

# SPIDER SPECIES DISCOVERY AND DELIMITATION: TAXONOMY IN THE 21<sup>ST</sup> CENTURY

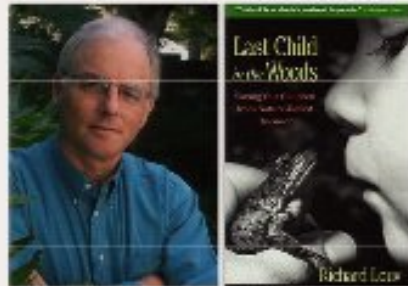


Jason E. Bond  
East Carolina University  
Department of Biology &  
North Carolina Center for  
Biodiversity

North Carolina  
Center For  
Biodiversity



The North Carolina Center for Biodiversity Presents



Richard Louv  
7 pm, Friday April 15<sup>th</sup>  
C307 Science and Technology  
Building,  
East Carolina University

"LAST CHILD IN THE WOODS: Saving Our Children From Nature-Deficit Disorder" has stimulated an international conversation about the relationship between children and nature.

Earth Day Celebration

- Returning to Nature -

10 AM- 1 PM, Saturday April 16<sup>th</sup>

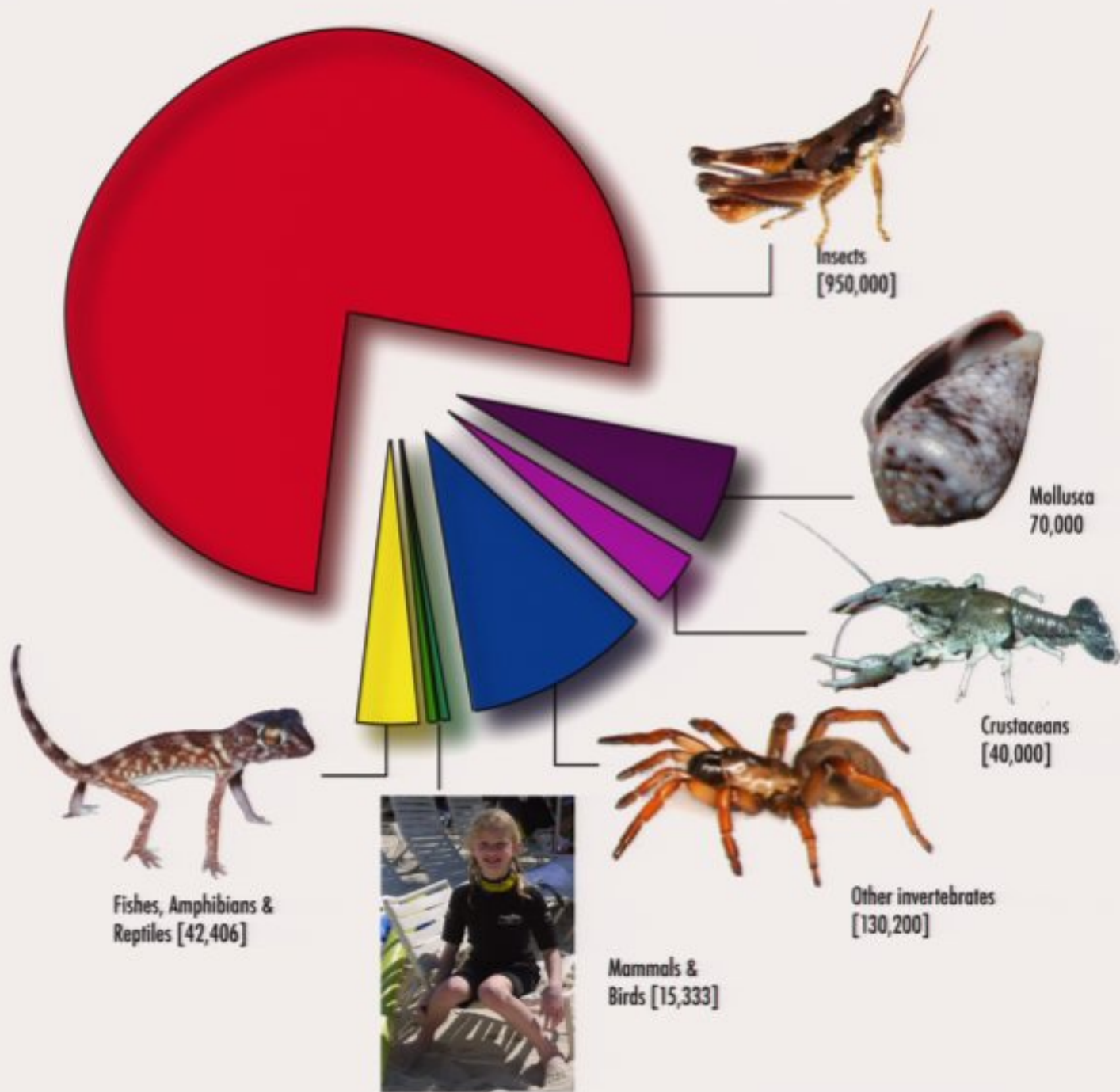
River Park North

Parking at Greenville Utilities



Visit Greenville's natural jewel to return to nature. After a welcome by Richard Louv, you can follow your own path, join NC Center for Biodiversity faculty for nature walks, and visit numerous environmental exhibits and River Park North's Walter L. Stasavich Science & Nature Center. All events are free!

Partners: Thomas Harriot College of Arts and Sciences - Dept. of Biology - Dept. of Chemistry - Brody School of Medicine - Dept. of Pediatrics - Center for Sustainable Tourism - Institute for Coastal Science and Policy - Dept. of Health Education and Promotion - College of Health and Human Performance - College of Education - Dept. of Mathematics, Science, and Instructional Technology Education - Greenville Parks and Recreation - Go-Science - A Time for Science Nature and Science Learning Center - D. H. Conley High School - Dept. of Geography - Emerald Energy NC - Acacia's Tipoy Teapot- Pamlico-Tar River Foundation - Dept. of Geological Sciences - FROGGS

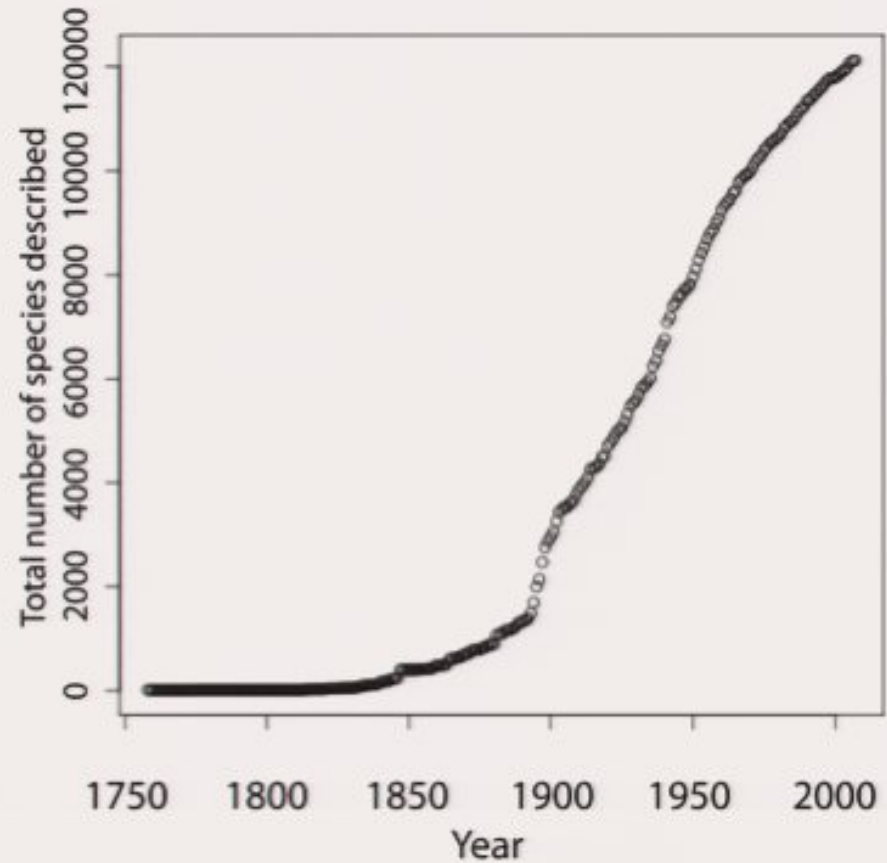
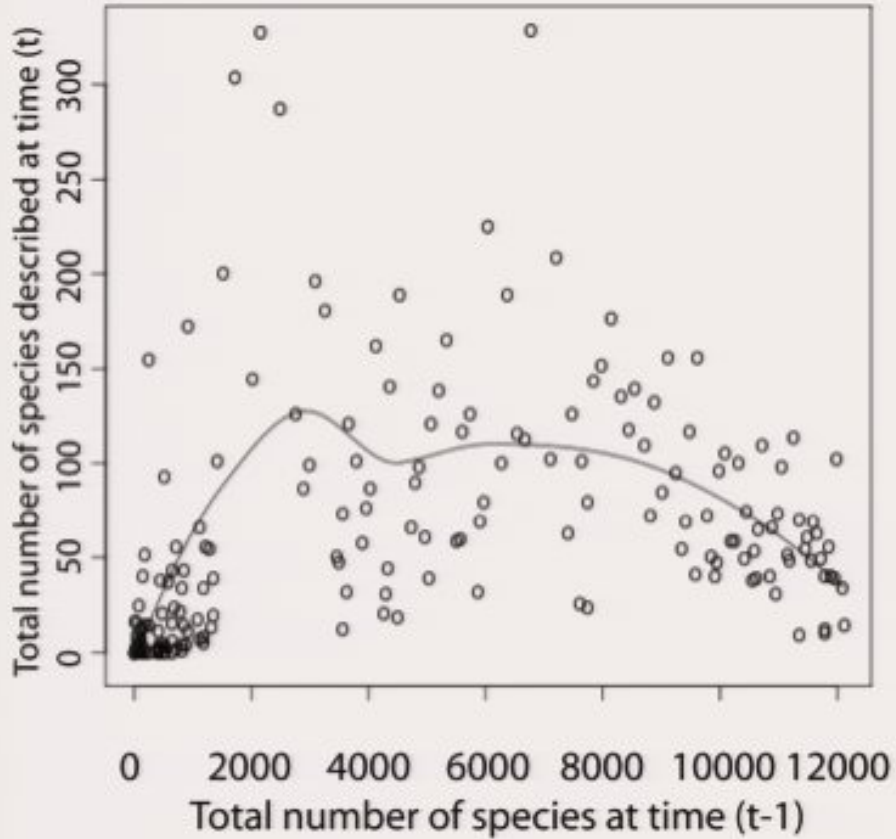


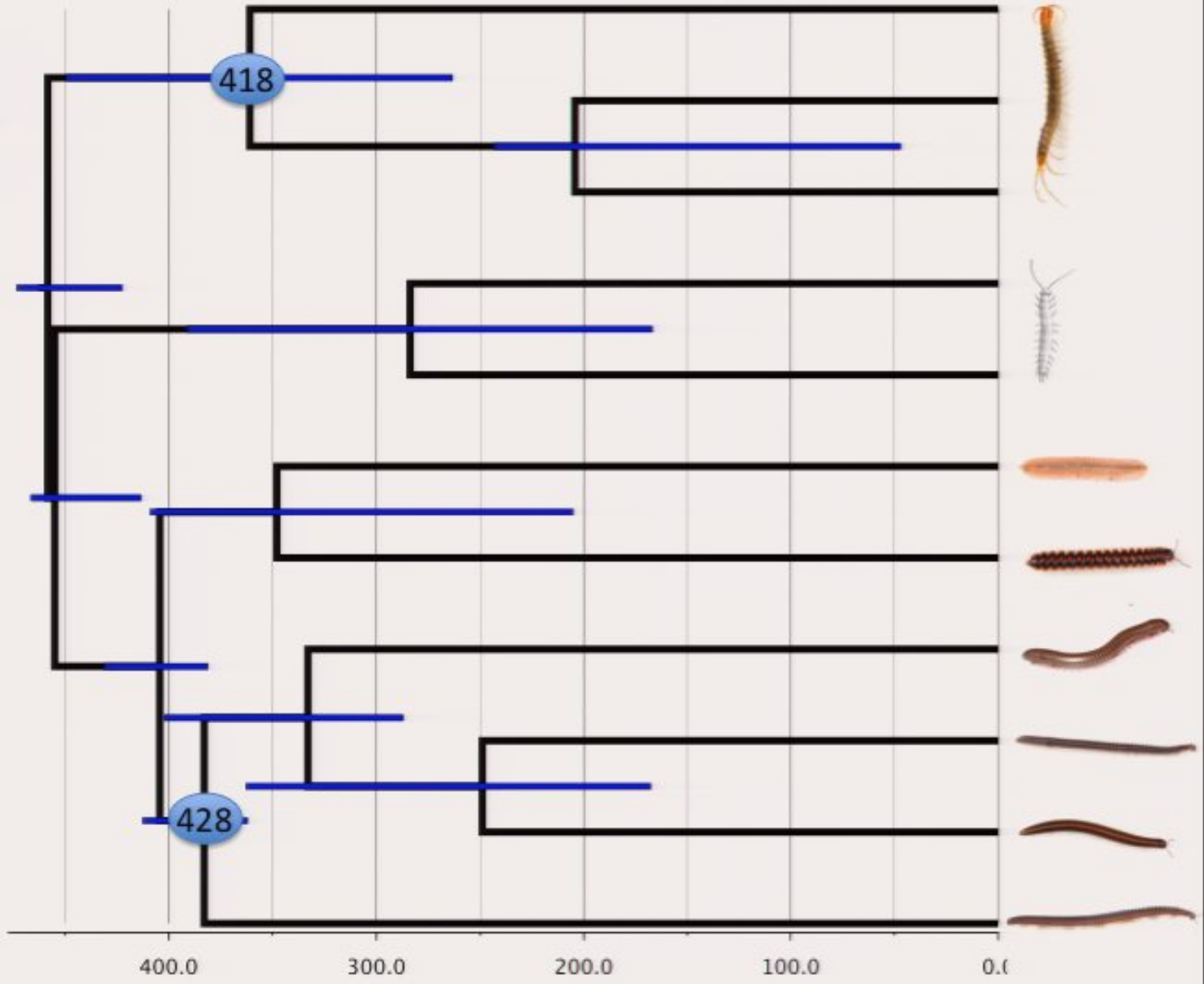
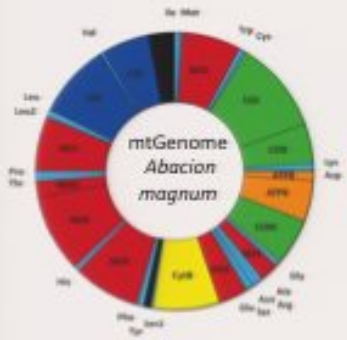




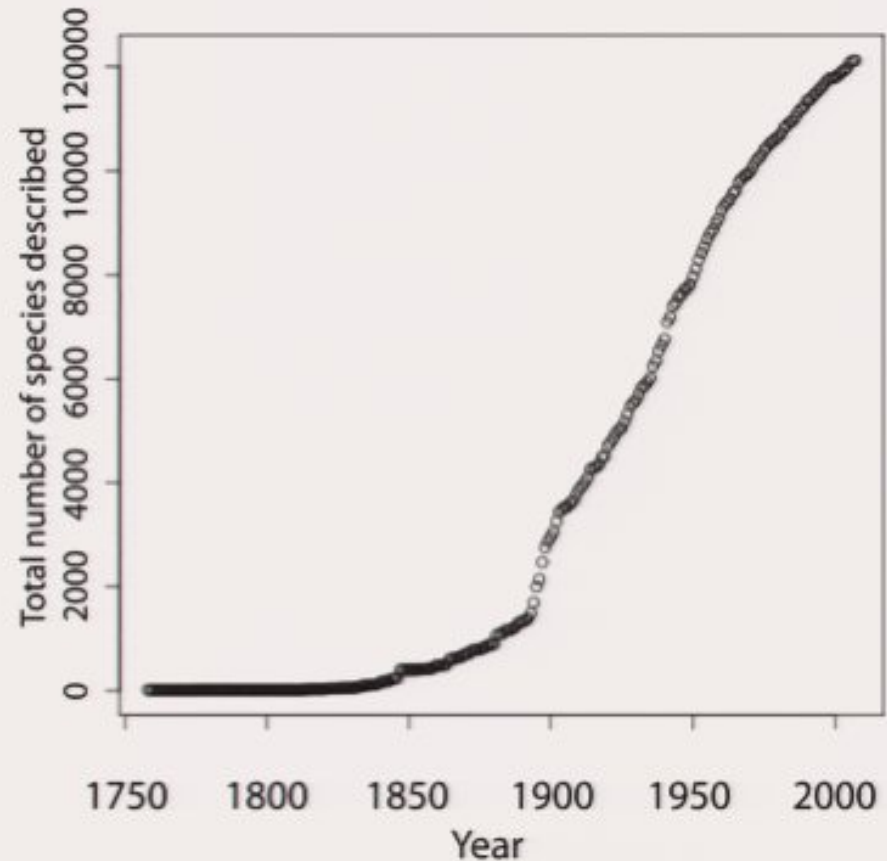
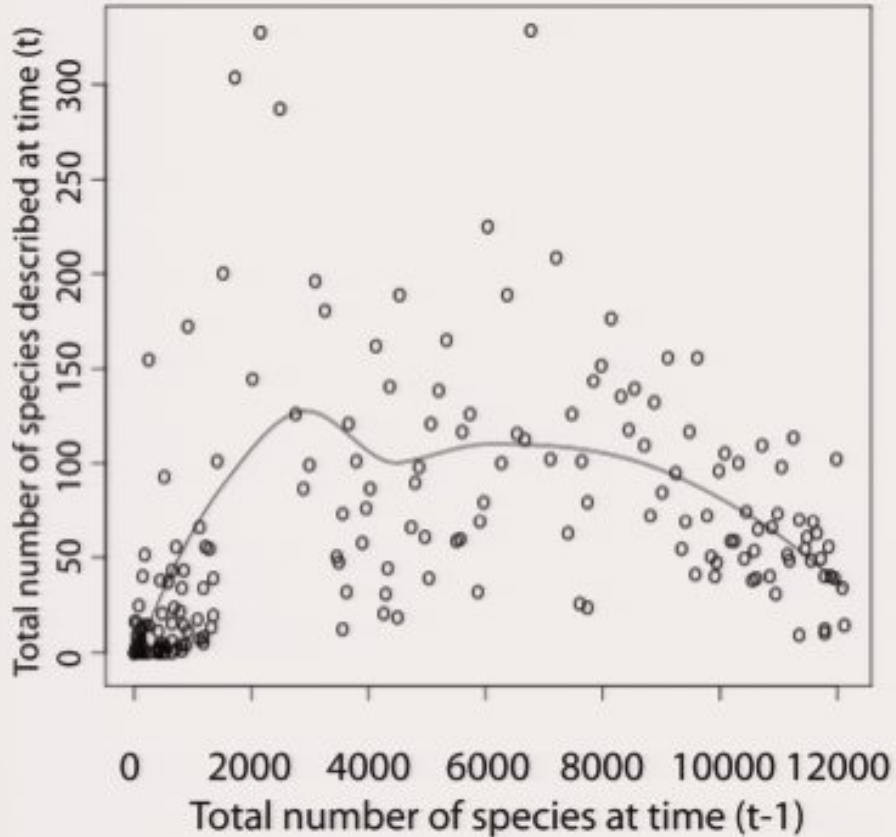


# Millipede Diversity

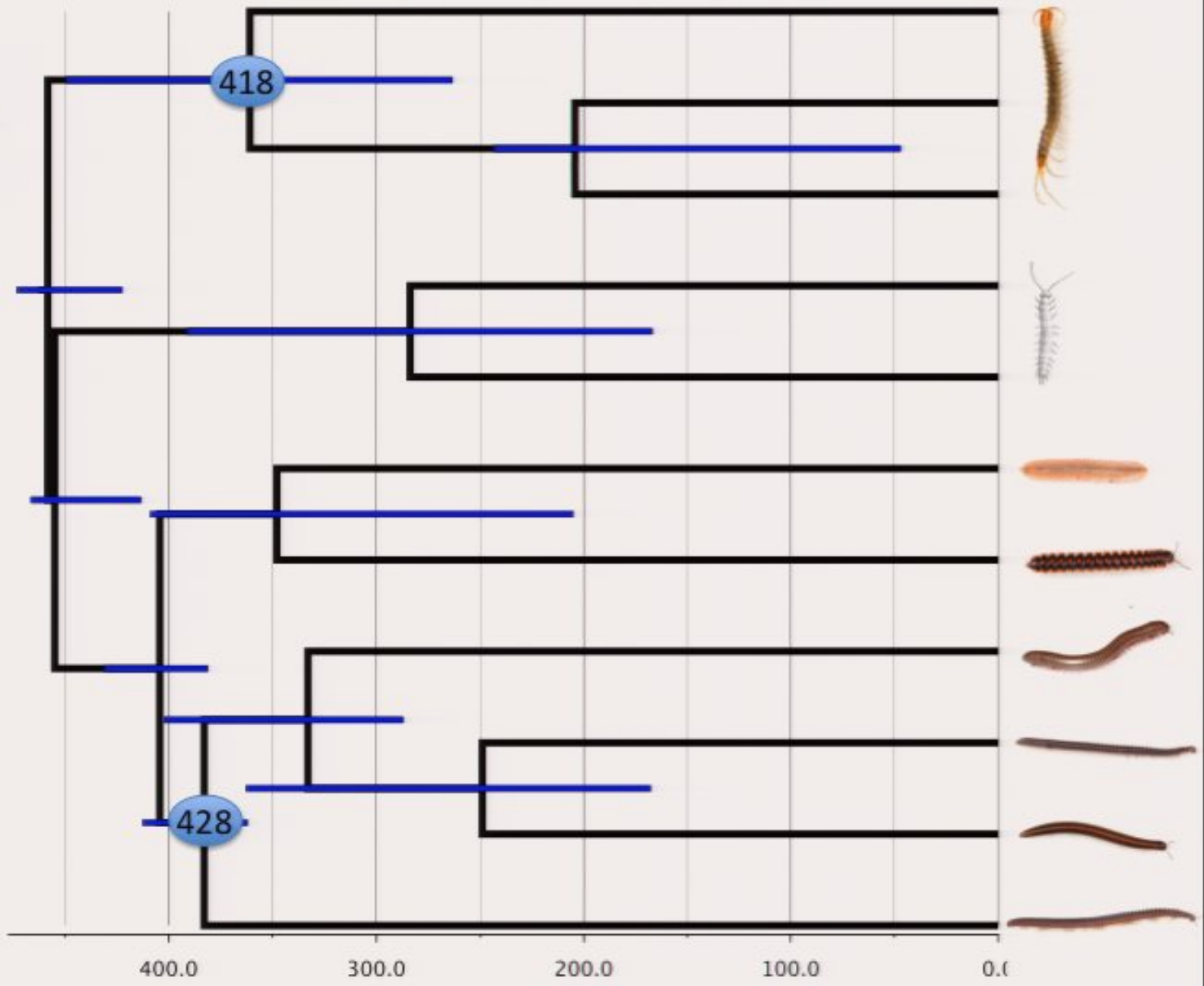
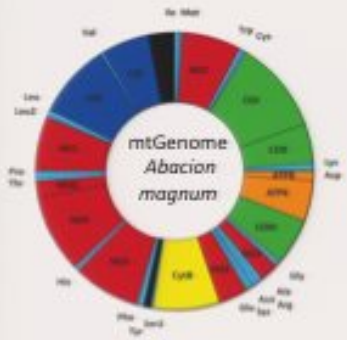




