

Species ranges, niche overlap and niche trait evolution in *Austrolebias* annual killifish

Tom JM Van Dooren

Institute for Ecology and Environmental Sciences iEES Paris
Sorbonne University
Team Phenotypic Variability and Adaptation VPA

Leiden 2019

tvdooren@gmail.com

tomvandooren.eu

greenkillies.org/blog





2012

Neofundulus cf. paraguayensis



2012

Austrolebias monstrosus



2012

Papilliolebias bitteri
Trigonectes aplocheiloïdeus



2012



2012



2012

A. vandenbergi



2012

Started Latest Headlines Vrienden zoeken R: Reorder Levels of a ...

Bourgogne zoekt Nederlandse huisart...

rividavia salta - Google Maps

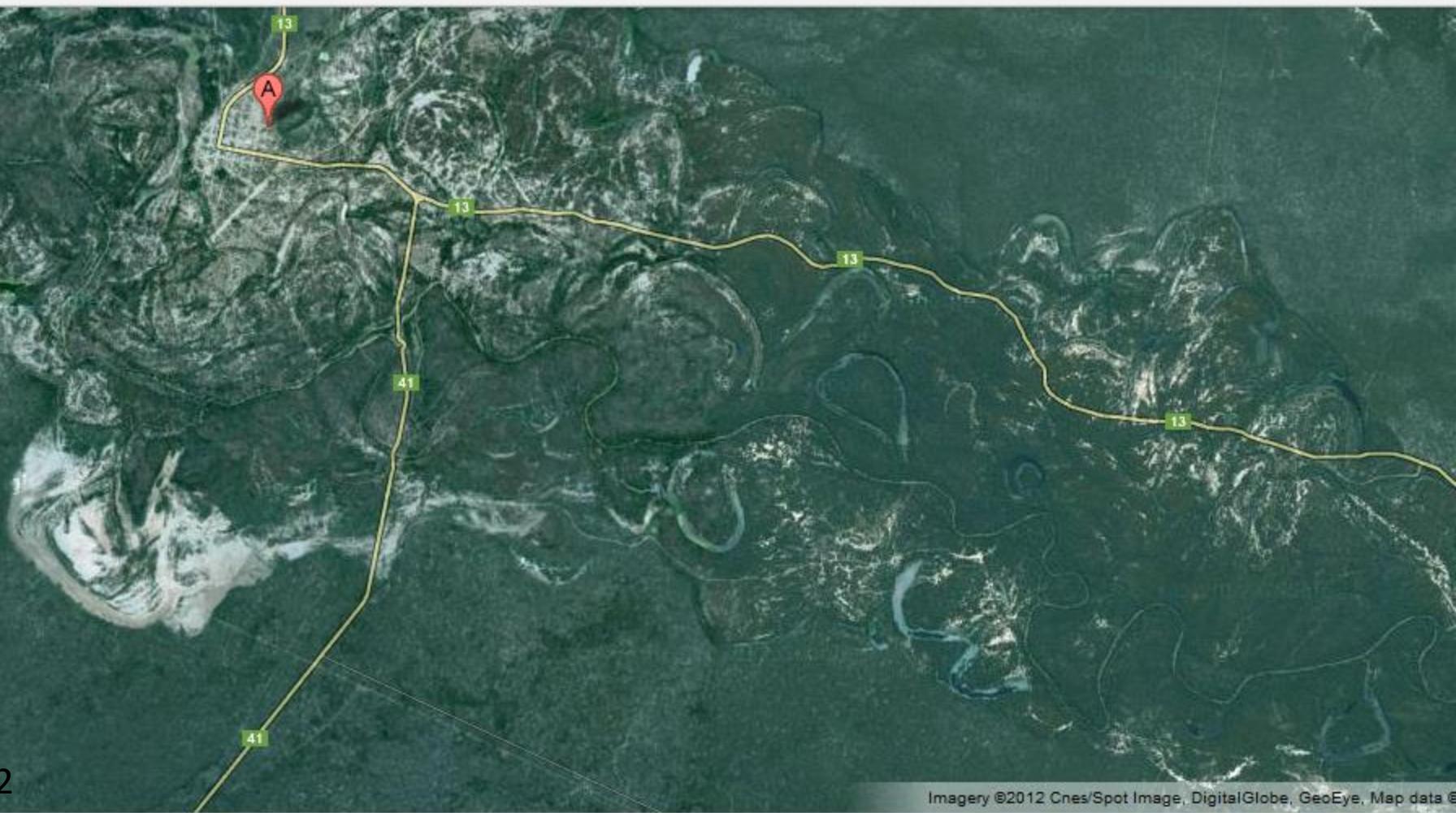
Images Maps Play YouTube News Gmail Drive Calendar More

rividavia salta



Tom Van Dooren

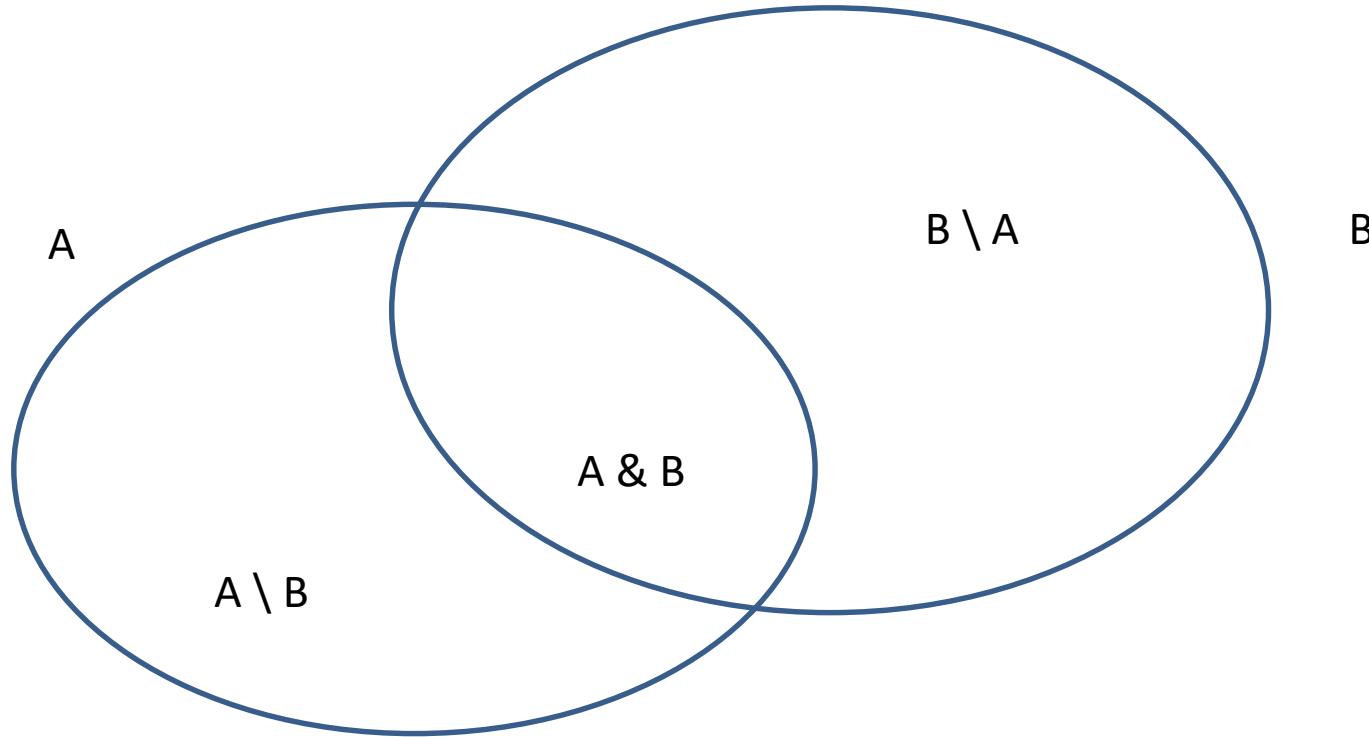
0



2012

Imagery ©2012 Cnes/Spot Image, DigitalGlobe, GeoEye. Map data ©

Ecology



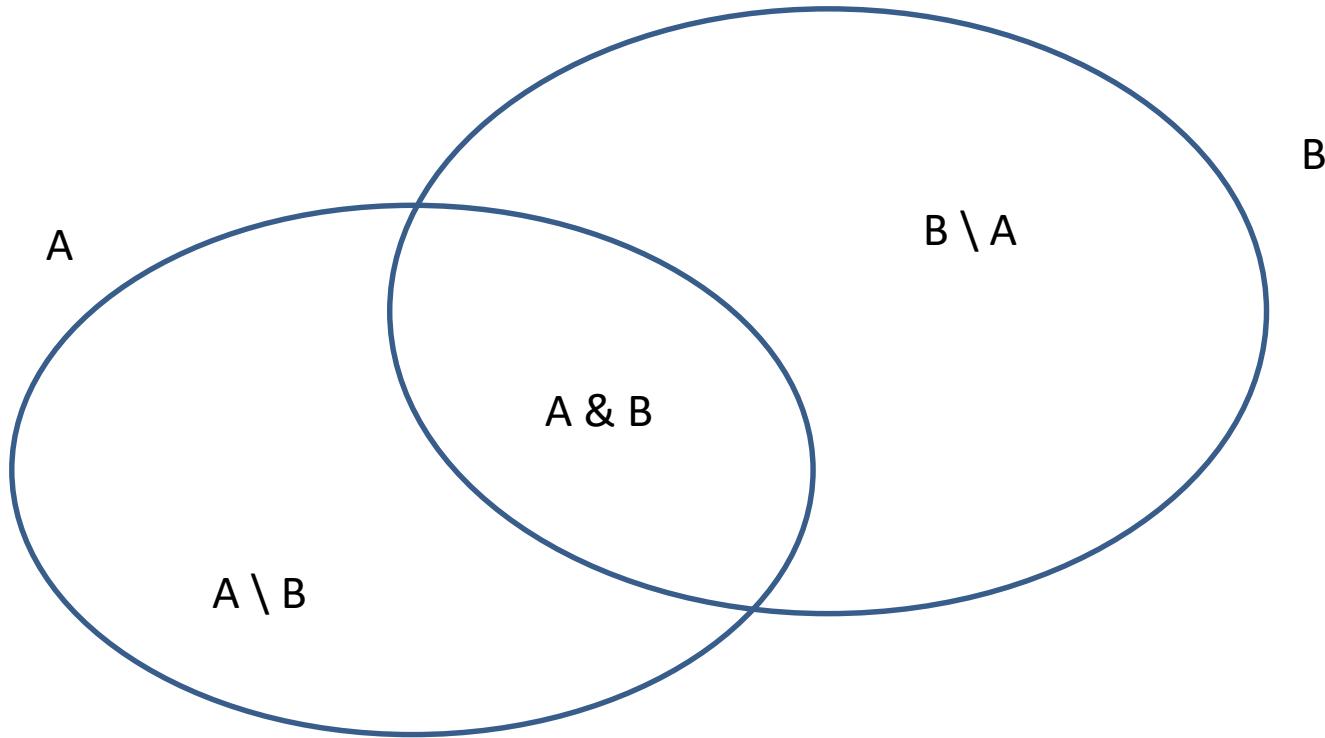
Ranges and range overlap:

No stable coexistence possible without phenotypic differences

Unified neutral theory of biodiversity (Hubbell)

Project range changes with changes in environmental variables

Evolution



Ranges and range overlap:

Modes of speciation (allopatric / parapatric / sympatric)

Niche trait evolution: niche traits calculated from range information

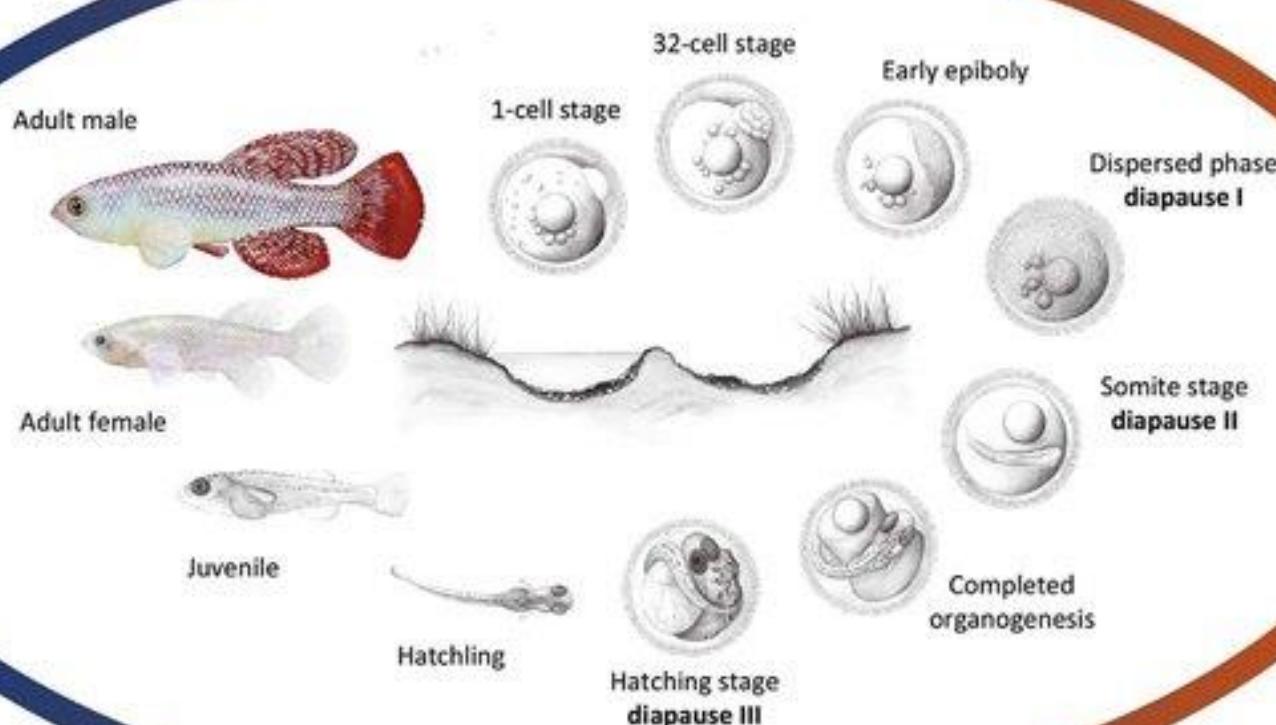
Reconstruct or project range changes over evolutionary time

