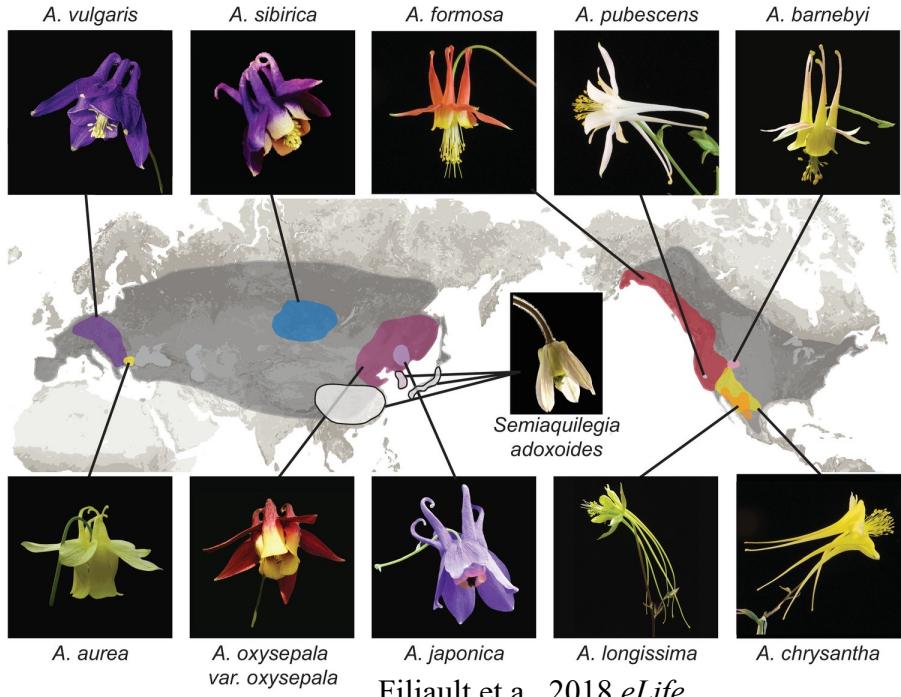
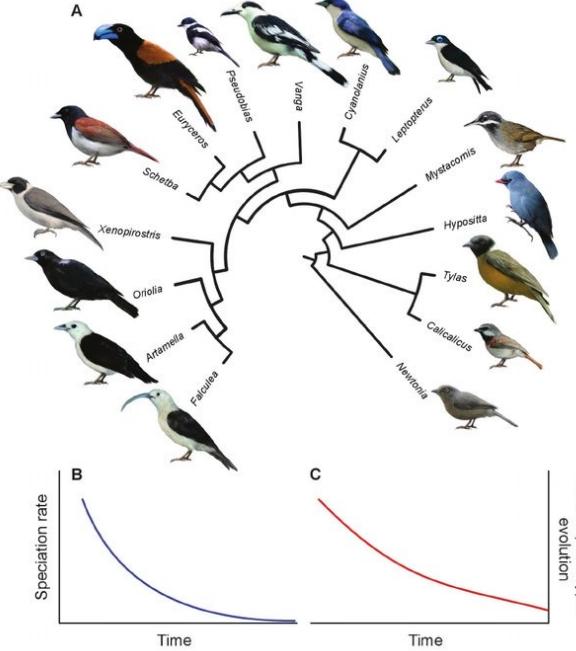
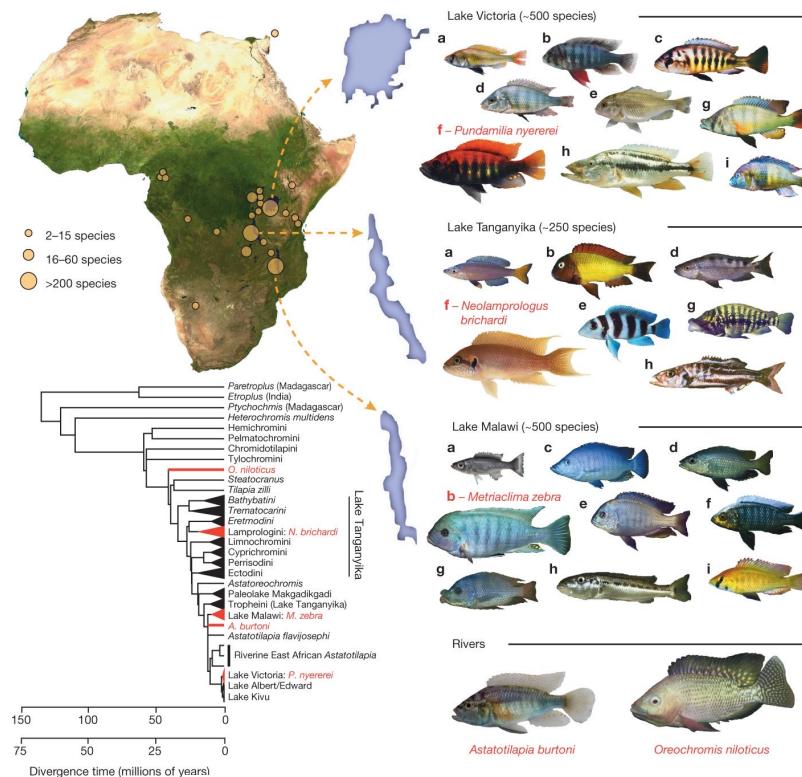


# Introducción a modelos State-Speciation-Extinción (SSE)

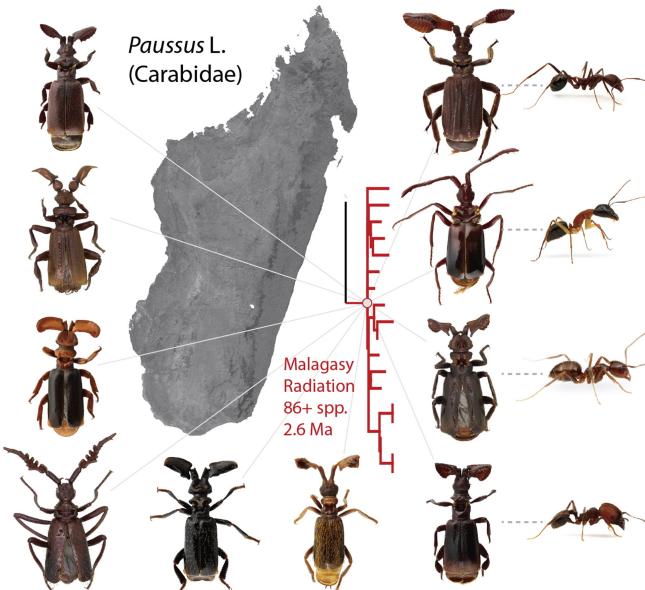
Moen & Morlon, 2014 *PLoS Biology*



Filiault et al., 2018 *eLife*

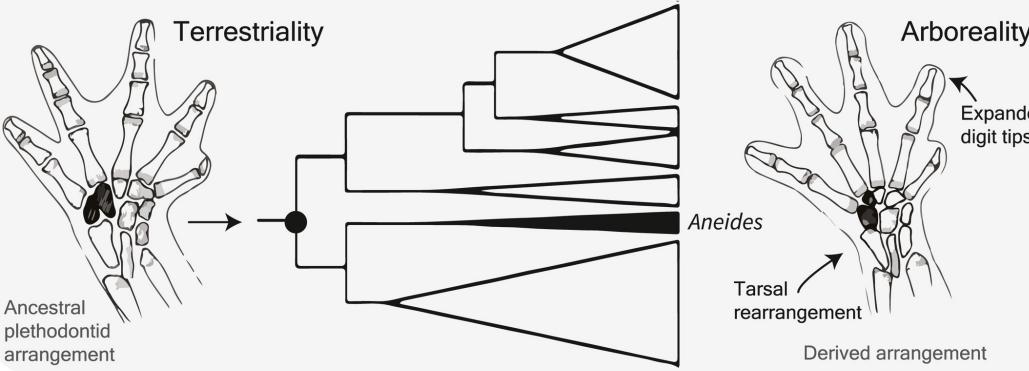


Moore & Robertson, 2014 *Current Biology*

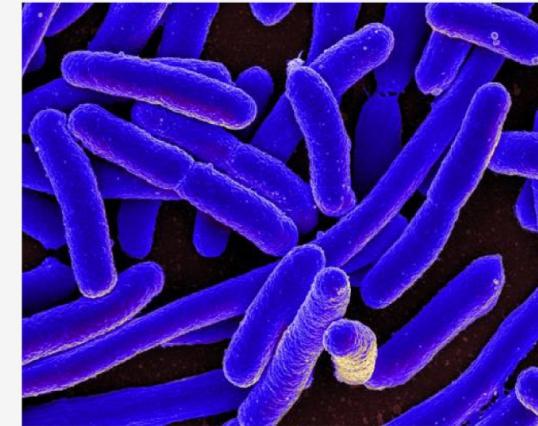
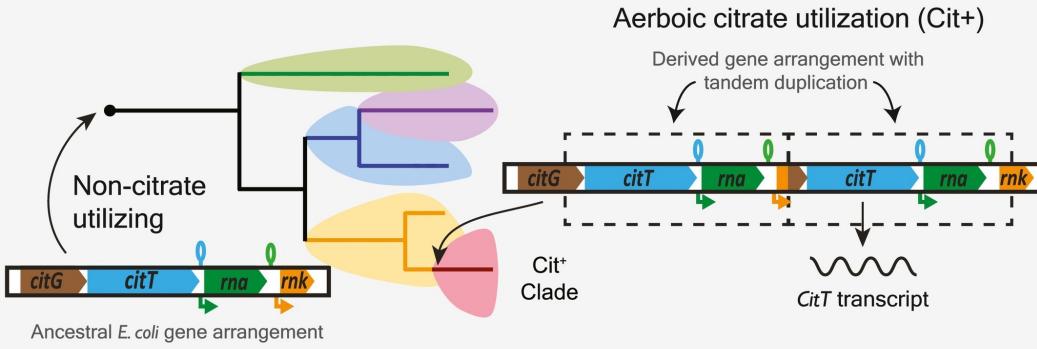


Brawand et al., 2014 *Nature*

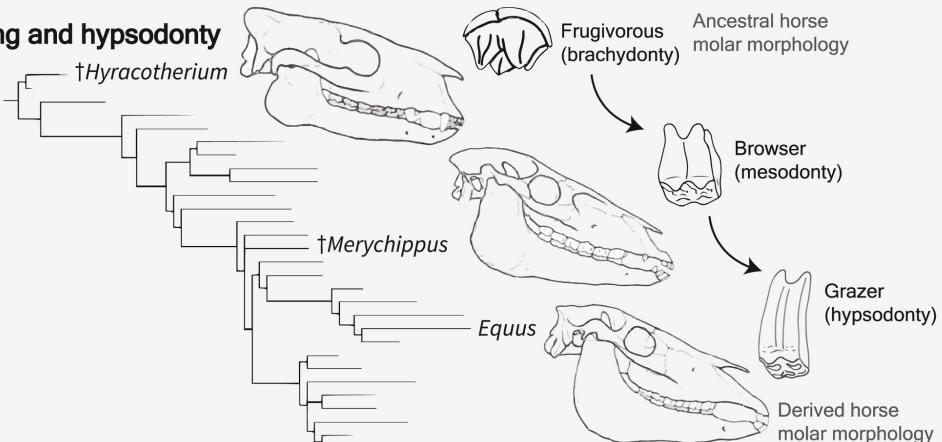
### (A) Arboreality and digit modification

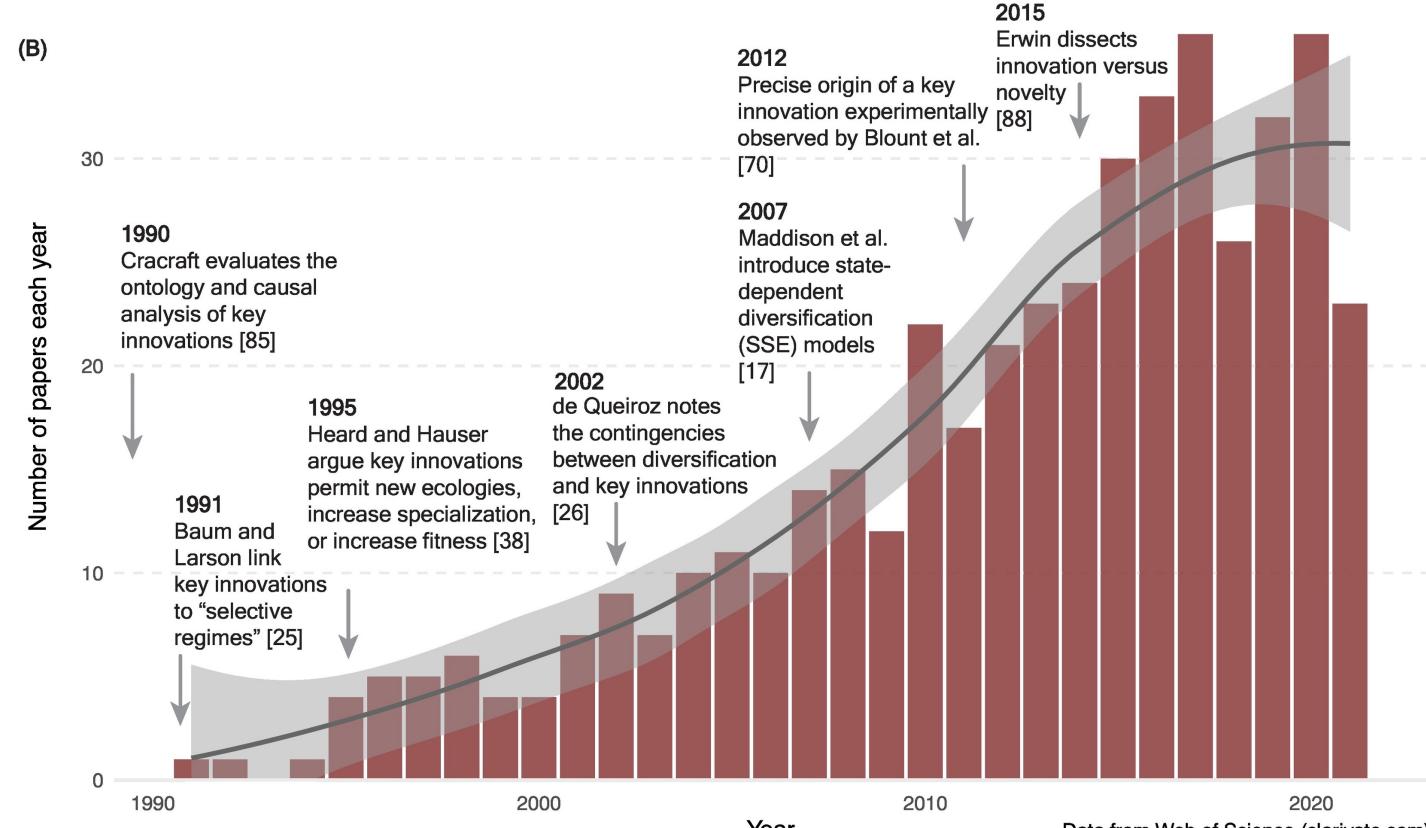
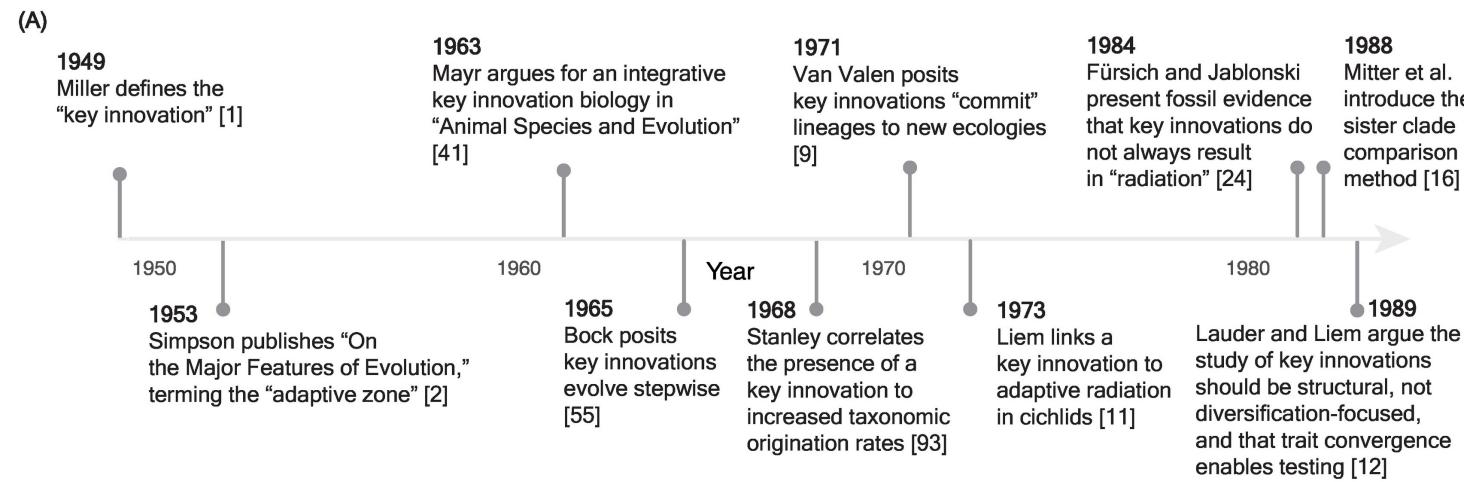