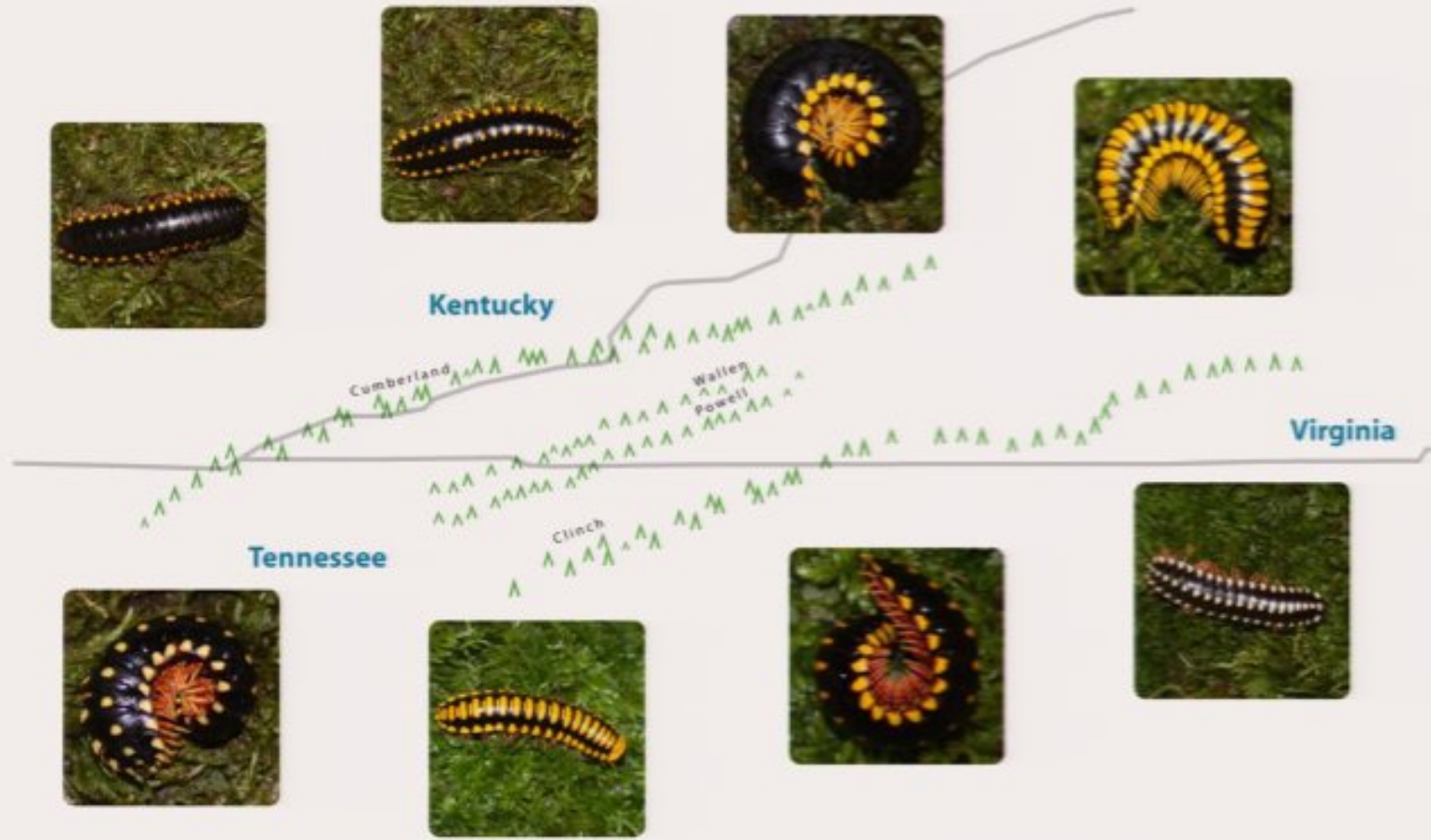
# Millipede Diversity



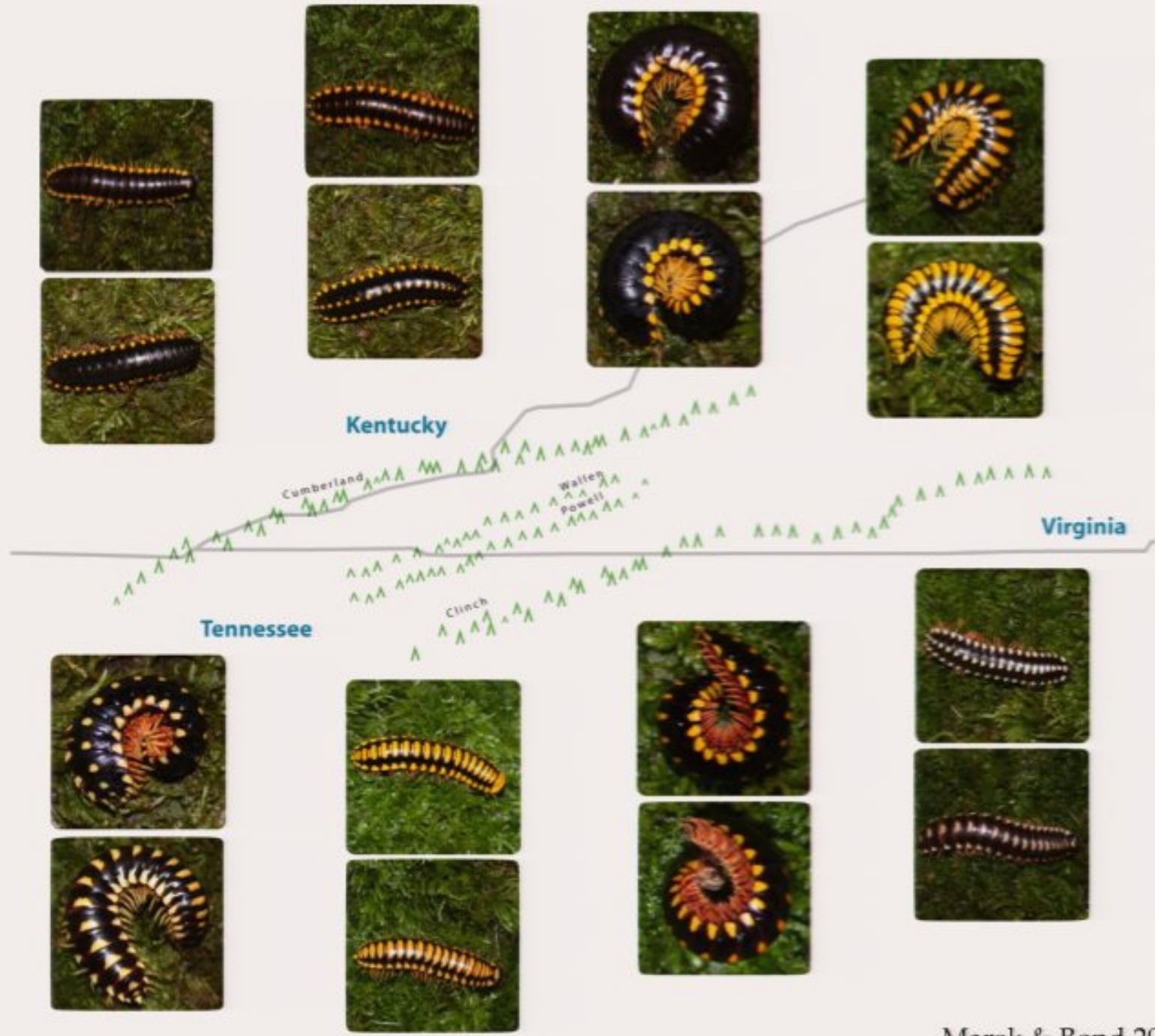


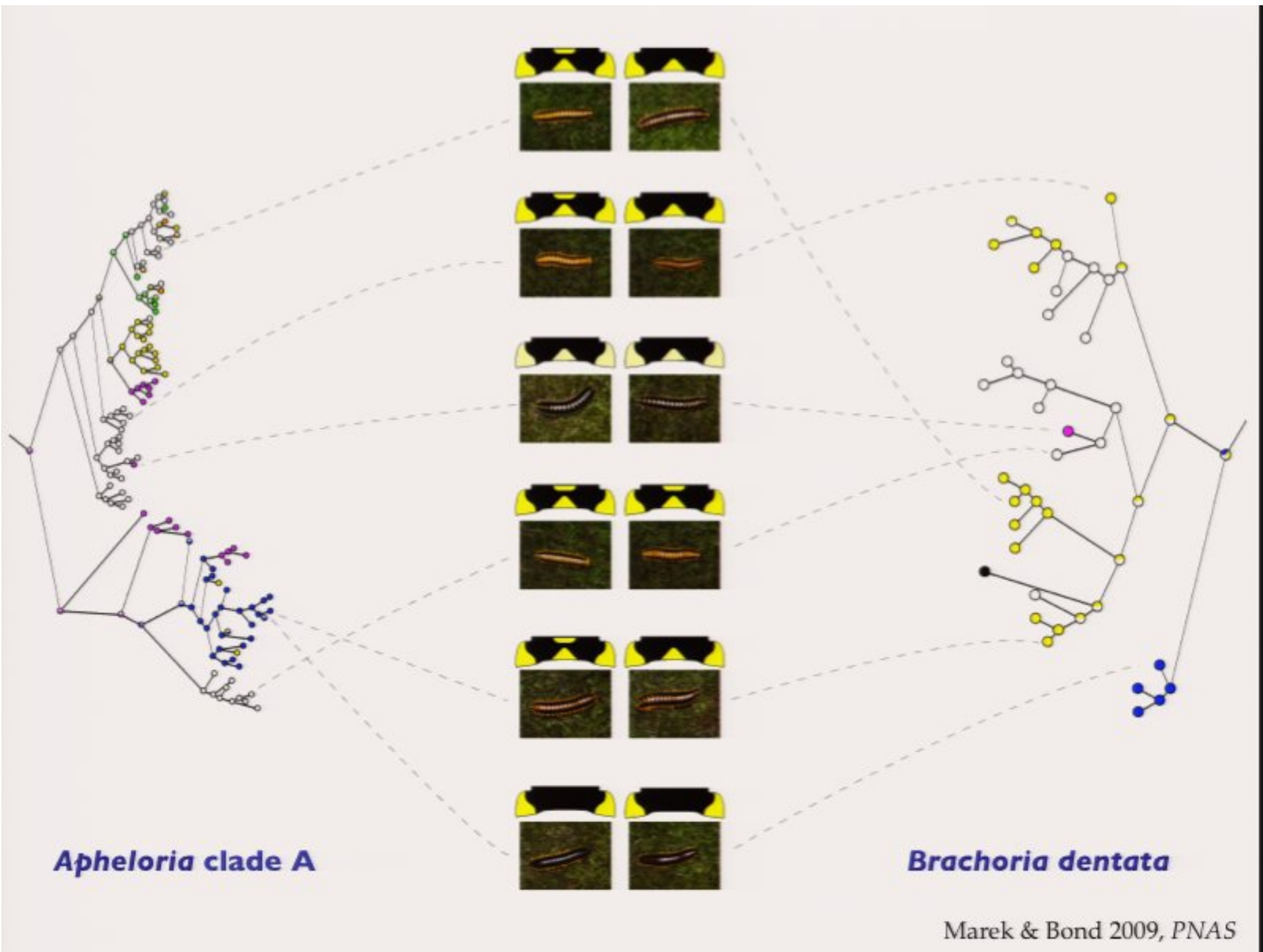














# A Müllerian mimicry ring in Appalachian millipedes

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Edited by May R. Berenbaum, University of Illinois at Urbana-Champaign, Urbana, IL, and approved April 10, 2009 (received for review October 17, 2008)

Few biological phenomena provide such an elegant and straightforward example of evolution by natural selection as color mimicry among unrelated organisms. By mimicking the appearance of a heavily defended aposematic species, members of a second species gain protection from predators and, potentially, enhanced fitness. Mimicking a preexisting warning advertisement is economical because a potentially costly novel one can be avoided; simultaneously, the addition of more aposematic individuals enhances the overall warning effect. The better-known mimetic systems comprise tropical taxa, but here, we show a remarkable example of color mimicry in 7 species of blind, cyanide-generating millipedes endemic to the Appalachian Mountains of temperate North America. Because these millipedes lack eyes, there is no sexual selection or intraspecific signaling for coloration, providing an ideal system for mimicry studies. We document a Müllerian symbiosis where unrelated species vary in color and pattern over geographical space but appear identical where they co-occur. By using spectral color data, estimations of evolutionary history, and detailed field observations of species abundance, we test 4 predictions of Müllerian mimicry theory and begin to unravel the story of an elaborate mimetic diversification in the forests of Appalachia.

aposematic | reflectance | Apheloriini | Diplopoda | Brachoria

Müllerian mimicry, a shared coloration system in which all participant species are defended (1), is the more commonly documented mimicry phenomenon. Batesian mimicry, in contrast, is a form where one species is undefended and the other is defended (2). Müllerian theory predicts mutualism between species and positive frequency dependence whereby “honest” warning signals (backed up by antipredation defense) are maximized to reinforce a shared signal (3, 4). Alternatively, Batesian mimicry predicts negative frequency dependence whereby an “honest” signal is copied by a “dishonest” signal. Batesian and Müllerian mimics in nature are exemplified by tropical Amazonian butterflies, which compose diverse and fantastically complex systems (1–4).

Apheloriine millipedes, endemic to the forests of temperate North America, are aposematic (i.e., their appearance signals to predators that they are unprofitable prey). Each individual can secrete 18-fold the amount of hydrogen cyanide necessary to kill pigeon-sized birds (5, 6). Cyanogenesis occurs in 2 internal glands—one secreting the stable precursor mandelonitrile, and the other secreting the enzyme hydroxynitrile lyase (7). Their admixture creates the cyanide, and the millipede opens a muscle-actuated valve to squirt it through lateral gland openings called ozopores. Apheloriine millipede aposematism involves a conspicuous display of color patterns that vary in hue, including yellow, red, orange, and pink (Fig. 1).

For more than 30 years, scientists have postulated that color mimicry occurs within communities of Apheloriini in the Appalachian Mountains of the eastern United States (8, 9). Extensive field observations by P.E.M. suggest that certain apheloriine millipedes constitute complex mimicry rings, where variable aposematic hues and patterns are shared among sympatric species. However, these hypotheses have never been formally tested within the context of a comparative evolutionary framework. Because all apheloriines produce cyanide, a Müllerian

mimetic system is considered to be operable in this millipede tribe in the Appalachian Mountains.

We report the discovery and evaluate the evolutionary dynamics of an intricate Müllerian mimicry complex among 7 apheloriine species endemic to the valleys and ridges of the Appalachian Mountains. Species in this group are differentiated by the structure of male genitalia. Color and pattern vary considerably within species, and co-occurring species often appear identical (Fig. 1). Some sympatric populations have up to 5 conimic species within an area less than 50 m<sup>2</sup> (video of mimicry community from site 1, Stone Mountain, Virginia; Movie S1). The evolutionary phenomenon of geographical covariation in color and pattern between apheloriine species parallels exemplary cases in butterfly species from the Amazon. This mimicry ring phenomenon in millipedes agrees with the theory of mimetic divergence that states a mimic species converges over evolutionary time with a preestablished, widespread, and variably colored model species (4).

Apheloriine millipedes are ideal models for studying aposematism and mimicry for several reasons. First, they are abundant and have high endemic species diversity; up to 43 individuals comprising 5 unique species can be found in a single 50-m<sup>2</sup> area. Second, apheloriines display extremely variable colors and patterns both within and between species. Third, there is no known diet-color correlation: all co-occurring species feed on decaying leaves of the same deciduous tree species (tulip-poplar, maple, and oak). Fourth, all apheloriines—indeed, the entire order Polydesmida—lack eyes. Thus, there is no sexual selection for coloration or any other intraspecific color signaling. Instead, coloration appears to be linked solely and directly to warning colors and mimicry. This is perhaps the most exciting aspect of using apheloriine millipedes as models to study aposematism. Their coloration provides a controlled and isolated view of warning signaling and mimetic resemblance. To study this mimetic symbiosis in millipedes, we investigated 7 species endemic to the Appalachian Mountains as a model system to test the following predictions of Müllerian mimicry: (i) species share the same aposematic signal, (ii) a shared signal is not attributable to close evolutionary relatedness, (iii) rarer species tend to mimic the most abundant and/or most highly defended model, and (iv) the mimicry varies geographically as a function of the model's geographical variation in color pattern.

## Results

The study species are endemic to the mountainous confluence of Virginia, Kentucky, and Tennessee. We surveyed 2 species of *Apheloria* (*A.* clade A and *A.* clade B) and 5 species of *Brachoria* (*B. corda*, *B. dentata*, *B. insolita*, *B. mendota*, and *B.* species “n”). Together, these comprise all of the region's known apheloriines.

Author contributions: P.E.M. and J.E.B. designed research; P.E.M. performed research; P.E.M. analyzed data; and P.E.M. and J.E.B. wrote the paper.

The authors declare no conflict of interest.

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## A revision of the Appalachian millipede genus *Brachoria* Chamberlin, 1939 (Polydesmida: Xystodesmidae: Apheloriini)

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The apheloriine millipede genus *Brachoria* as presented here comprises 34 species distributed throughout the south-eastern US Appalachian Mountains. Members of this genus are blind (like all millipedes in the order Polydesmida), large (4–6 cm in length), and display conspicuous aposomatic coloration in yellow, red, orange, and violet. Many *Brachoria* species participate in Müllerian mimicry rings with co-occurring Apheloriini, in particular with species in the genus *Apheloria*. Some areas contain five co-mimic species of Apheloriini and a high local density totalling 43 individuals per 50 m<sup>2</sup>. Since the first revision in 1959, workers have suggested that many more species were awaiting discovery in the Cumberland Mountains. Here I present a taxonomic revision and describe ten new species: *Brachoria badbranchensis*, *Brachoria blackmountainensis*, *Brachoria campervehenensis*, *Brachoria cumberlandmountainensis*, *Brachoria flammpes*, *Brachoria grapevinensis*, *Brachoria guntermountainensis*, *Brachoria hendrixsoni*, *Brachoria sheart*, and *Brachoria virginia*. Five of these new species occur in the Cumberland Mountain Thrust Block region and five occur elsewhere throughout the Appalachian Highlands in eastern Kentucky, north-eastern Alabama, southern West Virginia, south-western Virginia, and the Blue Ridge Mountains of Tennessee. A molecular phylogeny of *Brachoria* species is well supported at deeper divergences, corresponds closely with geography, and is used as a phylogenetic basis for the taxonomy presented here.

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doi: 10.1111/j.1096-3642.2010.00633.x

ADDITIONAL KEYWORDS: aposomatic – biodiversity – Cumberland Mountains – Diplopoda – southeastern US – genitalia evolution – mimicry – molecular phylogeny – taxonomy – Valley and Ridges.

### INTRODUCTION

The genus *Brachoria* as presented here is the third largest millipede genus in the US, with 34 described species (*Cleidogona* and *Pseudotremis* are the largest with 80 and 47, respectively). The genus encompasses an impressive and colourful fauna distributed throughout the Appalachian mixed mesophytic forests. Many species in the genus display conspicuous warning coloration that evolved to warn predators of toxic cyanide defence secretions. Most species

share a striking resemblance with co-occurring species (frequently with those in the genus *Apheloria*) and represent a widespread diversification of mimetic colour forms throughout Appalachia (Marok & Bond, 2009). On Stone Mountain in Virginia, for example, four *Brachoria* and one *Apheloria* species co-occur in a single 50-m<sup>2</sup> area, where they display a strong mimetic resemblance. These brightly coloured Müllerian mimics (i.e. a mimetic system where all species involved are toxic, in contrast to Batesian mimicry, where one species is nontoxic and the other is toxic) often achieve high local densities – up to 43 millipedes per 50 m<sup>2</sup>, as is the case on Stone Mountain.

The Diplopoda (millipedes) encompass an incredible estimated diversity. There are 12 000 described

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near Bad Branch, about 30 m above (west of) the water. Another population of *B. badbranchensis* occurs on the north slope of Pine Mountain in James E. Bickford Nature Preserve (see *B. gracilipes* for habitat details there). One other xystodesmid encountered sympatrically at the Bad Branch locality is *Apheloria virginianensis corrugata* (Wood, 1864), which has a mimetic resemblance with *B. badbranchensis*. Other xystodesmids encountered on the nature preserve were *B. splendida*, *B. gracilipes*, *Pleurodema flavipes* Rafinesque, 1820, and undescribed species of *Nannaria*. Note: individuals of *B. badbranchensis* may easily be confused in the field with *A. v. corrugata*, *B. splendida*, *B. gracilipes*, and *P. flavipes* because of similarity in colour patterns, but can be distinguished from the other *Brachoria* species by the diagnostic characters and from *A. v. corrugata* and *P. flavipes* by the presence of the following characters (viewed with a 20 $\times$  loupe). Acropodite with midlength transverse groove, cingulum. Acropodite, when ventrally viewed, fancy 7-shaped (Fig. 4B). Acropodite not circular like in *A. v. corrugata*. Acropodite distinctly bent anteromedially at 60°, one-ninth its length from the profemur, not straight as in *P. flavipes*. Acropodite projecting straight from the profemur, whereas in *P. flavipes* (and other individuals in the tribe Rhysodesmini) the acropodite is bent at 90° from the profemur. *Nannaria* is easy to distinguish; it has an olive drab colour and a body length about two-thirds of that of *B. badbranchensis*.

**Distribution:** Known only from the type locality and James E. Bickford Nature Preserve near the town of Pine Mountain. The closest known *Brachoria* species, *B. hoffmani*, occurs about 15 air km north-east in Jefferson National Forest near Pound Gap, Wise

County, Virginia. *Brachoria insidiosa* occurs about 22 air km south-east in Norton City, Virginia.

