2010 | https://doi.org/10.1111/j.1365-294X.2009.04514.x

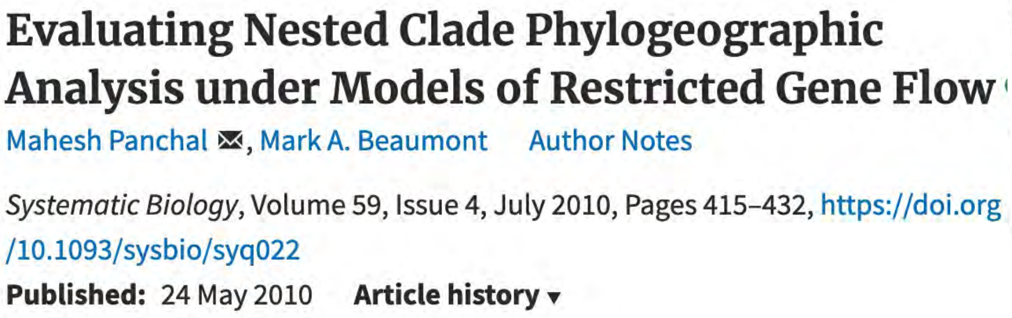


NEWS AND VIEWS† | Free Access

In defence of model-based inference in phylogeography

MARK A. BEAUMONT, RASMUS NIELSEN, CHRISTIAN ROBERT, JODY HEY, OSCAR GAGGIOTTI, LACEY KNOWLES, ARNAUD ESTOUP, MAHESH PANCHAL, JUKKA CORANDER, MIKE HICKERSON, SCOTT A. SISSON , NELSON FAGUNDES, LOUNÈS CHIKHI, PETER BEERLI, RENAUD VITALIS, JEAN-MARIE CORNUET, JOHN HUELSENBECK, MATTHIEU FOLL, ZIHENG YANG, FRANCOIS ROUSSET, DAVID BALDING, LAURENT EXCOFFIER ... See fewer authors ^

First published: 18 January 2010 | https://doi.org/10.1111/j.1365-294X.2009.04515.x | Citations: 118



Evaluating Nested Clade Phylogeographic Analysis under Models of Restricted Gene Flow

Mahesh Panchal ✉, Mark A. Beaumont Author Notes

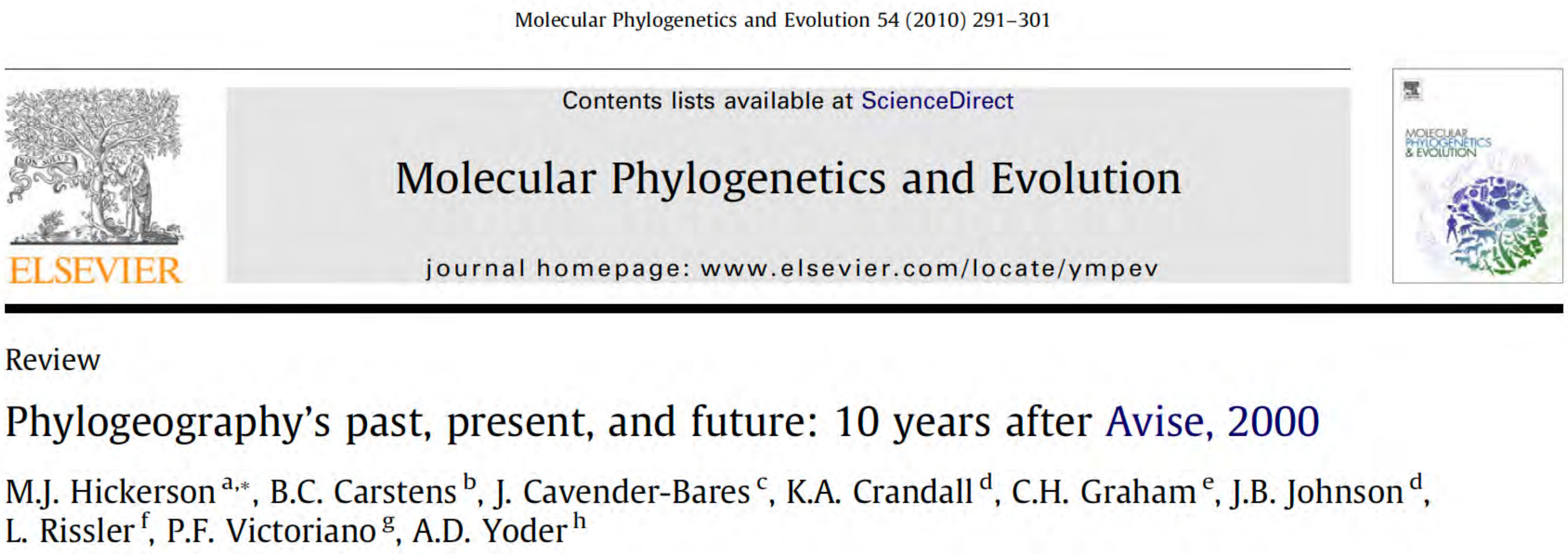
Systematic Biology, Volume 59, Issue 4, July 2010, Pages 415–432, https://doi.org/10.1093/sysbio/syq022

Published: 24 May 2010 **Article history** ▾

Coherent and incoherent inference in phylogeography and human evolution

Alan R. Templeton ✉ Authors Info & Affiliations

March 22, 2010 107(14)6376-6381 https://doi.org/10.1073/pnas.0910647107



Molecular Phylogenetics and Evolution 54 (2010) 291–301

Contents lists available at ScienceDirect

Molecular Phylogenetics and Evolution

journal homepage: www.elsevier.com/locate/ympev

ELSEVIER

Review

Phylogeography's past, present, and future: 10 years after Avise, 2000

M.J. Hickerson[a,*], B.C. Carstens[b], J. Cavender-Bares[c], K.A. Crandall[d], C.H. Graham[e], J.B. Johnson[d], L. Rissler[f], P.F. Victoriano[g], A.D. Yoder[h]

- NCPA *fue* el método paradigmático de la era descriptiva
- NCPA *representó* un marco estadístico para inferir historia demográfica directamente de genealogías
- Sin embargo, igualar la genealogía con la demografía puede generar sobre-interpretaciones cuando se ignora la estocasticidad del coalescente
- En la nueva era, la genealogía *no* es el foco, sino que es un paso intermedio que conecta la demografía con un modelo coalescente explícito

Approximate Bayesian Computation

Approximate Bayesian Computation in Population Genetics FREE

Mark A Beaumont, Wenyang Zhang, David J Balding

Genetics, Volume 162, Issue 4, 1 December 2002, Pages 2025–2035, https://doi.org/10.1093/genetics/162.4.2025

Approximate Bayesian Computation in Evolution and Ecology

Annual Review of Ecology, Evolution, and Systematics

Vol. 41:379-406 (Volume publication date December 2010)
First published online as a Review in Advance on August 10, 2010
https://doi.org/10.1146/annurev-ecolsys-102209-144621

Mark A. Beaumont

MOLECULAR ECOLOGY

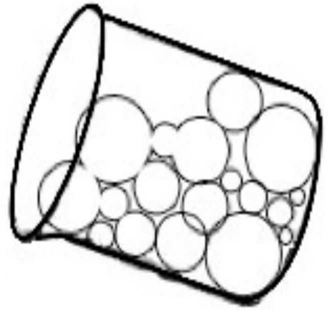
Molecular Ecology (2010) **19**, 2609–2625 doi: 10.1111/j.1365-294X.2010.04690.x

INVITED REVIEW

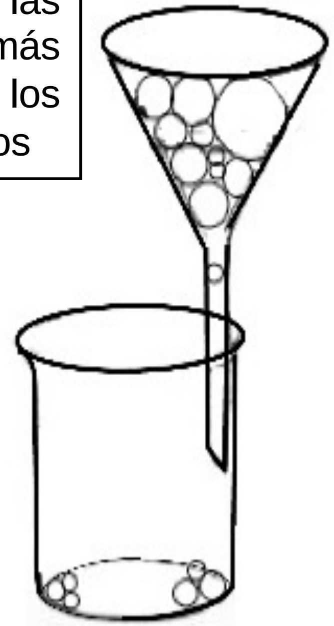
ABC as a flexible framework to estimate demography over space and time: some cons, many pros

G. BERTORELLE,* A. BENAZZO* and S. MONA*†‡

Simulación de datos a partir de distribuciones a priori de parámetros

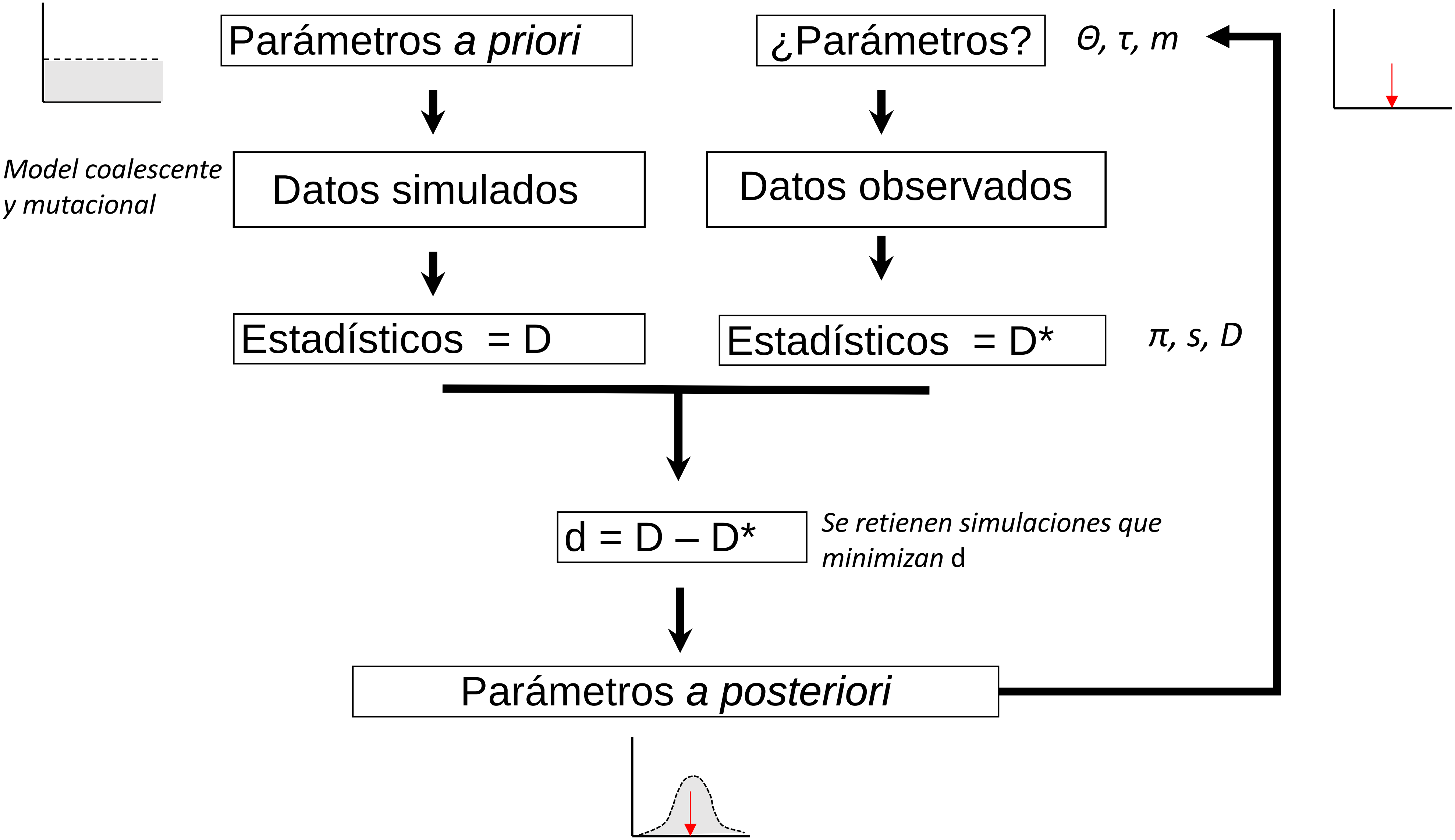


Aceptación de las simulaciones más similares a los datos observados



Estimación de parámetros y comparación de modelos a partir de simulaciones retenidas

Approximate Bayesian Computation



Parámetros *a priori*

¿Parámetros?

Θ, τ, m

Model coalescente y mutacional

Datos simulados

Datos observados

Estadísticos = D

Estadísticos = D*

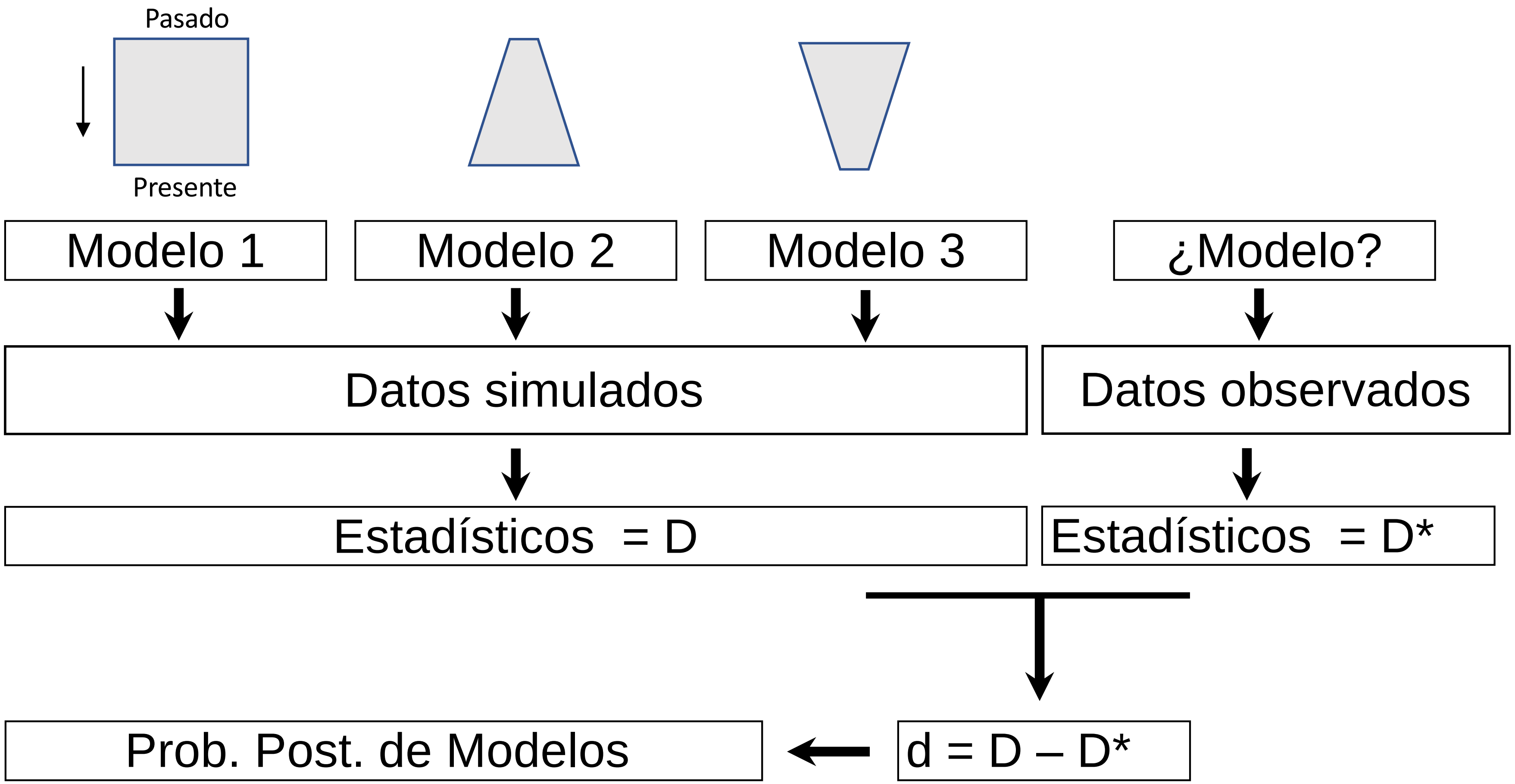
π, s, D

d = D – D*

Se retienen simulaciones que minimizan d

Parámetros *a posteriori*

Approximate Bayesian Computation



Pasado

Presente

Modelo 1

Modelo 2

Modelo 3

¿Modelo?

Datos simulados

Datos observados

Estadísticos = D

Estadísticos = D*

Prob. Post. de Modelos

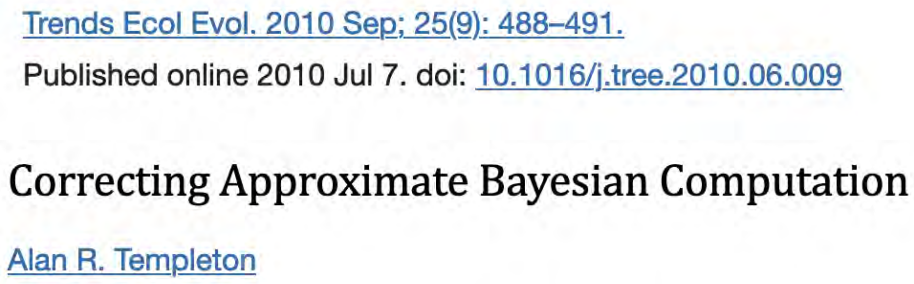
d = D – D*

Controversias con ABC

Review > Trends Ecol Evol. 2010 Jul;25(7):410-8. doi: 10.1016/j.tree.2010.04.001. Epub 2010 May 18.

Approximate Bayesian Computation (ABC) in practice

Katalin Csilléry [1], Michael G B Blum, Oscar E Gaggiotti, Olivier François



Trends Ecol Evol. 2010 Sep; 25(9): 488–491.

Published online 2010 Jul 7. doi: 10.1016/j.tree.2010.06.009

Correcting Approximate Bayesian Computation

Alan R. Templeton

Incoherent phylogeographic inference

James O. Berger, Stephen E. Fienberg, Adrian E. Raftery, and Christian P. Robert ✉ Authors Info & Affiliations

September 24, 2010 | 107(41)E157 | https://doi.org/10.1073/pnas.1008762107

Reply to Berger et al.: Improving ABC

Alan R. Templeton ✉ Authors Info & Affiliations

September 24, 2010 | 107(41)E158 | https://doi.org/10.1073/pnas.1009012107

Lack of confidence in approximate Bayesian computation model choice

Christian P. Robert ✉, Jean-Marie Cornuet, Jean-Michel Marin, and Natesh S. Pillai Authors Info & Affiliations

August 29, 2011 | 108(37)15112-15117 | https://doi.org/10.1073/pnas.1102900108

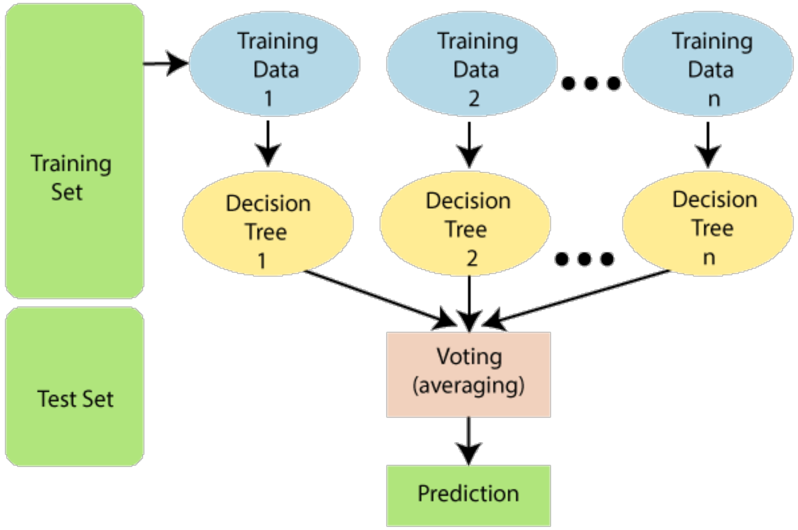
Selección de modelos con “Machine learning”

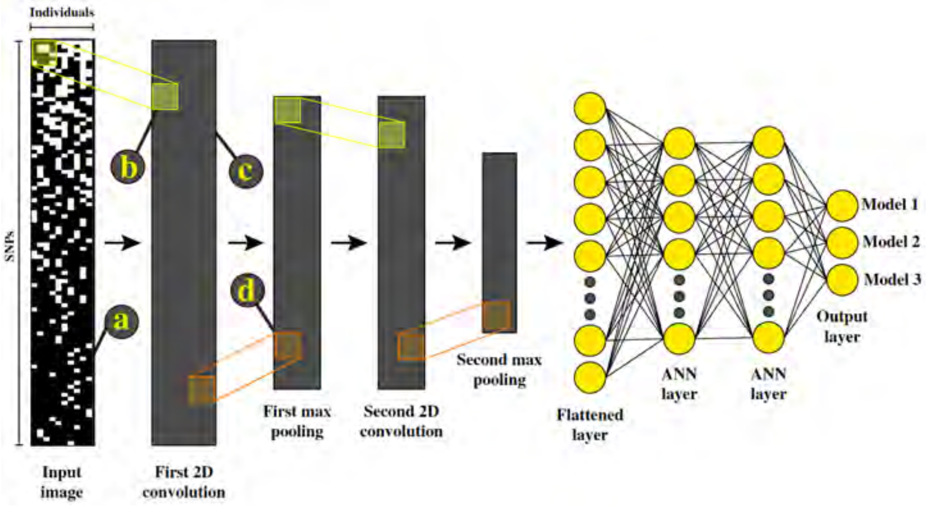
Reliable ABC model choice via random forests FREE

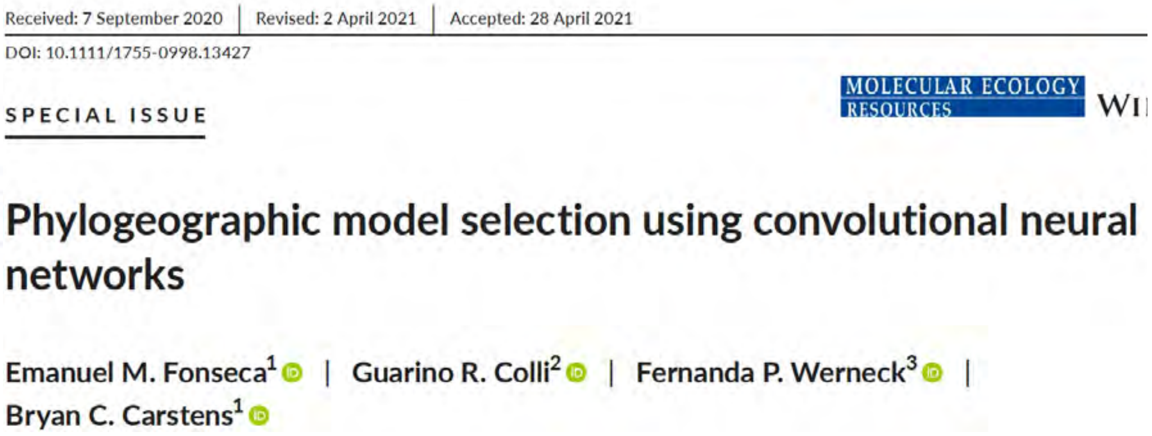
Pierre Pudlo, Jean-Michel Marin ✉, Arnaud Estoup, Jean-Marie Cornuet,
Mathieu Gautier, Christian P. Robert Author Notes