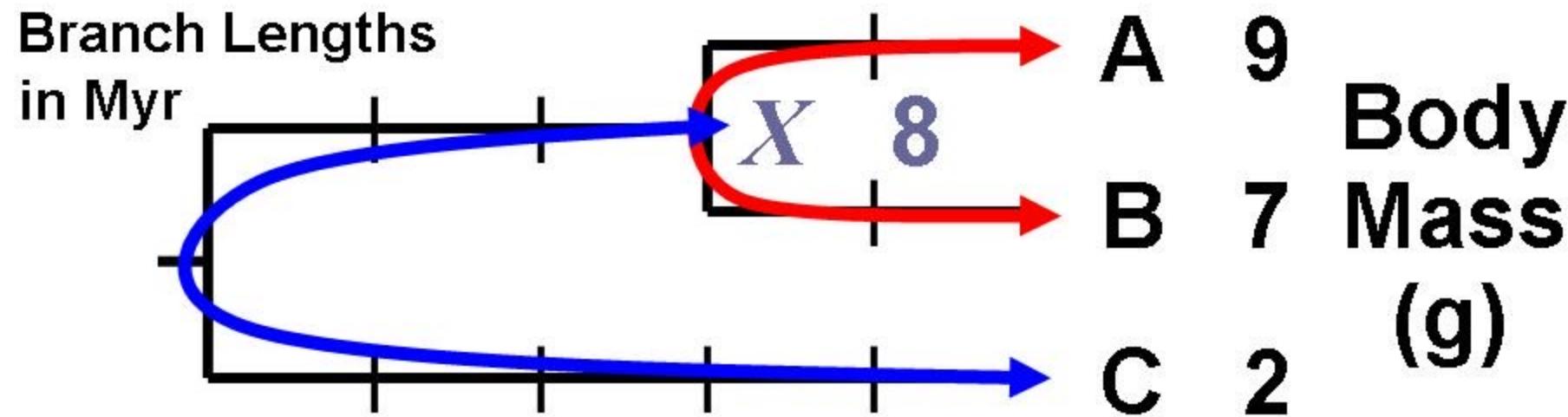
### (B) Citrate utilization and promoter capture



### (C) Grazing and hypsodonty







**Identify and Compute Independent Contrasts**

**Compute square roots of sums of (corrected) branch lengths = S.D.**

Contrast	Value	S.D.
----------	-------	------

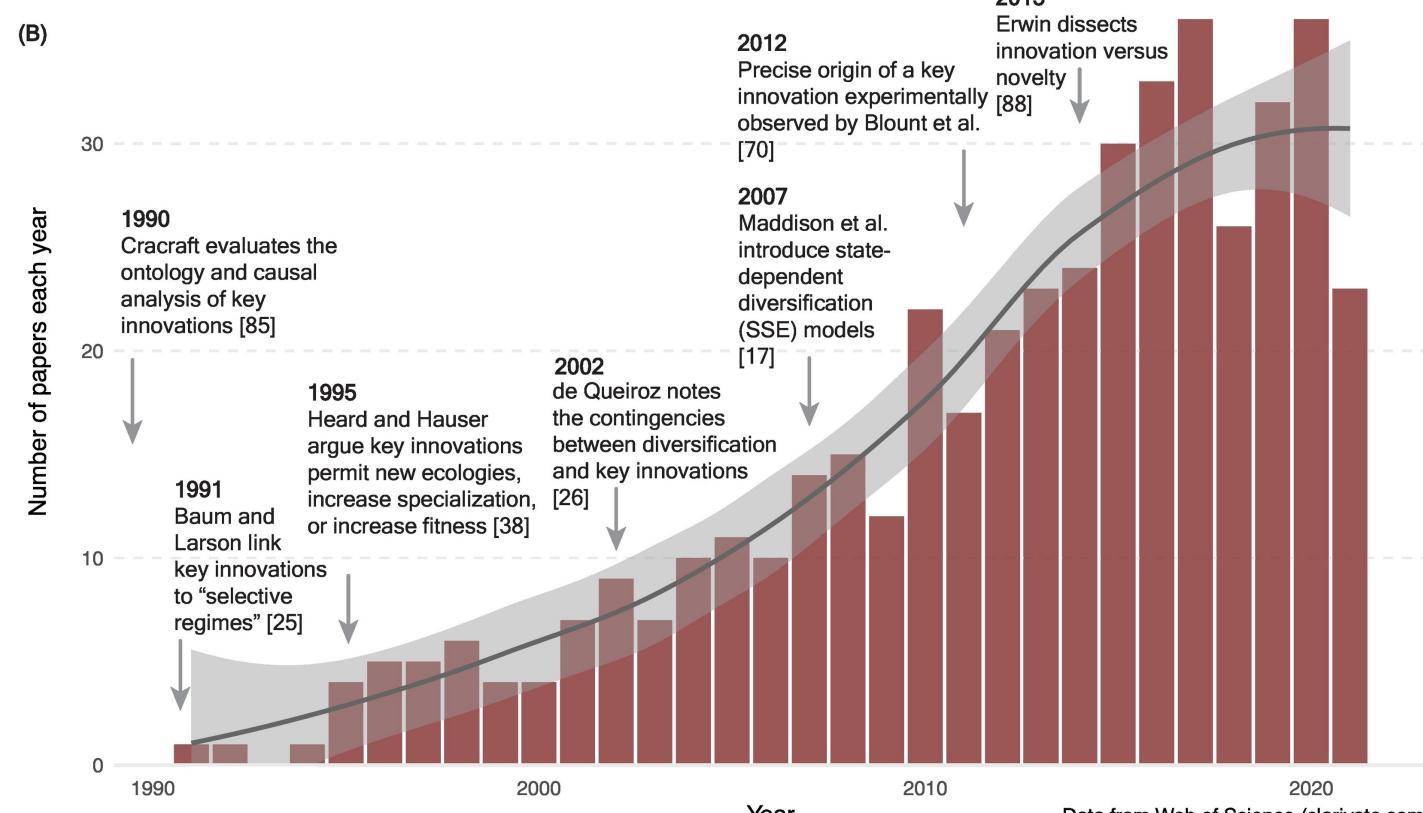
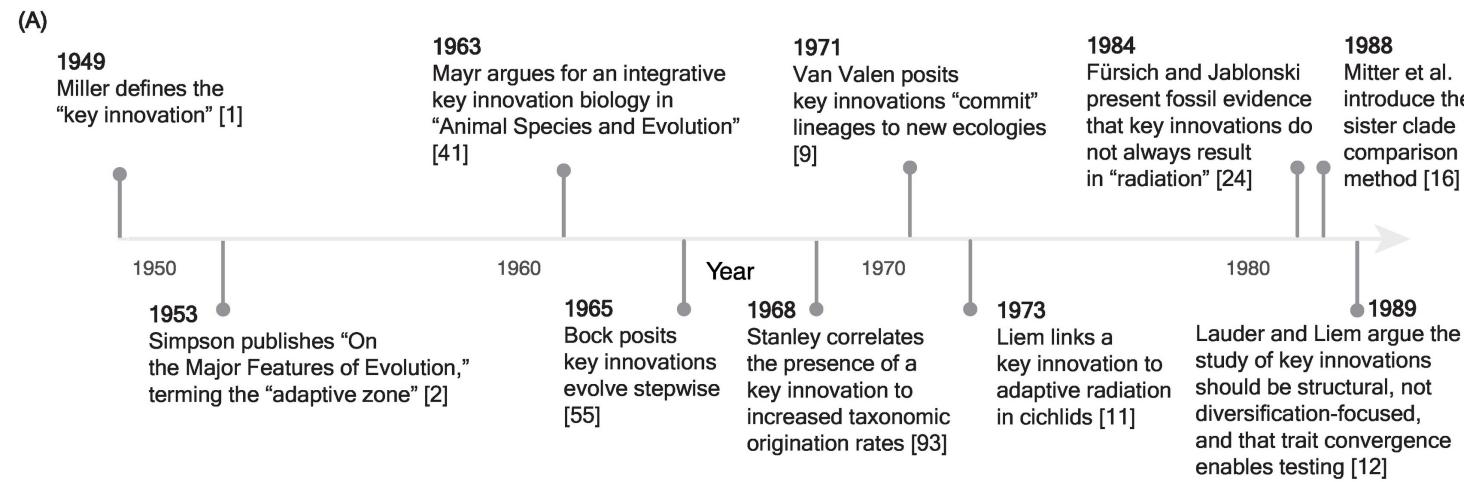
<b>A-B</b>	<b>2</b>	<b>2</b>
------------	----------	----------