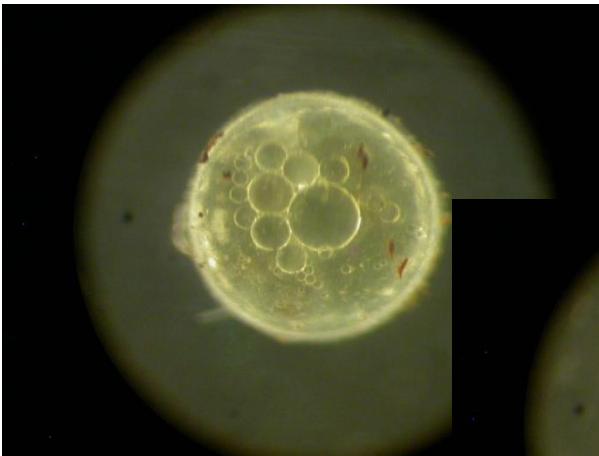
Annual killifish: fish with an egg bank

In the lab: a lot of individual variation in life histories

Rainy season

Dry season





blastula – dispersed cells

Diapause I



somites

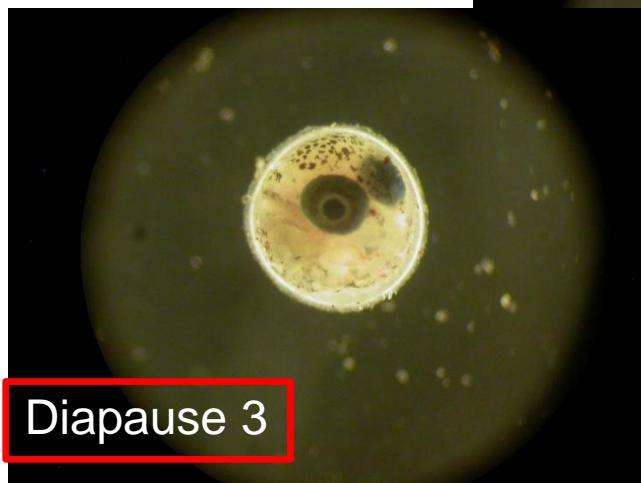
Diapause 2



head formation

Strategy determination
is relatively accessible,
observable

Three developmental
arrests possible



seemingly ready to hatch

Diapause 3

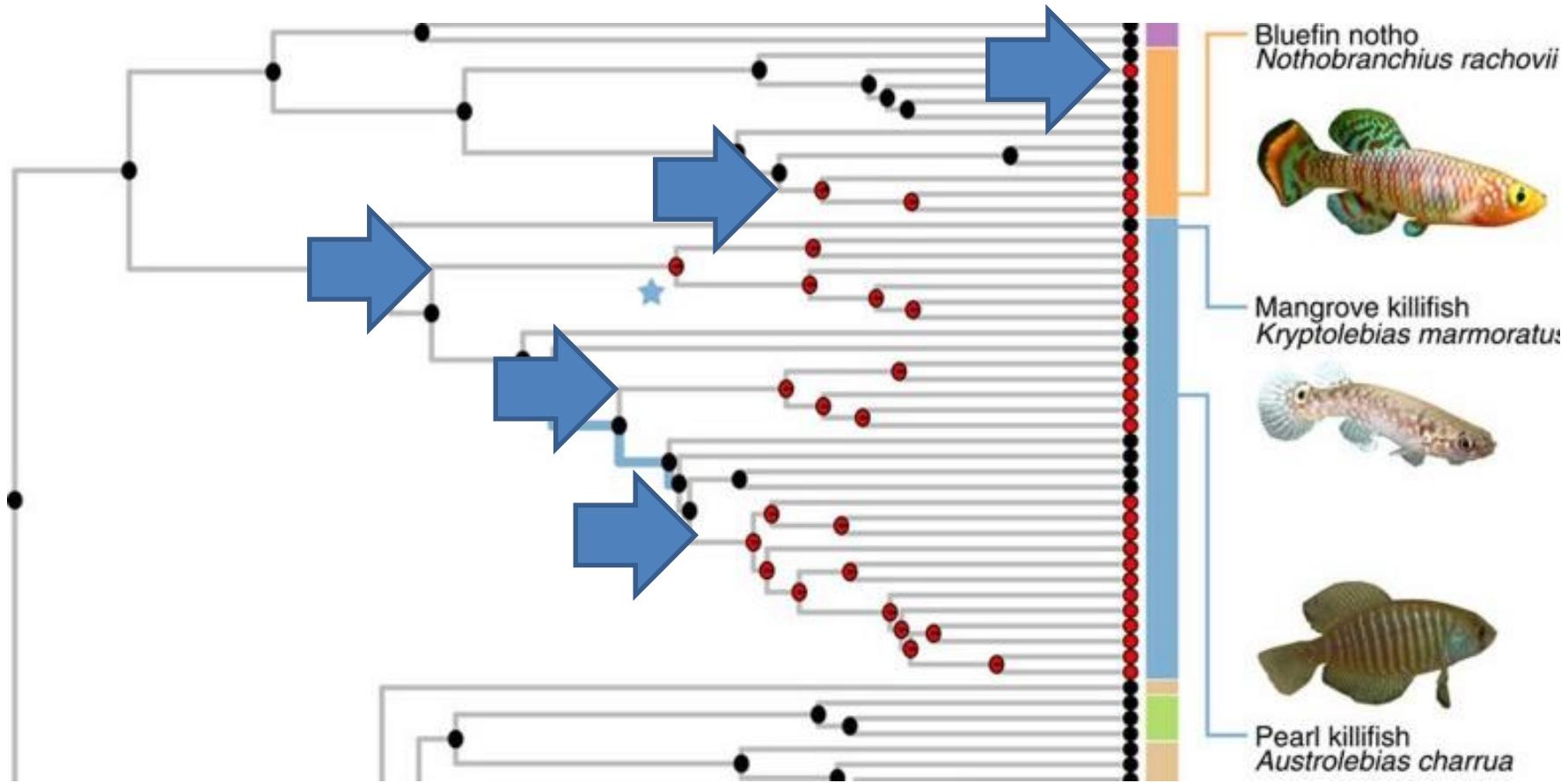
apparently complete but small



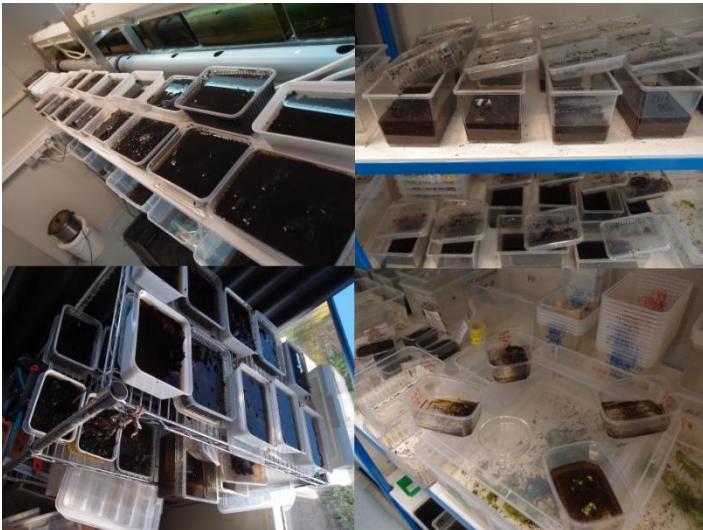
Delaying strategies
Diapause = developmental arrest
remain in the same developmental stage

Diapause has evolved repeatedly in killifish (Cyprinodontiformes):

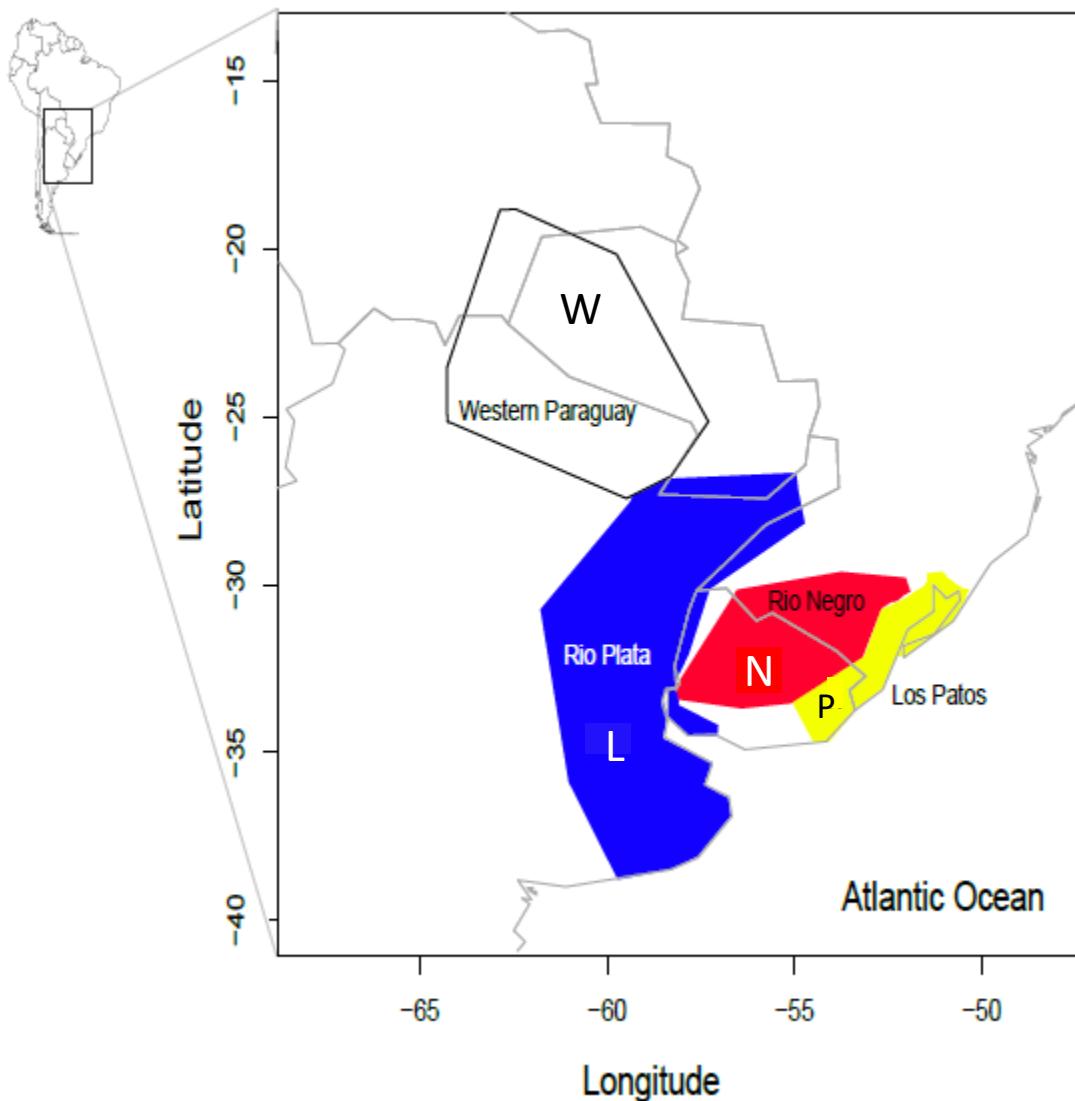
5 times

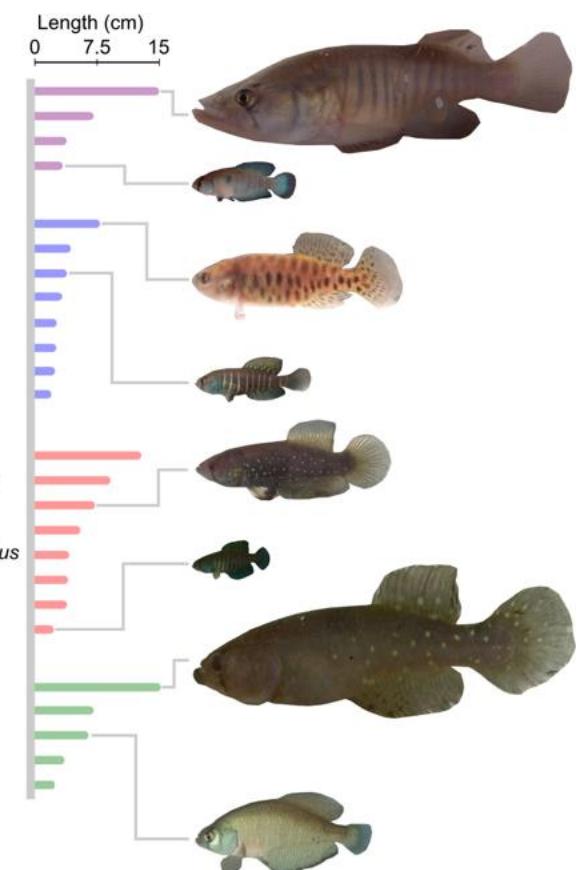
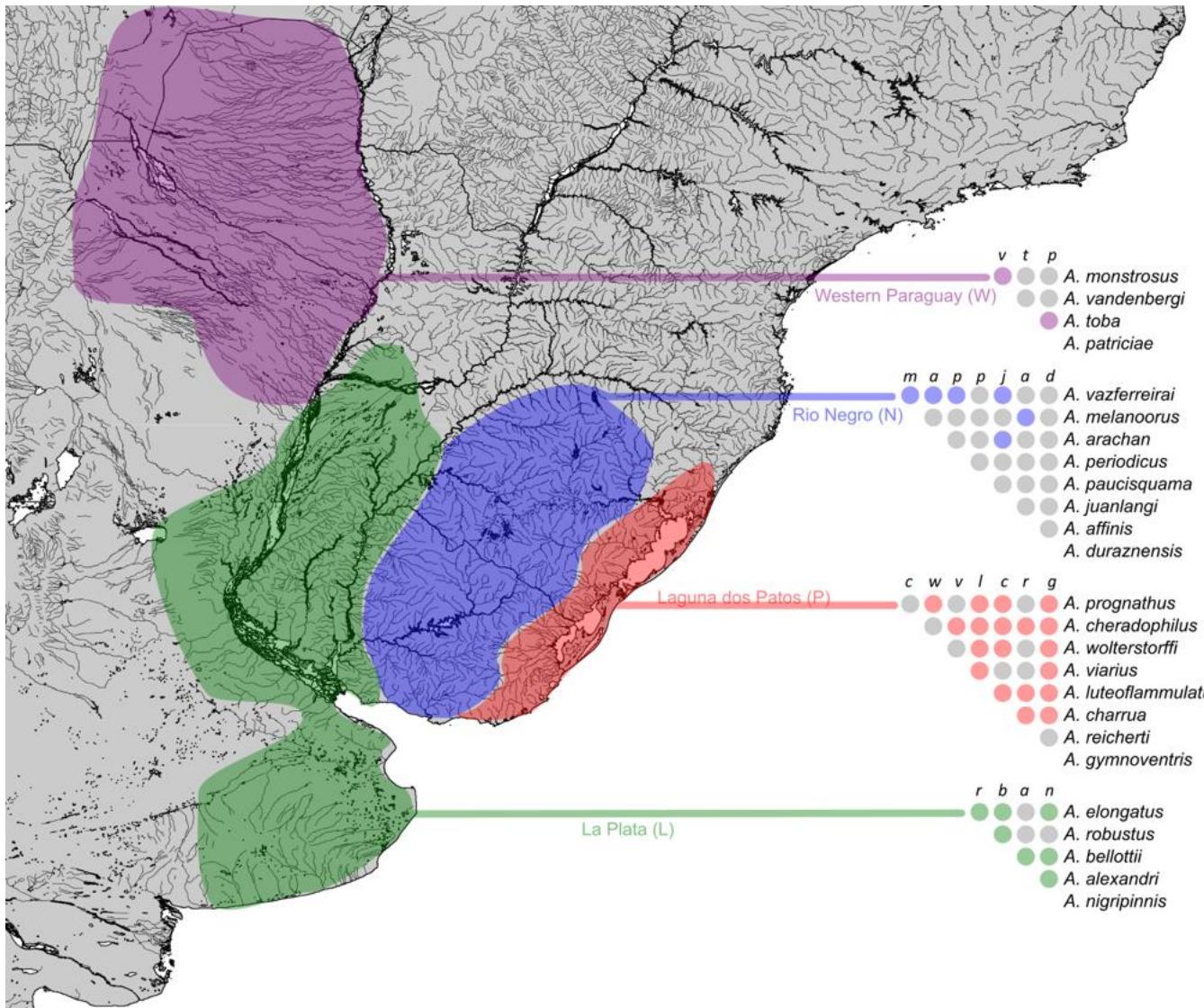


South-American *Austrolebias* killifish ecology



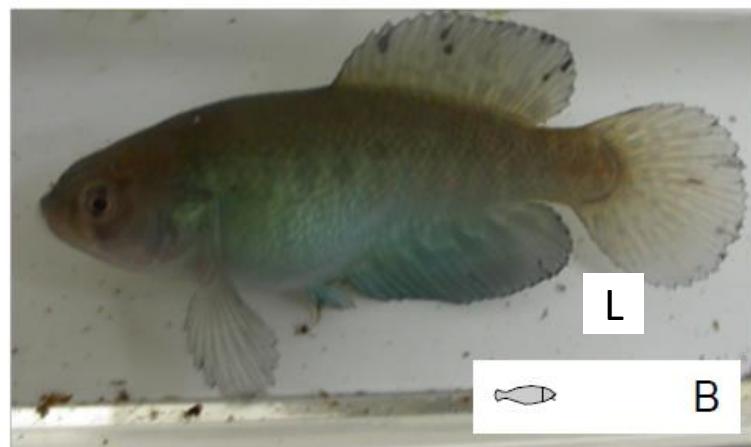
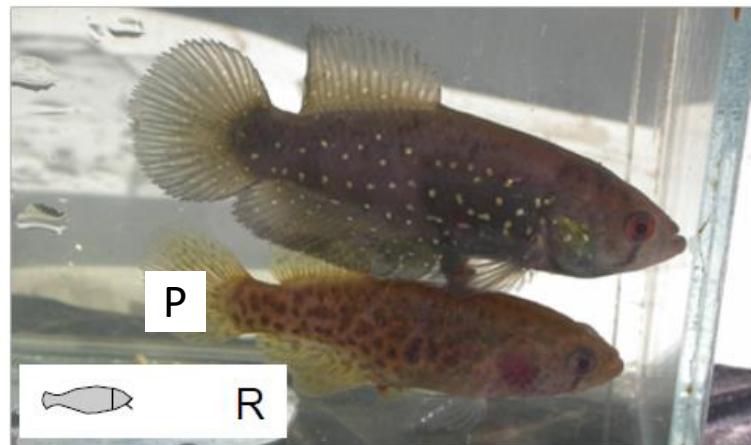
Ranges: primarily considered are **areas of endemism** (Costa 2010)
all extant (current) species described in 2010 exclusive to one such area





Large and small species. Some large species are piscivores of small ones.

Coexistence with other annual fish genera limited to W and P areas of endemism
(ignoring immigrants from rivers into temporary ponds)



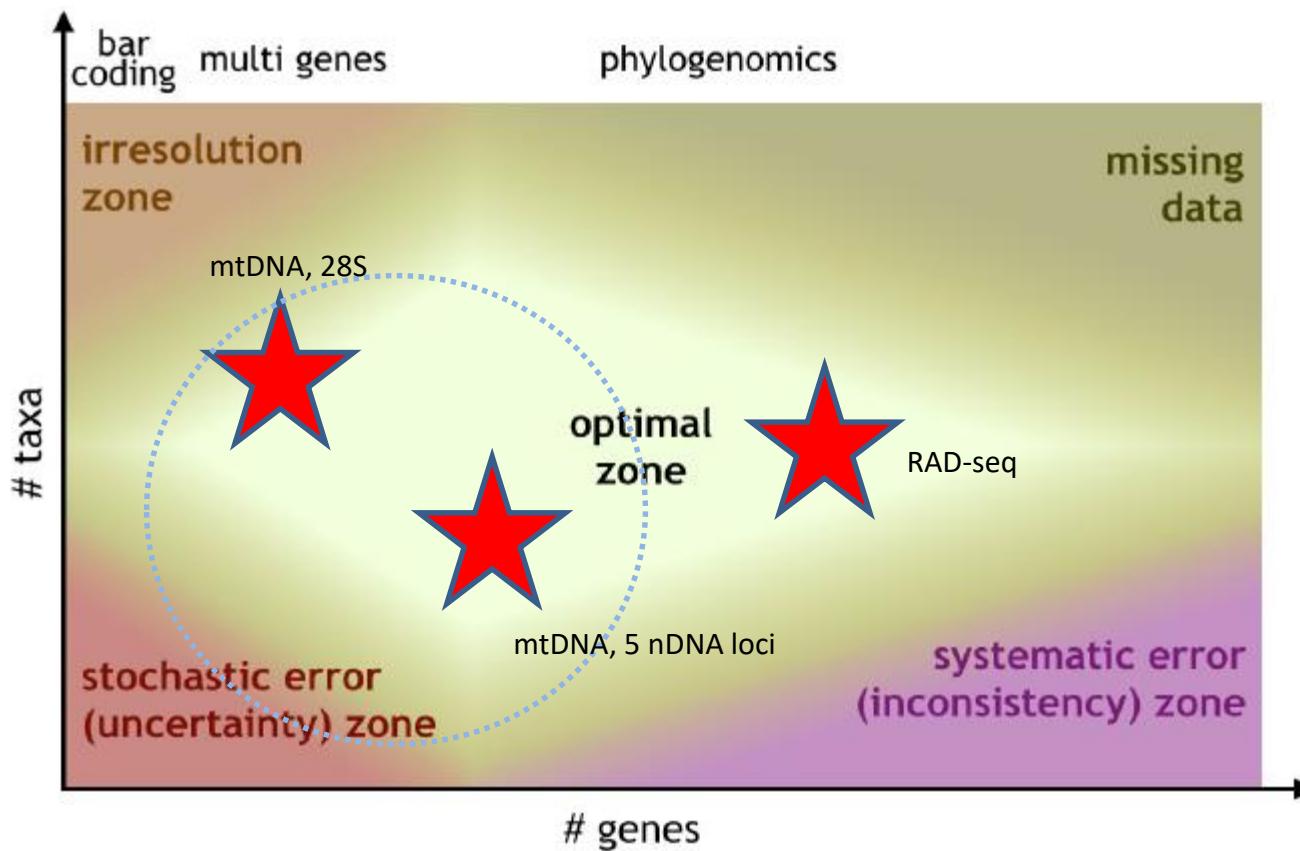
Todo cambia



Which phylogenetic trees are the most reliable to build models with?

