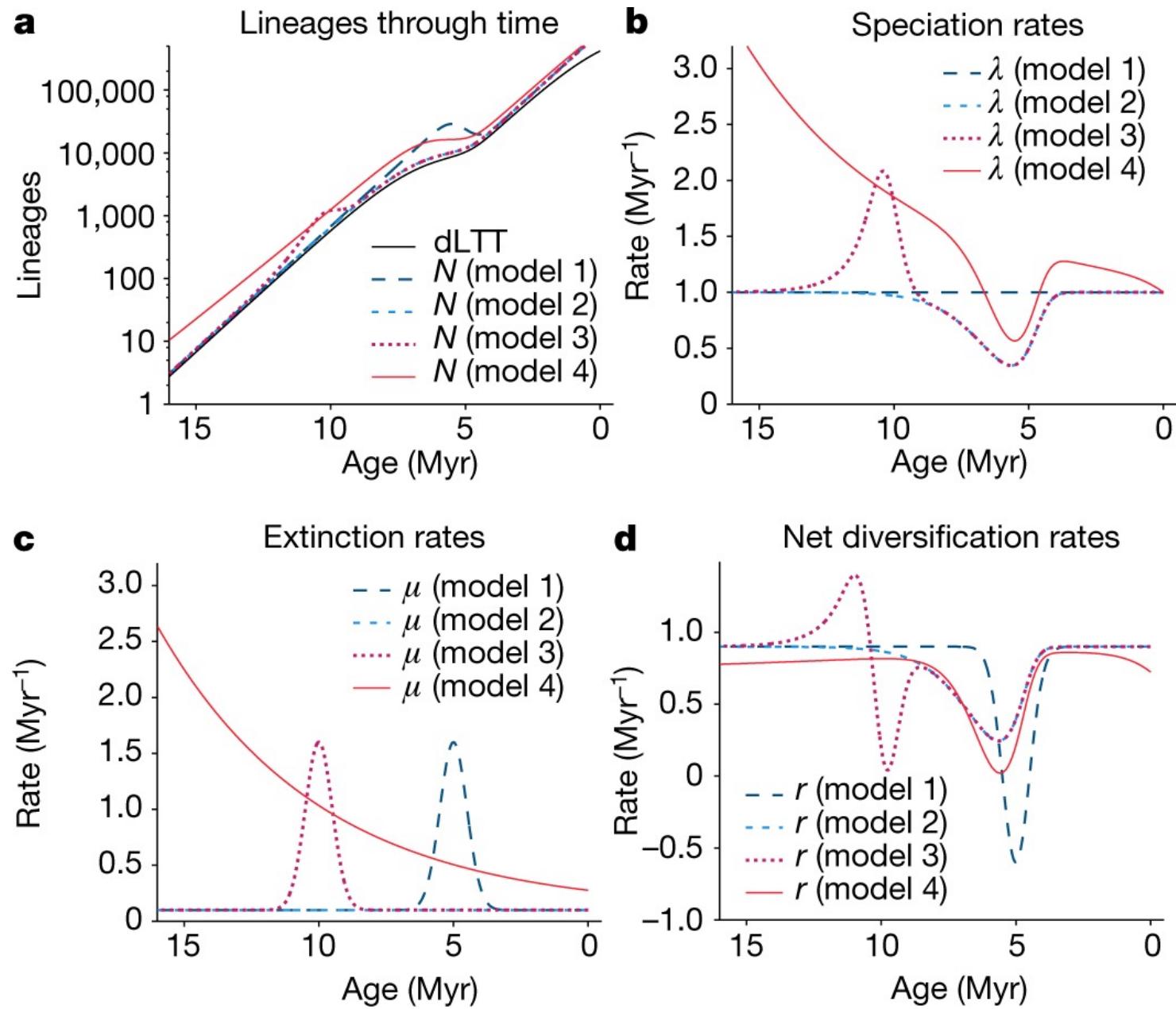


Modelación de escenarios geológicos o estratificados e incorporación del registro fósil

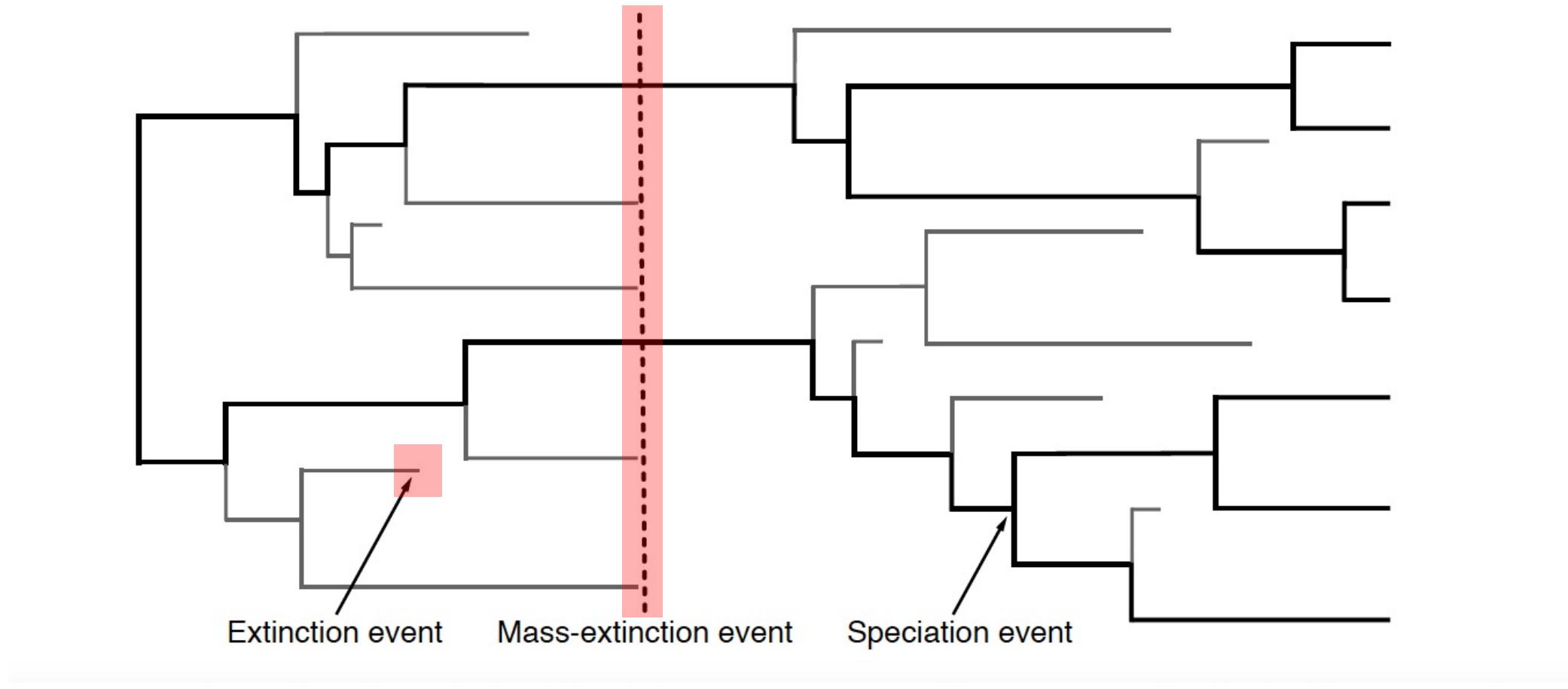
Introducción a la Biogeografía Paramétrica
Semana 2

Dra. Karen López y Dra. Marysol Trujano









Höhna et al., 2016; *Systematic Biology*

Earth's "mass extinctions"

During the last 500 million years, Earth has experienced five periods when at least half the living creatures were wiped out

Syst. Biol. 62(2):264–284, 2013

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DOI:10.1093/sysbio/sys092

Advance Access publication November 28, 2012

Treating Fossils as Terminal Taxa in Divergence Time Estimation Reveals Ancient Vicariance Patterns in the Palpimanoid Spiders

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⁴Department of Integrative Biology, University of California, 1005 Valley Life Sciences Building #3140, Berkeley, CA 94720, USA; and ⁵Department of Biology, San Francisco State University, 1600 Holloway Avenue, San Francisco, California 94132, USA

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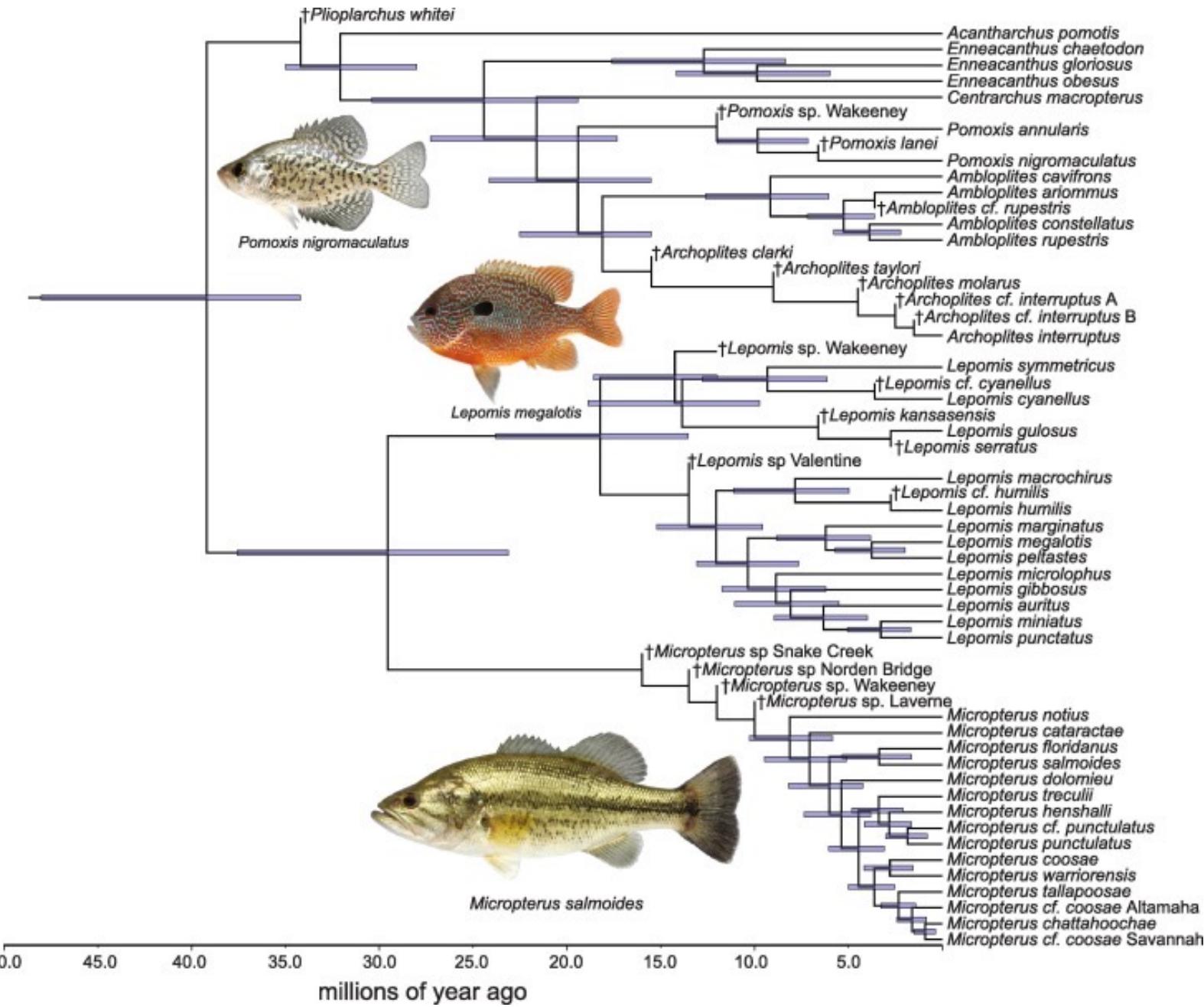
Received 29 February 2012; reviews returned 2 November 2012; accepted 20 November 2012

Associate editor: Elizabeth Jockusch



Sources: National Geographic, Encyclopedia Britannica, scientific studies

© AFP



Molecular data

#NEXUS
begin data;

dimensions ntax=2 nchar=15;
format datatype=DNA gap=-;

