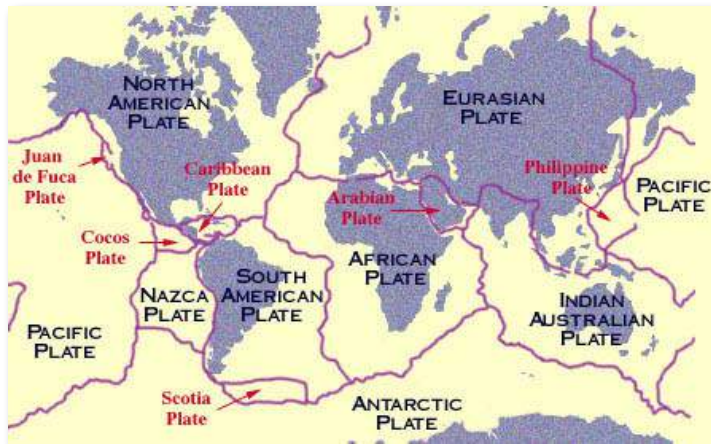


# Historical Biogeography

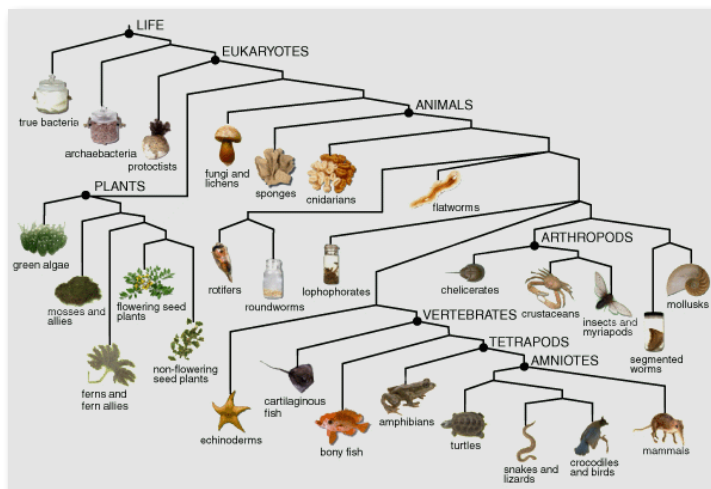
How do you choose between dispersalist and vicariance models?

Two important scientific advances – in the study of **earth history** and **organismal history** - revolutionized historical biogeography



## 1. Acceptance of plate tectonics

Up until the 1960s, most persons considered the earth's crust to be fixed. Finally, in the 1960s the geological evidence was at hand that made continental drift irrefutable.

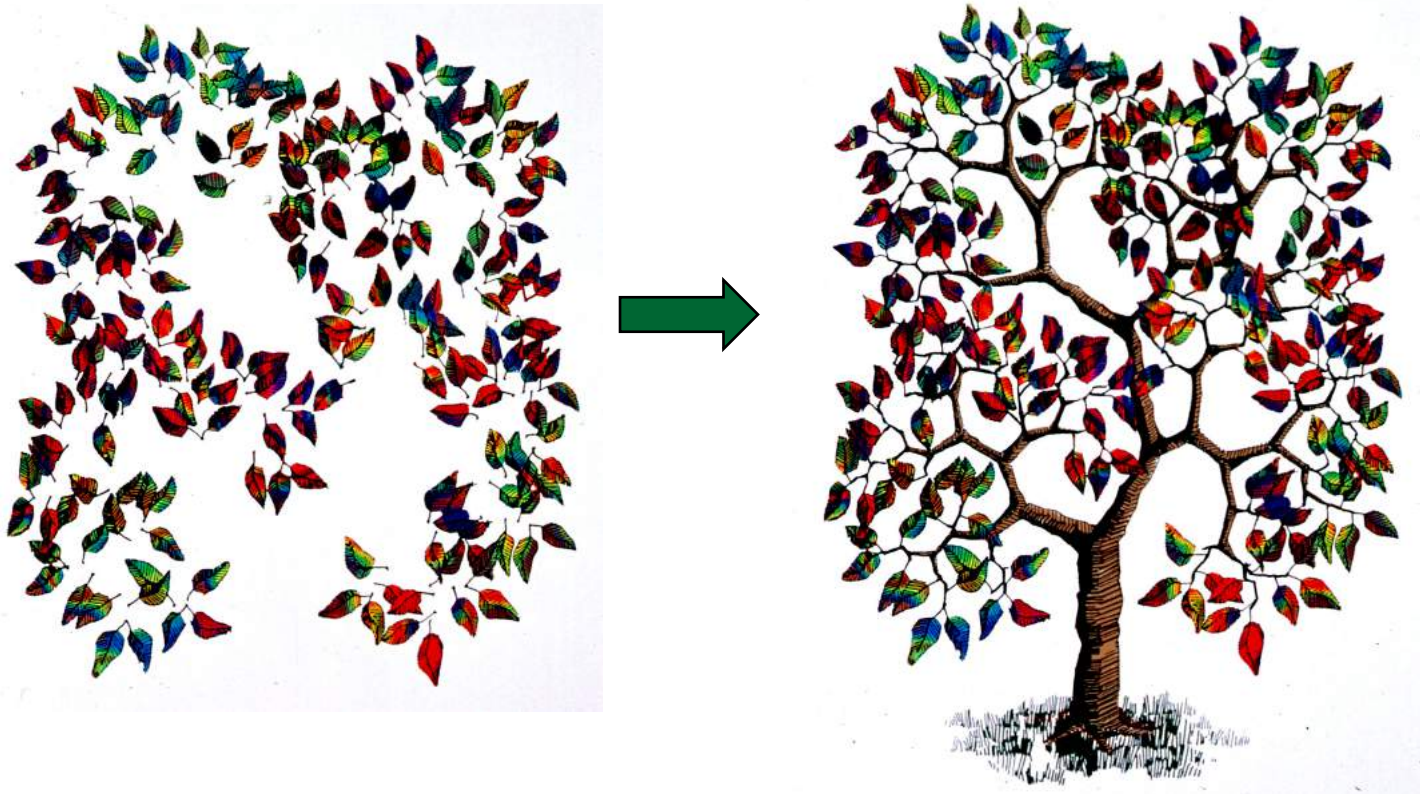


## 2. Development of new phylogenetic methods

Willi Hennig (1950) introduced the modern concepts of phylogenetic theory (first published in 1956). Using this methodology, hypotheses of historical lineages of species could be reconstructed.

# Phylogenetics

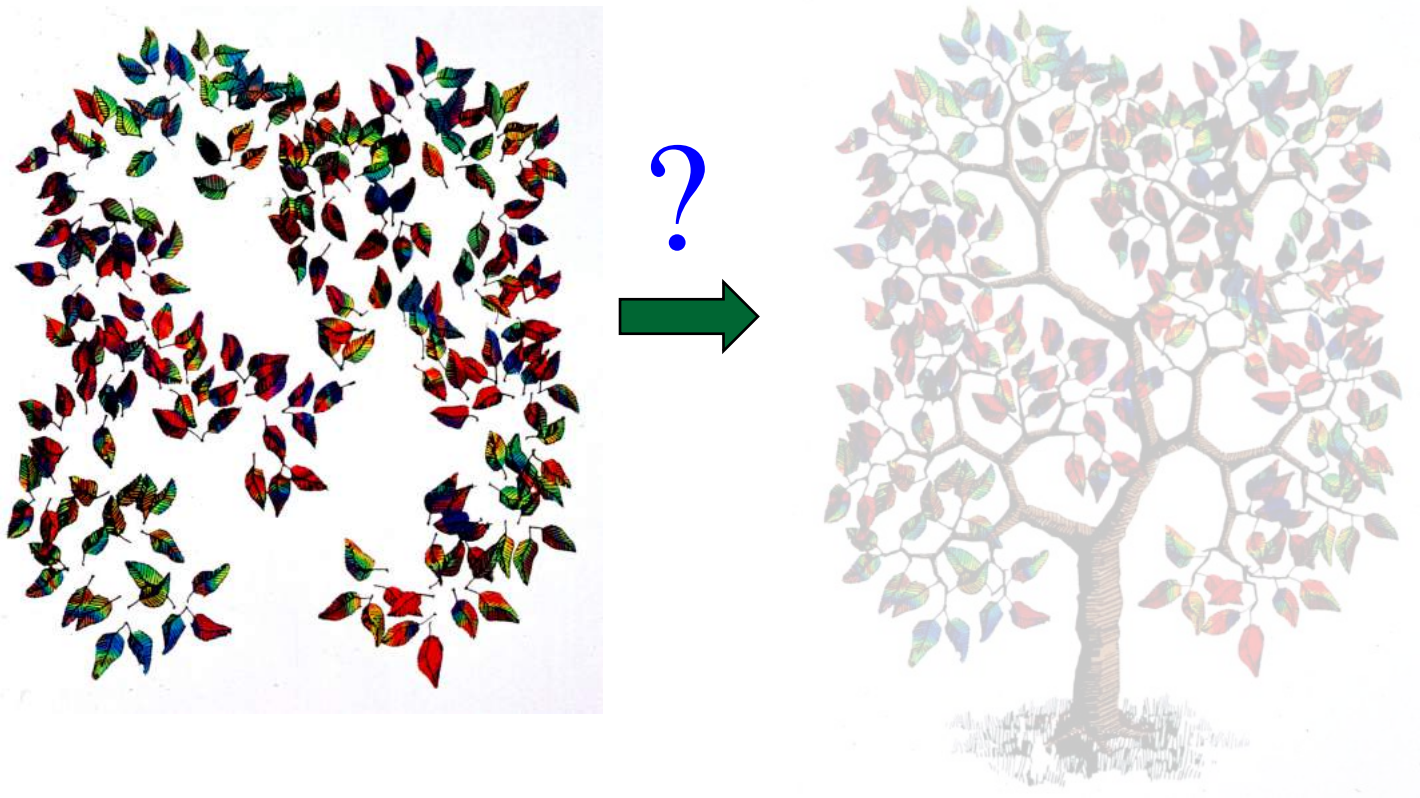
Before linking biogeography with phylogenetics, we need to take a closer look at how to estimate the “tree”



Usually we only have information on the “leaves” – or extant living species – and estimating the “tree” with its “branches” is not easy

# Phylogenetics

Before linking biogeography with phylogenetics, we need to take a closer look at how to estimate the “tree”

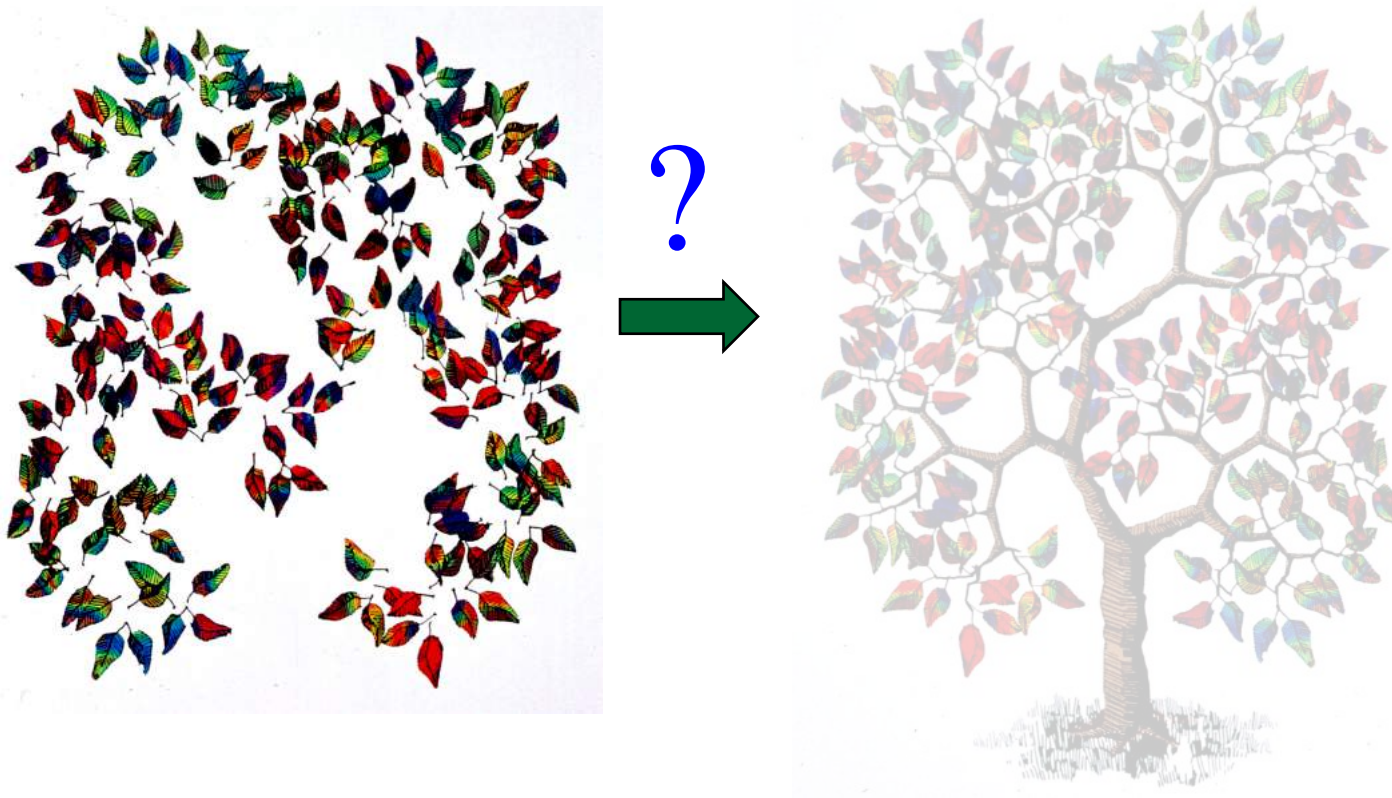


Usually we only have information on the “leaves” – or extant living species – and estimating the “tree” with its “branches” is not easy



# Phylogenetics

Before linking biogeography with phylogenetics, we need to take a closer look at how to estimate the “tree”