Bioinformatics, Volume 32, Issue 6, 15 March 2016, Pages 859–866, https://doi.org/10.1093/bioinformatics/btv684

Published: 20 November 2015 **Article history** ▾







Received: 7 September 2020 | Revised: 2 April 2021 | Accepted: 28 April 2021
DOI: 10.1111/1755-0998.13427

SPECIAL ISSUE

MOLECULAR ECOLOGY RESOURCES WI

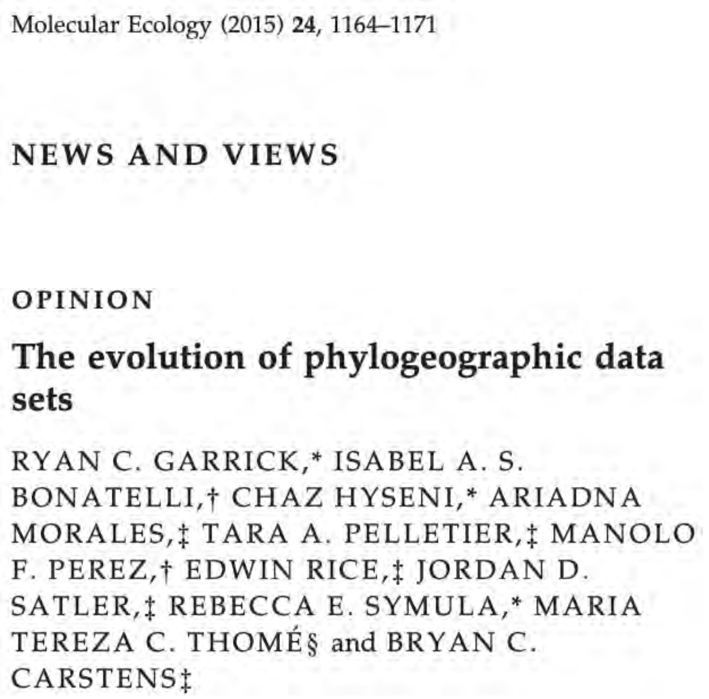
Phylogeographic model selection using convolutional neural networks

Emanuel M. Fonseca[1] | Guarino R. Colli[2] | Fernanda P. Werneck[3] |
Bryan C. Carstens[1]

Selección de modelos con “Machine learning”

Nuevos tipos de datos

- mtDNA: RFLP
- Microsatélites
- Secuencias de ADN
- Locus vs. Loci
- Subrepresentación genómica: SNPs
- (RADseq, UCEs)
- Genomas completos



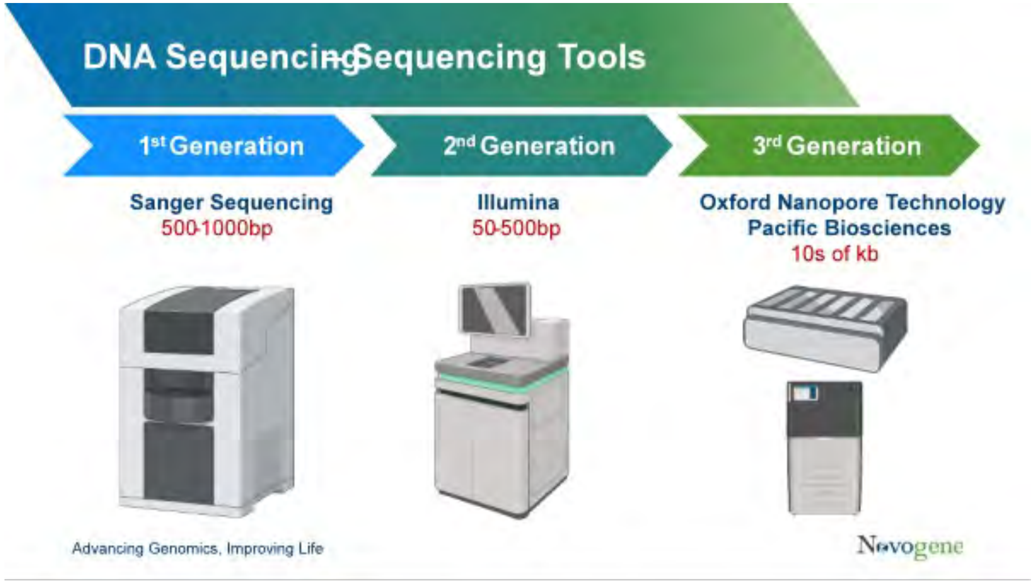
Molecular Ecology (2015) **24**, 1164–1171

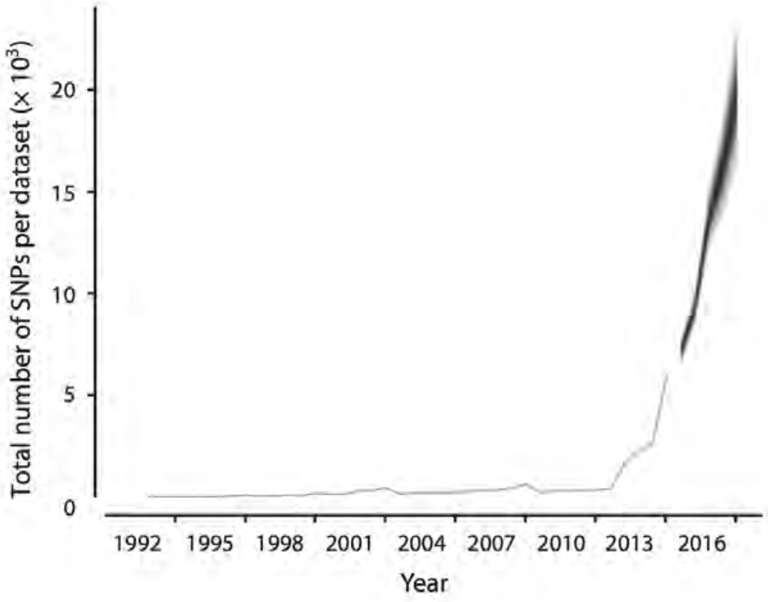
NEWS AND VIEWS

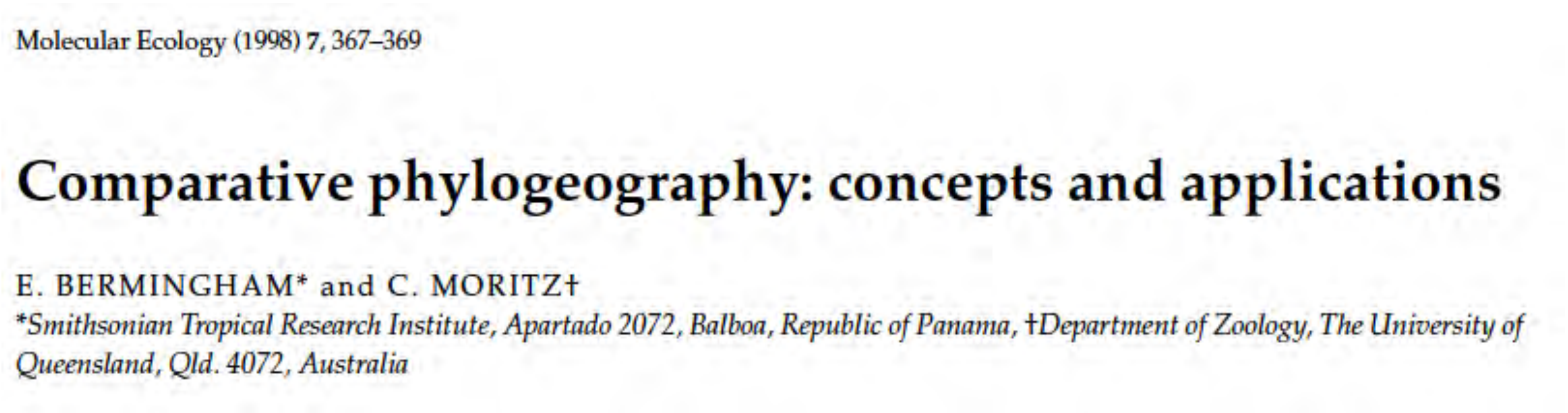
OPINION

The evolution of phylogeographic data sets

RYAN C. GARRICK,* ISABEL A. S. BONATELLI,† CHAZ HYSENI,* ARIADNA MORALES,‡ TARA A. PELLETIER,‡ MANOLO F. PEREZ,† EDWIN RICE,‡ JORDAN D. SATLER,‡ REBECCA E. SYMULA,* MARIA TEREZA C. THOMÉ§ and BRYAN C. CARSTENS‡







Molecular Ecology (1998) 7, 367–369

Comparative phylogeography: concepts and applications

E. BERMINGHAM* and C. MORITZ†
*Smithsonian Tropical Research Institute, Apartado 2072, Balboa, Republic of Panama, †Department of Zoology, The University of Queensland, Qld. 4072, Australia

'… describe la evolución de paisajes y permite el análisis de los efectos de la historia y la geografía sobre la estructura de las comunidades de organismos a niveles locales y regionales'

Congruencia temporal

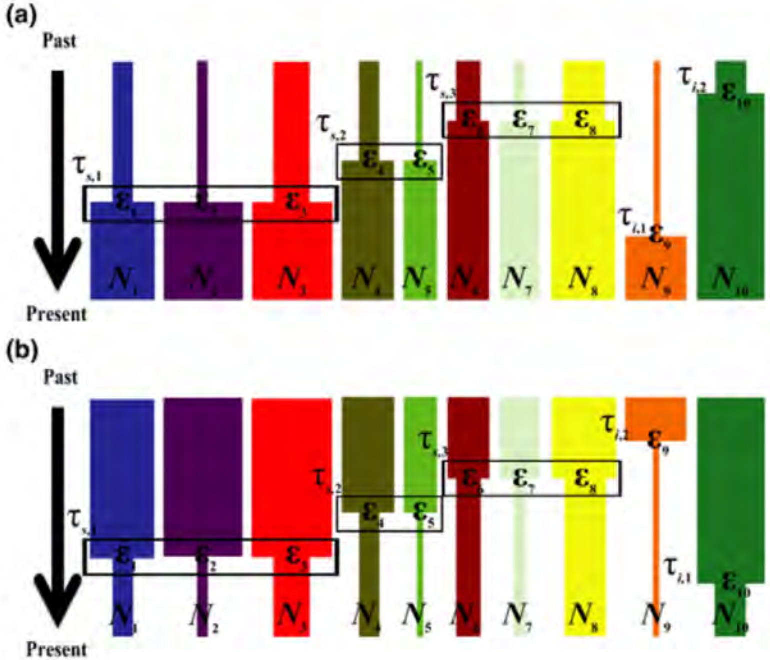
Congruencia espacial

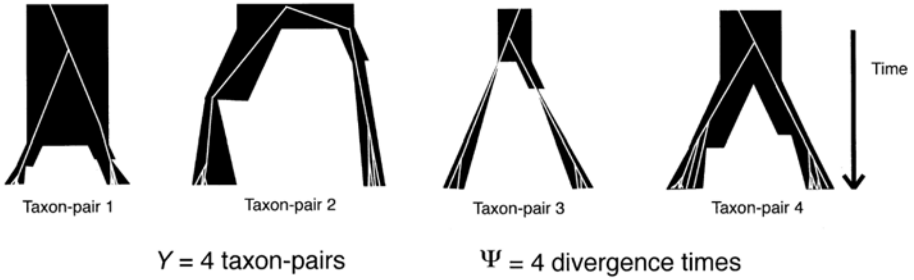
	Si	No
Si	Factores causales locales que afectaron comunidades enteras	Factor causal recurrente que afectaron comunidades locales en diferentes momentos
No	Factores causales globales que afectaron comunidades en diferentes regiones	Diferentes factores causales locales y en el tiempo

Evolution, 60(12), 2006, pp. 2435–2453

TEST FOR SIMULTANEOUS DIVERGENCE USING APPROXIMATE BAYESIAN COMPUTATION

MICHAEL J. HICKERSON,[1,2] ELI A. STAHL,[3,4] AND H. A. LESSIOS[5,6]





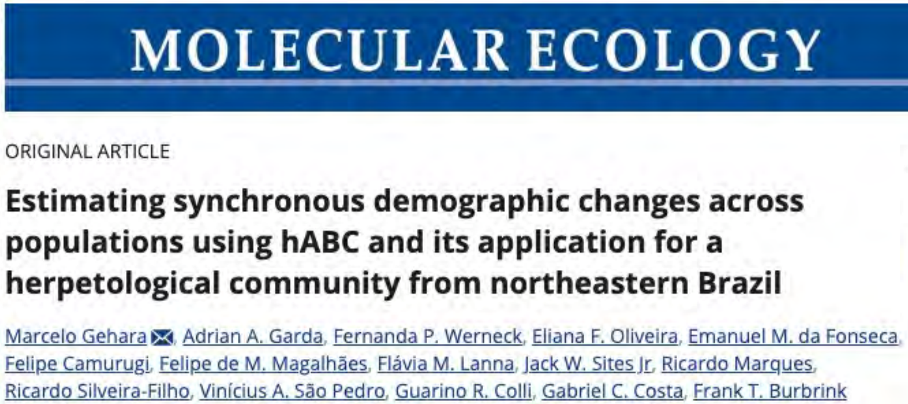

MOLECULAR ECOLOGY RESOURCES

RESOURCE ARTICLE | Open Access

MULTI-DICE: R package for comparative population genomic inference under hierarchical co-demographic models of independent single-population size changes

Alexander T. Xue, Michael J. Hickerson

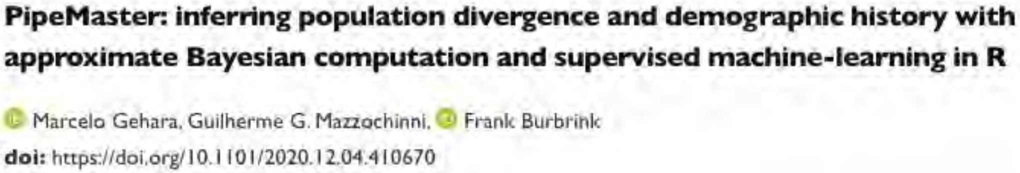
First published: 27 April 2017 | https://doi.org/10.1111/1755-0998.12686 | Citations: 22


MOLECULAR ECOLOGY

ORIGINAL ARTICLE

Estimating synchronous demographic changes across populations using hABC and its application for a herpetological community from northeastern Brazil

Marcelo Gehara, Adrian A. Garda, Fernanda P. Werneck, Eliana F. Oliveira, Emanuel M. da Fonseca, Felipe Camurugi, Felipe de M. Magalhães, Flávia M. Lanna, Jack W. Sites Jr, Ricardo Marques, Ricardo Silveira-Filho, Vinícius A. São Pedro, Guarino R. Colli, Gabriel C. Costa, Frank T. Burbrink


PipeMaster: inferring population divergence and demographic history with approximate Bayesian computation and supervised machine-learning in R

Marcelo Gehara, Guilherme G. Mazzochinni, Frank Burbrink

doi: https://doi.org/10.1101/2020.12.04.410670

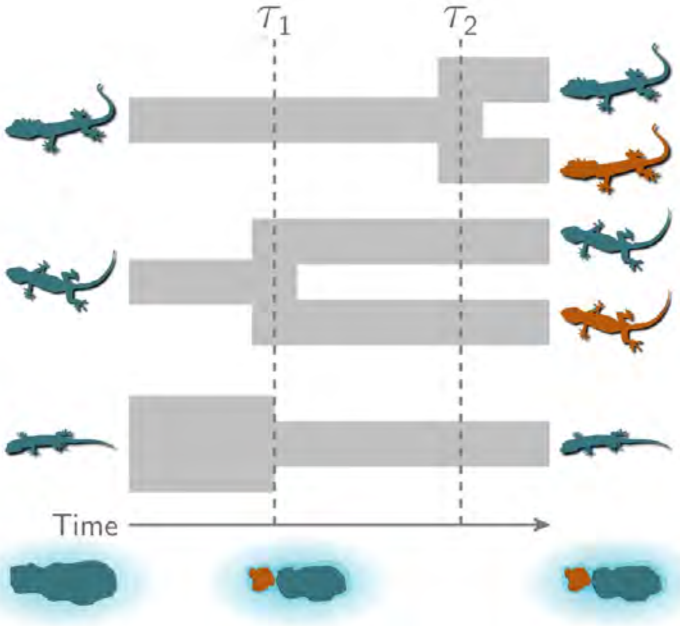
Full Bayesian Comparative Phylogeography from Genomic Data

Jamie R Oaks

Systematic Biology, Volume 68, Issue 3, May 2019, Pages 371–395,
https://doi.org/10.1093/sysbio/syy063

Ecoevolity

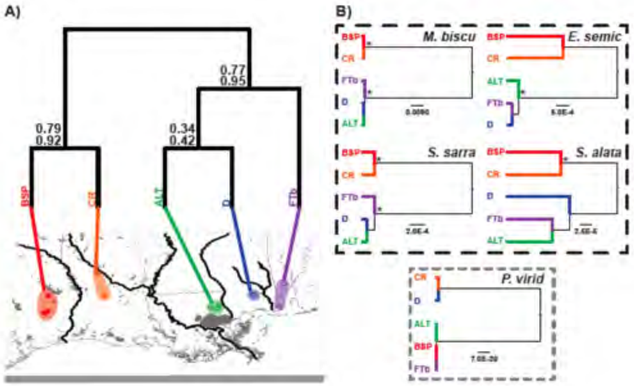
Estimating evolutionary coevality



> Evolution. 2016 May;70(5):1105-19. doi: 10.1111/evo.12924. Epub 2016 Apr 29.

Phylogeographic concordance factors quantify phylogeographic congruence among co-distributed species in the Sarracenia alata pitcher plant system

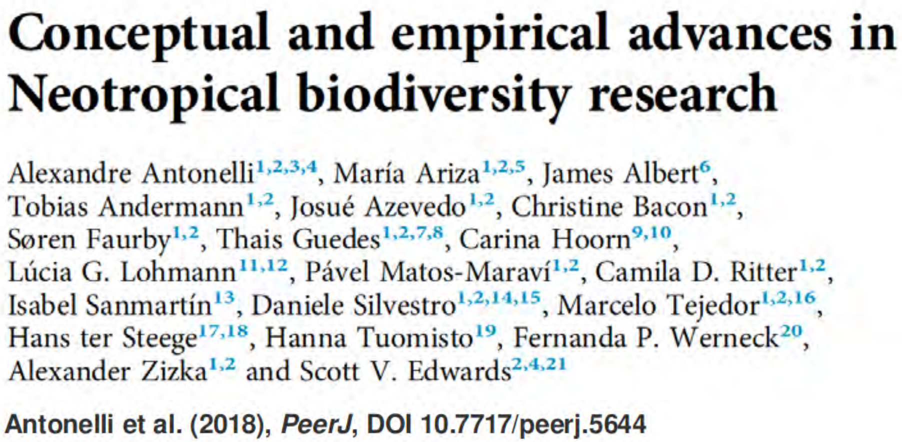
Jordan D Satler [1], Bryan C Carstens [2]



Filogeografía predictiva

- Trait-based phylogeography (Knowles)
- Sullivan et al integrating life history traits

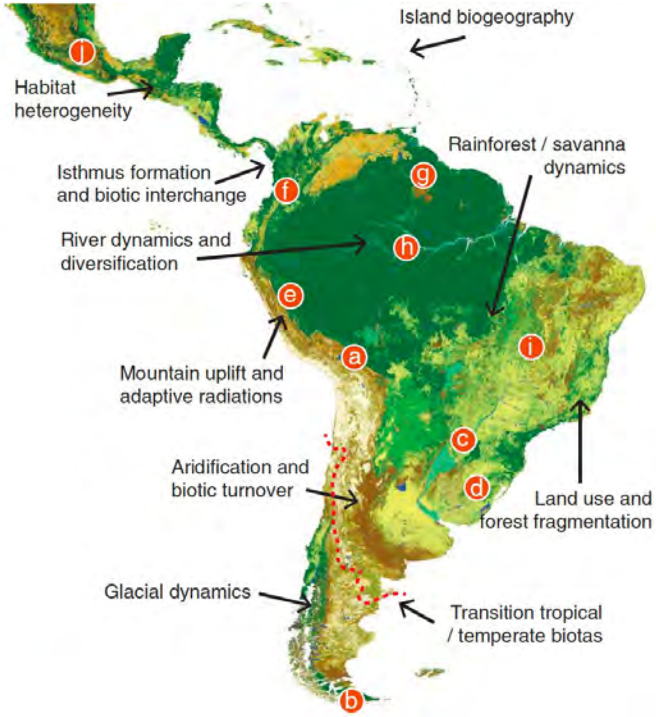
Filogeografía en la Región Neotropical



Conceptual and empirical advances in Neotropical biodiversity research

Alexandre Antonelli[1,2,3,4], María Ariza[1,2,5], James Albert[6],
Tobias Andermann[1,2], Josué Azevedo[1,2], Christine Bacon[1,2],
Søren Faurby[1,2], Thais Guedes[1,2,7,8], Carina Hoorn[9,10],
Lúcia G. Lohmann[11,12], Pável Matos-Maraví[1,2], Camila D. Ritter[1,2],
Isabel Sanmartín[13], Daniele Silvestro[1,2,14,15], Marcelo Tejedor[1,2,16],
Hans ter Steege[17,18], Hanna Tuomisto[19], Fernanda P. Werneck[20],
Alexander Zizka[1,2] and Scott V. Edwards[2,4,21]

Antonelli et al. (2018), *PeerJ*, DOI 10.7717/peerj.5644



- Especies distribuidas en ”transbiomas”: anuros (232 spp., 17%), escamados (482 spp., 23%)