Taxon_a agtttaccctgattgcatacatgt
Taxon_b agtttacgctgattggatgttagct

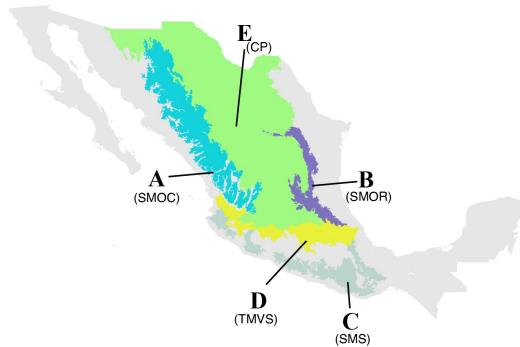
Morphological data

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format datatype=standard

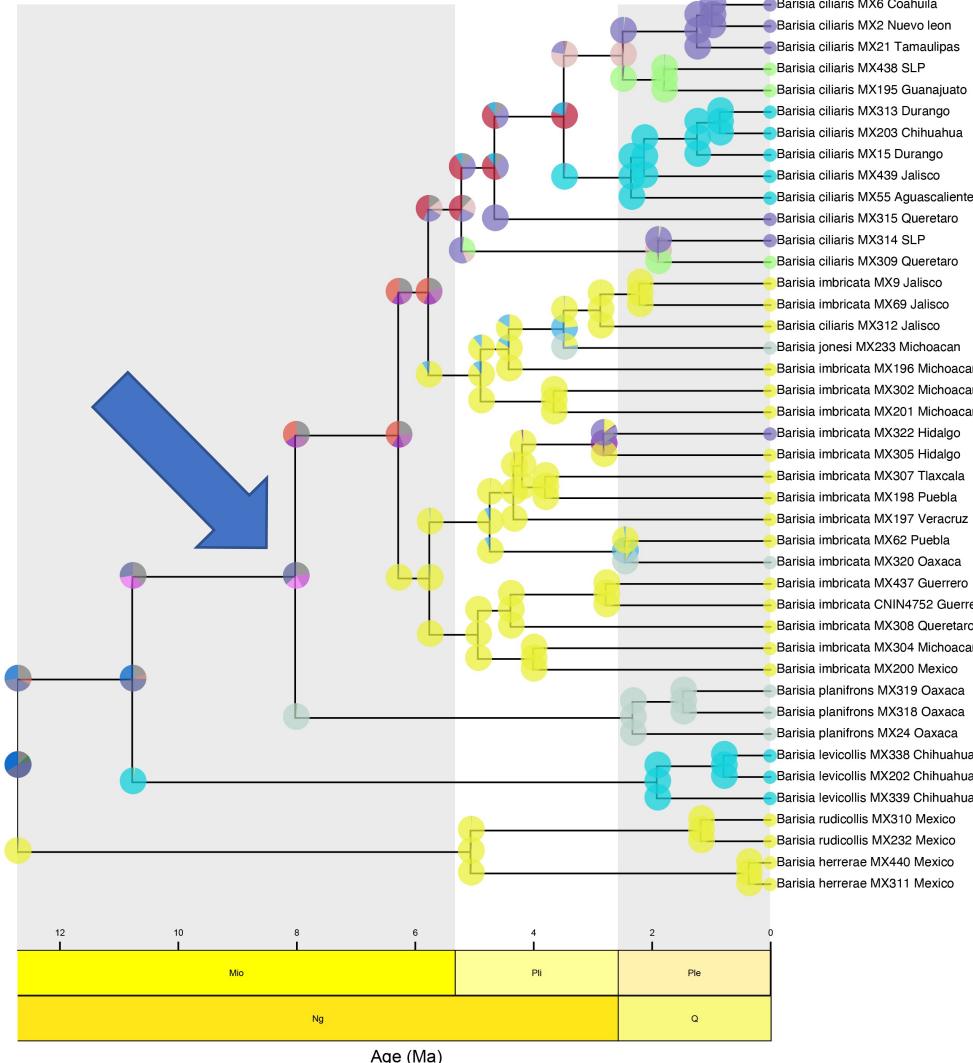
symbols="01" gap=-;

Taxon_a 0101110101200301010
Taxon_b 0101310101200301011



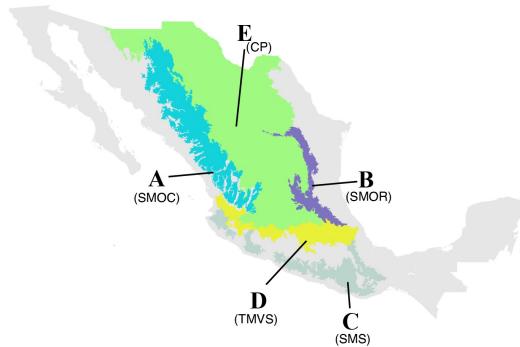
State

A	ABDE	AE	BDE	CE
AB	ABE	B	BE	D
ABC	AC	BCD	C	DE
ABCDE	ACD	BCDE	CD	E
ABCE	AD	BD	CDE	other

 $Q =$

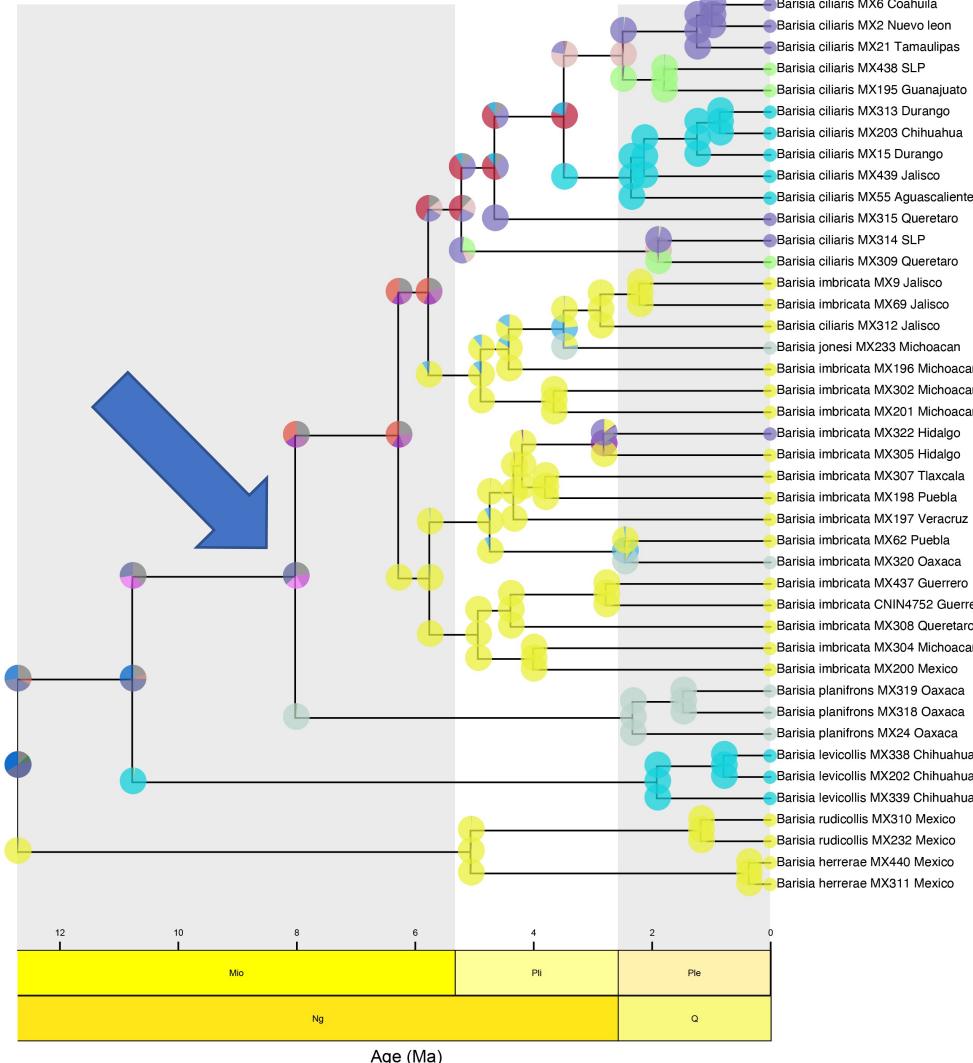
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B	e_B	0	-	0	d_{BA}	0	d_{BC}	0
C	e_C	0	0	-	0	d_{CA}	d_{CB}	0
AB	0	e_B	e_A	0	-	0	0	$d_{AC} + d_{BC}$
AC	0	e_C	0	e_A	0	-	0	$d_{AB} + d_{CB}$
BC	0	0	e_C	e_B	0	0	-	$d_{BA} + d_{CA}$
ABC	0	0	0	0	e_C	e_B	e_A	-

include: Constrain a node to contain at least the areas specified. For example, fossil include foo = 011 will constrain the node foo (specified with mrca) to the distributions 111 and 011.



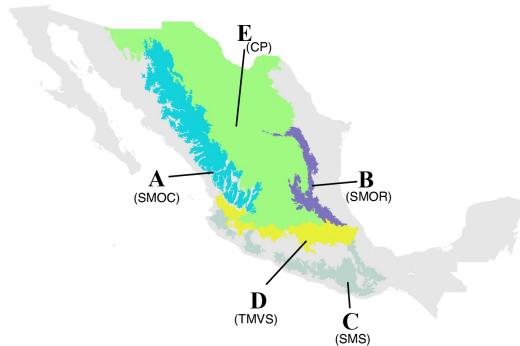
State

A	ABDE	AE	BDE	CE
AB	ABE	B	BE	D
ABC	AC	BCD	C	DE
ABCDE	ACD	BCDE	CD	E
ABCE	AD	BD	CDE	other

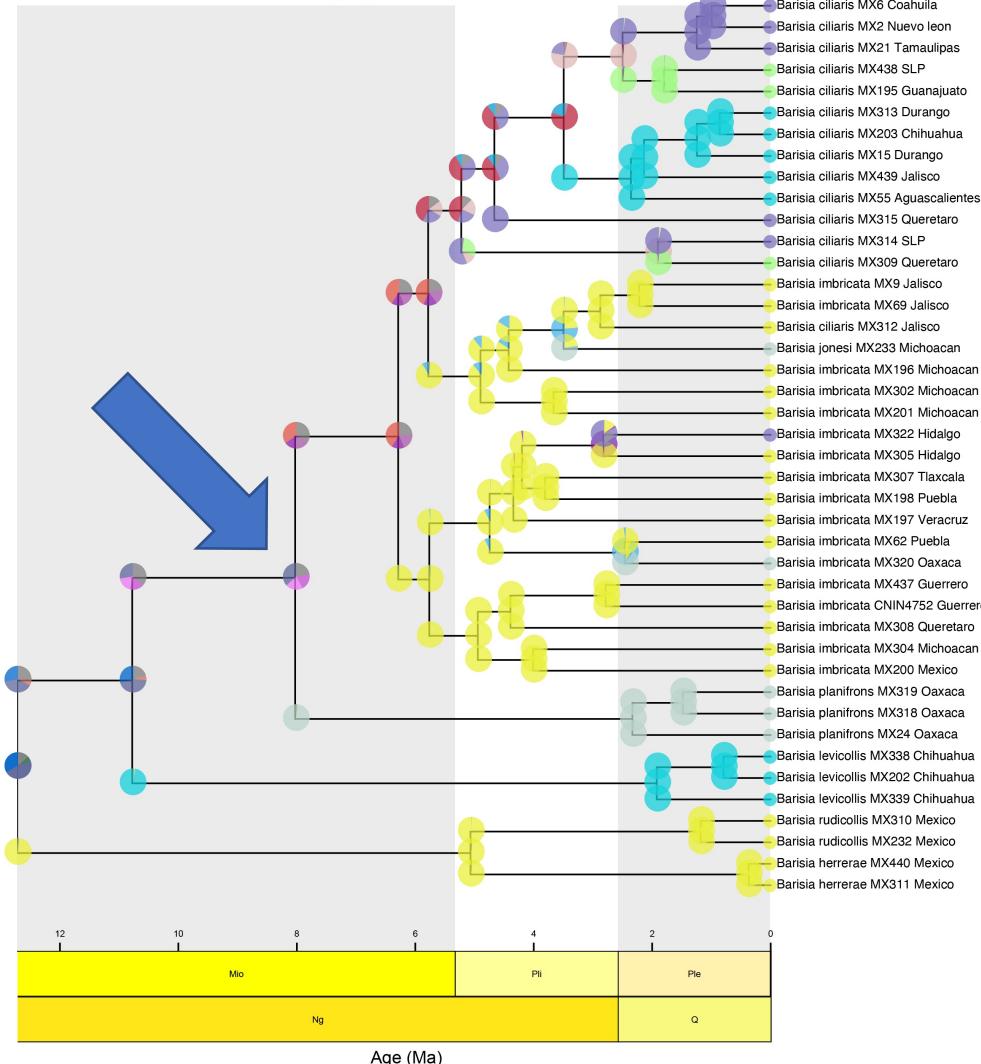


exclude: Constrain a node to contain *none* of the areas specified. For example, fossil exclude foo = 001 will exclude the distributions 001, 011, 101, and 111 from node foo.