Usually we only have information on the “leaves” – or extant living species – and estimating the “tree” with its “branches” is not easy

# Phylogenetics

Willi Hennig (entomologist) and Walter Zimmerman (botanist) developed formal methods for reconstructing phylogenies

Hennig's book "*Phylogenetic Systematics*" was translated into English and introduced the method of phylogenetics called **cladistics**



**WILLI HENNIG**

## **Phylogenetic Systematics**

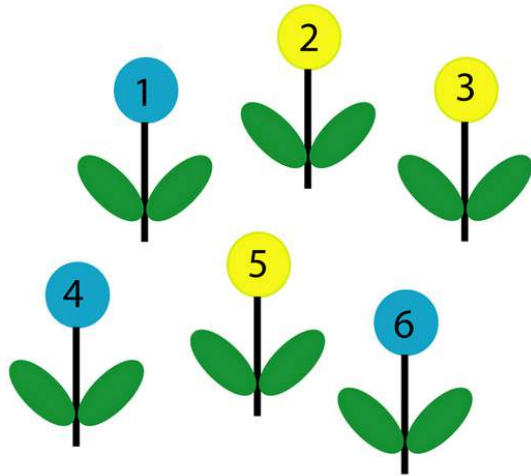
(1950) 1966

TRANSLATED BY D. DWIGHT DAVIS AND RAINER ZANGERL

Foreword by Donn E. Rosen, Gareth Nelson, and Colin Patterson

UNIVERSITY OF ILLINOIS PRESS Urbana Chicago London

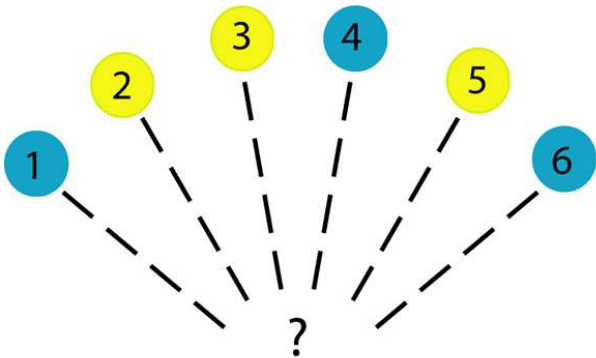
# Phylogenetics



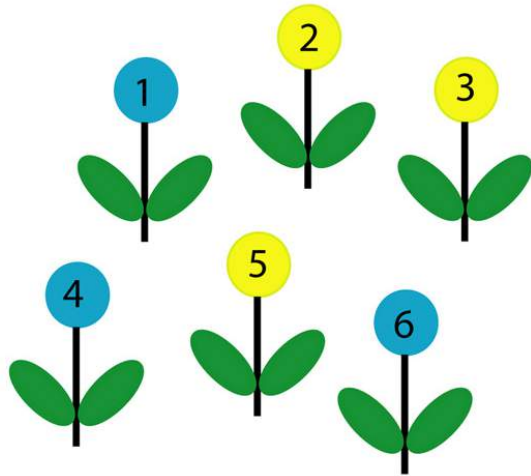
Cladistics forms groups based on **shared-derived characters** or synapomorphies

Are the blue flowers **derived** (apomorph) or are they **primitive** (plesiomorph)?

How are these 6 species of genus *Oppositifolia* related?

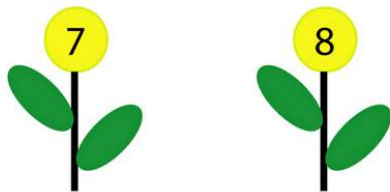


# Phylogenetics



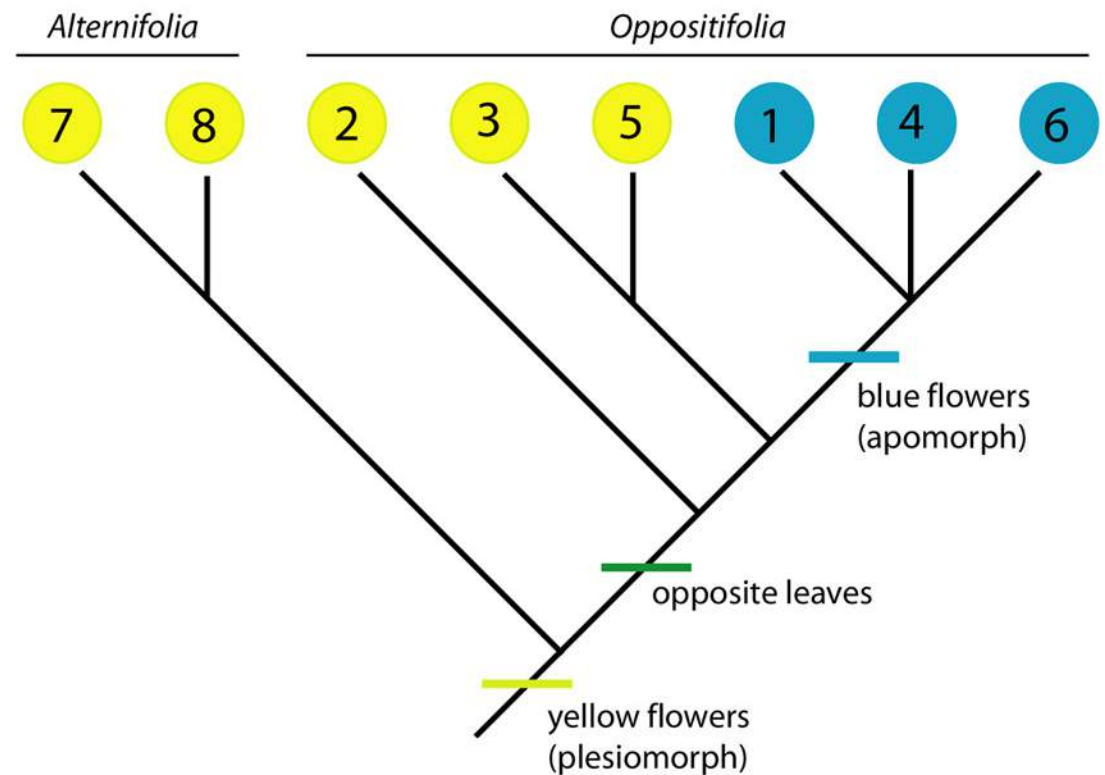
How are these 6 species of genus *Oppositifolia* related?

Use the genus *Alternifolia* as an **outgroup** to polarize the characters in the **ingroup**



Cladistics forms groups based on shared-derived characters or synapomorphies

Are the blue flowers derived (apomorph) or are they primitive (plesiomorph)?

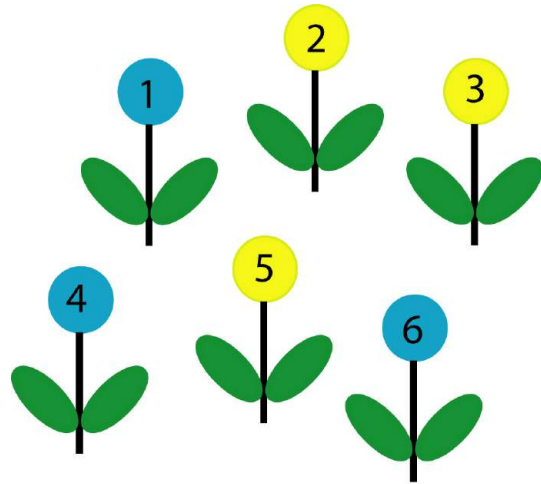


# Phylogenetics

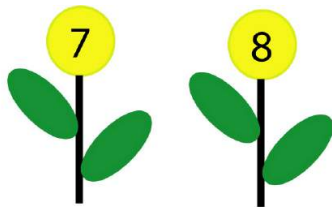
What if **convergences** or **reversals** have taken place in evolution?



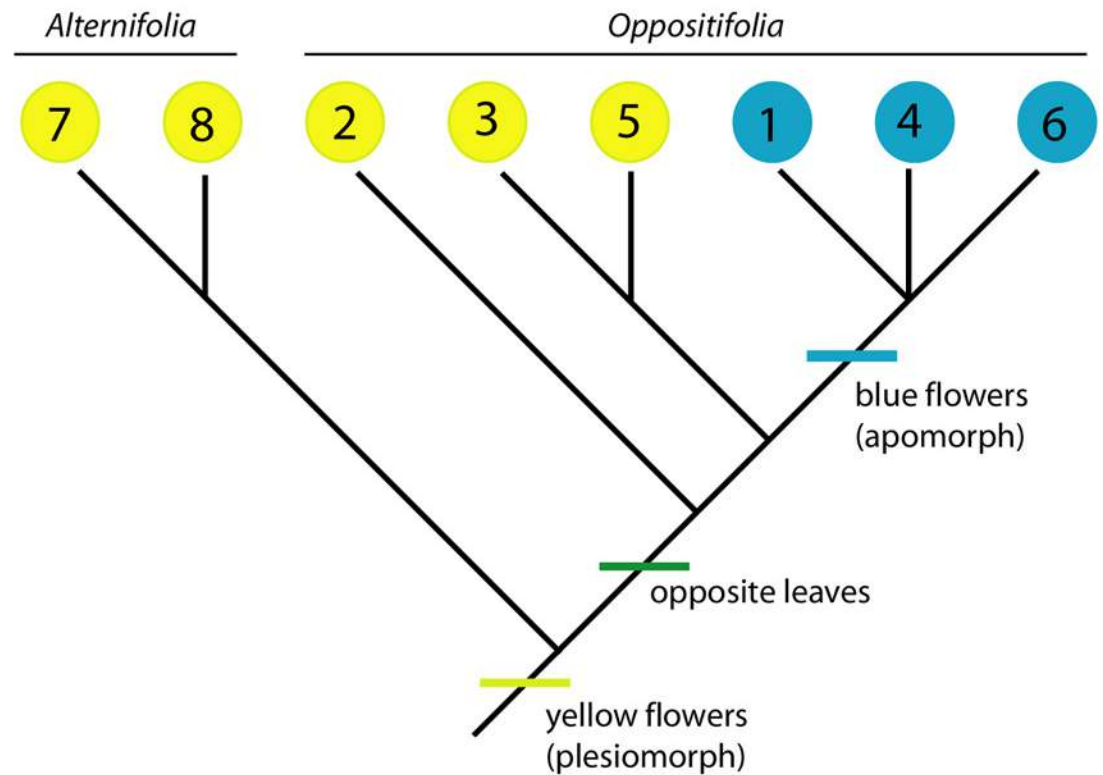
*Where does this belong?*



*Oppositifolia species*



*Alternifolia species*



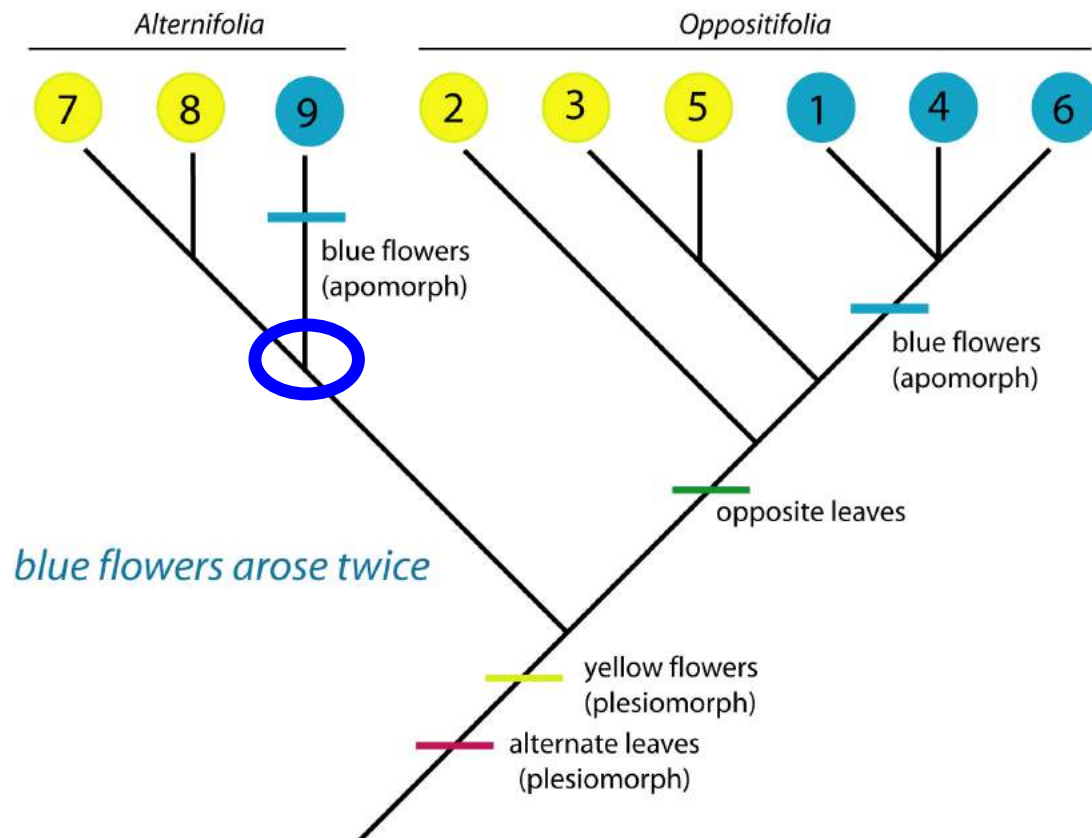


# Phylogenetics

What if **convergences** or **reversals** have taken place in evolution?