<b>X-C</b>	<b>6</b>	<b>3</b>
------------	----------	----------

**Standardized Contrast**

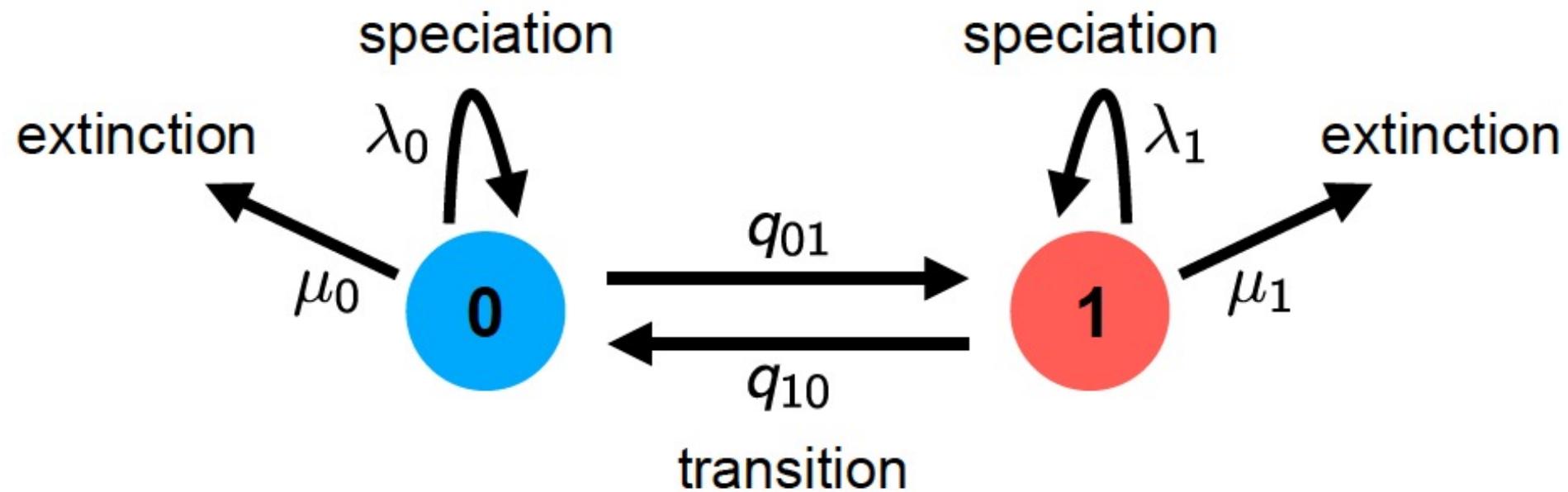
<b>1</b>
----------

<b>2</b>
----------



# BiSSE

Maddison et al., 2007;  
*Systematic Biology*



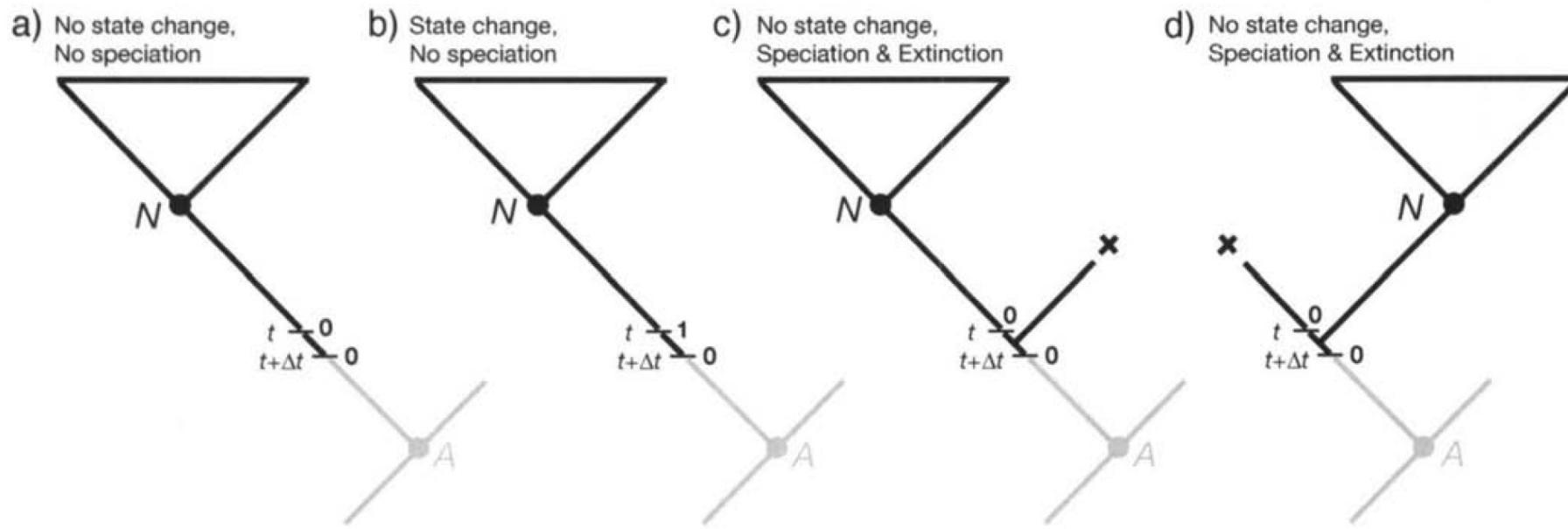
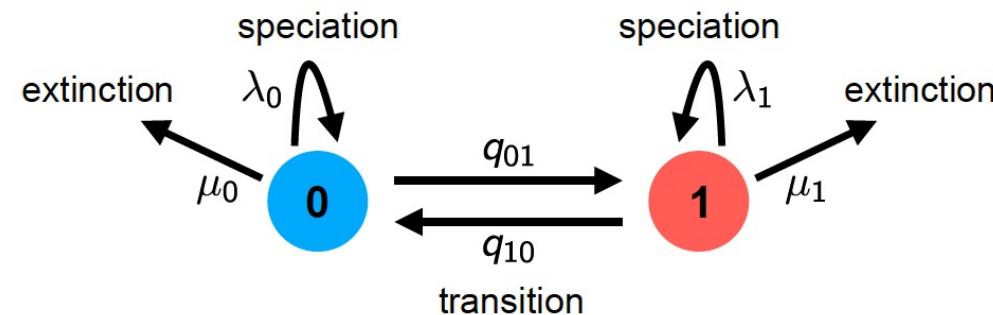
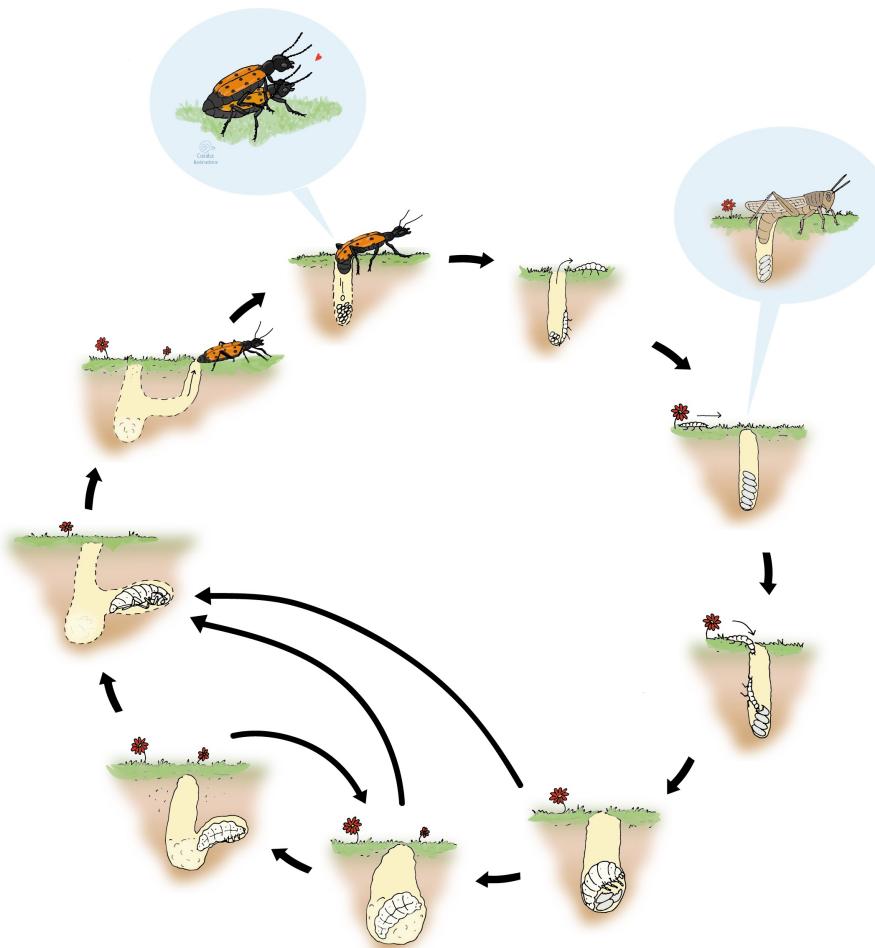
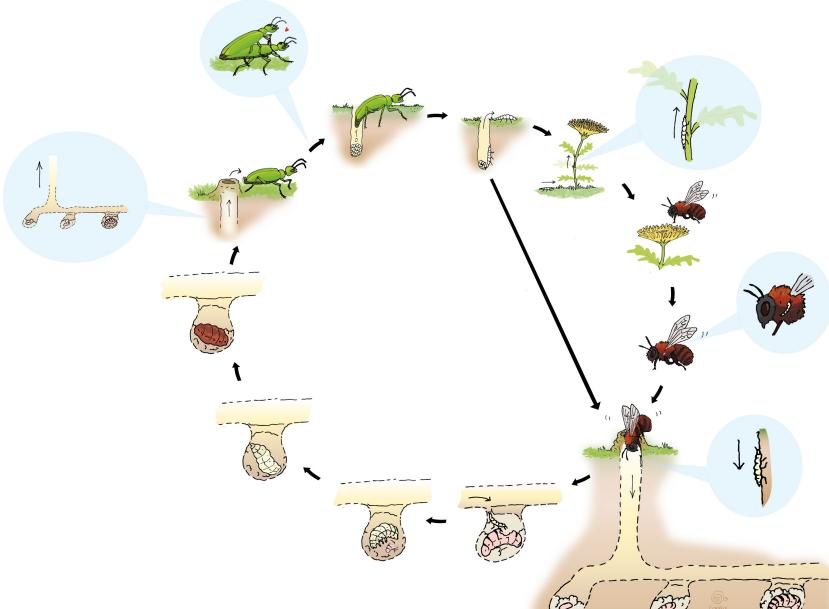
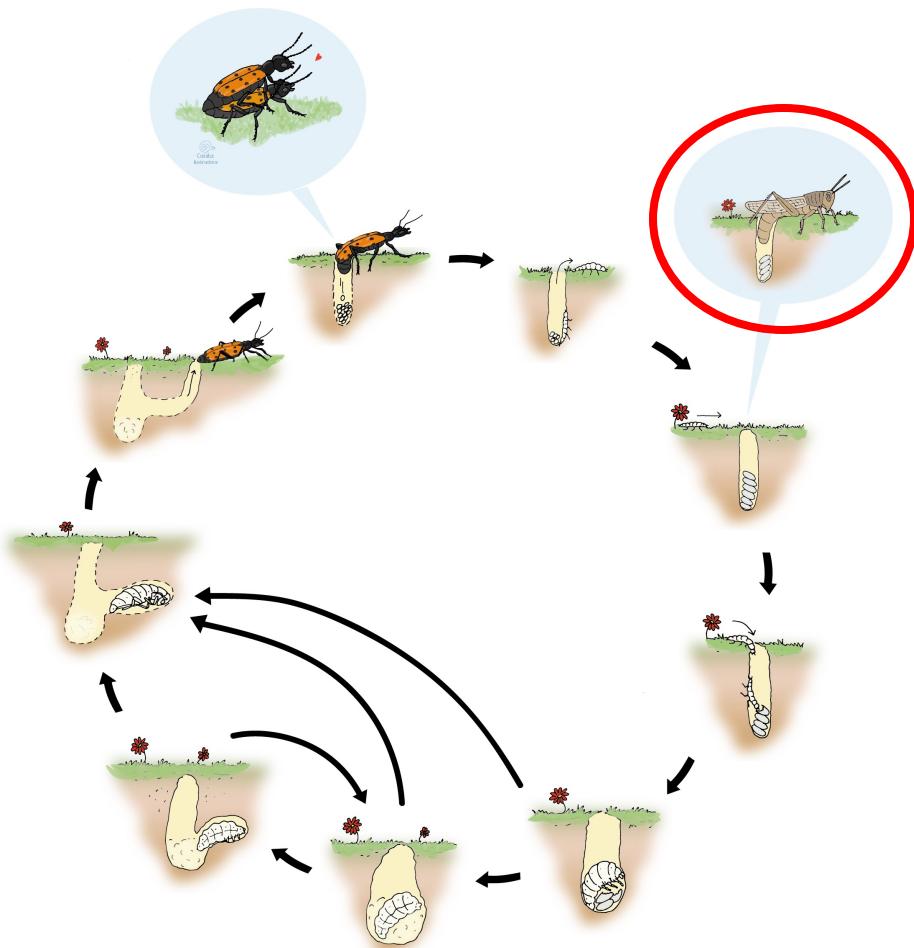
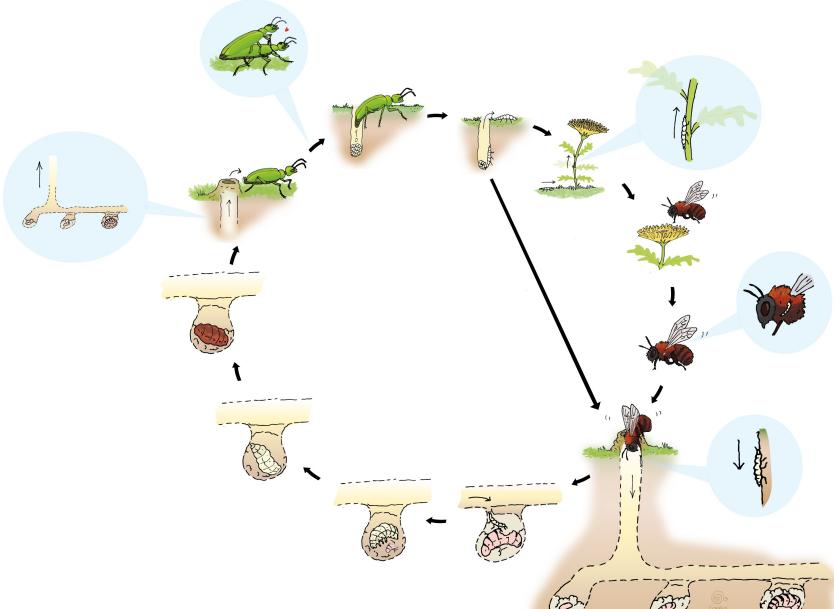
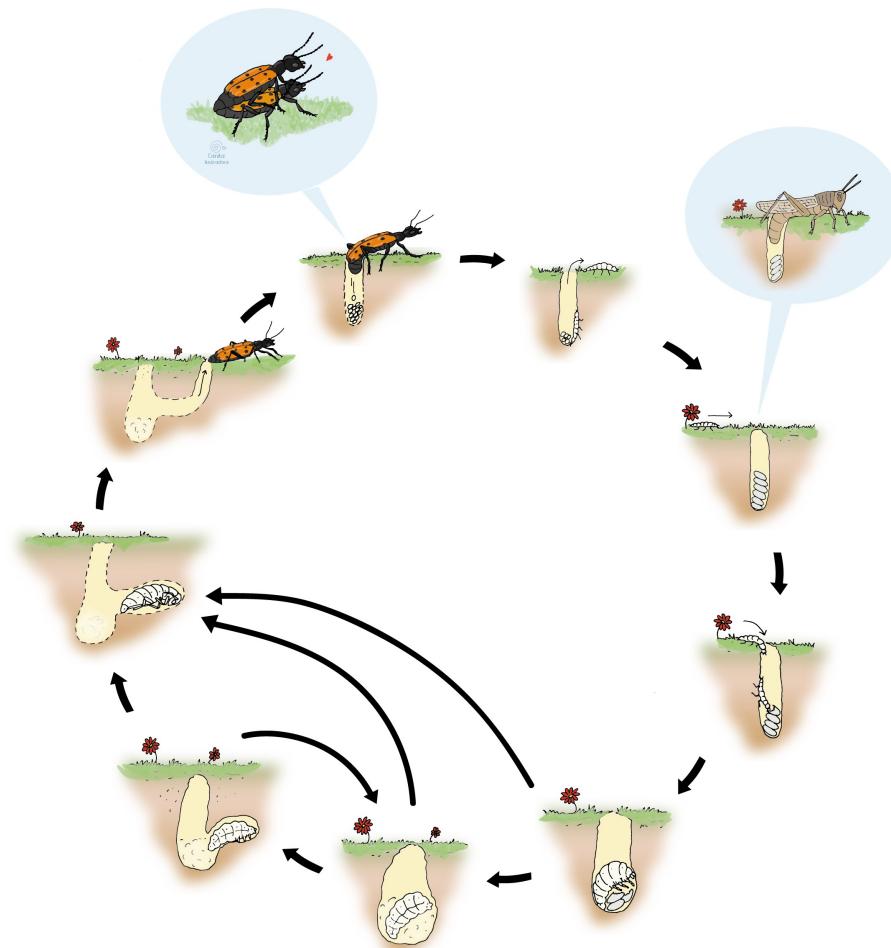
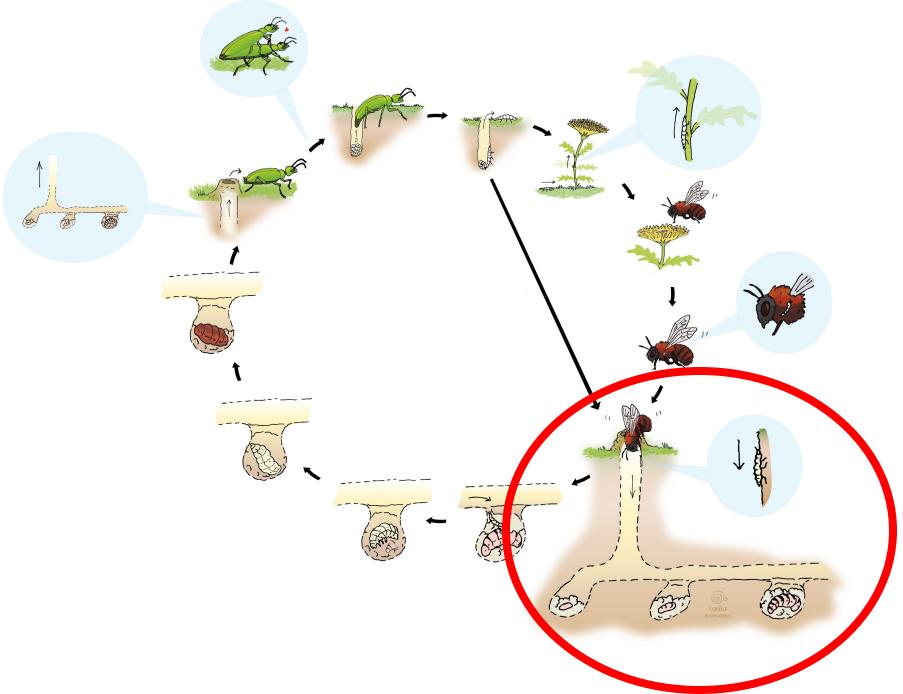


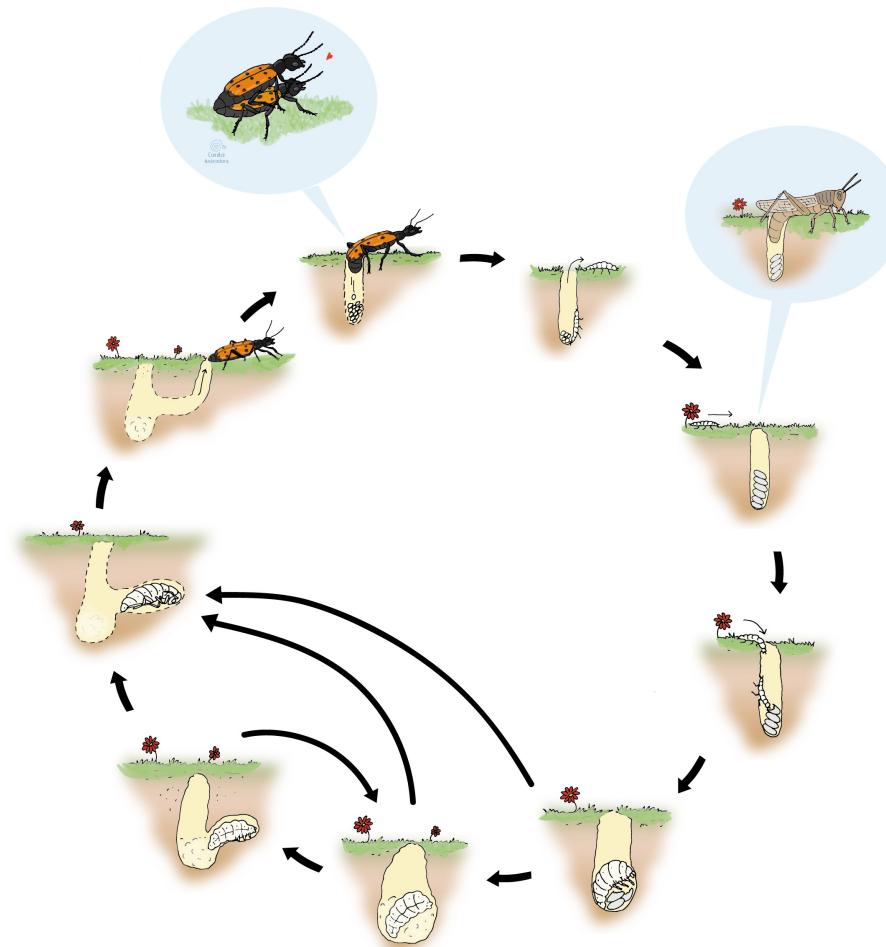
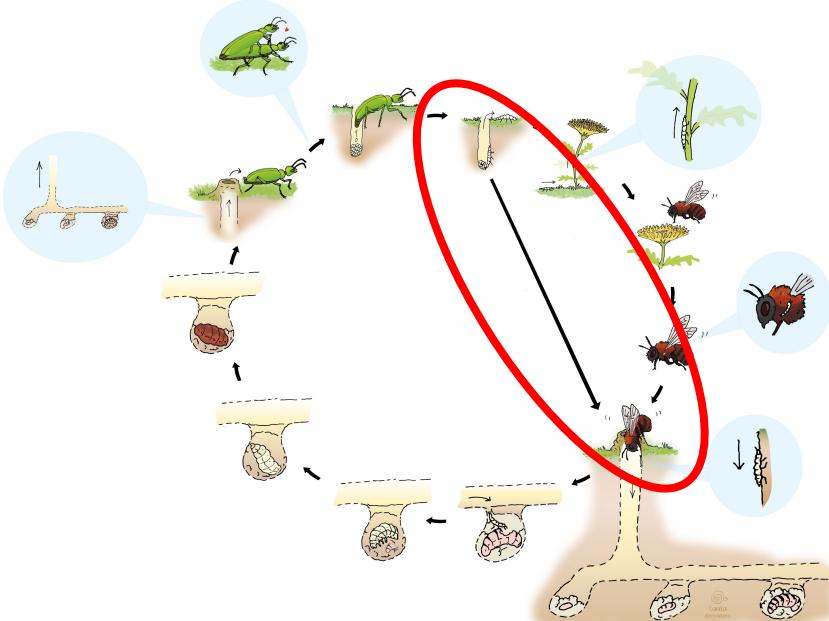
FIGURE 2. Alternative scenarios by which a lineage with state 0 at time  $t+\Delta t$  on the branch might yield clade descended from node N but no other living descendants.

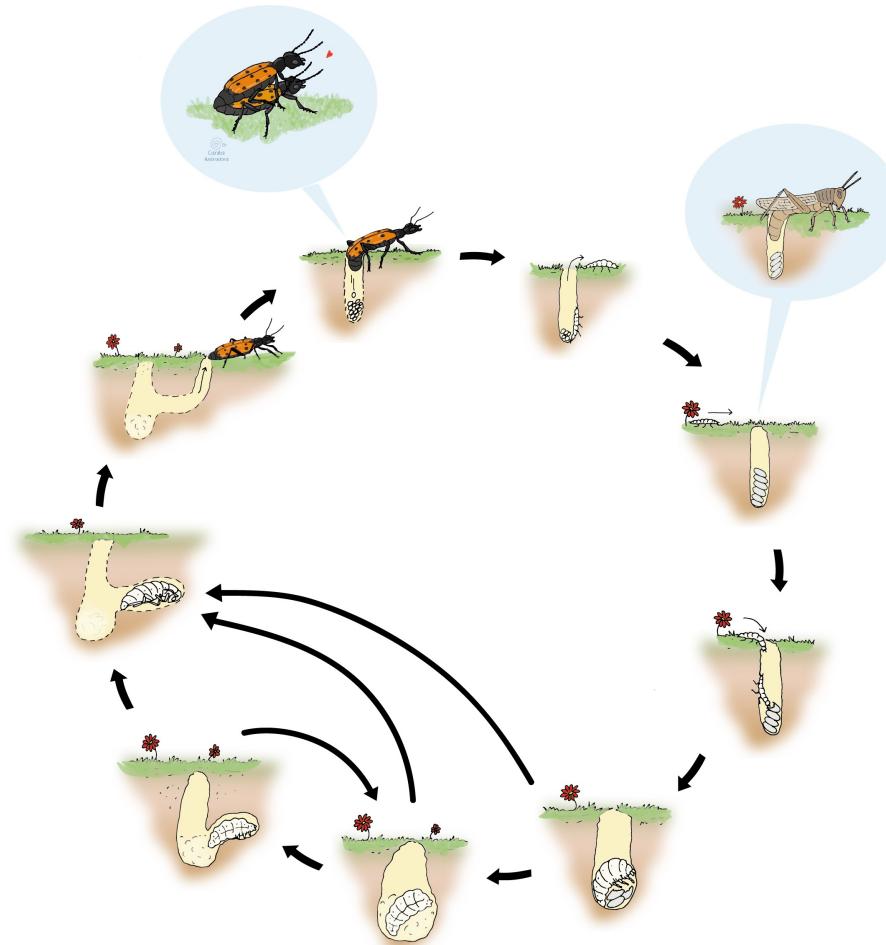
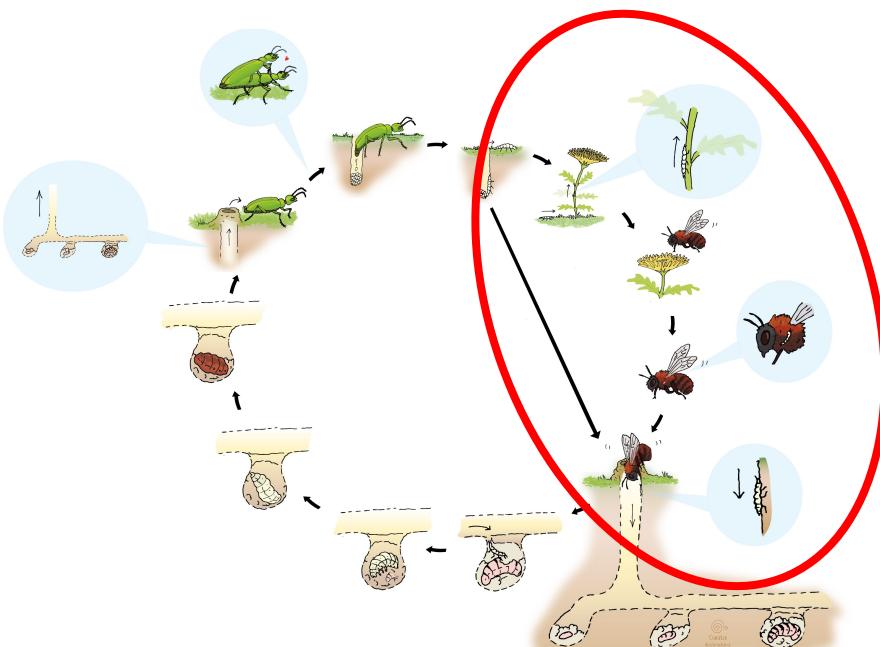