Not totally self-evident which phylogenetic tree(s) are most suitable for comparative analysis and biogeographical reconstructions

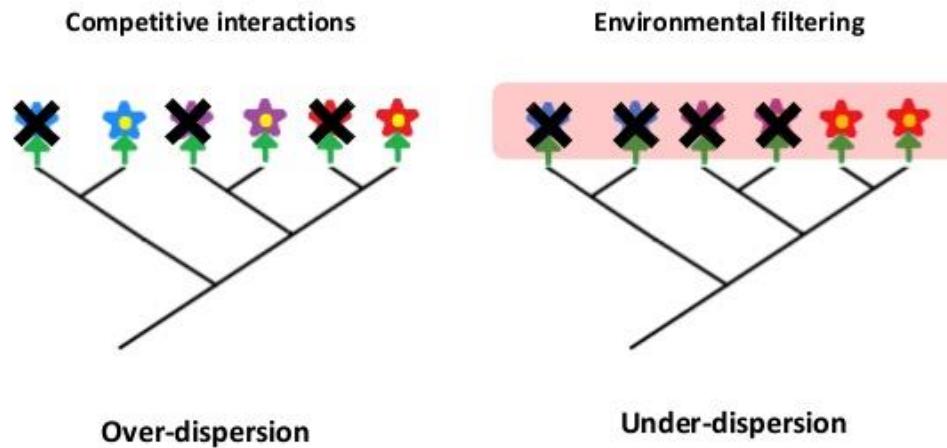
Which trees are most reliable to build models with?



Community Phylogenetics

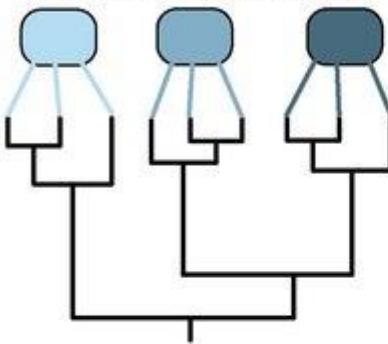
PHYLOGENIES AND COMMUNITY ECOLOGY

Campbell O. Webb¹, David D. Ackerly², Mark A. McPeek³,
and Michael J. Donoghue¹

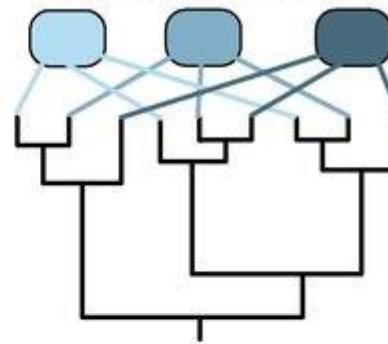


Webb *et al.* 2002 Annu Rev Ecol Syst

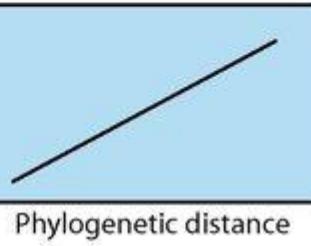
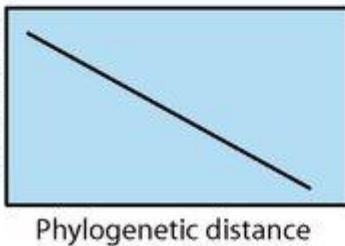
A) Environmental filtering/
phylogenetically clustered



B) Niche differentiation/
phylogenetically dispersed



Coexistence/
co-occurrence





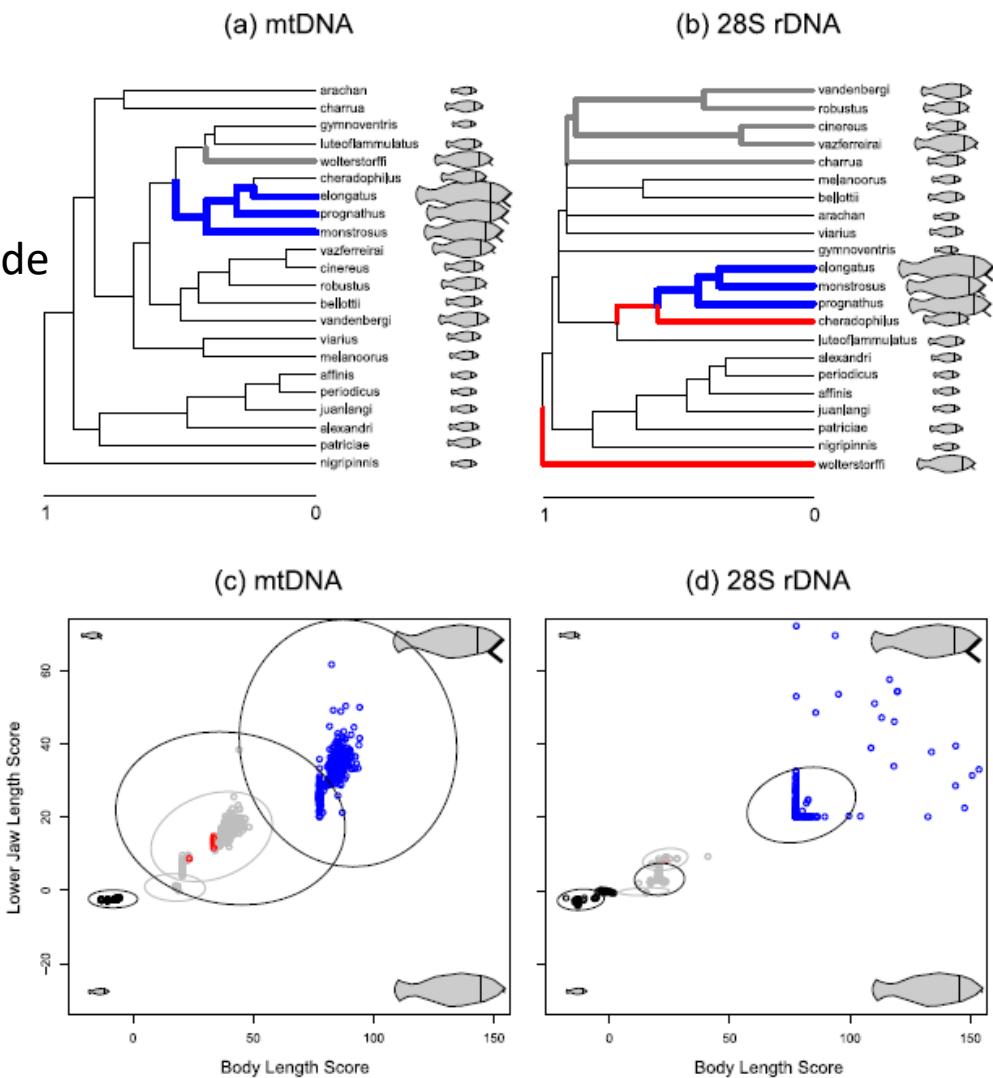
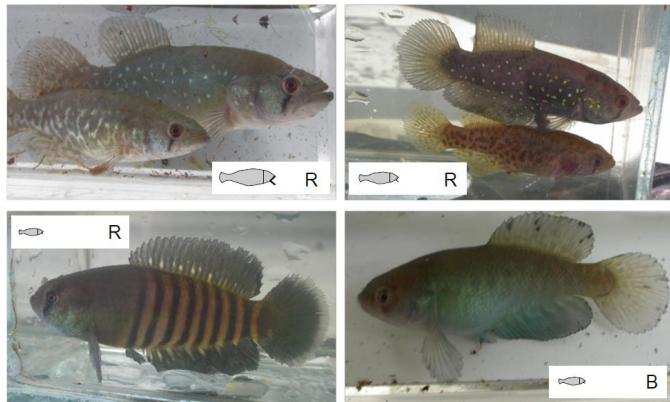
size and jaw data from Costa (2006) revision

Large sizes evolved three times

No vicariance involved in speciation

Largest specialized piscivores in one clade

Selection regime shifts significant
(after a lot of simulation and
resampling work)



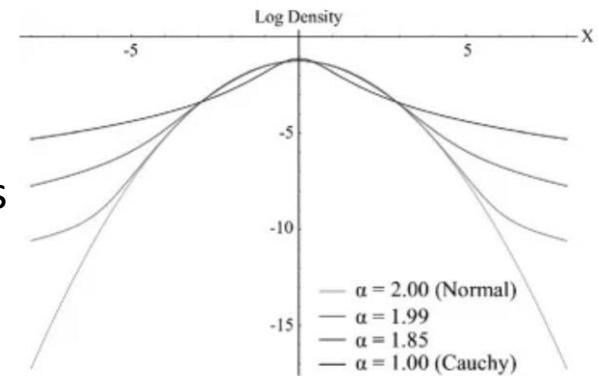
large sizes evolved three times

stable traits (Elliot and Mooers 2014)

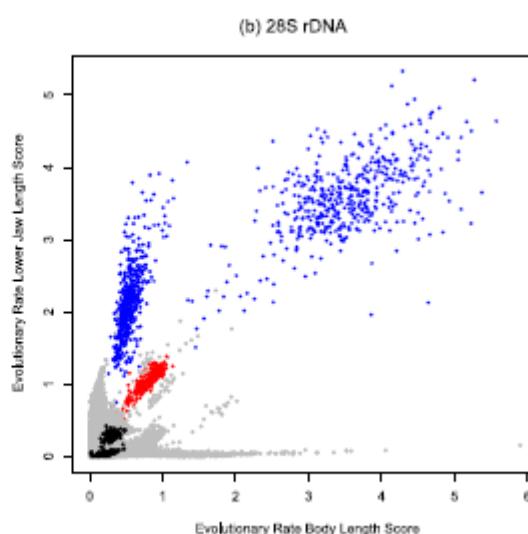
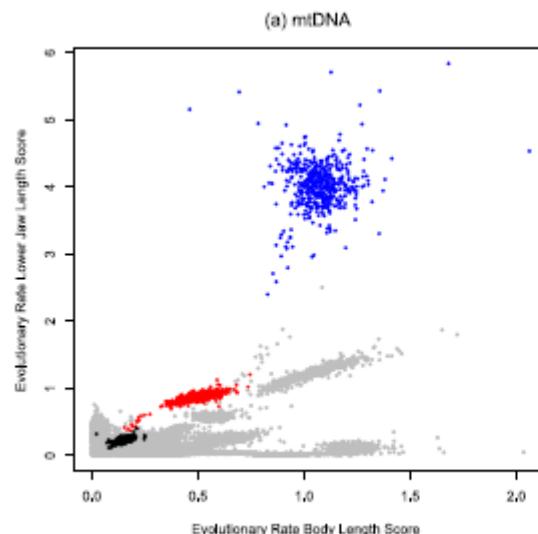
distribution modelling of evolutionary changes along trees
distributions for trait changes with fat tails

→ larger changes more likely

Models fitted across posterior of tree distributions

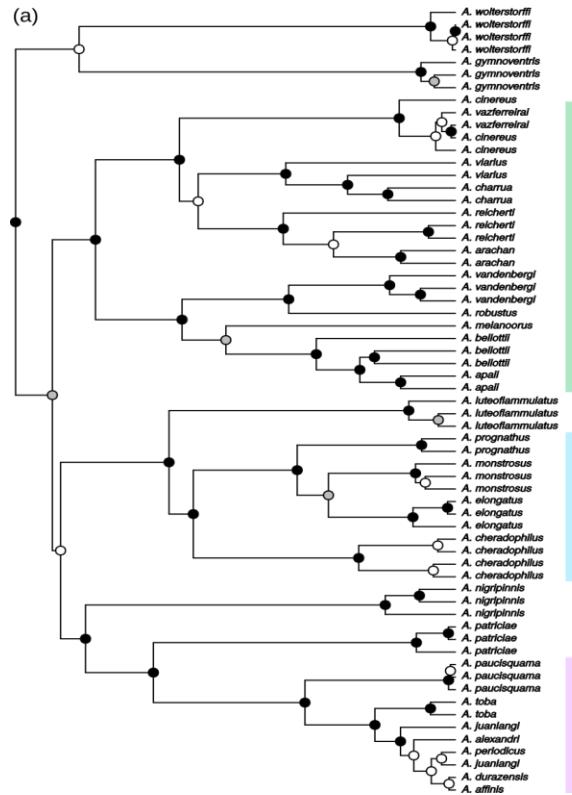


Changes on branches towards specialized piscivores
systematically rank among fastest changes

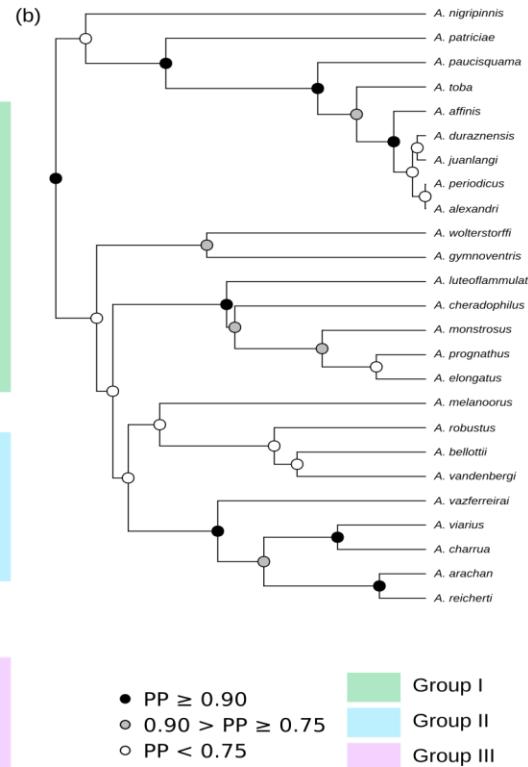




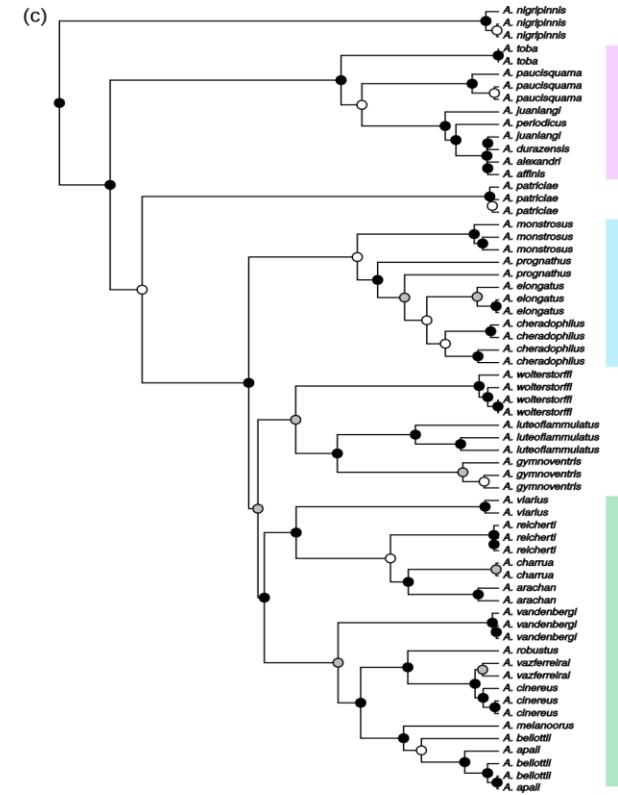
nDNA concatenated



coalescent



mtDNA concatenated



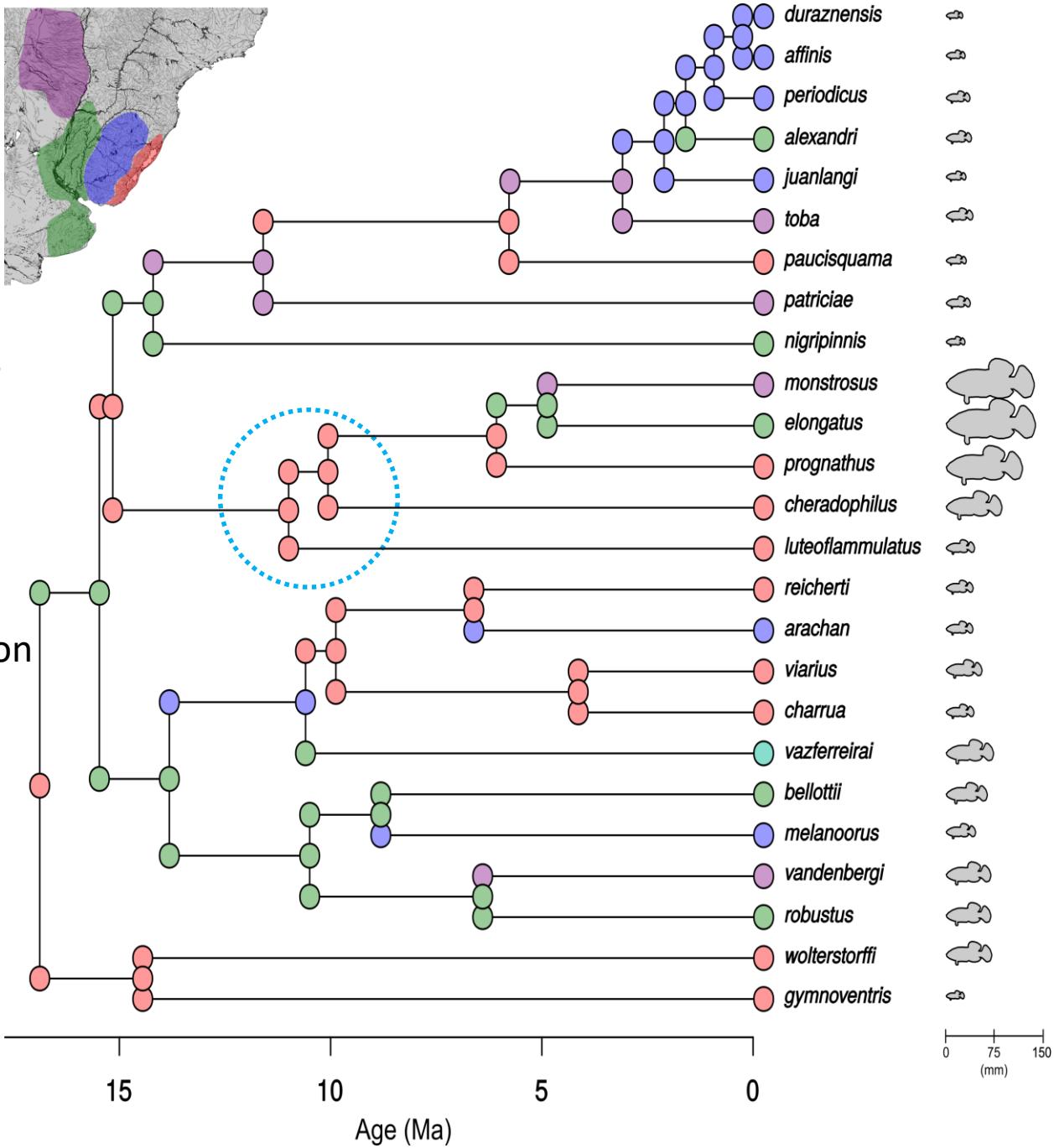
Maximum clade credibility trees from Bayesian analyses coalescent using *BEAST
lack circles indicate a posterior probability (PP) from 0.90 – 1.00 and grey circles indicate a PP from 0.75 to 0.90.
Highlighted, colour-coded regions represent three major clades that are recovered in all trees.