*Where does this belong?*



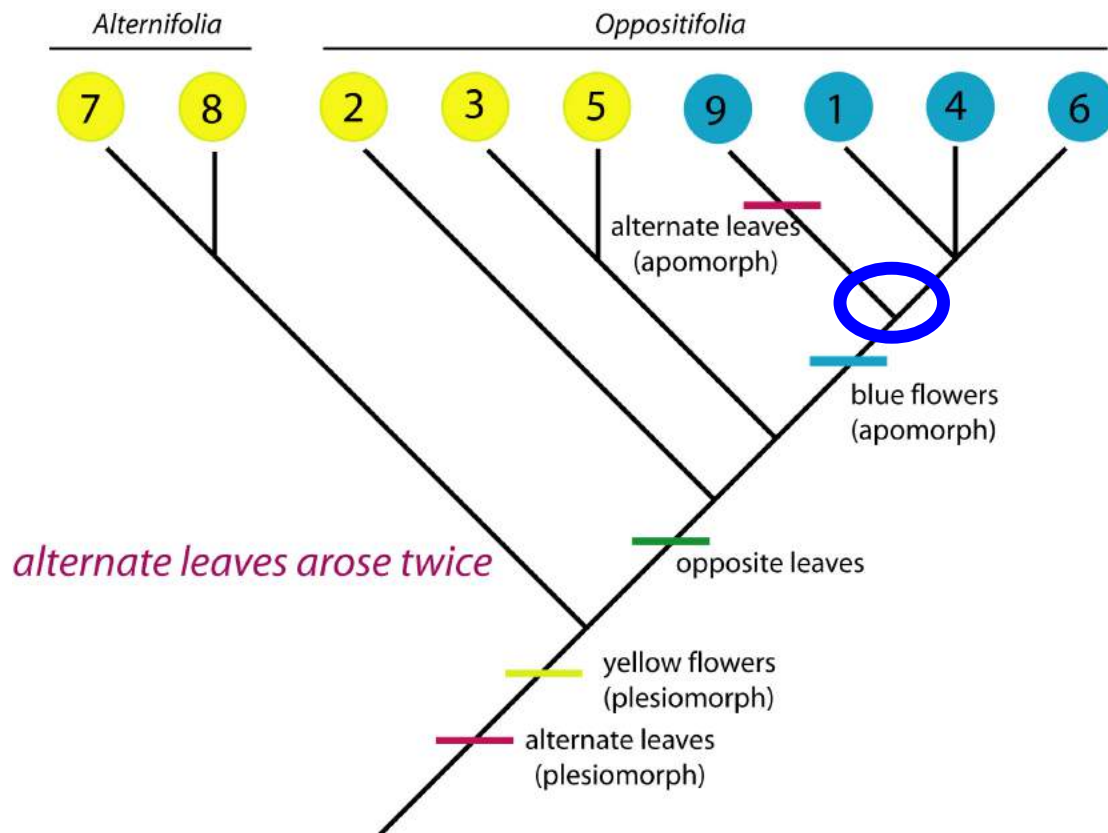
1. Belongs with other alternate leaved species; but **blue flowers have evolved twice independently**

# Phylogenetics



What if **convergences** or **reversals** have taken place in evolution?

*Where does this belong?*



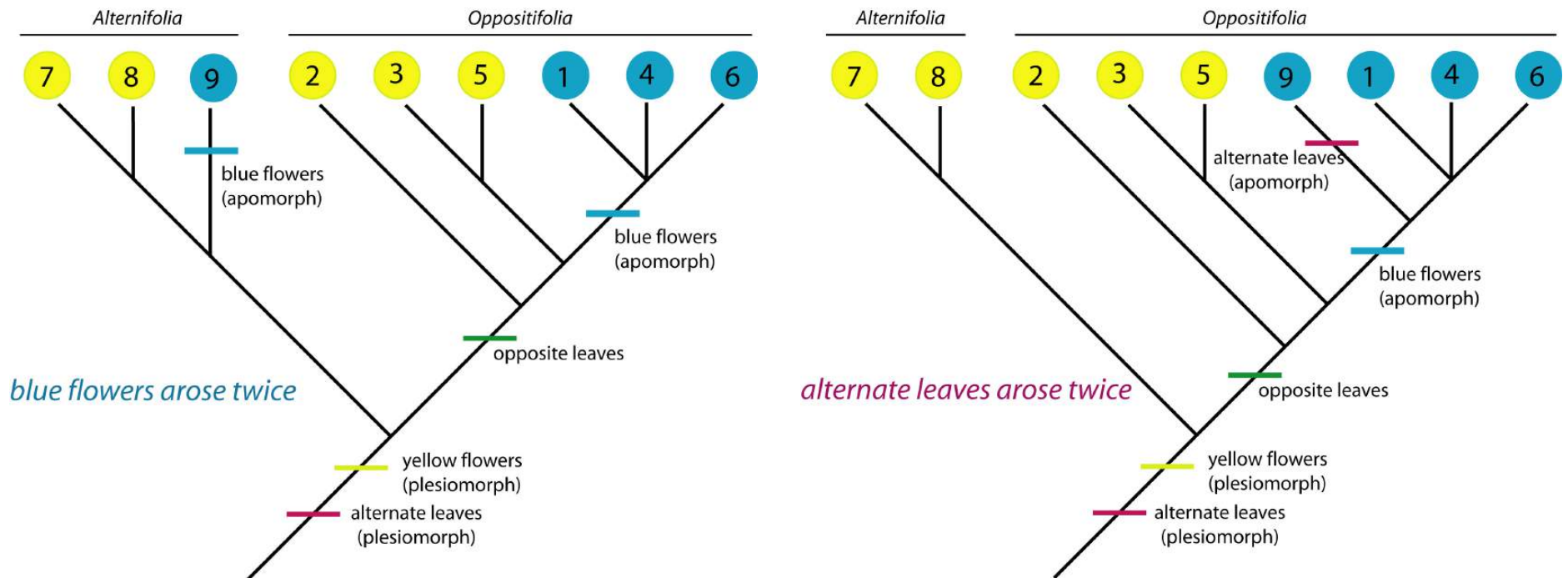
2. Belongs with other blue flowered species; but **reversal back to alternate leaves** has occurred

# Phylogenetics

What if convergences or reversals have taken place in evolution?

Both of these phylogenetic trees are equally likely based on **parsimony** — they both require one extra step

Maximum parsimony, maximum likelihood, etc. used as **optimality criteria** in phylogenetics to choose which of potentially many different trees is best



# Phylogenetics

The data matrix has **taxa** each scored for as many **characters** as possible

	<i>char 1</i>	<i>char 2</i>	<i>etc.</i>	(morphology)	(DNA)	(geography)
<i>taxon 1</i>	1	1	0	0	0	1
<i>taxon 2</i>	1	1	0	0	0	0
<i>etc.</i>	0	1	0	0	0	0
(populations)	0	1	0	0	0	0
(species)	0	0	0	0	1	0
(families)	0	0	1	1	1	0
	0	0	1	1	1	0
	0	0	1	1	1	0

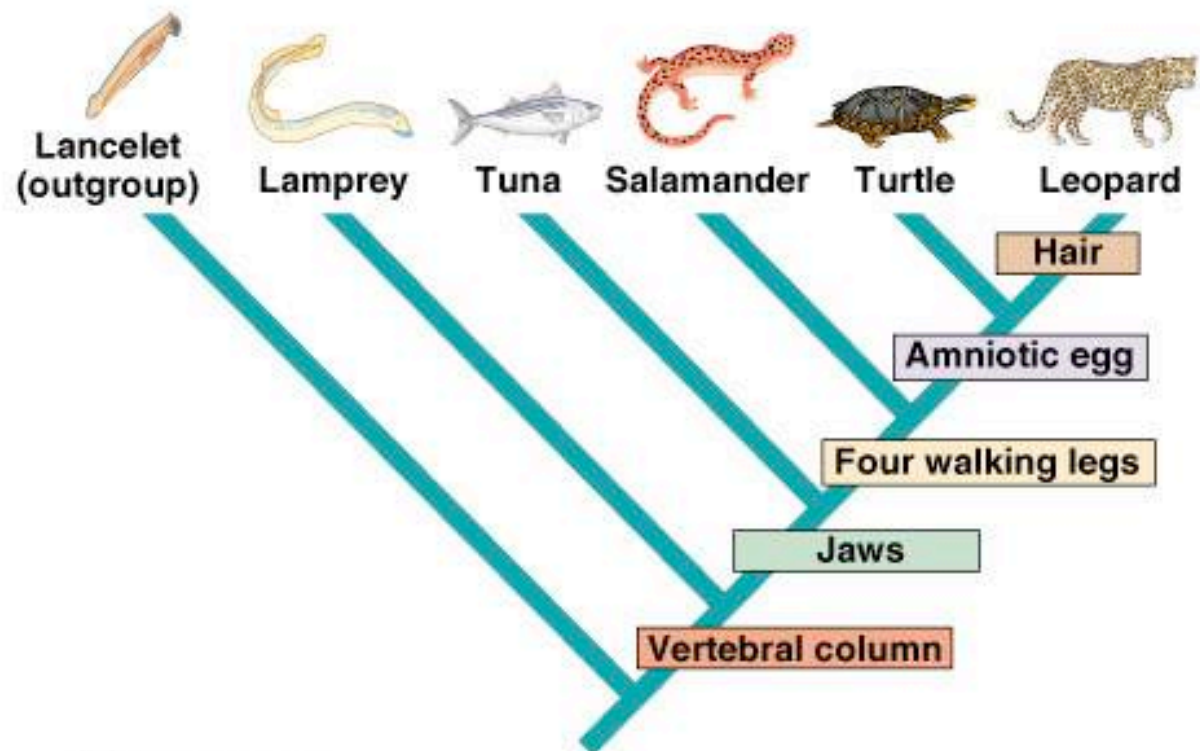


# Constructing Phylogenetic Trees

<https://www.youtube.com/watch?v=pwQWecIbsIc>

CHARACTERS	TAXA					
	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Hair	0	0	0	0	0	1
Amniotic (shelled) egg	0	0	0	0	1	1
Four walking legs	0	0	0	1	1	1
Jaws	0	0	1	1	1	1
Vertebral column (backbone)	0	1	1	1	1	1

(a) Character table



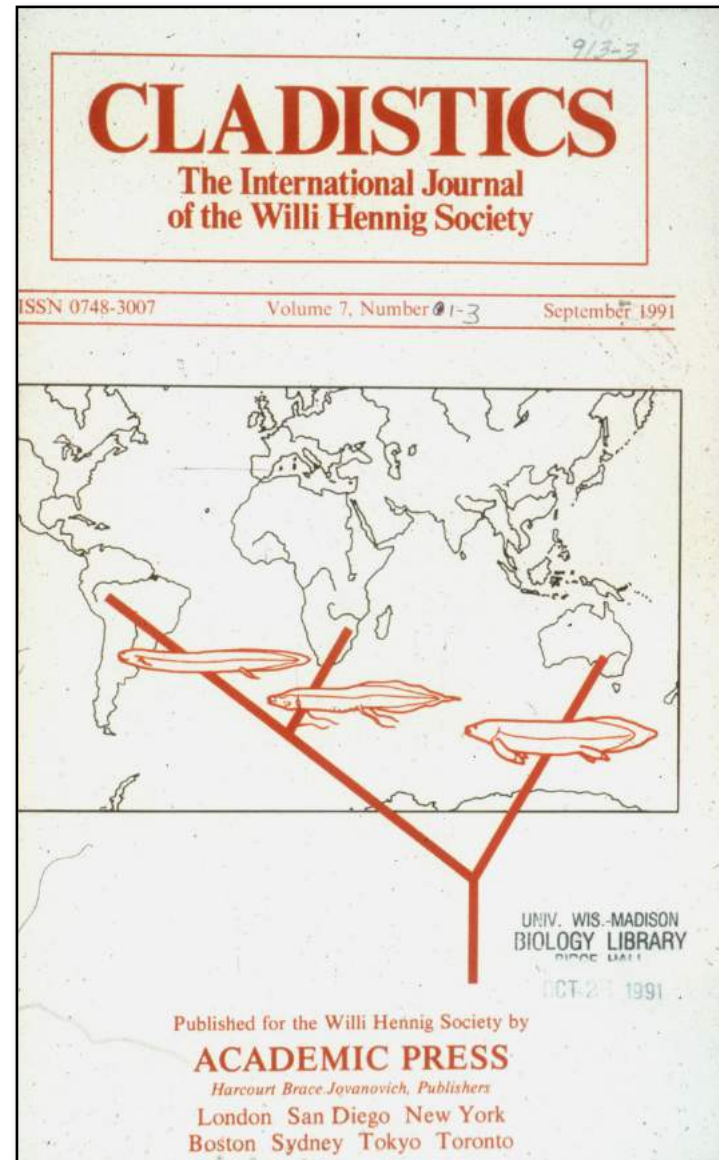
(b) Cladogram

# Phylogenetics

*“If philosophy is the devil’s whore, as Martin Luther once quipped, then biogeography and biological systematics are fast becoming Old Nick’s bordello”* (Craw, 1988b)

Phylogenetics and historical biogeography are now intimately intertwined . . .