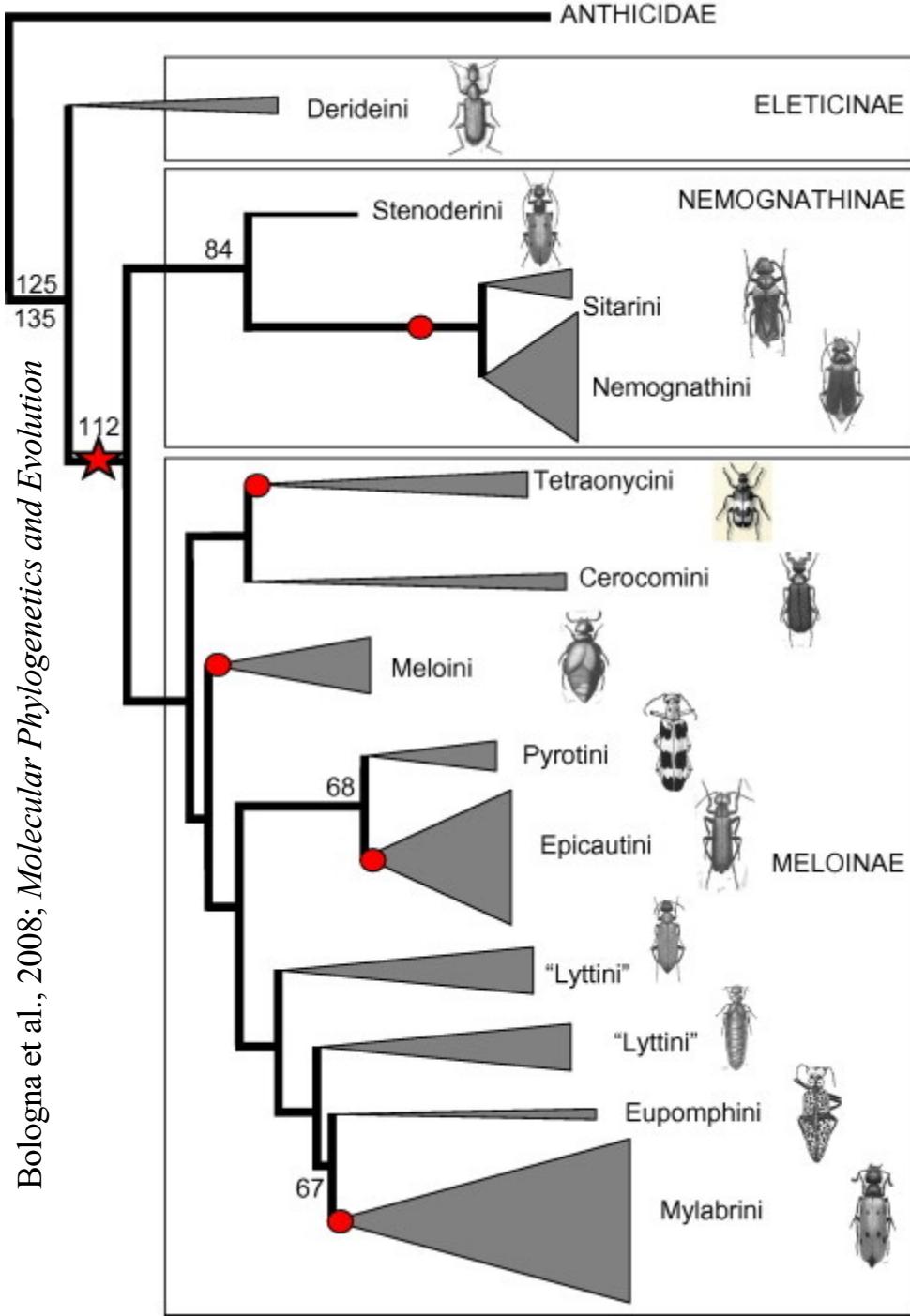


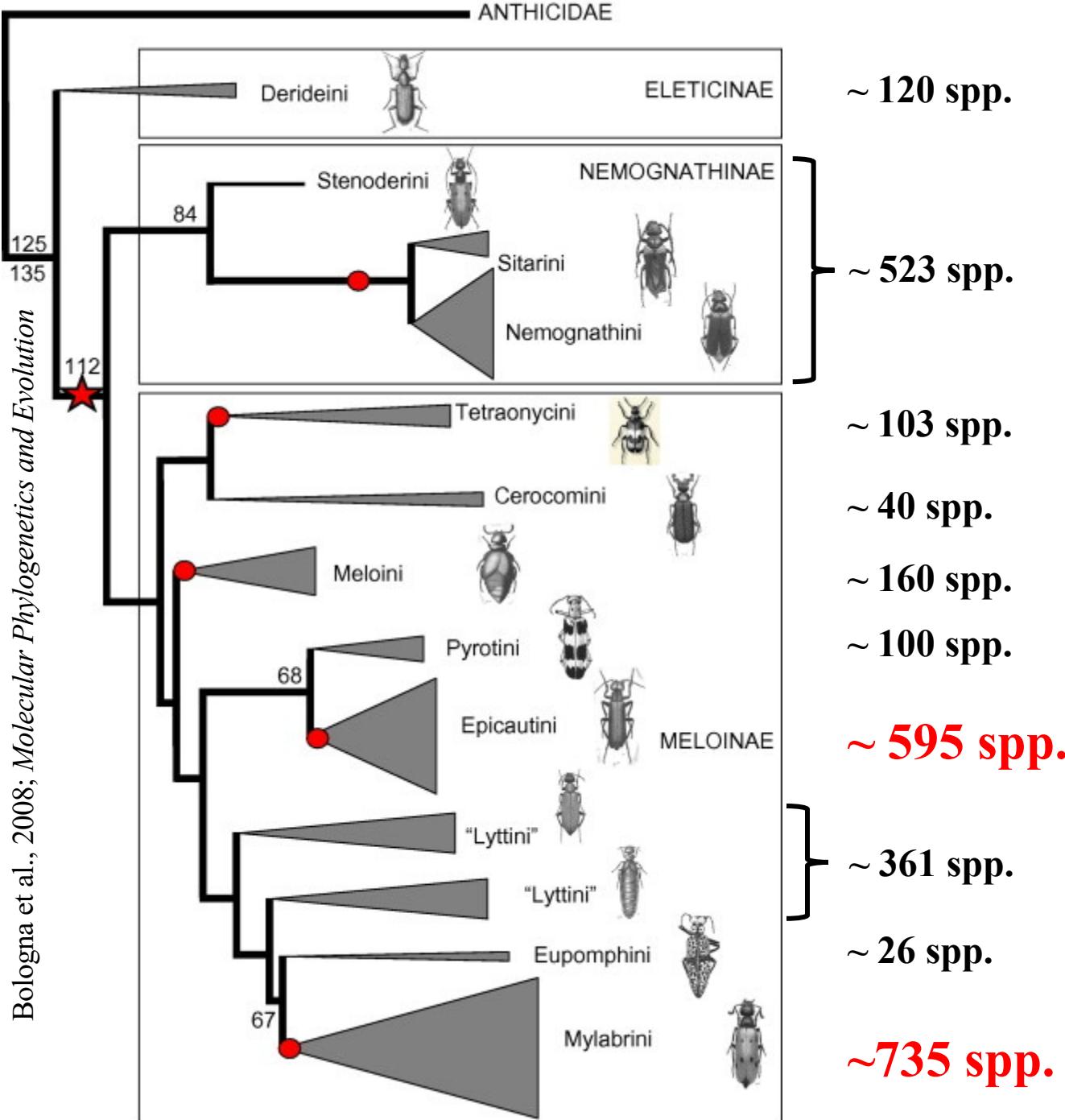












~ 120 spp.

~ 523 spp.

~ 103 spp.

~ 40 spp.

~ 160 spp.

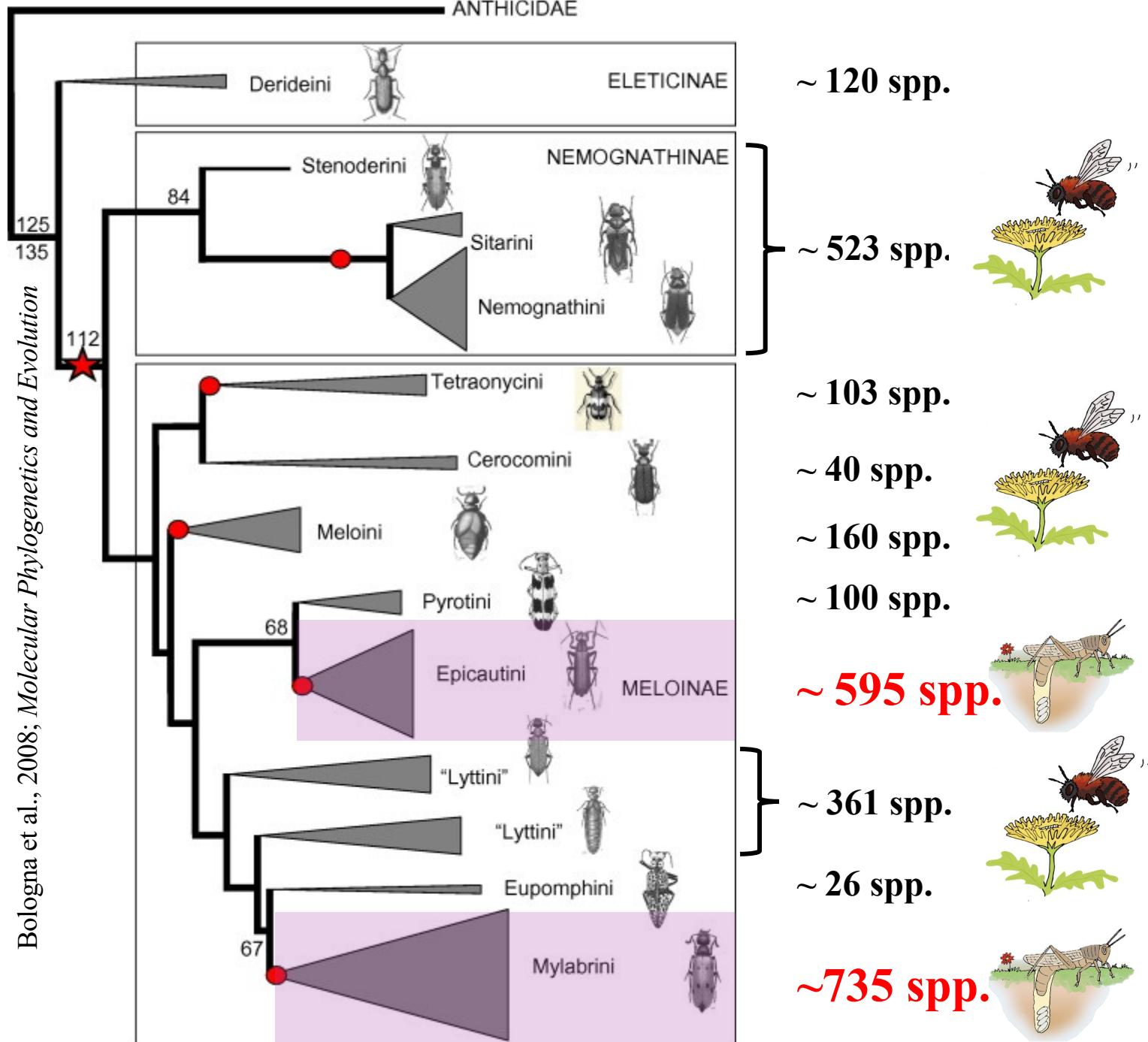
~ 100 spp.

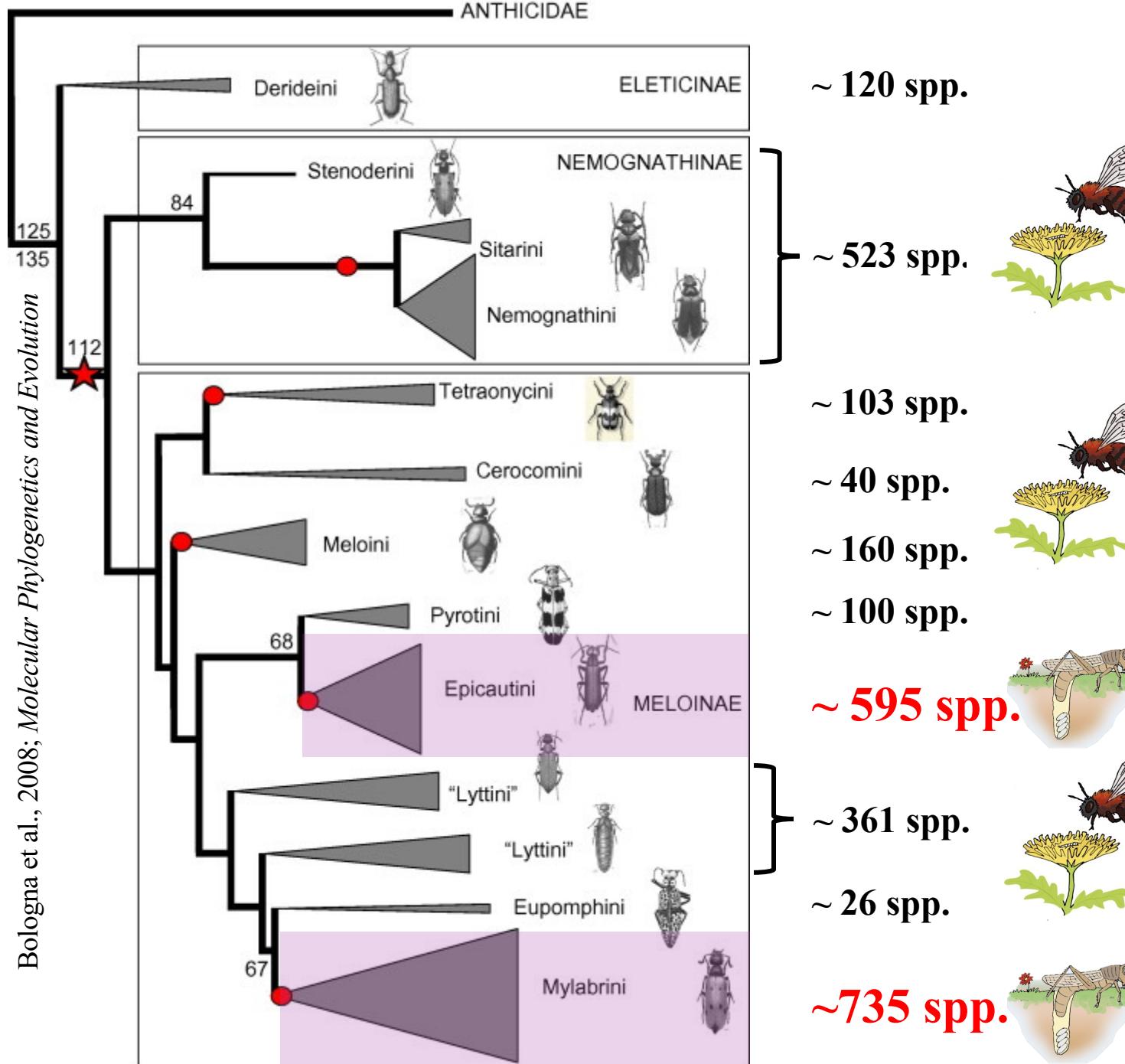
~ 595 spp.

~ 361 spp.

~ 26 spp.

~735 spp.





~ 120 spp.



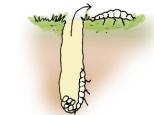
~ 523 spp.



~ 103 spp.



~ 40 spp.



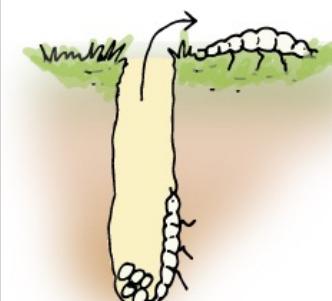
~ 160 spp.



~ 100 spp.



~ 595 spp.