	\emptyset	A	B	C	AB	AC	BC	ABC
\emptyset	-	0	0	0	0	0	0	0
A	e_A	-	0	0	d_{AB}	d_{AC}	0	0
B	e_B	0	-	0	d_{BA}	0	d_{BC}	0
C	e_C	0	0	-	0	d_{CA}	d_{CB}	0
AB	0	e_B	e_A	0	-	0	0	$d_{AC} + d_{BC}$
AC	0	e_C	0	e_A	0	-	0	$d_{AB} + d_{CB}$
BC	0	0	e_C	e_B	0	0	-	$d_{BA} + d_{CA}$
ABC	0	0	0	0	e_C	e_B	e_A	-

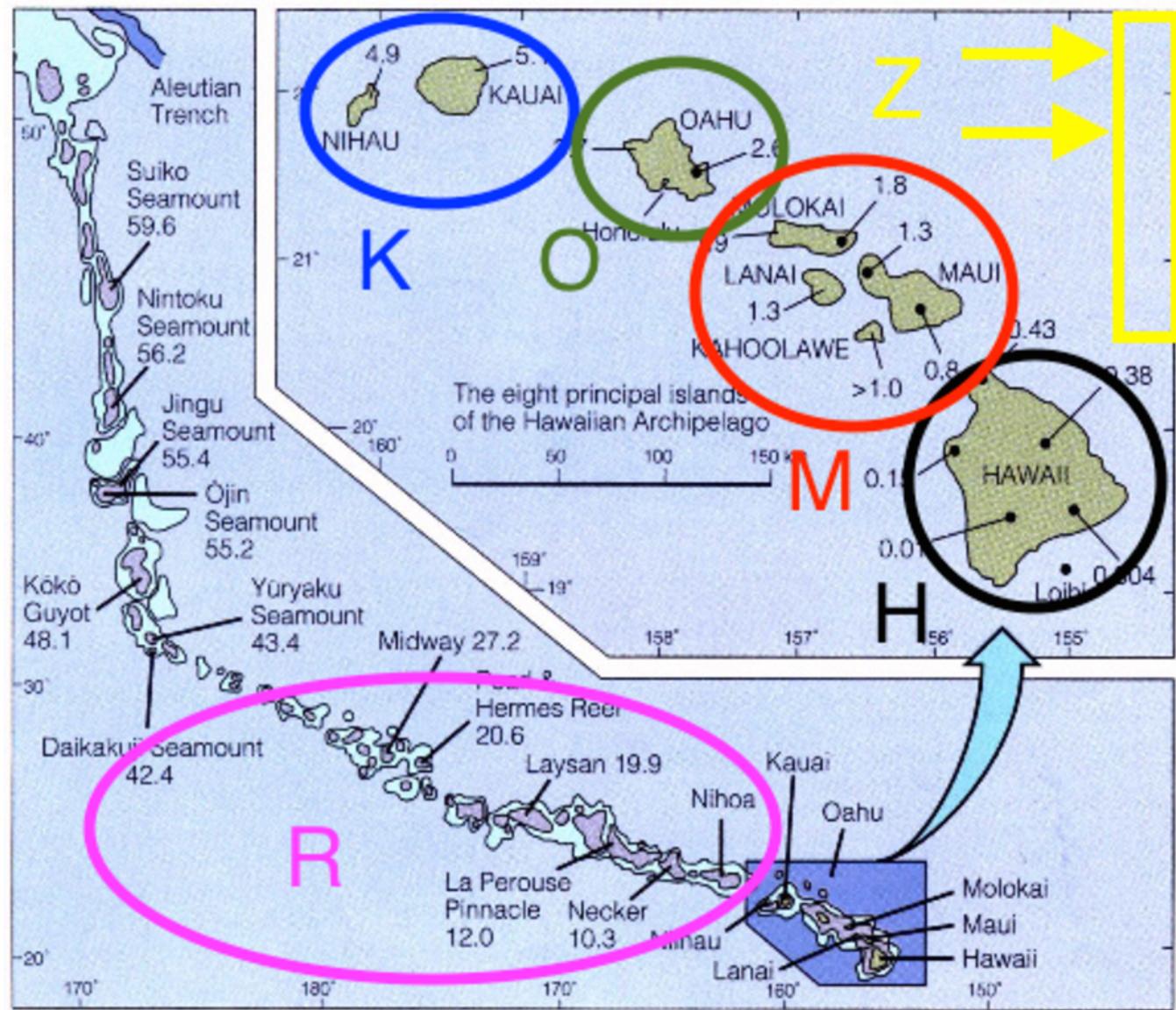


State														
A	ABDE	AE	BDE	CE	D									
AB	ABE	B	BE											
ABCD	AC	BCD	C	DE										
ABCDE	ACD	BCDE	CD	E										
ABCE	AD	BD	CDE											



fixed: Constrain a node to be exactly the distribution specified. For example, fossil fixed foo = 011 will constrain the node foo to the distribution 011.

$Q =$	\emptyset	A	B	C	AB	AC	BC	ABC
\emptyset	-	0	0	0	0	0	0	0
A	e_A	-	0	0	d_{AB}	d_{AC}	0	0
B	e_B	0	-	0	d_{BA}	0	d_{BC}	0
C	e_C	0	0	-	0	d_{CA}	d_{CB}	0
AB	0	e_B	e_A	0	-	0	0	$d_{AC} + d_{BC}$
AC	0	e_C	0	e_A	0	-	0	$d_{AB} + d_{CB}$
BC	0	0	e_C	e_B	0	0	-	$d_{BA} + d_{CA}$
ABC	0	0	0	0	e_C	e_B	e_A	-



$Q =$	\emptyset	A	B	C	AB	AC	BC	ABC
\emptyset	—	0	0	0	0	0	0	0
A	e_A	—	0	0	d_{AB}	d_{AC}	0	0
B	e_B	0	—	0	d_{BA}	0	d_{BC}	0
C	e_C	0	0	—	0	d_{CA}	d_{CB}	0
AB	0	e_B	e_A	0	—	0	0	$d_{AC} + d_{BC}$
AC	0	e_C	0	e_A	0	—	0	$d_{AB} + d_{CB}$
BC	0	0	e_C	e_B	0	0	—	$d_{BA} + d_{CA}$
ABC	0	0	0	0	e_C	e_B	e_A	—

Matriz Q

T1:

	\emptyset	A	B	AB
\emptyset	-	0	0	0
A	e_A	-	0	d_{AB}
B	e_B	0	-	d_{BA}
AB	0	e_B	e_A	-

$Q =$

Matriz Conectividad

1 1 0
1 1 0
0 0 0

T2:

	\emptyset	A	B	C	AB	AC	BC	ABC
\emptyset	-	0	0	0	0	0	0	0
A	e_A	-	0	0	d_{AB}	d_{AC}	0	0
B	e_B	0	-	0	d_{BA}	0	d_{BC}	0
C	e_C	0	0	-	0	d_{CA}	d_{CB}	0
AB	0	e_B	e_A	0	-	0	0	$d_{AC} + d_{BC}$
AC	0	e_C	0	e_A	0	-	0	$d_{AB} + d_{CB}$
BC	0	0	e_C	e_B	0	0	-	$d_{BA} + d_{CA}$
ABC	0	0	0	0	e_C	e_B	e_A	-