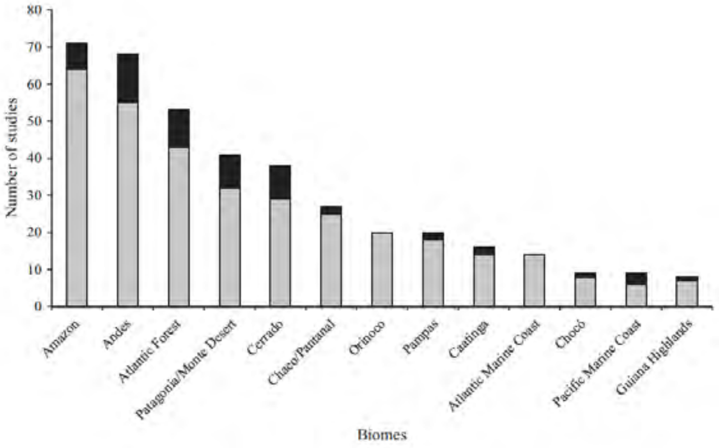
MOLECULAR ECOLOGY

Molecular Ecology (2012) doi: 10.1111/mec.12164

INVITED REVIEW AND META-ANALYSES

Phylogeographical patterns shed light on evolutionary process in South America

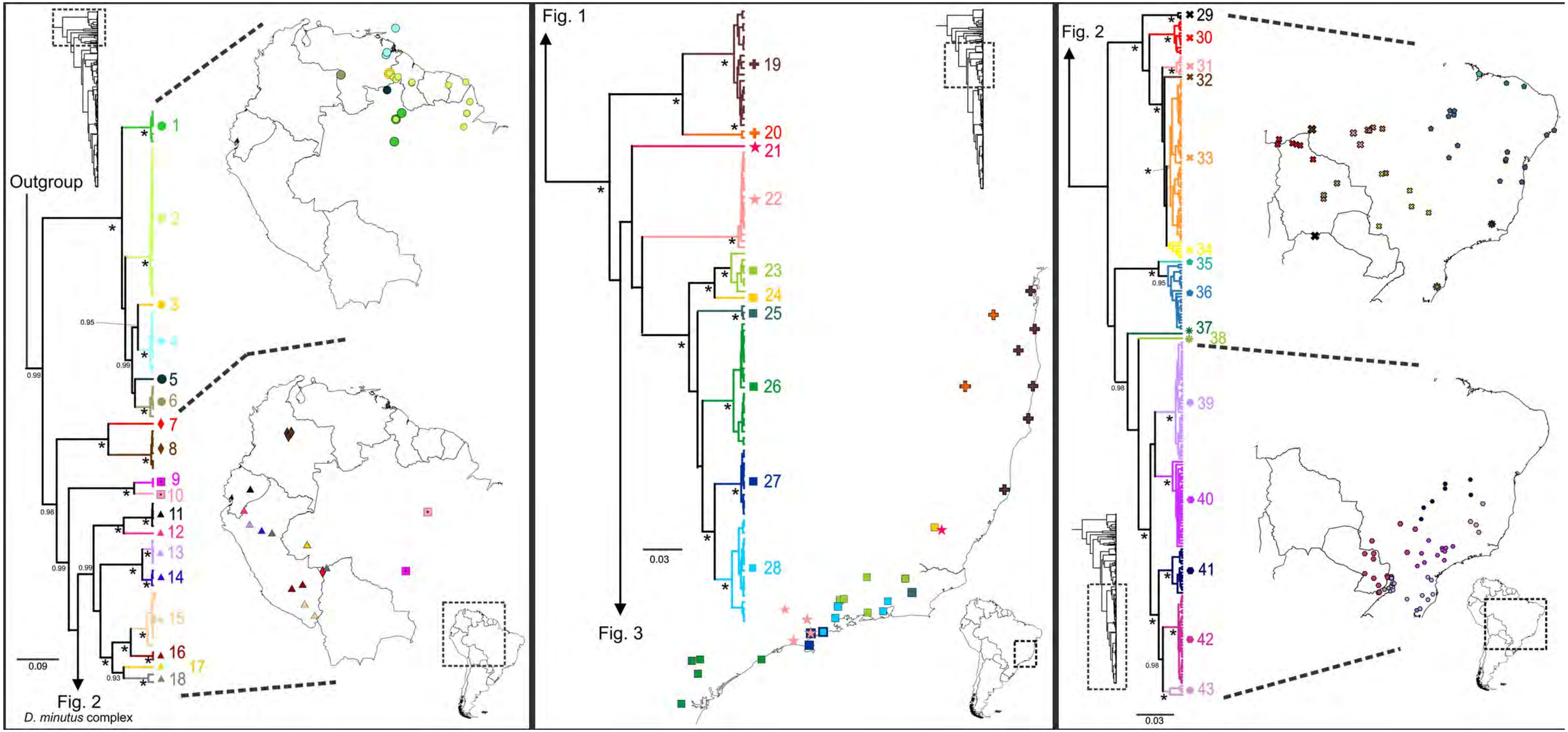
A. C. TURCHETTO-ZOLET,* F. PINHEIRO,† F. SALGUEIRO‡ and C. PALMA-SILVA†
*Programa de Pós-Graduação em Genética e Biologia Molecular, Departamento de Genética, IB/UFRGS, 91501-970, Porto Alegre, RS, Brazil, †Instituto de Botânica, Av. Miguel Stefano 3687, Agua Funda, 04301-902, São Paulo, SP, Brazil, ‡Departamento de Botânica, UNIRIO, 22290-240, Rio de Janeiro, RJ, Brazil

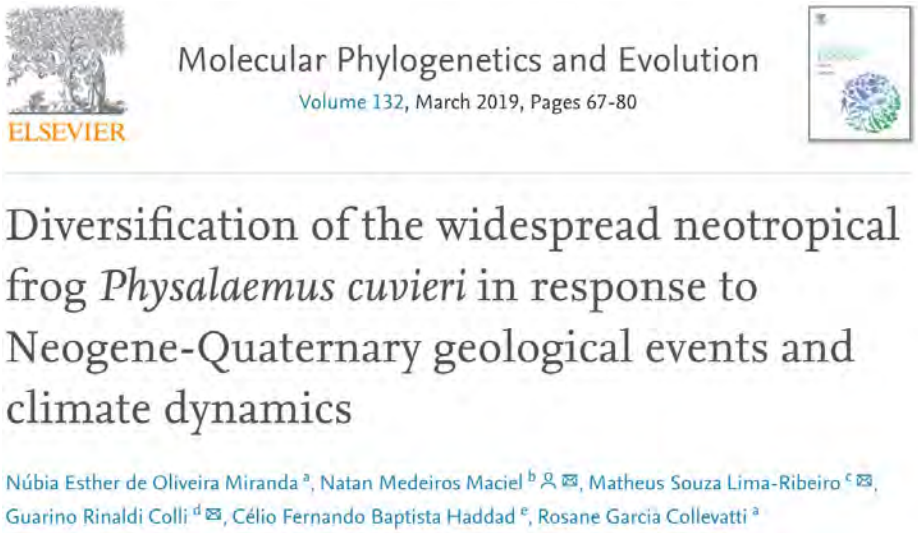


High Levels of Diversity Uncovered in a Widespread Nominal Taxon: Continental Phylogeography of the Neotropical Tree Frog *Dendropsophus minutus*

Marcelo Gehara ✉, Andrew J. Crawford, Victor G. D. Orrico, Ariel Rodríguez, Stefan Lötters, Antoine Fouquet, Lucas S. Barrientos, Francisco Brusquetti, Ignacio De la Riva, Raffael Ernst, Giuseppe Gagliardi Urrutia, Frank Glaw, Juan M. Guayasamin, [...], Jörn Köhler [view all]

Published: September 10, 2014 • https://doi.org/10.1371/journal.pone.0103958

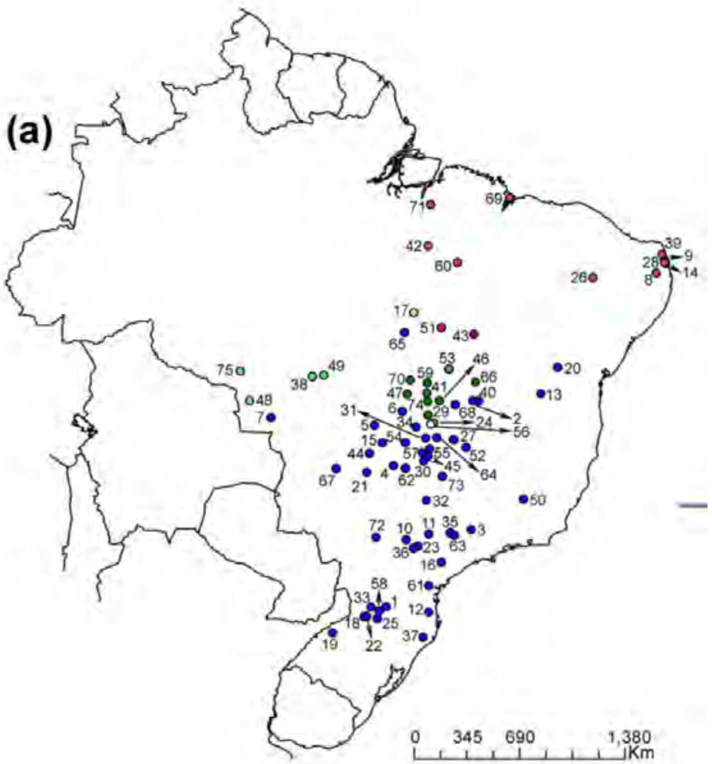


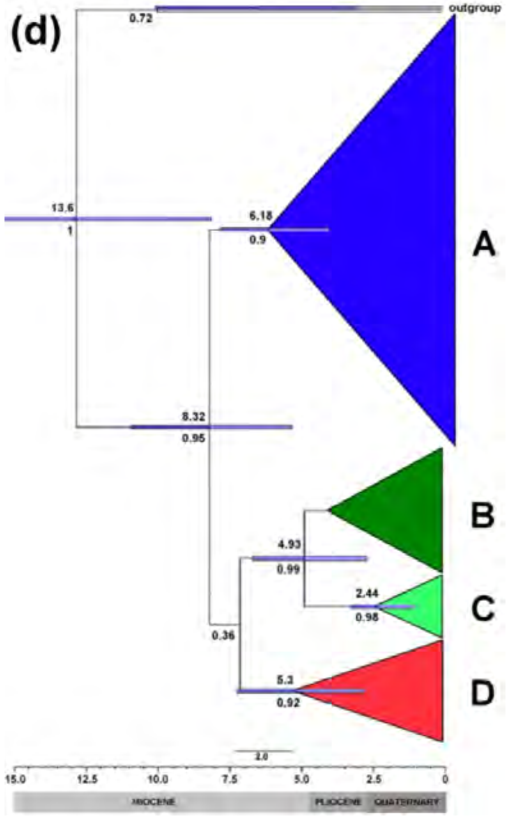


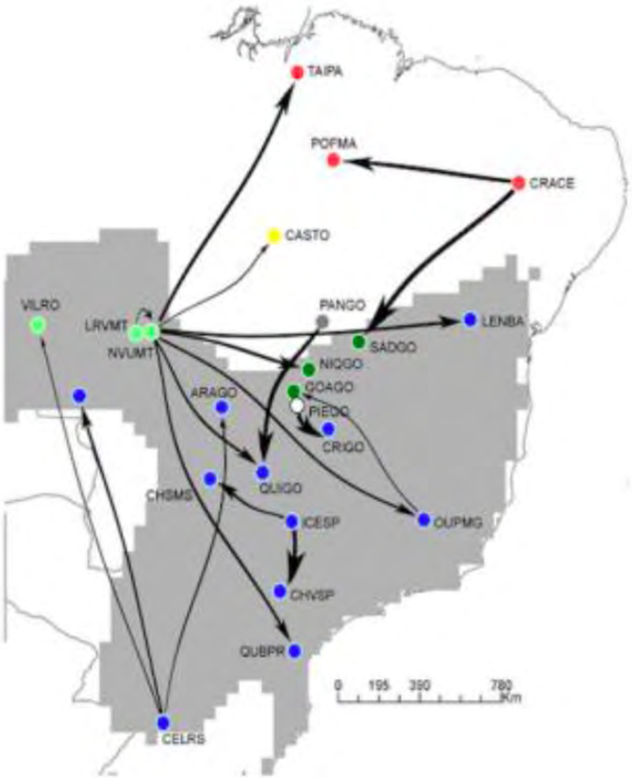
Molecular Phylogenetics and Evolution
Volume 132, March 2019, Pages 67-80

Diversification of the widespread neotropical frog *Physalaemus cuvieri* in response to Neogene-Quaternary geological events and climate dynamics

Núbia Esther de Oliveira Miranda [a], Natan Medeiros Maciel [b], Matheus Souza Lima-Ribeiro [c], Guarino Rinaldi Colli [d], Célio Fernando Baptista Haddad [e], Rosane Garcia Collevatti [a]



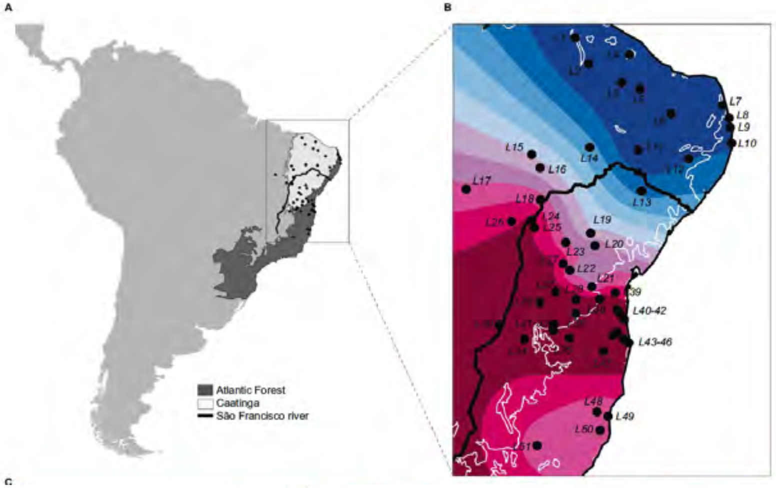


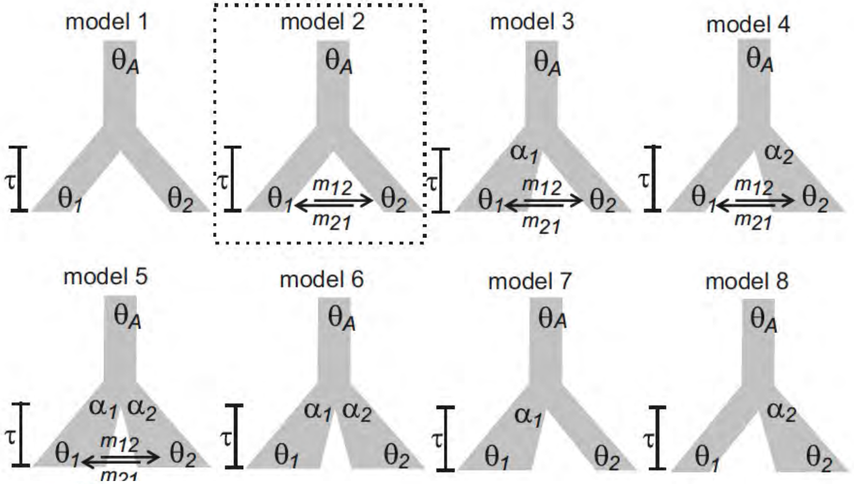


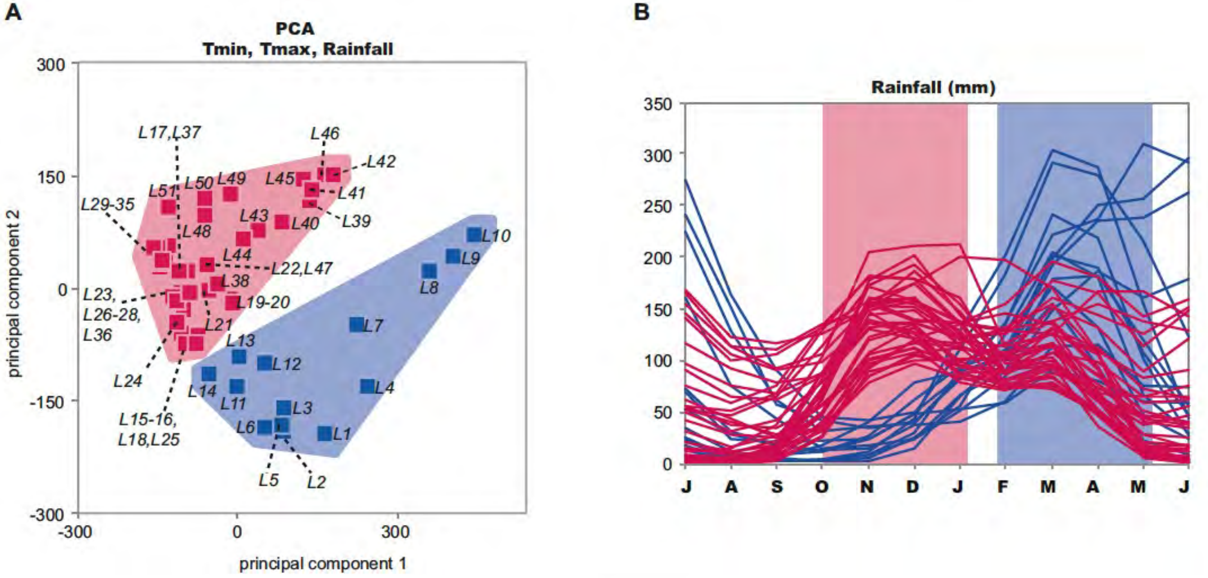
ARTICLE

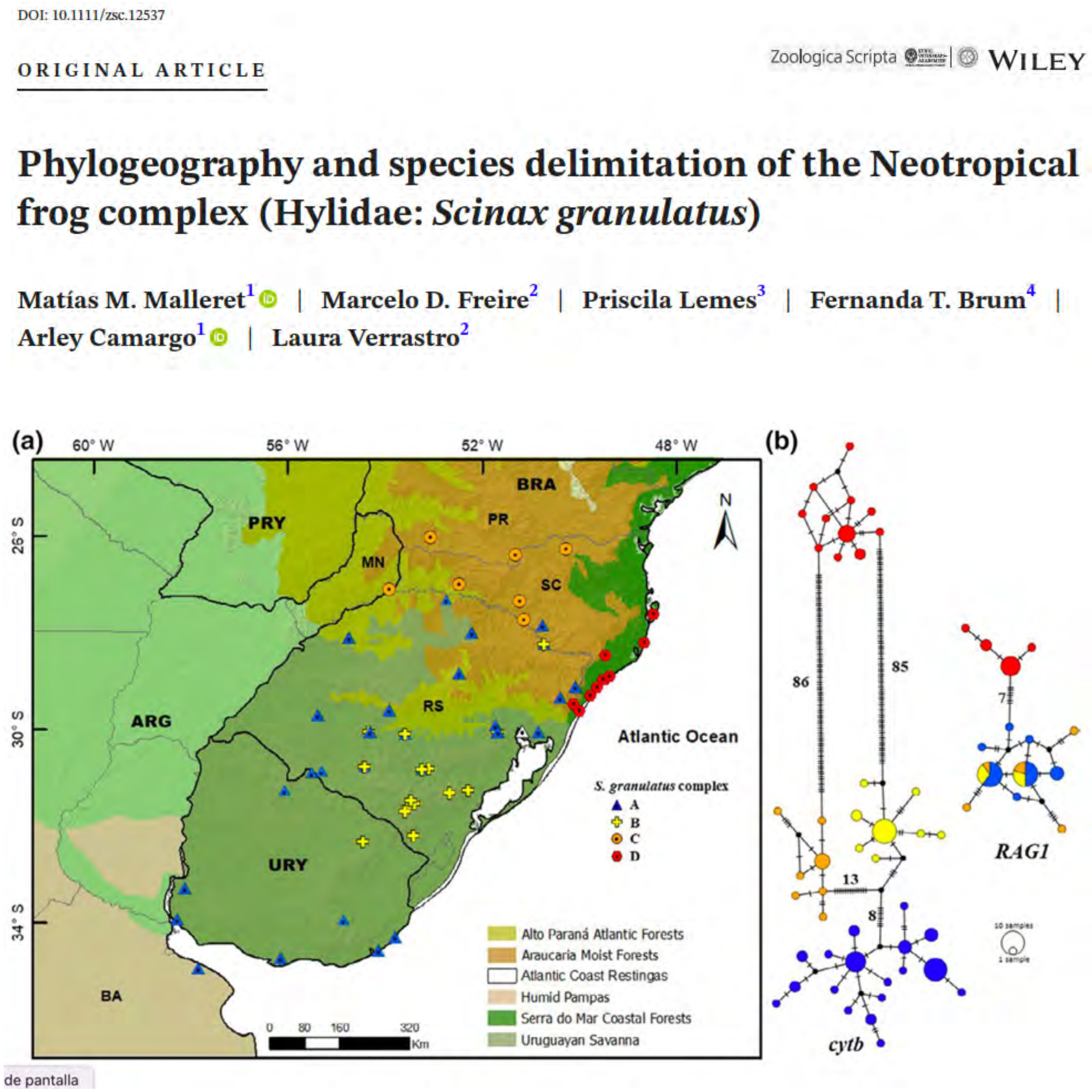
A role of asynchrony of seasons in explaining genetic differentiation in a Neotropical toad

Maria Tereza C. Thomé[1,2]✉, Bryan C. Carstens[1], Miguel Trefaut Rodrigues[3], Pedro Manoel Galetti Jr[4], João Alexandrino[5] and Célio F. B. Haddad[2]









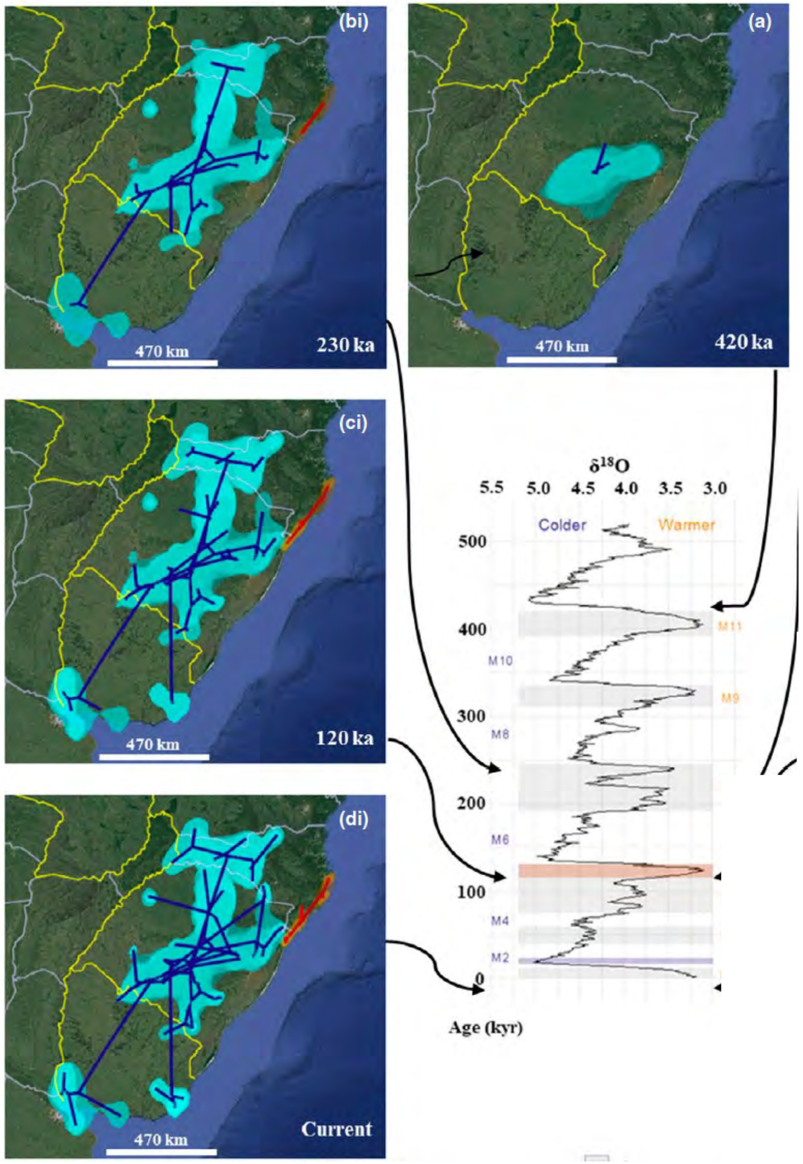
DOI: 10.1111/zsc.12537

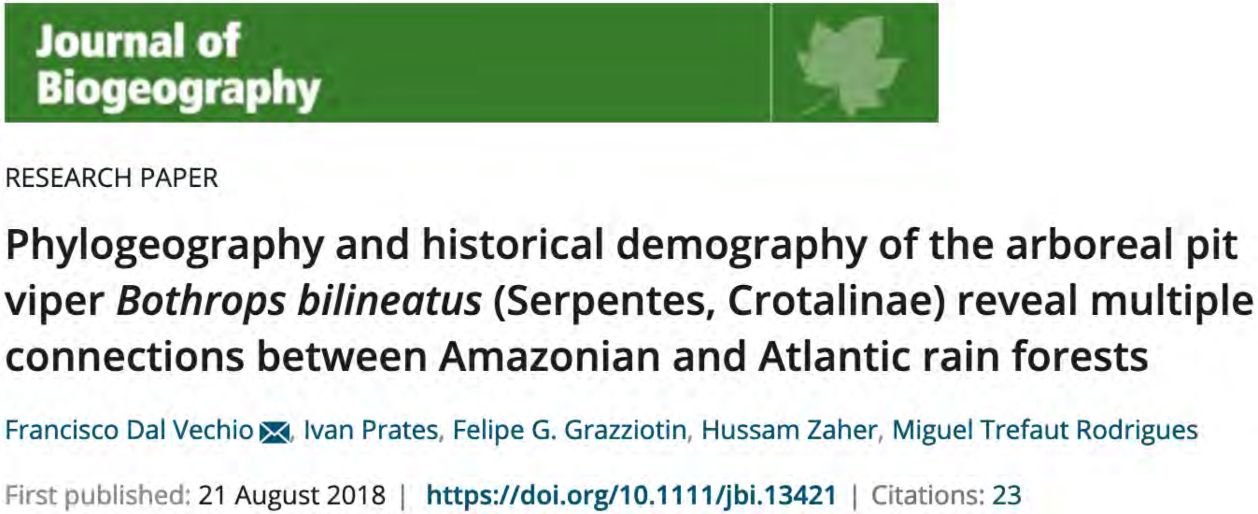
ORIGINAL ARTICLE

Zoologica Scripta | WILEY

Phylogeography and species delimitation of the Neotropical frog complex (Hylidae: *Scinax granulatus*)