. . . and now becoming a sanctified marriage with the use of DNA – molecular phylogenetics



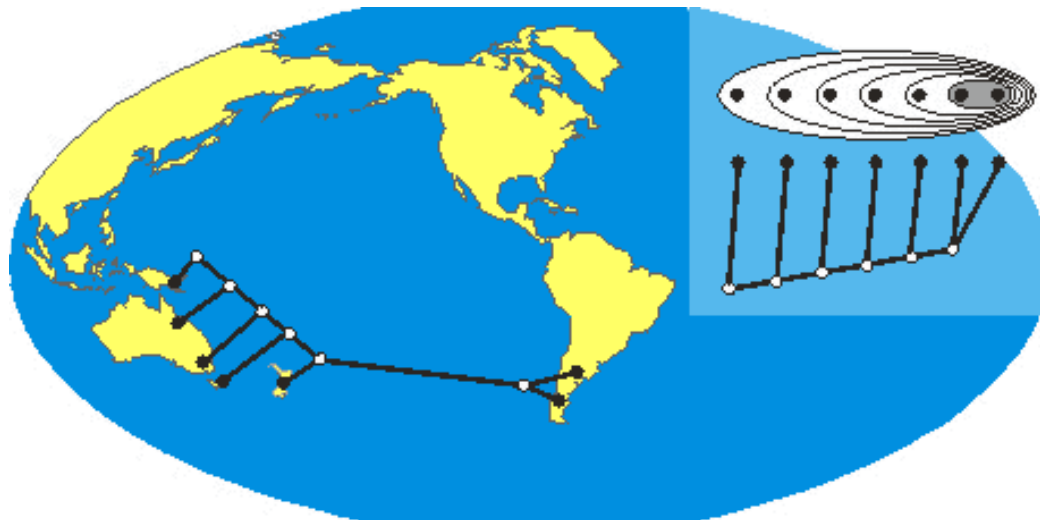
# Phylogenetic Biogeography

Phylogenetic biogeography was the first explicit attempt to connect relationships of taxa to biogeography

Initially attempted by Willi Hennig (1968), the formulation of the method was done by the Swedish zoologist Lars Brundin and his students



Brundin, Lars (I) (Sweden, Chironomidae)  
XII International Congress of Entomology,  
London, July, 1964

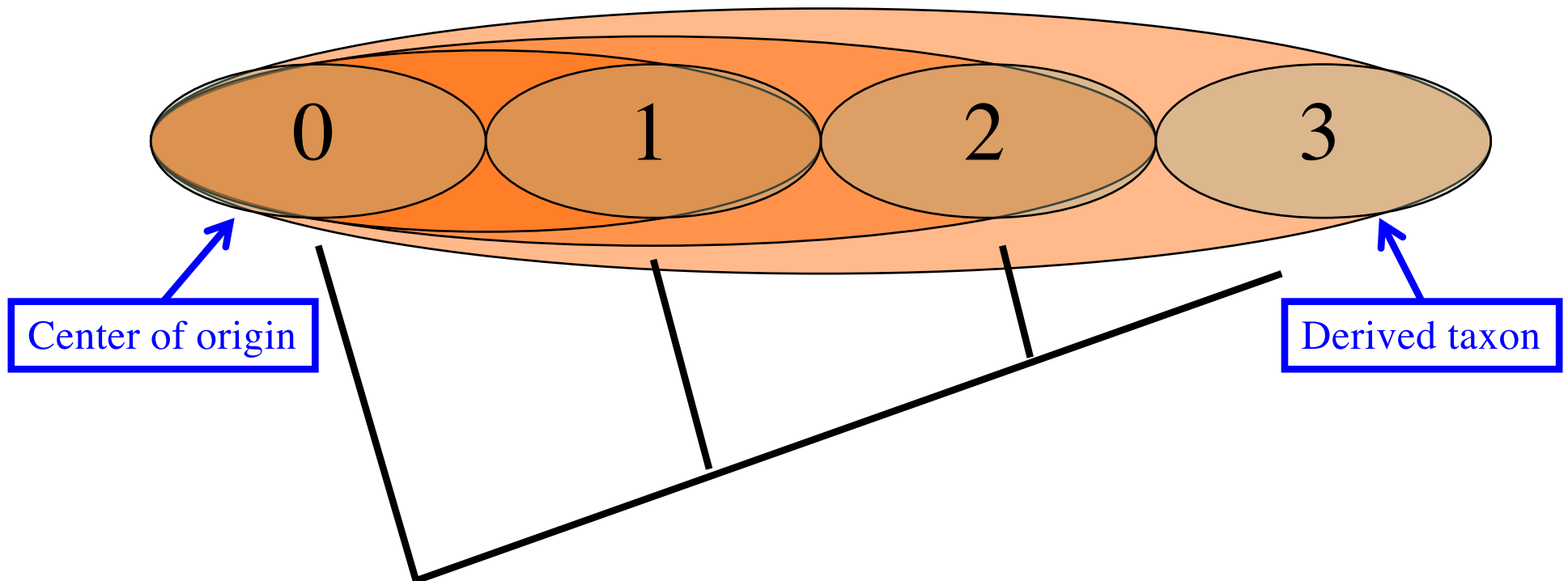


- Phylogenetic hypothesis
- “Progression rule, and Deviation rule”
- Centers of origin
- Intermediate between dispersalism and cladistic biogeography

# Phylogenetic Biogeography

- *Progression rule:*      **0 → 1 → 2 → 3**

The *primitive members of a taxon are found closer to its center of origin* than more derived ones. "Peripheral allopatric speciation".

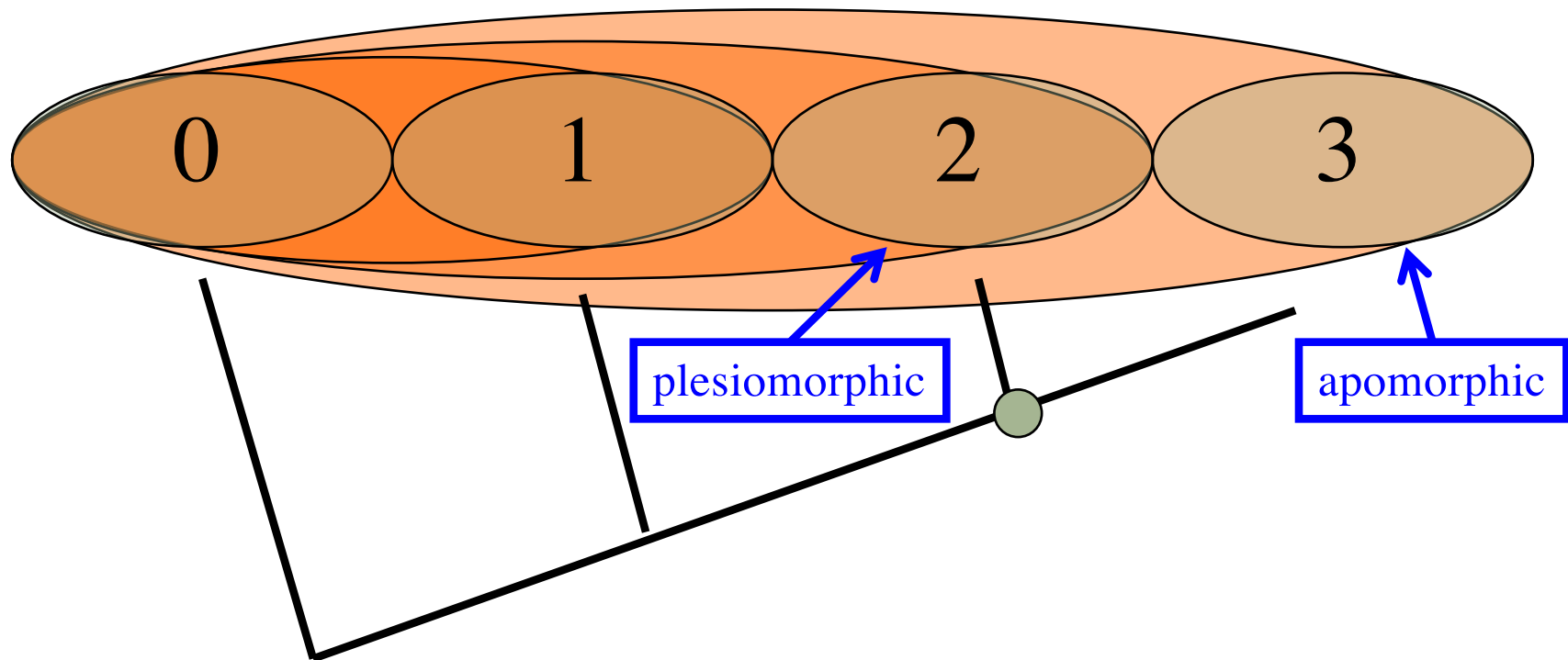




# Phylogenetic Biogeography

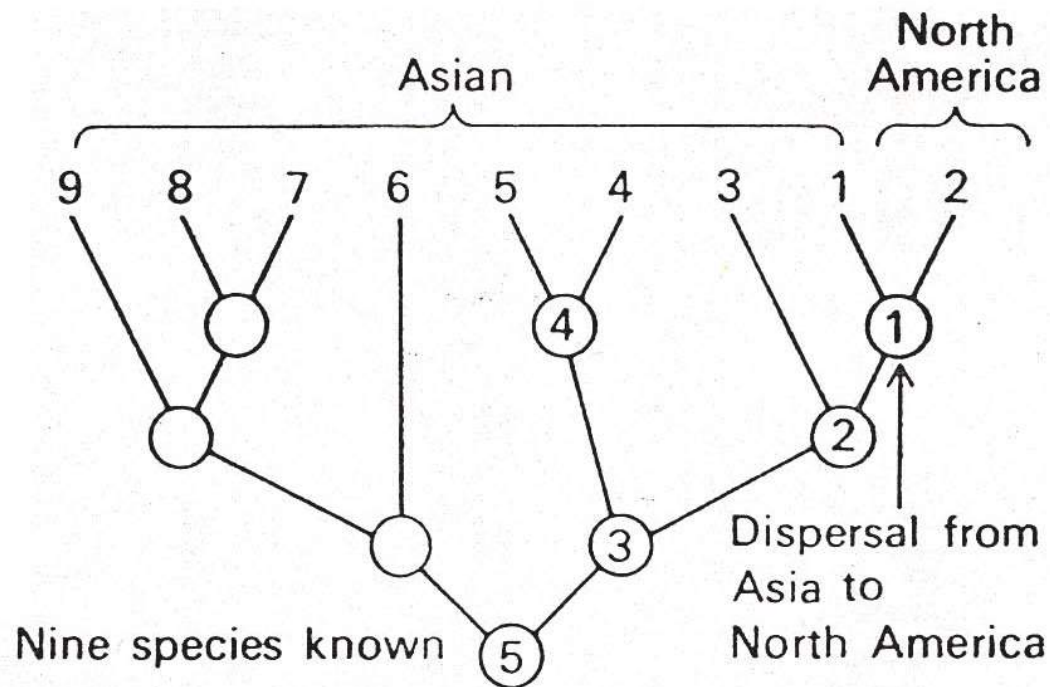
- *Deviation rule:*

Between two sister-species, the more *plesiomorphic* species is the one present in the *original* area, whereas the more *apomorphic* is the one that *dispersed*



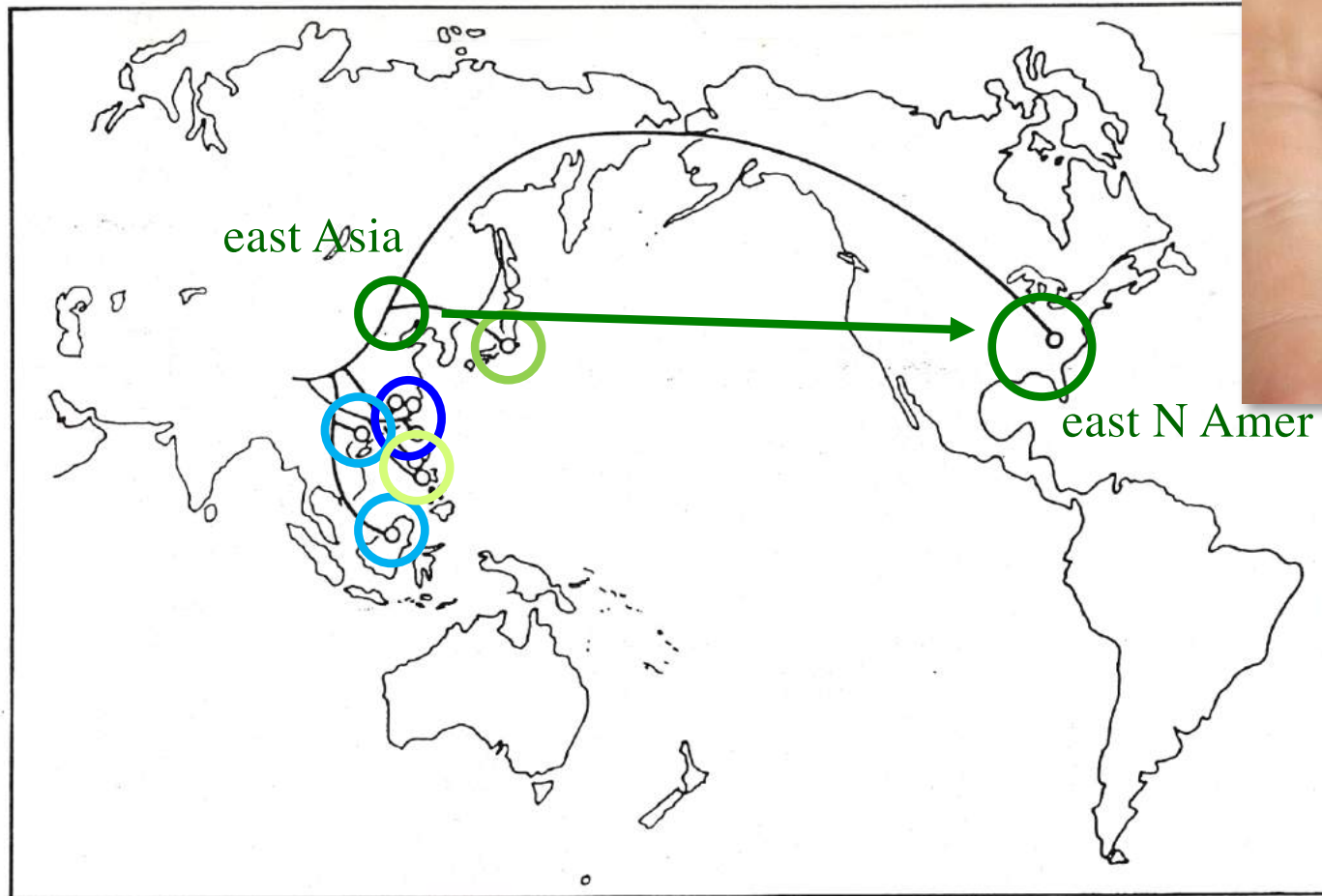
# Phylogenetic Biogeography

Cladogram used with the two rules to find *center of origin* and patterns of *dispersal*