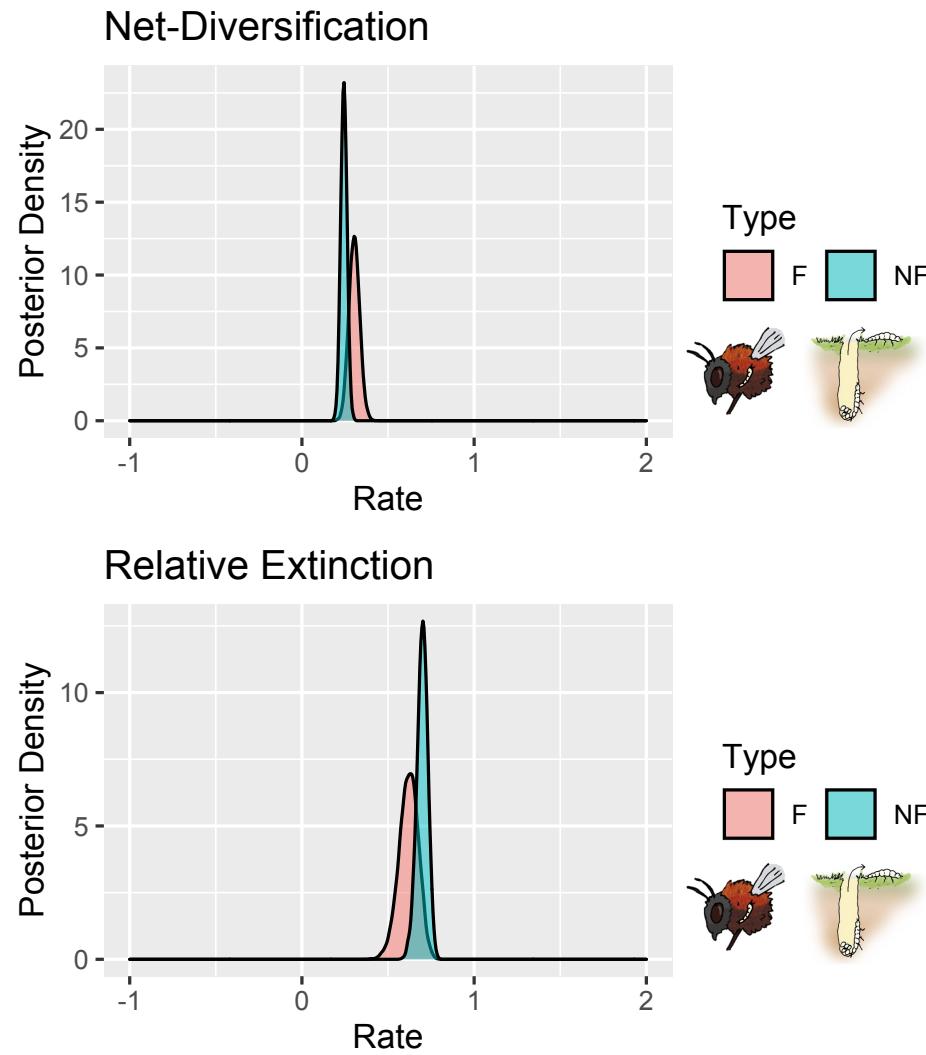
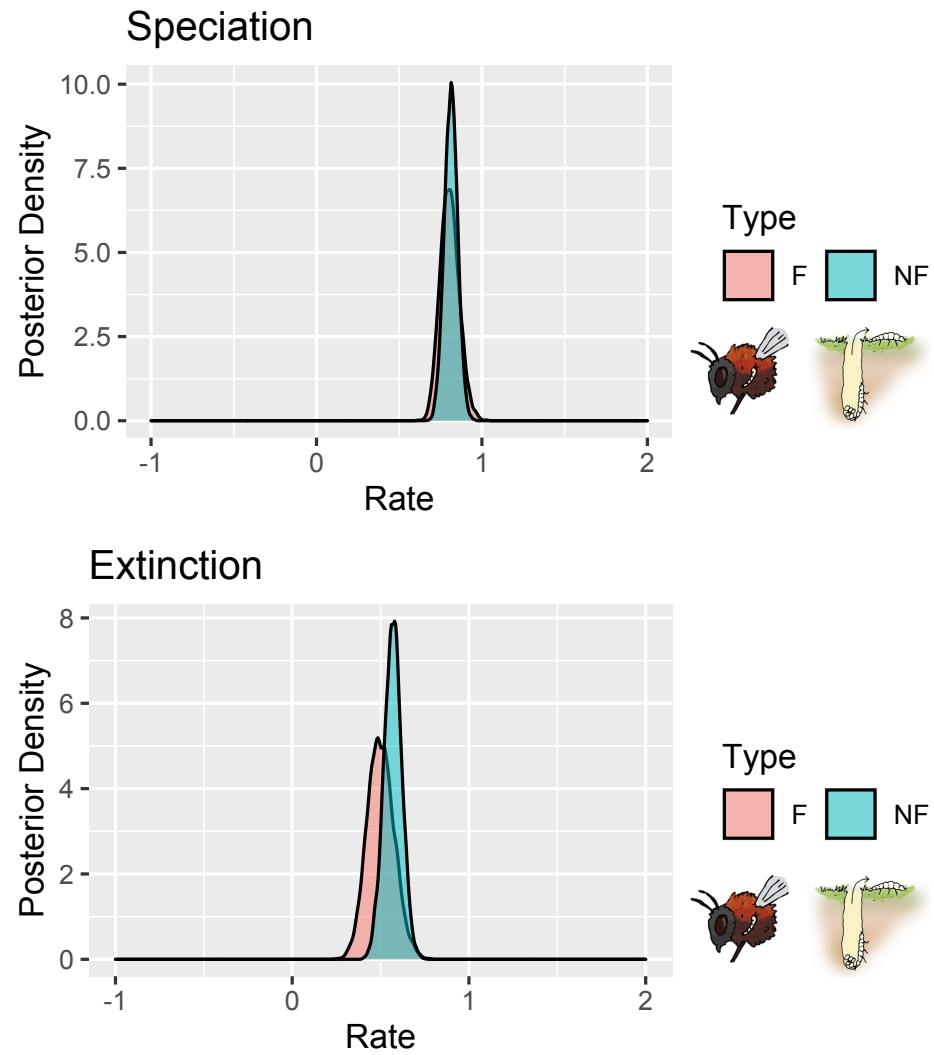


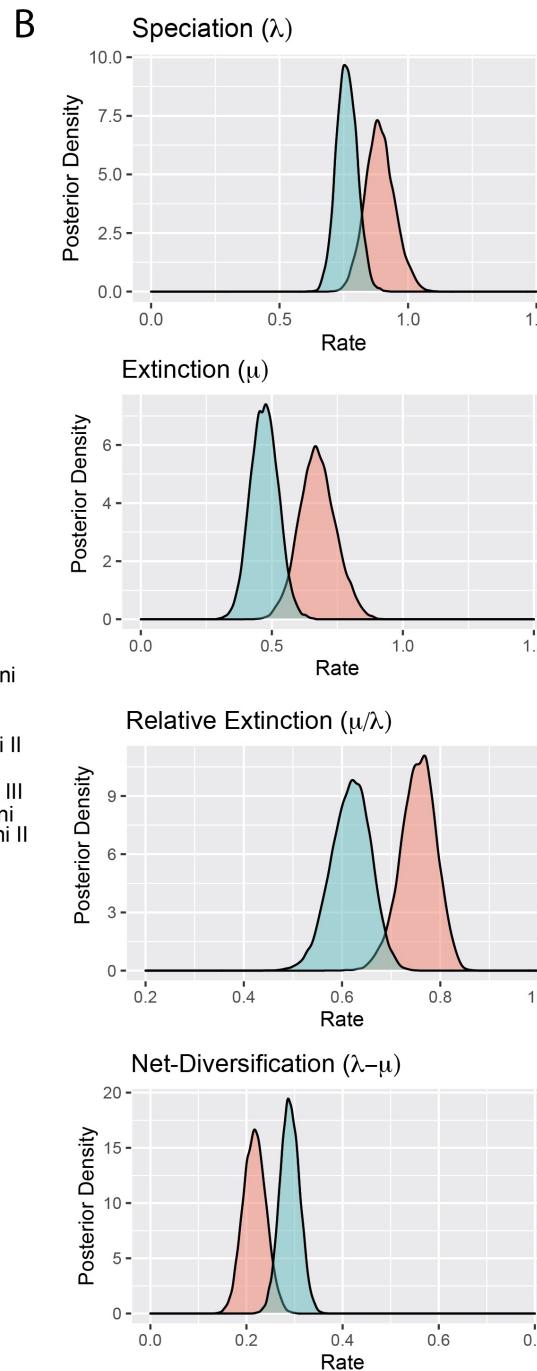
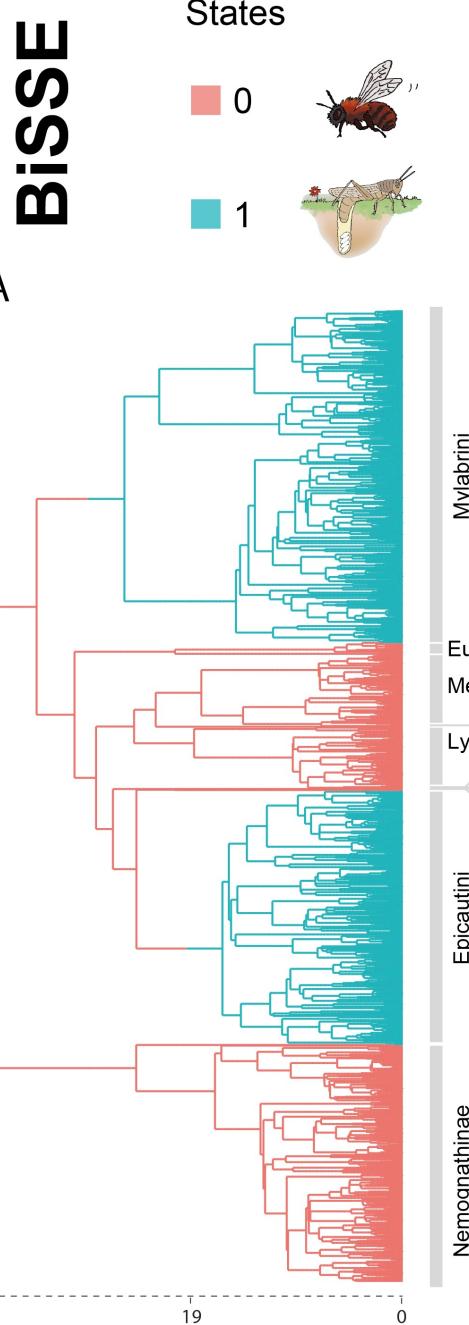
~ 361 spp.

~ 26 spp.

~ 735 spp.

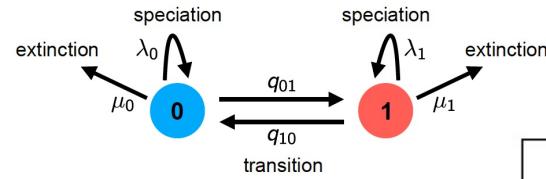
# BiSSE: foresia





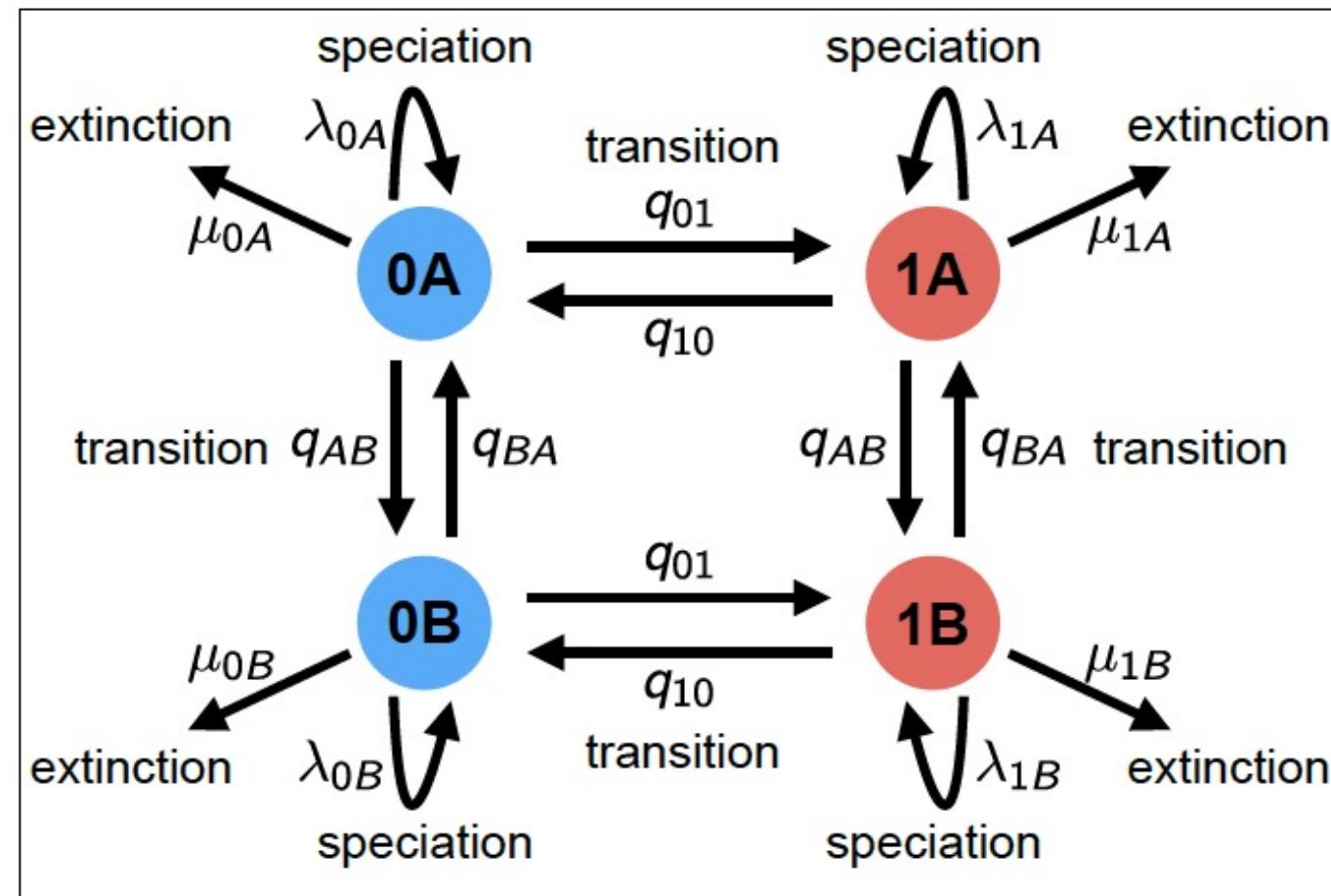
# BiSSE

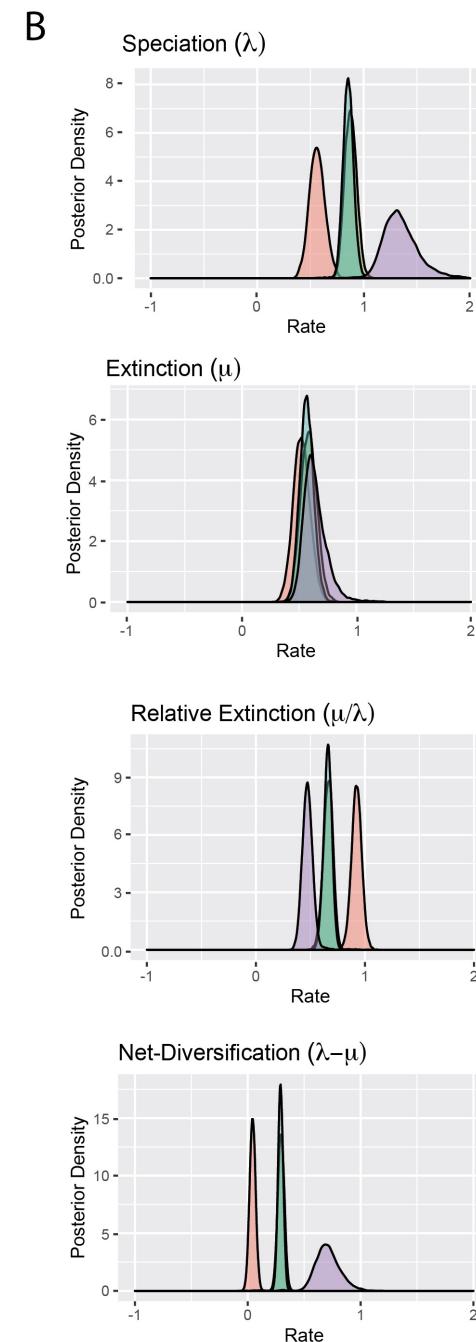
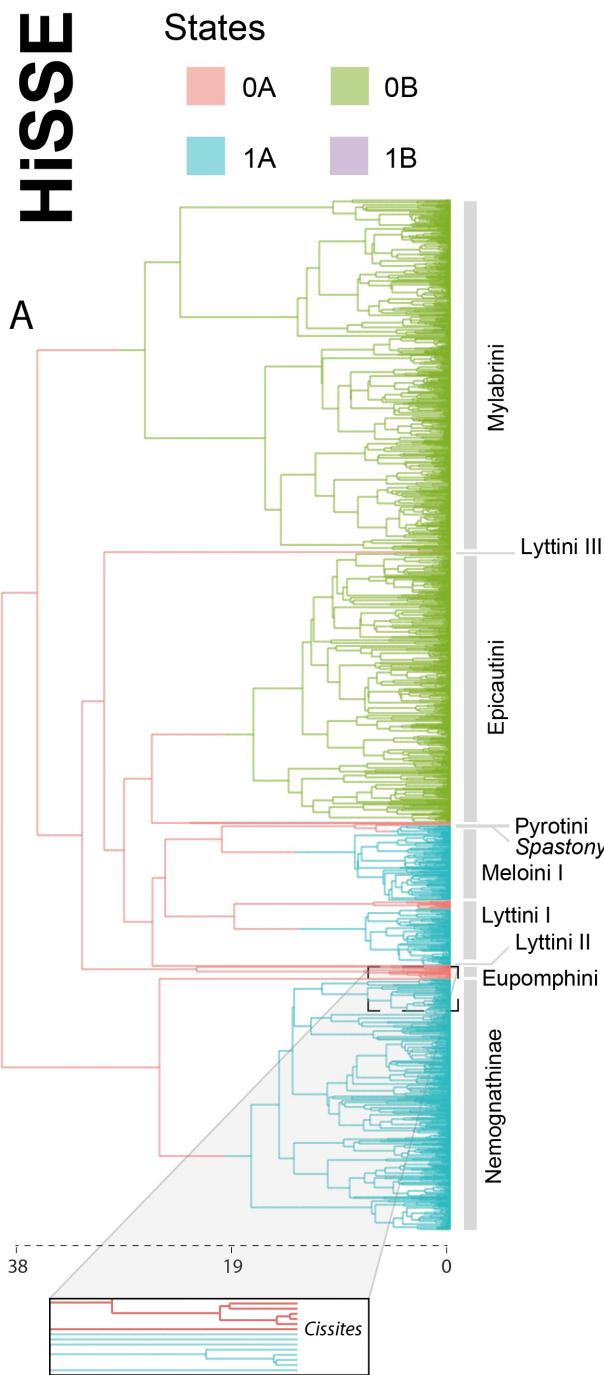
Maddison et al., 2007;  
*Systematic Biology*