**Material examined:** Type specimens. ♂ holotype (FMNH-INS43054\*: EU127873), 1♀ paratype (FMNH-INS43055), 1♂ paratype (USNM, SPC001049) from Kentucky, Letcher County, Bad Branch Nature Preserve, Preserve Trail, above falls, about 2.0 trail km north of junction with KY-932 (37.08020°N, -82.77232°W, 683 m), 29.vii.2006, 15:00 [collector (coll): P. Marek]. Nontype specimens. Kentucky: 5♂ (SPC001065, 76-79), Harlan County, north slope of Pine Mountain, James E. Bickford Nature Preserve, Pine Mountain Settlement School (36.94733°N, -83.18072°W, 577 m), 8.v.2007, 12:00 (colls: P. Marek, C. Hall, D. and M. Benner, J. Staubach, and E. Keyser). 1♂ (A8708), Letcher County, about 6.4 km east-south-east of Whitesburg, along Bad Branch Creek, off KY-932 (37.0677°N, -82.7707°W), 11.vi.2001 (coll: R. Shelley).

**Etymology:** This species is named after Bad Branch, a pleasing stream with a nice waterfall in Bad Branch State Nature Preserve, one of the many wonderful nature preserves in Kentucky. (The specific name is a feminine adjective derived from the type locality.)

***BRACHORIA BLACKMOUNTAINENSIS* SP. NOV.**  
 'THE BLACK MOUNTAIN MIMIC MILLIPEDE'  
 (FIG. 5A-D, FIG. 39D-F)

**Diagnosis:** Adult males of *B. blackmountainensis* are distinct from other *Brachoria* species based on the combination of: Exoskeleton. Caudolateral corners, paranota 1-13 broadly rounded, lateral margins 1-4 angled cephalically. Gonopods. Gonopodal acropodite

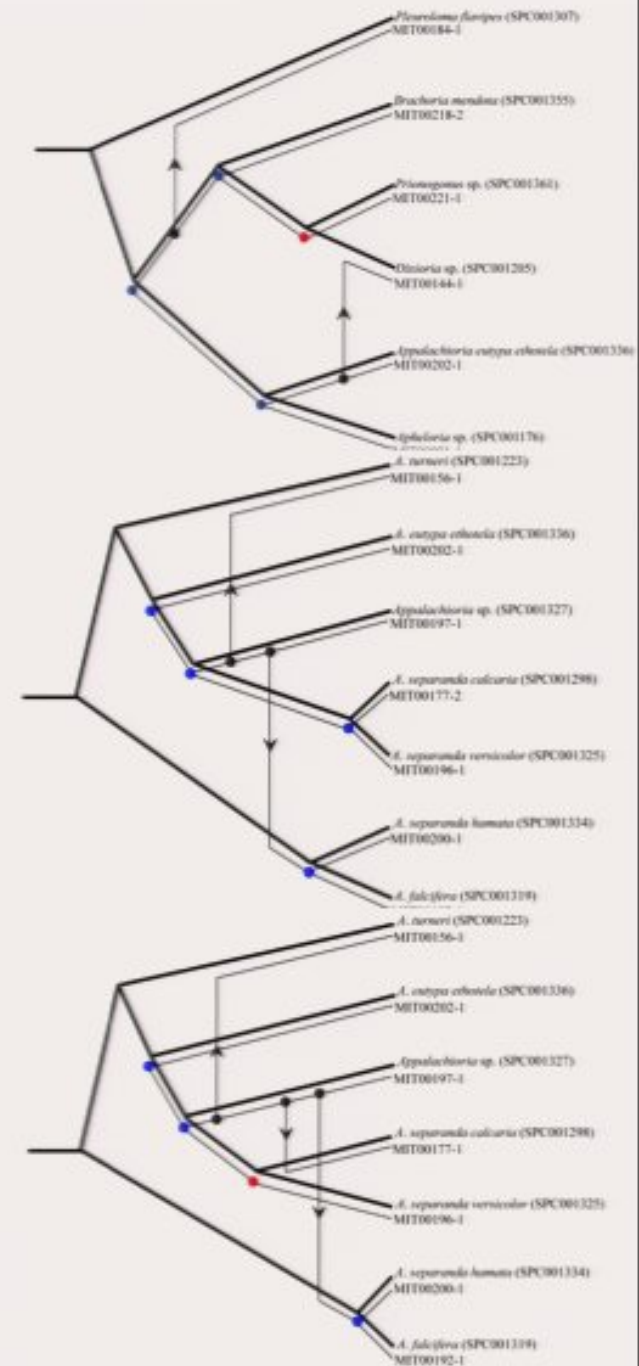
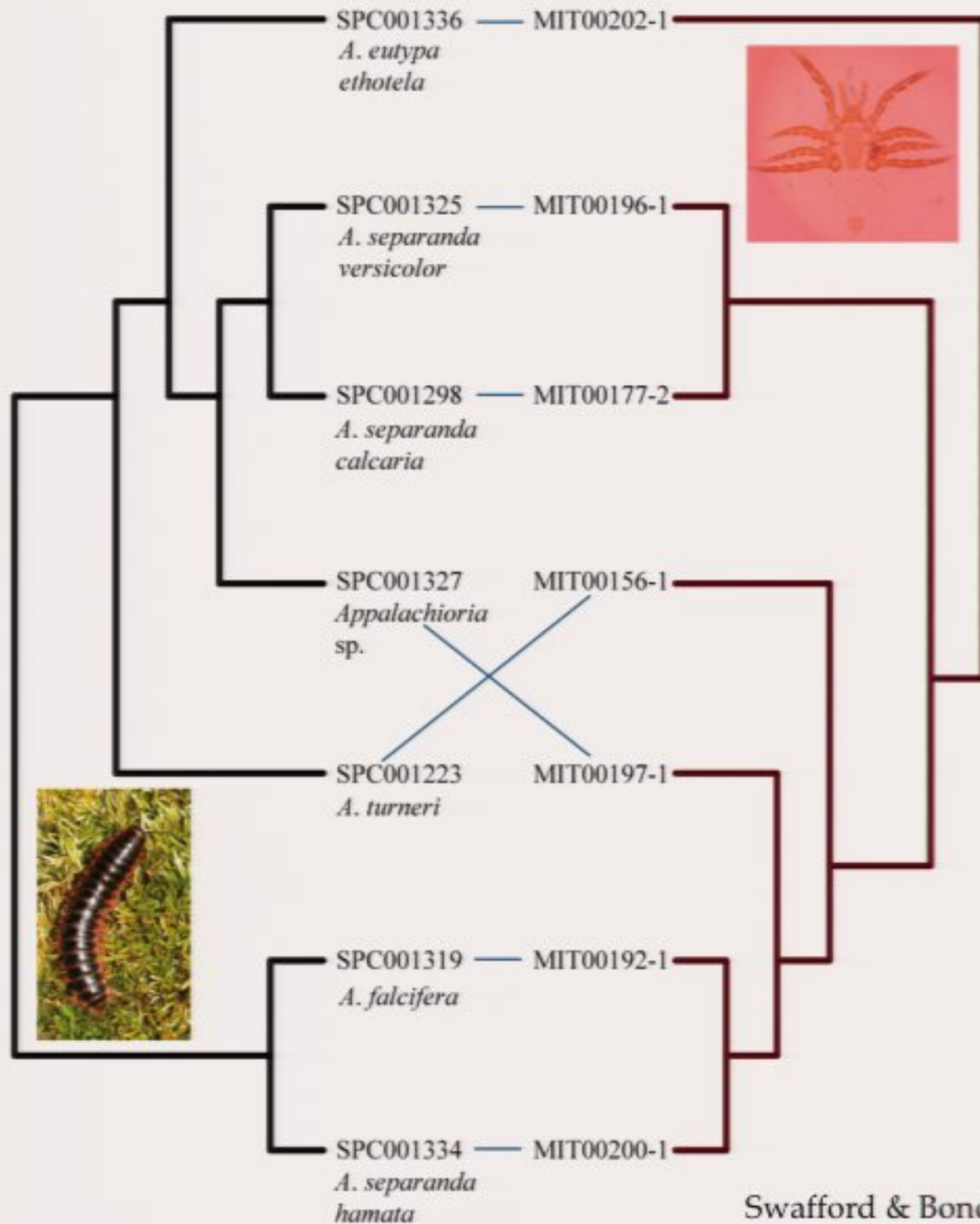


Figure 5. *Brachoria blackmountainensis* sp. nov. A-D, holotype specimen gonopods: A, left male gonopod, anterior view; B, left male acropodal apex, magnified; C, left male gonopod, medial; D, same, posterior (acropodite length = 2.05 mm).

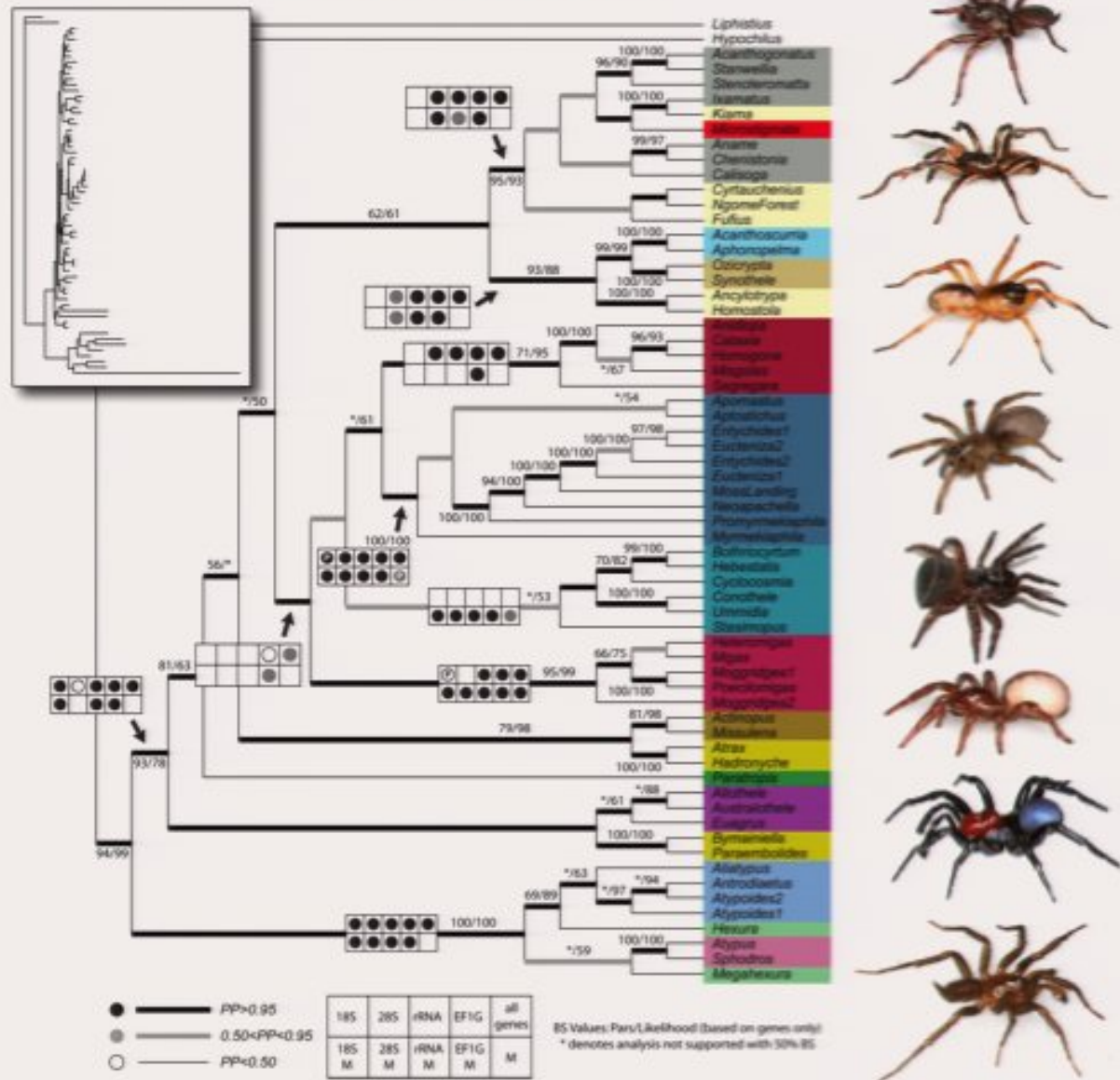


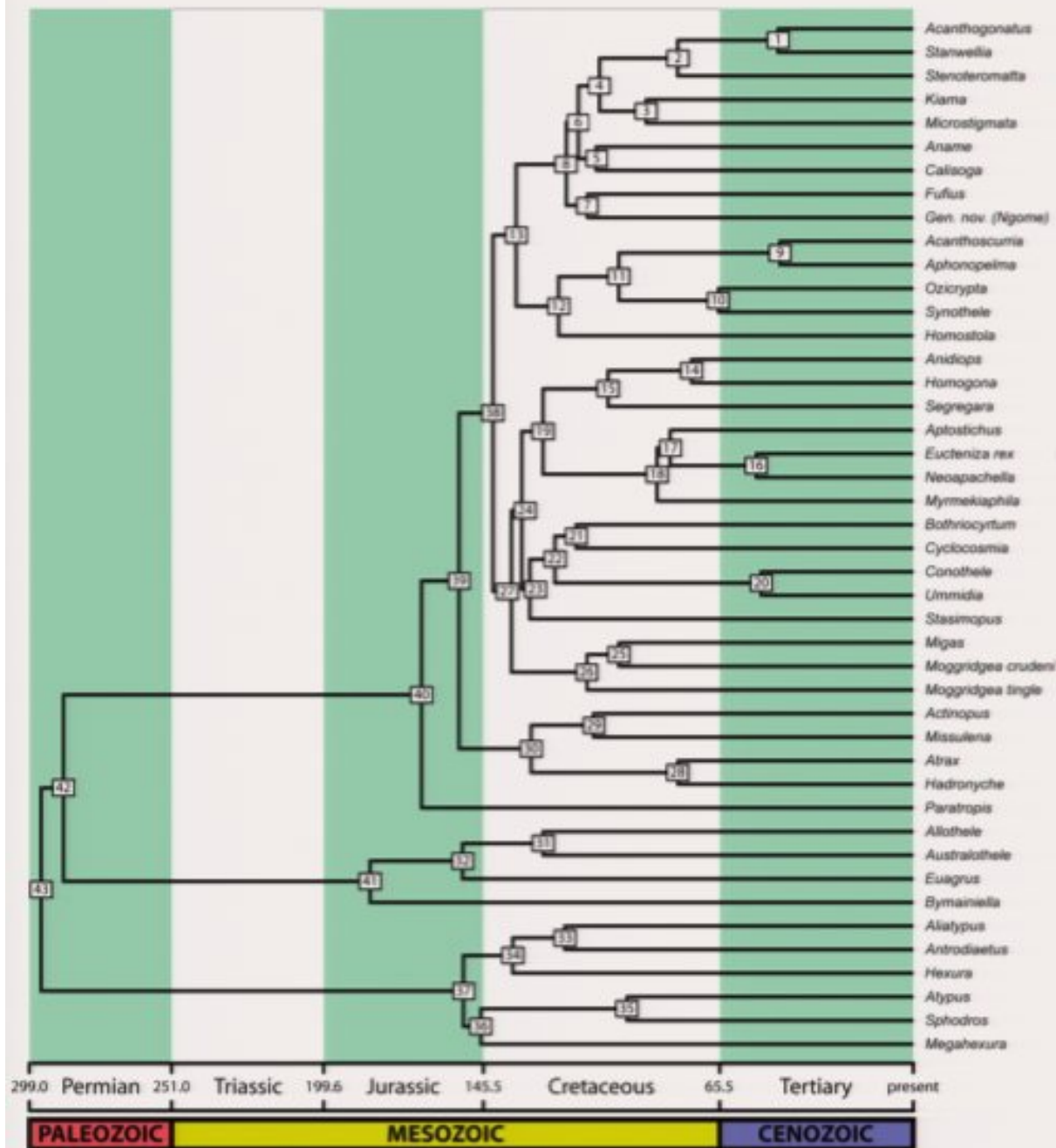
**Figure 2.** Top, *Bruchoria* species left male acropodites (with setae removed): (left) medial view and (right) magnified apical view. A–C, gonopod scanning electron micrographs, labelled with key anatomical features. A, 'bulky' gonopod from *Bruchoria splendida* (SPC000171), scale bar = 1 mm; B, 'narrow' gonopod from *Bruchoria hendrixsoni* (SPC000219), scale bar = 1 mm; C, acropodite from *B. hendrixsoni*, magnified view of cingulum and prostatic groove. D, *Bruchoria initialis* gonopod diagram, colour-coded by region – dashed lines indicate junctions between (moving distally from the prefemur) the precingular region, postcingular region, and apex. Abbreviations: ap, acropodite; ax, acropodite apex; cx, caxilla; cg, cingulum; cx, coxa; post-cg, postcingular region of acropodite; pre-cg, precingular region of acropodite; pf, prefemur; pp, prefemoral process; ps, prostatic groove. The gonopod comprises the acropodite, prefemur, and coxa.





# Spider infraorder Mygalomorphae: trapdoor spiders, funnel web spiders, tarantulas and their relatives





Bond et al. in review







Figures 10–12.—Photos of burrow entrance behavior of adult females of *Ummidia* at Las Cruces, Costa Rica. 10, Spider in foraging posture at night; arrows point to claws, from left to right, of right leg II, right leg I, right pedipalp, left pedipalp, and left leg I touching entrance rim; 11, Spider attempting to close door with fangs and claws of pedipalps, legs I, and legs II; 12, Spider attempting to close fully opened door with claws and fangs while anchoring itself in burrow with legs III.



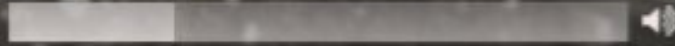
Figures 3–5.—Photos of burrows of adult females of *Ummidia* at Las Cruces, Costa Rica. 3, Entrance with trapdoor propped open to show small broken silk seal and small old door attached to upper surface of functional trapdoor; 4, Side view of burrow and trapdoor excavated (same as in Fig. 3) in 1992, with female (upper wall of upper end of burrow has collapsed so that door is shifted from its normal position); 5, Side view of burrow excavated in 1993, with female, showing nearly vertical hinge and upper surface of partly open trapdoor.

















## Scientists name diving beetle for Colbert

Thursday, 14 May 2009



by Carol Hughes

"What has six legs and is way cooler than a spider?" asks a riddle on the cover of a birthday card sent to Stephen Colbert by entomologists Quentin Wheeler at Arizona State University and Kelly Miller at the University of New Mexico.

The answer—*Agaporomorphus colberti*—is a diving beetle from Venezuela named by Wheeler and Miller to honor Colbert, the satirical host and executive producer of Comedy Central's "The Colbert Report."

Knowing Colbert's fondness for recognition (there's his popular segment on the show: "Who's Not Honoring Me Now") and for presents, the scientists sent the political satirist a framed print of the beetle as a birthday gift to mark his 45th birthday on May 13.

"Last year, Stephen shamelessly asked the science community to name something cooler than a spider to honor him. His top choices were a giant ant or a laser lion. While those would be cool species to

discover, our research involves beetles, and they are 'way cooler' than a spider any day," Wheeler says.









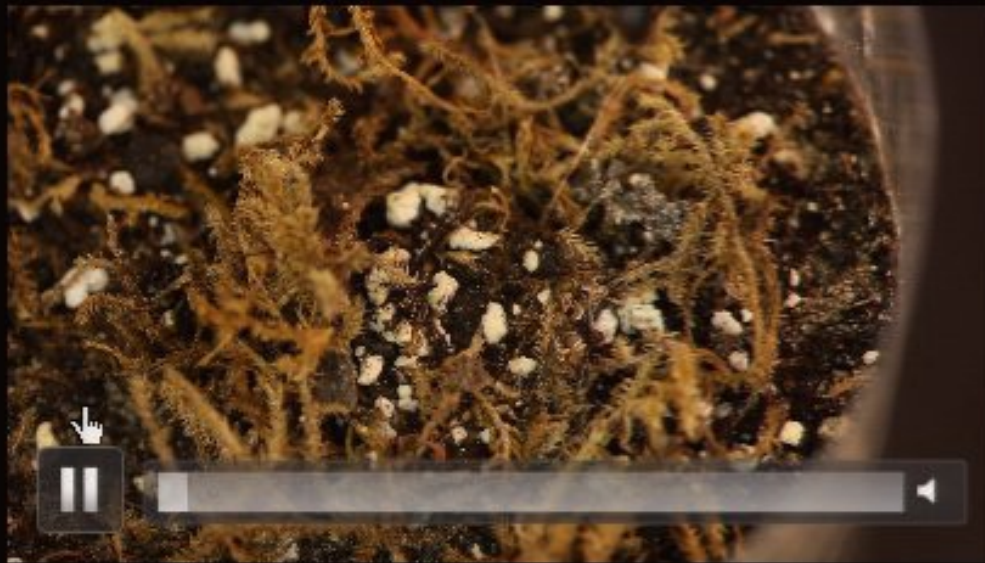
















































































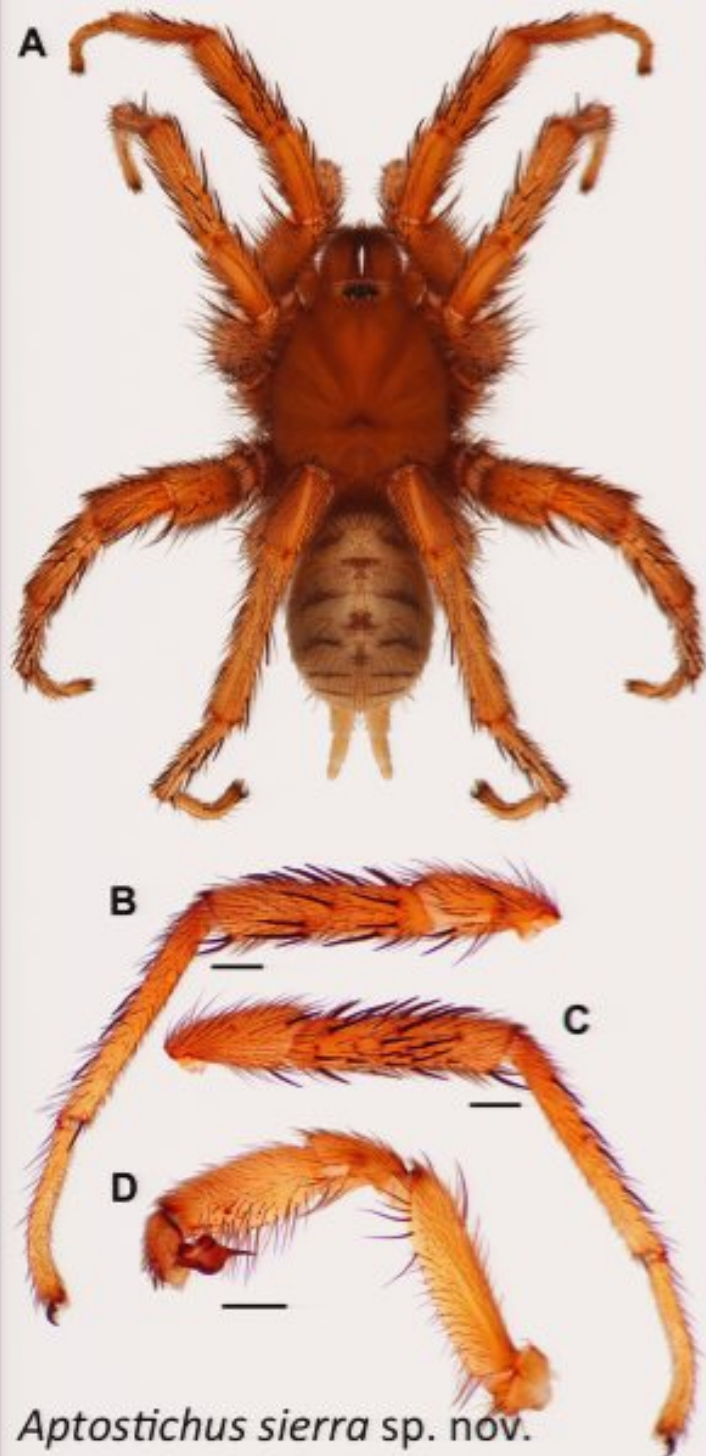








*Aptostichus kumeyaay* sp. nov.