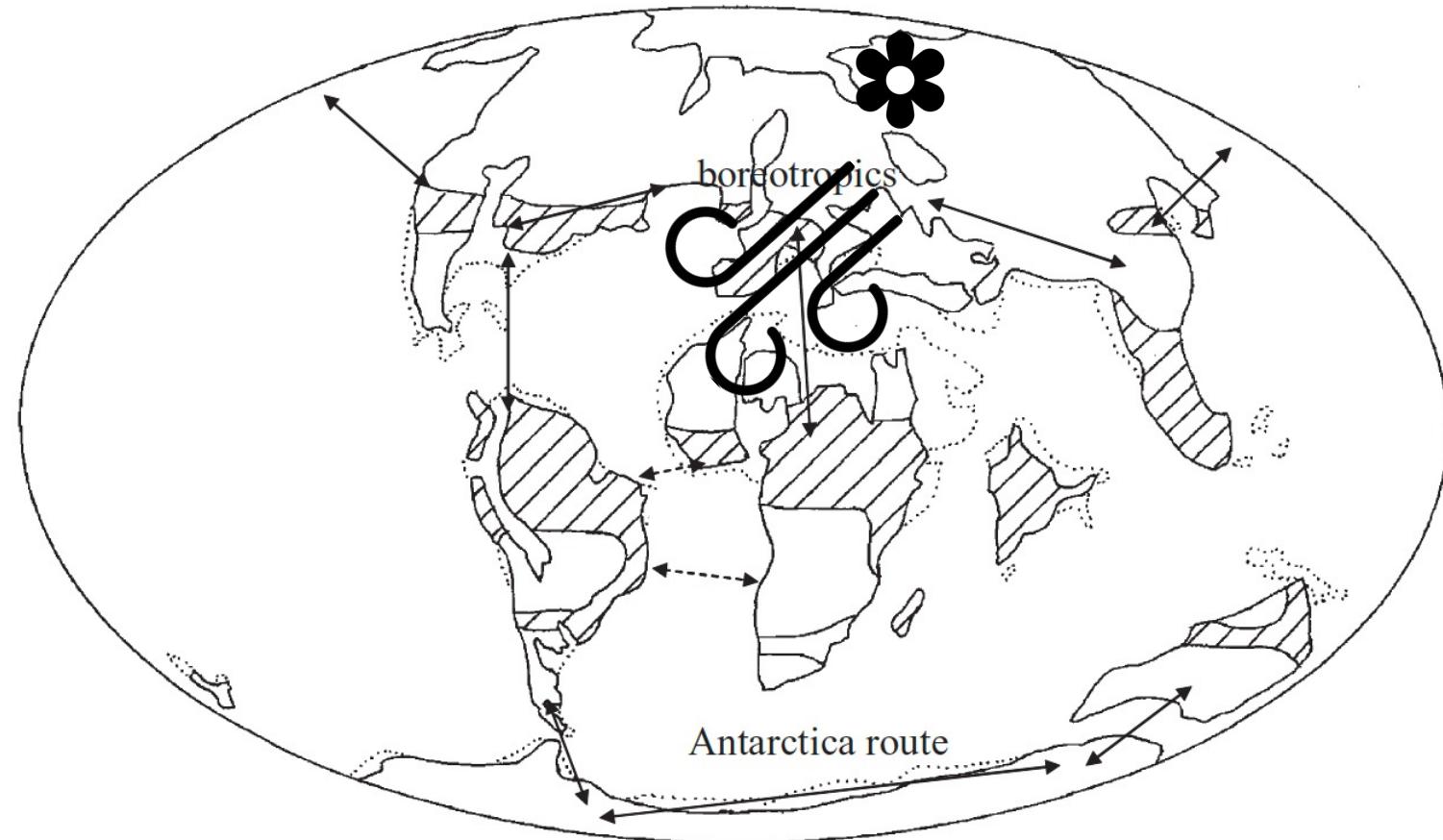
1 1 1
1 1 1
1 1 1

Expansiones del modelo DEC y sus limitaciones

Introducción a la Biogeografía Paramétrica
Semana 2

Dra. Karen López y Dra. Marysol Trujano

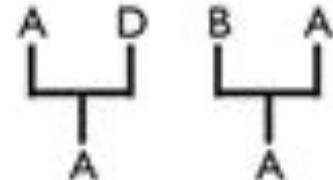
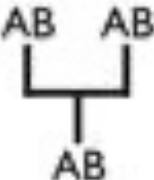
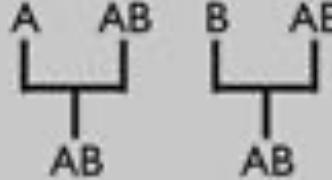
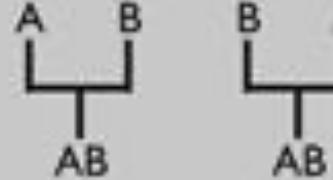
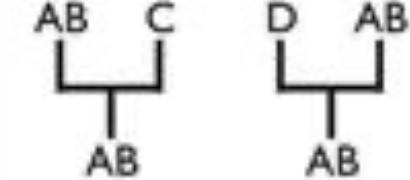
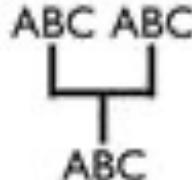
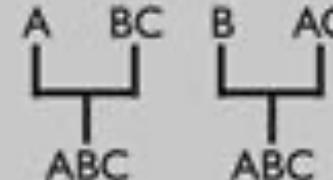
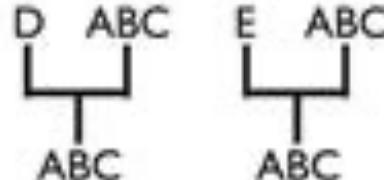
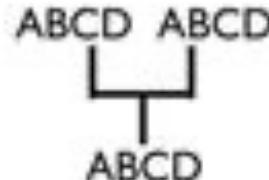
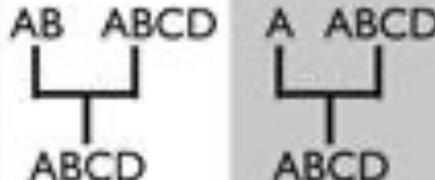
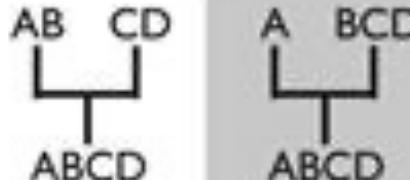
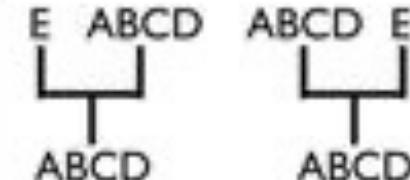
Pennington & Dick, 2004



	\emptyset	A	B	C	AB	AC	BC	ABC
$\mathbf{Q} =$	\emptyset	—	0	0	0	0	0	0
	A	e_A	—	0	0	d_{AB}	d_{AC}	0
	B	e_B	0	—	0	d_{BA}	0	d_{BC}
	C	e_C	0	0	—	0	d_{CA}	d_{CB}
	AB	0	e_B	e_A	0	—	0	$d_{AC} + d_{BC}$
	AC	0	e_C	0	e_A	0	—	$d_{AB} + d_{CB}$
	BC	0	0	e_C	e_B	0	0	$d_{BA} + d_{CA}$
	ABC	0	0	0	0	e_C	e_B	—

Types of speciation, and example descendant ranges:

Matzke, 2014 Sys Bio

Ancestral ranges:	Sympatric (range copying)	Sympatric (subset)	Vicariance	Founder Event
A		--	--	
AB				
ABC				
ABCD				

DEC

DEC+J

Model Selection in Historical Biogeography Reveals that Founder-Event Speciation Is a Crucial Process in Island Clades

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Received 19 September 2013; reviews returned 14 July
Associate Editor: Frank Anderson

DOI: 10.1111/jbi.13173

PERSPECTIVE

WILEY  Journal of Biogeography

Conceptual and statistical problems with the DEC+J model of founder-event speciation and its comparison with DEC via model selection

Abstract

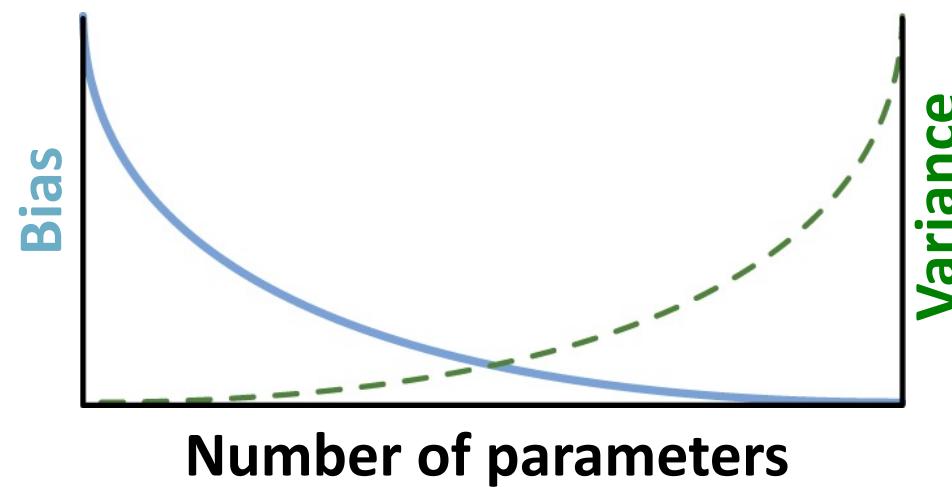
Phylogenetic studies of geographic range evolution are increasingly using statistical model selection methods to choose among variants of the dispersal-extinction-cladogenesis (DEC) model, especially between DEC and DEC+J, a variant that emphasizes “jump dispersal,” or founder-event speciation, as a type of cladogenetic range inheritance scenario. Unfortunately, DEC+J is a poor model of founder-event speciation, and statistical comparisons of its likelihood with DEC are inappropriate. DEC and DEC+J share a conceptual flaw: cladogenetic events of range inheritance at ancestral nodes, unlike anagenetic events of dispersal and local extinction along branches, are not modelled as being probabilistic with respect to time. Ignoring this probability factor artificially inflates the contribution of cladogenetic events to the likelihood, and leads to underestimates of anagenetic, time-dependent range evolution. The flaw is exacerbated in DEC+J because not only is jump dispersal allowed, expanding the set of cladogenetic events, its probability relative to non-jump events is assigned a free parameter j that when maximized precludes the pos-

1 | INTRODUCTION

In historical biogeographic studies that infer ancestral geographic ranges on phylogenetic trees, a particularly notable trend is the increasing use of statistical model selection, particularly in choosing between the dispersal-extinction-cladogenesis (DEC) model of range evolution (Ree, Moore, Webb, & Donoghue, 2005; Ree & Smith, 2008) and a variant called DEC+J (Matzke, 2014a). The impetus for DEC+J was a perceived shortcoming of DEC in island systems, namely, that it fails to consider “founder event” or “jump dispersal” speciation, in which new lineages are directly established by colonization without the intermediate existence of a widespread ancestor (Clark et al., 2008). DEC+J differs from DEC in allowing this kind of speciation scenario to be posited at internal nodes of the phylogeny, and includes a free parameter j that weights the contribution of such events to the likelihood of the data, observed species ranges at the tips of the tree.

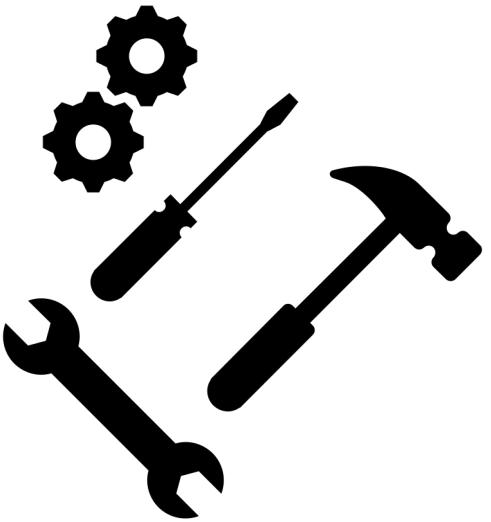
Model selection

- Adding more parameters *always* improves the fit of the model to the observed data (reduces bias in estimates)
- But more parameters leads to greater variance in the estimates of those parameters
 - Is the improvement in model fit worth the cost of adding a parameter?



Ventajas y limitaciones

- Integran la dimensión temporal
- Se incorpora el error asociado
- Se puede discriminar entre escenarios con métodos estadísticos (LRT, Bayes Factor, AIC)
- Pueden integrar diferentes fuentes de evidencia
- Costosos computacionalmente
- Limitado por el número de áreas aunque...
- Coste de parámetros
- No diferencia entre tipos de dispersion aunque...



BioGeoBears

Lagrange-DEC C++ version

Syst. Biol. 72(1):242–248, 2023
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<https://doi.org/10.1093/sysbio/syad002>
Advance Access Publication January 27, 2023

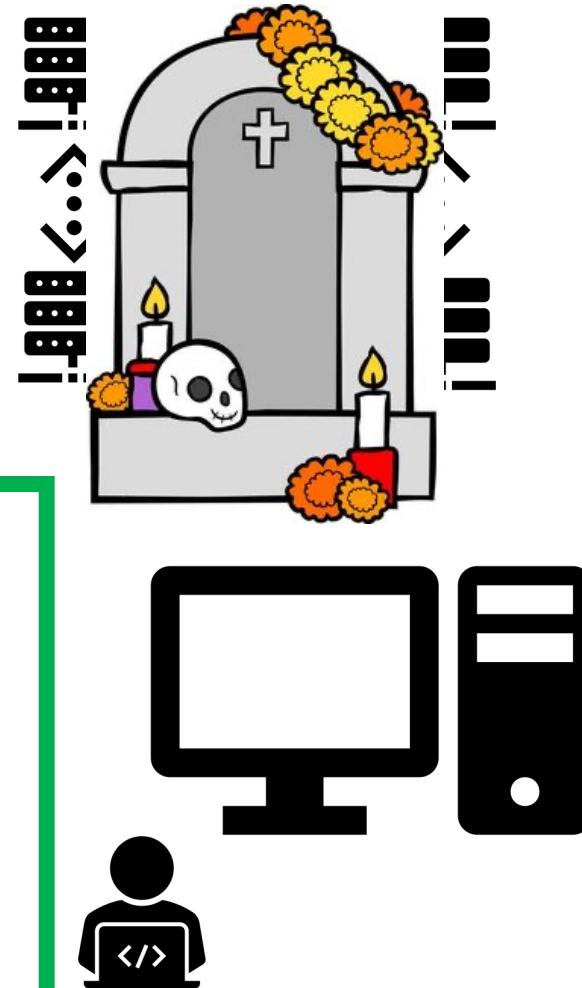
Lagrange-NG: The next generation of Lagrange

BEN BETTISWORTH^{1,*} STEPHEN A. SMITH² , AND ALEXANDROS STAMATAKIS^{1,3}

¹Computational Molecular Evolution Group, Heidelberg Institute for Theoretical Studies, Heidelberg, Germany
²Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, United States
³Institute for Theoretical Informatics, Karlsruhe Institute of Technology, Karlsruhe, Germany

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E-mail: ben.bettisworth@h-its.org

Received 21 April 2022; reviews returned 9 January 2023; accepted 20 January 2023
Associate Editor: James Allard