# HiSSE

Maddison and FitzJohn 2015;  
*Systematic Biology*





# Stochastic Character Mapping of State-Dependent Diversification Reveals the Tempo of Evolutionary Decline in Self-Compatible Onagraceae Lineages

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Help

William A Freyman ✉, Sebastian Höhna

*Systematic Biology*, Volume 68, Issue 3, May 2019, Pages 505–519, <https://doi.org/10.1093/sysbio/syy078>

**Published:** 26 November 2018      **Article history** ▾



PDF



“ Cite

# 1 Hidden state models improve the adequacy of state-dependent diversification approaches

## 2 using empirical trees, including biogeographical models

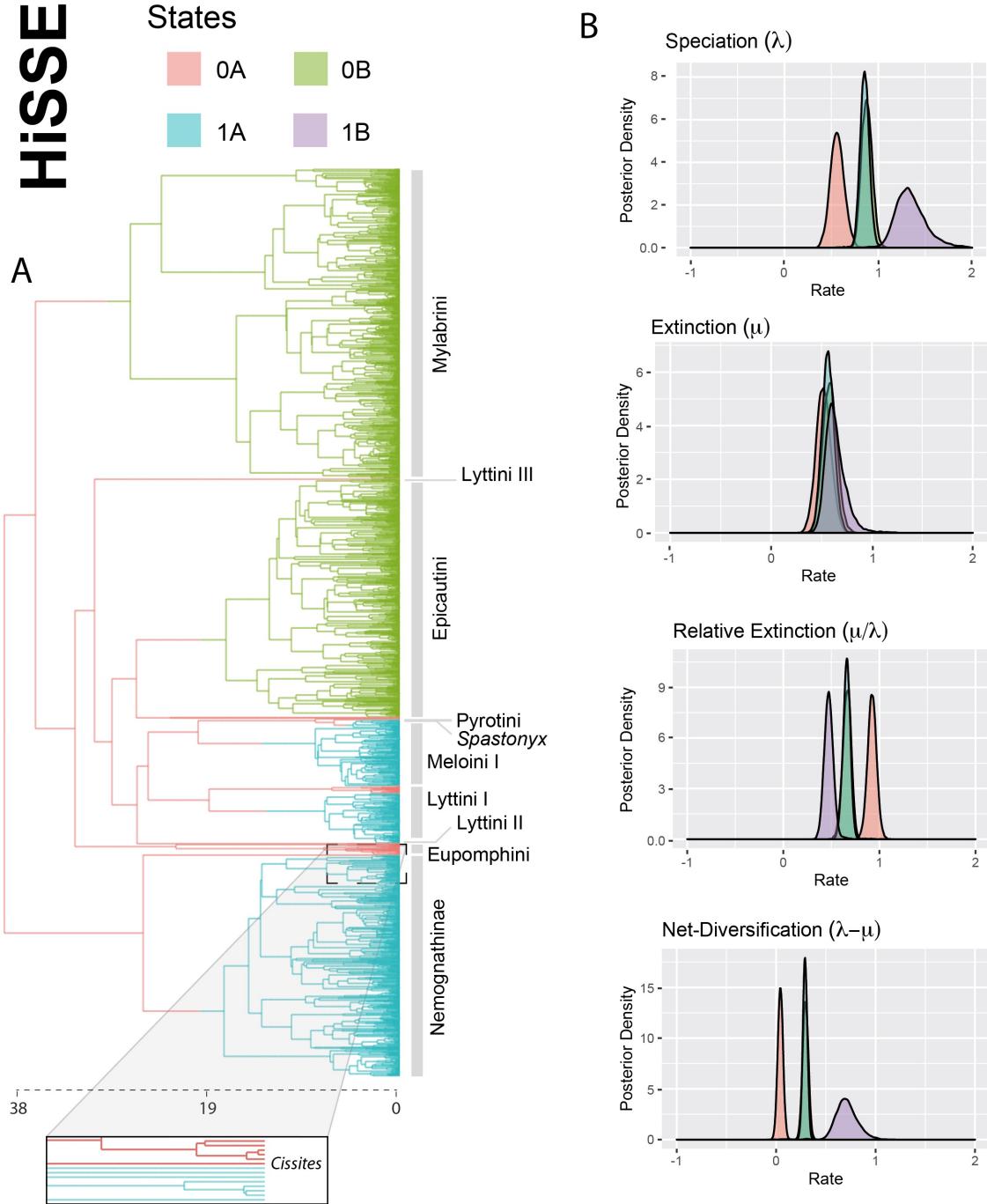
<sup>3</sup> Daniel S. Caetano<sup>1,3</sup>, Brian C. O'Meara<sup>2</sup>, and Jeremy M. Beaulieu<sup>1</sup>

<sup>4</sup> <sup>1</sup>Department of Biological Sciences, University of Arkansas, Fayetteville AR 72701.

<sup>5</sup> <sup>2</sup>Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville TN

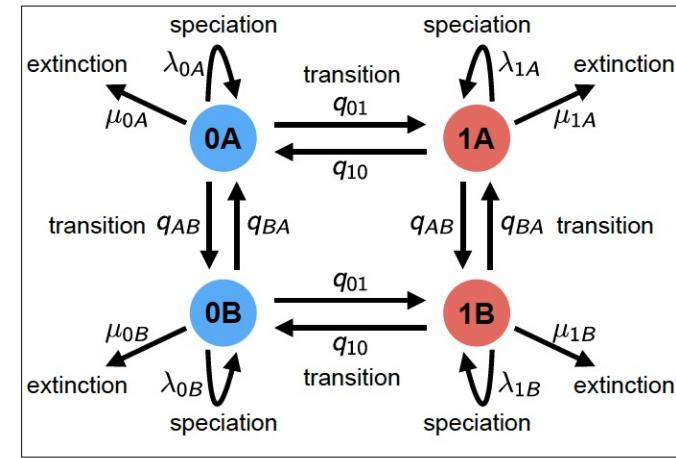
6 37996-1610

<sup>7</sup> <sup>3</sup>Author for correspondence: Daniel S. Caetano. Email: dcaetano@uark.edu



JOURNAL ARTICLE  
Stochastic Character Mapping of State-Dependent Diversification Reveals the Tempo of Evolutionary Decline in Self-Compatible Onagraceae Lineages  
William A Freymann, Sebastian Höhna  
Systematic Biology, Volume 68, Issue 3, May 2019, Pages 505–519, <https://doi.org/10.1093/sysbio/syy078>  
Published: 26 November 2018 Article history ▾ PDF Help

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- (1) if the diversification rates varied between 0 and 1, but not between hidden states a and b, we could conclude that shifts in mating system explained all diversification rate heterogeneity
- (2) if the diversification rates did not vary between 0 and 1, but did vary between hidden states a and b we could conclude that there were background rate changes unassociated with mating system and that mating system evolution was not associated with rate shifts; or
- (3) if the diversification rates varied both between 0/1 and between hidden states a/b, then depending on the phylogenetic pattern of the hidden states they could represent the different long and short term consequences of the loss of SI

# Stochastic Character Mapping of State-Dependent Diversification Reveals the Tempo of Evolutionary Decline in Self-Compatible Onagraceae Lineages

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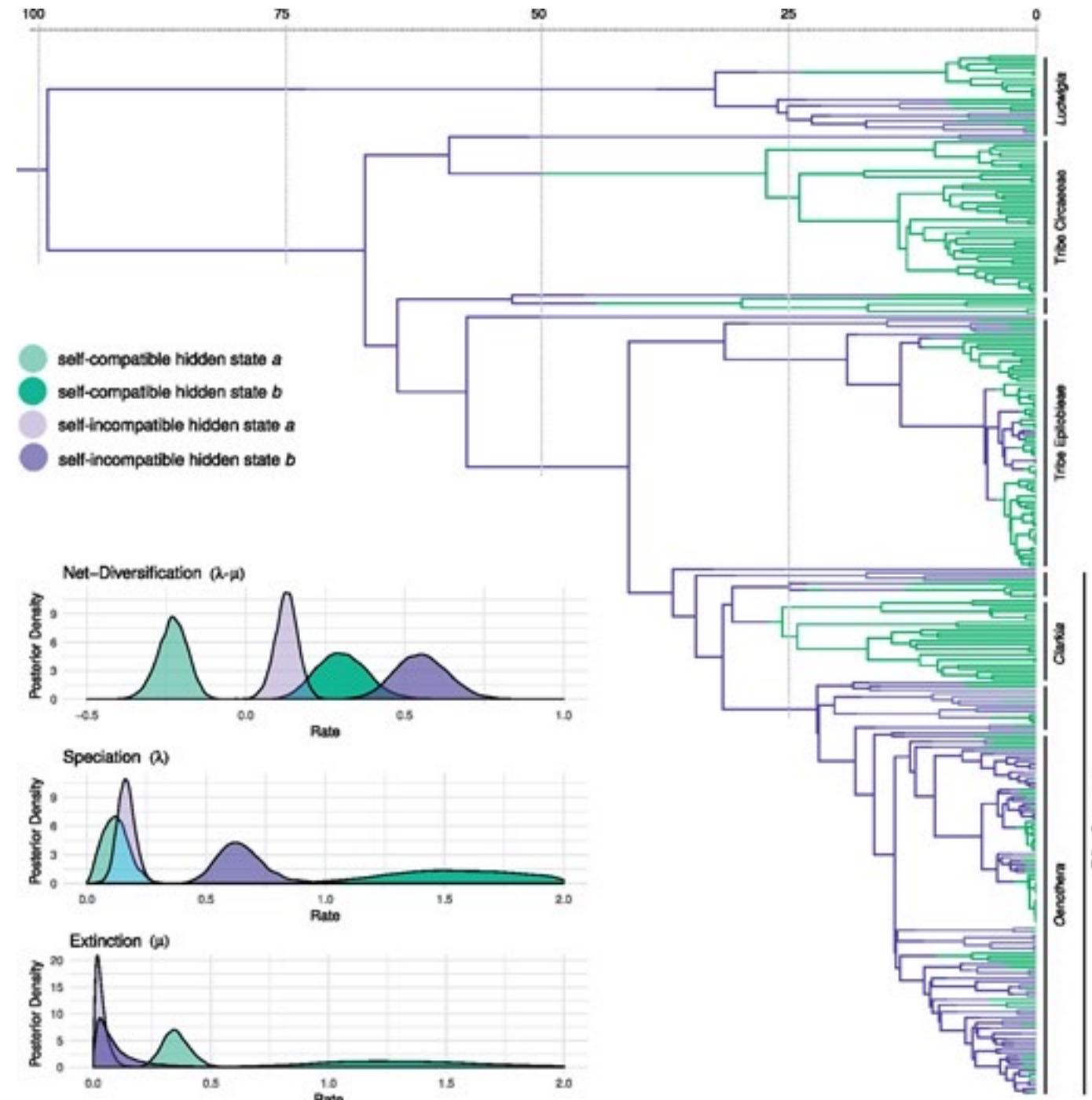
William A Freyman ✉, Sebastian Höhna

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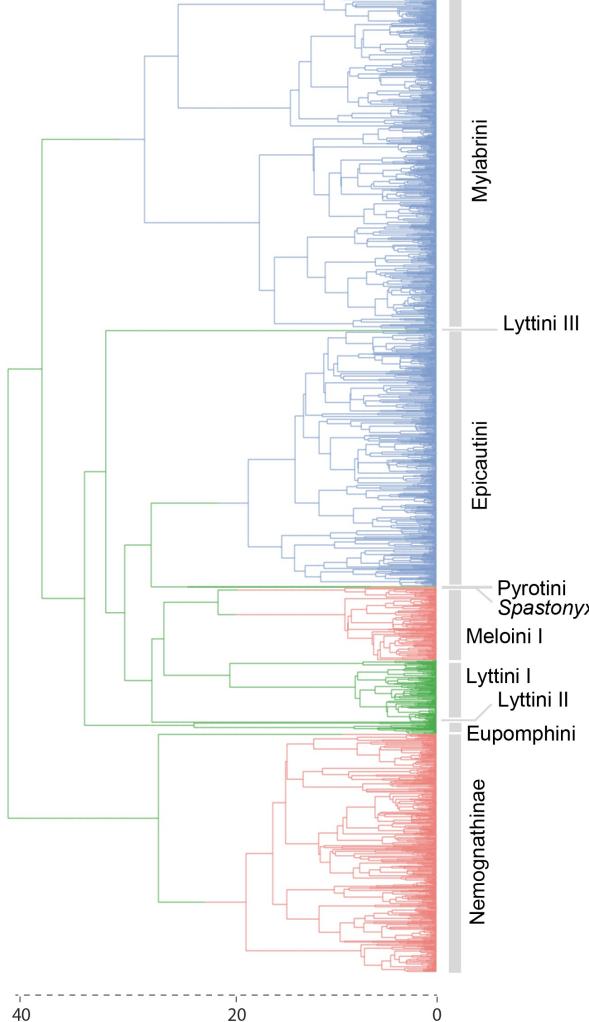
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- (1) if the diversification rates varied between 0 and 1, but not between hidden states a and b, we could conclude that shifts in mating system explained all diversification rate heterogeneity
- (2) if the diversification rates did not vary between 0 and 1, but did vary between hidden states a and b we could conclude that there were background rate changes unassociated with mating system and that mating system evolution was not associated with rate shifts; or
- (3) if the diversification rates varied both between 0/SI and between hidden states a/b, then depending on the phylogenetic pattern of the hidden states they could represent the different long and short term consequences of the loss of SI