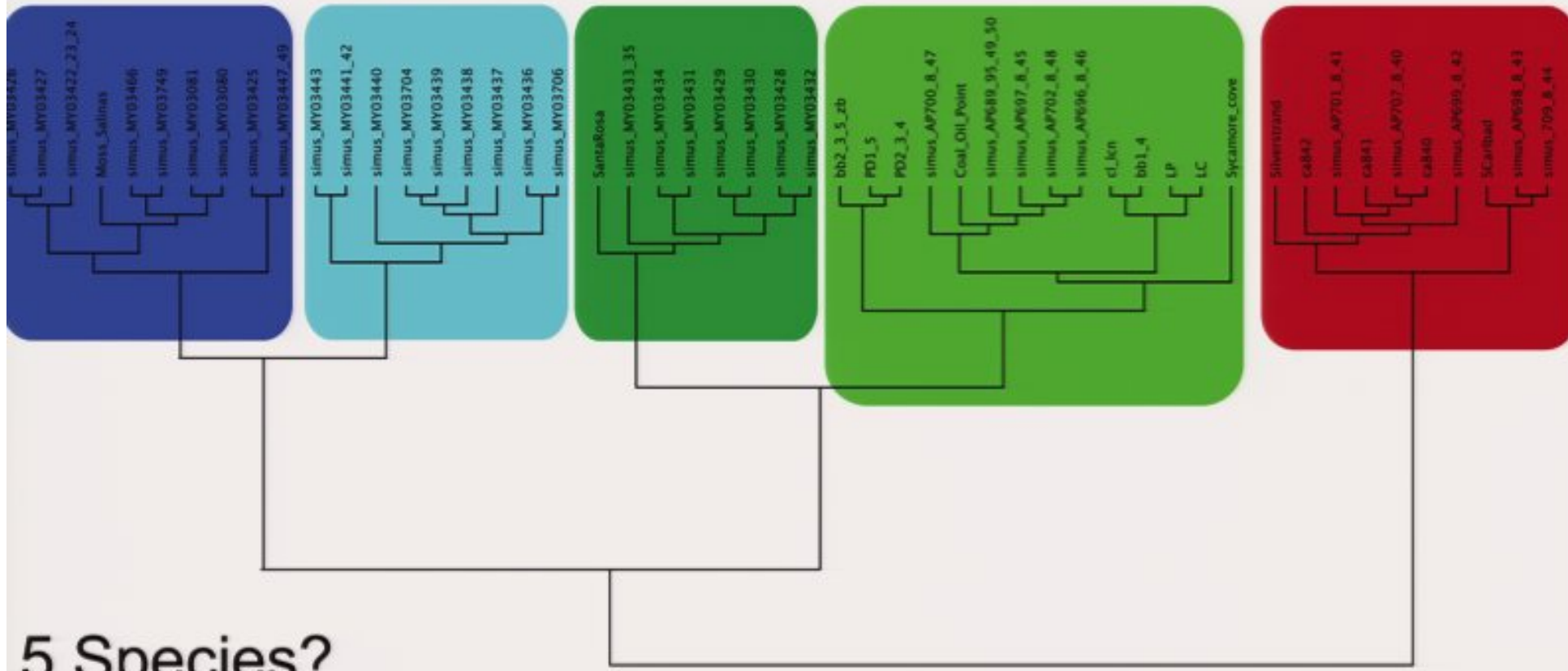
*Aptostichus sierra* sp. nov.





• **Reanalysis of Bond et al. 2001, *Mol. Ecol.***

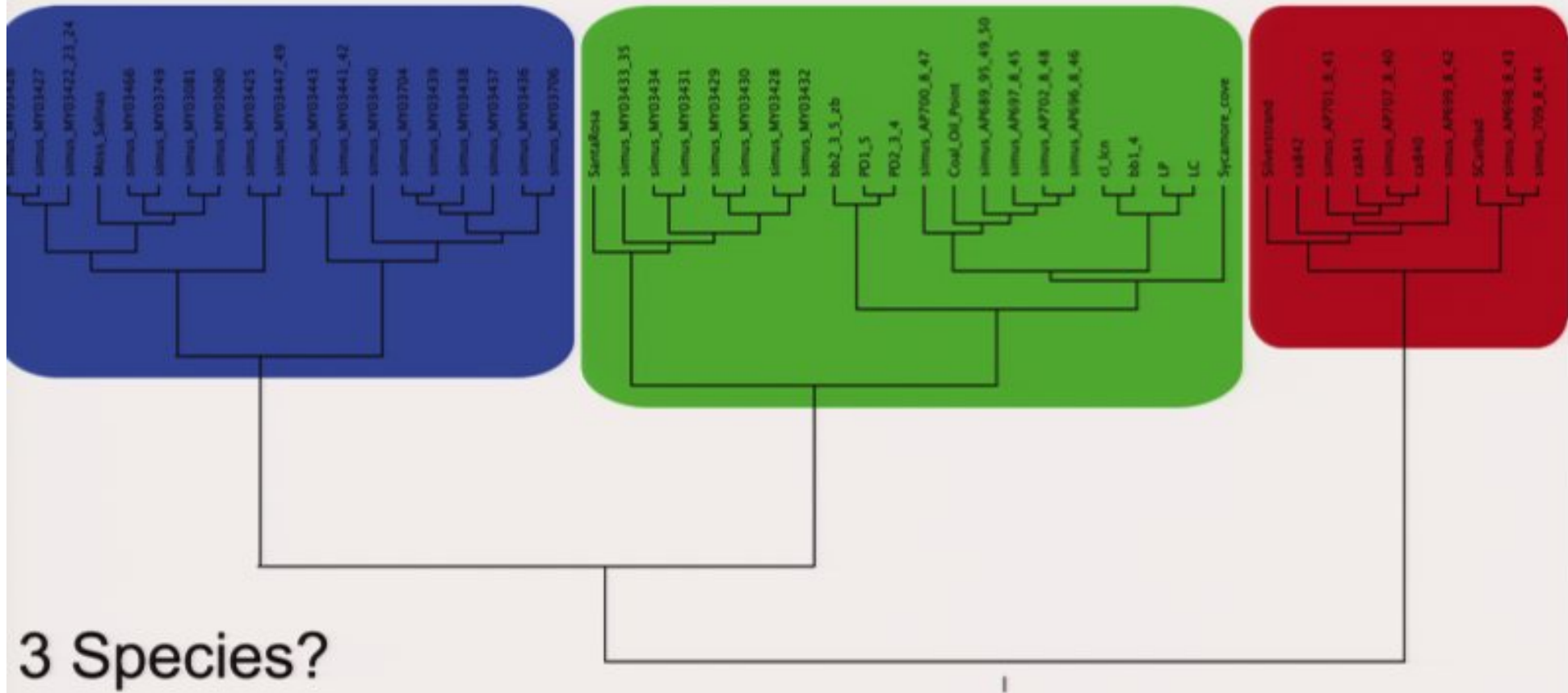
- 75 individuals, 51 haplotypes, 25 populations
  - 1,345 bp 12S-tRNA val-16S
  - RAxML: 100 random add seq reps, 100 bootstrap reps
- $\ln = -3955.477173$ ; all major nodes > 95% bootstrap support



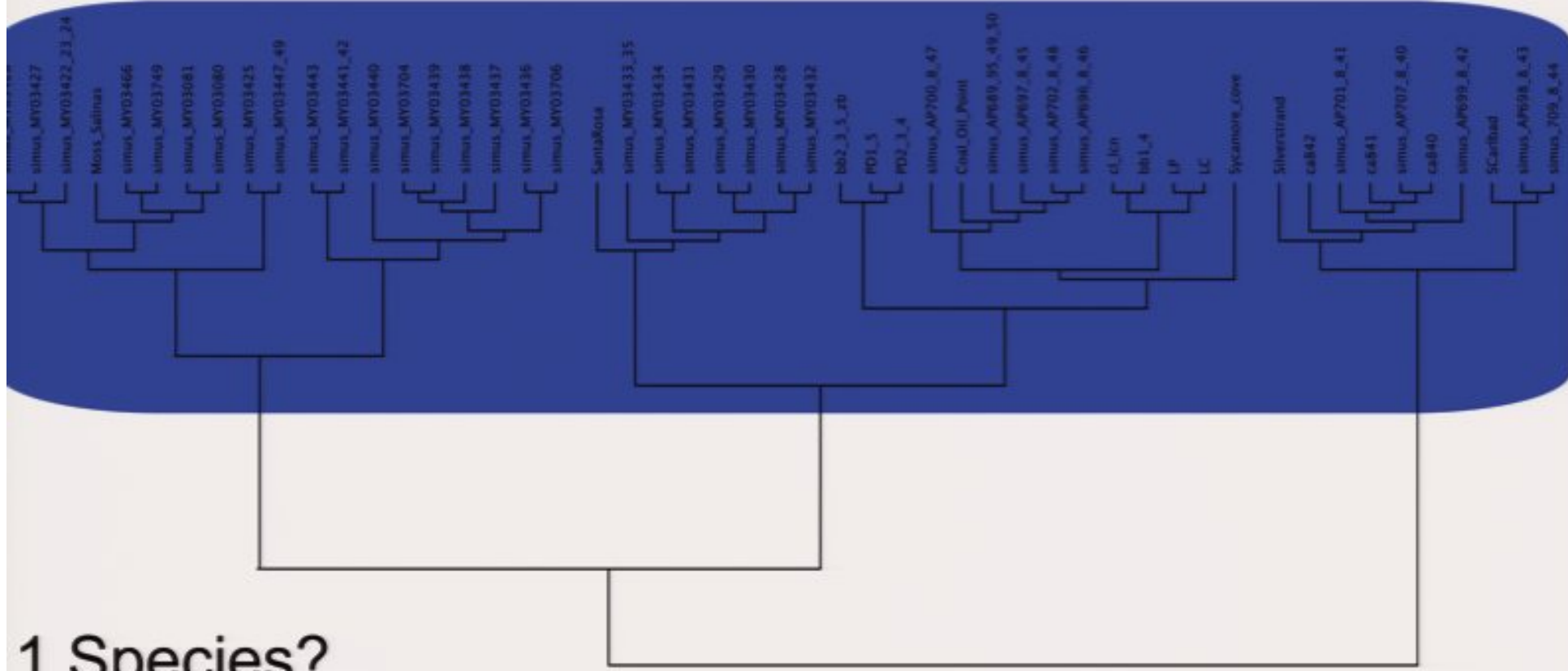
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3 Species?



> 16% uncorrected pairwise difference



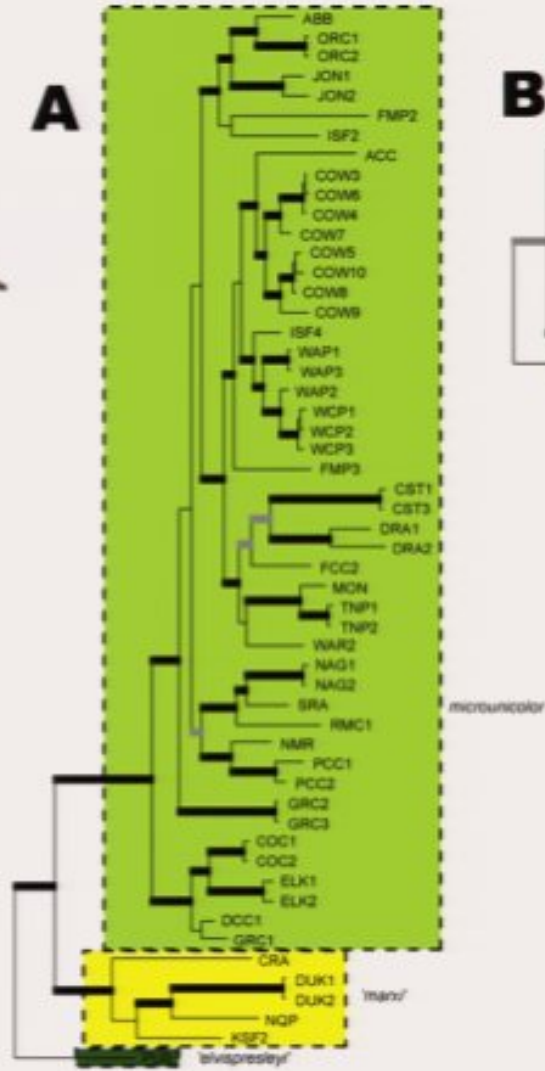
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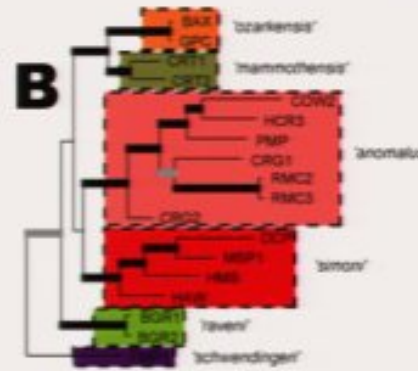




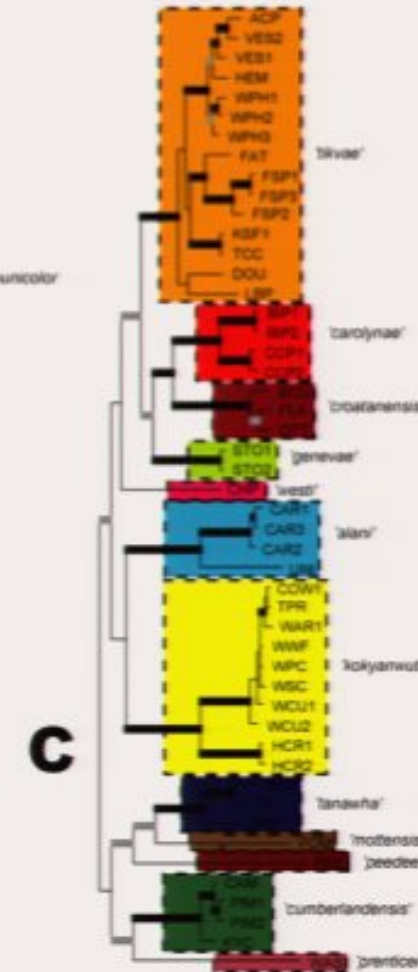
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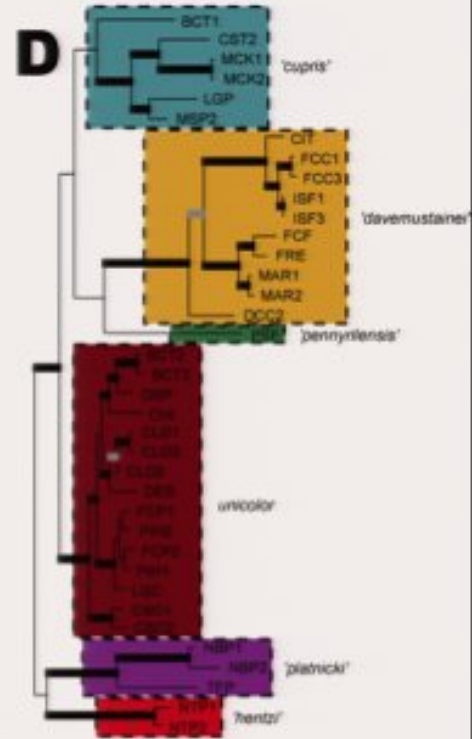
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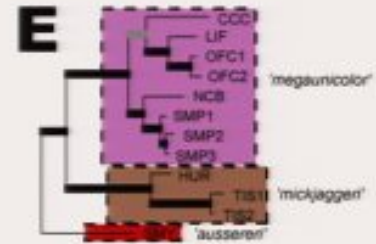
**C**



**D**



**E**

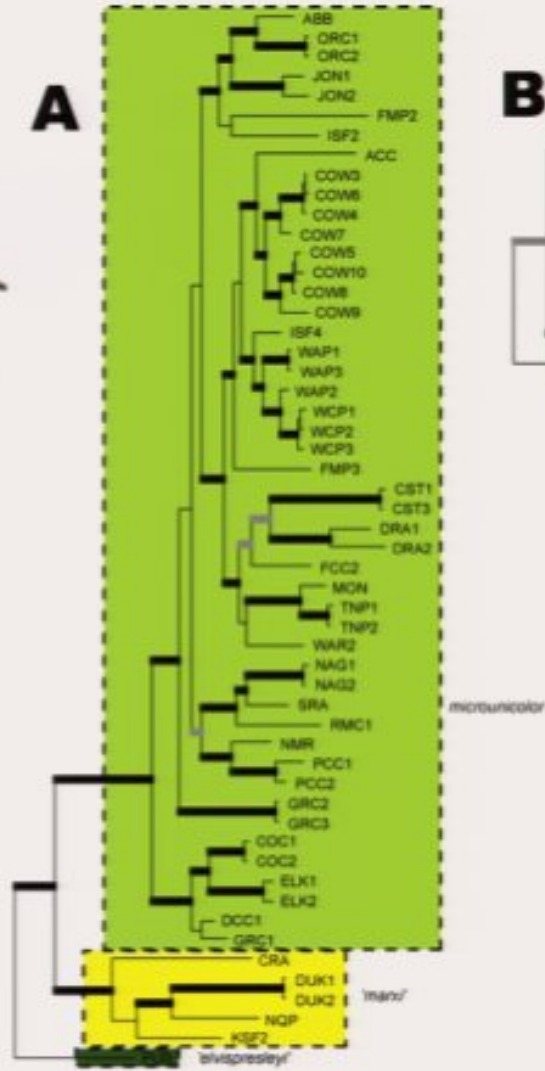


Hendrixson & Bond in prep

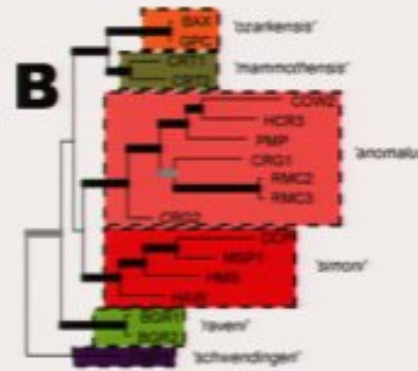




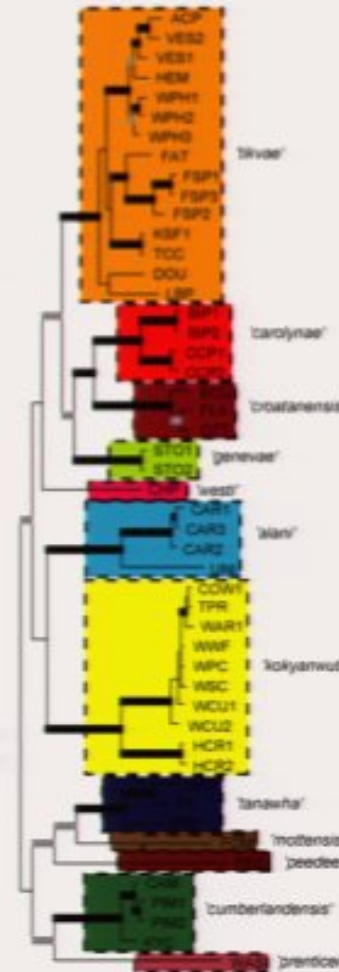
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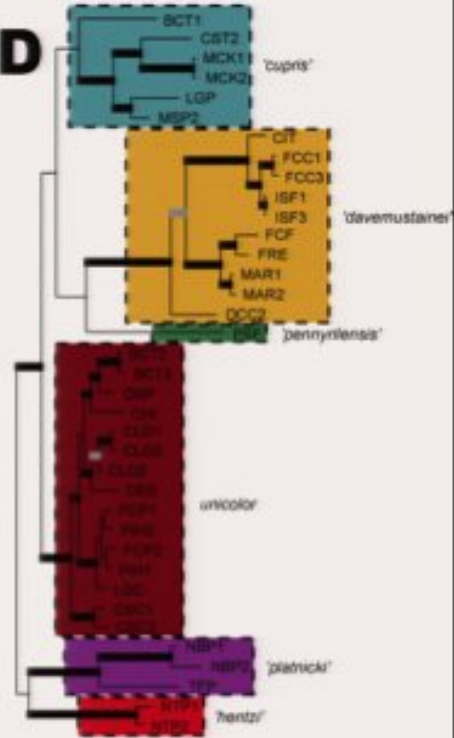
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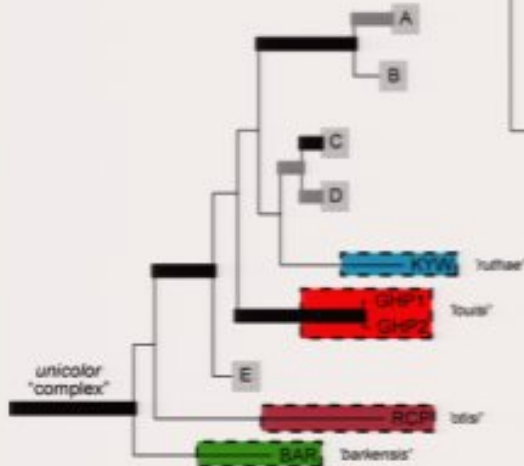
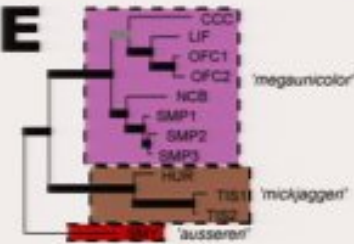
**C**



**D**



**E**









# Phylogeny and Classification of the Trapdoor Spider Genus *Myrmekiaphila*: An Integrative Approach to Evaluating Taxonomic Hypotheses

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## Abstract

**Background:** Revised by Bond and Platnick in 2007, the trapdoor spider genus *Myrmekiaphila* comprises 11 species. Species delimitation and placement within one of three species groups was based on modifications of the male copulatory device. Because a phylogeny of the group was not available these species groups might not represent monophyletic lineages; species definitions likewise were untested hypotheses. The purpose of this study is to reconstruct the phylogeny of *Myrmekiaphila* species using molecular data to formally test the delimitation of species and species-groups. We seek to refine a set of established systematic hypotheses by integrating across molecular and morphological data sets.