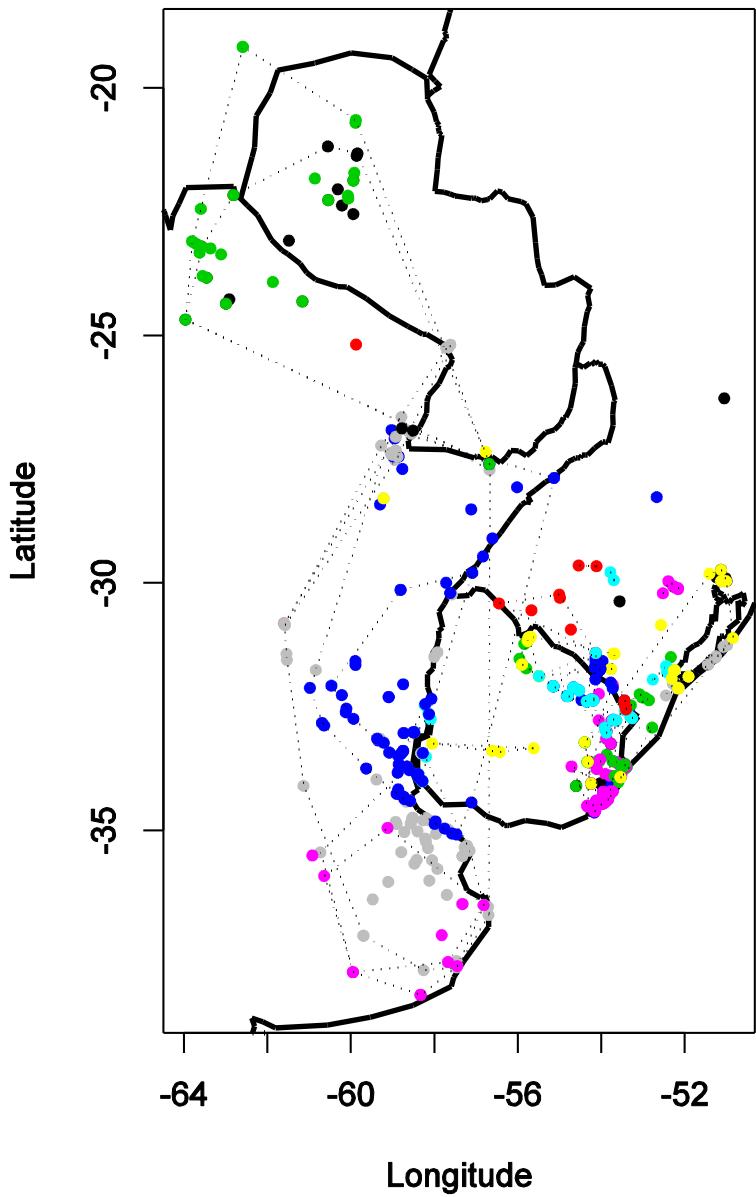
biogeographic reconstruction,
areas of endemism

using BioGeoBears
(Matzke 2013)

potentially sympatric speciation
of two clades of large species

Chaco W invaded four times
independently

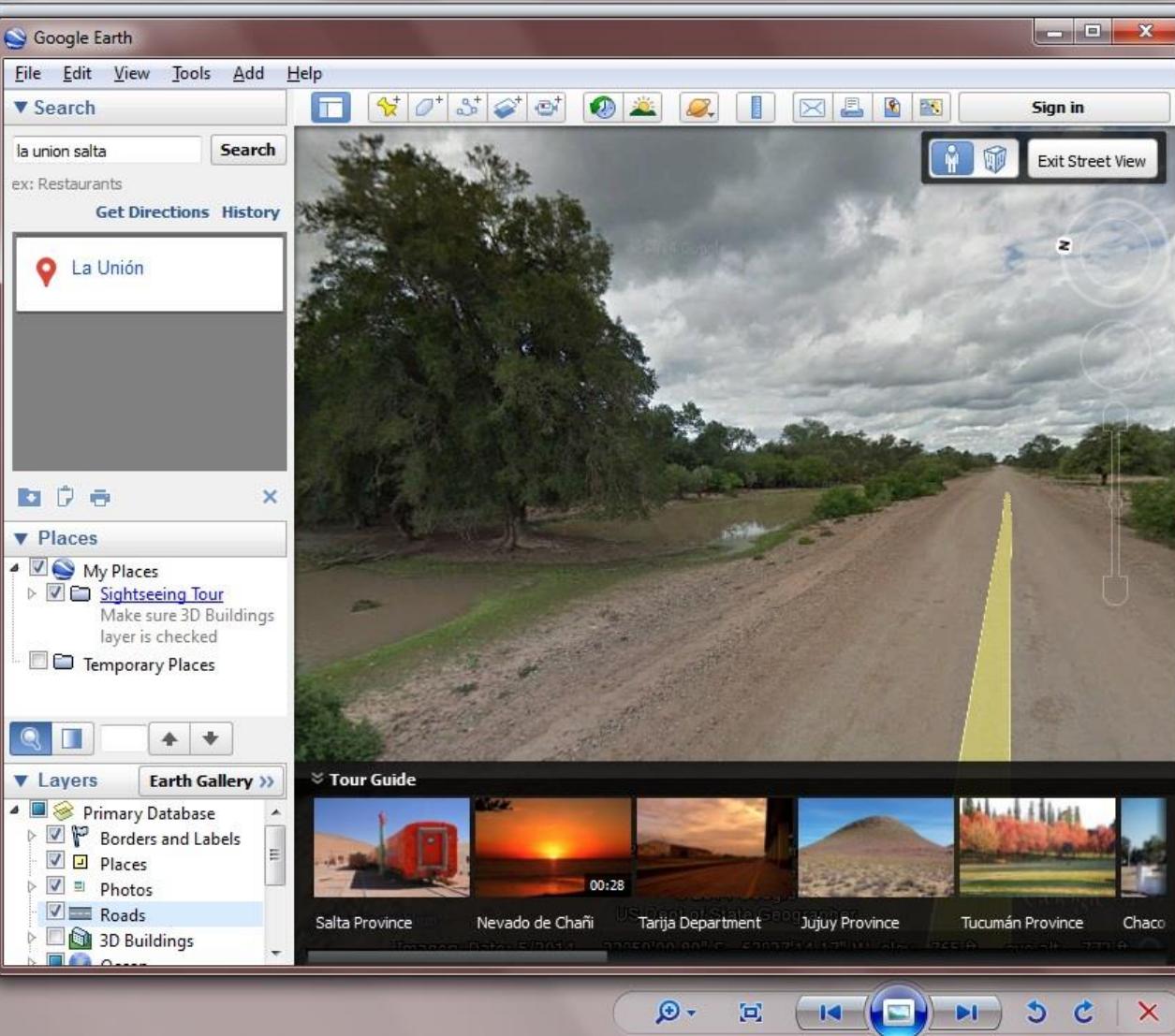




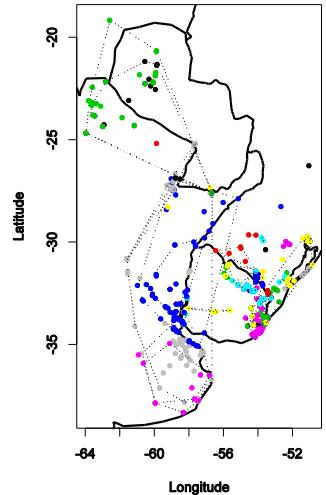
Nearly all known *Austrolebias* locations

verified and synonyms resolved, updated continually, analysed until March 2017





What are the environments experienced?
What are the environmental differences between locations?



- Environmental variables:
 - Worldclim climatic data
 - 10 soil composition variables
 - two variables for river basin characteristics

Ranges × environmental variables:

Niche trait calculations: environmental variables "typical" for a species

~ OMI (Outlying Mean Index, Dolédec et al 2000):

Standardized environmental variables at each spatial cell

Weighted by abundance of a species and averaged

PCA on the result to characterise variability between species

- We **don't** have abundance data, species have different trophic roles

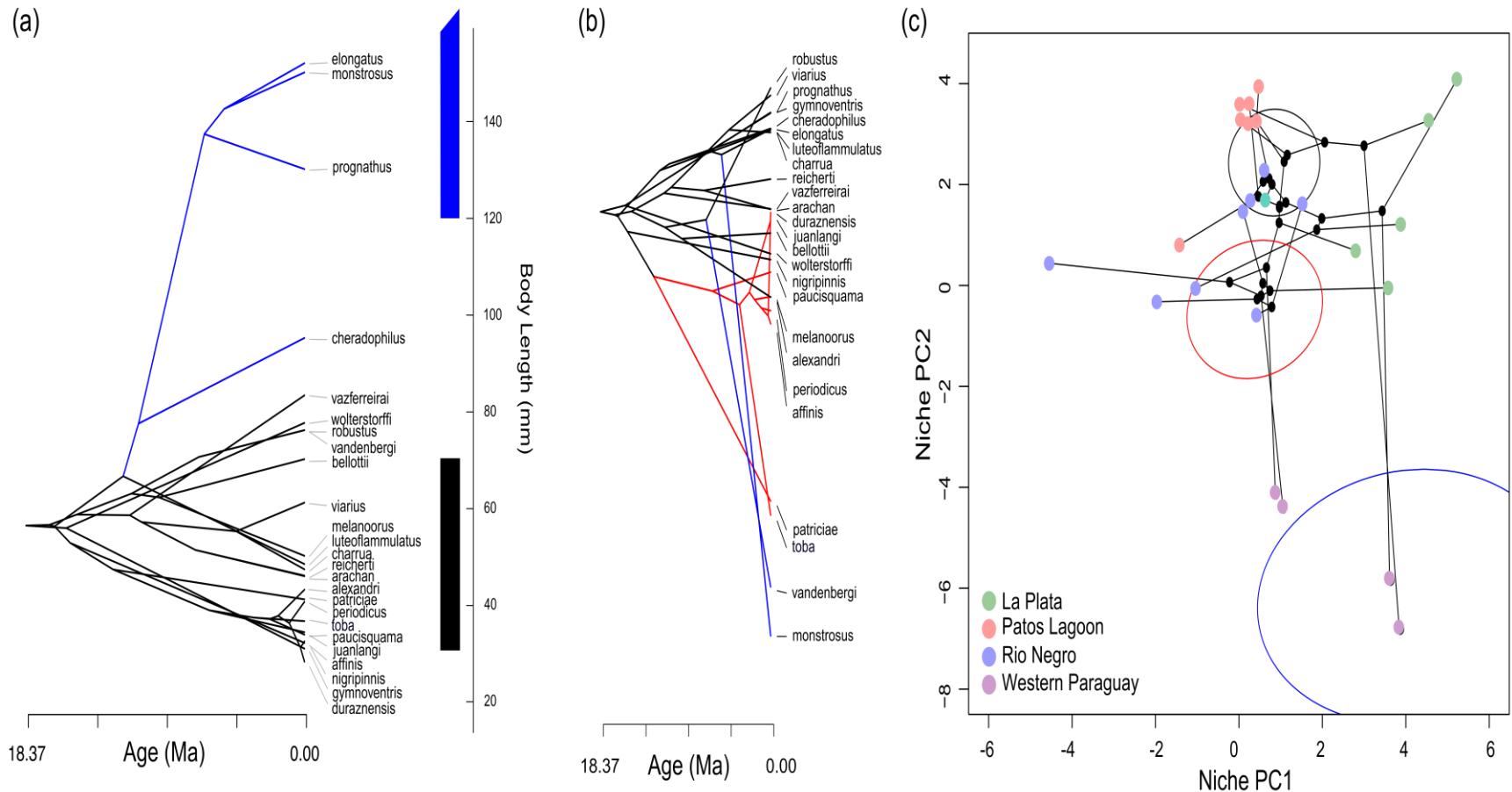
→ NICHE TRAITS

Standardized environmental variables at each capture location of a species

PCA on all species averages

First two scores retained as niche traits

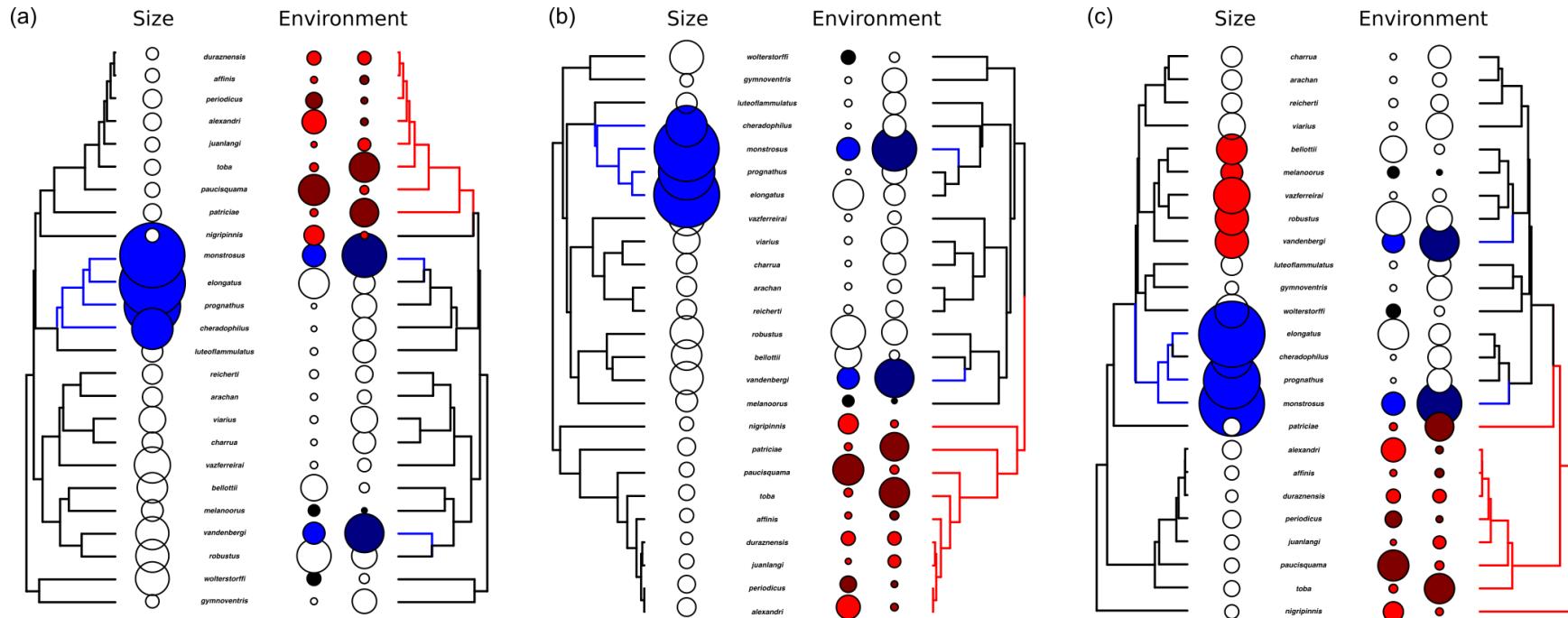
Niche traits somewhat related to areas of endemism