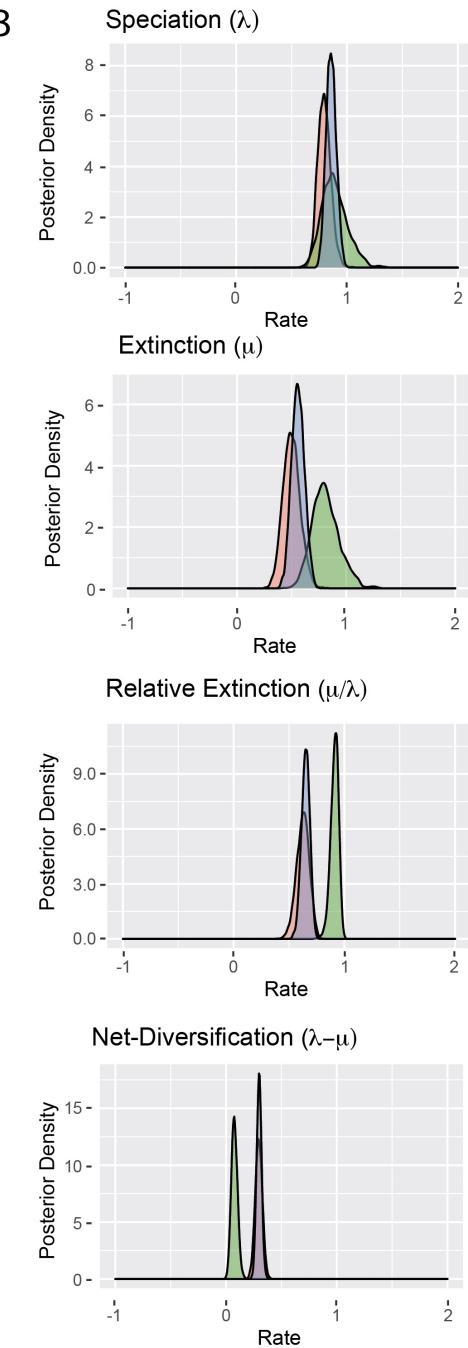


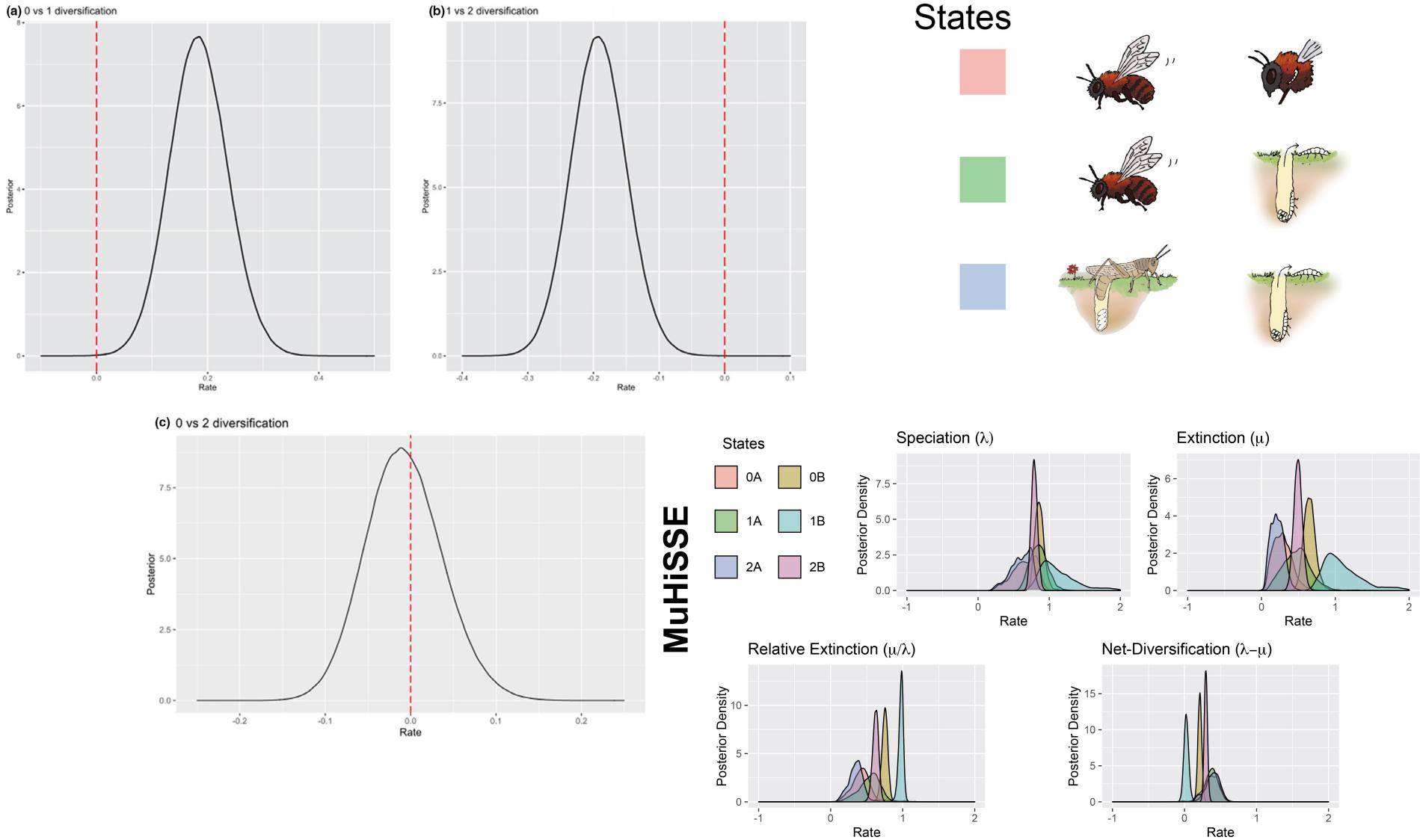
# MusSSE

A



B





# Character-Independent Model

JOURNAL ARTICLE

## Detecting Hidden Diversification Shifts in Models of Trait-Dependent Speciation and Extinction

Jeremy M. Beaulieu ✉, Brian C. O'Meara   Author Notes

PDF

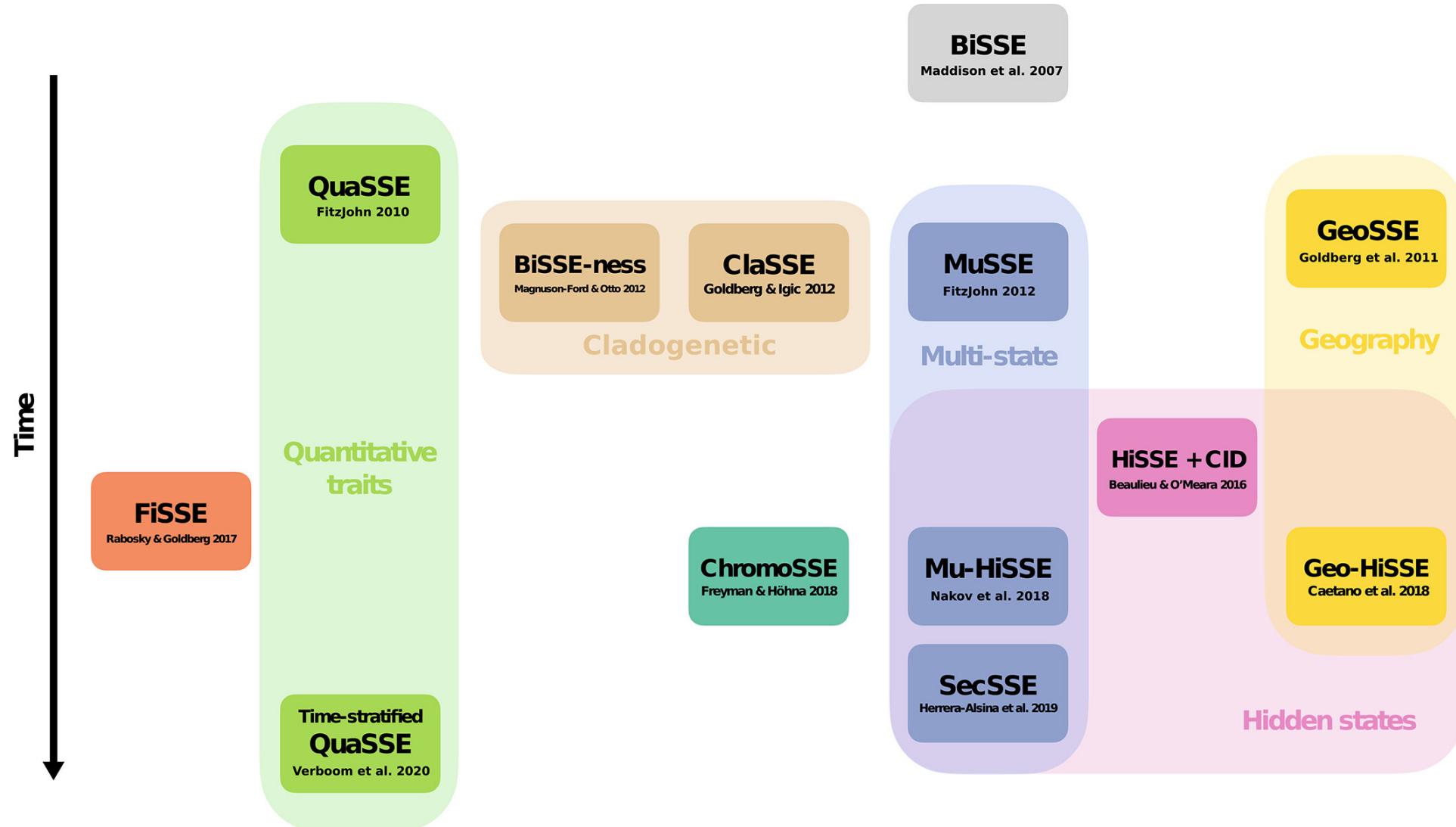
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Systematic Biology, Volume 65, Issue 4, July 2016, Pages 583–601, <https://doi.org/10.1093/sysbio/syw022>

Published: 25 March 2016   Article history ▾

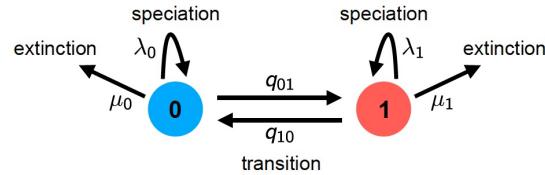
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$$Q = \begin{matrix} 0A \\ 0B \\ 0C \\ 0D \\ 1A \\ 1B \\ 1C \\ 1D \end{matrix} \left[ \begin{array}{ccccccccc} - & q_{0A \rightarrow 0B} & q_{0A \rightarrow 0C} & q_{0A \rightarrow 0D} & q_{0A \rightarrow 01} & 0 & 0 & 0 \\ q_{0B \rightarrow 0A} & - & q_{0B \rightarrow 0C} & q_{0B \rightarrow 0D} & 0 & q_{0B \rightarrow 1B} & 0 & 0 \\ q_{0D \rightarrow 0A} & q_{0C \rightarrow 0B} & - & q_{0C \rightarrow 0D} & 0 & 0 & q_{0C \rightarrow 1C} & 0 \\ q_{0D \rightarrow 0A} & q_{0D \rightarrow 0B} & q_{0D \rightarrow 0C} & - & 0 & 0 & 0 & q_{0D \rightarrow 1D} \\ q_{1B \rightarrow 0A} & 0 & 0 & 0 & - & q_{1A \rightarrow 1B} & q_{1A \rightarrow 1C} & q_{0A \rightarrow 1D} \\ 0 & q_{1B \rightarrow 0B} & 0 & 0 & q_{1B \rightarrow 1A} & - & q_{1B \rightarrow 1C} & q_{1B \rightarrow 1D} \\ 0 & 0 & q_{0C \rightarrow 0C} & 0 & q_{1C \rightarrow 1A} & q_{1C \rightarrow 1B} & - & q_{1C \rightarrow 1D} \\ 0 & 0 & 0 & q_{1D \rightarrow 0D} & q_{1D \rightarrow 1A} & q_{1D \rightarrow 1B} & q_{1D \rightarrow 1C} & - \end{array} \right]$$



# BiSSE

Maddison et al., 2007;  
*Systematic Biology*



1 Potential survival of some, but not all, diversification methods

2 Running title (40 characters max): Diversification method survival

3 Authors: Brian C. O'Meara<sup>1\*</sup> and Jeremy M. Beaulieu<sup>2</sup>

4 Affiliations:

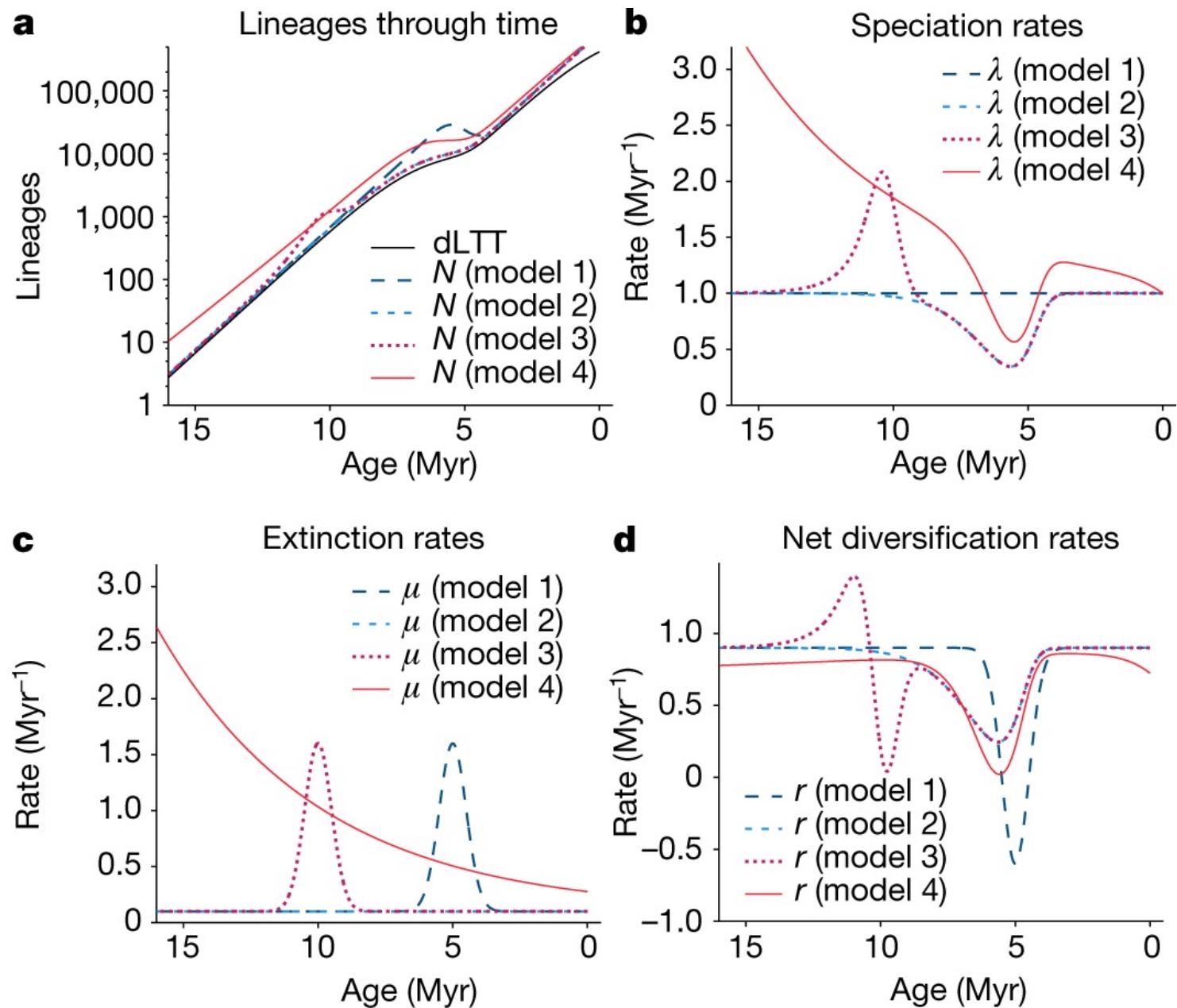
<sup>1</sup>Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, Tennessee, 37996-1610 USA

<sup>2</sup>Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas, 72701 USA

\*Corresponding author: Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, Tennessee, 37996-1610 USA; email: bomeara@utk.edu

Author contributions: BCO and JMB take equal responsibility for the contents of this article.

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# Cladogenetic State change Speciation and Extinction (ClaSSE)

Introducción a la Biogeografía Paramétrica  
Semana 2

Dra. Karen López y Dra. Marysol Trujano

# TEMPO AND MODE IN PLANT BREEDING SYSTEM EVOLUTION

Emma E. Goldberg, Boris Igić

*Evolution*, Volume 66, Issue 12, 1 December 2012, Pages 3701–3709, <https://doi.org/10.1111/j.1558-5646.2012.01730.x>

Published: 01 December 2012

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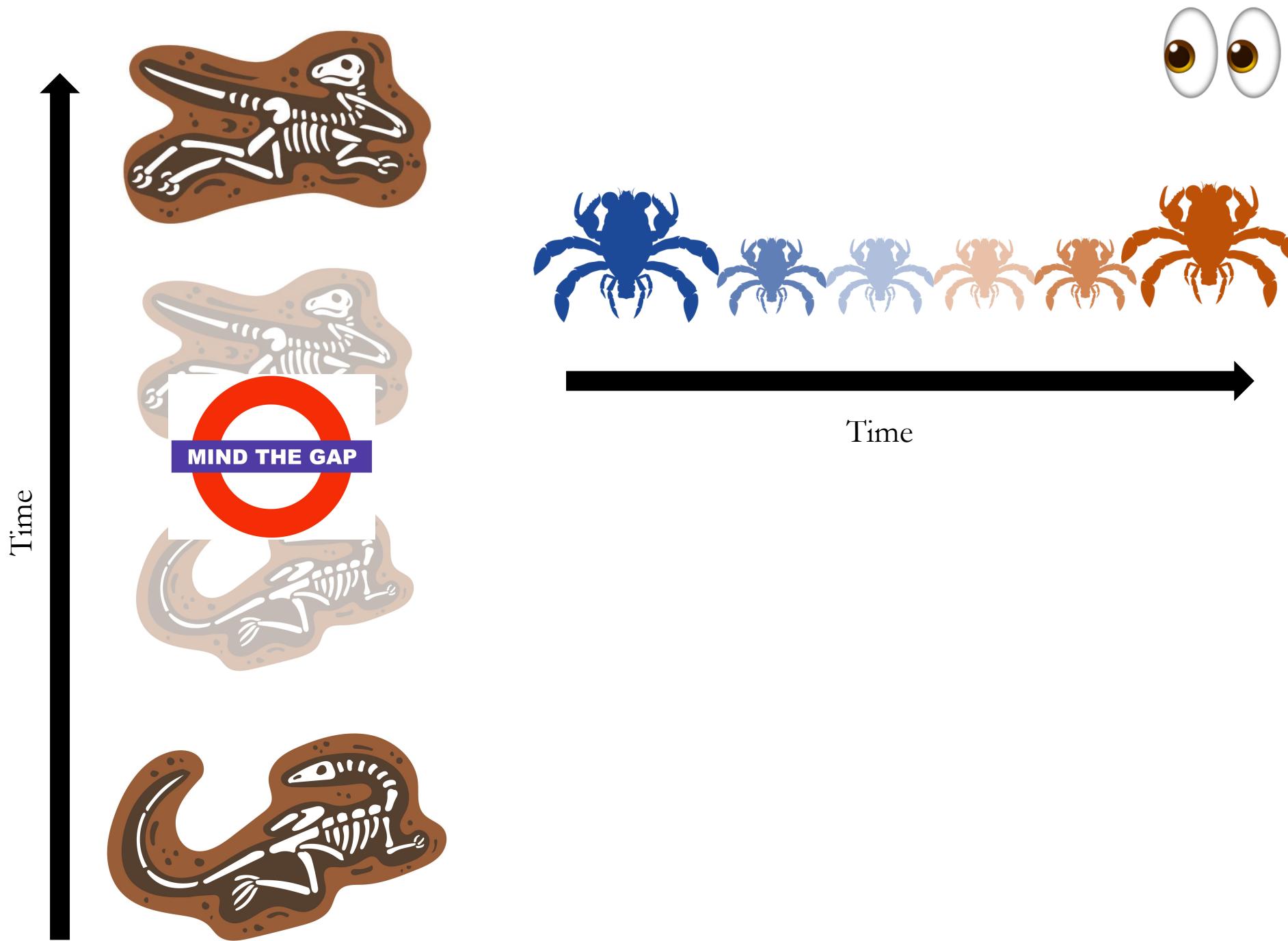
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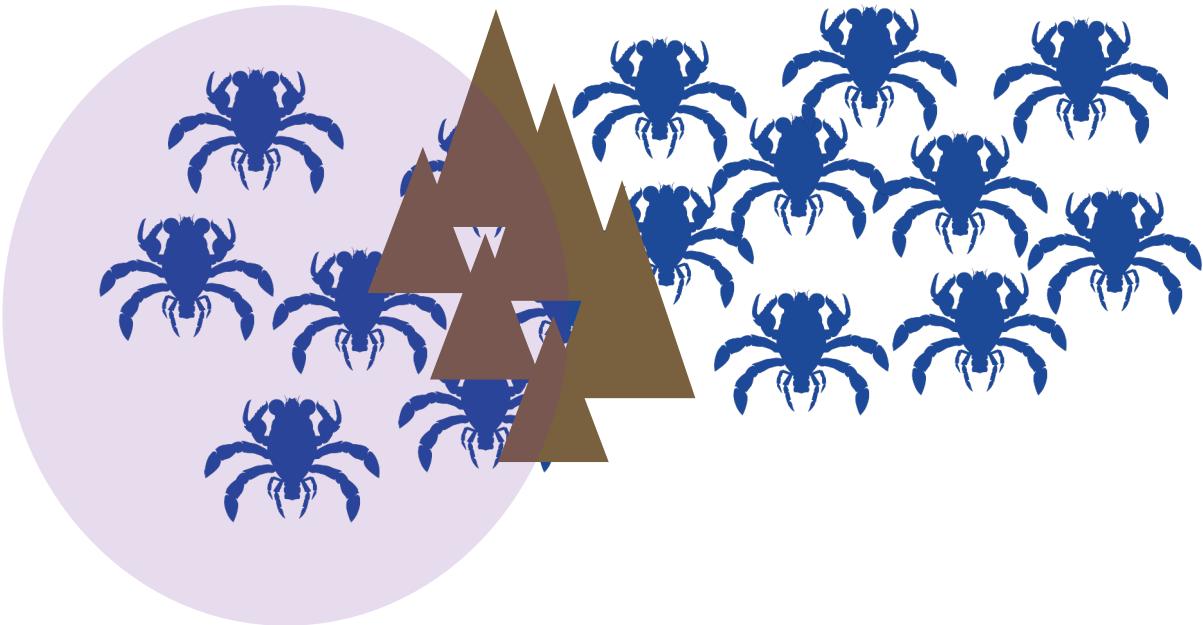
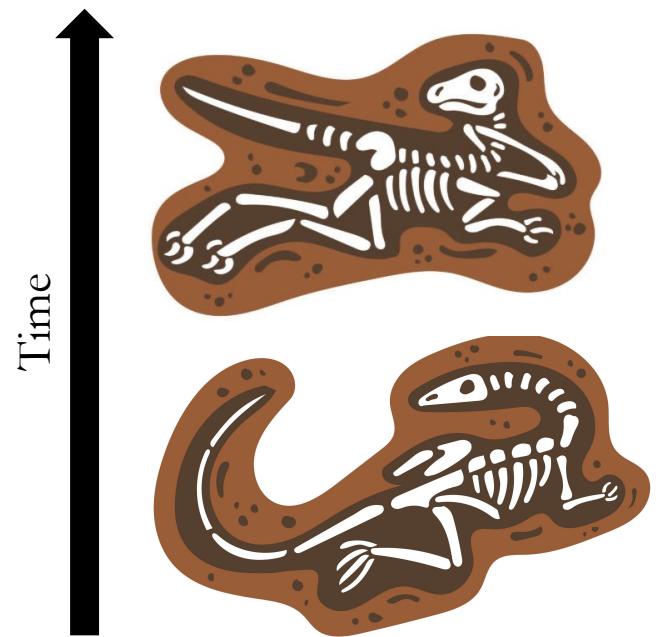
## Abstract