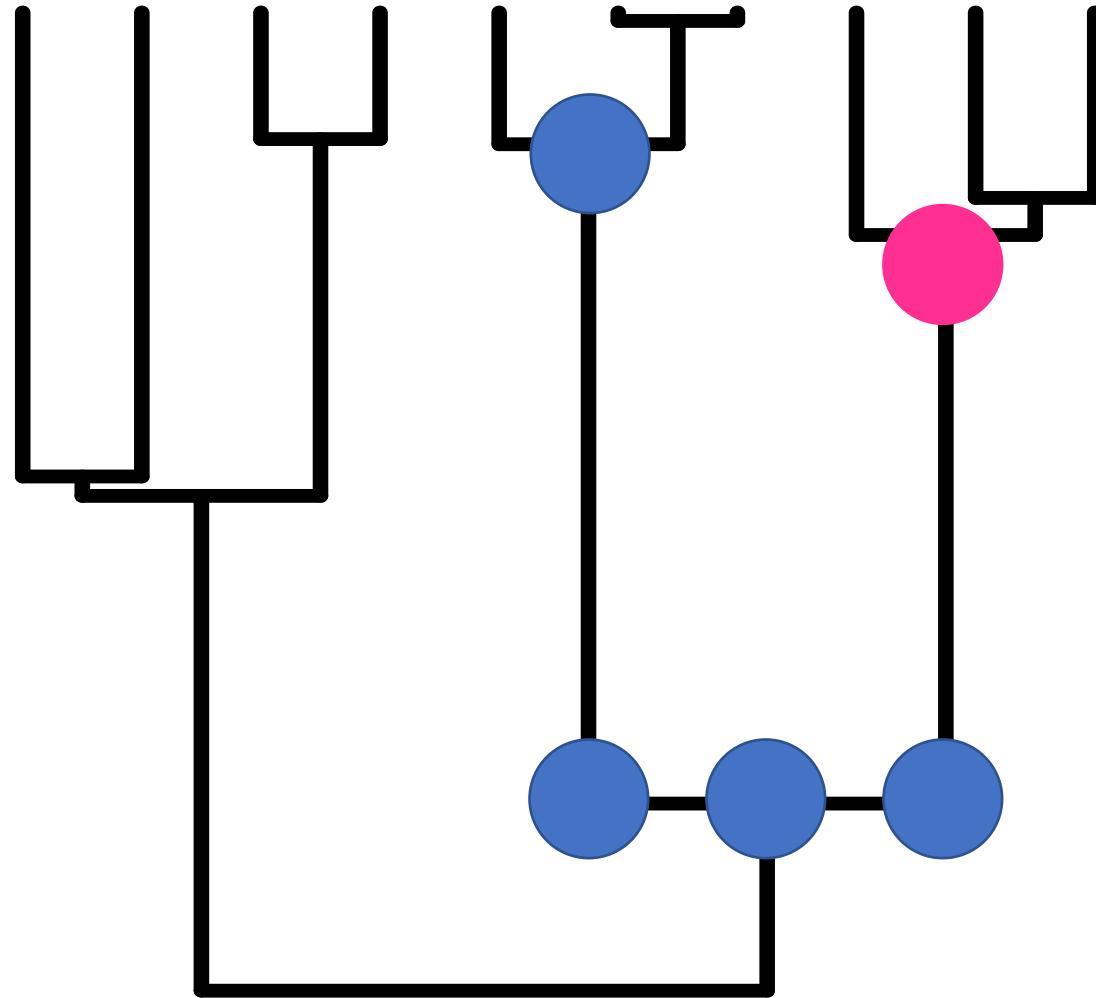


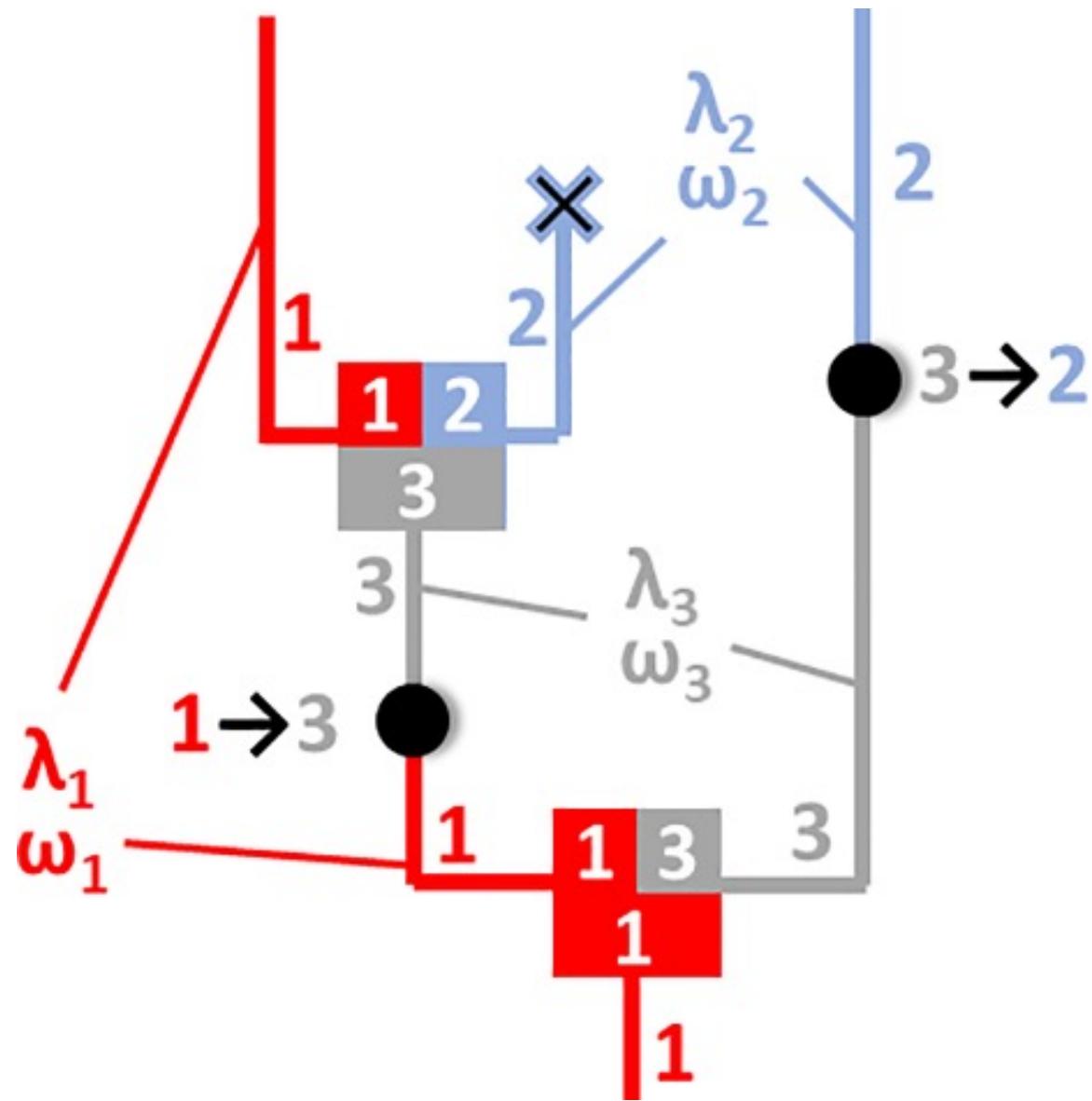
Abstract.— Computing ancestral ranges via the Dispersion Extinction and Cladogenesis (DEC) model of biogeography is characterized by an exponential number of states relative to the number of regions considered. This is because the DEC model requires computing a large matrix exponential, which typically accounts for up to 80% of overall runtime. Therefore, the kinds of biogeographical analyses that can be conducted under the DEC model are limited by the number of regions under consideration. In this work, we present a completely redesigned efficient version of the popular tool Lagrange which is up to 49 times faster with multithreading enabled, and is also 26 times faster when using only one thread. We call this new version Lagrange-NG (Lagrange-Next Generation). The increased computational efficiency allows Lagrange-NG to analyze datasets with up to 100 regions in a reasonable amount of time (e.g., 10 min).

Ventajas y limitaciones

- Integran la dimensión temporal
- Se incorpora el error asociado
- Se puede discriminar entre escenarios métodos estadísticos (LRT, Bayes Factor)
- Pueden integrar diferentes fuentes de evidencia
- Costosos computacionalmente
- Limitado por el número de parámetros
- Diferencia entre los niveles de dispersión
- aunque...

Limitaciones conceptuales





Speciation with a $3 \rightarrow (1, 2)$ transition
(occurs with rate λ_{312})

Speciation with a $1 \rightarrow (1, 3)$ transition
(occurs with rate λ_{113})

Extinction in state 2
(occurs with rate ω_2)