**Methods and Findings:** Phylogenetic analyses comprising Bayesian searches were conducted for a mtDNA matrix composed of contiguous 12S rRNA, tRNA-val, and 16S rRNA genes and a nuclear DNA matrix comprising the glutamyl and prolyl tRNA synthetase gene each consisting of 1348 and 481 bp, respectively. Separate analyses of the mitochondrial and nuclear genome data and a concatenated data set yield *M. torreyi* and *M. millerae* paraphyletic with respect to *M. coreyi* and *M. howelli* and polyphyletic *fluvistilis* and *foliata* species groups.

**Conclusions:** Despite the perception that molecular data present a solution to a crisis in taxonomy, studies like this demonstrate the efficacy of an approach that considers data from multiple sources. A DNA barcoding approach during the species discovery process would fail to recognize at least two species (*M. coreyi* and *M. howelli*) whereas a combined approach more accurately assesses species diversity and illuminates speciation pattern and process. Concomitantly these data also demonstrate that morphological characters likewise fail in their ability to recover monophyletic species groups and result in an unnatural classification. Optimizations of these characters demonstrate a pattern of "Dollo evolution" wherein a complex character evolves only once but is lost multiple times throughout the group's history.

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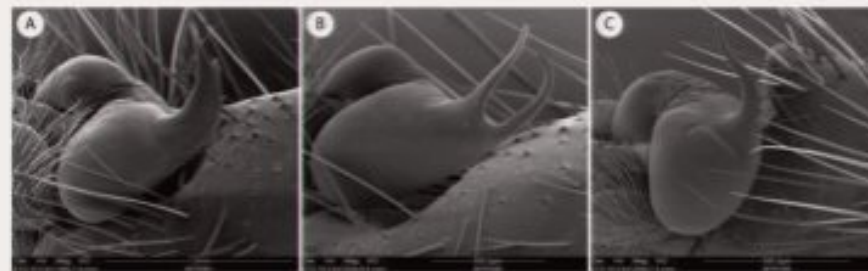
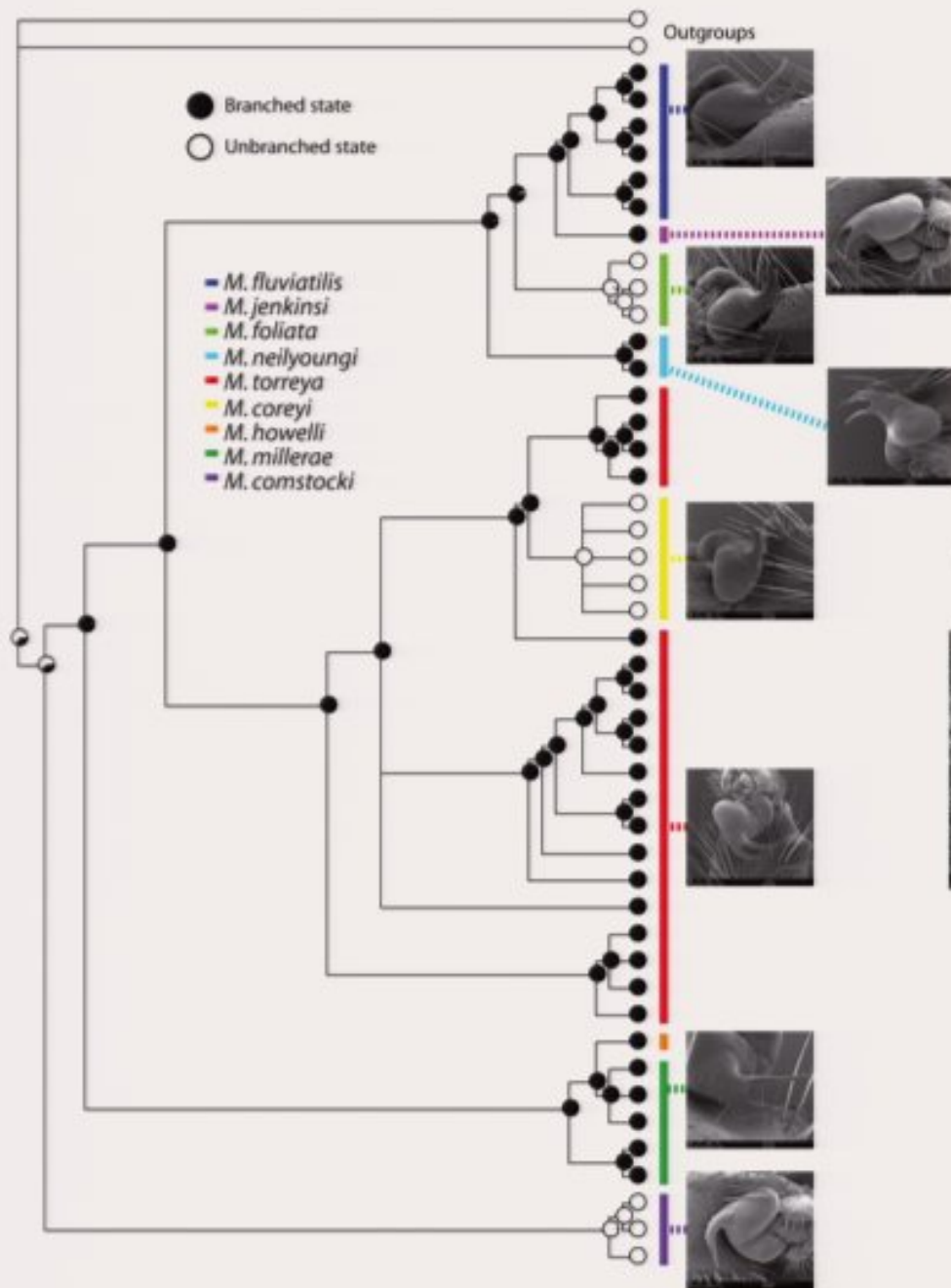
## Introduction

*Unfortunately, in the domain of people using an immediate passion, the molecular identification of species is fraught with the same obstacles and inconsistencies that plague morphological judgments of species boundaries.* [1]

Advances in molecular biology over the past decades continue to shape the nature of systematics and taxonomy. One of the most prevalent examples of how species identification and discovery has changed is through the employment of DNA barcoding [2], an approach considered by many as a universal remedy to the "crisis" in traditional taxonomy and the only opportunity to complete an inventory of all life on the planet [3]. Briefly, DNA barcoding or DNA taxonomy is the utilization of a single gene region, in animals often the cytochrome *c oxidase I (cod)* gene of the

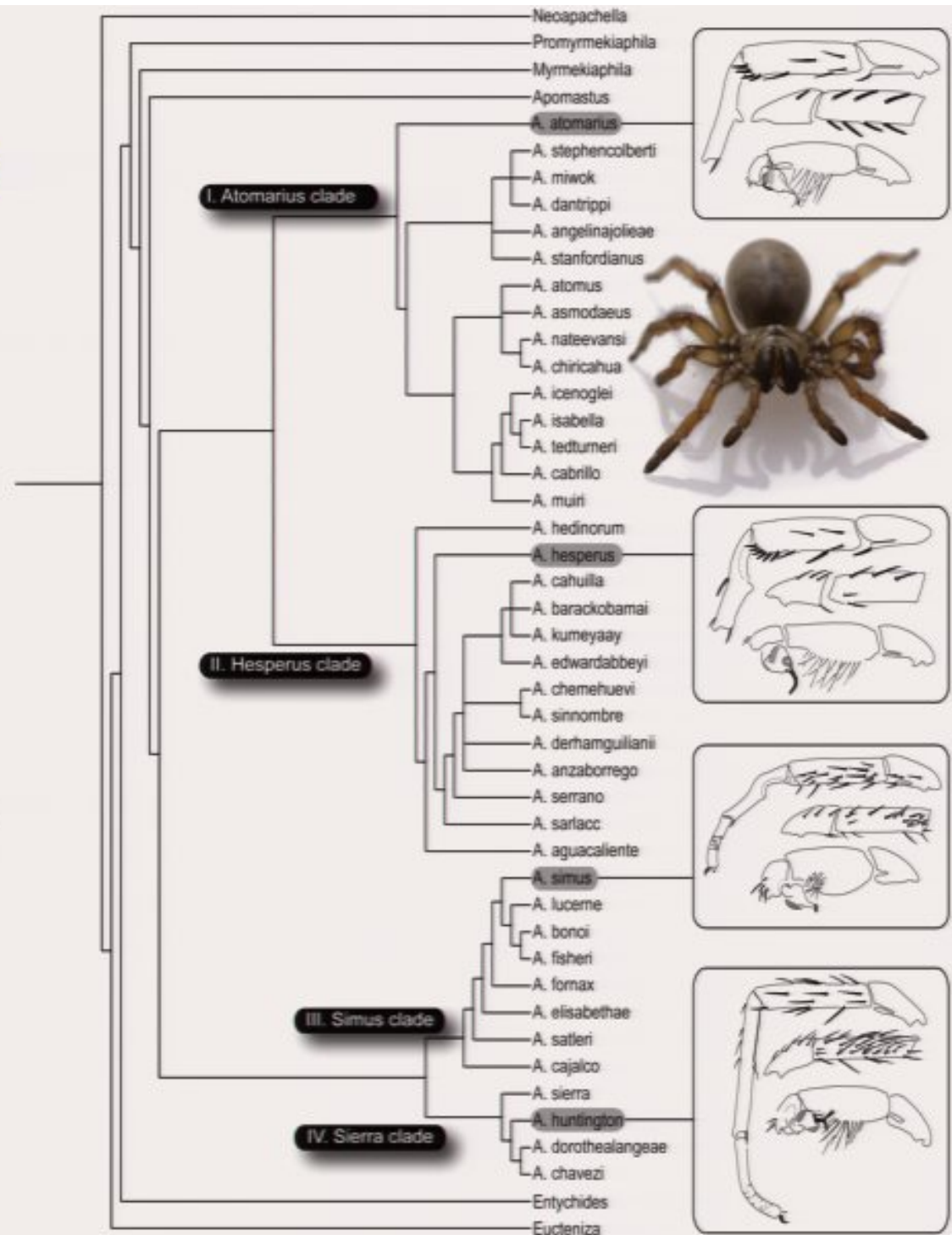
mitochondrial genome, to identify species [4]. DNA barcoding is considered by some a remedy to the idea that traditional alpha taxonomy is time intensive and is a dwindling expertise; that is, there are too few taxonomists to document earth's biodiversity within a reasonable time period.

In general, DNA barcoding or DNA taxonomy could be seen as a simplistic approach to the taxonomic enterprise. Consequently, recent attempts to refine DNA taxonomy have sought to objectively delimitate species based on divergence values, the expectations of a particular diversification-extinction process, or other criteria related to gene tree-species tree construction (e.g., [5,6]). While DNA barcoding and DNA taxonomy have detractors that would be expected of any single marker system, particularly one based on mitochondrial sequences (e.g., [7–10]), the insights provided by molecular sequence data have proven invaluable with respect to enhancing our understanding of speciation pattern and process [11] and distinguishing cryptic



# *Aptostichus* Simon

- Distributed throughout California
- 40 species; 33 new
- Morphology based phylogeny
  - 73 characters
  - PAUP\* 4b10
    - Goloboff fit  $k=7$
    - 1000 Random addition sequence replicates
  - 835 trees, 239 steps,  $CI=0.35$ ,  $RI=0.76$











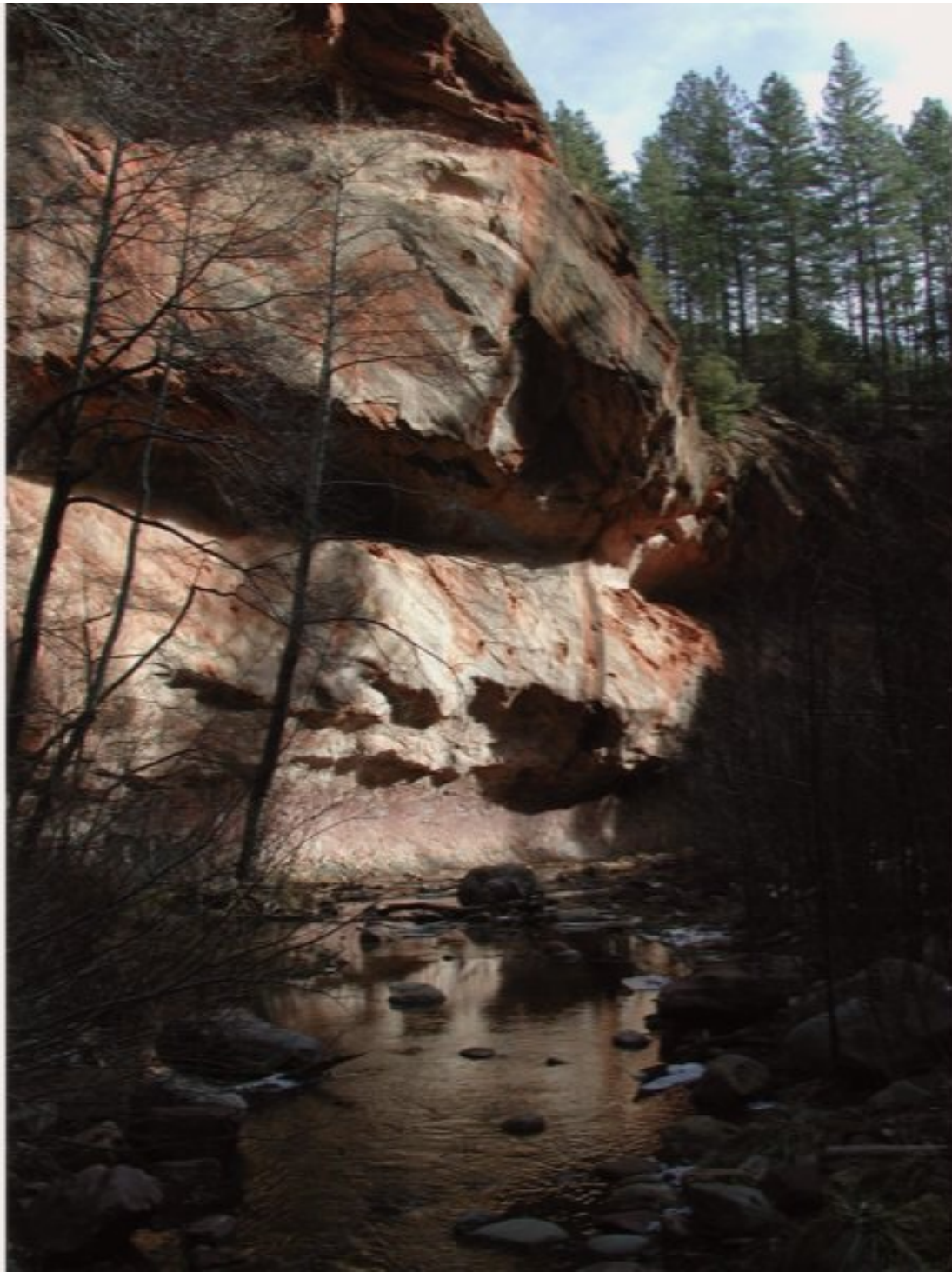








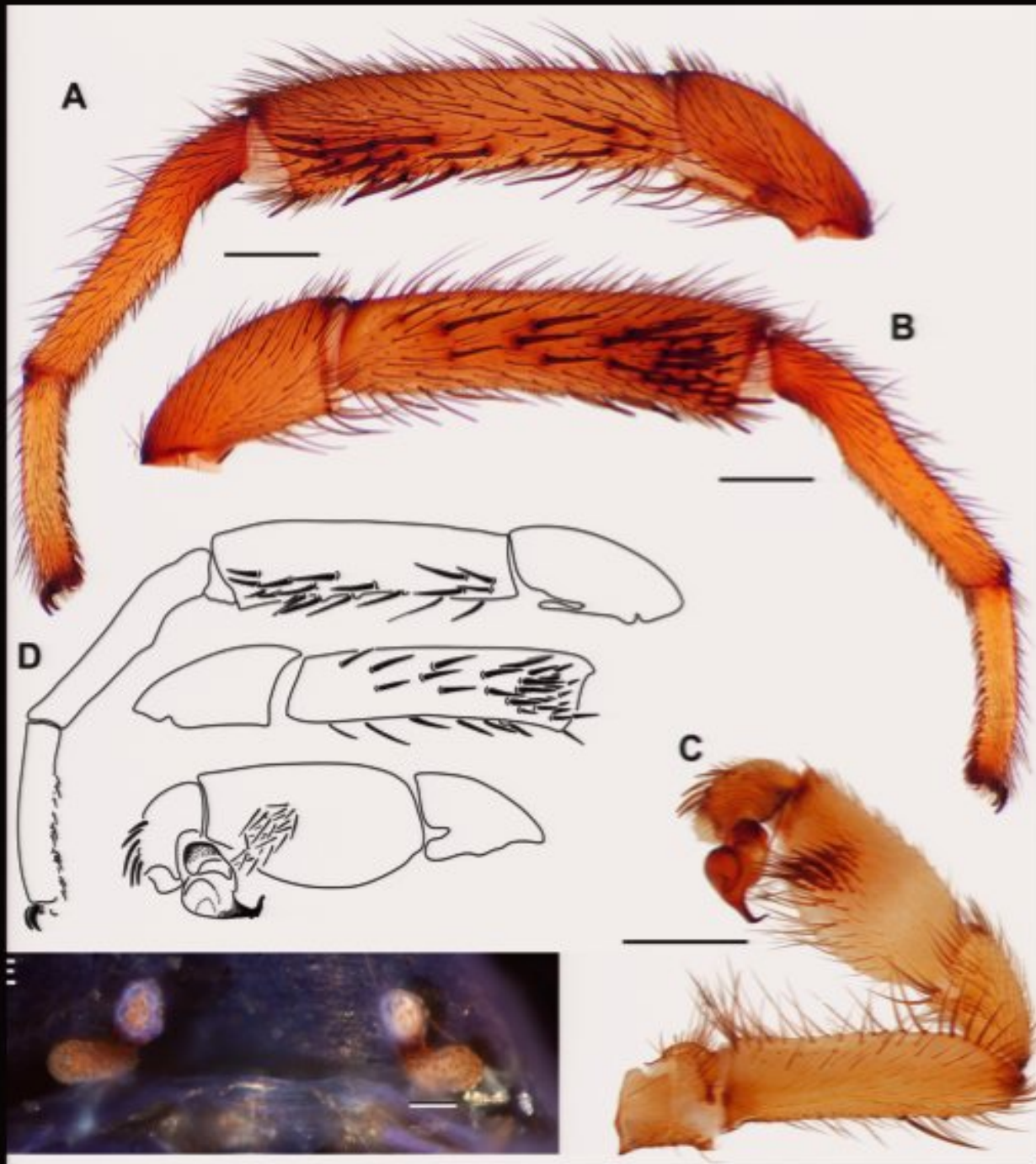








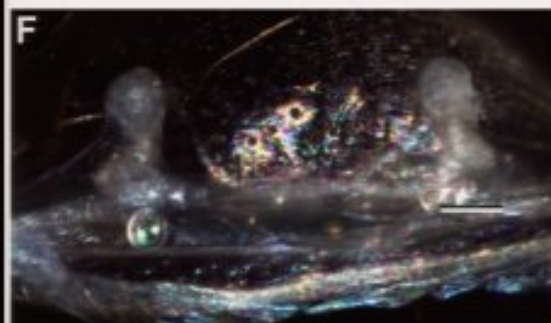
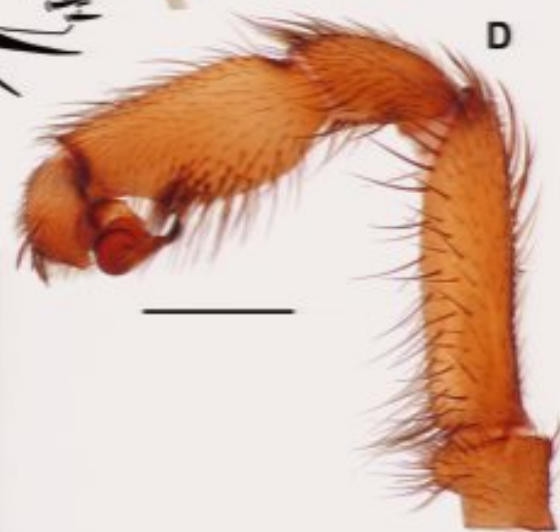
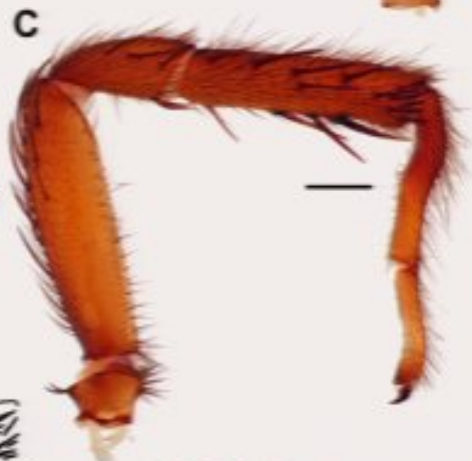
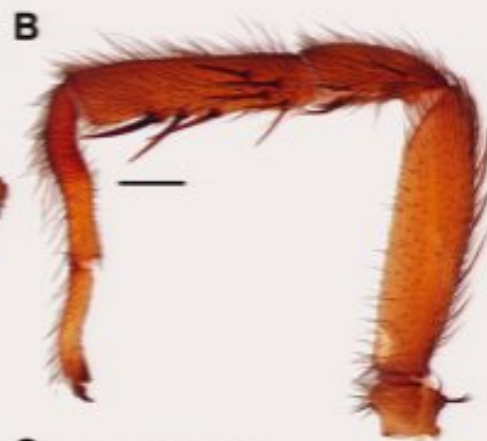