Cladogram for the nine species of *Wormaldia* (caddis flies) — Ross, 1974

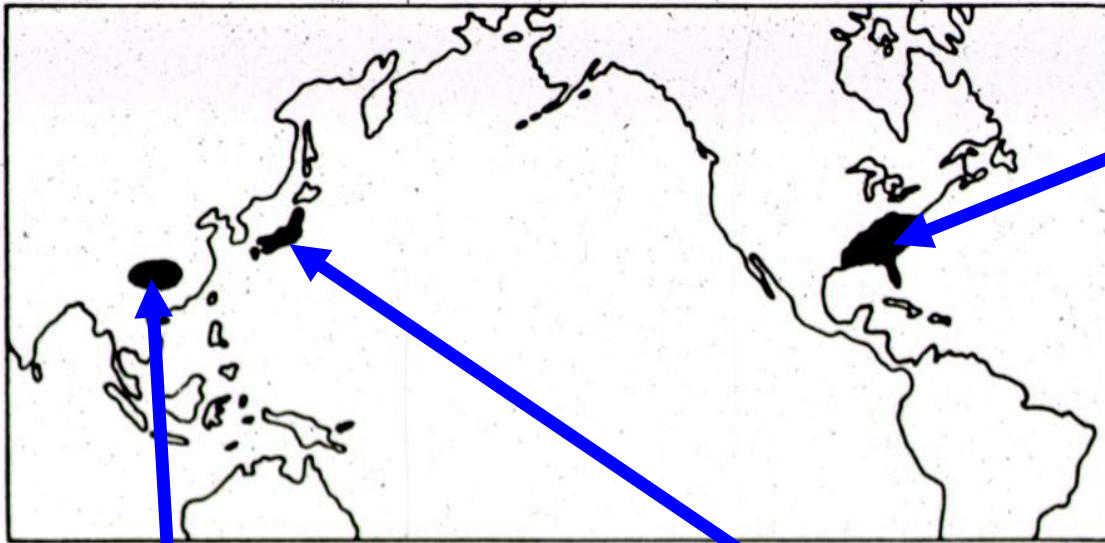
# Phylogenetic Biogeography



Note center of origin  
and dispersal events  
and one LDD event

Distribution and phylogeny of *Wormaldia* (caddis flies) — Ross, 1974

# Phylogenetic Biogeography



*Stewartia malacodendron*  
Theaceae - tea family



*Stewartia sinensis*



*Stewartia pseudocamellia*

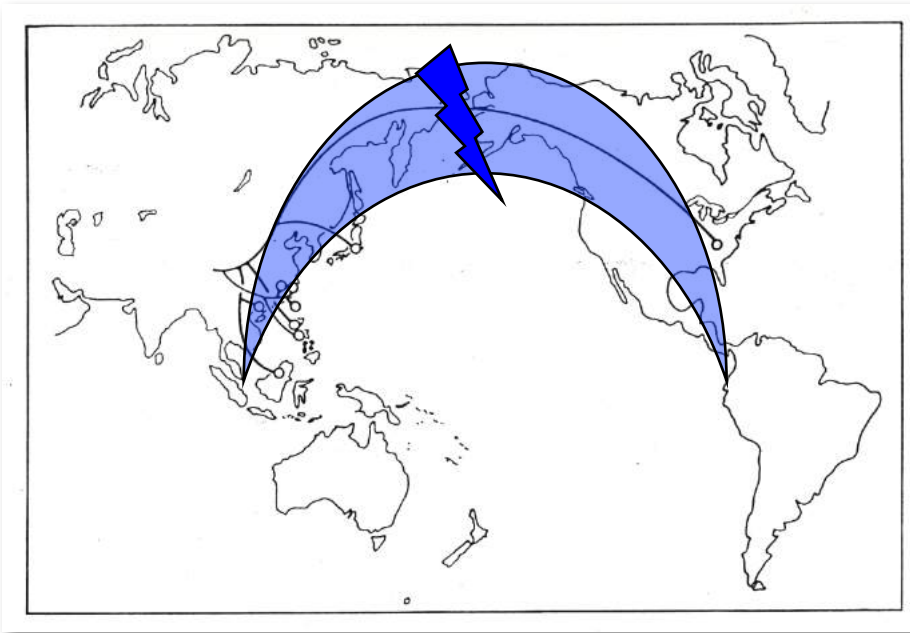
But there are **many** animals and plants with this same distribution!

All explained by separate centers of origins and dispersal events?



# Cladistic Biogeography

One breakthrough in the application of phylogenetics to biogeography - **cladistic biogeography** - came with the efforts of biogeographers such as Donn Rosen, Gareth Nelson, and Norm Platnick in their interpretation of these examples



They would interpret such a pattern as the caddis flies in a different way —

Once **continuous biota** . . .

and then **vicariance** explains this particular distribution *just as well*

# Cladistic Biogeography

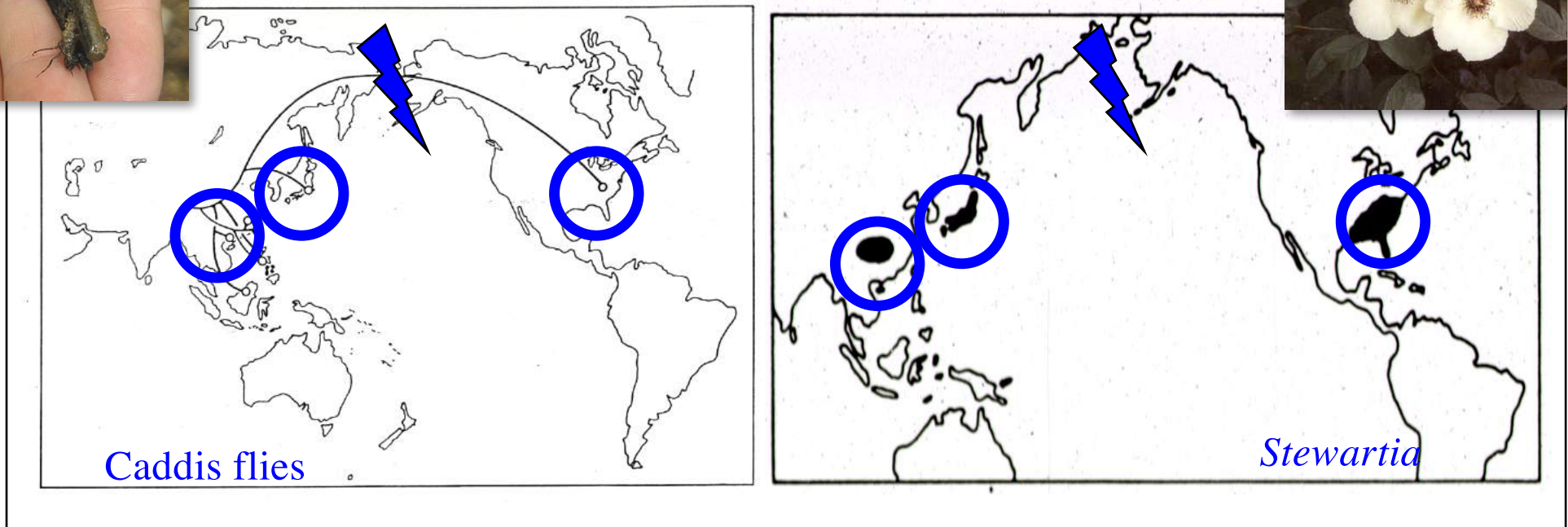
One breakthrough in the application of phylogenetics to biogeography - **cladistic biogeography** - came with the efforts of biogeographers such as Donn Rosen, Gareth Nelson, and Norm Platnick in their interpretation of these examples



Distributional data are insufficient to resolve decisively either **dispersal** or **vicariance** as the cause of a particular disjunct distribution pattern

# Cladistic Biogeography

if general pattern . . . then invoke vicariance!

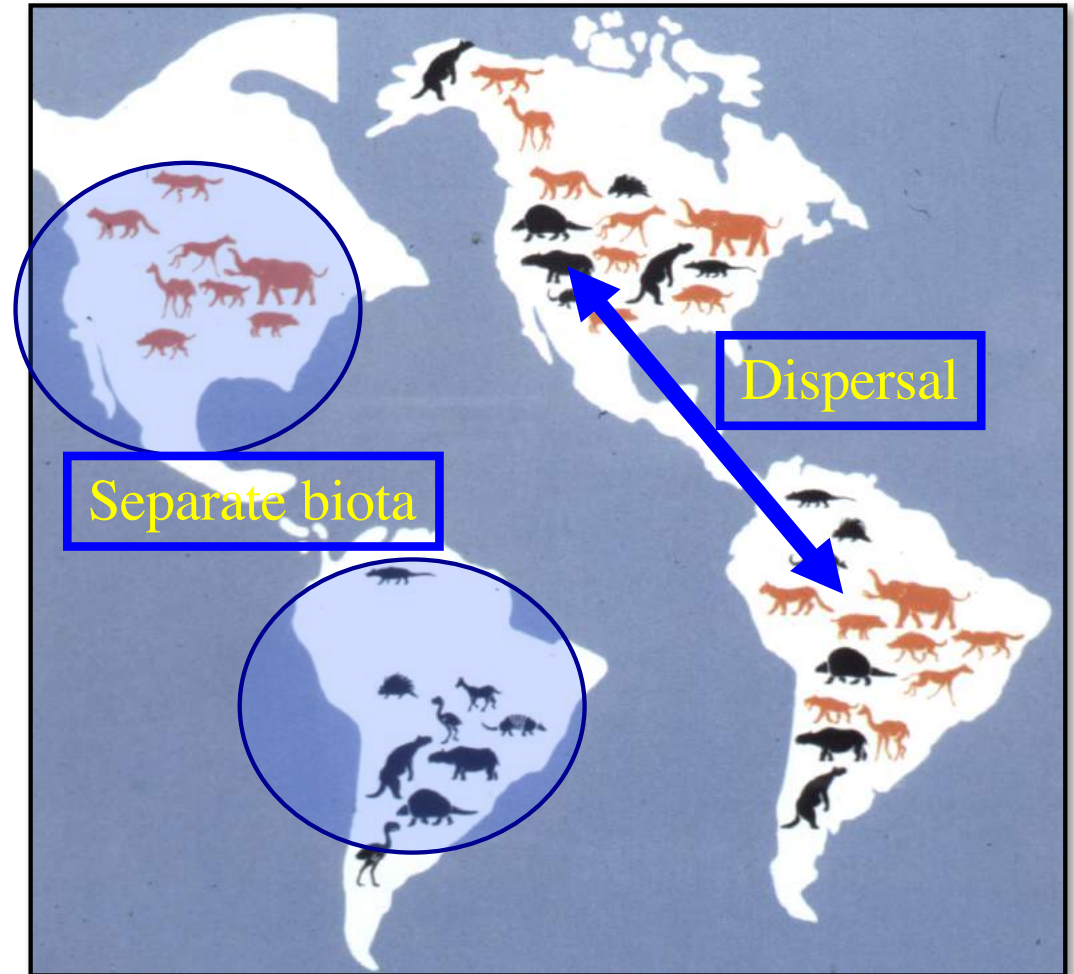


Platnick and Nelson (1978) argued that “*one should not worry about the cause of a particular distribution but whether or not it conforms to a general pattern of relationships shown by other groups of taxa endemic to the areas occupied*”

# Cladistic Biogeography

Aside: perhaps these two ideas should be considered ends of a spectrum:

Completion of Panama land bridge allowed **migration/dispersal** of quite unrelated animal and plant taxa into the two Americas . . .



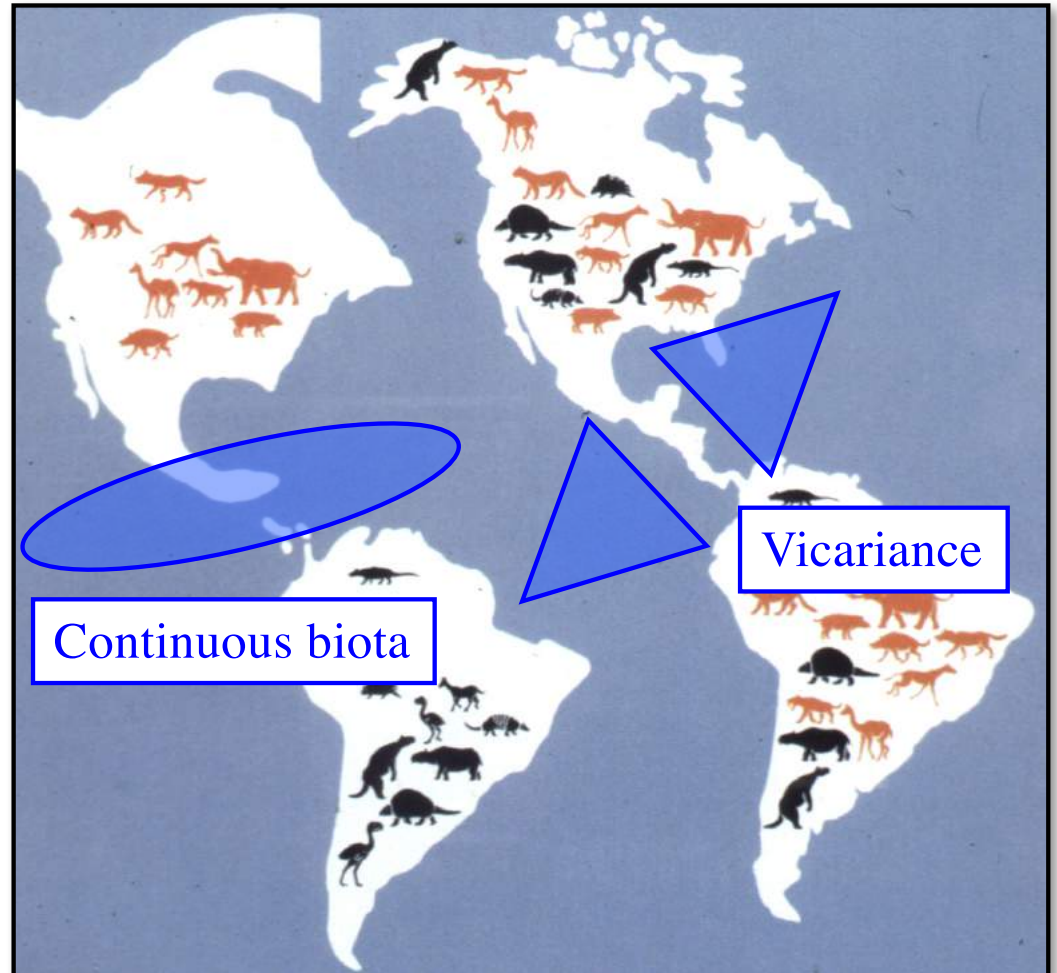


# Cladistic Biogeography

Aside: perhaps these two ideas should be considered ends of a spectrum:

Completion of Panama land bridge allowed **migration/dispersal** of quite unrelated animal and plant taxa into the two Americas . . .