Size data: maximum male size among field records

Surface (Ingram and Mahler) modelling of shifts in selection regimes

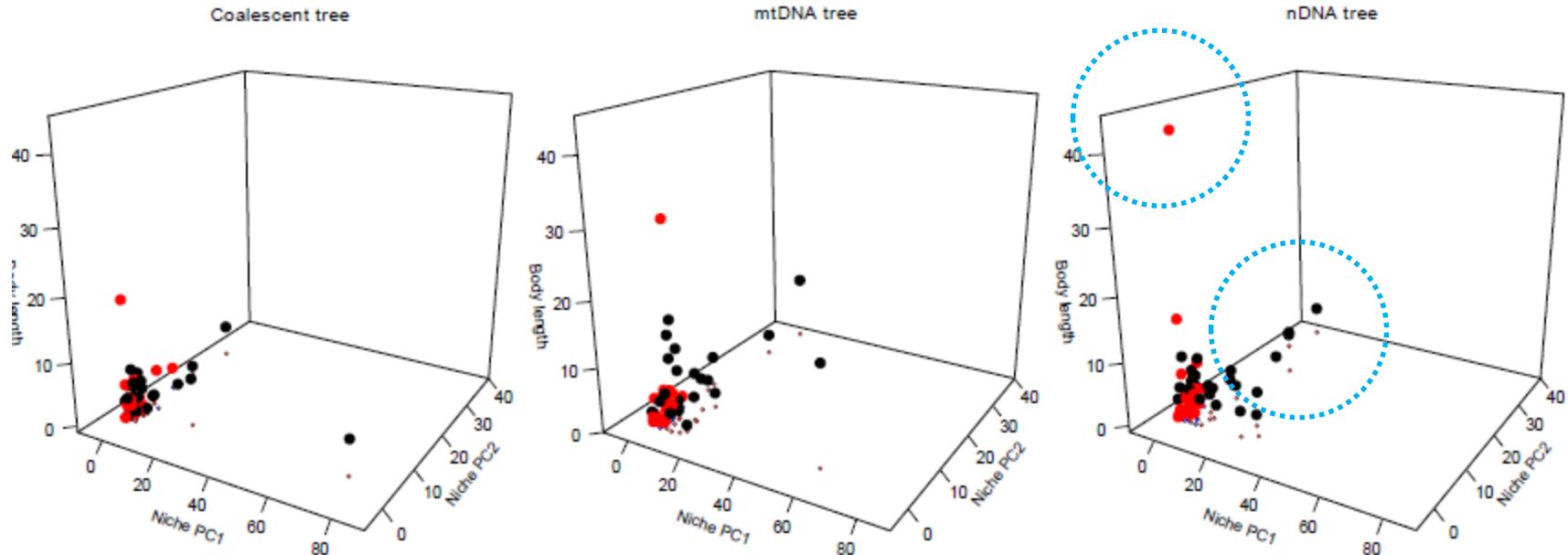
size (length) and Niche traits PC1 and PC2



Size data: maximum male size among field records

stabletraits (Elliot and Mooers 2014) again

rapid evolution at trait shifts



The Western Paraguay area of endemism has been invaded repeatedly
similar niche traits shifts in at least two species, *A. monstrosus* *A. vandenbergi*

Todo cambia

Salta: Se pavimentarán 45 km de la Ruta 13 en Rivadavia

La obra se realizará por medio del Fondo de Reparación Histórica con la inversión de 50 millones más otros 30 millones que aportará Vialidad de la Provincia

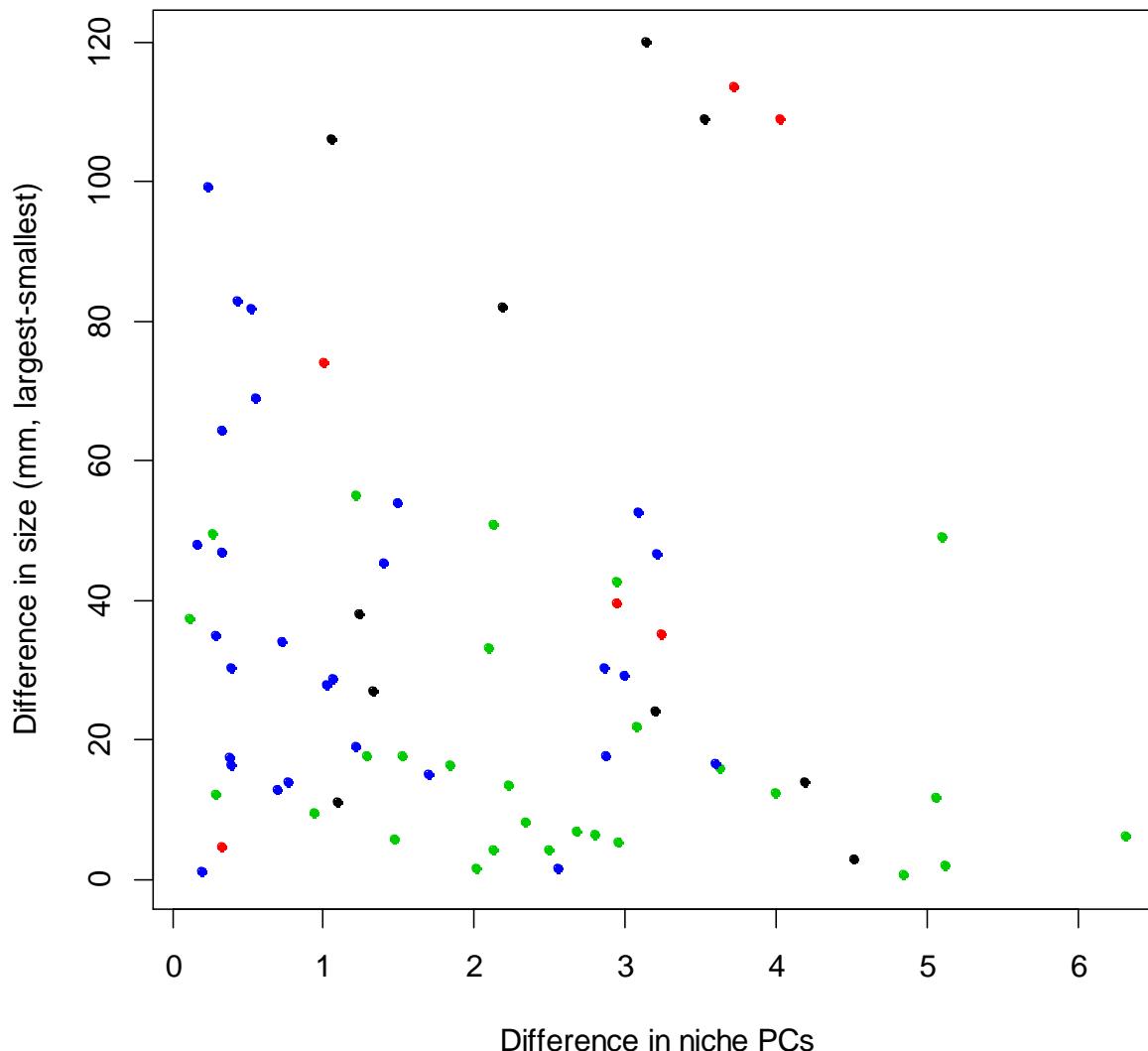


Una localidad salteña, última en ranking de ciudades ambientales del Conicet

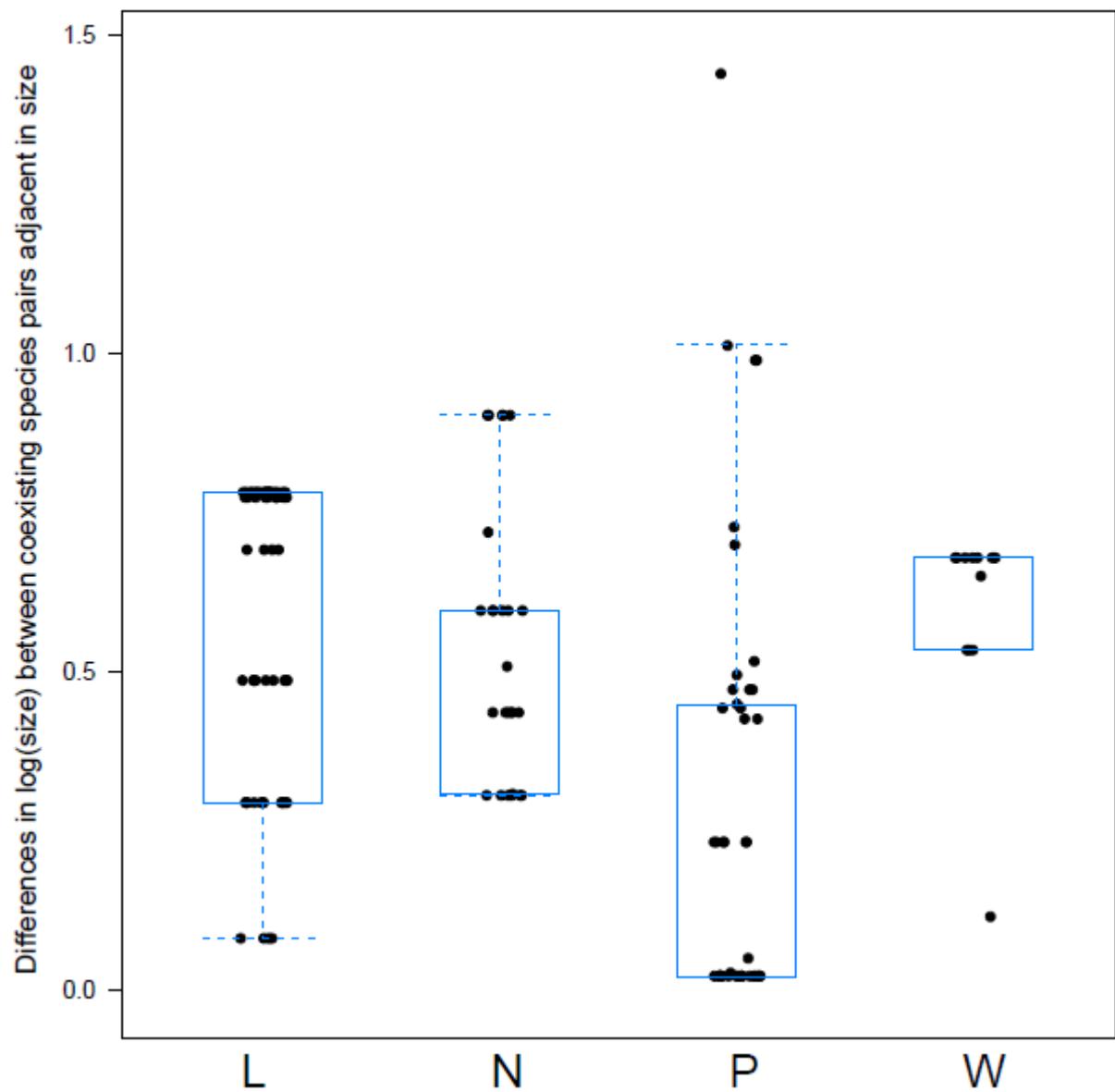
Investigadores del Conicet elaboraron un índice en base a los problemas ambientales y los recursos naturales y sociales de 511 partidos del país



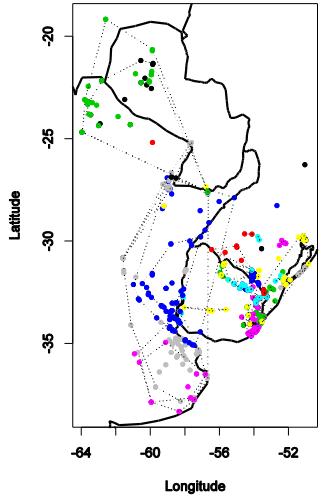
Does size divergence allow coexistence in otherwise similar niches?



Does size divergence allow coexistence in otherwise similar niches?



- global river basin shapefile 500 m threshold
- Maxent species distribution modelling of all species with data

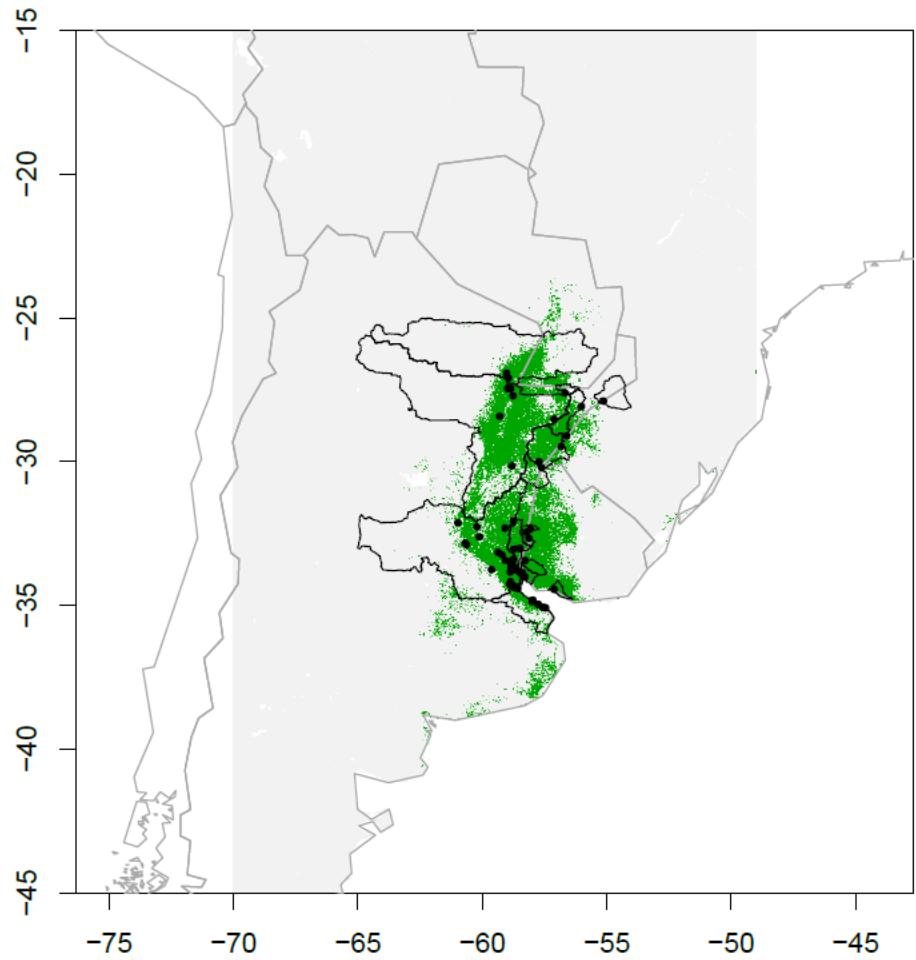
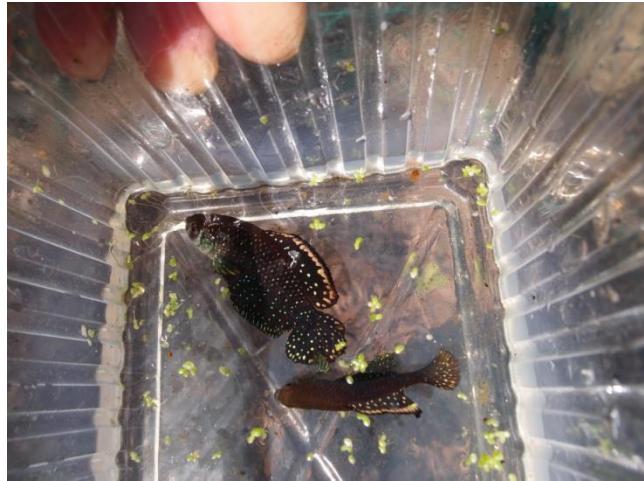


Environmental variables:

- Worldclim climatic data
- 10 soil composition variables
- two variables for river basin characteristics
- unstandardized PCA before model fitting
- Background points: roadside points

Using library dismo in R (beautiful tool)

Austrolebias nigripinnis



From ranges to **range overlaps**

an alternative way to assess odds of speciation modes

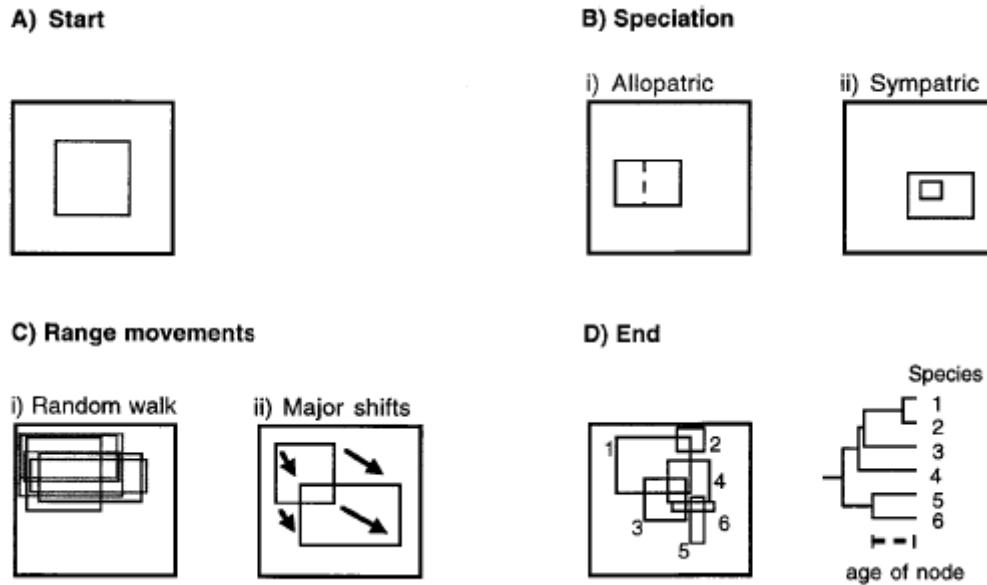
Using detailed range predictions or data

VOL. 155, NO. 4 THE AMERICAN NATURALIST APRIL 2000

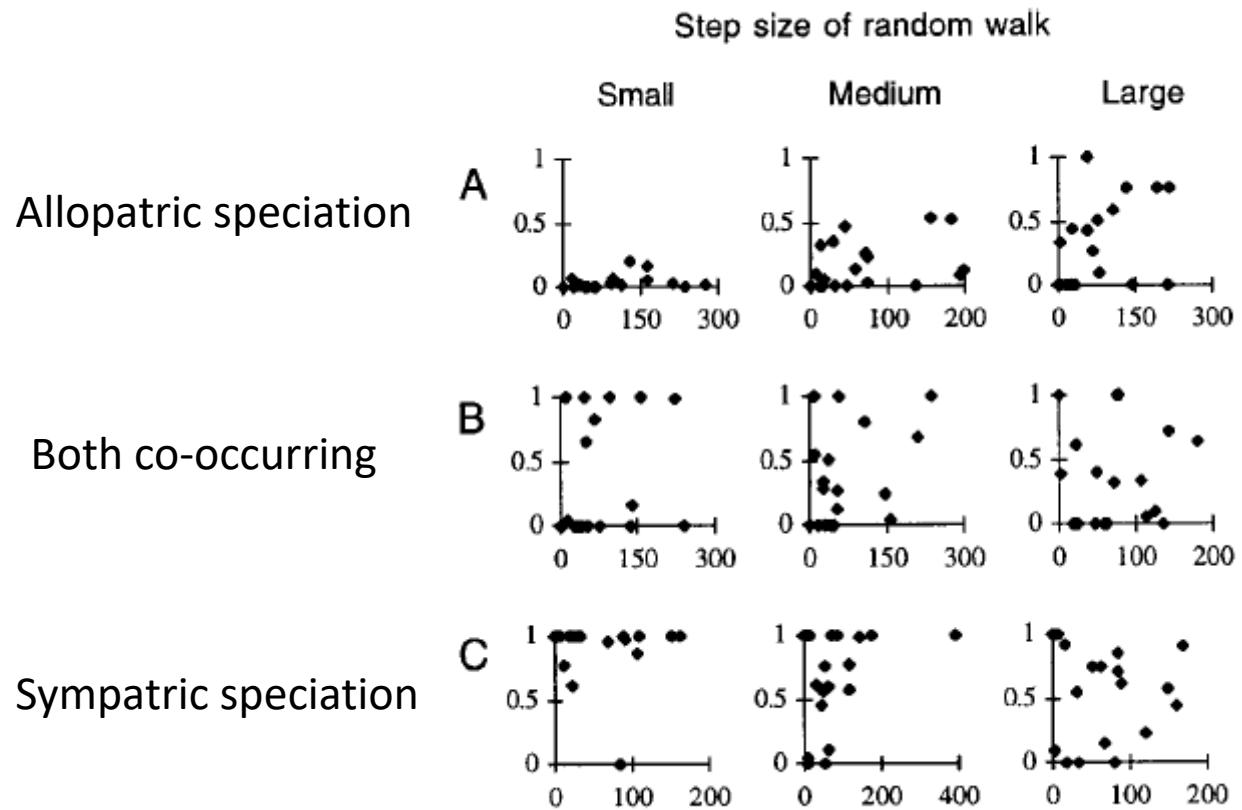
Detecting the Geographical Pattern of Speciation from Species-Level Phylogenies

Timothy G. Barraclough^{1,*} and Alfried P. Vogler^{1,2,†}

Simulations of speciation events and range shifts at cladogenetic events and in between speciations (anagenetic)



Predictions from simulations on the dependence of range overlap on node age
overlap: part of range of the smallest range among a pair of species
occupied by both species



One intercept or more?