Matías M. Malleret[1] | **Marcelo D. Freire**[2] | **Priscila Lemes**[3] | **Fernanda T. Brum**[4] | **Arley Camargo**[1] | **Laura Verrastro**[2]





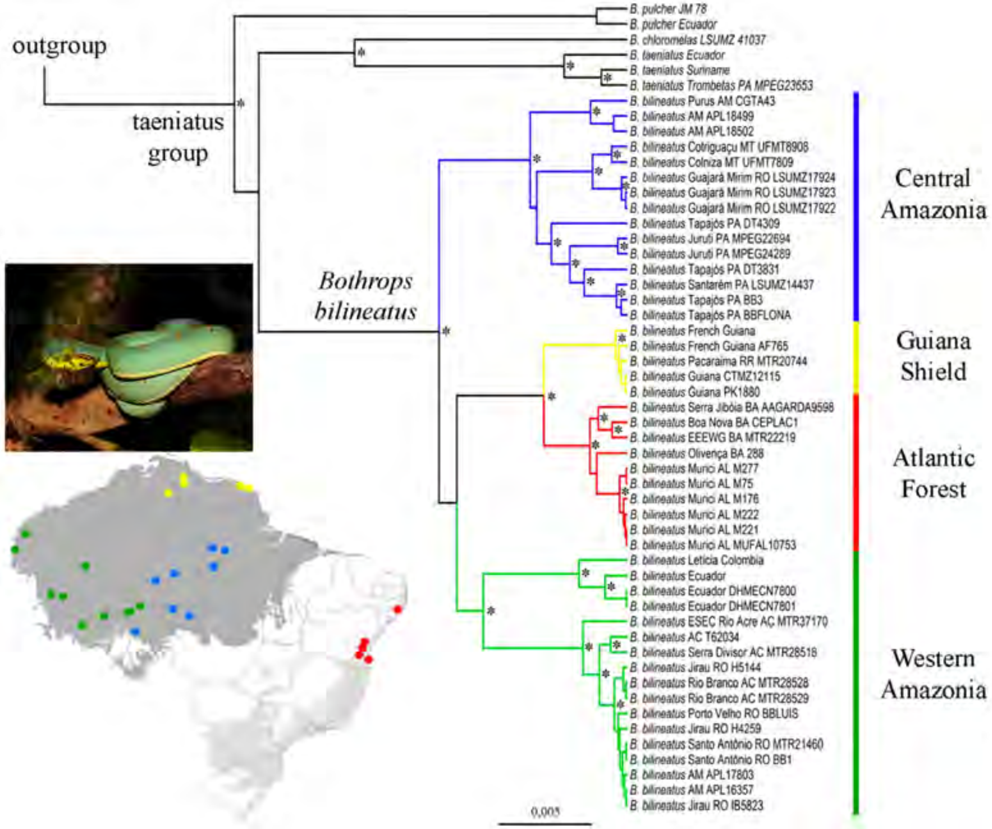
Journal of Biogeography

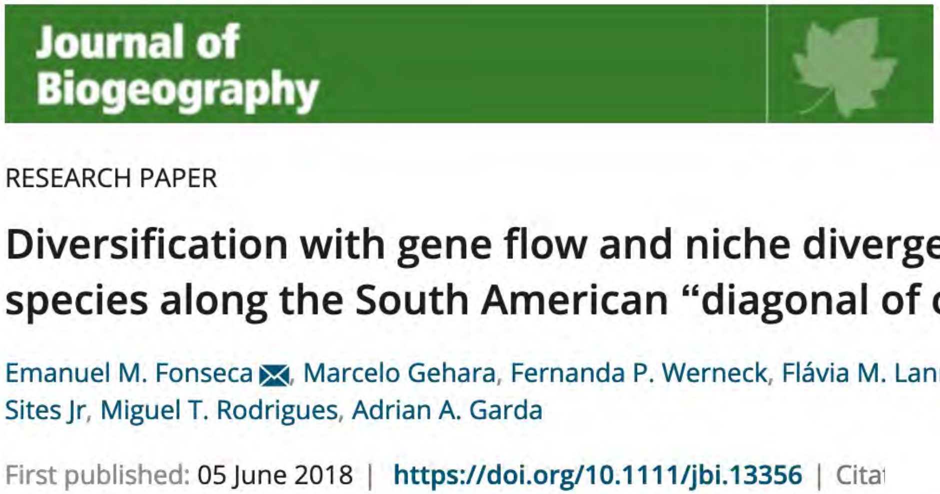
RESEARCH PAPER

Phylogeography and historical demography of the arboreal pit viper *Bothrops bilineatus* (Serpentes, Crotalinae) reveal multiple connections between Amazonian and Atlantic rain forests

Francisco Dal Vechio ✉, Ivan Prates, Felipe G. Grazziotin, Hussam Zaher, Miguel Trefaut Rodrigues

First published: 21 August 2018 | https://doi.org/10.1111/jbi.13421 | Citations: 23





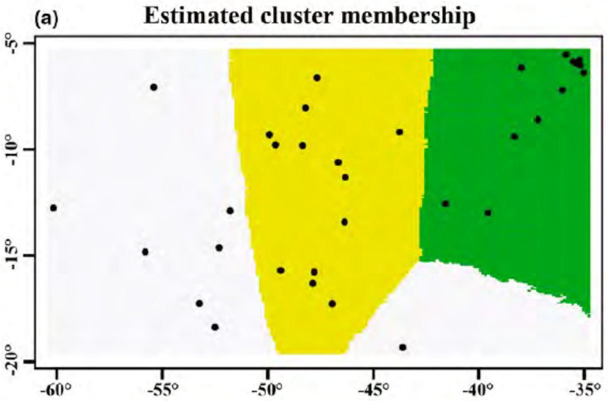
Journal of Biogeography

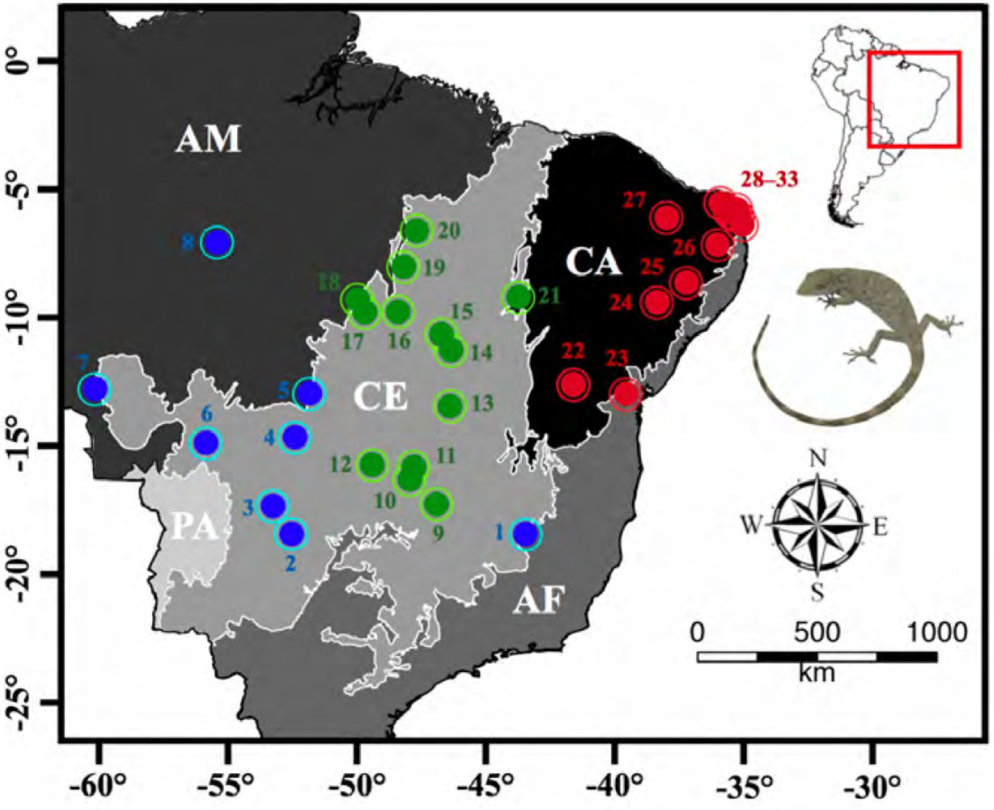
RESEARCH PAPER

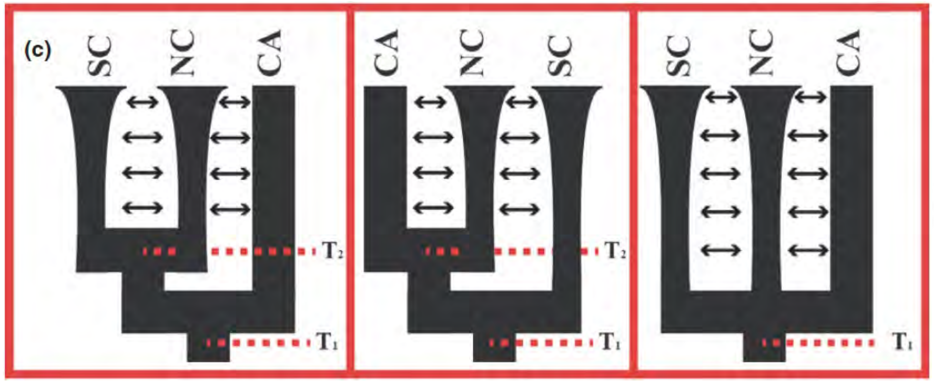
Diversification with gene flow and niche divergence in a lizard species along the South American “diagonal of open formations”

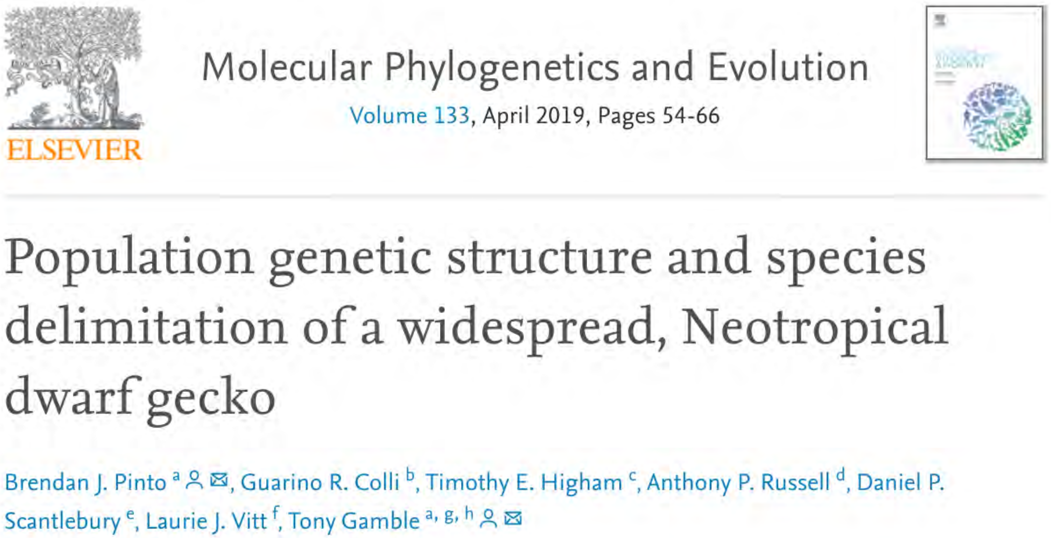
Emanuel M. Fonseca, Marcelo Gehara, Fernanda P. Werneck, Flávia M. Lanna, Guarino R. Colli, Jack W. Sites Jr, Miguel T. Rodrigues, Adrian A. Garda

First published: 05 June 2018 | https://doi.org/10.1111/jbi.13356 | Cita





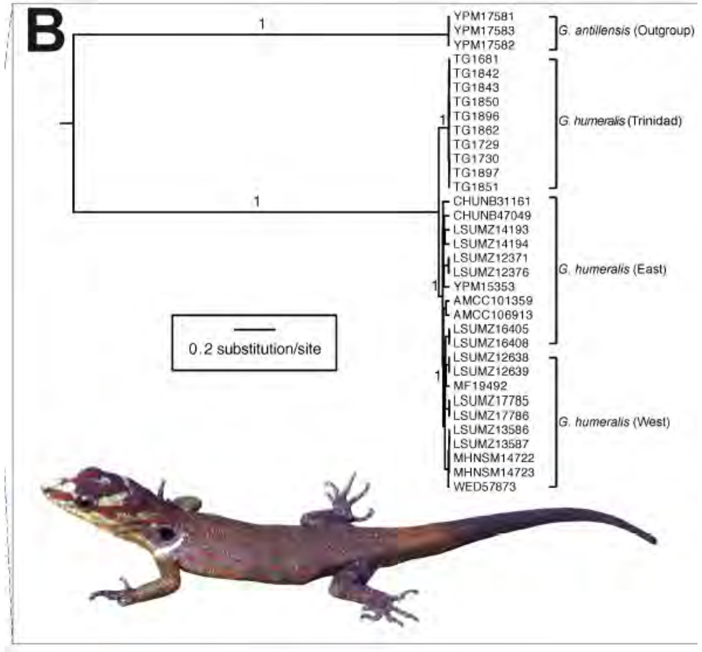


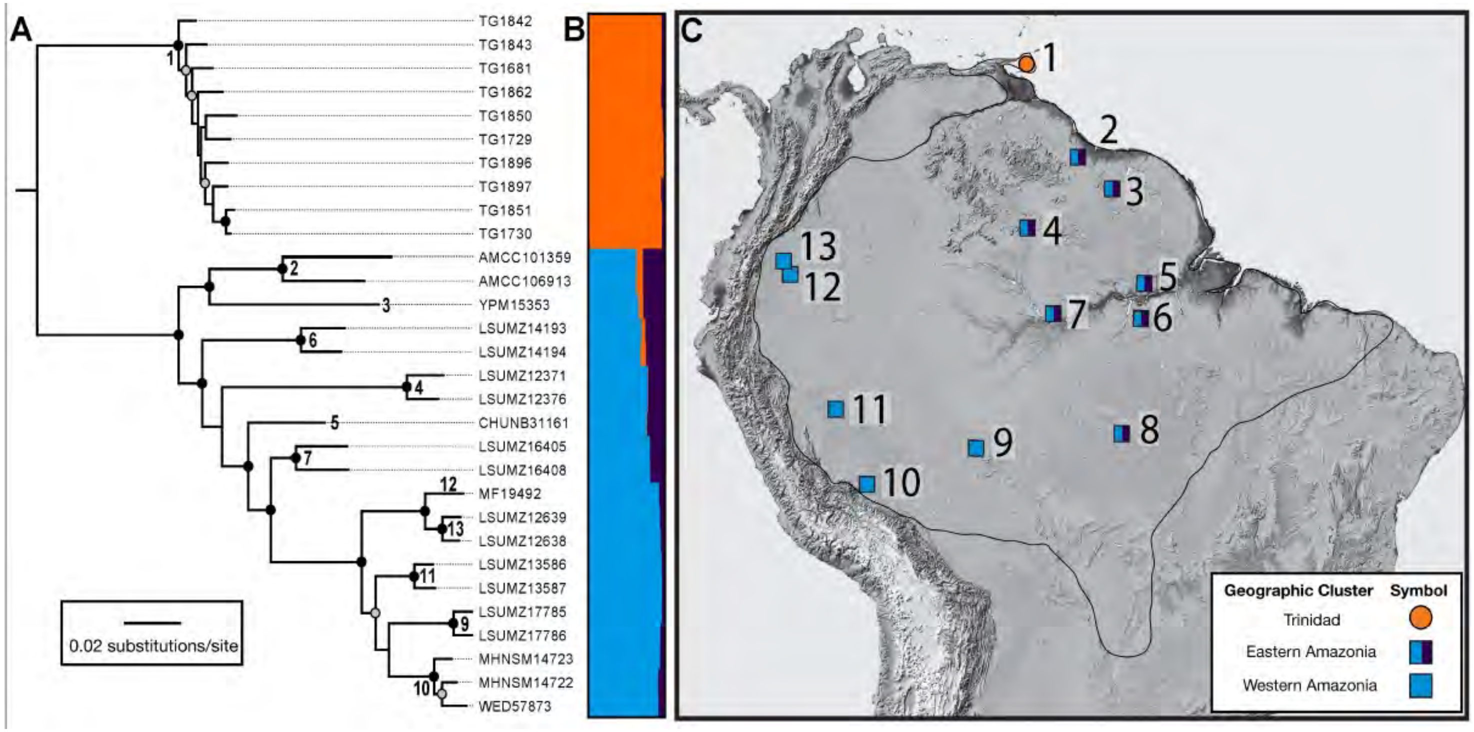


Molecular Phylogenetics and Evolution
Volume 133, April 2019, Pages 54-66

Population genetic structure and species delimitation of a widespread, Neotropical dwarf gecko

Brendan J. Pinto [a] ✉, Guarino R. Colli [b], Timothy E. Higham [c], Anthony P. Russell [d], Daniel P. Scantlebury [e], Laurie J. Vitt [f], Tony Gamble [a, g, h] ✉

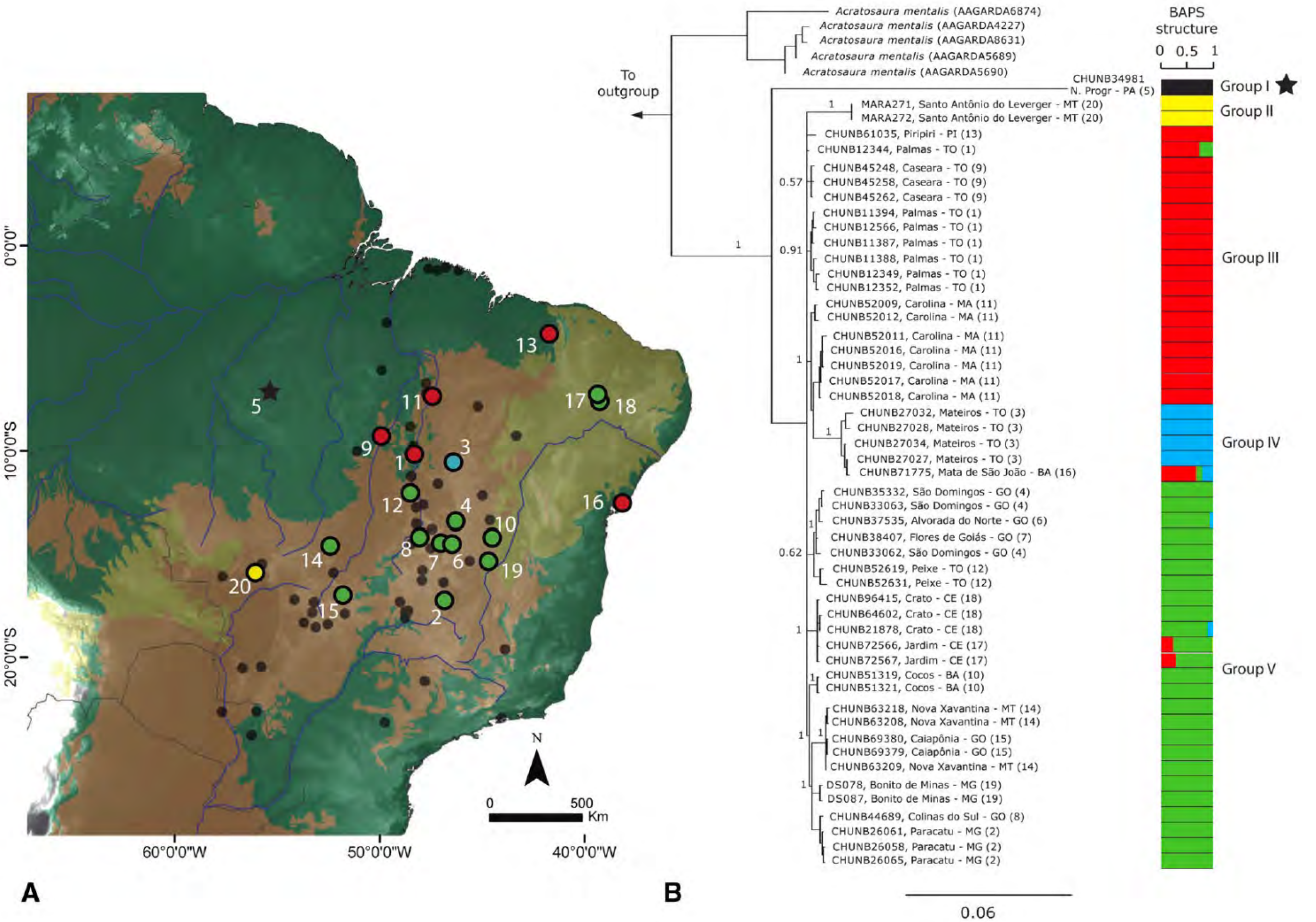




Pleistocene expansion and connectivity of mesic forests inside the South American Dry Diagonal supported by the phylogeography of a small lizard*

Roger Maia D. Ledo, Fabricius M. C. B. Domingos, Lilian G. Giugliano, Jack W. Sites Jr, Fernanda P. Werneck, Guarino R. Colli

First published: 19 April 2020 | https://doi.org/10.1111/evo.13978 | Citations: 3