Classic questions about trait evolution—including the directionality of character change and its interactions with lineage diversification—intersect in the study of plant breeding systems. Transitions from self-incompatibility to self-compatibility are frequent, and they may proceed within a species (“anagenetic” mode of breeding system change) or in conjunction with speciation events (“cladogenetic” mode of change). We apply a recently developed phylogenetic model to the nightshade family Solanaceae, quantifying the relative contributions of these two modes of evolution along with the

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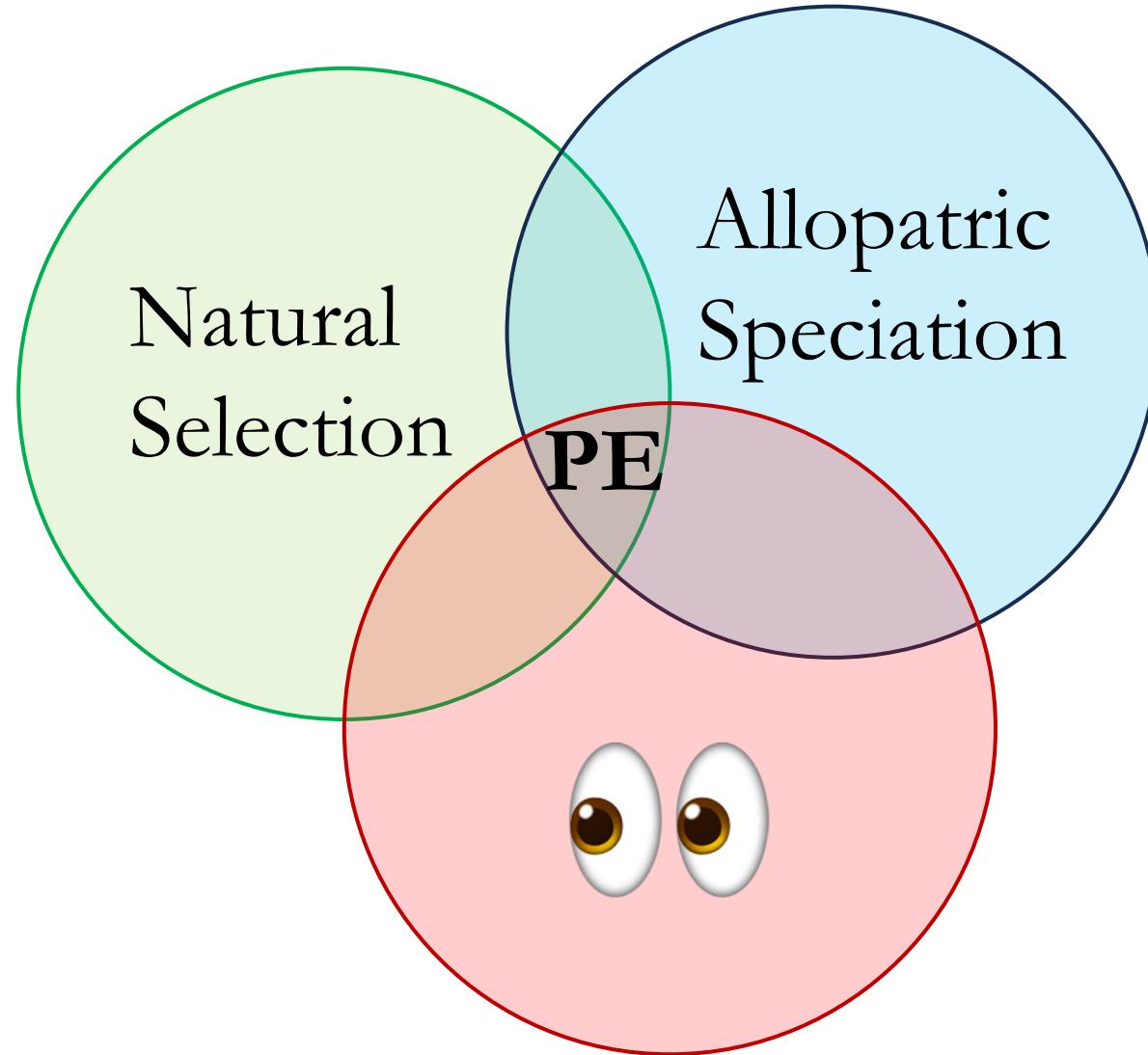
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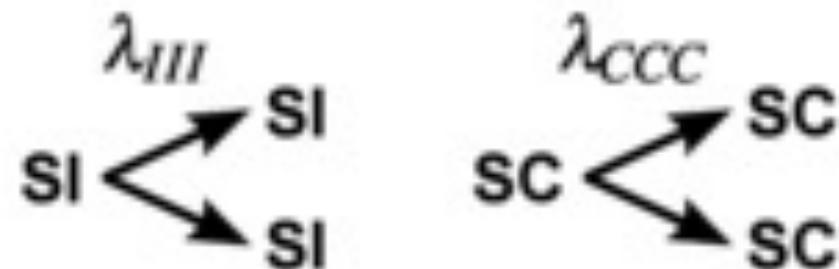


# Punctuated Equilibria (PE)

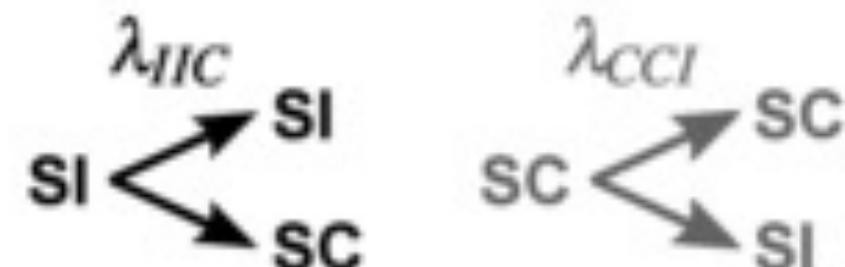
1970s by Eldredge  
and Gould



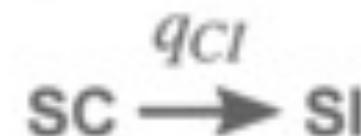
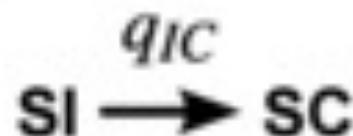
Cladogenesis, no state change  
(BiSSE & ClaSSE)



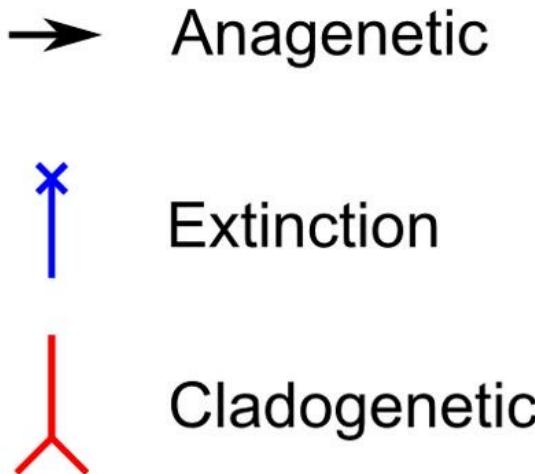
Cladogenetic state change  
(ClaSSE only)



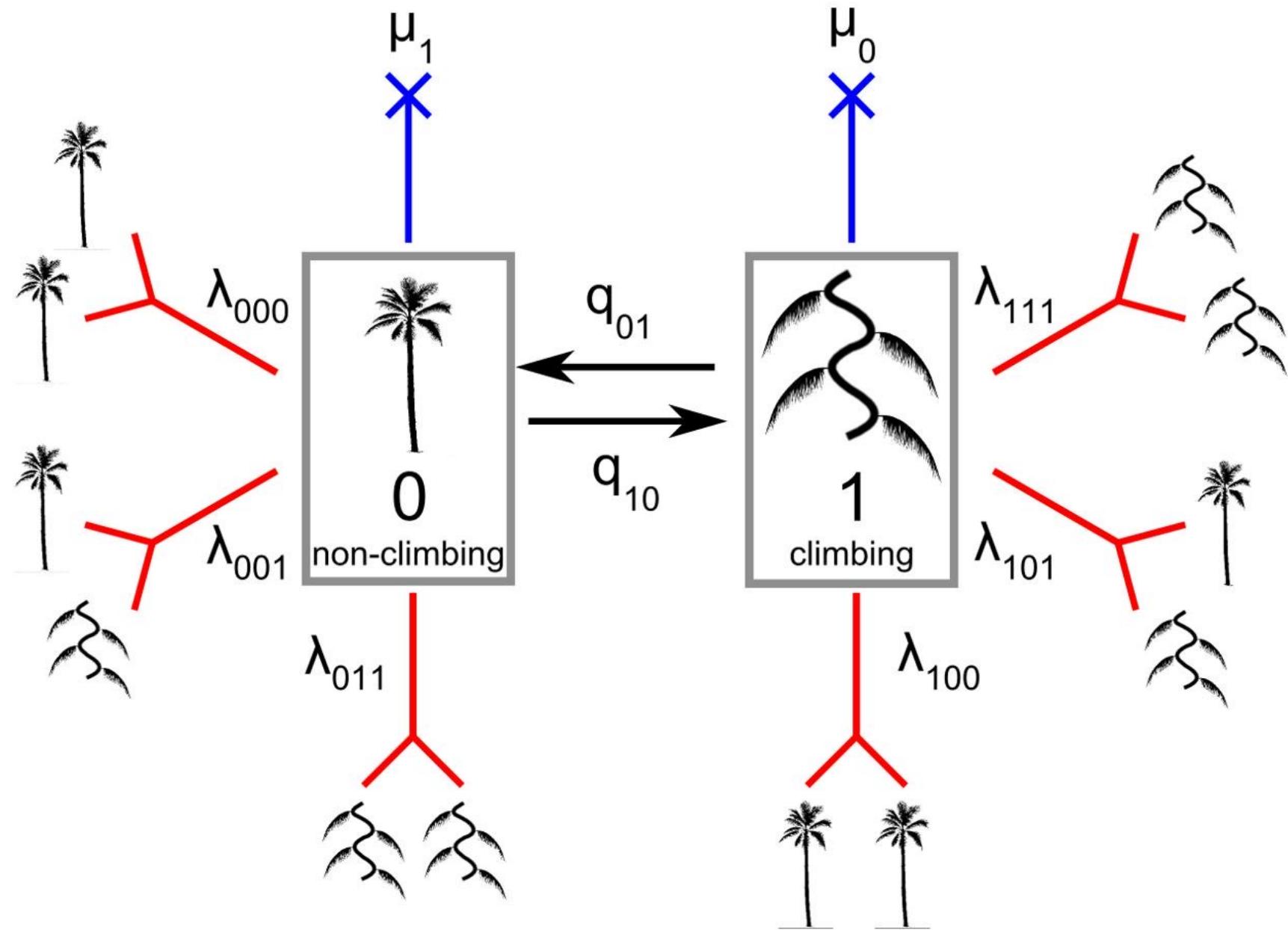
Anagenetic state change (BiSSE & ClaSSE)



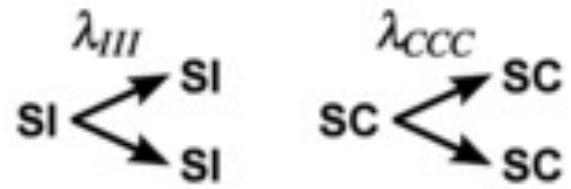
# ClaSSE



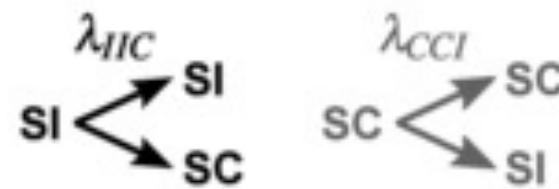
Couvreur et al., 2015; Frontiers



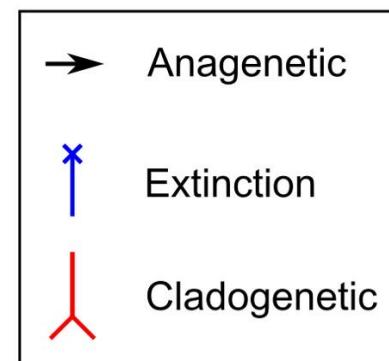
Cladogenesis, no state change  
(BiSSE & ClaSSE)



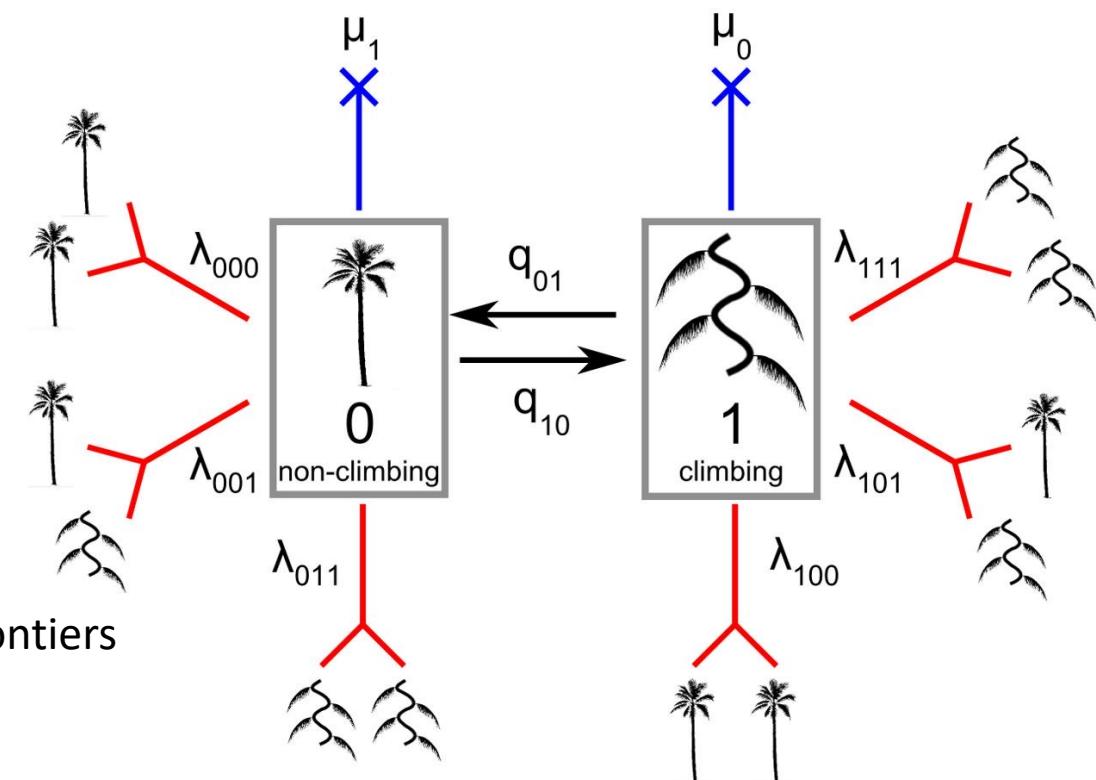
Cladogenetic state change  
(ClaSSE only)



Anagenetic state change (BiSSE & ClaSSE)



Couvreur et al., 2015; Frontiers



$0 = 00 =$  the null state with no range

$1 = 01 =$  Area A only

$2 = 10 =$  Area B only

$3 = 11 =$  both areas AB

state,range
0,0000
1,1000
2,0100
3,0010
4,0001
5,1100
6,1010
7,0110
8,1001
9,0101
10,0011
11,1110
12,1101
13,1011
14,0111
15,1111