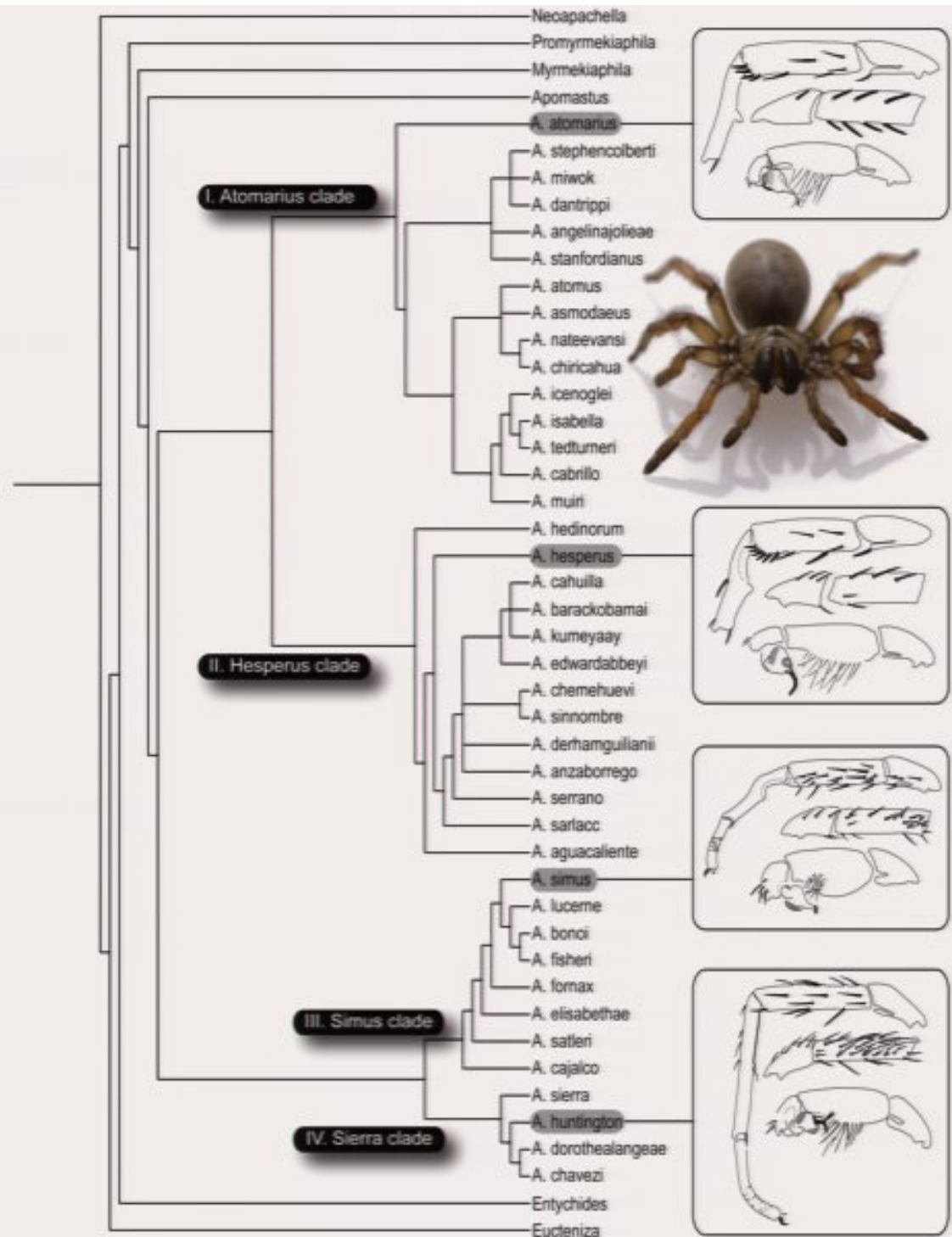






# *Aptostichus* Simon

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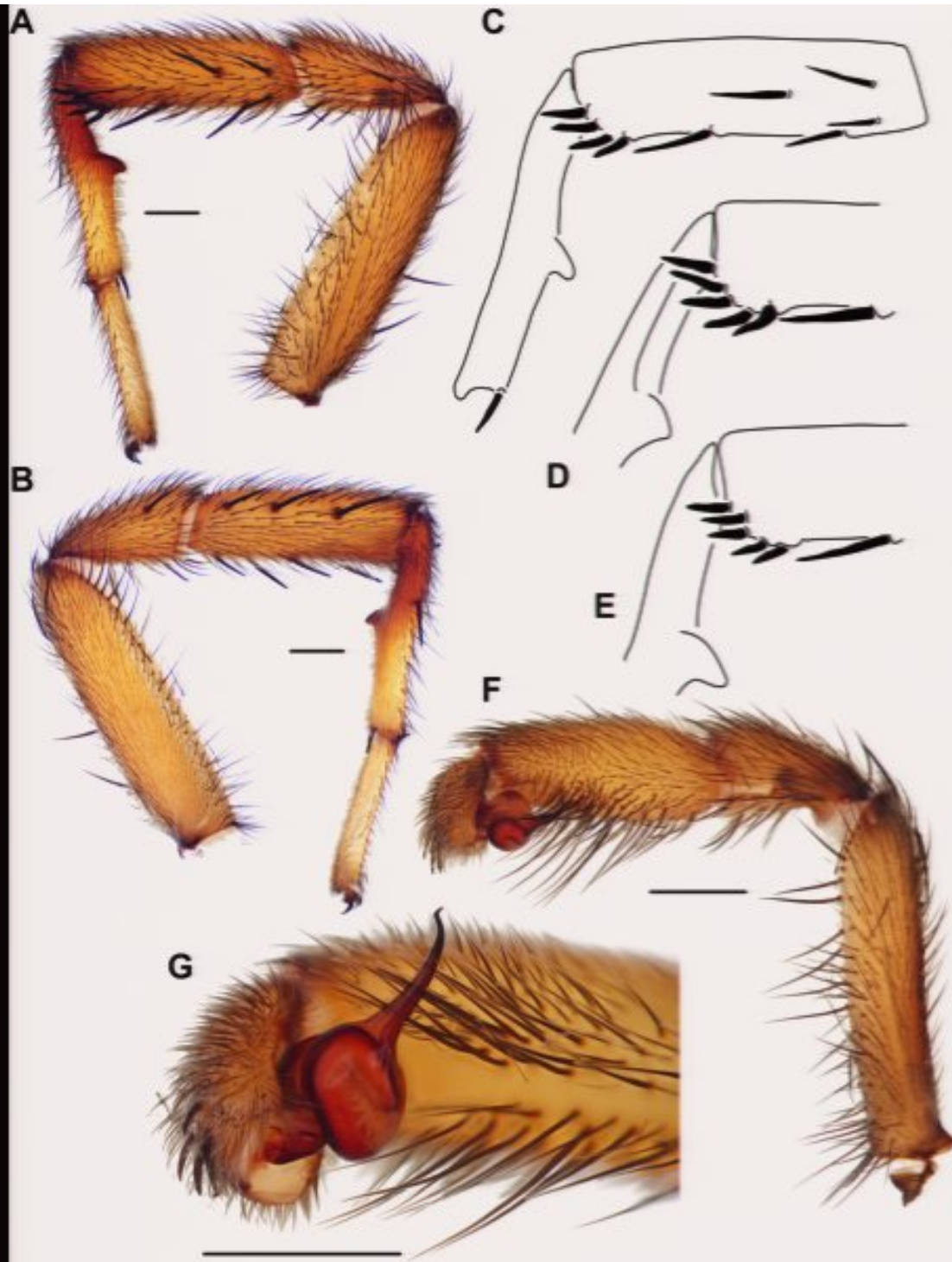
- *Aptostichus atomarius*
  - Geographically widespread throughout California
  - Habitat diversity
  - Morphological stasis

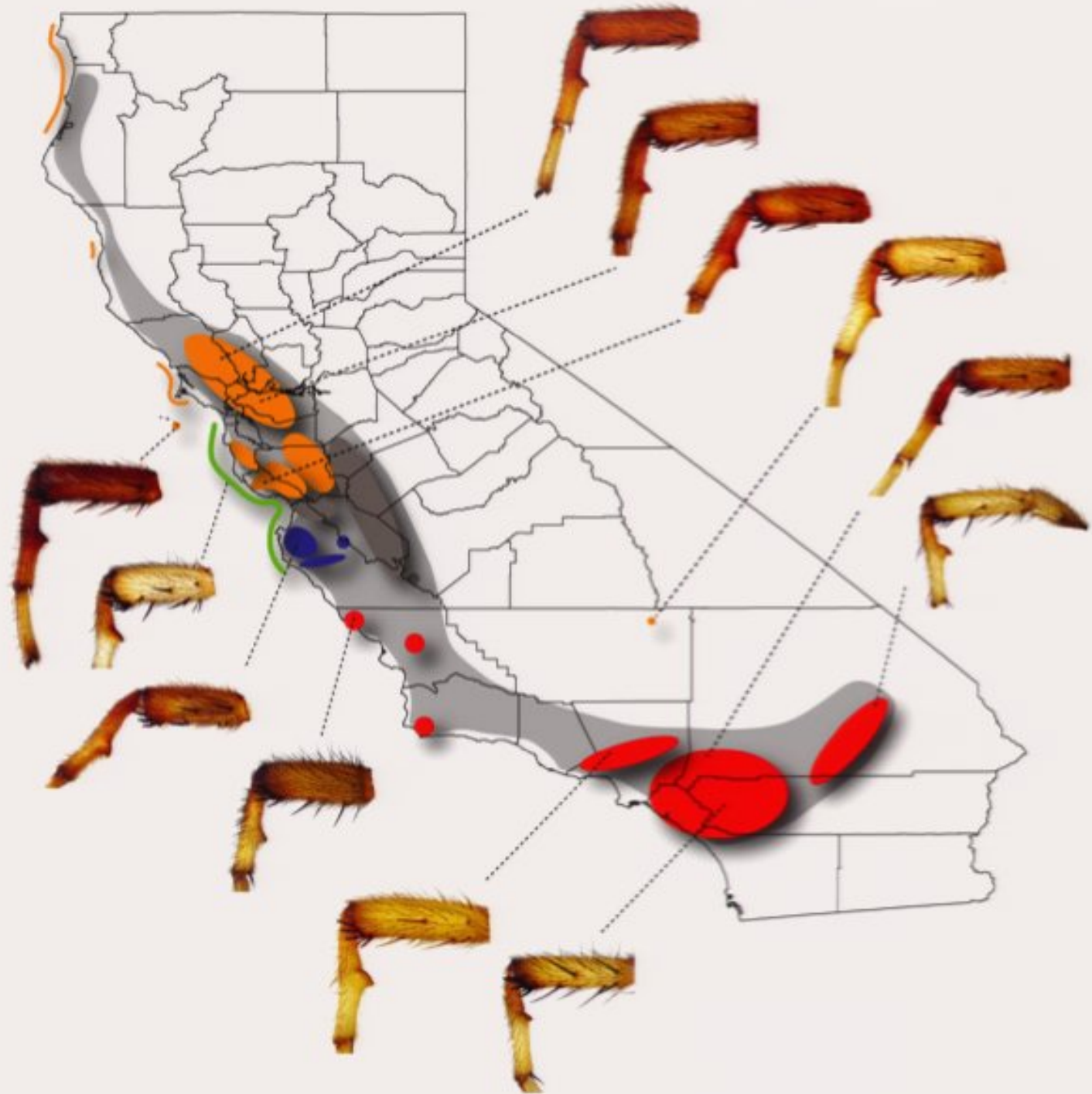




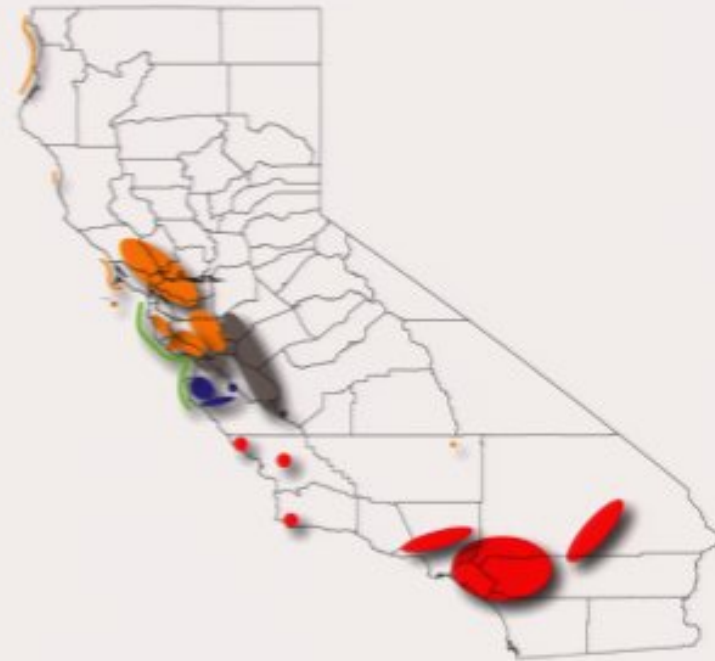
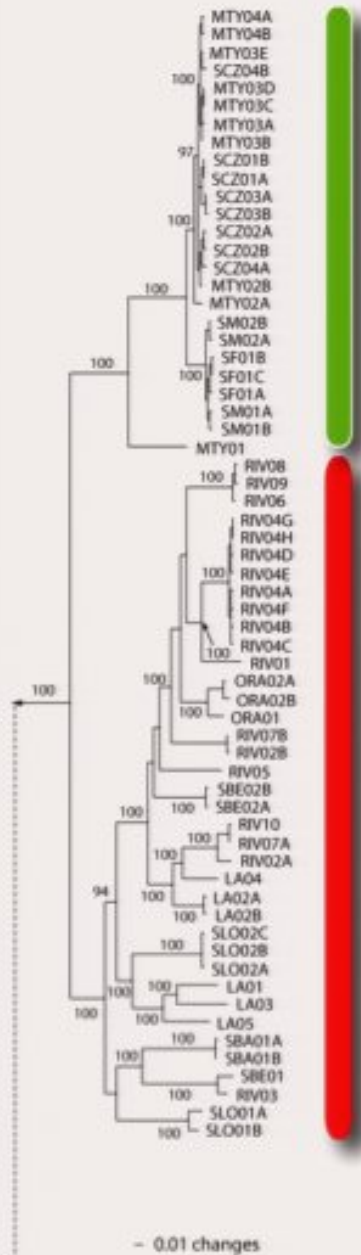
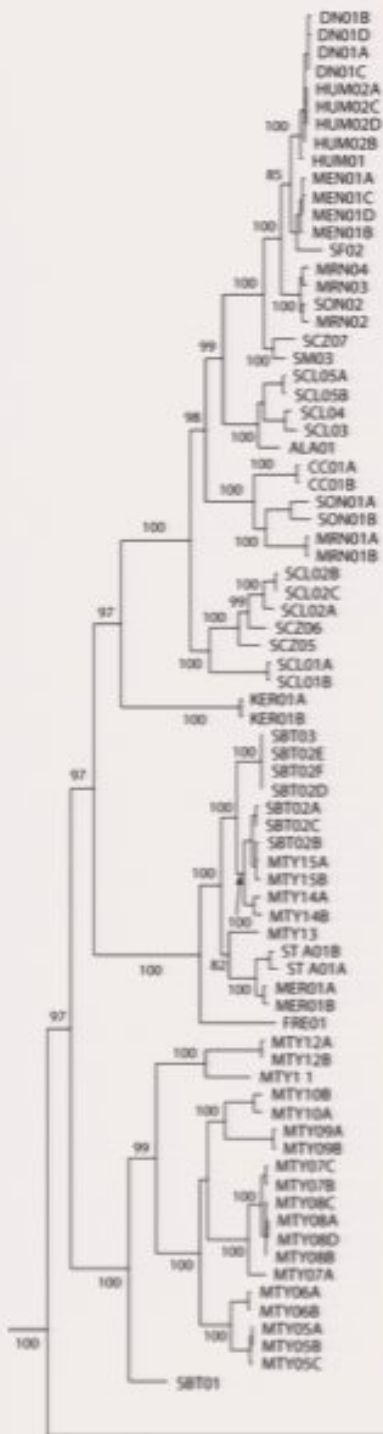










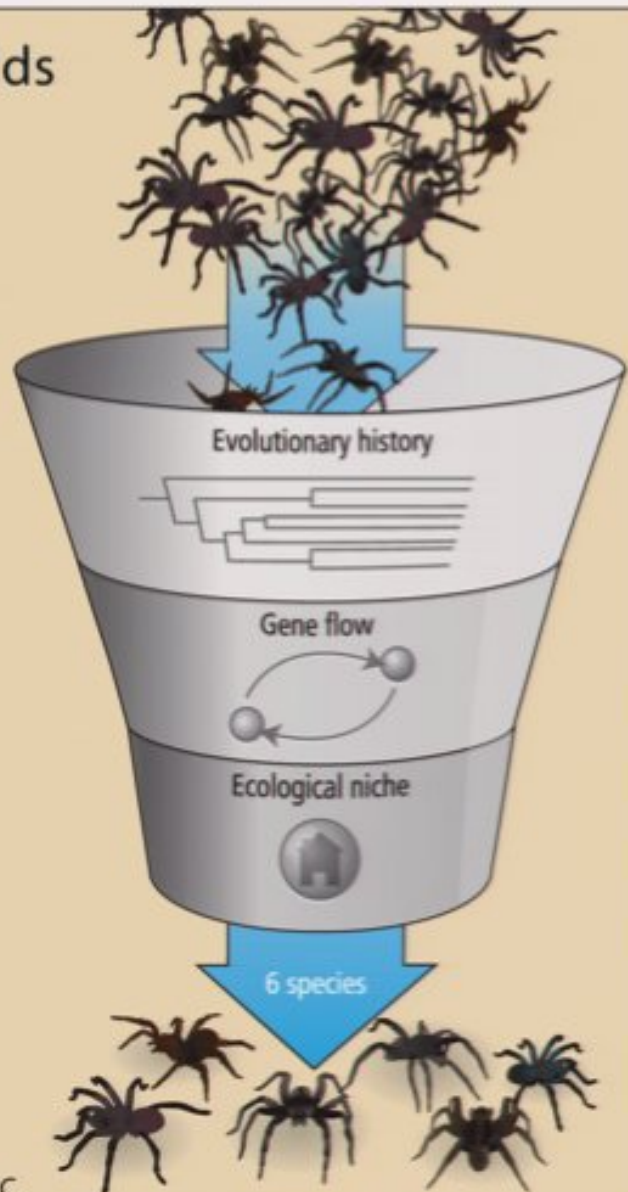


- **mtDNA genealogy**
  - ~1500 bp: 12S, tRNA, 16S
  - 11 outgroup species
  - 167 individuals from 75 localities
  - Bayesian inference
    - 3 partitions (GTR +  $\Gamma$  + I)
    - MrBayes 3.1.2
    - 3 million generations
    - Ln = -31256.83
  - Highly structured geographically
  - Divergent genetically (> 23%)

[A UNIFIED APPROACH]

## The Best of All Worlds

Because of the turmoil, some researchers have begun to create phylogenetic classifications by looking beyond evolutionary history and combining it with molecular, ecological, behavioral and biological data. As an example, Jason Bond and one of his students at East Carolina University studied a genus of spider, *Promyrmekeiaphila* (above) found in California. They studied the spider's evolutionary history and ecological role and sequenced the genes of 222 spiders at 78 sites, using the full collection of information to group the animals into six species.



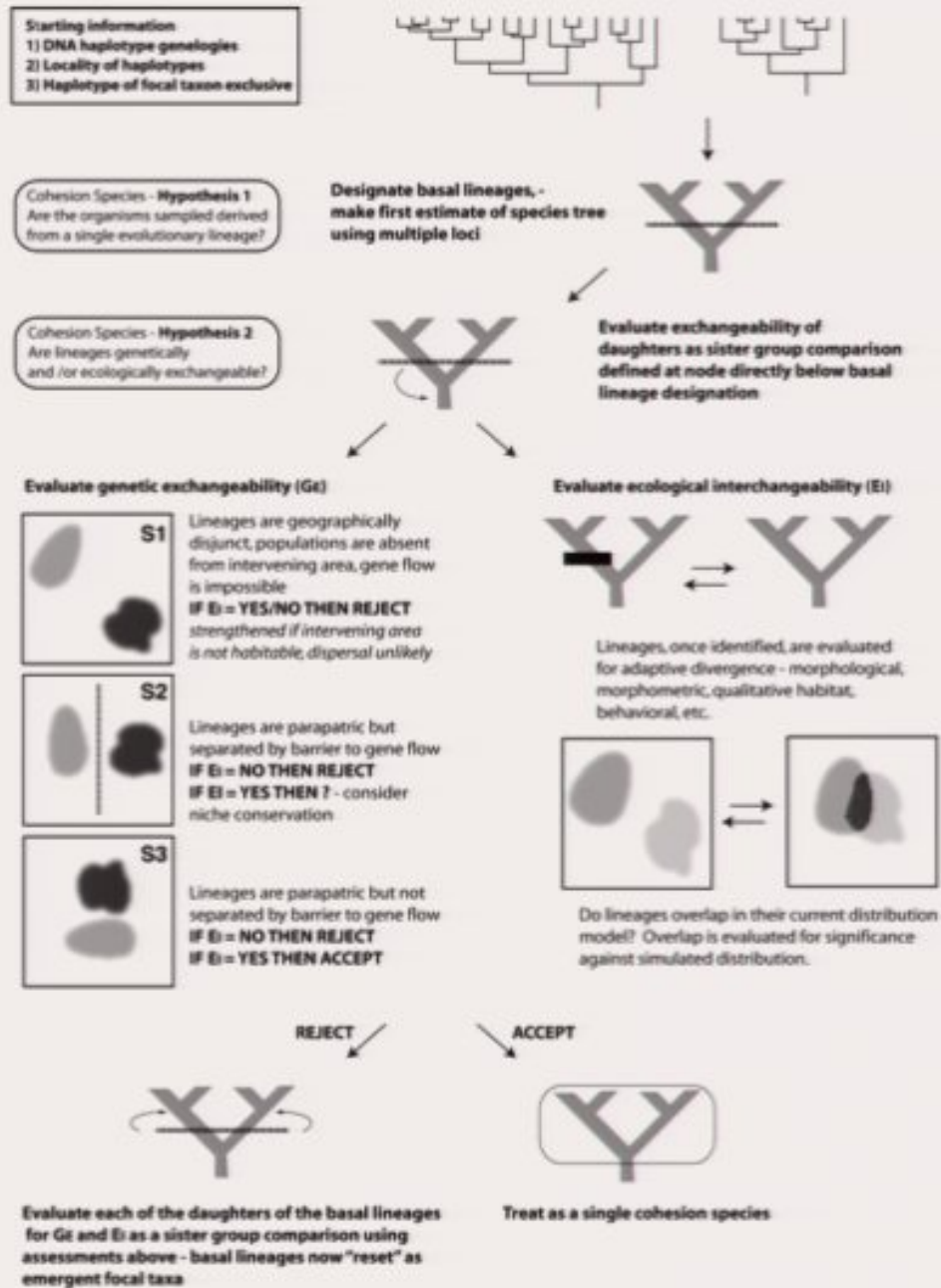


Figure 2

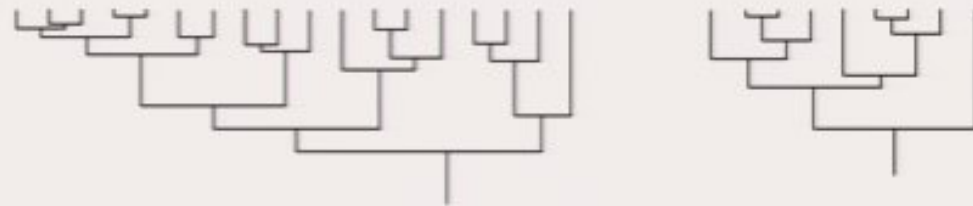


**Starting information**

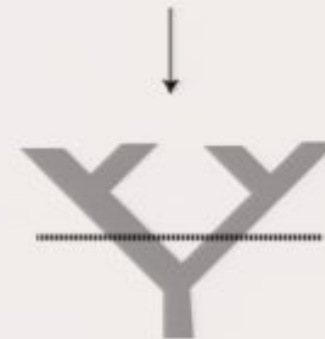
- 1) DNA haplotype genealogies
- 2) Locality of haplotypes
- 3) Haplotype of focal taxon exclusive

**Cohesion Species - Hypothesis 1**

Are the organisms sampled derived from a single evolutionary lineage?