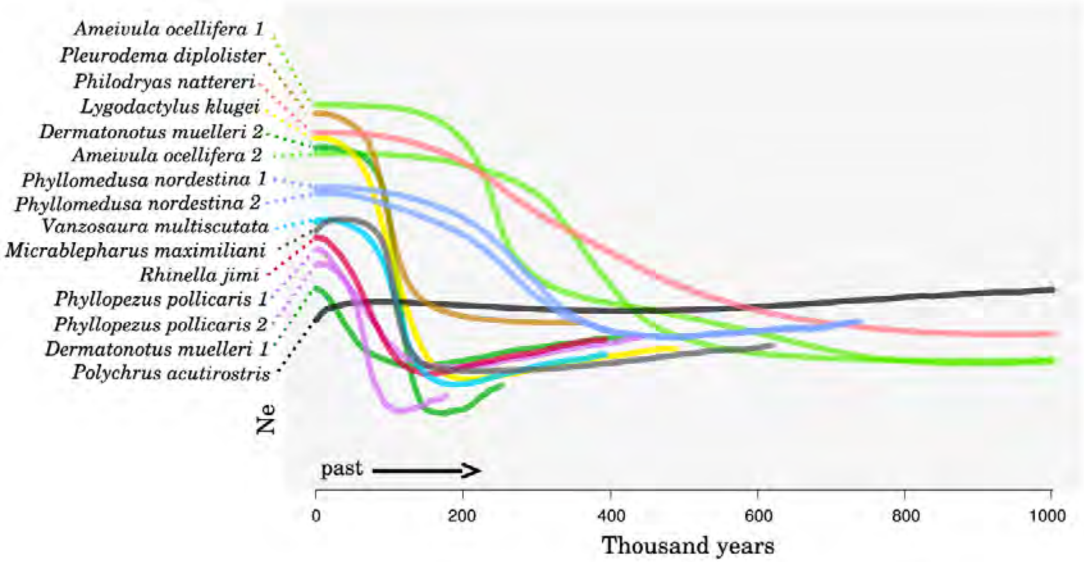
Received: 4 November 2016 | Revised: 30 May 2017 | Accepted: 2 July 2017
DOI: 10.1111/mec.14239

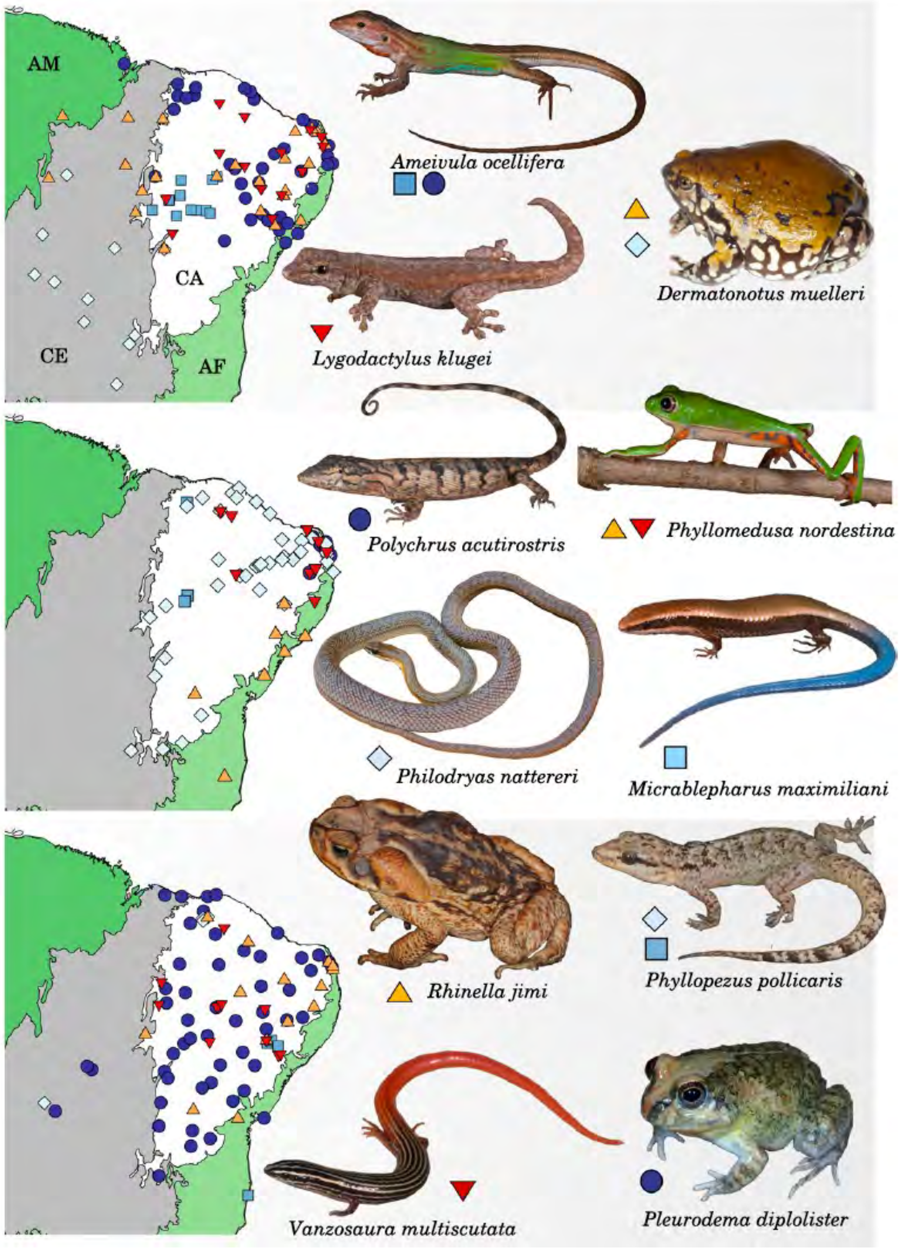
ORIGINAL ARTICLE

WILEY MOLECULAR ECOLOGY

Estimating synchronous demographic changes across populations using hABC and its application for a herpetological community from northeastern Brazil

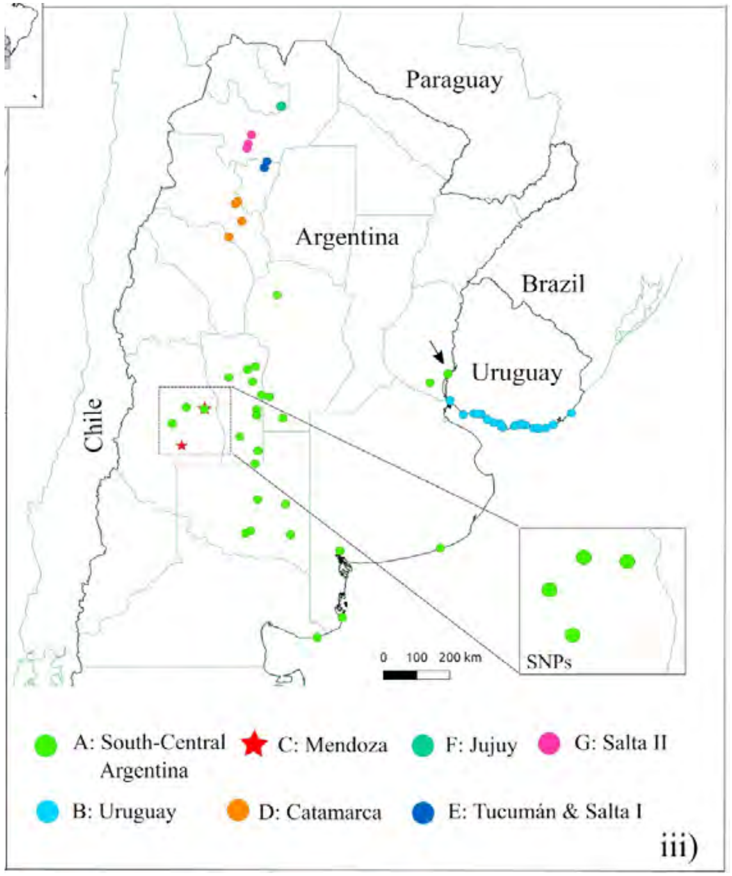
Marcelo Gehara[1] | Adrian A. Garda[2] | Fernanda P. Werneck[3] | Eliana F. Oliveira[4,5] | Emanuel M. da Fonseca[4] | Felipe Camurugi[6] | Felipe de M. Magalhães[6] | Flávia M. Lanna[4] | Jack W. Sites Jr[7] | Ricardo Marques[6] | Ricardo Silveira-Filho[6] | Vinícius A. São Pedro[4,8] | Guarino R. Colli[9] | Gabriel C. Costa[10] | Frank T. Burbrink[1]

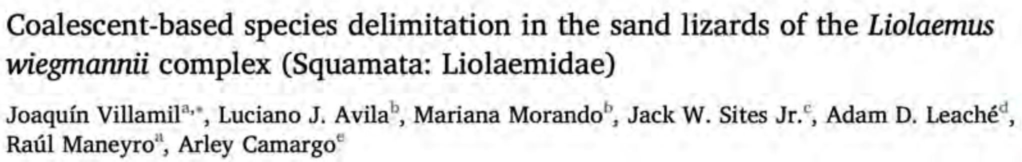




Filogeografía del complejo *Liolaemus wiegmannii*

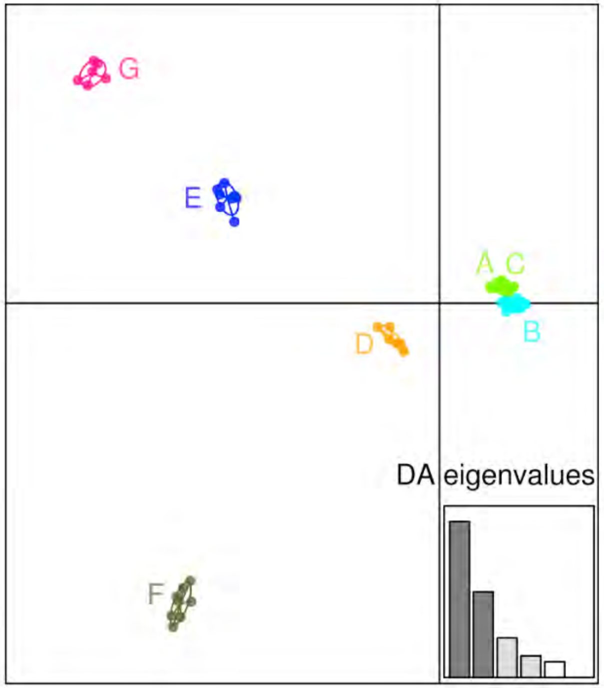
- Dr. Joaquín Villamil: Postdoc CONICET (Puerto Madryn, Argentina)



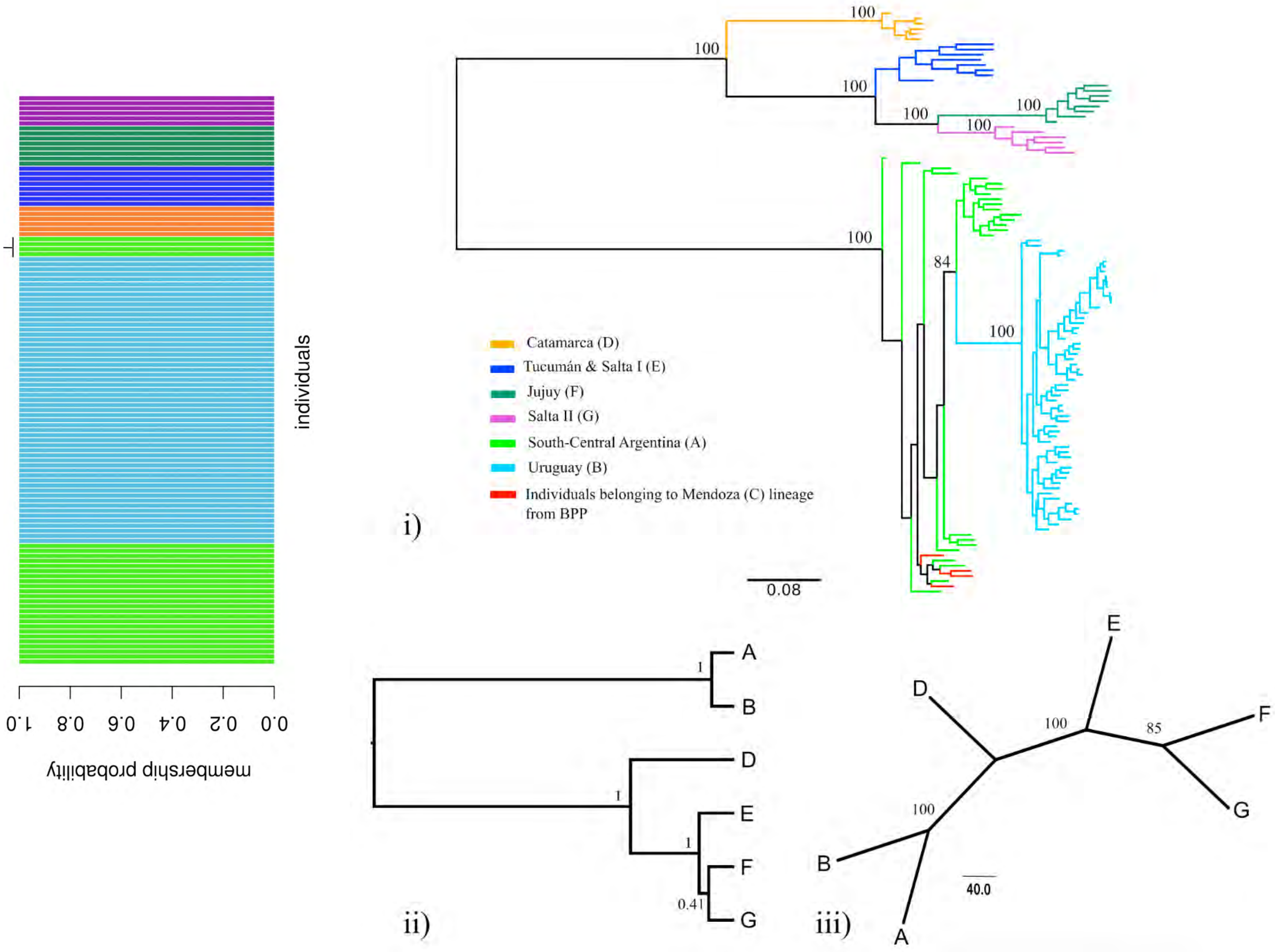


Coalescent-based species delimitation in the sand lizards of the *Liolaemus wiegmannii* complex (Squamata: Liolaemidae)

Joaquín Villamil[a,*], Luciano J. Avila[b], Mariana Morando[b], Jack W. Sites Jr.[c], Adam D. Leaché[d], Raúl Maneyro[a], Arley Camargo[e]



Filogeografía del complejo *Liolaemus wiegmannii*



Filogeografía de *Leptodactylus latinasus*

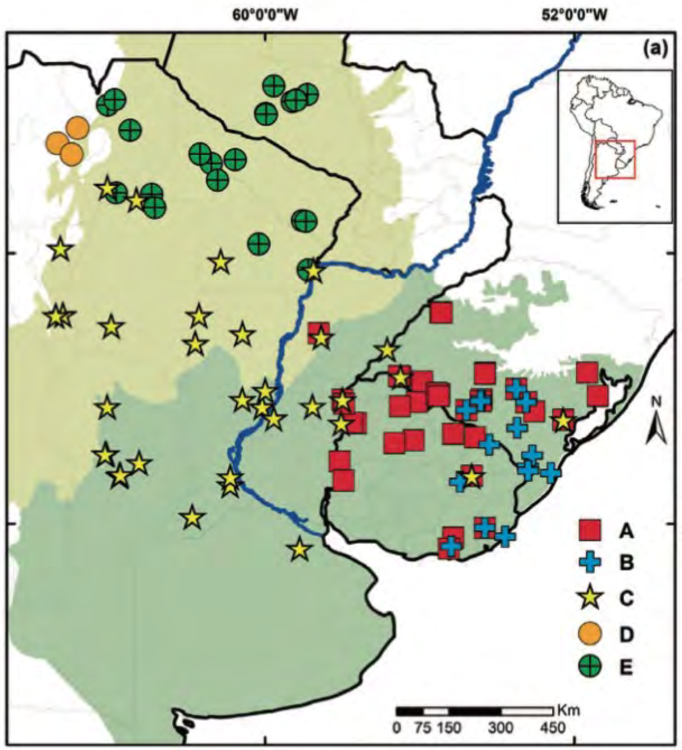
- Dr. Matías Malleret: Postdoc CONICET (Posadas, Argentina)

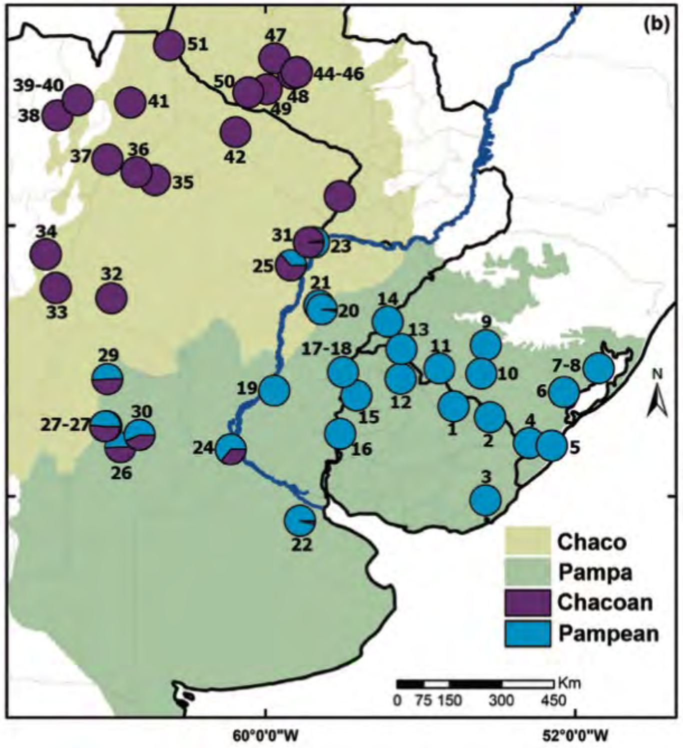
Journal of Biogeography

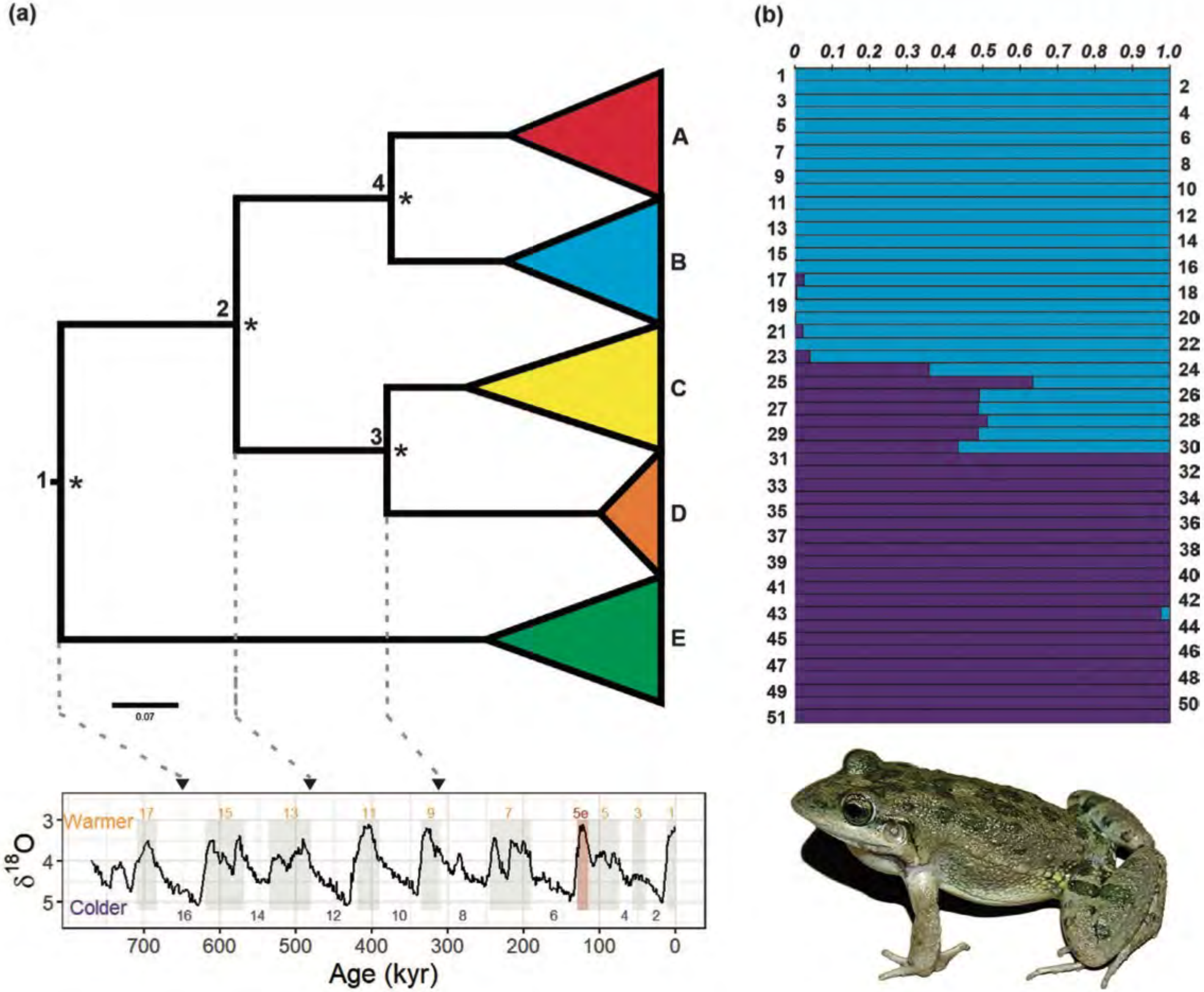
RESEARCH ARTICLE

Rivers, Environment, and Climate: Shaping an Oven Frog's Evolution in the Chaco and Pampa Lowlands of South America

Matías M. Malleret[1,2,3] | Diego Baldo[3] | Priscila Lemes[4] | Francisco Brusquetti[5] | Laura Verrastro[2] | Arley Camargo[1]