Biogeografía basada en procesos

Evolución de la línea de investigación: Biogeografía histórica

Usted
está aquí



Dispersionismo
y centros de
origen

Vicarianza y
Biogeografía
cladista

Biogeografía
basada en
procesos

Biogeografía
probabilística

Biogeografía
Next
generation

Dispersionismo y centros de origen

Dispersión

Criterios para determinar
el centro de origen

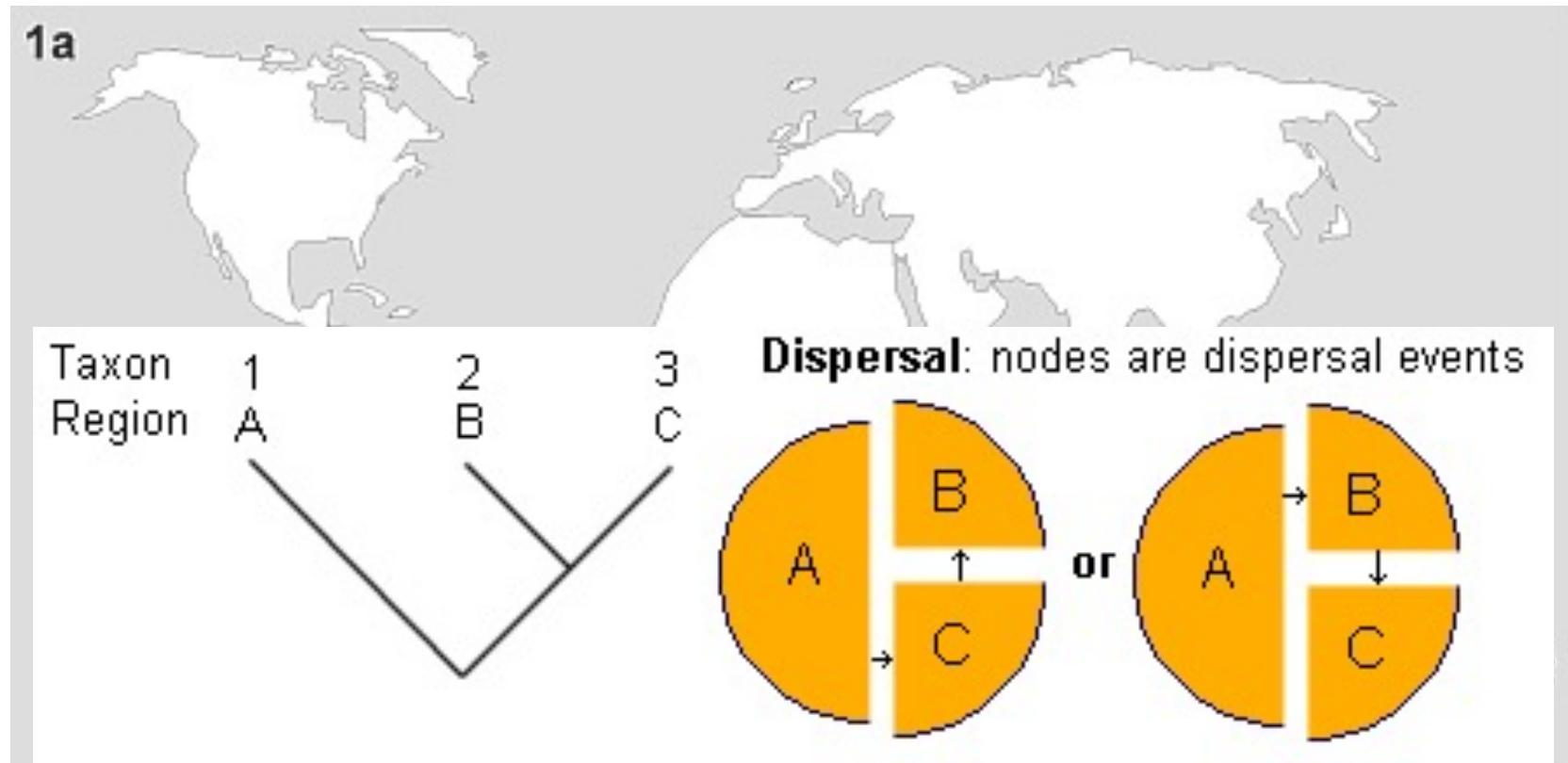
Estabilidad geográfica

Deficiencias metodológicas

Criterio parsimonia

Proceso biológico

Dispersión



Vicarianza y Biogeografía cladista

Vicarianza

Tectónica de placas

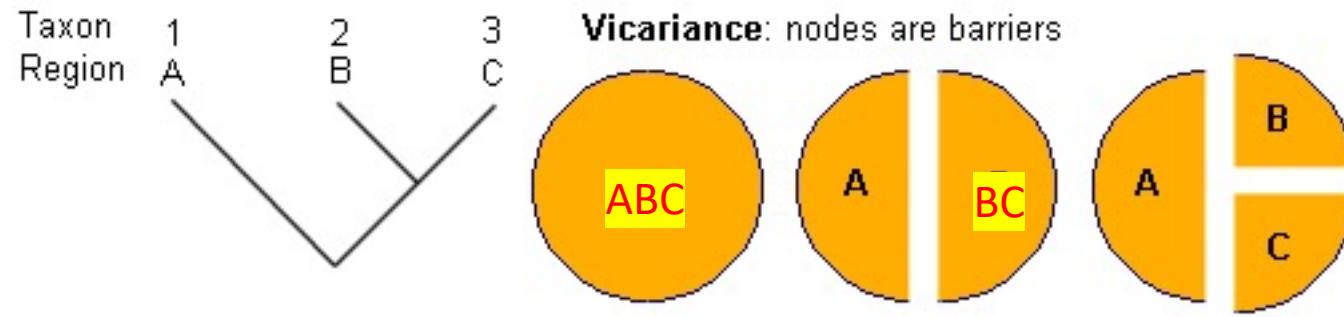
Tierra y biota evolucionan juntos

Deficiencias metodológicas

Criterio parsimonia

Procesos biológicos

Dispersión + vicarianza



Biogeografía basada en procesos

Incorpora explícitamente los Procesos en la reconstrucción

Criterio parsimonia

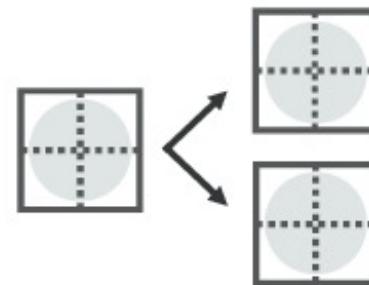
Costes a procesos

Busca patrones filogenéticamente Conservados

Deficiencias metodológicas

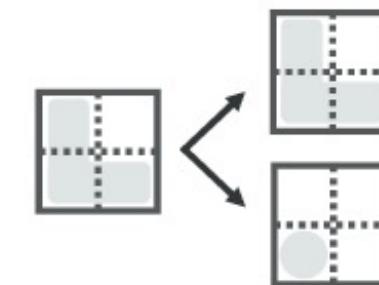
Procesos biológicos:
Dispersión + vicarianza
+ extirpación (extinción)
+ duplicación (especiación *in situ*)

Speciation within-area



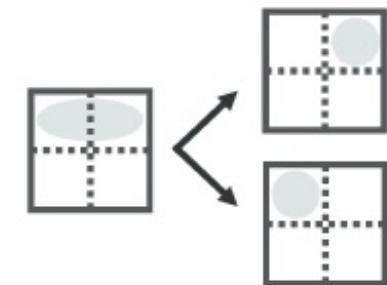
Range before Range after

Speciation within-area subset



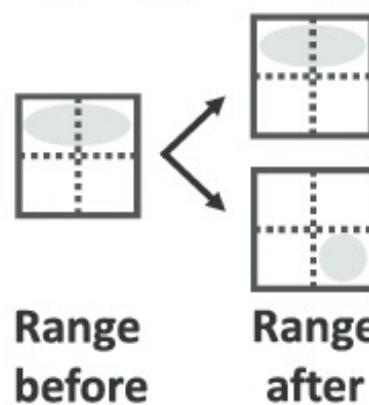
Range before Range after

Vicariance



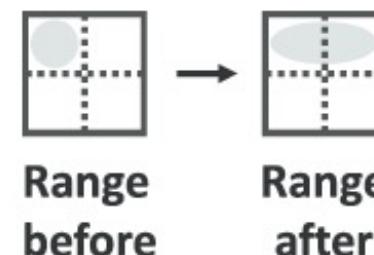
Range before Range after

Founder Event



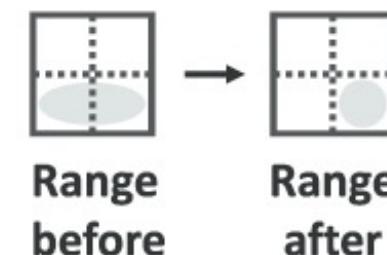
Range before Range after

Range Expansion



Range before Range after

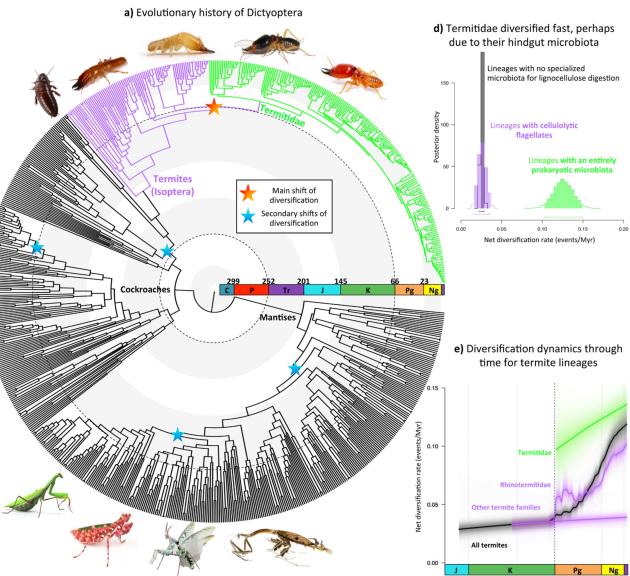
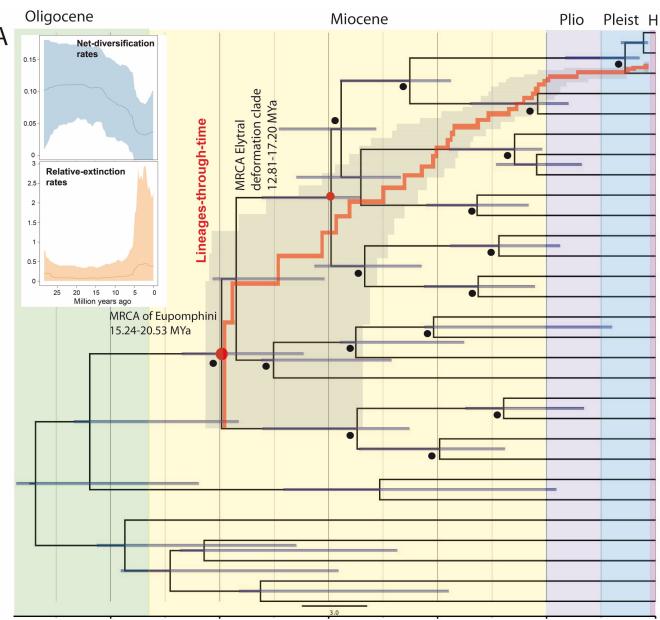
Range Contraction