**Designate basal lineages, -  
make first estimate of species tree  
using multiple loci**



Cohesion Species - **Hypothesis 2**  
Are lineages genetically  
and /or ecologically exchangeable?



Evaluate exchangeability of  
daughters as sister group comparison  
defined at node directly below basal  
lineage designation

### Evaluate genetic exchangeability (GE)



S1

Lineages are geographically  
disjunct, populations are absent  
from intervening area, gene flow  
is impossible

**IF  $E_i$  = YES/NO THEN REJECT**  
*strengthened if intervening area  
is not habitable, dispersal unlikely*



S2

Lineages are parapatric but  
separated by barrier to gene flow

**IF  $E_i$  = NO THEN REJECT**  
**IF  $E_i$  = YES THEN ?** - consider  
niche conservation

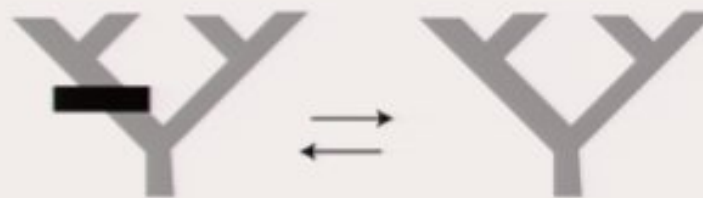


S3

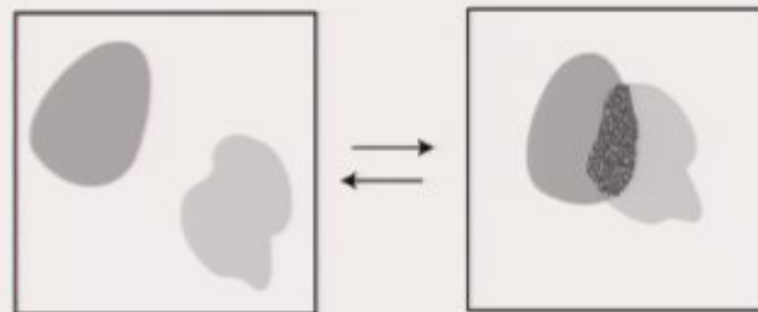
Lineages are parapatric but not  
separated by barrier to gene flow

**IF  $E_i$  = NO THEN REJECT**  
**IF  $E_i$  = YES THEN ACCEPT**

### Evaluate ecological interchangeability ( $E_i$ )



Lineages, once identified, are evaluated  
for adaptive divergence - morphological,  
morphometric, qualitative habitat,  
behavioral, etc.



Do lineages overlap in their current distribution  
model? Overlap is evaluated for significance  
against simulated distribution.

**REJECT**



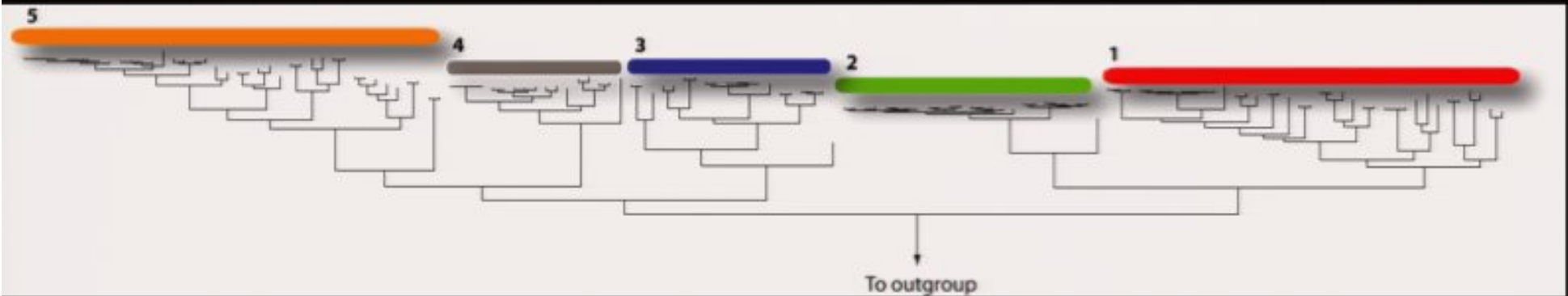
**Evaluate each of the daughters of the basal lineages for GE and EI as a sister group comparison using assessments above - basal lineages now "reset" as emergent focal taxa**

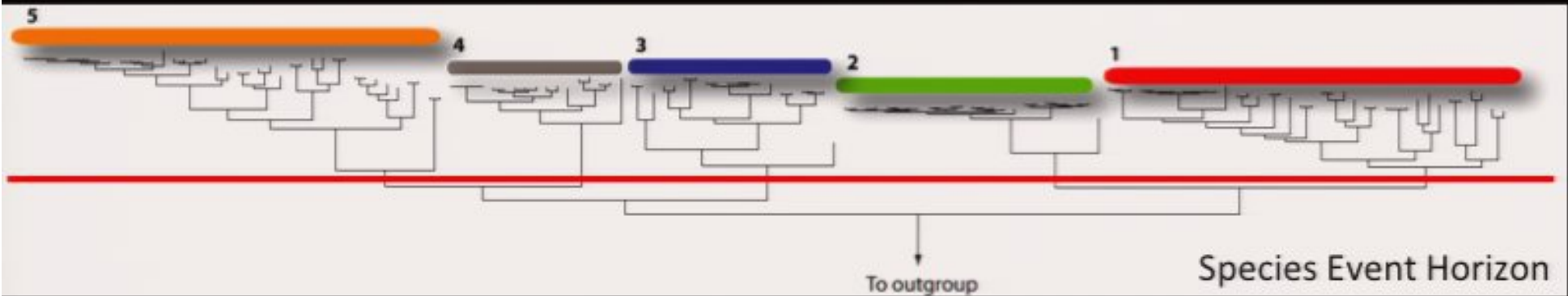
**ACCEPT**



**Treat as a single cohesion species**



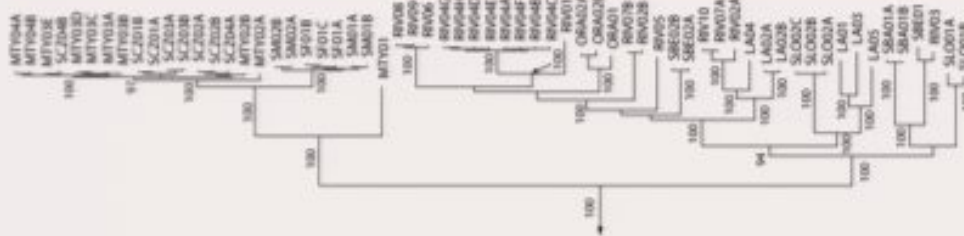


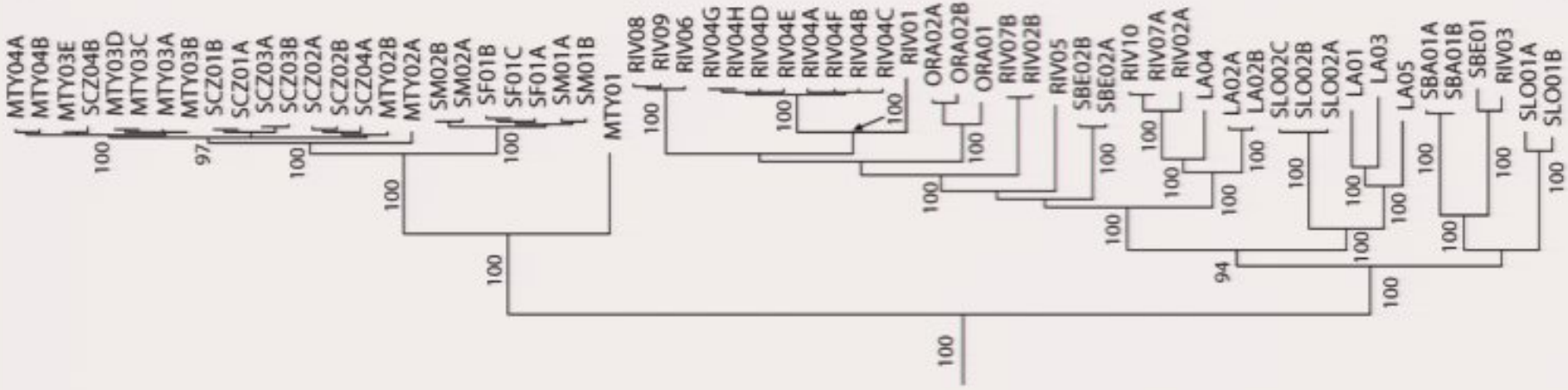




## • Clades 1 and 2

- Spatially non-overlapping
- Ecologically non-interchangeable
- Phenotypic differences



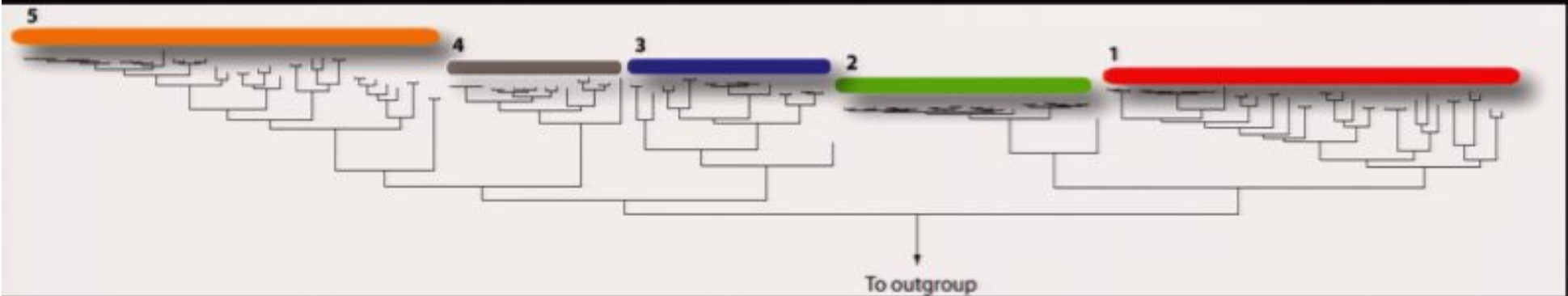


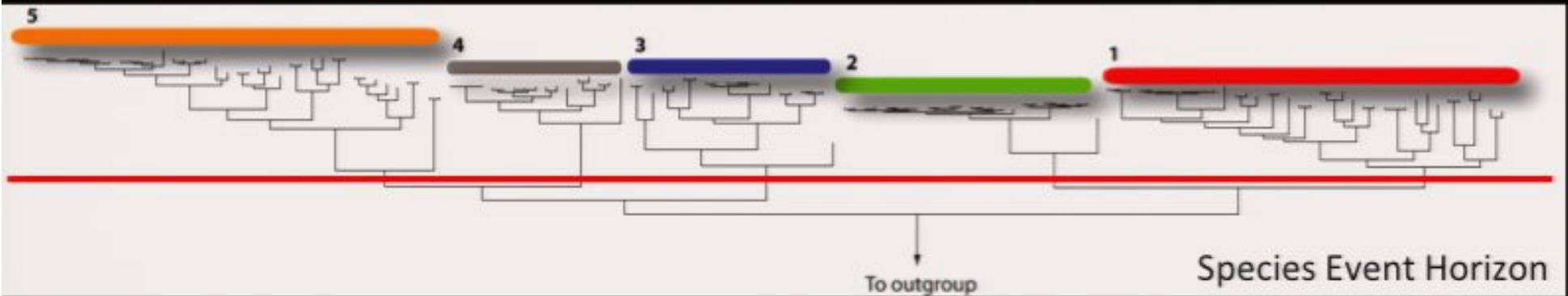




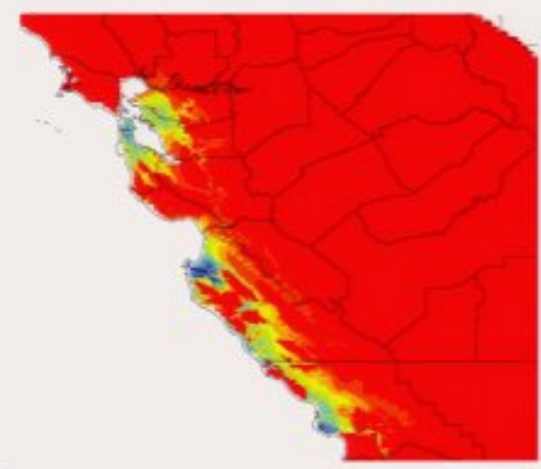
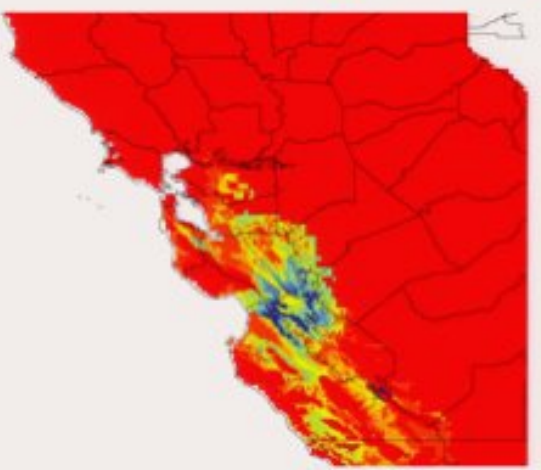
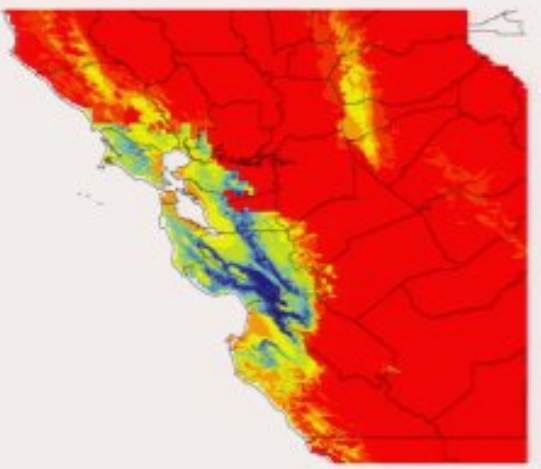
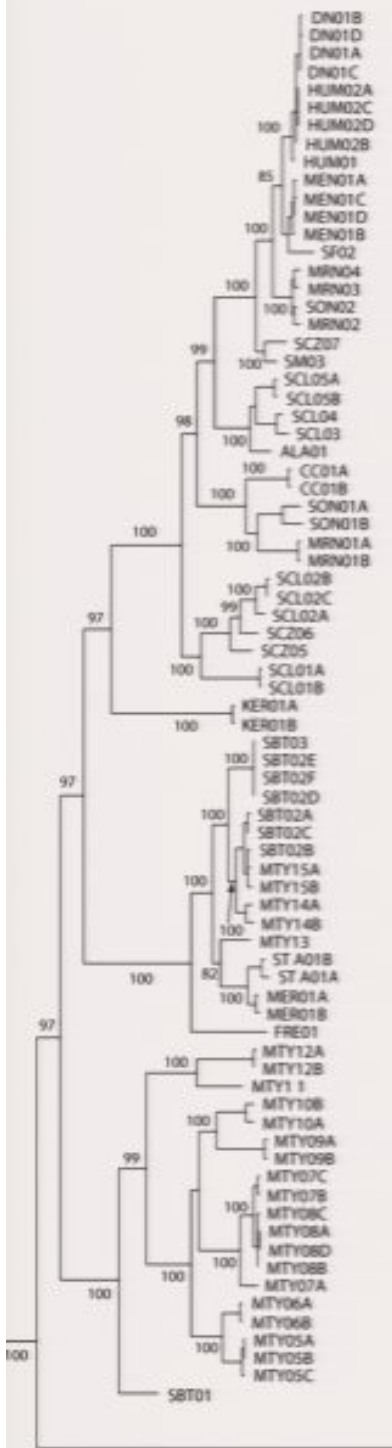


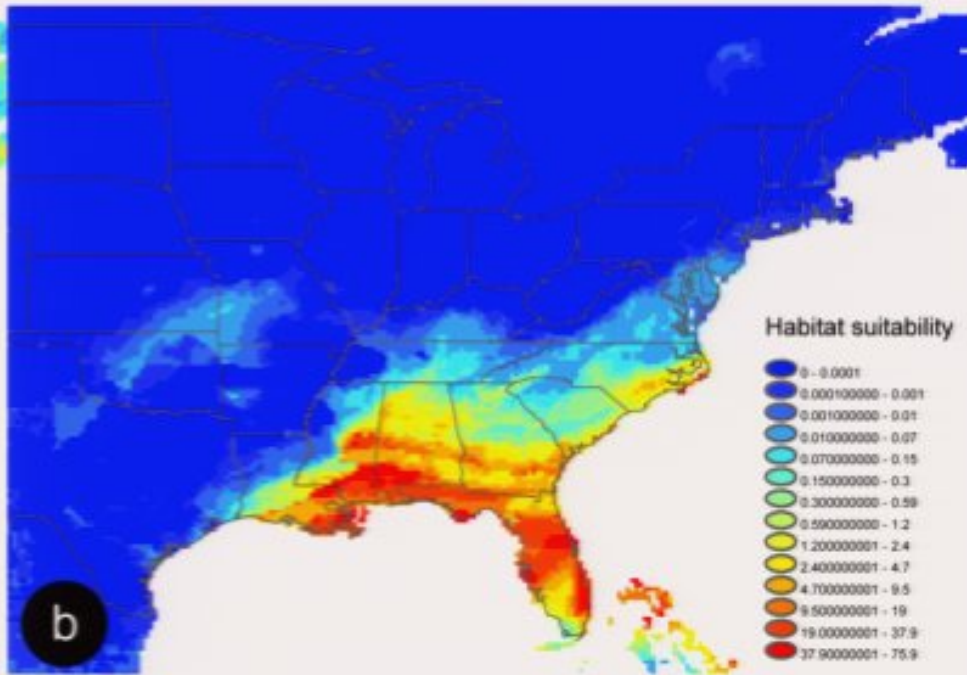
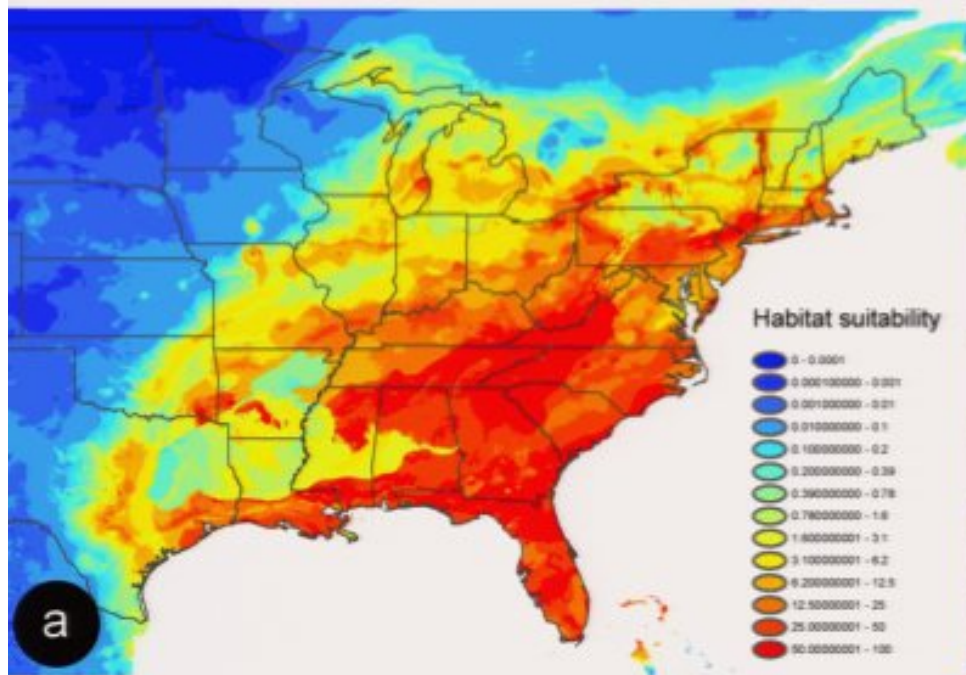