(a)
A
B
C
D
E
1
2
3
4
*
0.07
Warmer
Colder
δ18O
3
4
5
17
15
13
11
9
7
5e
5
3
1
16
14
12
10
8
6
4
2
700
600
500
400
300
200
100
0
Age (kyr)
(b)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1
3
5
7
9
11
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19
21
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35
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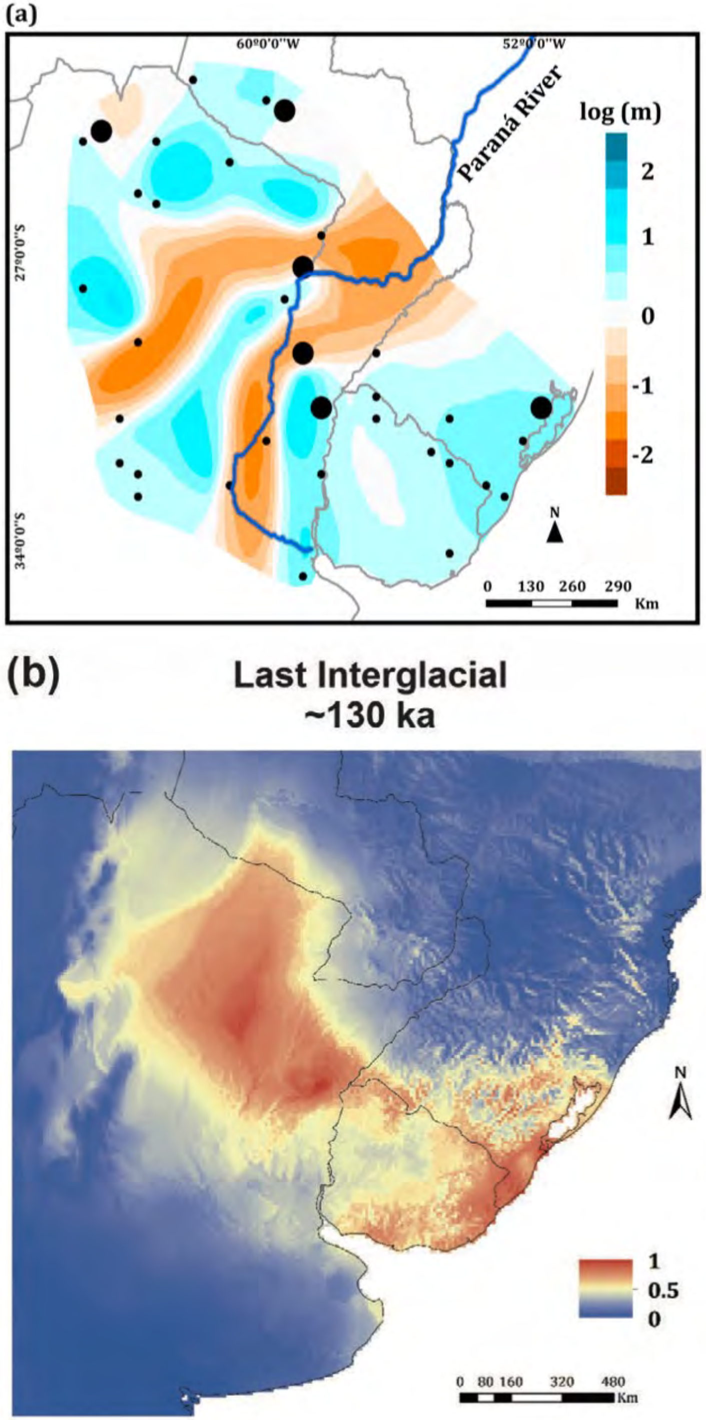
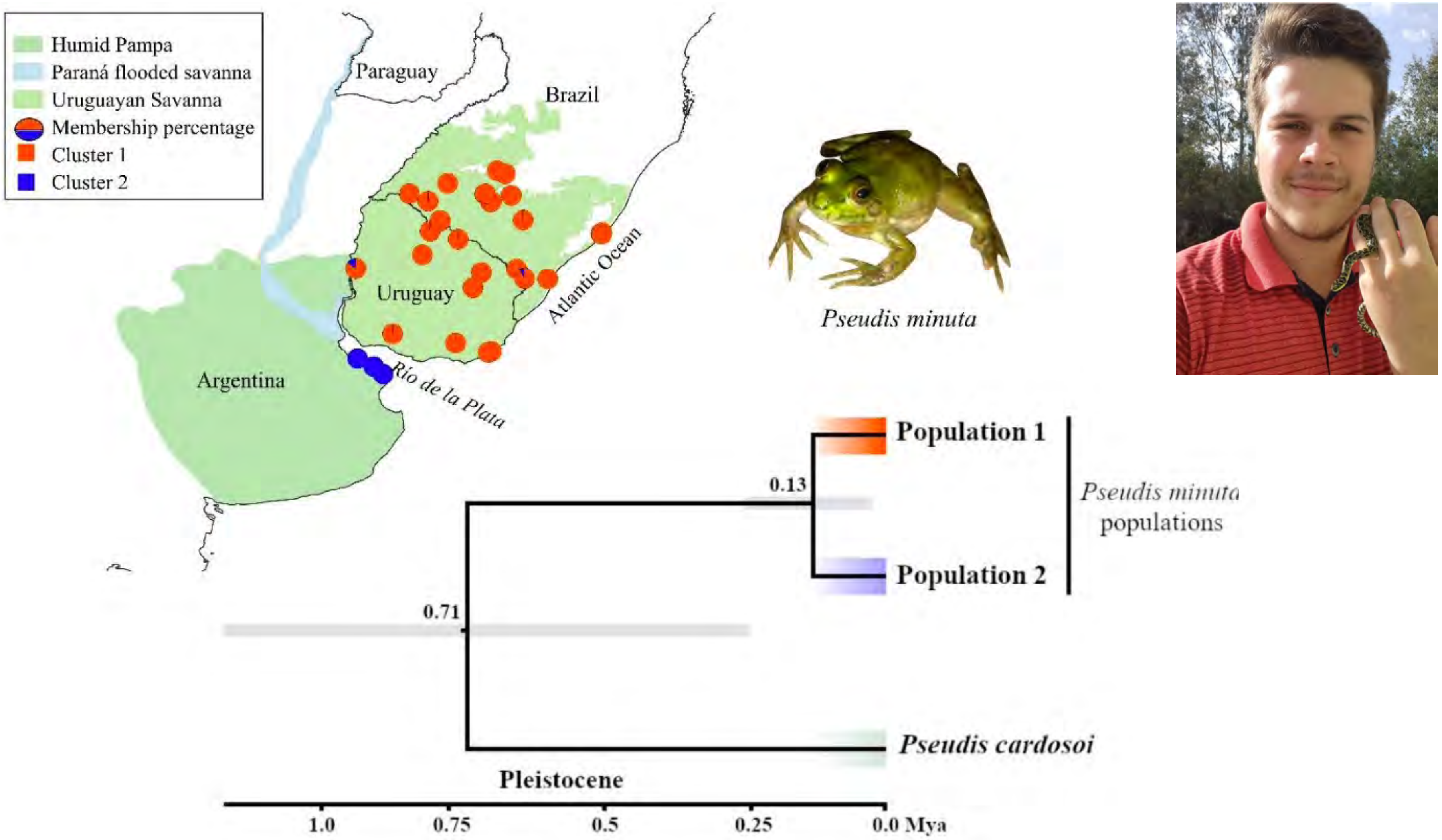
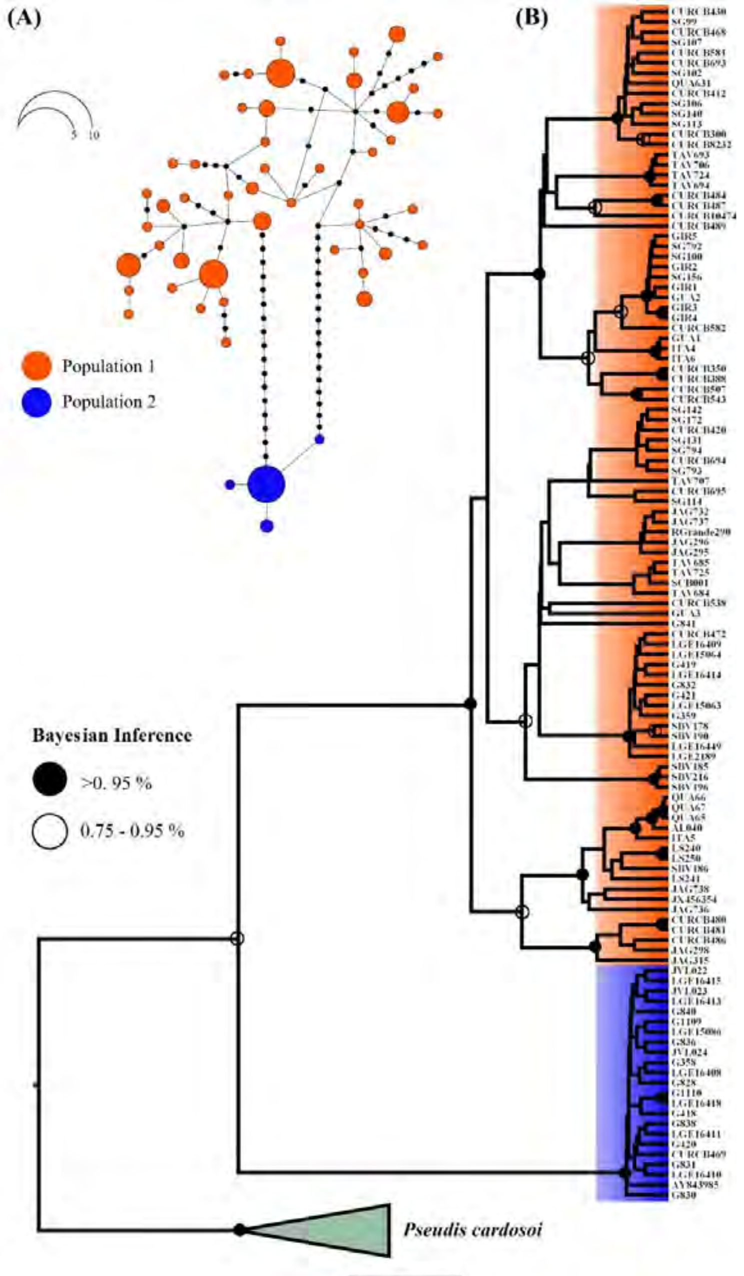

(a)
60º0'0''W
52º0'0''W
Paraná River
27º0'0''S
34º0'0''S
log (m)
2
1
0
-1
-2
N
0
130
260
290
Km
(b)
Last Interglacial
~130 ka
N
1
0.5
0
0
80
160
320
480
Km

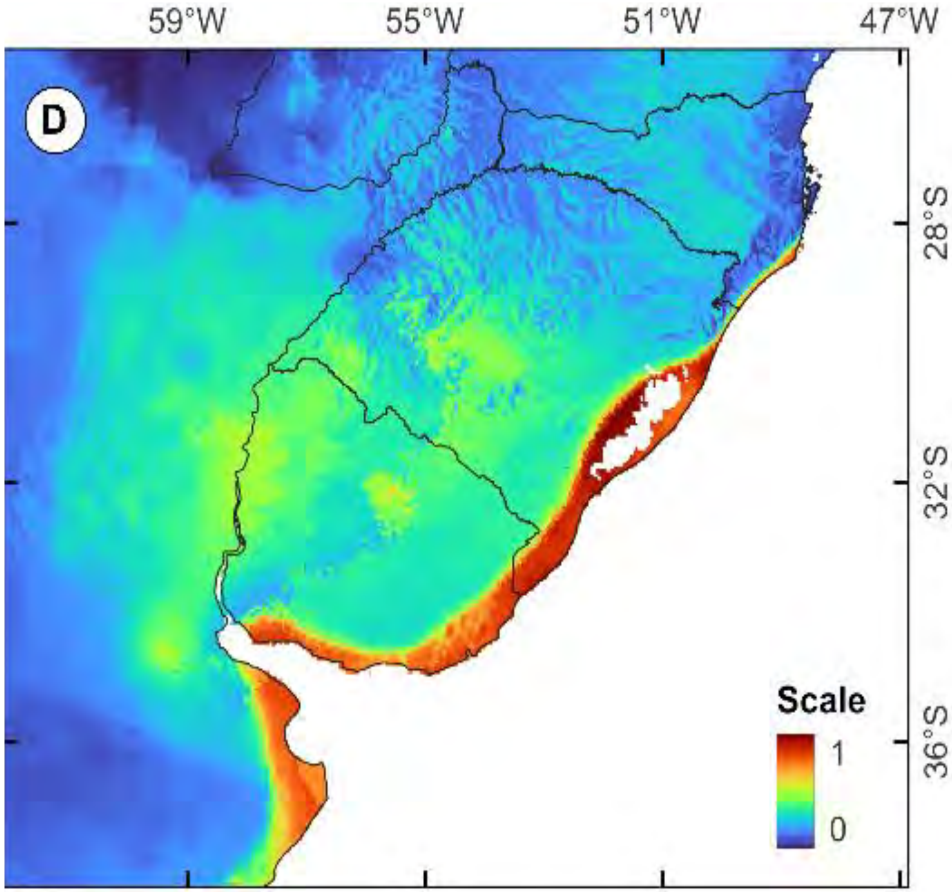
Filogeografía de *Pseudis minuta*

- Mag. Teilor Kroscevic: Doctorando en UFMG (Belo Horizonte, Brasil)

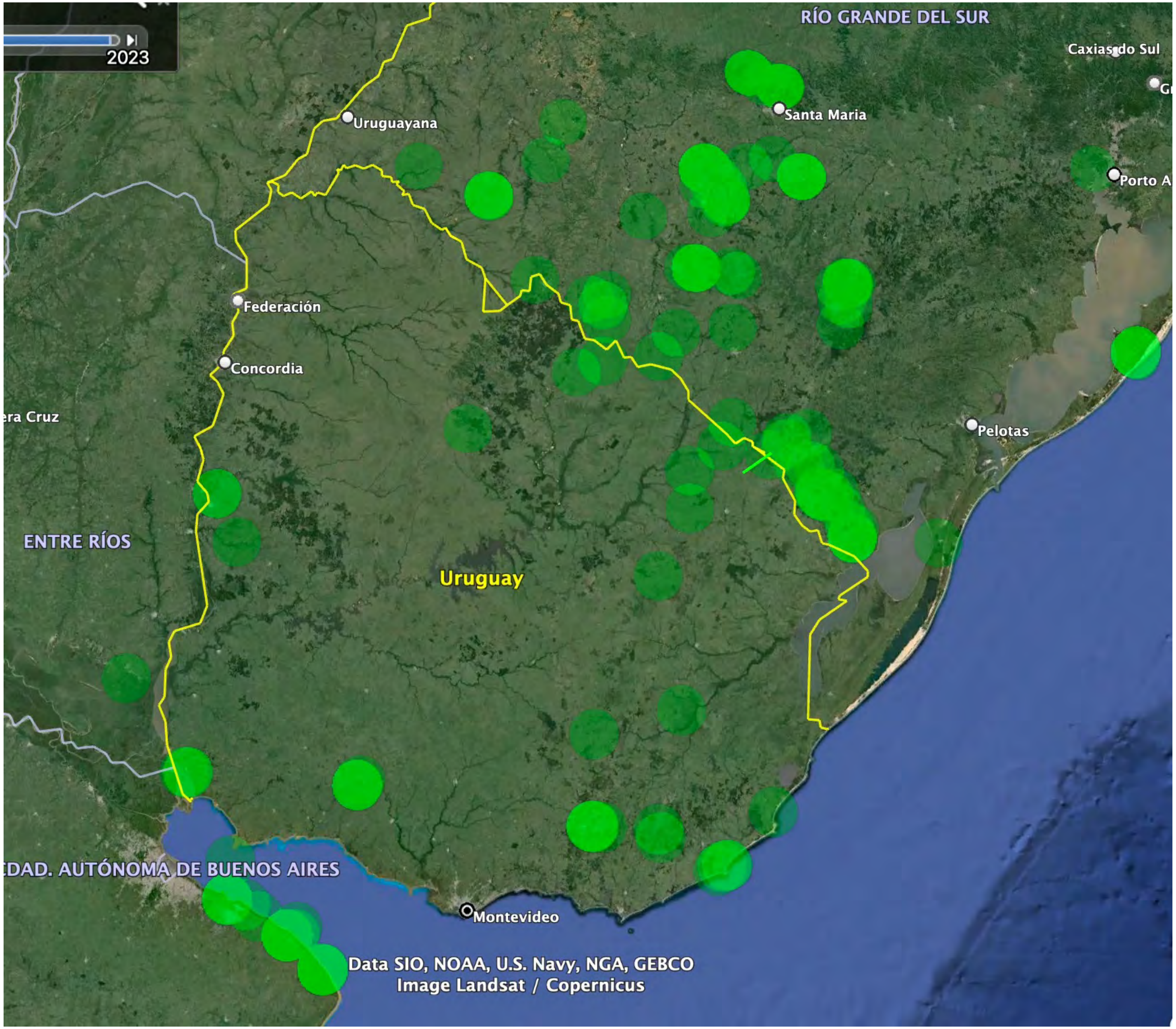


Filogeografía de *Pseudis minuta*



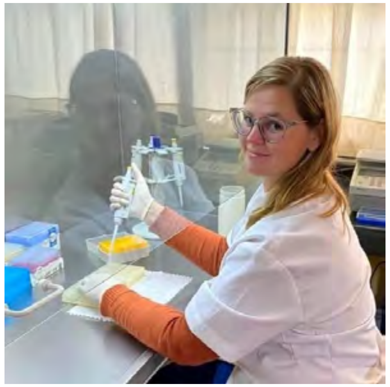


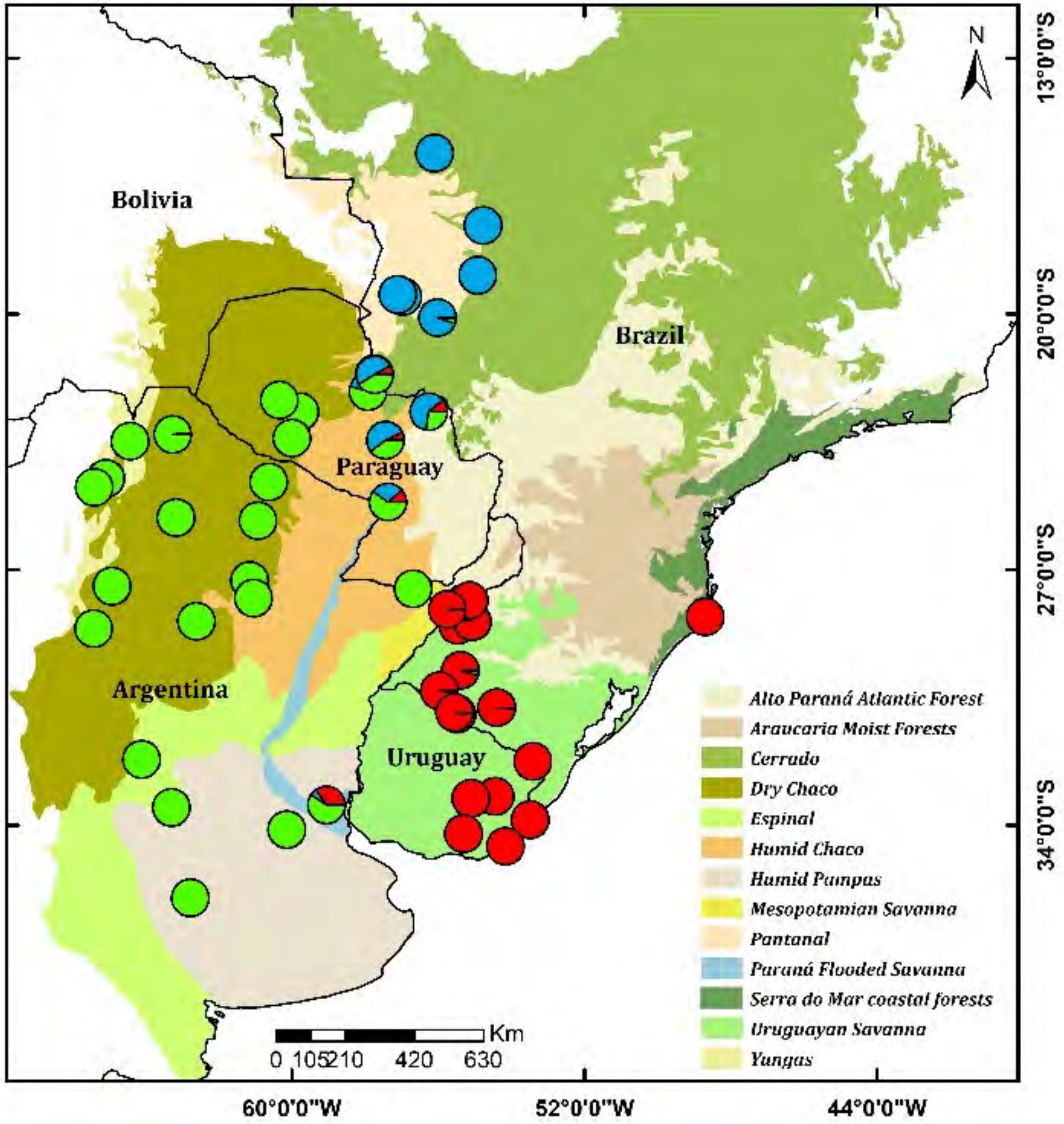
Filogeografía de *Pseudis minuta*



Filogeografía de *Physalaemus biligonigerus*

- Dra. Rosio Schneider (Postdoc CONICET Misiones, Argentina)

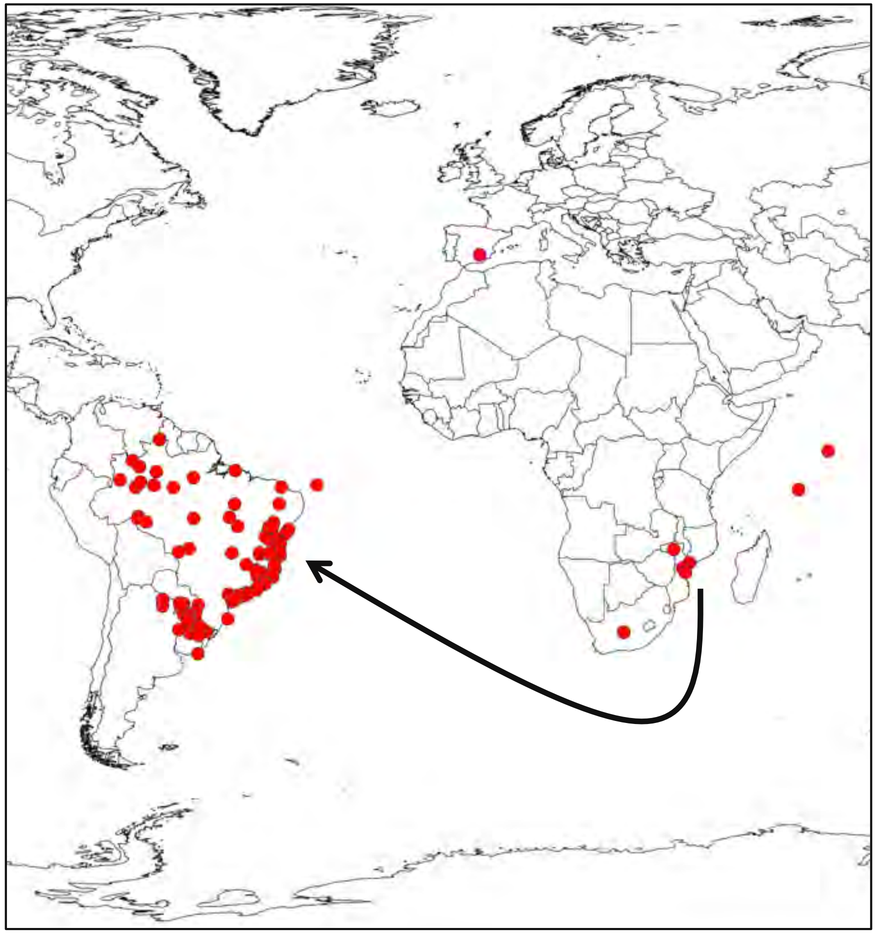


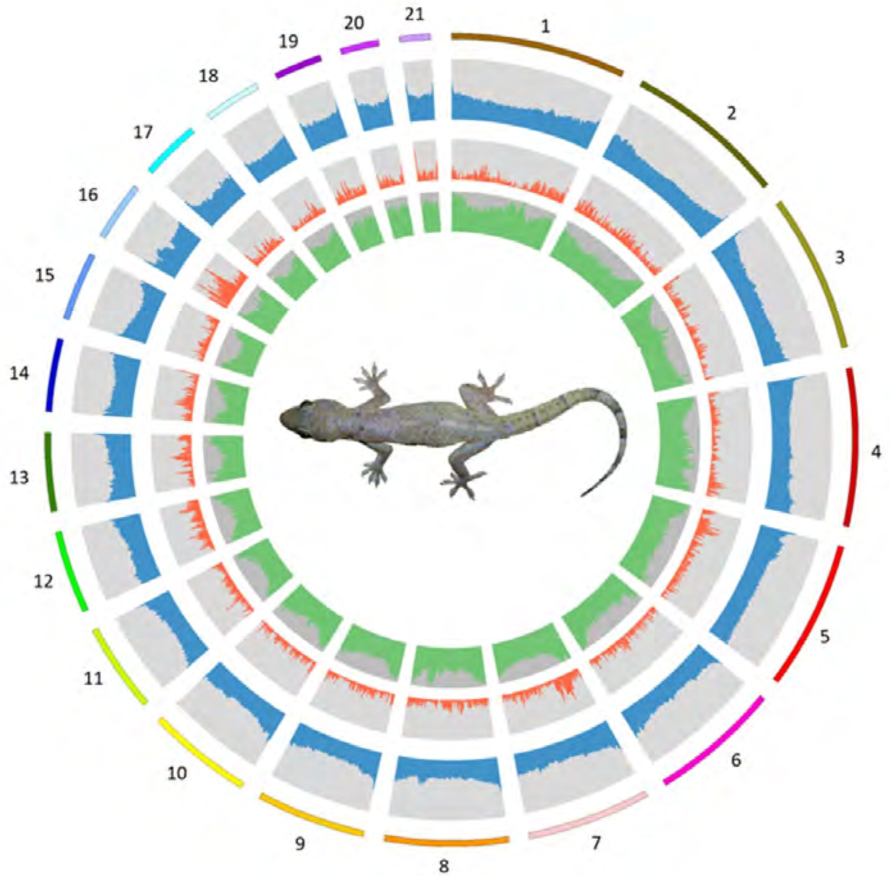


Filogeografía de *Hemidactylus mabouia*

- Mag. Mauro Martínez Villar:

  Doctorado UDELAR (Uruguay)

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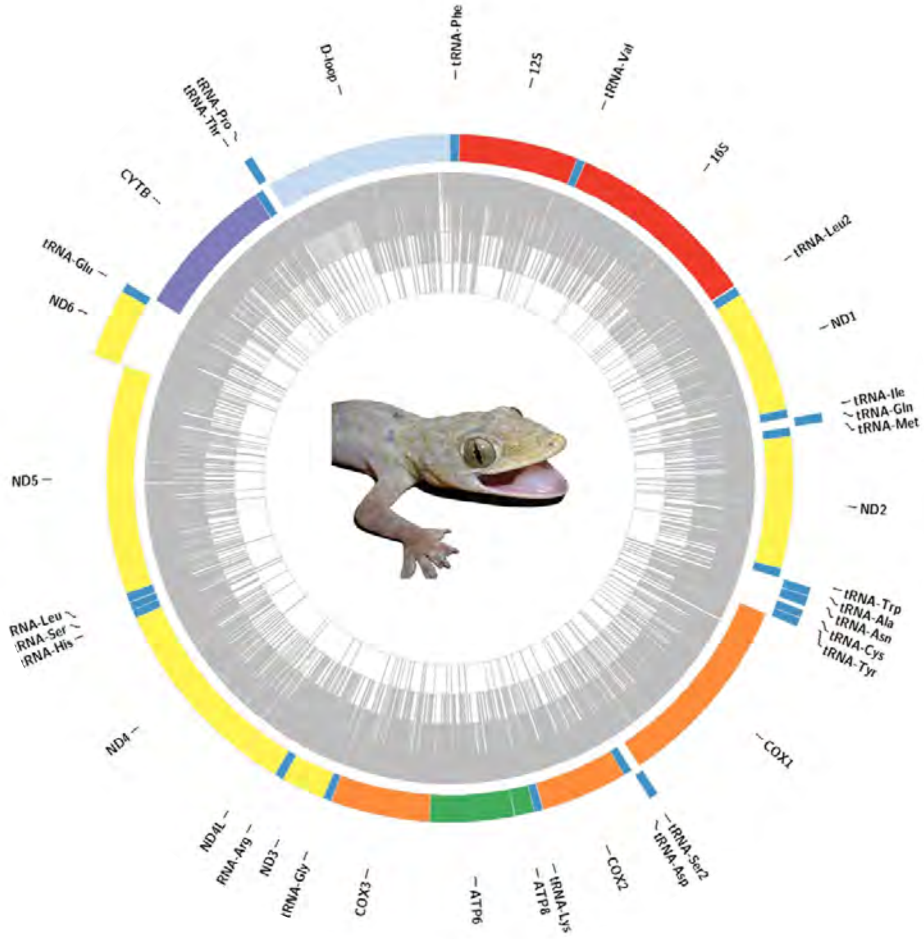
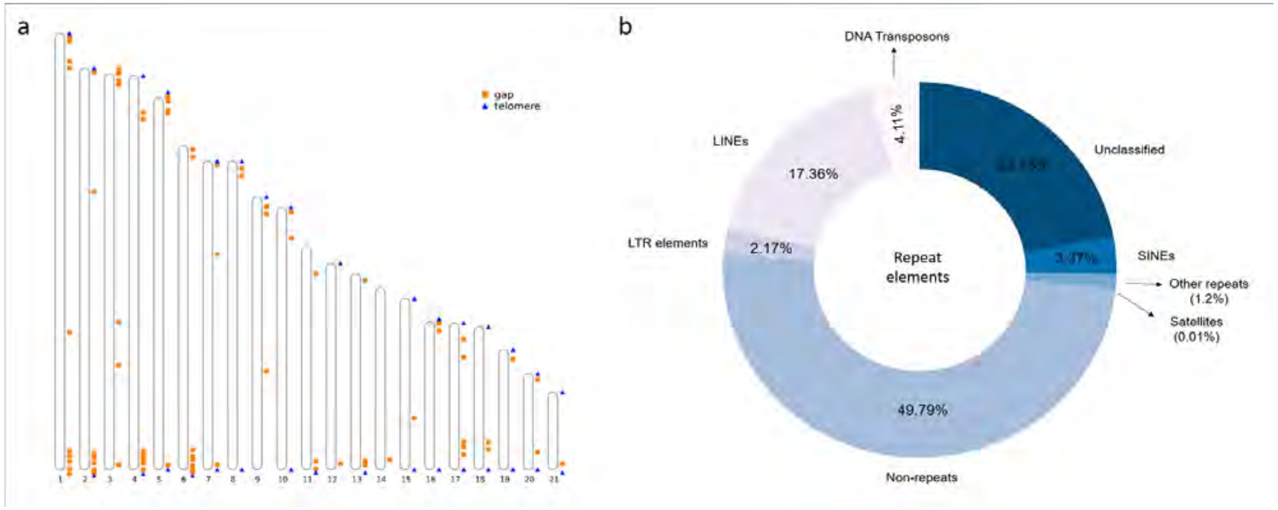

tRNA-Phe
12S
tRNA-Val
16S
tRNA-Leu2
ND1
tRNA-Ile
tRNA-Gln
tRNA-Met
ND2
tRNA-Trp
tRNA-Ala
tRNA-Asn
tRNA-Cys
tRNA-Tyr
COX1
tRNA-Ser2
tRNA-Asp
COX2
tRNA-Lys
ATP8
ATP6
COX3
tRNA-Gly
ND3
RNA-Arg
ND4L
ND4
RNA-Leu
RNA-Ser
tRNA-His
ND5
ND6
tRNA-Glu
CYTB
tRNA-Thr
tRNA-Pro
D-loop


a
gap
telomere
1
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3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
b
DNA Transposons
4.11%
LINEs
17.36%
Unclassified
LTR elements
2.17%
Repeat elements
3.37%
SINEs
Other repeats (1.2%)
Satellites (0.01%)
49.79%
Non-repeats

Filogeografía y conservación

- Proyecto CSIC I+D 2012 “Diversidad y conservación de anfibios y reptiles de las Quebradas del Norte” (2013–2015)
- Colaboración con FCien; dos tesistas de maestría

unesco

"Building peace in the minds of men and women"

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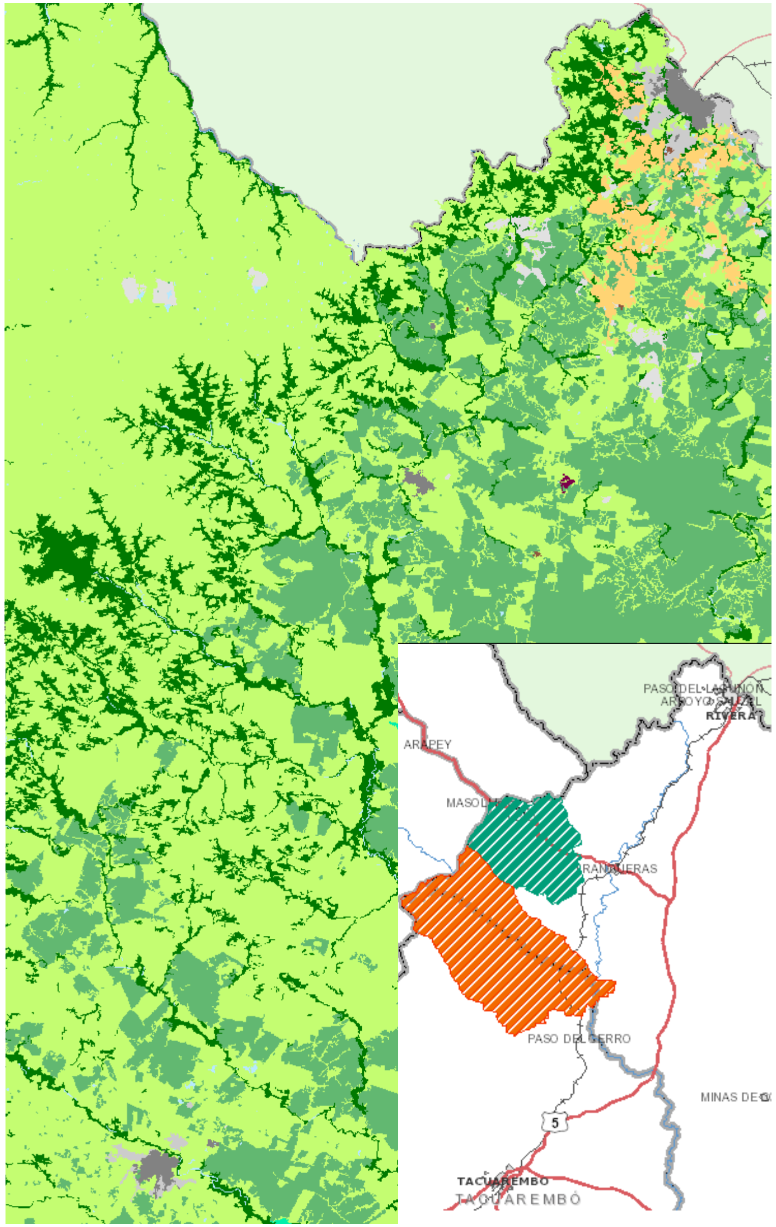
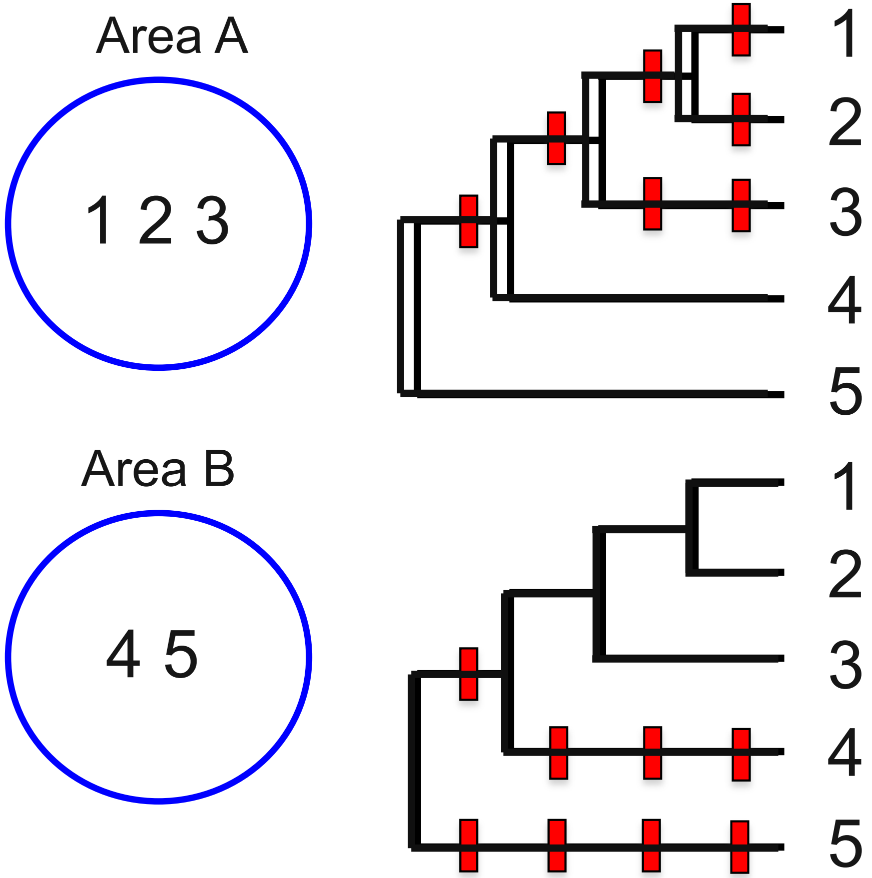
Bioma Pampa-Quebradas del Norte Biosphere Reserve, Uruguay



Diversidad Filogenética (DF)

- Cambios acumulados durante la historia evolutiva (“feature diversity”, Faith 1992)



3 especies
DF = 7

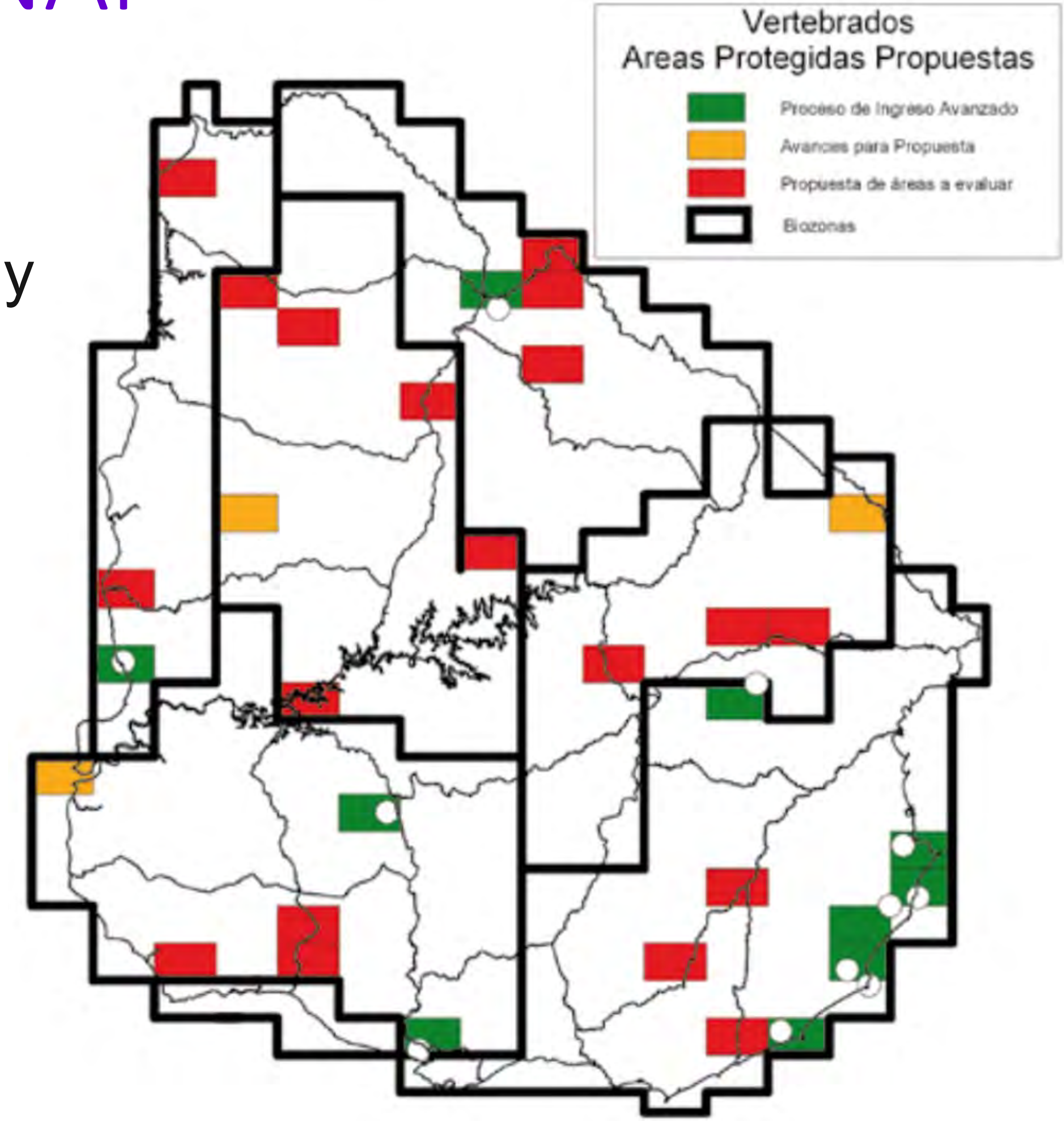
2 especies
DF = 8

Faith (1992) Biol. Conserv. 61:1-10

SNAP

- Criterios biológicos: riqueza de especies, grado de endemismo y amenaza; actividad antrópica y de naturalidad; patrimonios paisajísticos y culturales

- Factibilidad socio-política



Especies Focales

- *Homonota uruguayensis*

Limnomedusa

-
-

Leptodactylus latinasus

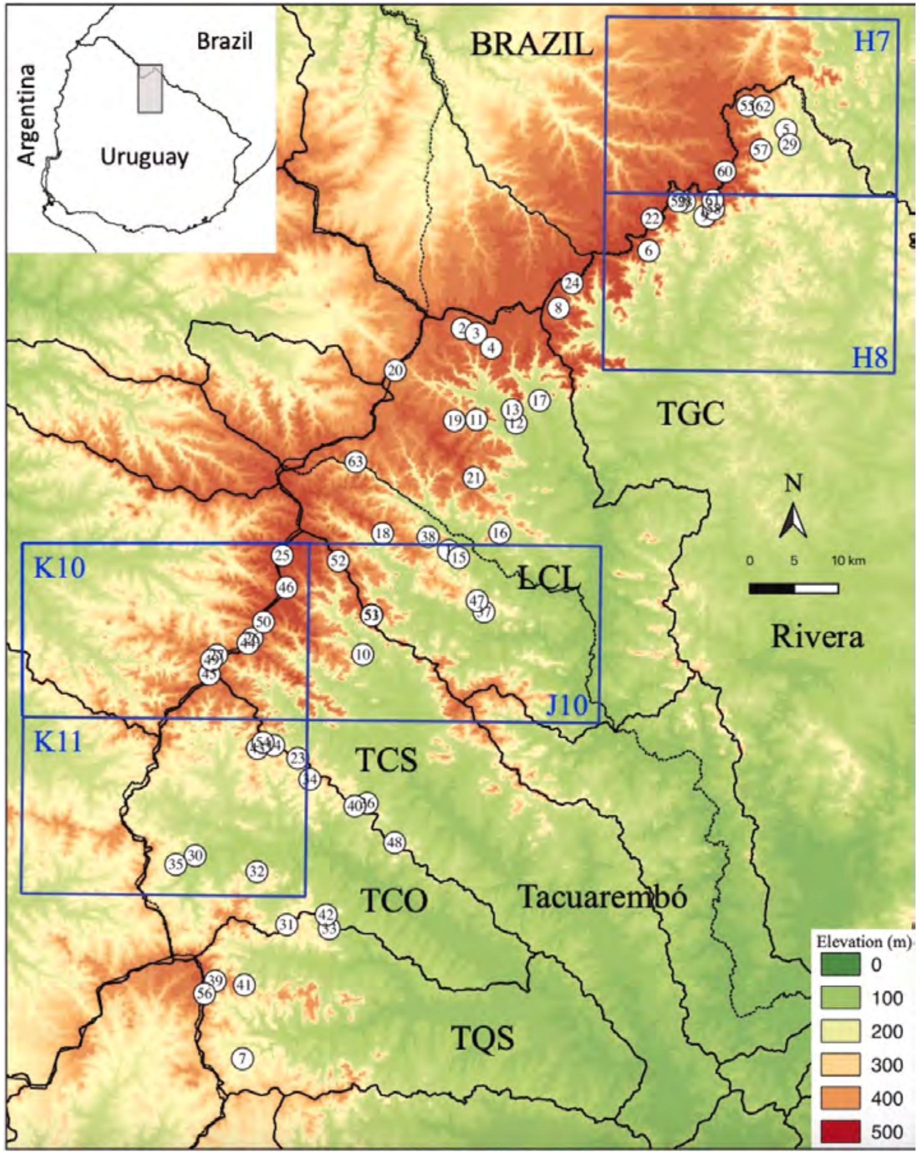
Contomastix lacertoides

Materiales y Métodos

- 78 *Homonota uruguayensis*, 26 *Contomastix lacertoides*, 67 *Limnomedusa macroglossa* y 28 *Leptodactylus latinasus*)
- Gen mitochondrial citocromo b
- Genealogías intraespecíficas
- Cálculo de PD global, de endemismo y complementariedad de 5 cuencas hidrográficas
- Valle del Lunarejo (VDL) en LCL es la única área protegida de las QDN:

(1) ¿Es LCL la cuenca con mayor PD?