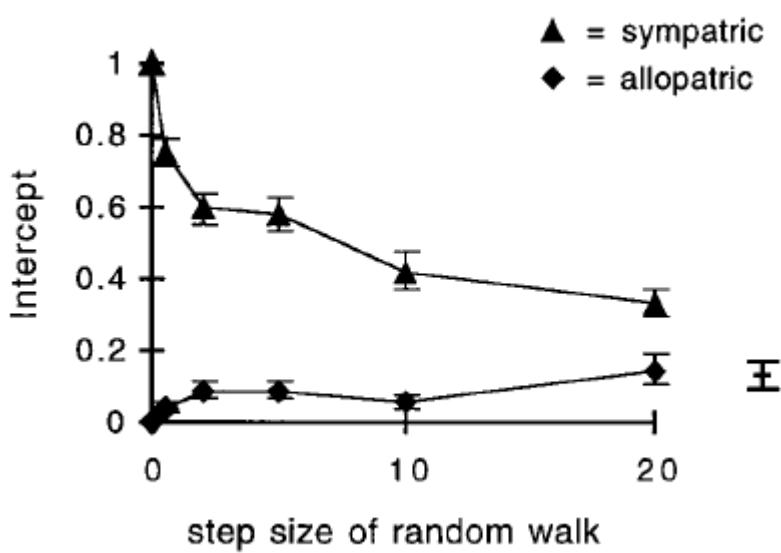
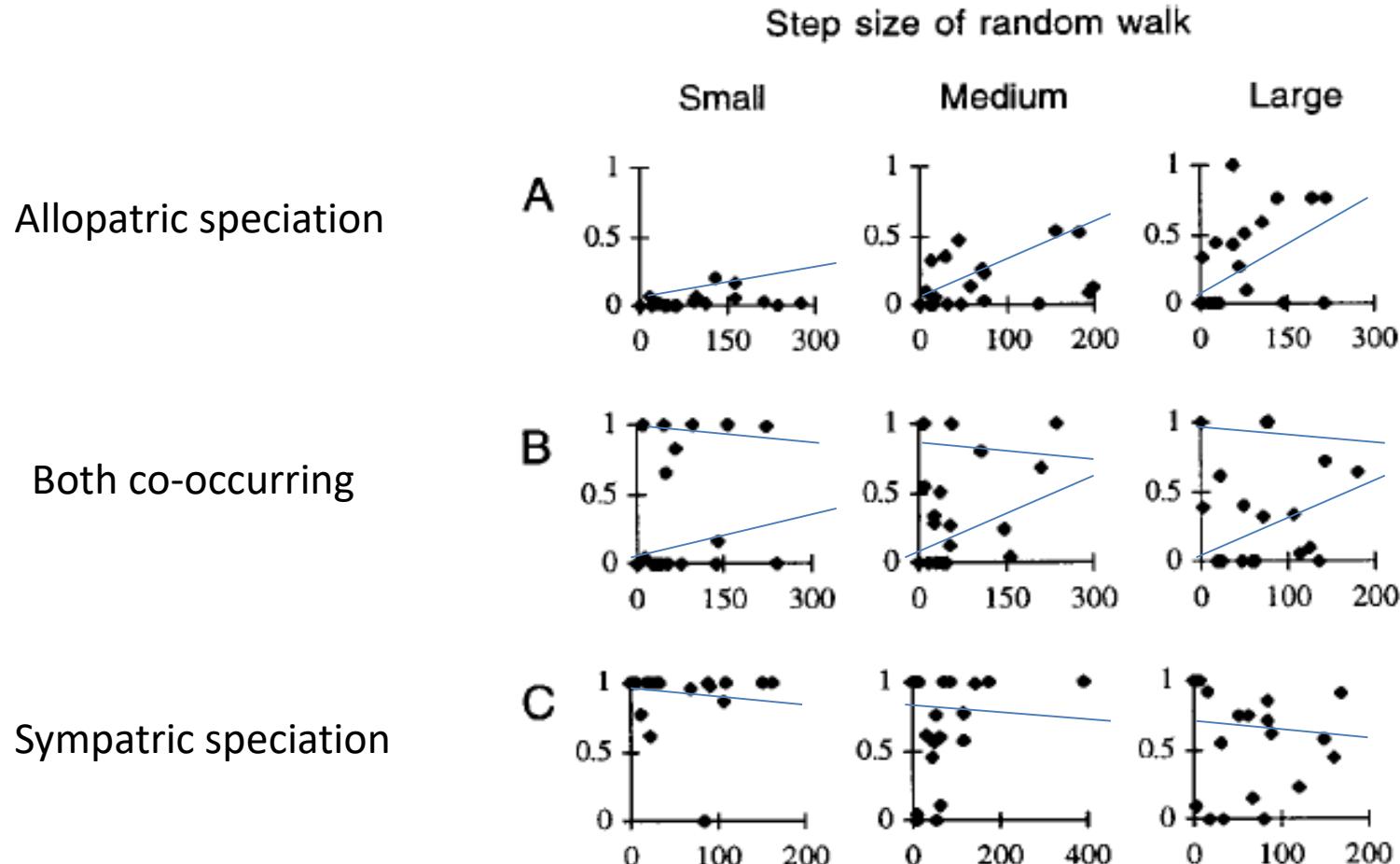


Table 1: Summary statistics for plots of the degree of sympatry against relative node age

Taxon	<i>n</i>	Spearman's rank test		Intercept	Standard error of intercept
		<i>r</i> _s	<i>P</i>		
Warblers	14	.66	.02	.054	+.120 -.052
Fairy wrens	11	.76	.02	.049	.091 -.045
Cranes	14	.54	.07	.012	.046 -.012
Auks	22	.63	.004	.011	.081 -.011
Swordtail fish	18	.47	.14	.024	.082 -.024
Fruitflies	19	.48	.001	.174	.185 -.127
Leafhoppers	35	.57	.06	.079	.080 -.054
Tiger beetles	12	.39	.21	.208	.147 -.116

Note: Intercepts were fitted by linear regression of arcsine transformed sympathy, hence the standard errors of the untransformed intercept are asymmetric; *n* = number of nodes.

We propose to use mixtures of regressions to
estimate **intercepts** and **slopes** for potentially different speciation modes
estimate the **proportion** of speciation events according each mode



Another proposal

Evolution, 60(3), 2006, pp. 601–615

THE GEOGRAPHY OF MAMMALIAN SPECIATION: MIXED SIGNALS FROM PHYLOGENIES AND RANGE MAPS

BENJAMIN M. FITZPATRICK¹ AND MICHAEL TURELLI²

Section of Evolution and Ecology and Center for Population Biology University of California, Davis, California 95616

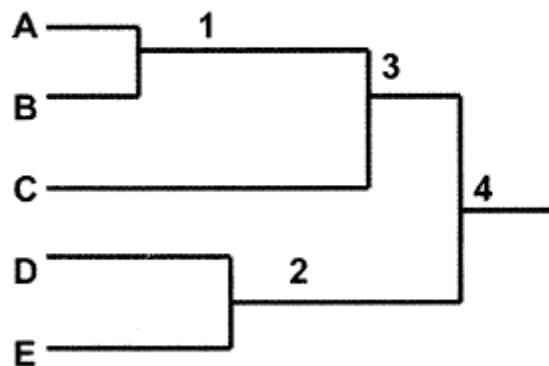
²E-mail: mturelli@ucdavis.edu

No predictions from simulations,
assuming range overlaps can be treated as traits of species

"we used nested averages of the pairwise overlaps between species in each clade"

$$\bar{o}_i = \sum_{j \in C_1} \sum_{k \in C_2} \left(\frac{1}{2}\right)^{n_{jk}-1} o_{jk}$$

Hypothetical Phylogeny



Independent Comparisons

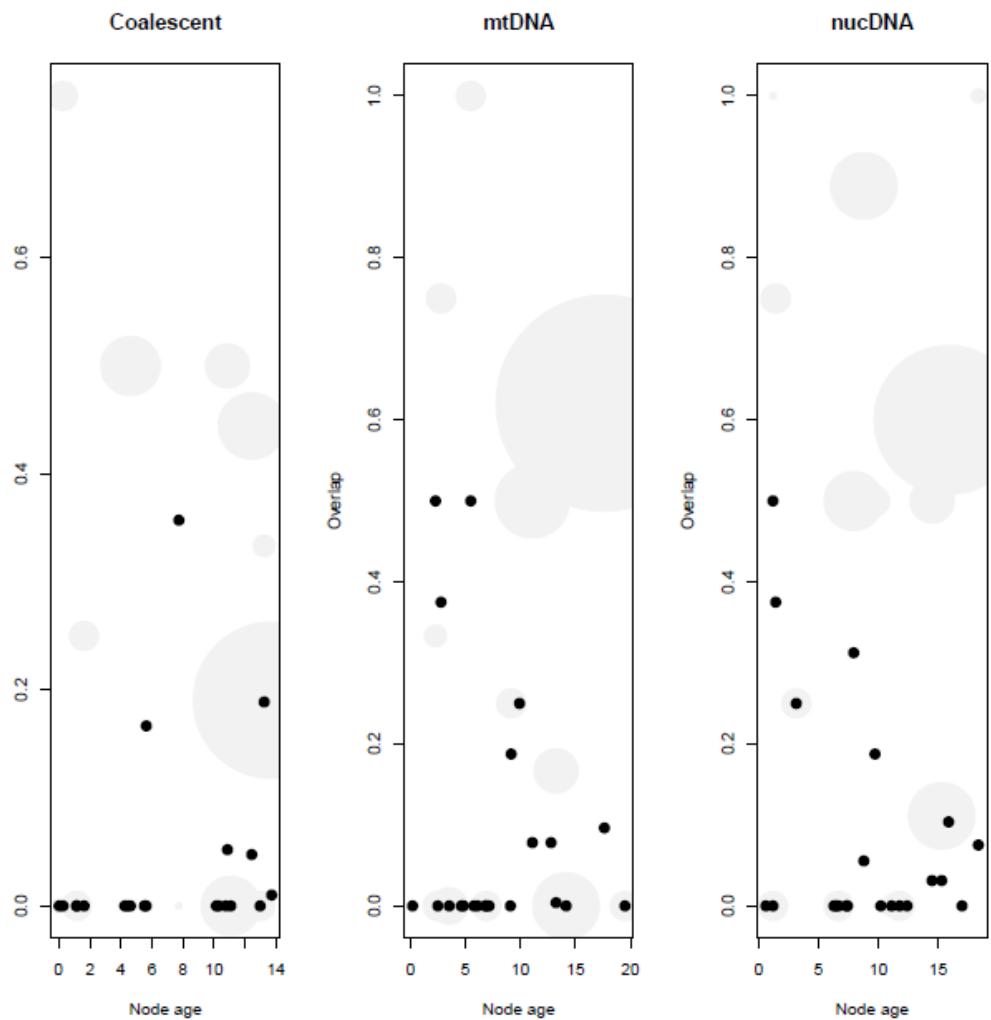
1: AxB

2: DxE

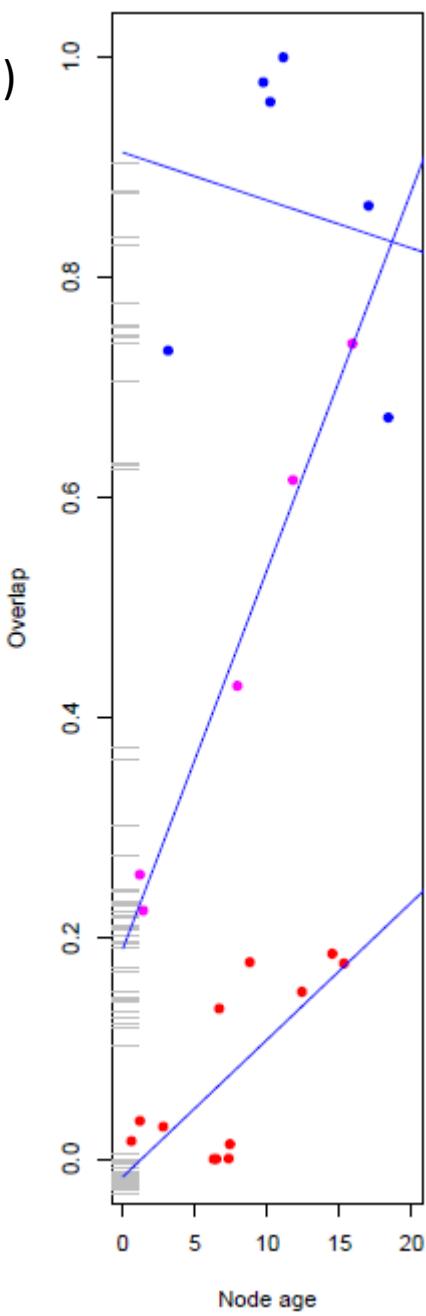
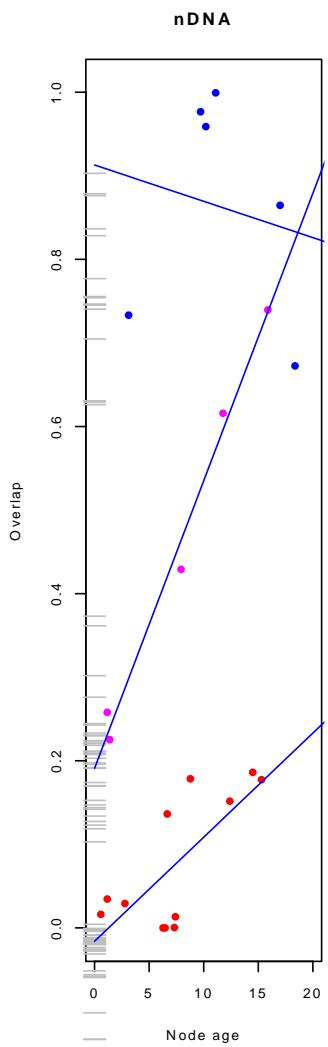
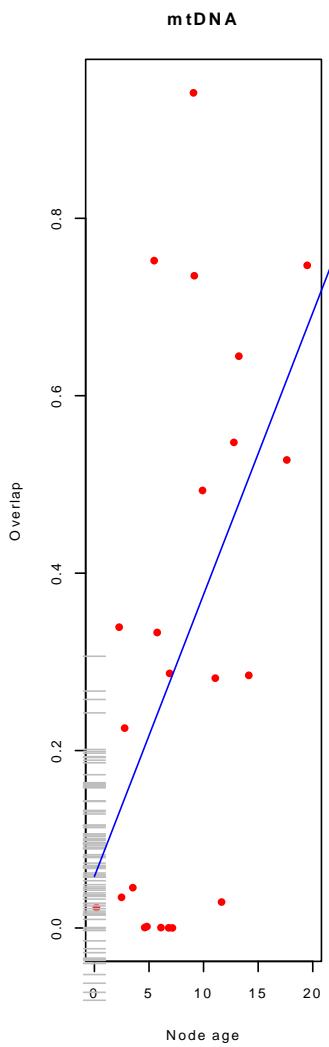
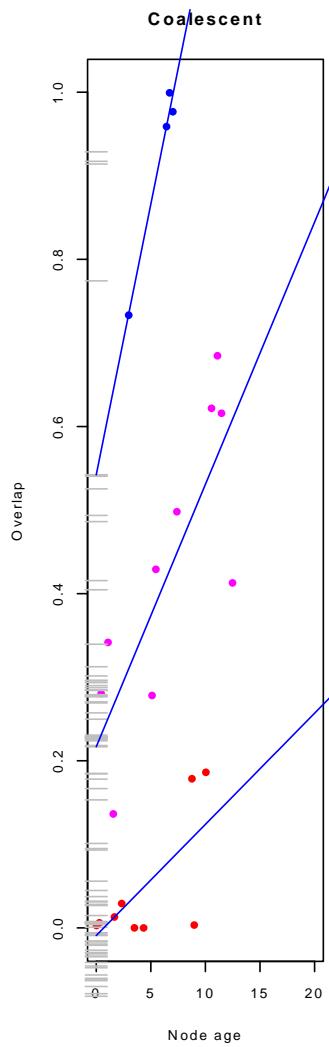
3: $\frac{Cx A + Cx B}{2}$