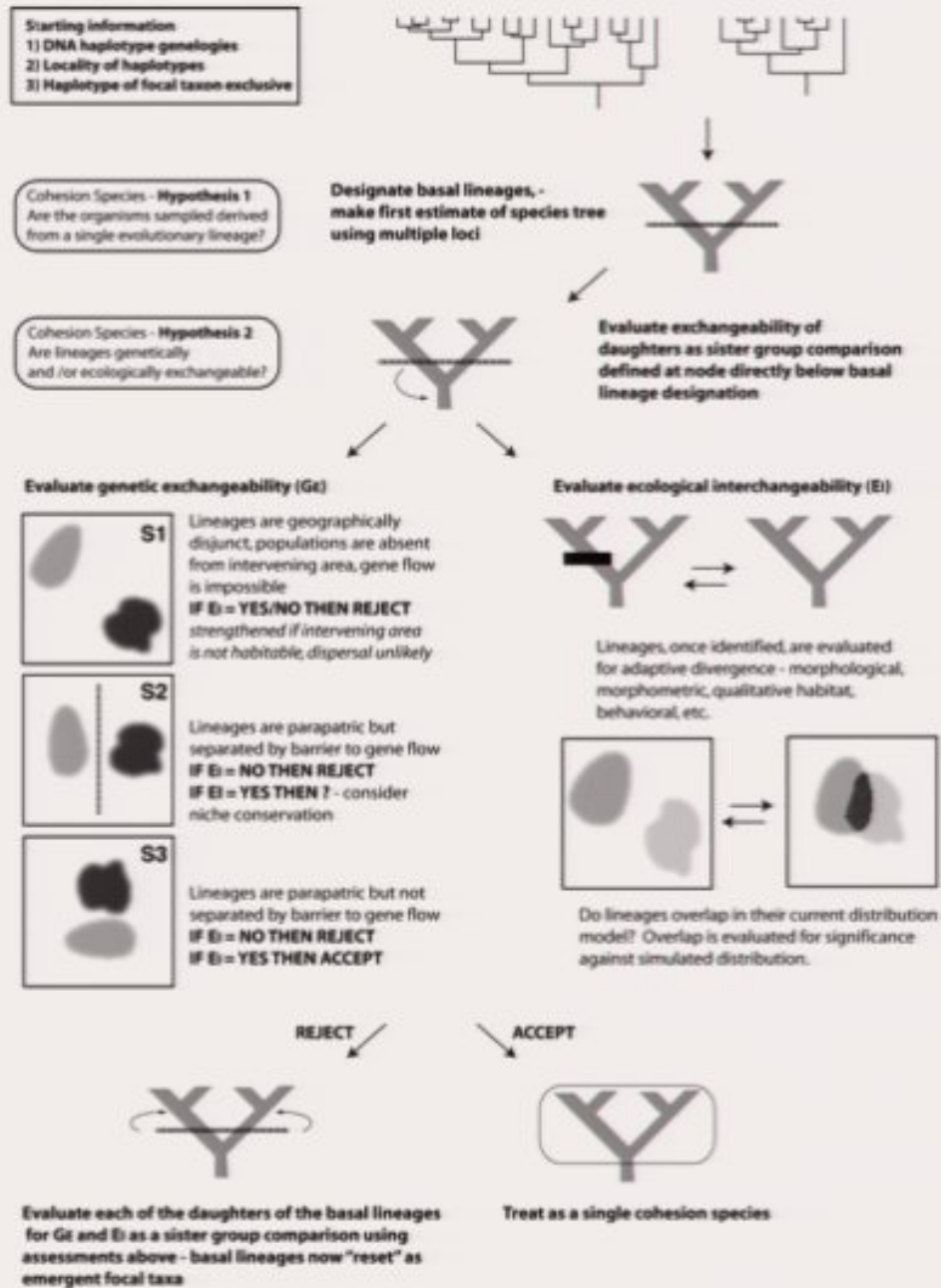
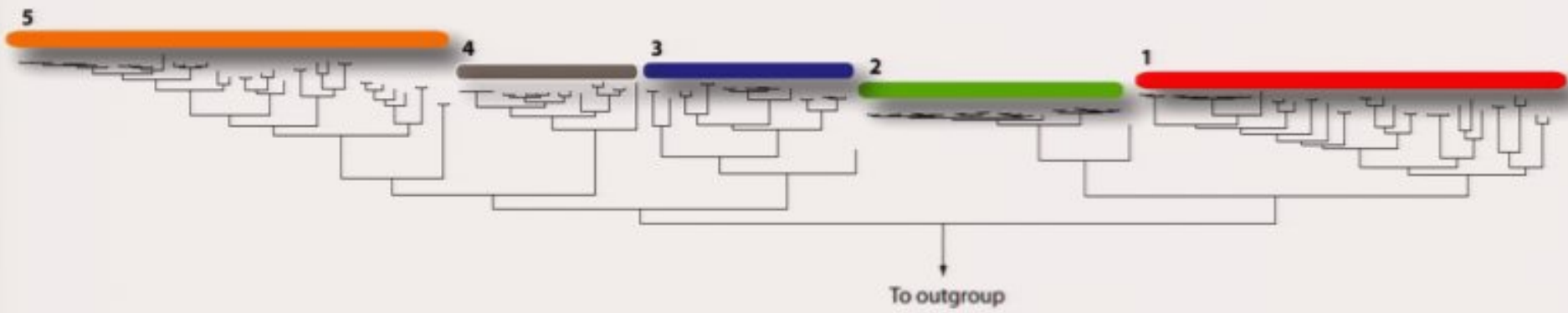
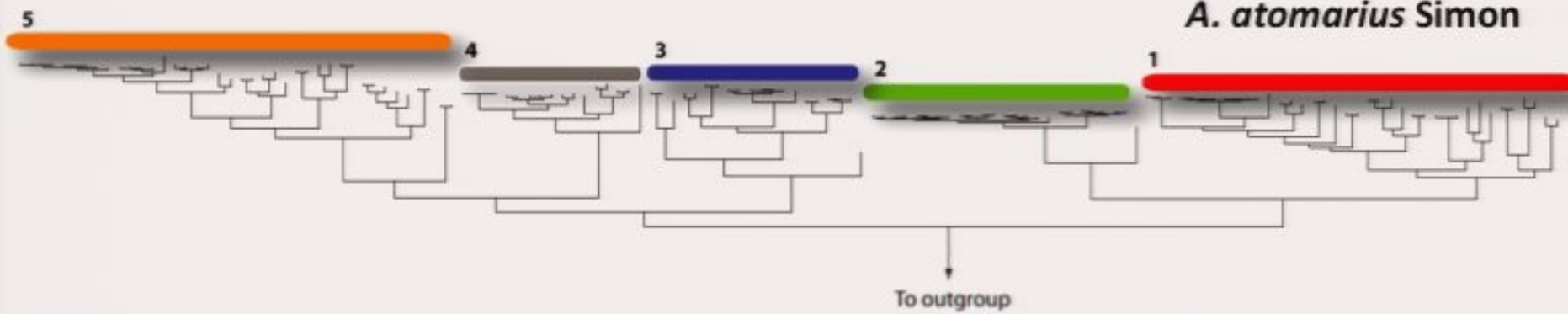
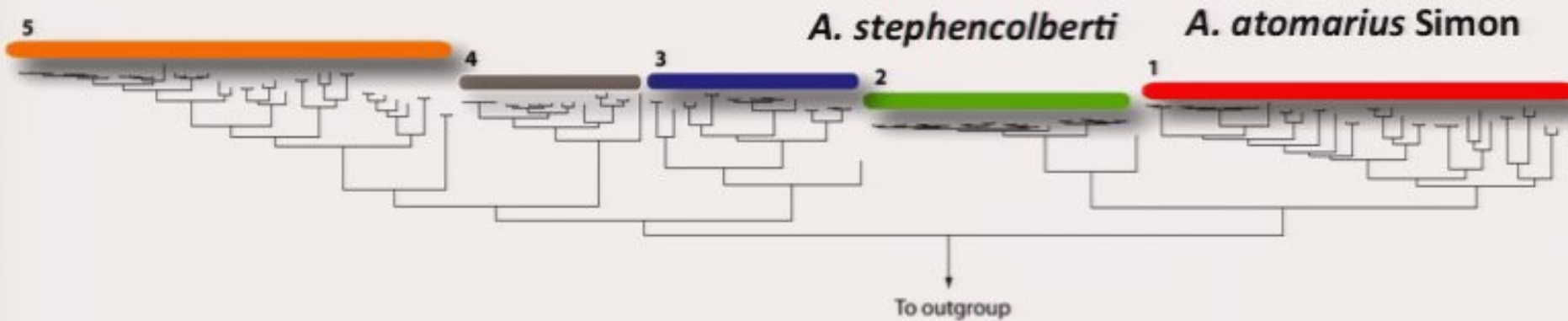


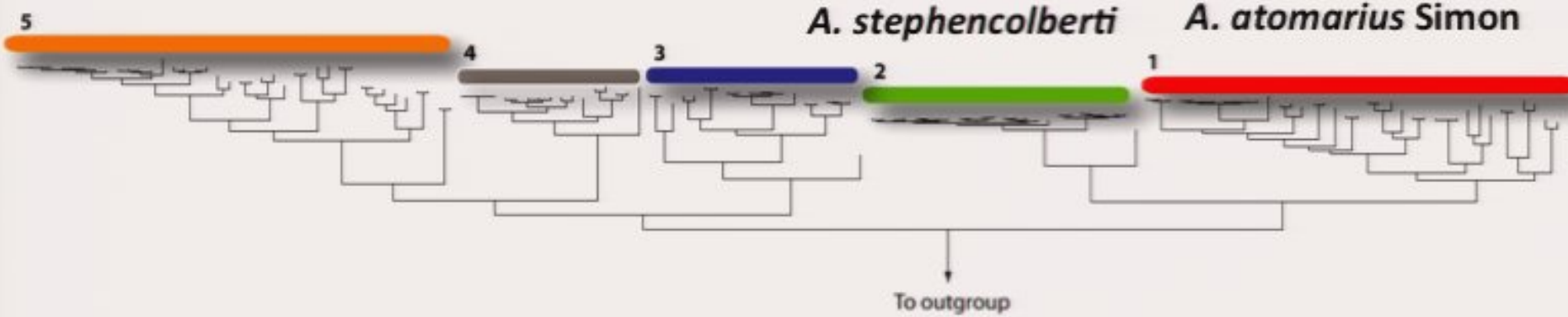
Figure 2

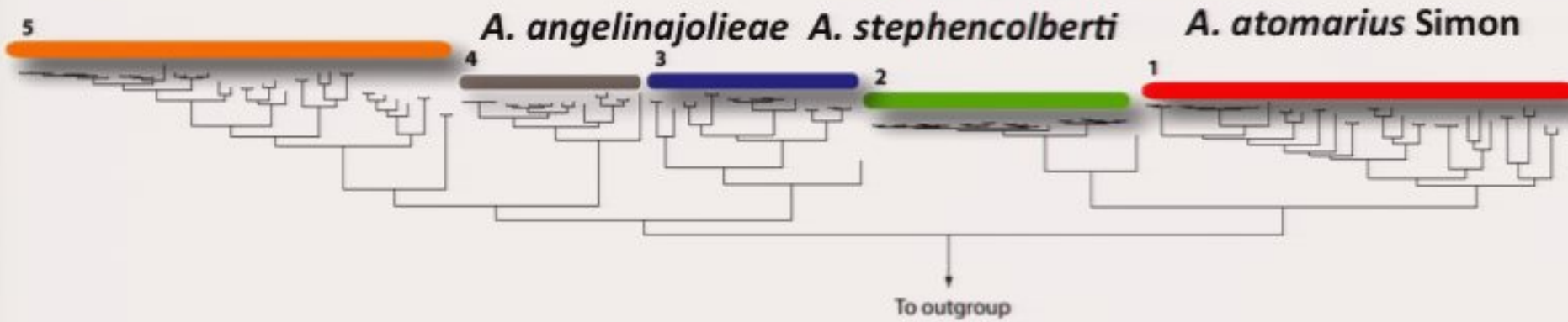




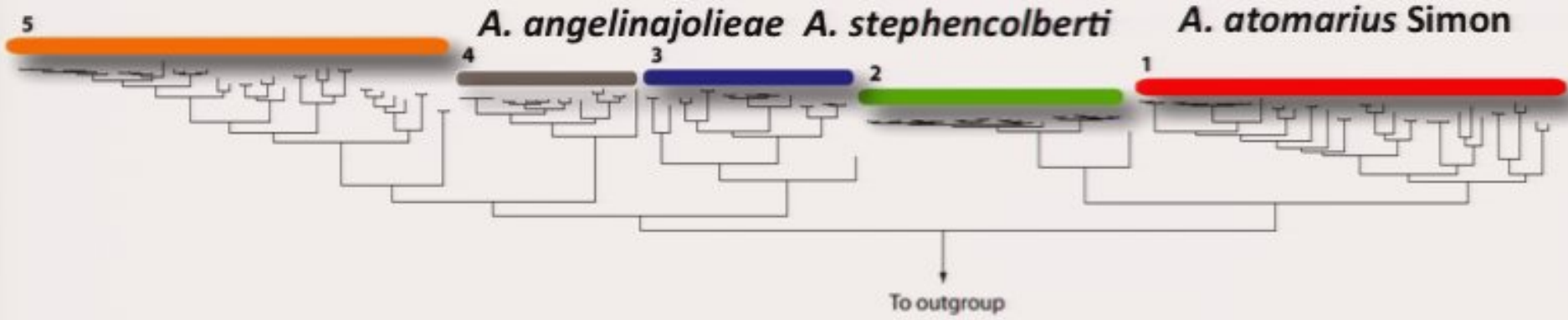
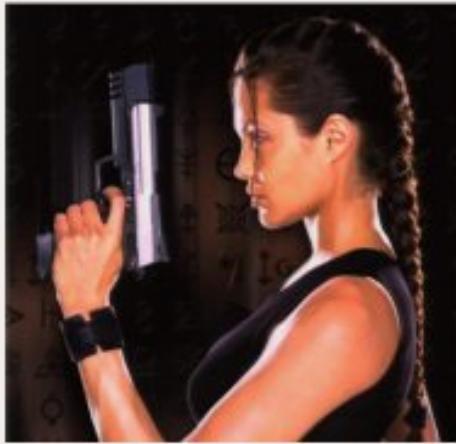










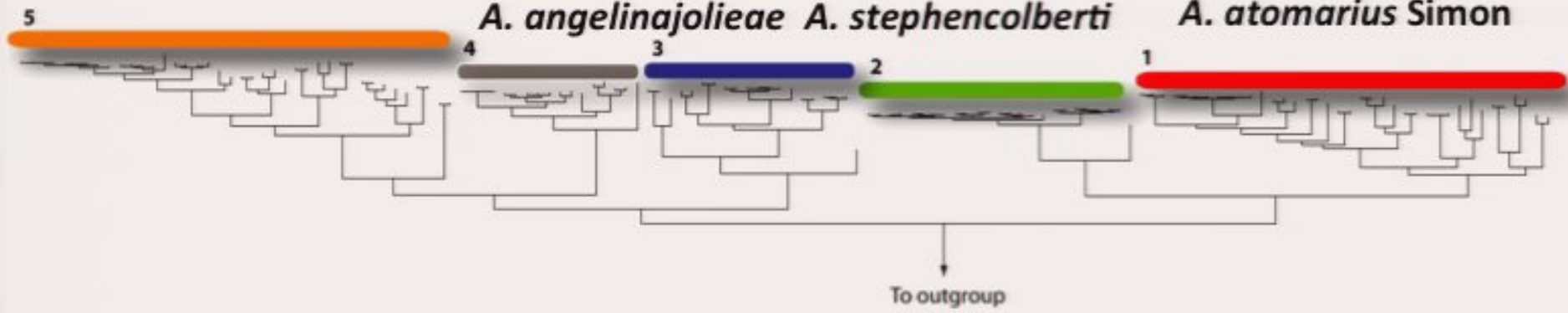




*A. stanfordianus* Smith

*A. angelinajolieae* *A. stephencolberti*

*A. atomarius* Simon



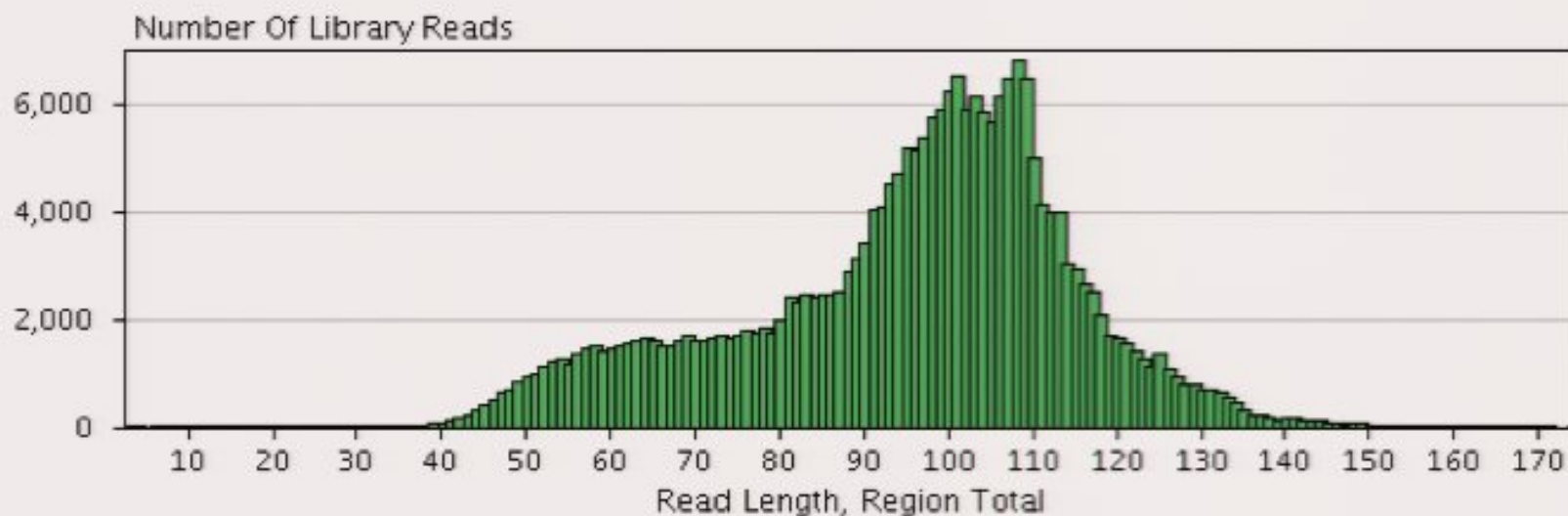
# What's the future hold for taxonomy?

- Probably more DNA barcoding...
  - Id specimens in faunistic studies, associate life history stages, works really for birds
  - clearly not a tool for species discovery
  - fails consistently when rigorously tested
  - see Meier (2008)
  - Soon will be obsolete (*sensu stricto*)
- Does taxonomy need to change in some fundamental way?

# Data from *Aptostichus stephencolberti*

TCAG (Library)	Region		Total
	1	2	
Raw Wells	573,078	595,672	1,168,750
Key Pass Wells	555,925	547,598	1,103,523
Passed Filter Wells	120,942	115,177	236,119
Total Bases	11,464,609	10,922,349	22,386,958
Length Average	94.80	94.83	94.81
Length Std Deviation	20.14	20.18	
Longest Reads Length	167	174	174
Shortest Reads Length	3	8	3
Median Reads Length	99.0	99.0	99.0

# of contigs (n >= 2)	11,514 unique
Multi-read contigs (n > 2)	5,962
Multi-read contigs >1 kb	24
Multi-read contigs >2 kb	3





# What's ahead?

- Probably more DNA barcoding and molecular reductionism...
  - Id specimens in faunistic studies, associate life history stages, works really for birds
  - clearly not a tool for species discovery
  - fails consistently when rigorously tested
  - see Meier (2008)
  - Soon will be obsolete (*sensu stricto*)
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Bond Lab | settings | change projects | my data | Logged in as [Jesse Bond](#) | my preferences | [Logout](#)

OTUs | Characters | Metrics | Content | **Material** | Measurements | DNA | Rats | Associations | Taxon names | Images | Ontology | Keys | Tags | Phylo

**Specimens** | Lists | List groups | Collecting Events | Distribution | Repositories | Geographical Names |  [Show List](#)  
[More options](#)

10/1/10

**Determinations**  
Click on an OTU to view all records for that OTU  

- [Aprostictus engelhardti](#)

**Identifiers**  


- Bond lab legacy identifier AP000279

**Repository/location**  
 Deposition location info: East Carolina University  
 Repository: CAS - USA, California, San Francisco, California Academy of Sciences

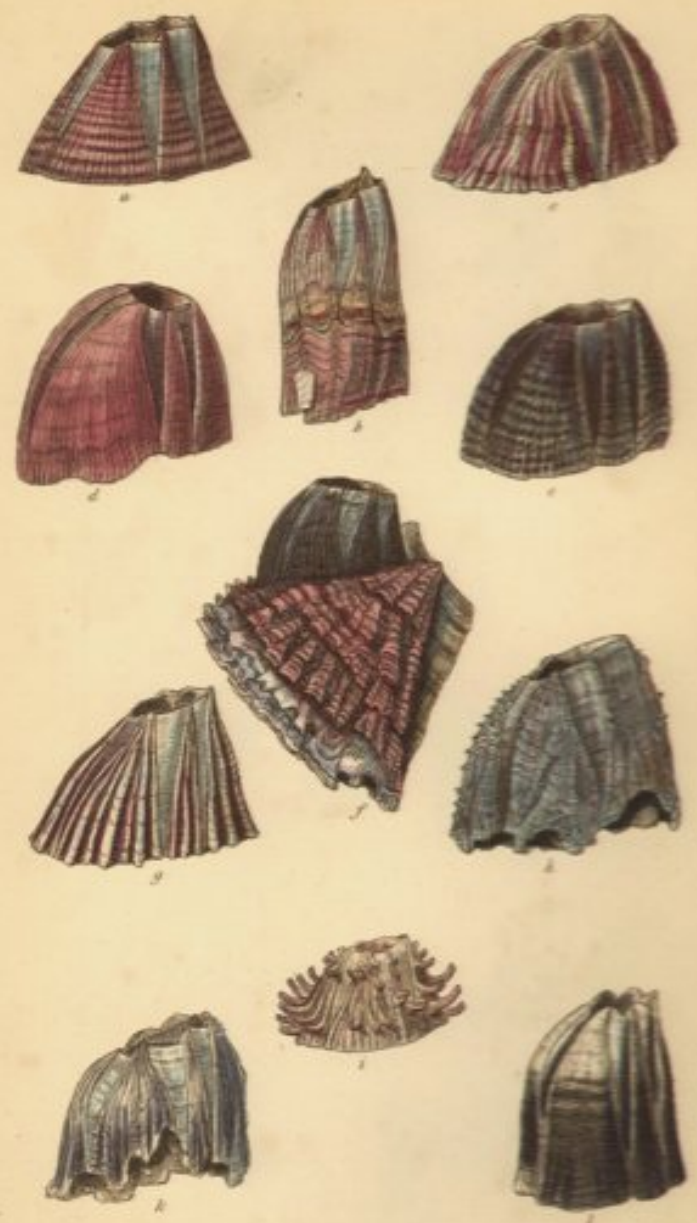
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 Stage: **larvae**   
 Diet source: **fish**   
 Preparation: **80% ETOH**   
 Parent (e.g. part of whole specimens):

**Recent details**  
 List number: **Jesse Bond**   
 Owner: **dummy dummy**   
 Created on: **20 days ago**   
 Last updated: **over 1 year ago**

Collecting Event with  
 United States, California, Monterey  
 Carlsbad Rd 6.5 miles southeast of Carmel  
 Valley Village, 2.6 miles south intersection with  
 Carmel Valley Rd  
 36.4275294, -121.982488W  
 150.82 meters  
 08.02.1974  
 W.R. Isenogle  
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BALANUS TINTINNACULUM.

George Sowerby

## EVOLUTIONARY BIOLOGY IN BIODIVERSITY SCIENCE, CONSERVATION, AND POLICY: A CALL TO ACTION

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