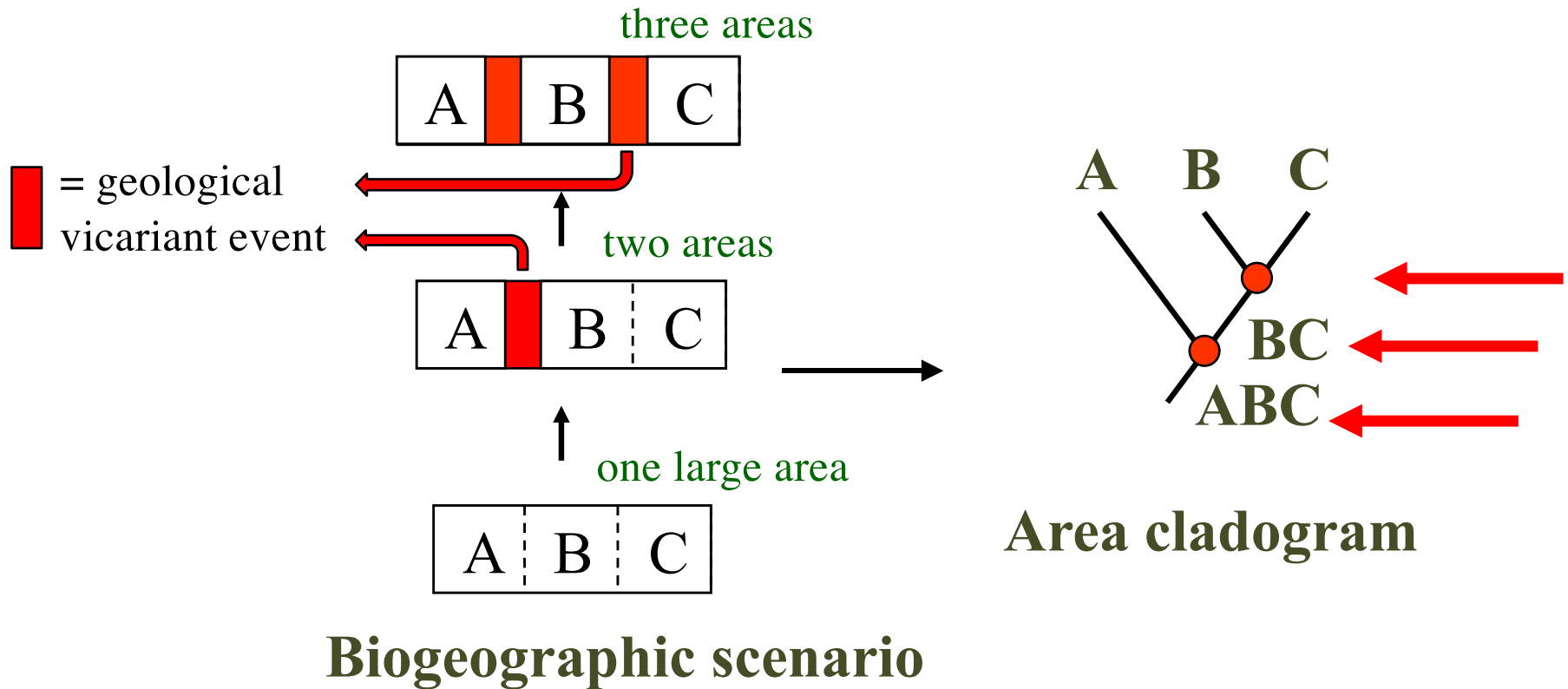
**and** at the same time provided a **vicariance event** in dividing a previously single community of marine organisms into separate Caribbean and East Pacific groups



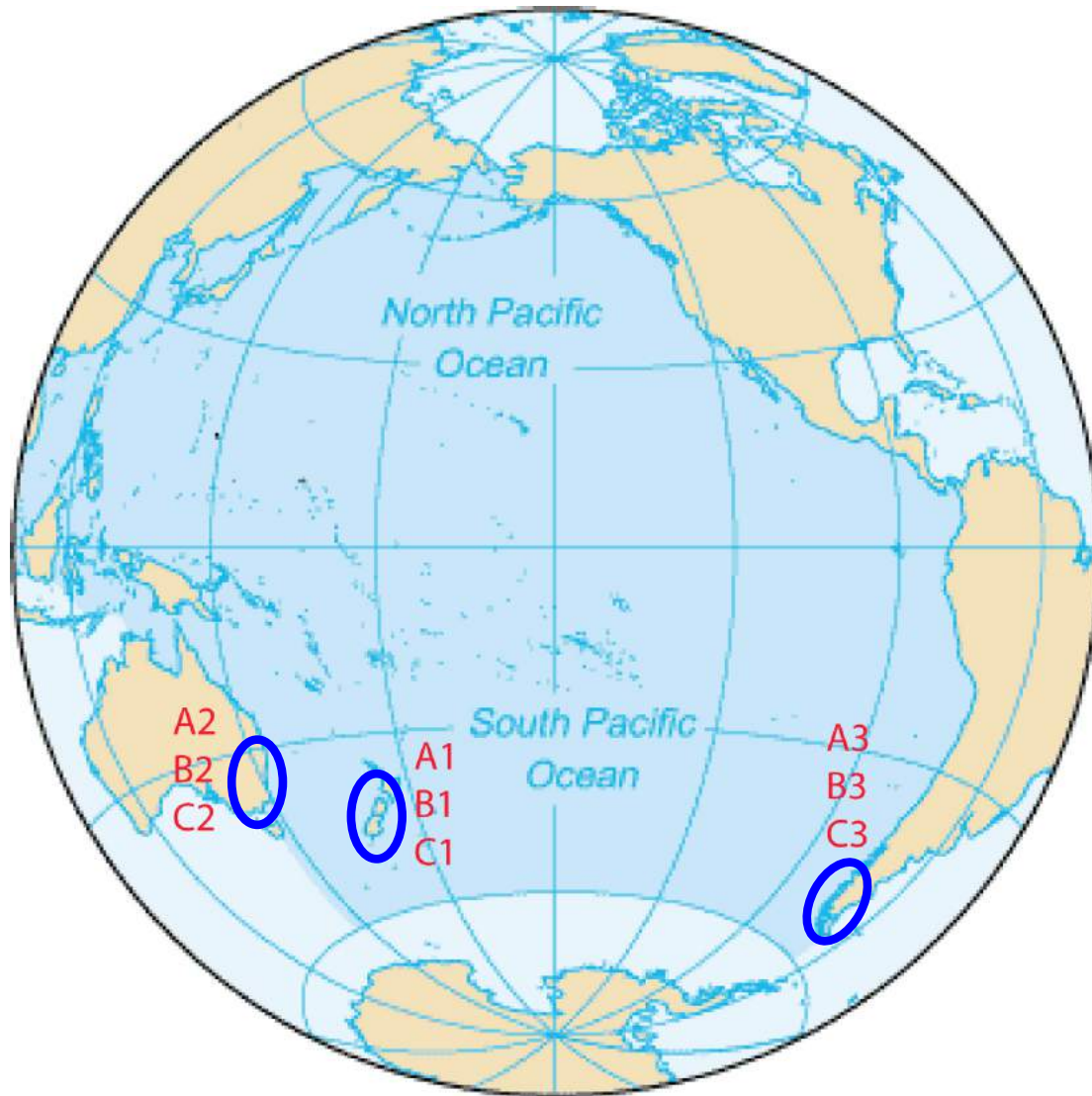


# Cladistic Biogeography

- Integration of **Plate tectonics** + **Vicariance** + **Cladistics**
- Correspondence between areas of distribution (A, B, C below) and phylogenetic relationships (Vicariance)



# Cladistic Biogeography



Step 1 — find  
monophyletic groups  
(A,B,C) with taxa  
occurring in 3 or more  
areas of endemism  
(1,2,3)

A



B

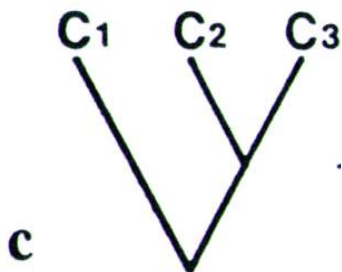
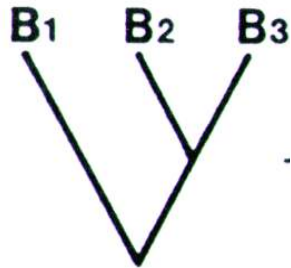
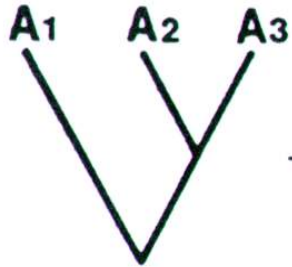


C



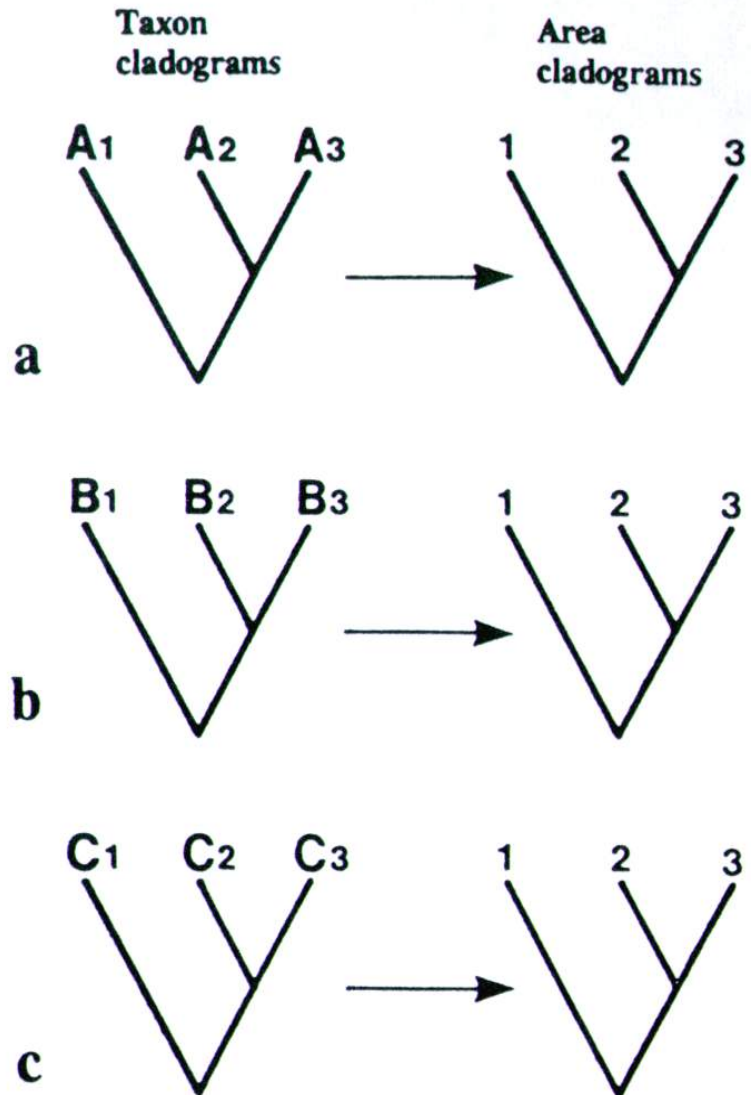
# Cladistic Biogeography

Taxon  
cladograms



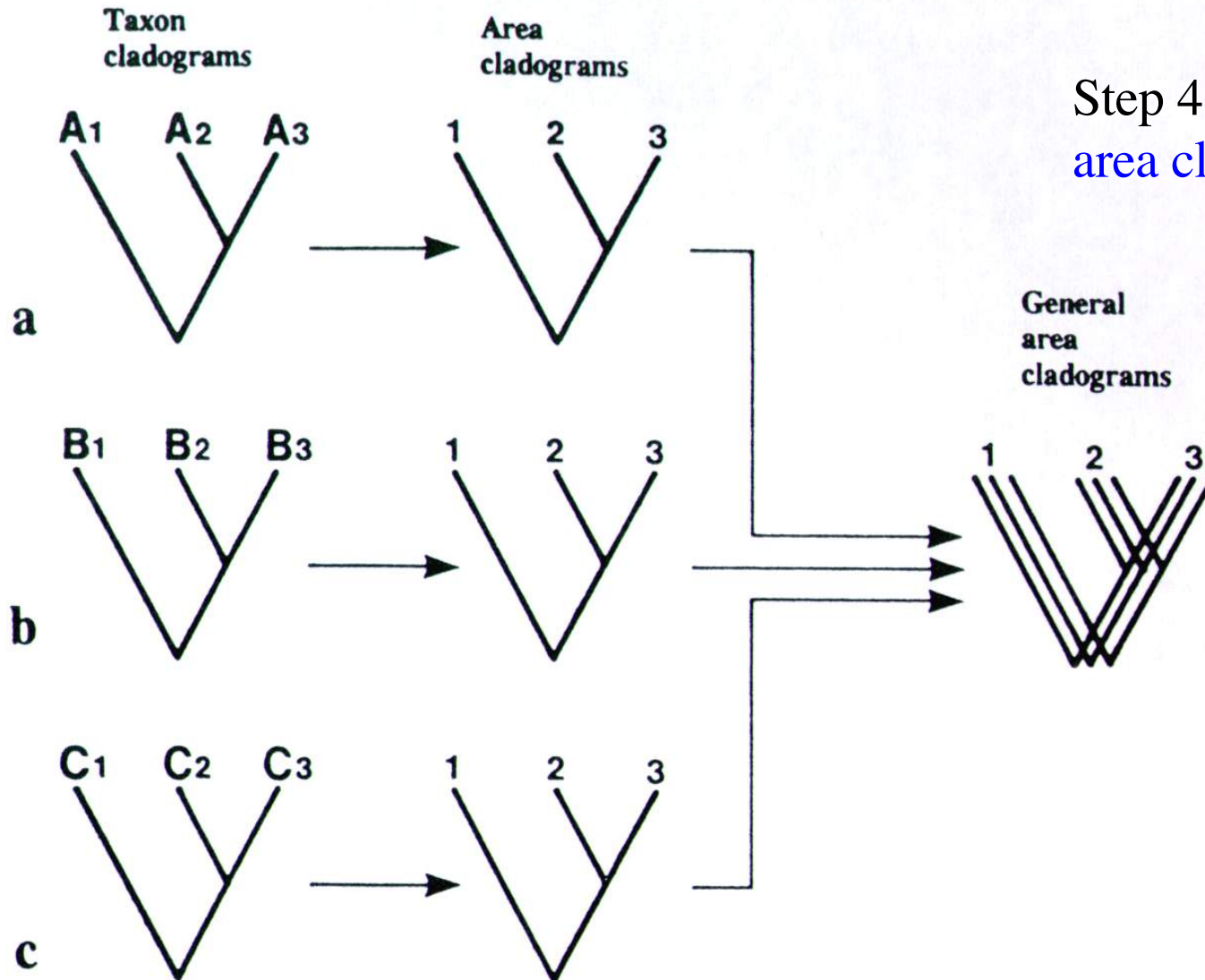
Step 2 — produce **taxon cladograms** for each group