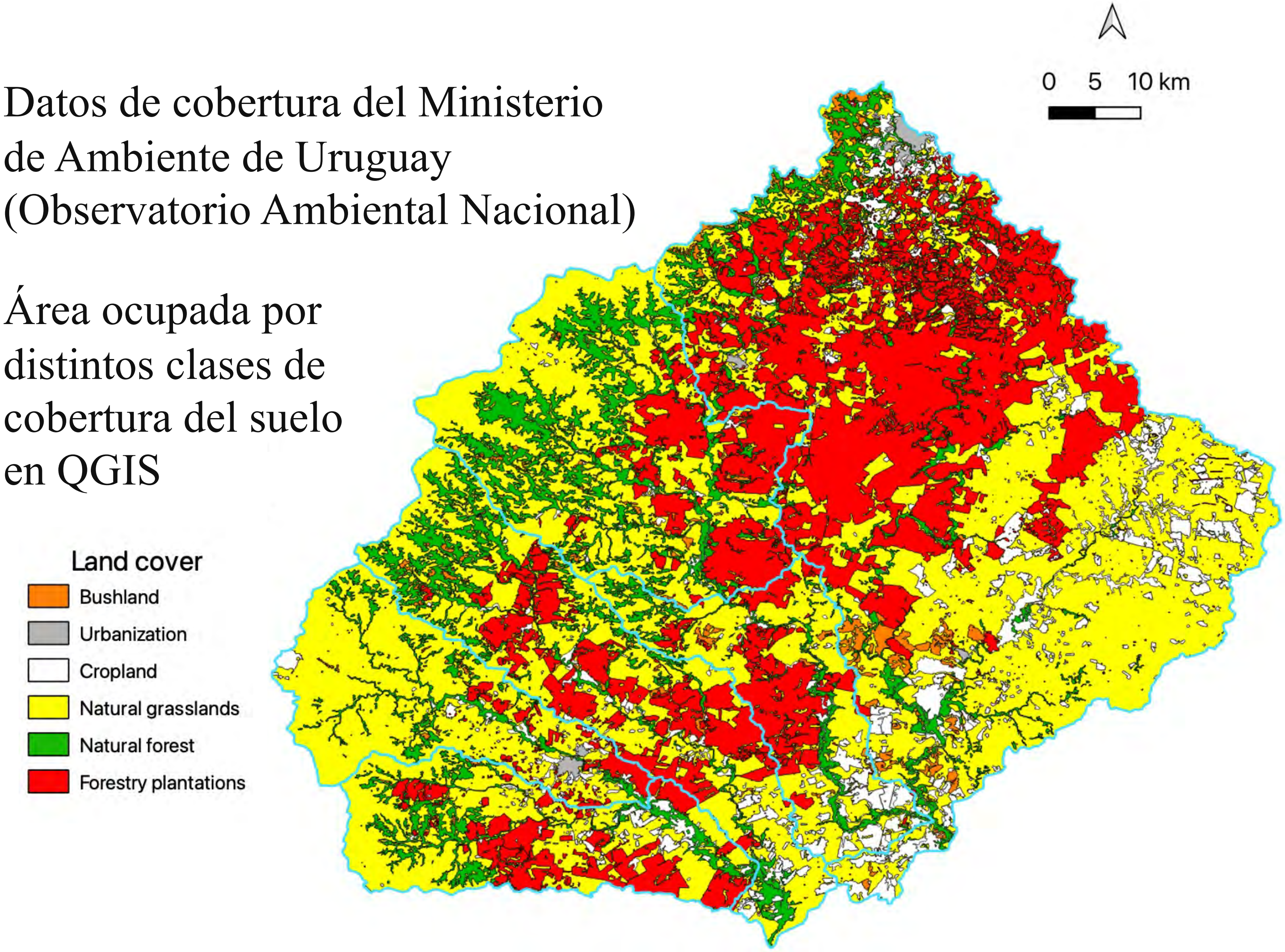
(2) ¿Cuál cuenca complementa mejor la PD de LCL?



TGC = Cuñapirú LCL = Lunarejo
TCS = Tres Cruces TCO = Tacuarembó
TQS = Tranqueras **VDL = Lunarejo**

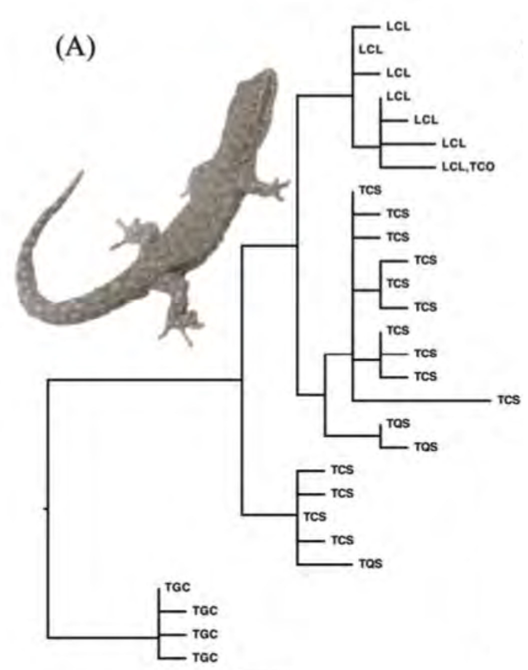
Cobertura del suelo

- Datos de cobertura del Ministerio de Ambiente de Uruguay (Observatorio Ambiental Nacional)
- Área ocupada por distintos clases de cobertura del suelo en QGIS

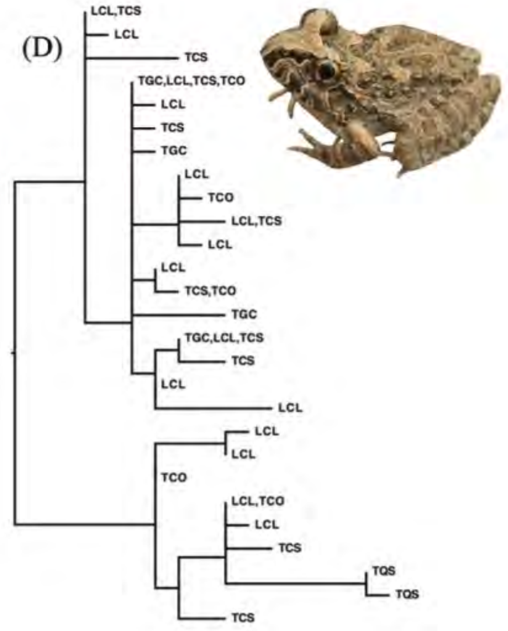


Resultados

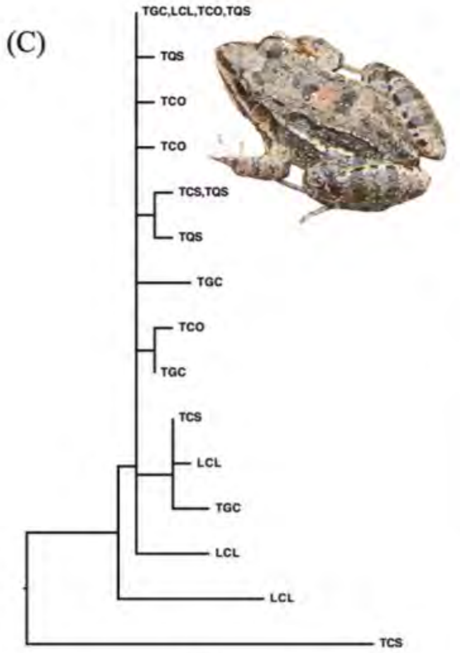
(A)



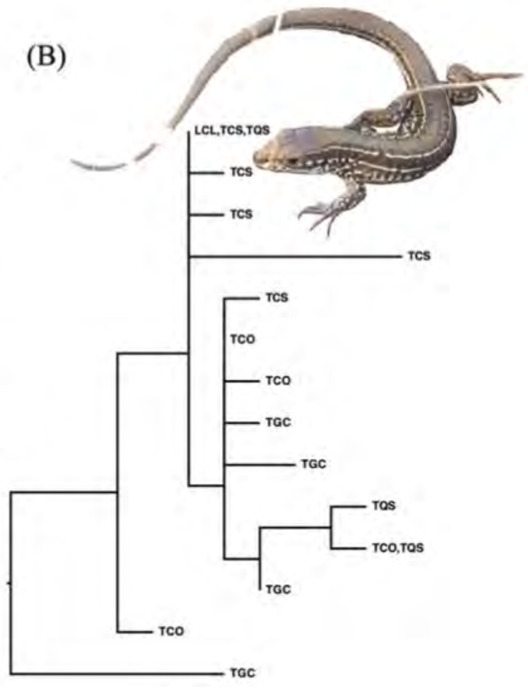
(D)



(C)

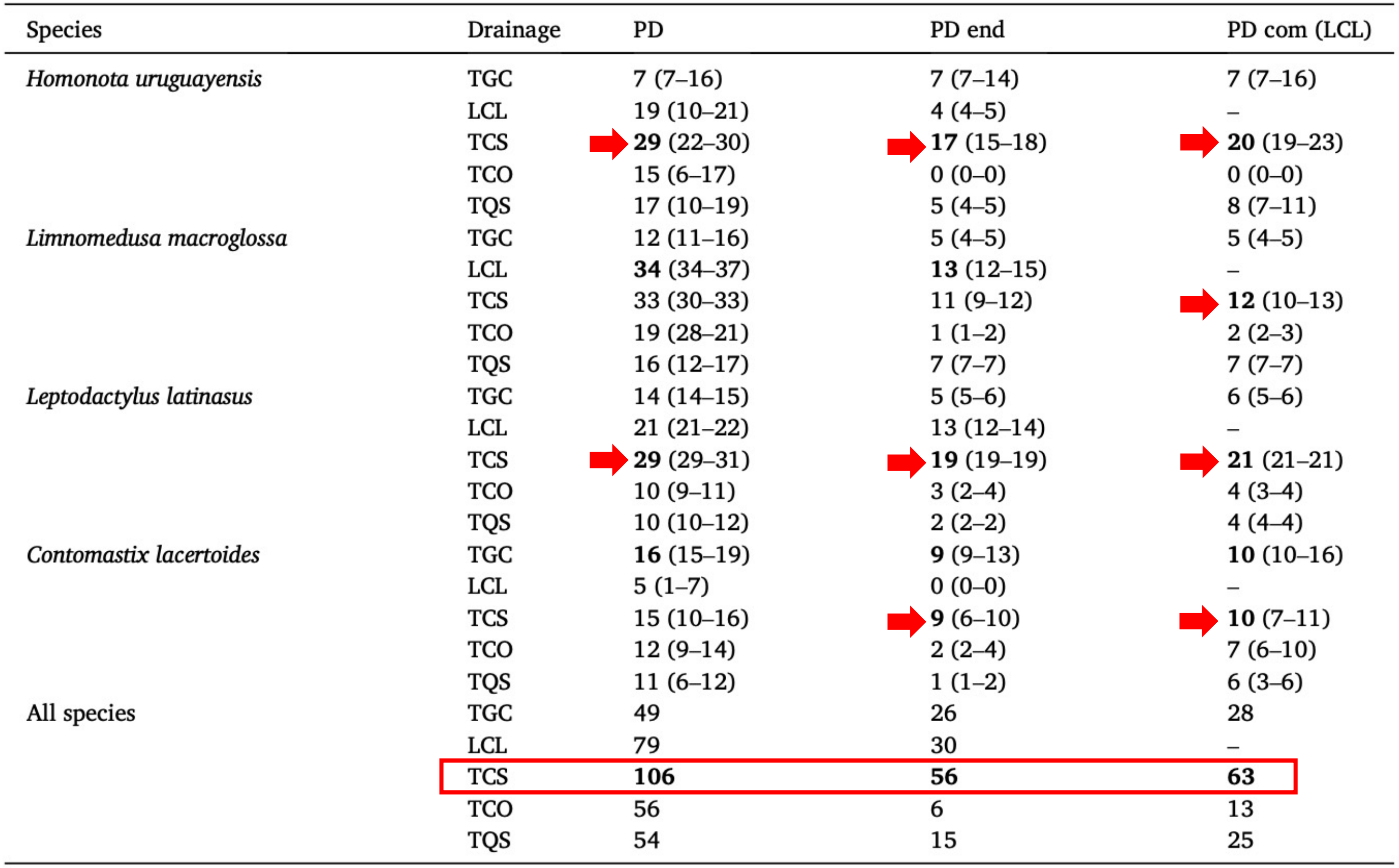


(B)



Resultados

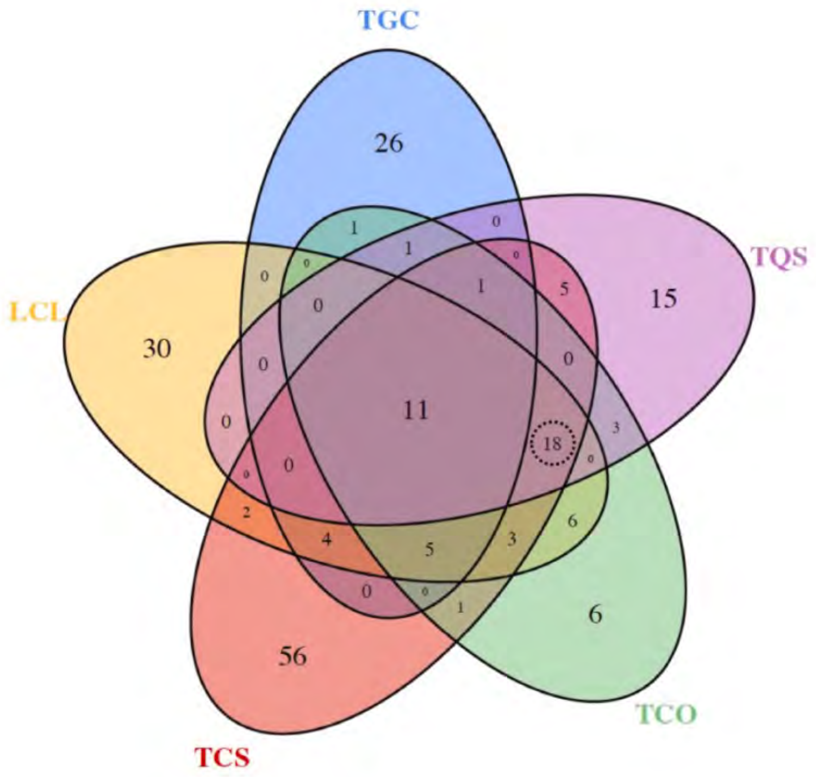
- Fuerte congruencia en patrones de PD entre especies
- Tres Cruces (TCS) es la Cuenca con PD más grande y la que mejor complementa la PD de LCL

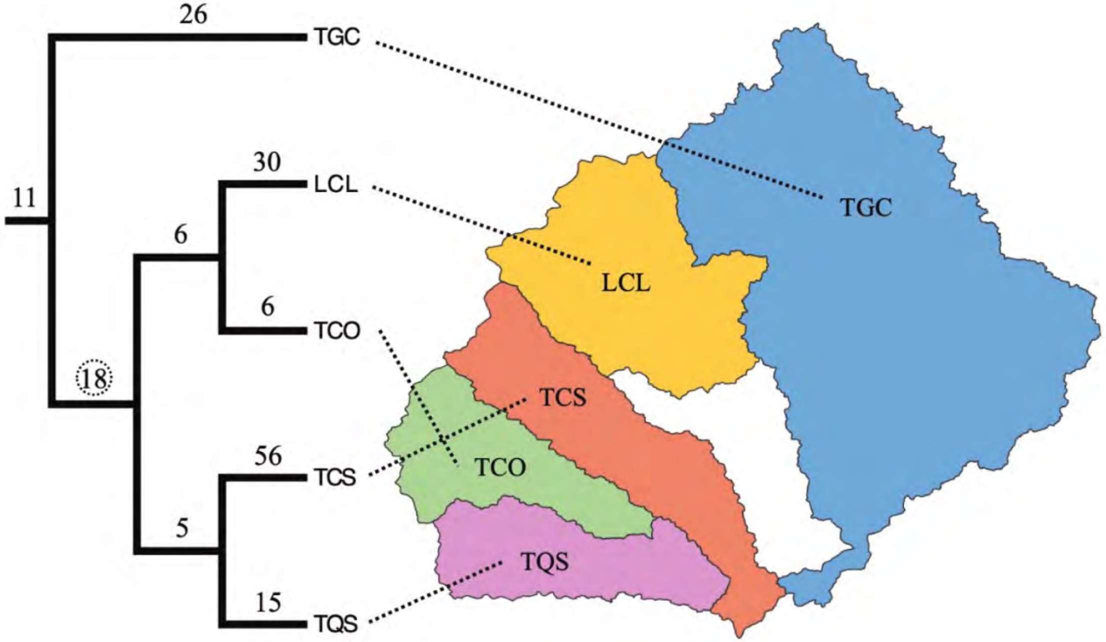


Species	Drainage	PD	PD end	PD com (LCL)
Homonota uruguayensis	TGC	7 (7–16)	7 (7–14)	7 (7–16)
	LCL	19 (10–21)	4 (4–5)	–
	TCS	➡ **29** (22–30)	➡ **17** (15–18)	➡ **20** (19–23)
	TCO	15 (6–17)	0 (0–0)	0 (0–0)
	TQS	17 (10–19)	5 (4–5)	8 (7–11)
Limnomedusa macroglossa	TGC	12 (11–16)	5 (4–5)	5 (4–5)
	LCL	**34** (34–37)	**13** (12–15)	–
	TCS	33 (30–33)	11 (9–12)	➡ **12** (10–13)
	TCO	19 (28–21)	1 (1–2)	2 (2–3)
	TQS	16 (12–17)	7 (7–7)	7 (7–7)
Leptodactylus latinasus	TGC	14 (14–15)	5 (5–6)	6 (5–6)
	LCL	21 (21–22)	13 (12–14)	–
	TCS	➡ **29** (29–31)	➡ **19** (19–19)	➡ **21** (21–21)
	TCO	10 (9–11)	3 (2–4)	4 (3–4)
	TQS	10 (10–12)	2 (2–2)	4 (4–4)
Contomastix lacertoides	TGC	**16** (15–19)	**9** (9–13)	**10** (10–16)
	LCL	5 (1–7)	0 (0–0)	–
	TCS	15 (10–16)	➡ **9** (6–10)	➡ **10** (7–11)
	TCO	12 (9–14)	2 (2–4)	7 (6–10)
	TQS	11 (6–12)	1 (1–2)	6 (3–6)
All species	TGC	49	26	28
	LCL	79	30	–
	TCS	**106**	**56**	**63**
	TCO	56	6	13
	TQS	54	15	25

Resultados

- La partición de PD dentro y entre cuencas muestra que la cuenca Cuñapirú (TGC) es la más diferenciada del resto

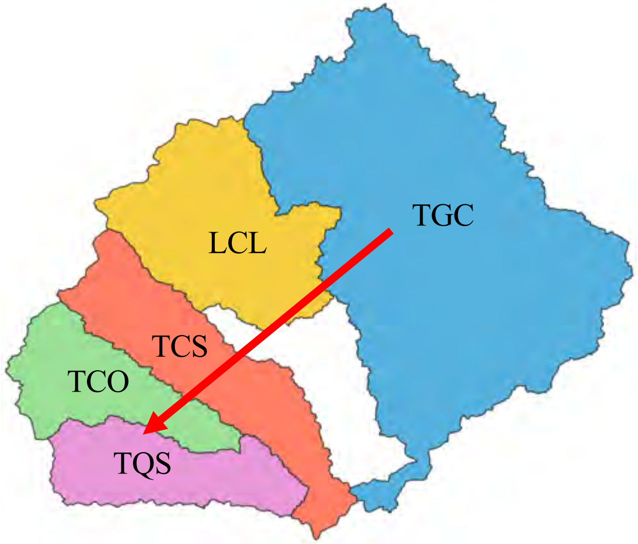




Resultados

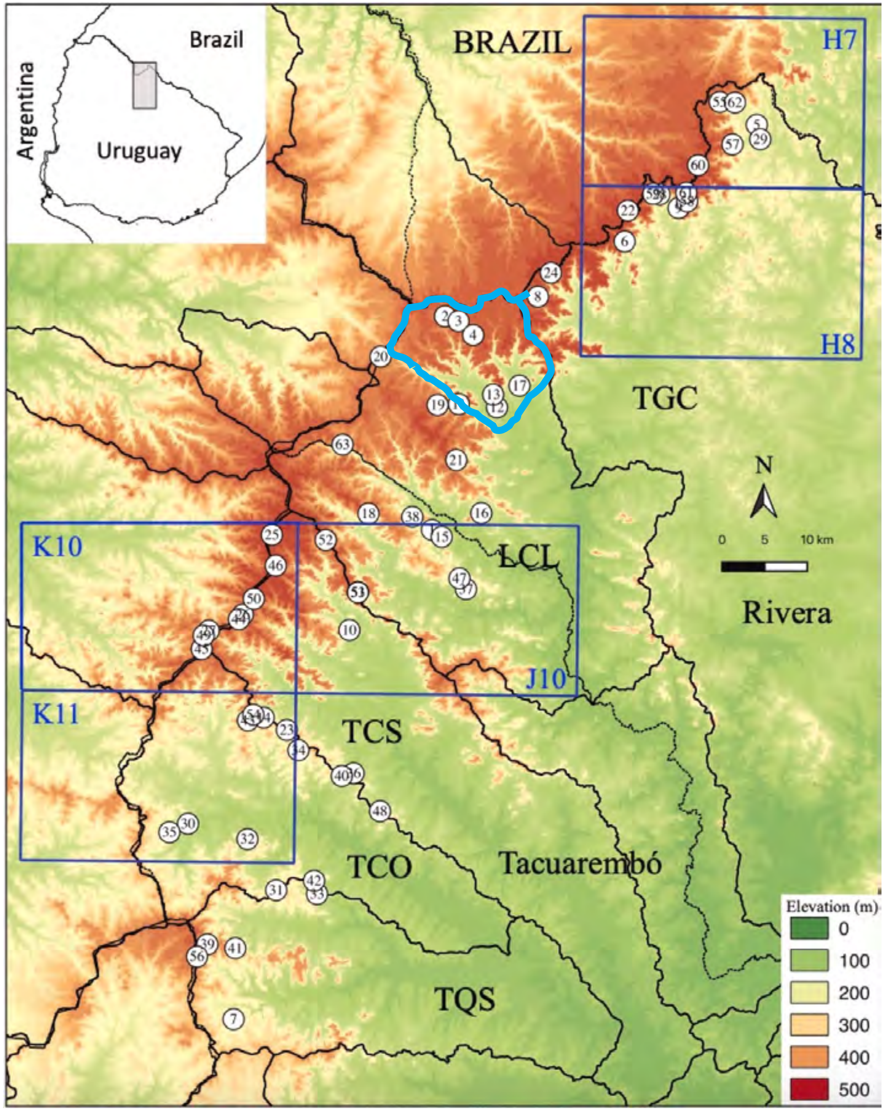
- Gradiente del NE al SO con incremento de la cobertura natural
- TCS tiene valores intermedios de antropización con la mayor contribución de bosque nativo
- TGC tiene una alta proporción de suelos antropizados con la mayor contribución de plantaciones forestales (*Eucalyptus* y *Pinus*)

Cuenca	Area (km^2)	Natural (km^2)	Antropizada (km^2)
TGC	1.112,7	599,4 (53,9%)	513,1 (46,1%)
LCL	1.019,7	865,5 (84,9%)	153,8 (15,1%)
TCS	420,4	383,4 (91,3%)	36,7 (8,7 %)
TCO	504,1	480,2 (95,3%)	23,8 (4,7%)
TQS	237,0	226,0 (95,3%)	11,0 (4,7%)



Discusión

- Patrones de PD congruentes: dispersión limitada y/o preferencias de habitat
- La priorización de TGC es consistente con vertebrados terrestes y plantas leñosas (Brazeiro et al. 2008, 2015)
- Expansión del SNAP incluyó la celda J10, contiene parcialmente a TCS (MVOTMA, 2015)
- Alta naturalidad de TCS pero alta antropización de TGS
- Evaluación de patrones de PD en otros taxa (ej.: *Scinax fuscovarius* y *Tropidurus catalanensis*)



Journal for Nature Conservation

Volume 75, October 2023, 126468

Conservation prioritization of the northern hills of Uruguay based on the intra-specific phylogenetic diversity of frogs and lizards

Arley Camargo[a], Ernesto Elgue[b], Claudia Fernández[b], Laura Lima[a], Raúl Maneyro[b]

Teléfono para el SNAP: dos ranas, un geko y una lagartija nos dan nuevas pistas para designar una nueva área protegida en el país

Publicado el 27 de septiembre de 2023

Escribe Martín Otheguy en Investigación científica

12 minutos de lectura

Estudio sobre diversidad filogenética de cuatro especies de las Quebradas del Norte, en Rivera y Tacuarembó, reveló que dos áreas presentan aportes muy valiosos para la biodiversidad de ese ecosistema único en el país, una de ellas en peligro por el avance de la urbanización y la forestación.

Laboratorio
Biogeografía
& Evolución

Gracias!

@bioevouy