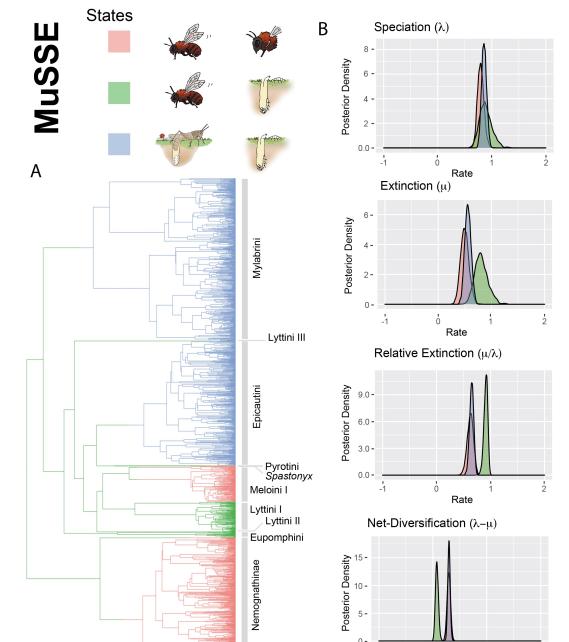
Range before Range after



López-Estrada et al., 2019

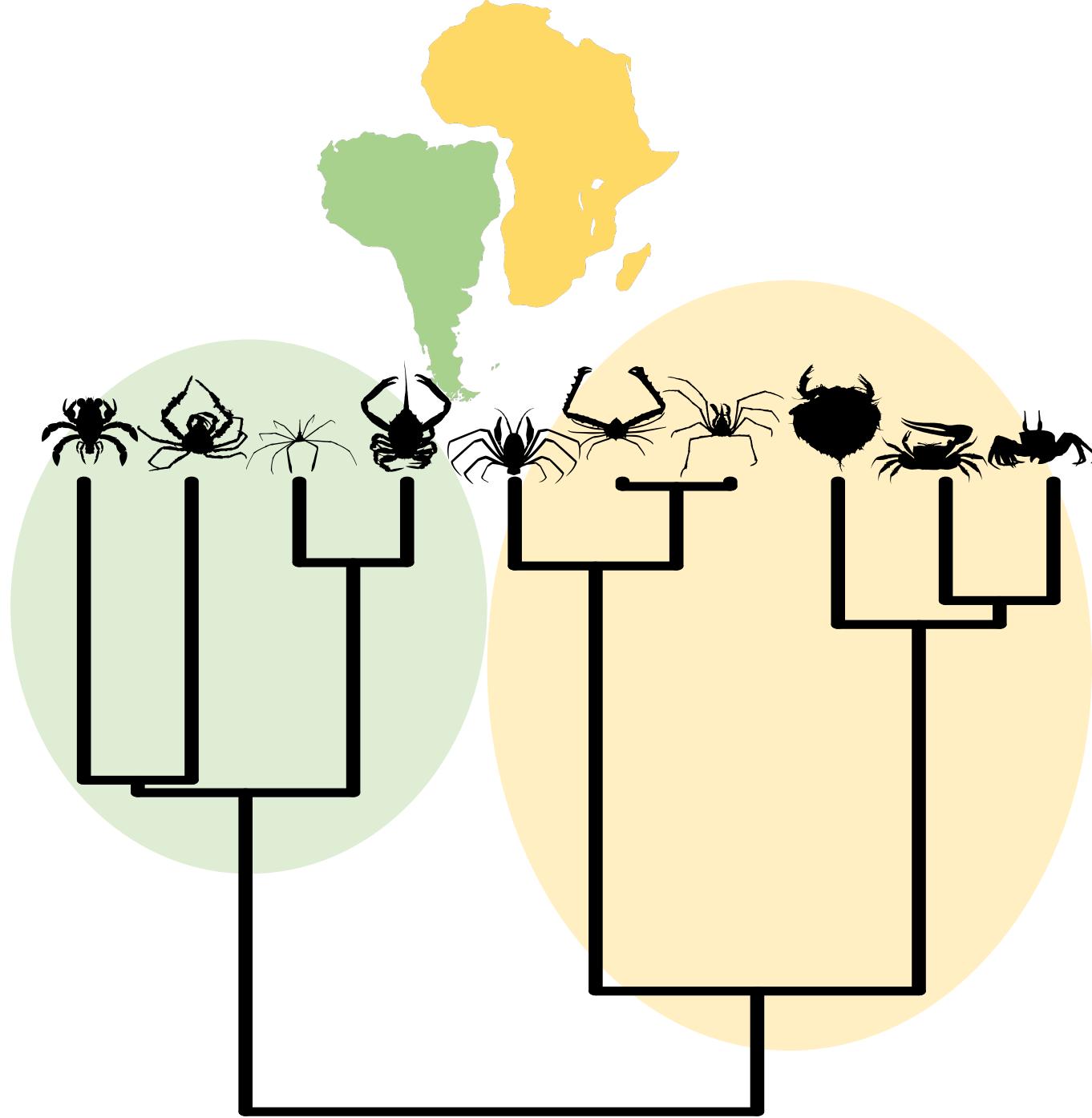


Legendre & Condamine, 2018



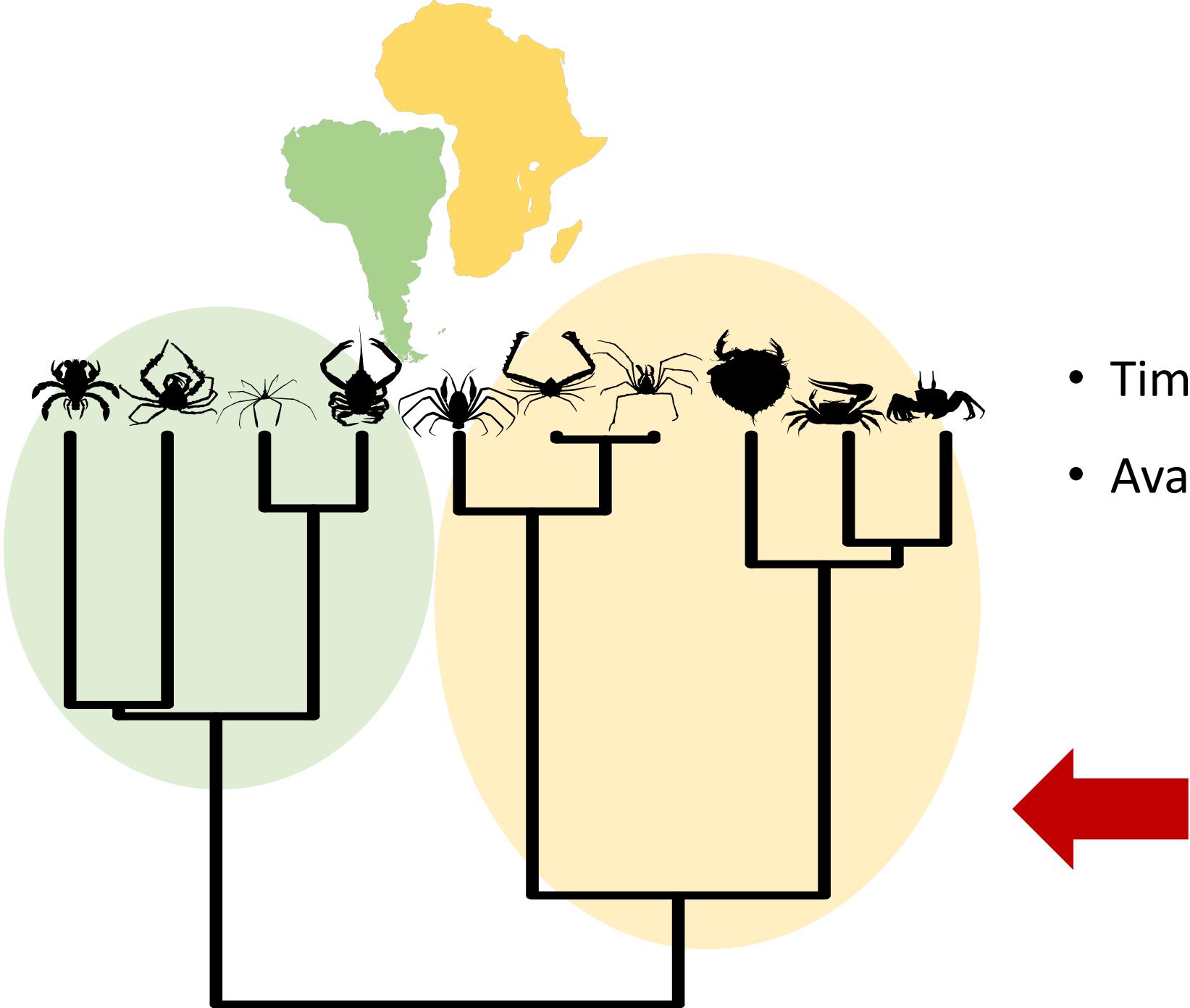
López-Estrada et al., 2022

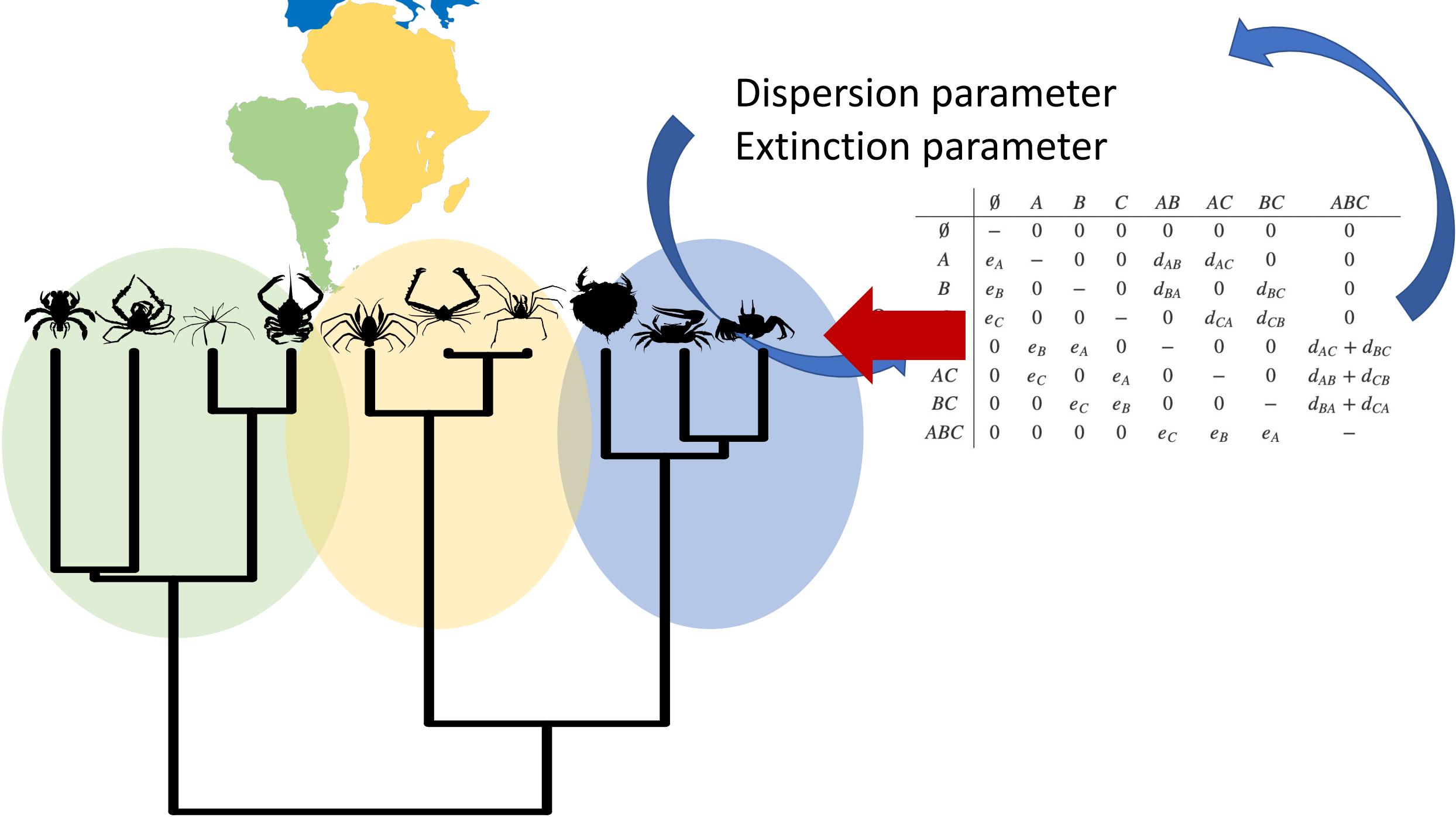
DEC Model Ree et al.



DEC Model

- Timing of lineages divergences
- Availability of connections





Areas:

A B
 C

	\emptyset	A	B	C	AB	AC	BC	ABC
\emptyset	-	0	0	0	0	0	0	0
A	e_A	-	0	0	d_{AB}	d_{AC}	0	0
B	e_B	0	-	0	d_{BA}	0	d_{BC}	0
C	e_C	0	0	-	0	d_{CA}	d_{CB}	0
AB	0	e_B	e_A	0	-	0	0	$d_{AC} + d_{BC}$
AC	0	e_C	0	e_A	0	-	0	$d_{AB} + d_{CB}$
BC	0	0	e_C	e_B	0	0	-	$d_{BA} + d_{CA}$
ABC	0	0	0	0	e_C	e_B	e_A	-

The number of possible states s is 2^r , where r is the number of regions .