# Cladistic Biogeography



Step 3 — produce **area cladograms** by replacing taxon names with areas

# Cladistic Biogeography

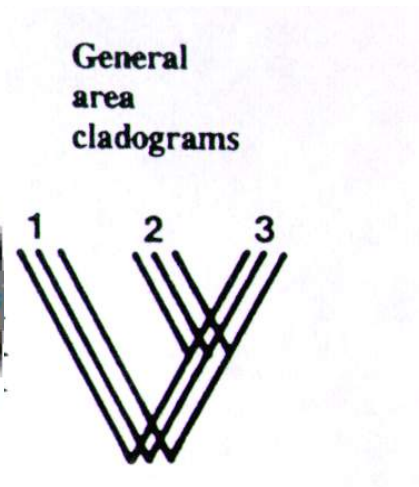
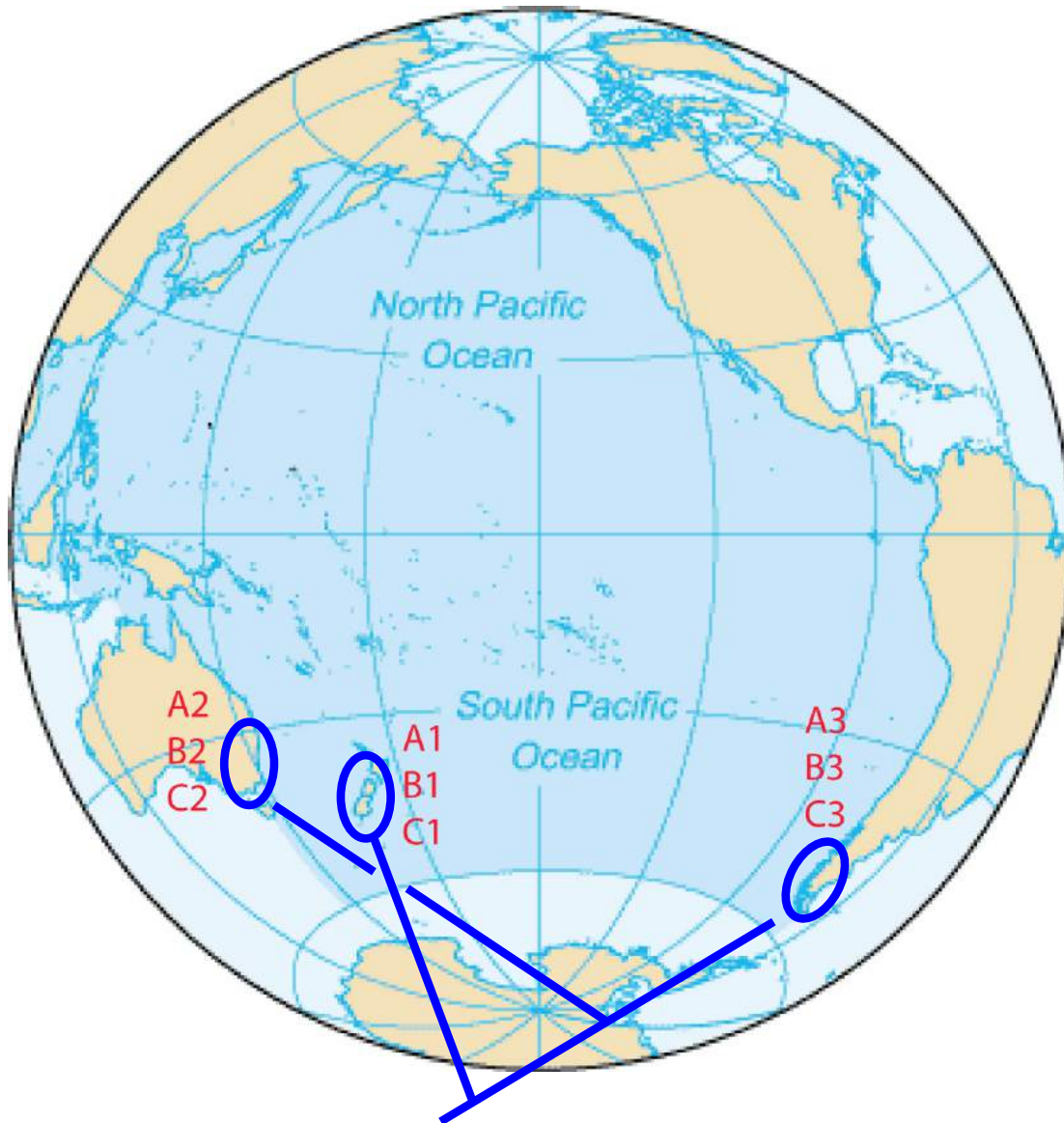


Step 4 — find **general area cladogram**

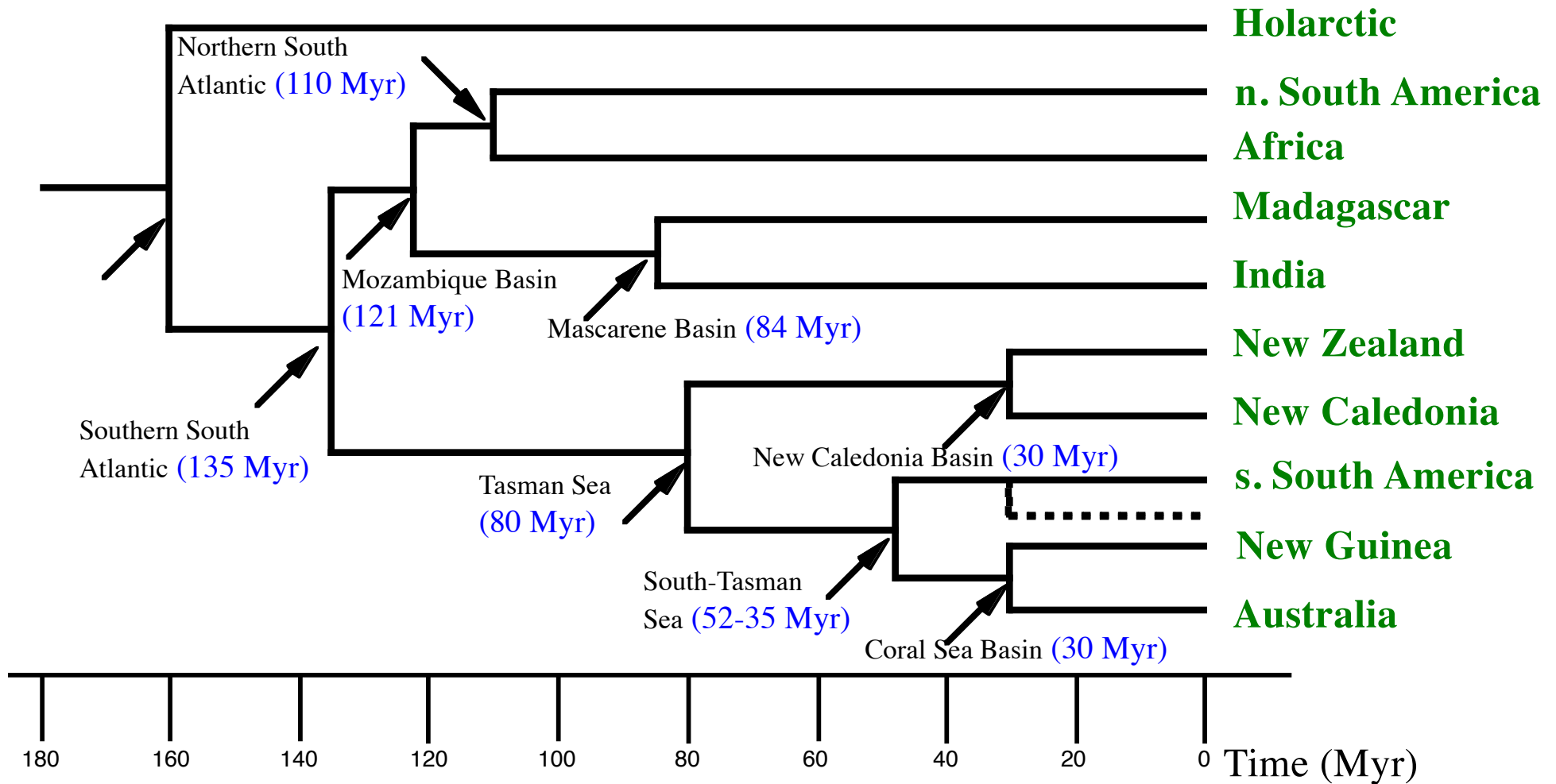


# Cladistic Biogeography

Step 4 — find **general area cladogram**

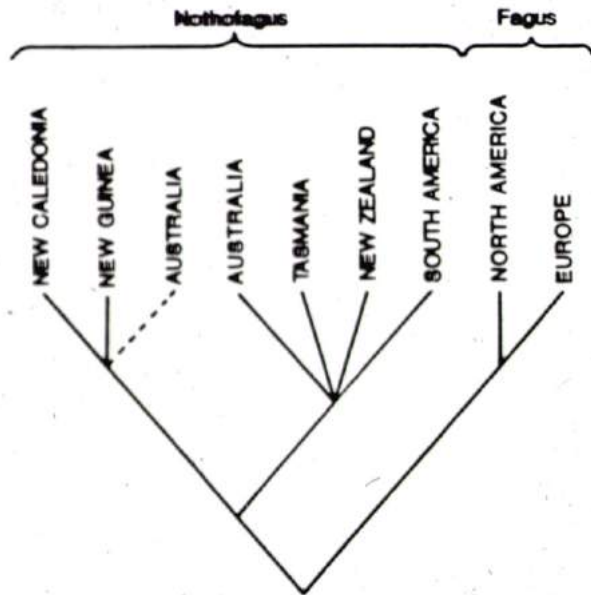


# Cladistic Biogeography

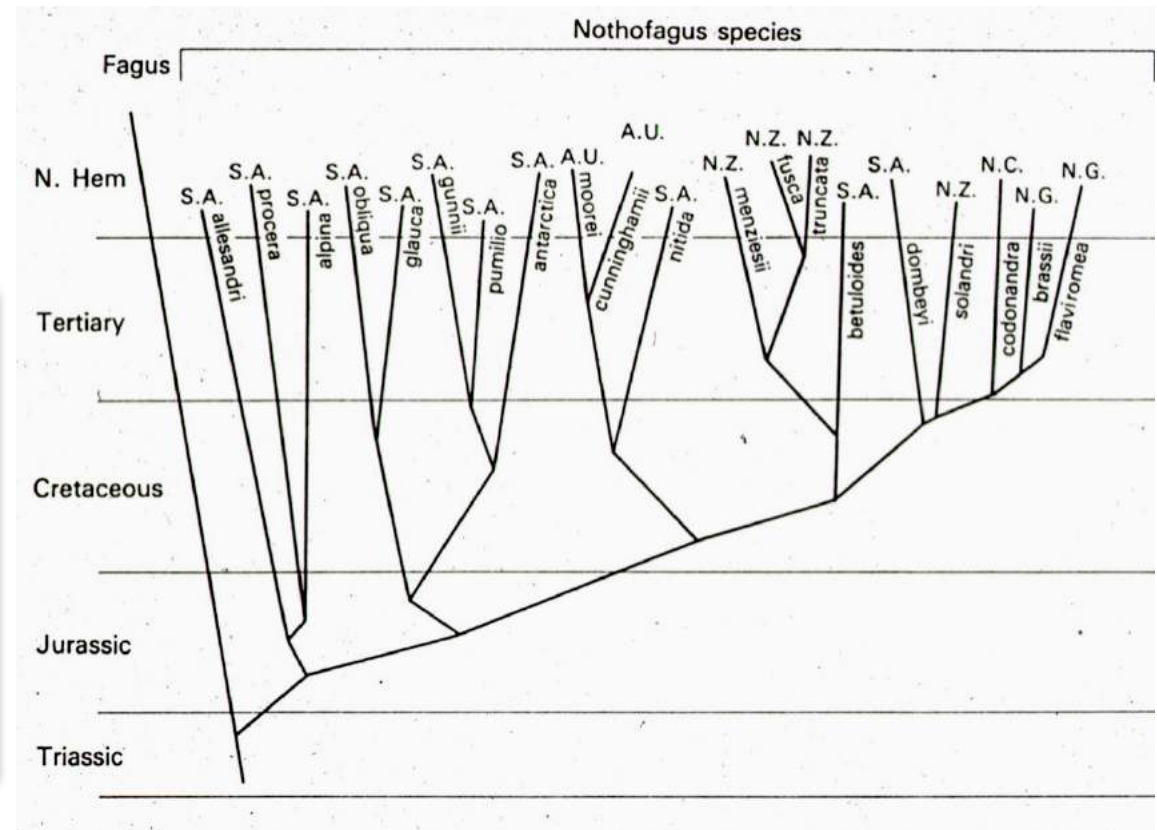


Step 5 — is general area cladogram supported by **geological area cladogram**?