4: $\frac{1}{2} \left(\frac{\frac{Ex A + Ex B}{2}}{2} + \frac{\frac{Dx A + Dx B}{2}}{2} + \frac{Cx E + Cx D}{2} \right)$

overlaps calculated from river basins
example of differences in overlap values
between Barraclough and Vogler (blobs)
and Fitzpatrick and Turelli (dots)

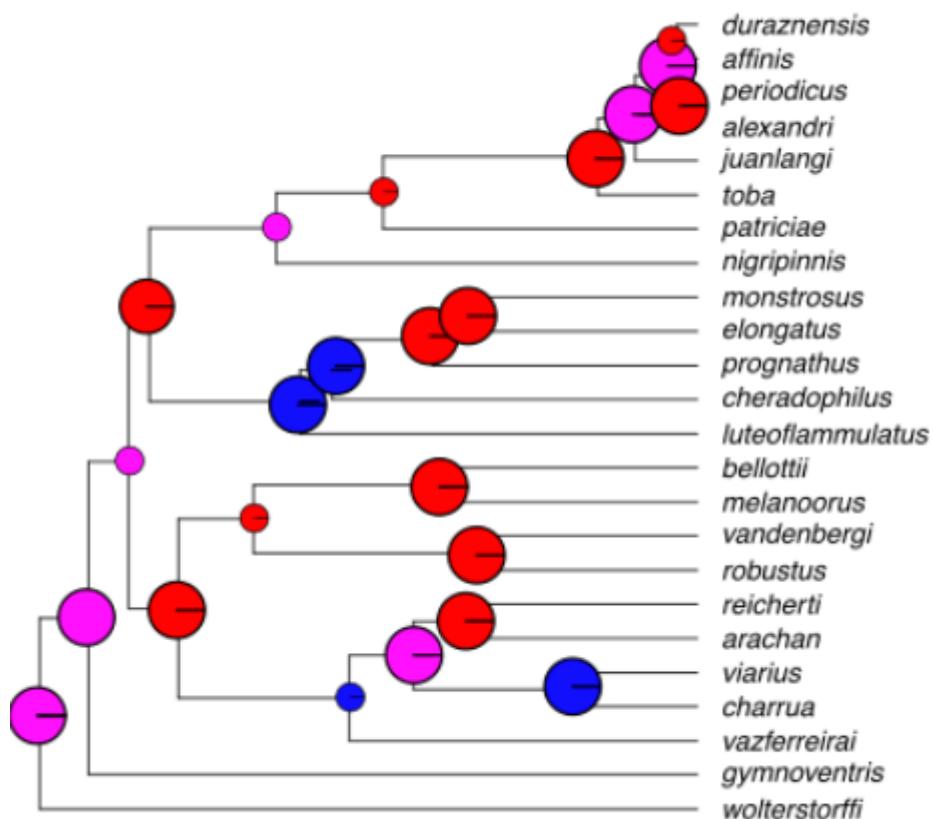


Austrolebias mixture regression using the R flexmix library (Leisch)

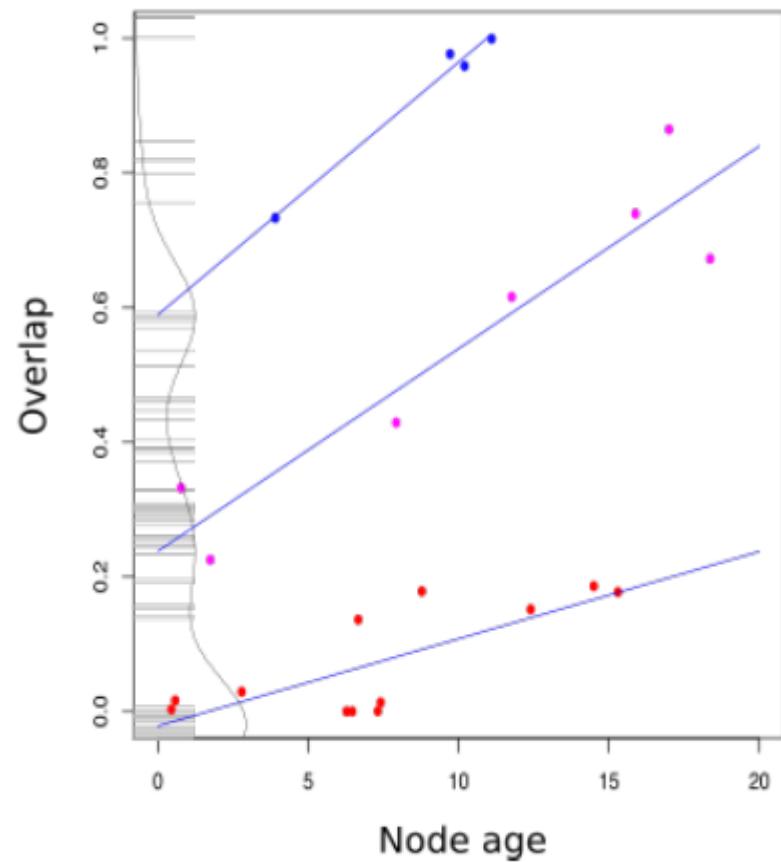


Predict node states using posterior probability per mixture component

A



B

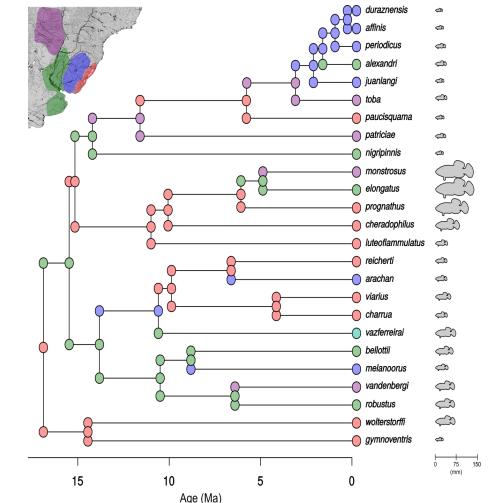


How reliable are these results?

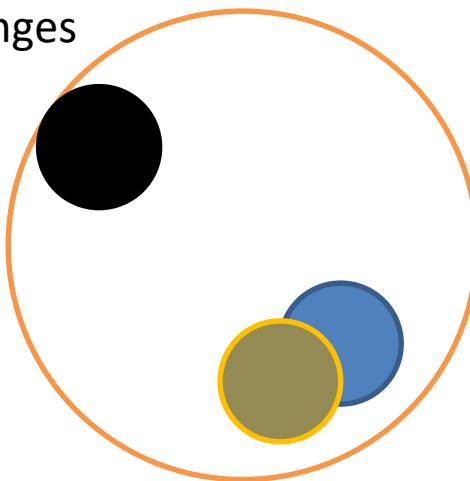
- Are there really three groups of speciation events?
- Are the posterior probabilities correct?

Simulations of cladogenetic and anagenetic
within- and between-area range changes

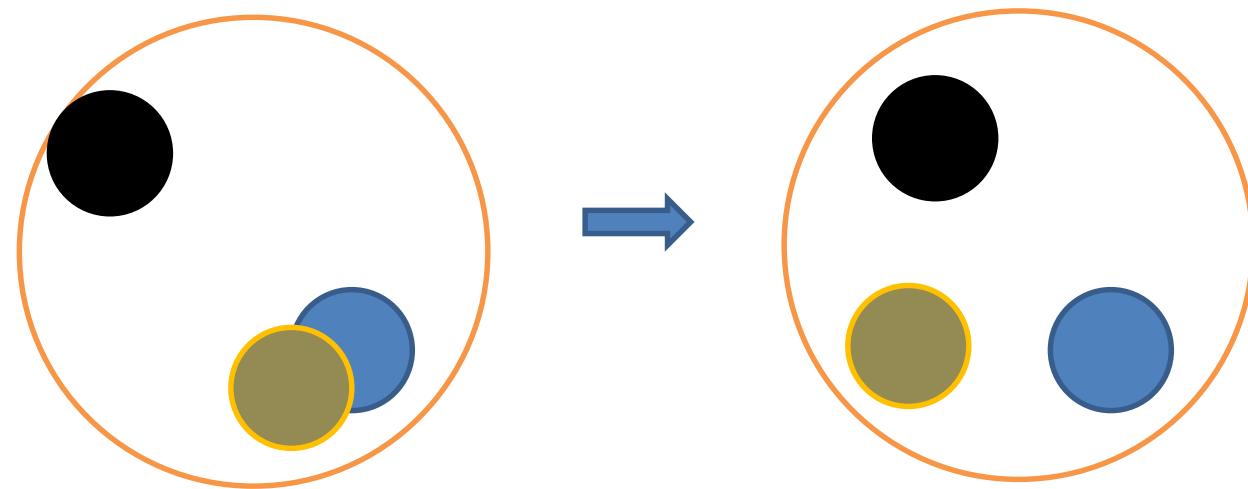
on the basis of the phylogenetic tree estimated
for the concatenated nDNA loci



An area of endemism with ranges



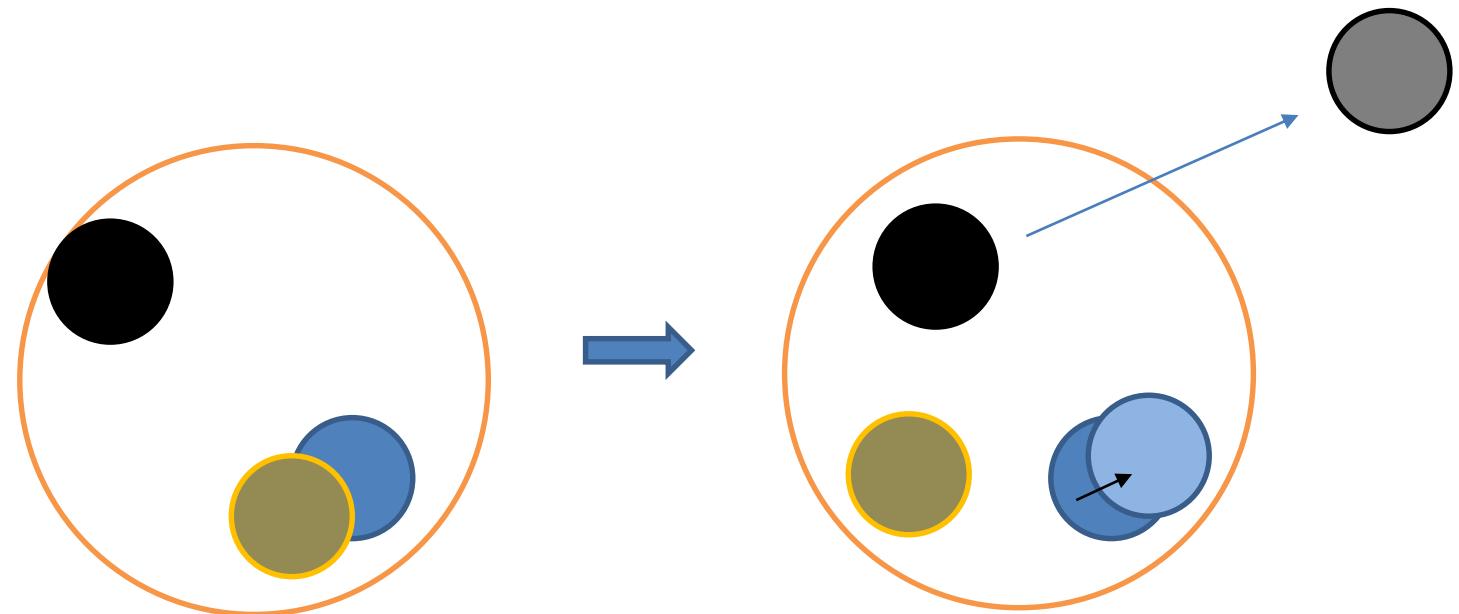
In between speciation events: random walks of ranges



At speciation events, different scenarios simulated:

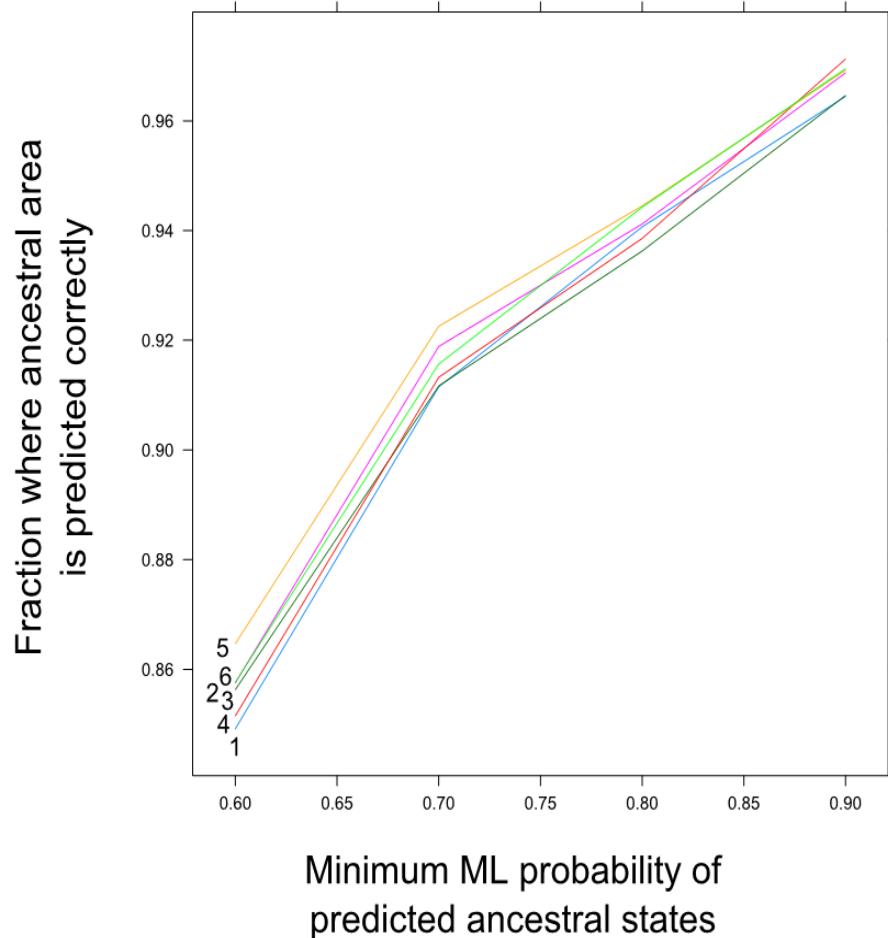
- (1) 50% jump dispersal and 50% allopatric speciation within area
- (2) 50% jump dispersal 25% allopatric speciation 25% parapatric speciation (0.2 overlap)
- (3) 50% jump dispersal 25% allopatric speciation 25% parapatric speciation (0.5 overlap)
- (4) 50% jump dispersal 25% allopatric speciation 25% sympatric speciation
- (5) 50% jump dispersal 25% parapatric speciation (0.2) 25% parapatric speciation (0.5 overlap)
- (6) 50% jump dispersal 25% 25% parapatric speciation (0.5) 25% sympatric speciation

200 simulations per combination of parameters

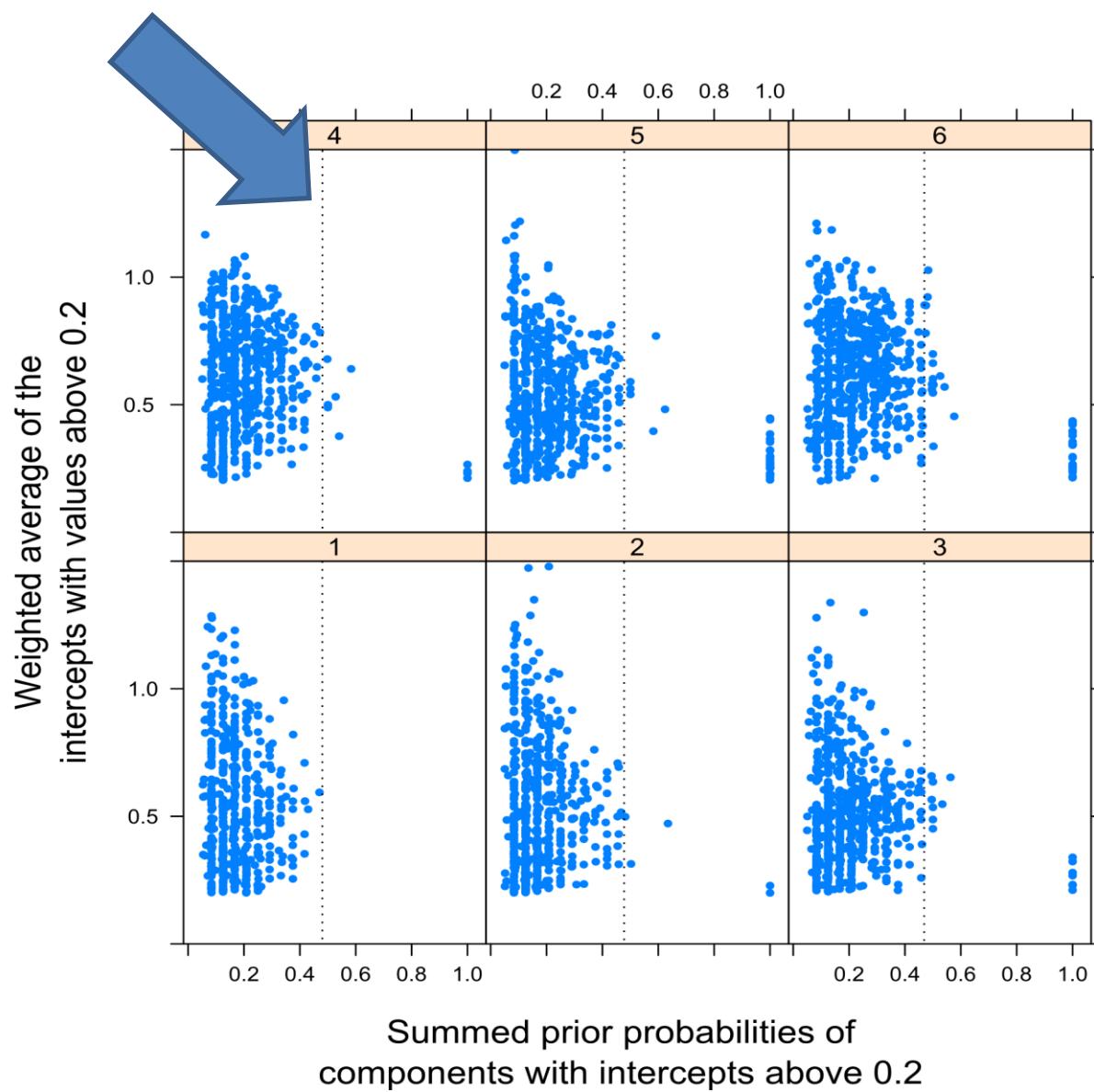


Do BioGeoBEARS on each simulation.