$$2^4 = 16$$

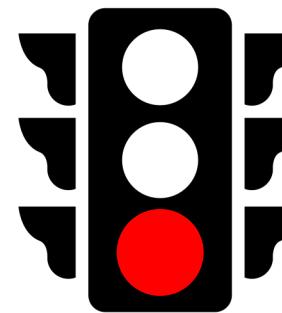
$$2^5 = 32$$

$$2^6 = 64$$

$$2^7 = 128$$

$$2^8 = 256$$

$$2^9 = 512$$



Anagenesis



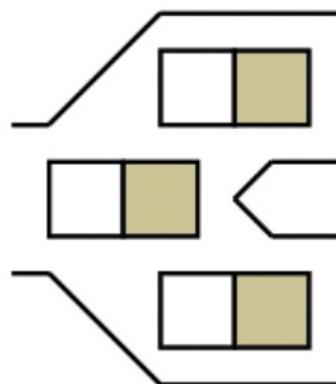
a. Dispersal



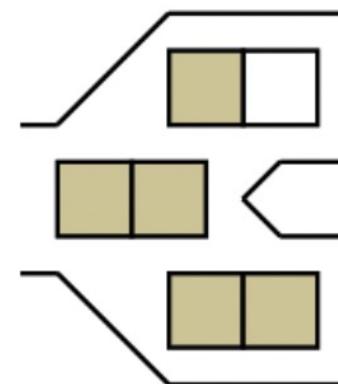
b. Extirpation

Time →
Time

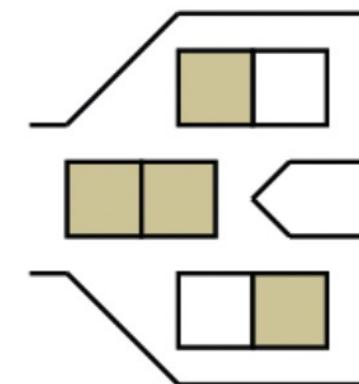
Cladogenesis



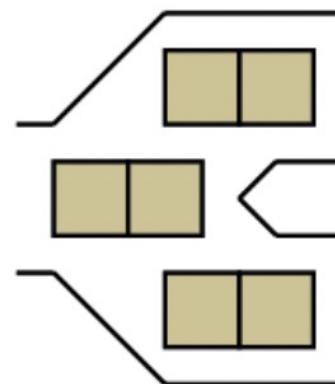
c. Narrow sympatry



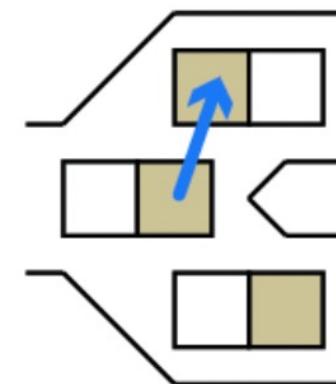
d. Subset sympatry



e. Allopatry

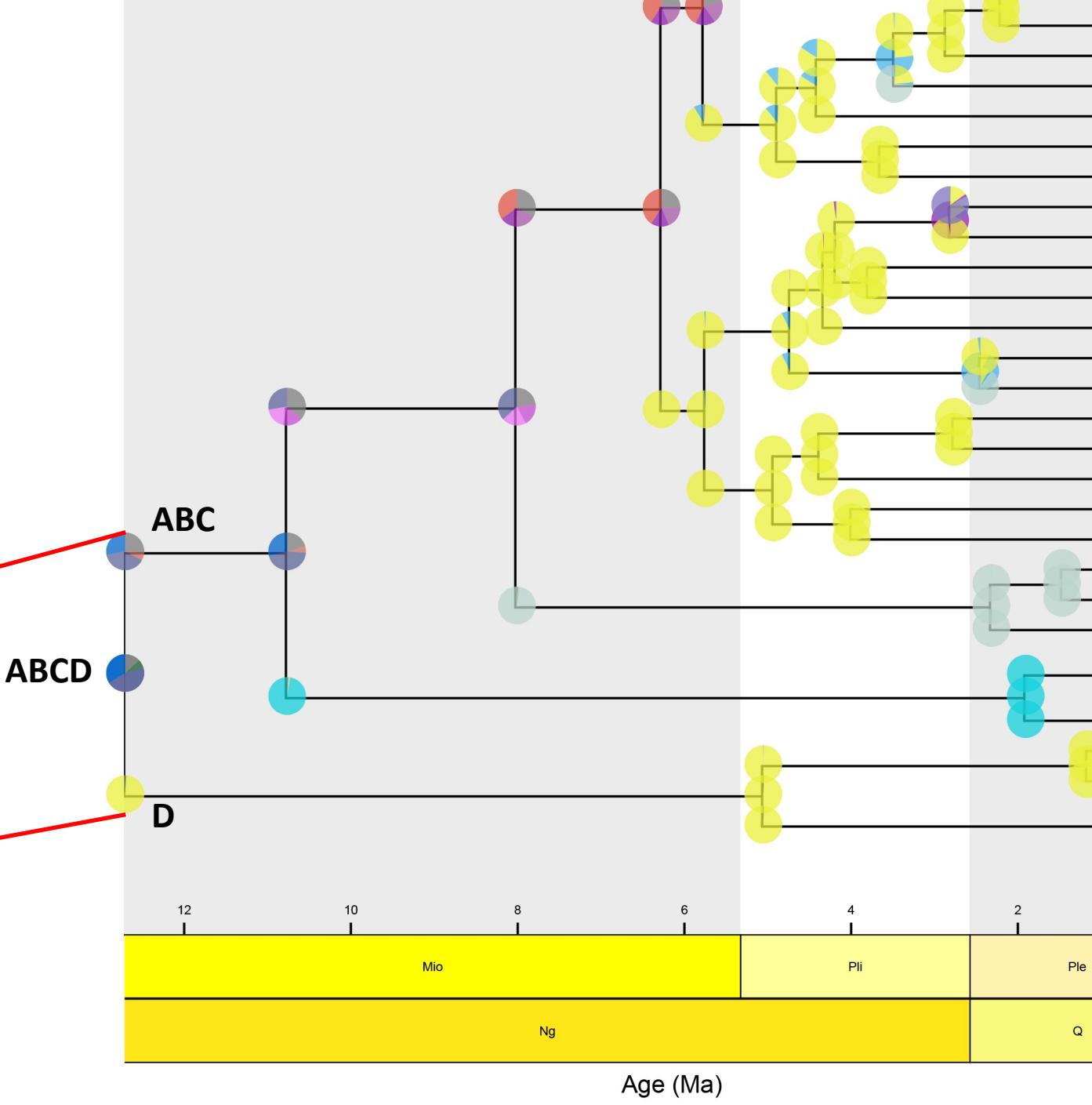
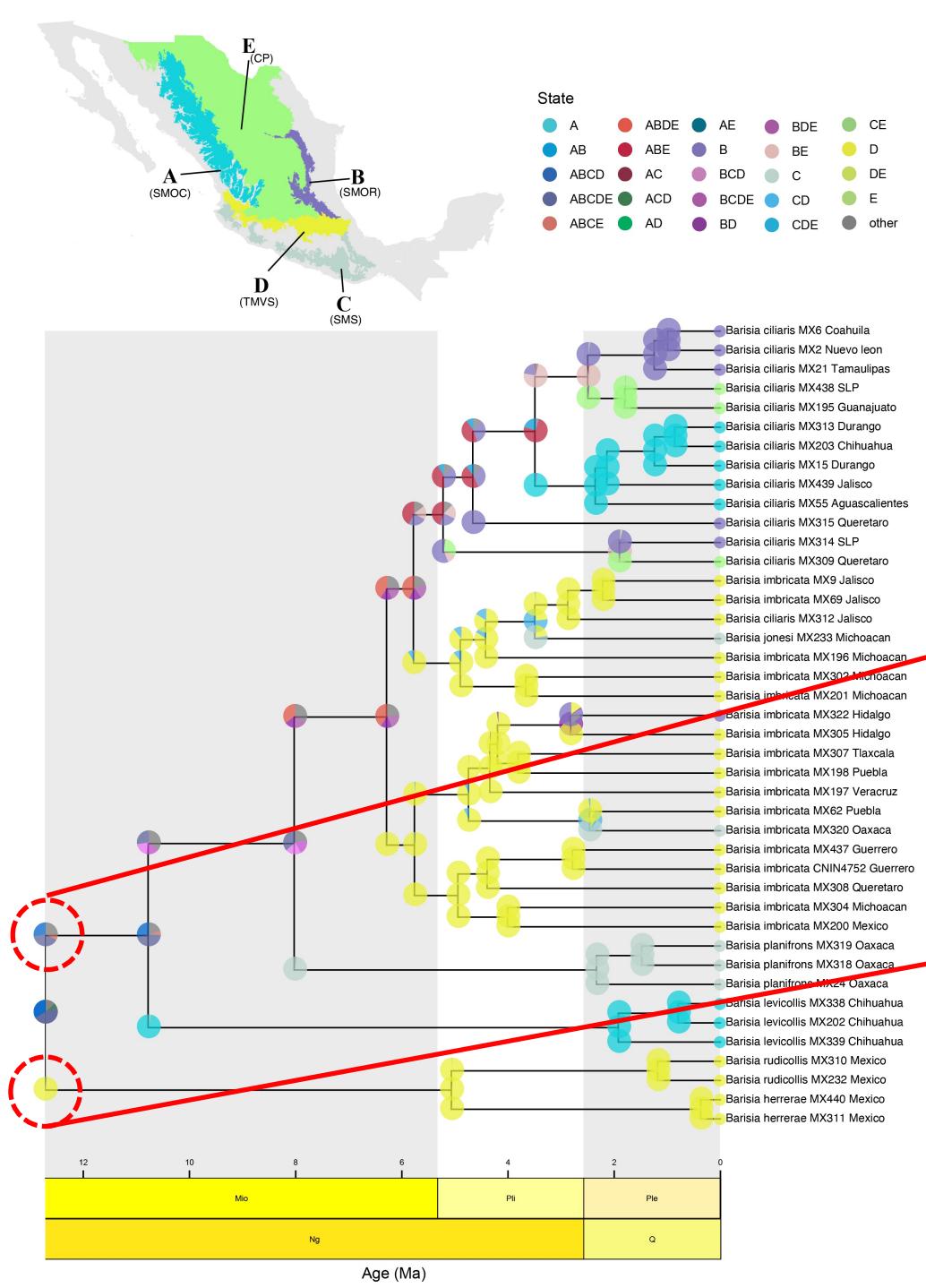


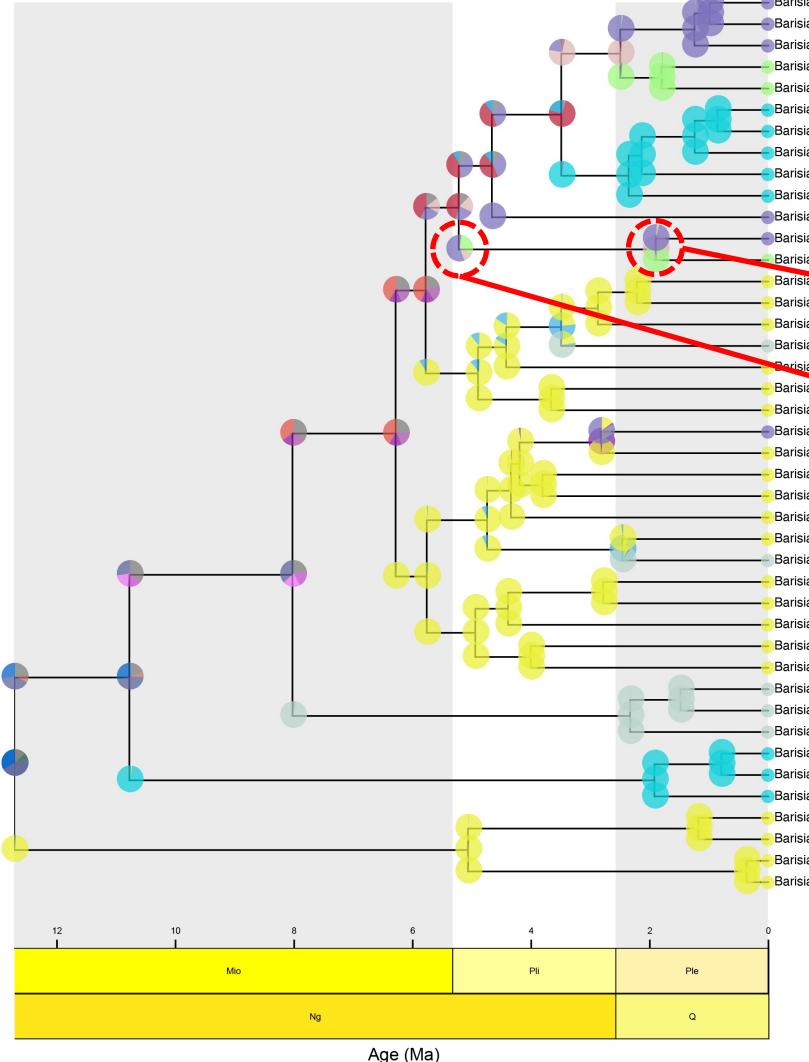
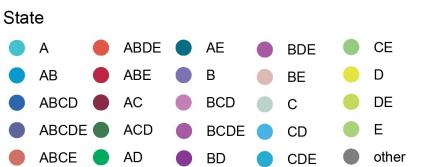
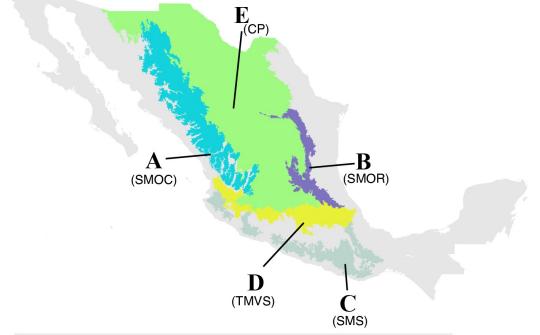
f. Full sympatry



g. Jump dispersal

Zaldivar-Riverón et al., In prep





Barisia ciliaris MX6 Coahuila
 Barisia ciliaris MX2 Nuevo leon
 Barisia ciliaris MX21 Tamaulipas
 Barisia ciliaris MX438 SLP
 Barisia ciliaris MX195 Guanajuato
 Barisia ciliaris MX313 Durango
 Barisia ciliaris MX203 Chihuahua
 Barisia ciliaris MX15 Durango
 Barisia ciliaris MX439 Jalisco
 Barisia ciliaris MX55 Aguascalientes
 Barisia ciliaris MX315 Queretaro
 Barisia ciliaris MX314 SLP
 Barisia ciliaris MX309 Queretaro
 Barisia imbricata MX9 Jalisco
 Barisia imbricata MX69 Jalisco
 Barisia ciliaris MX12 Jalisco
 Barisia jonesi MX23 Michoacan
 Barisia imbricata MX196 Michoacan
 Barisia imbricata MX302 Michoacan
 Barisia imbricata MX201 Michoacan
 Barisia imbricata MX322 Hidalgo
 Barisia imbricata MX305 Hidalgo
 Barisia imbricata MX307 Tlaxcala
 Barisia imbricata MX198 Puebla
 Barisia imbricata MX197 Veracruz
 Barisia imbricata MX62 Puebla
 Barisia imbricata MX320 Oaxaca
 Barisia imbricata MX437 Guerrero
 Barisia imbricata CNIN4752 Guerrero
 Barisia imbricata MX308 Queretaro
 Barisia imbricata MX304 Michoacan
 Barisia imbricata MX200 Mexico
 Barisia planifrons MX319 Oaxaca
 Barisia planifrons MX318 Oaxaca
 Barisia planifrons MX24 Oaxaca
 Barisia levicollis MX338 Chihuahua
 Barisia levicollis MX202 Chihuahua
 Barisia levicollis MX339 Chihuahua
 Barisia rudicollis MX310 Mexico
 Barisia rudicollis MX232 Mexico
 Barisia herrerae MX440 Mexico
 Barisia herrerae MX311 Mexico