Probability of correct assignment to ancestral area in BioGeoBEARS simulations
We should focus on nodes with large ML probabilities of a prediction



Value (0.47) in the data of the summed prior of the two components with intercepts > 0.2

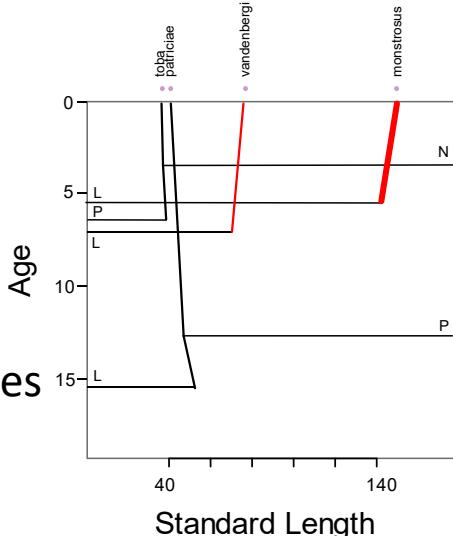


Scenario 1	Jump	Allopatric within		Scenario 4	Jump	Allopatric within	Sympatric
Predicted intercept ≤ 0.2	501	603		Predicted intercept ≤ 0.2	1020	533	583
Predicted intercept > 0.2	1047	1137		Predicted intercept > 0.2	1378	761	813
Scenario 2	Jump	Allopatric within	Parapatric	Scenario 5	Jump	Parapatric	Parapatric
Predicted intercept ≤ 0.2	644	331	369	Predicted intercept ≤ 0.2	1127	589	612
Predicted intercept > 0.2	917	490	489	Predicted intercept > 0.2	1561	886	865
Scenario 3	Jump	Allopatric within	Parapatric	Scenario 6	Jump	Parapatric	Sympatric
Predicted intercept ≤ 0.2	1096	597	587	Predicted intercept ≤ 0.2	1664	854	842
Predicted intercept > 0.2	1543	866	903	Predicted intercept > 0.2	1867	961	964

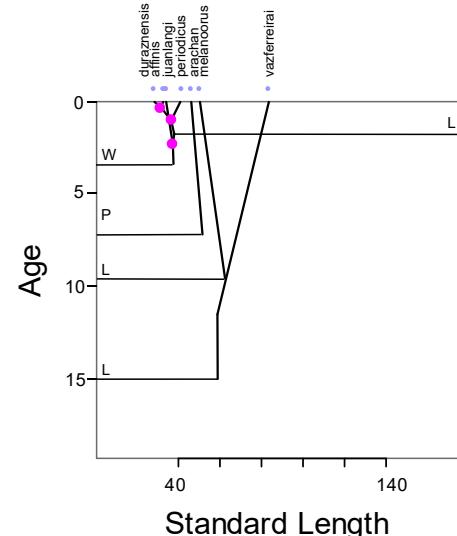
Communities/Assemblages/Areas
can have different (constructed) identities

that make us predict differences
in determinants of community ecology
between areas

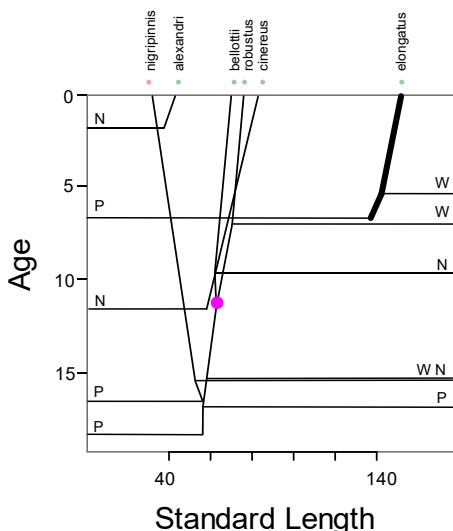
Western Paraguay



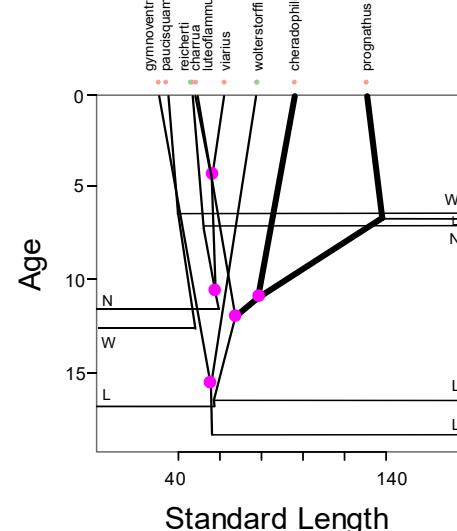
Negro



La Plata



Patos Lagoon



Original Article

Patterns of co-occurrences in a killifish metacommunity are more related with body size than with species identity

Andrés Canavero ✉, Daniel Hernández, Matías Zarucki, Matías Arim

First published: 06 November 2013 | <https://doi.org/10.1111/aec.12103> | Cited by: 6

Summary

Update community phylogenetics with more evolutionary and biogeographic modelling
More insightful view of ranges and niches in *Austrolebias*

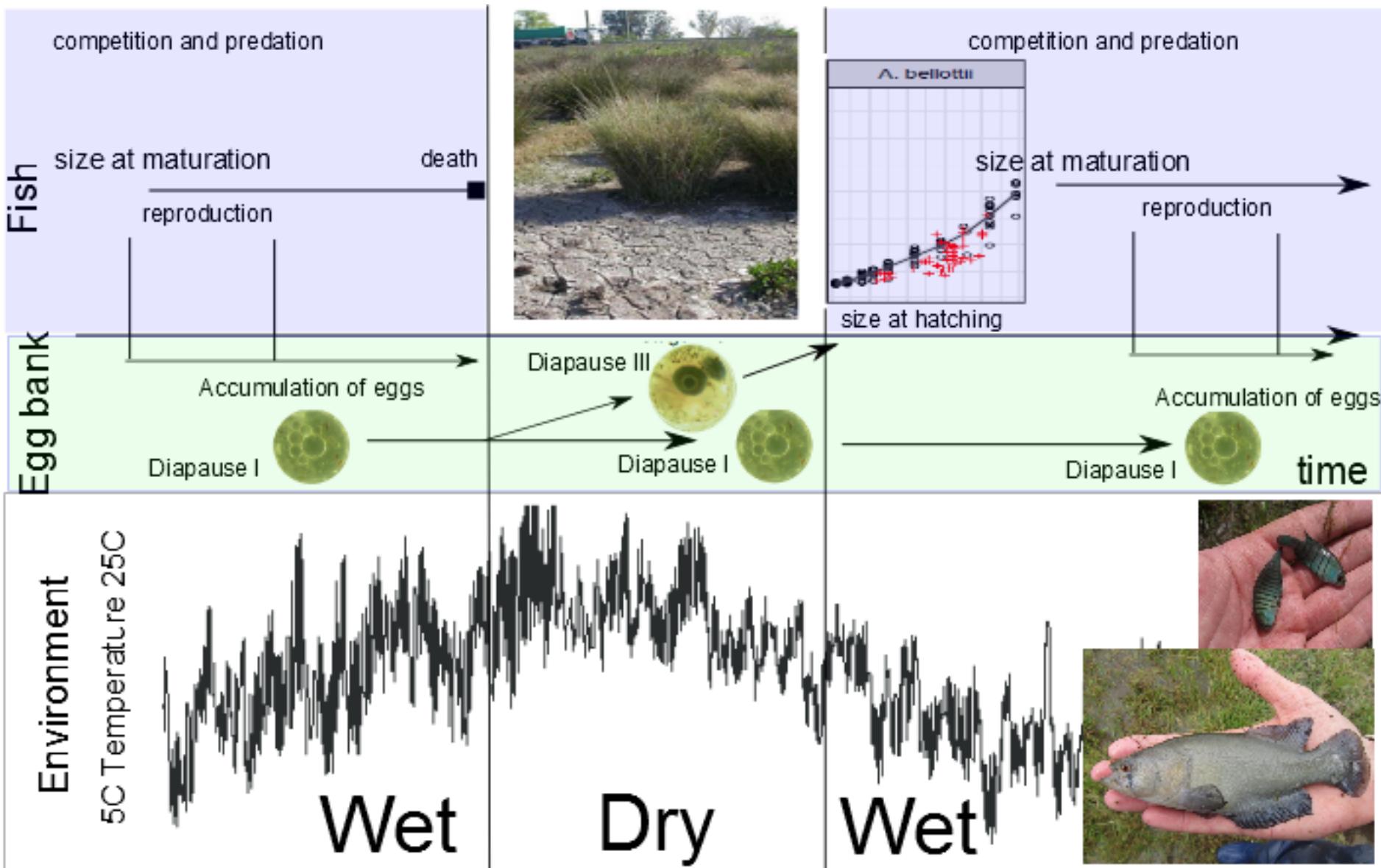
Repeated evolution of a similar niche shift
scope for eco-genetics

Niche shift involved in spread of piscivores & repeated assemblages with large differences

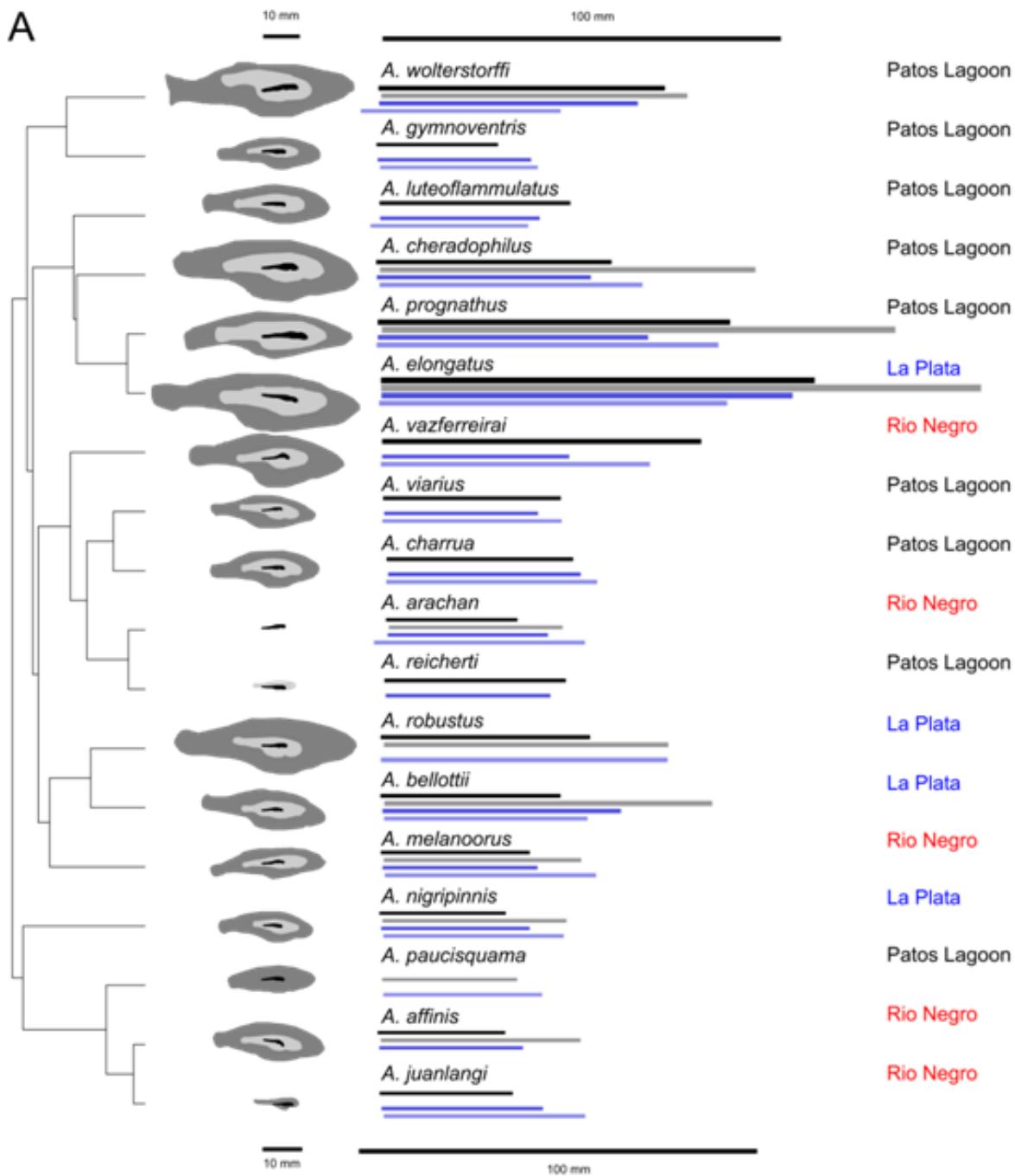
Introgression: we need to prepare to fit phylogenetic networks

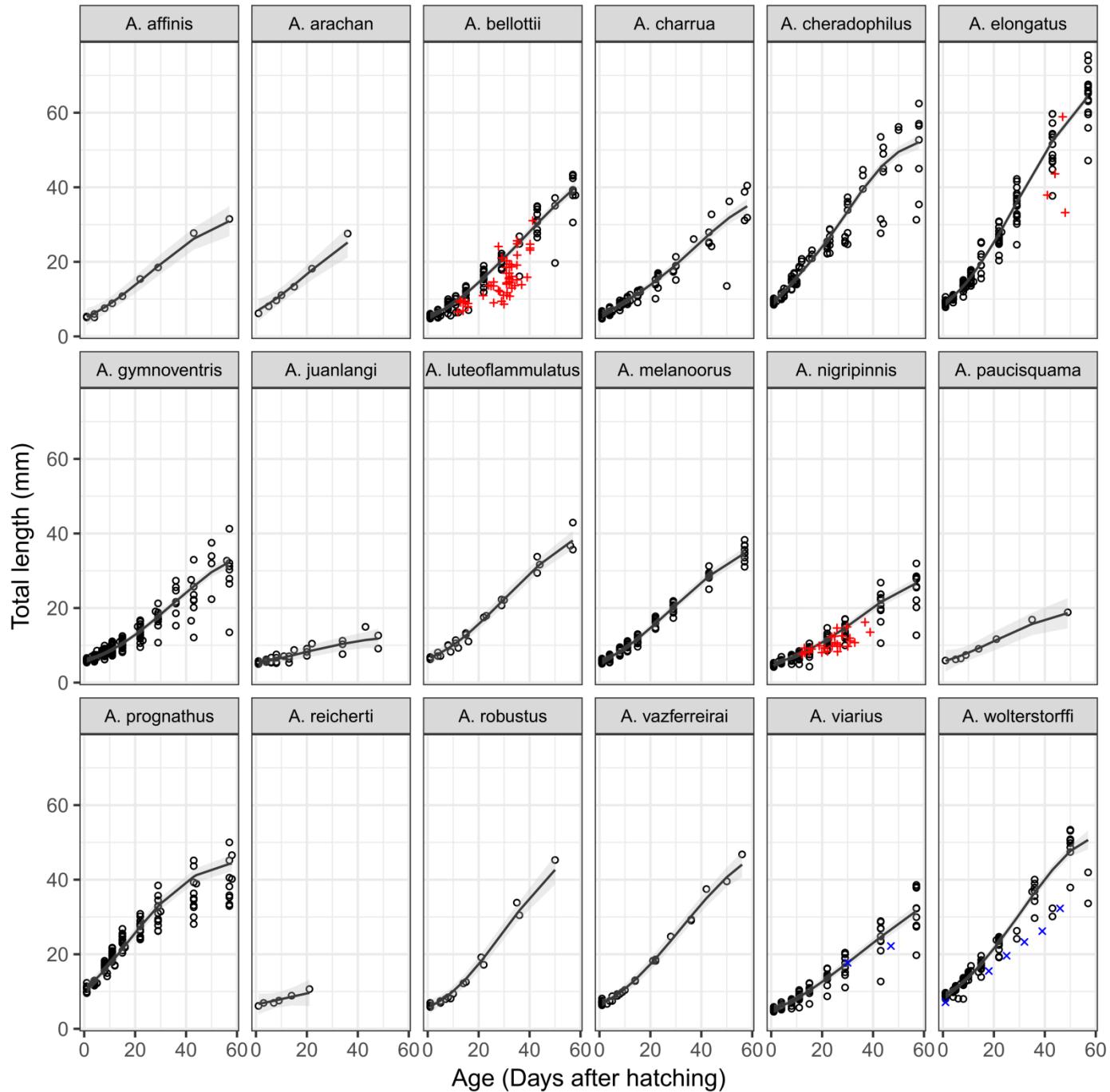
Modesty: replace "inference" by "predictions" and aim to propose new hypotheses for further testing

Check the mixture regressions with more simulations?
Or give up on the overlap regression method altogether?



A







Acknowledgements

Andrew Helmstetter
Martin Fourcade
Fabiana Cancino
Luis Lobo
Heber Salvia
Henri Thomassen
Vincent Savolainen
Femmie Smit
Erica, Amale, Luan

Schure-Beijerink-Popping Fund
Treub foundation
Killi-Data
NERC funding