# Cladistic Biogeography



Issue #1 — **cladogram accuracy**: biogeographic “story” is only as good as the “estimate” of relationships of the organisms (e.g., changing idea of *Nothofagus* phylogeny)



*Nothofagus betuloides*  
© J. Hyvönen

***Nothofagus* – southern beeches**

the plant example in cladistic biogeography



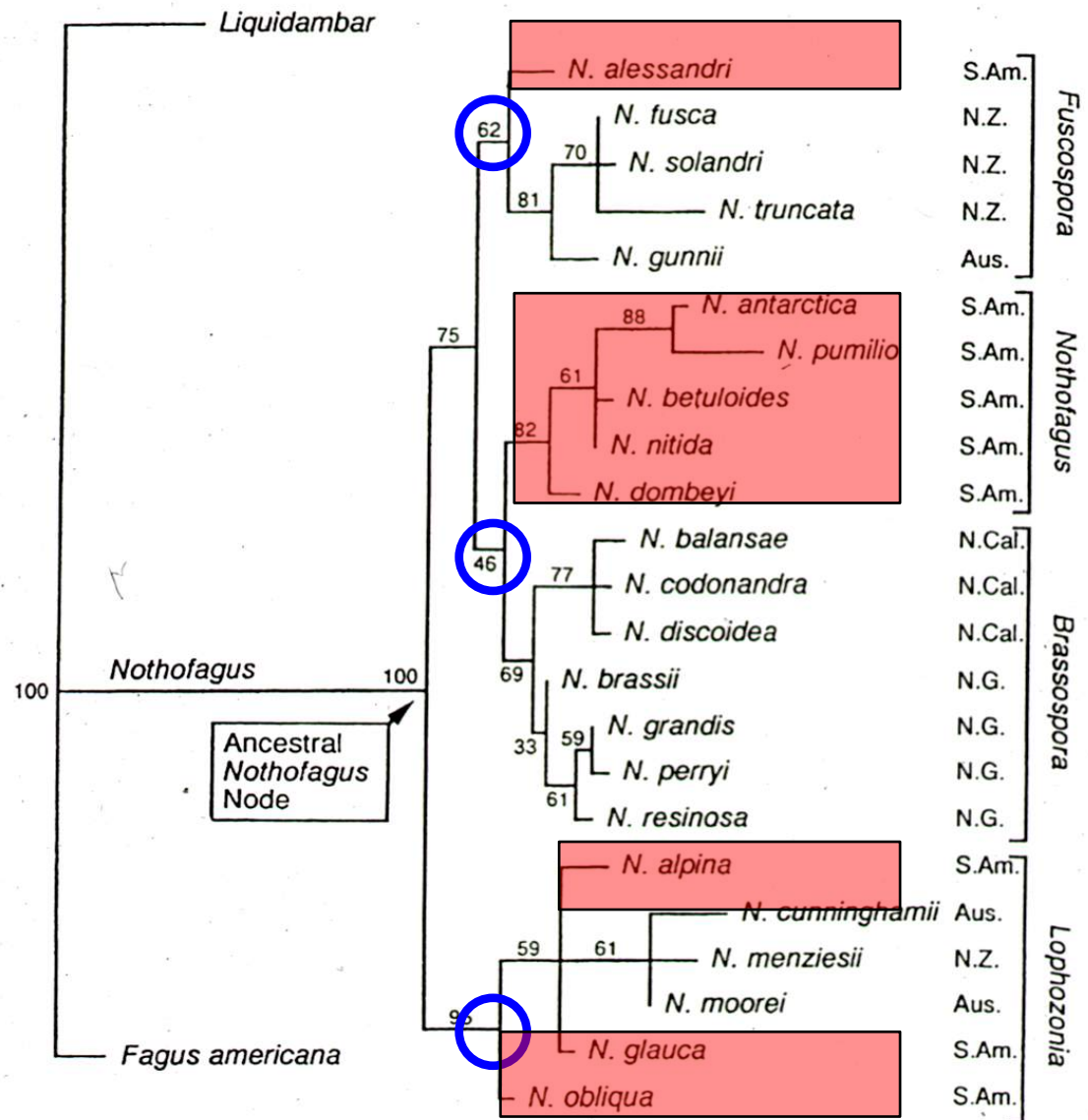
# Cladistic Biogeography

A recent molecular cladogram of *Nothofagus*; now there appears to be 3 lineages within *Nothofagus* that show independent Gondwanan vicariance with S. America splitting first



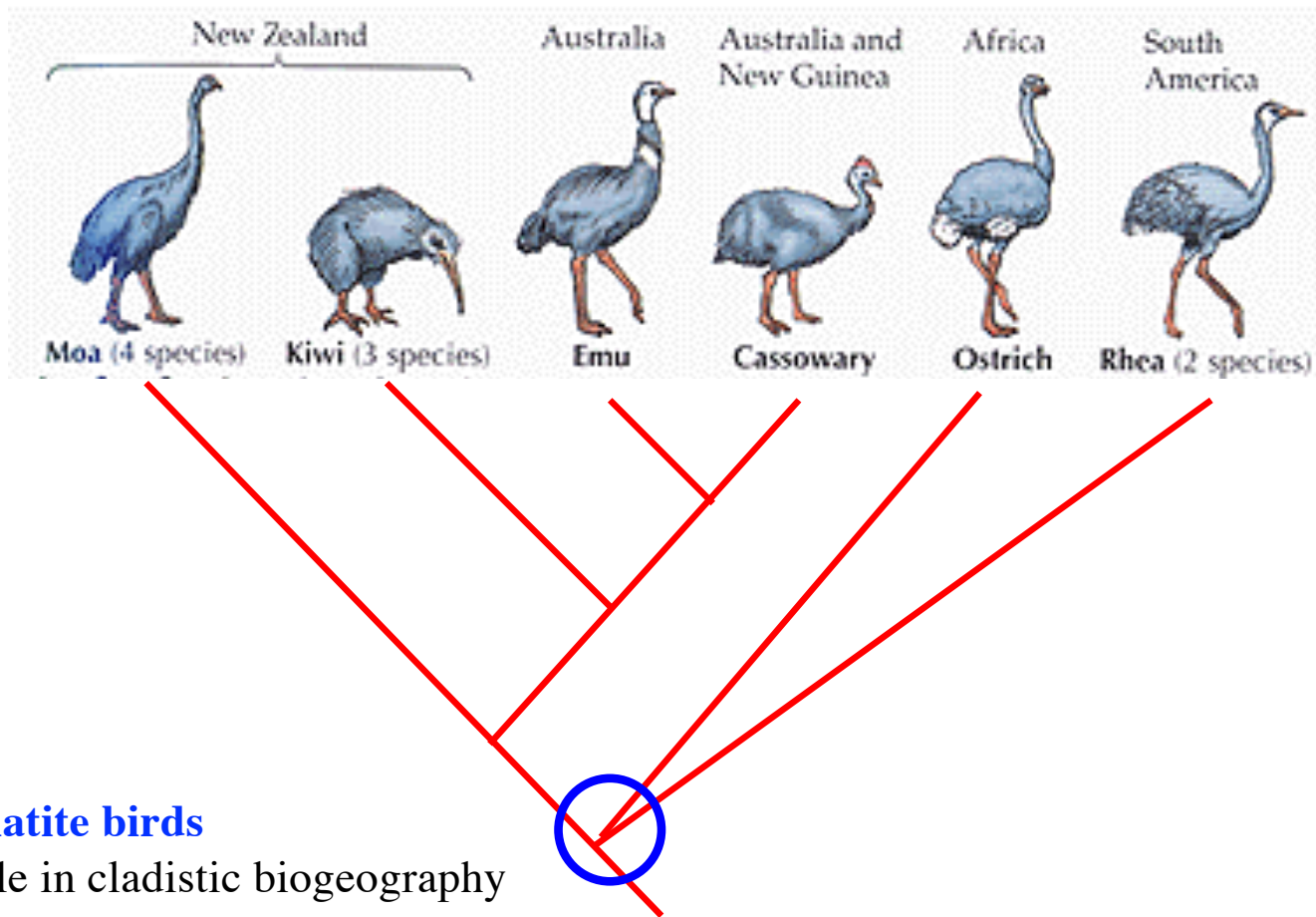
*Nothofagus* – southern beeches

the plant example in cladistic biogeography



# Cladistic Biogeography

Issue #2 — **unresolved cladogram**: therefore unknown area relationships



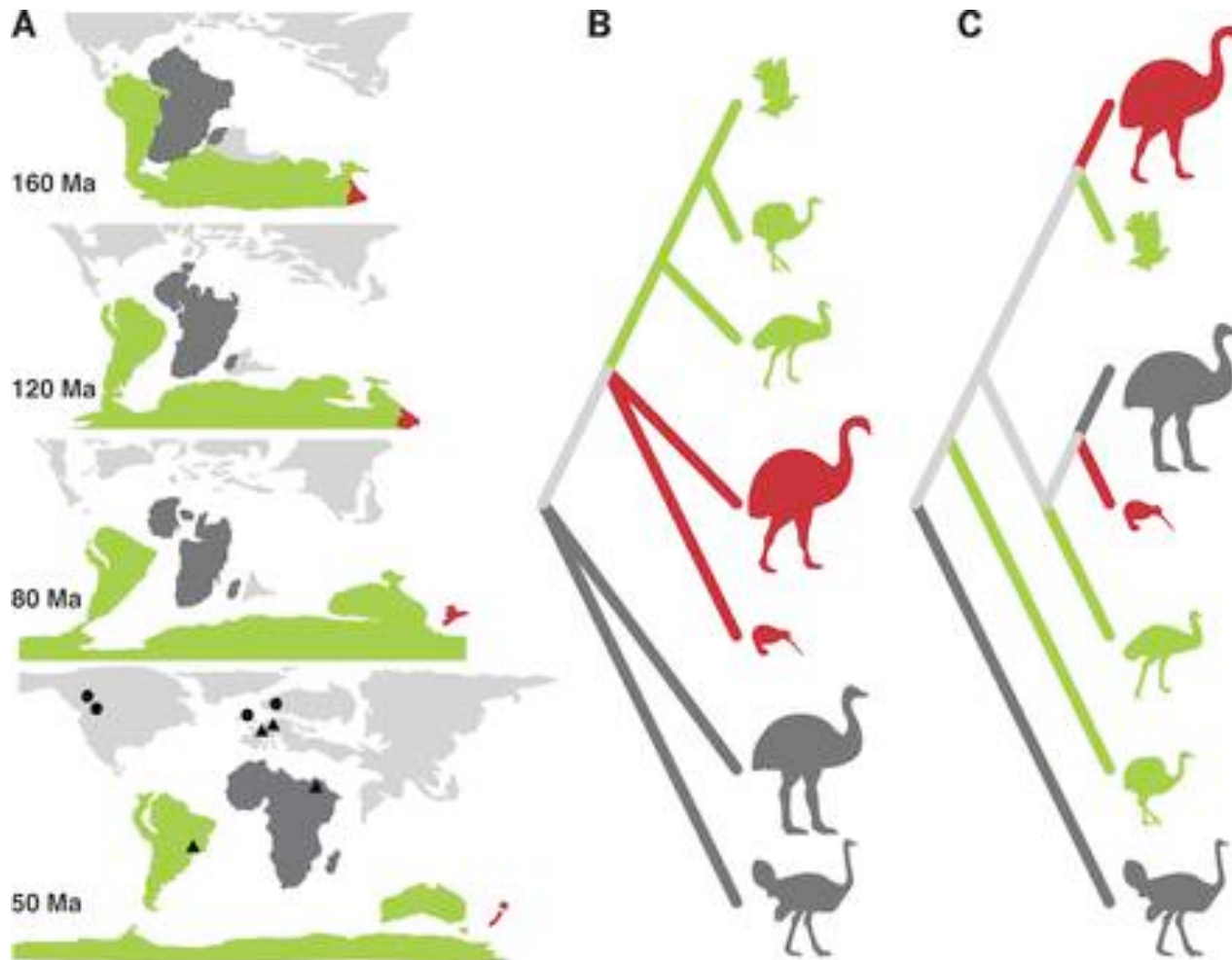
**Ratite birds**

*the animal example in cladistic biogeography*



# Cladistic Biogeography

Issue #2 — **unresolved cladogram**: therefore unknown area relationships



Also **cladogram accuracy!**

B. Geological story

C. Mitochondrial story  
(different from nuclear story)

*Science* 2014 Mitchell et al.

## Cladistic Biogeography

# Ancient DNA reveals elephant birds and kiwi are sister taxa and clarifies ratite bird evolution

Kieren J. Mitchell,<sup>1</sup> Bastien Llamas,<sup>1</sup> Julien Soubrier,<sup>1</sup> Nicolas J. Rawlence,<sup>1\*</sup>  
Trevor H. Worthy,<sup>2</sup> Jamie Wood,<sup>3</sup> Michael S. Y. Lee,<sup>1,4</sup> Alan Cooper<sup>1†</sup>

The evolution of the ratite birds has been widely attributed to vicariant speciation, driven by the Cretaceous breakup of the supercontinent Gondwana. The early isolation of Africa and Madagascar implies that the ostrich and extinct Madagascan elephant birds (Aepyornithidae) should be the oldest ratite lineages. We sequenced the mitochondrial genomes of two elephant birds and performed phylogenetic analyses, which revealed that these birds are the closest relatives of the New Zealand kiwi and are distant from the basal ratite lineage of ostriches. **This unexpected result strongly contradicts continental vicariance and instead supports flighted dispersal in all major ratite lineages.** We suggest that convergence toward gigantism and flightlessness was facilitated by early Tertiary expansion into the diurnal herbivory niche after the extinction of the dinosaurs.

# Cladistic Biogeography

Yonezawa et al. (2017) Phylogenomics and morphology of extinct paleognaths reveal the origin and evolution of the ratites. *Current Biology*

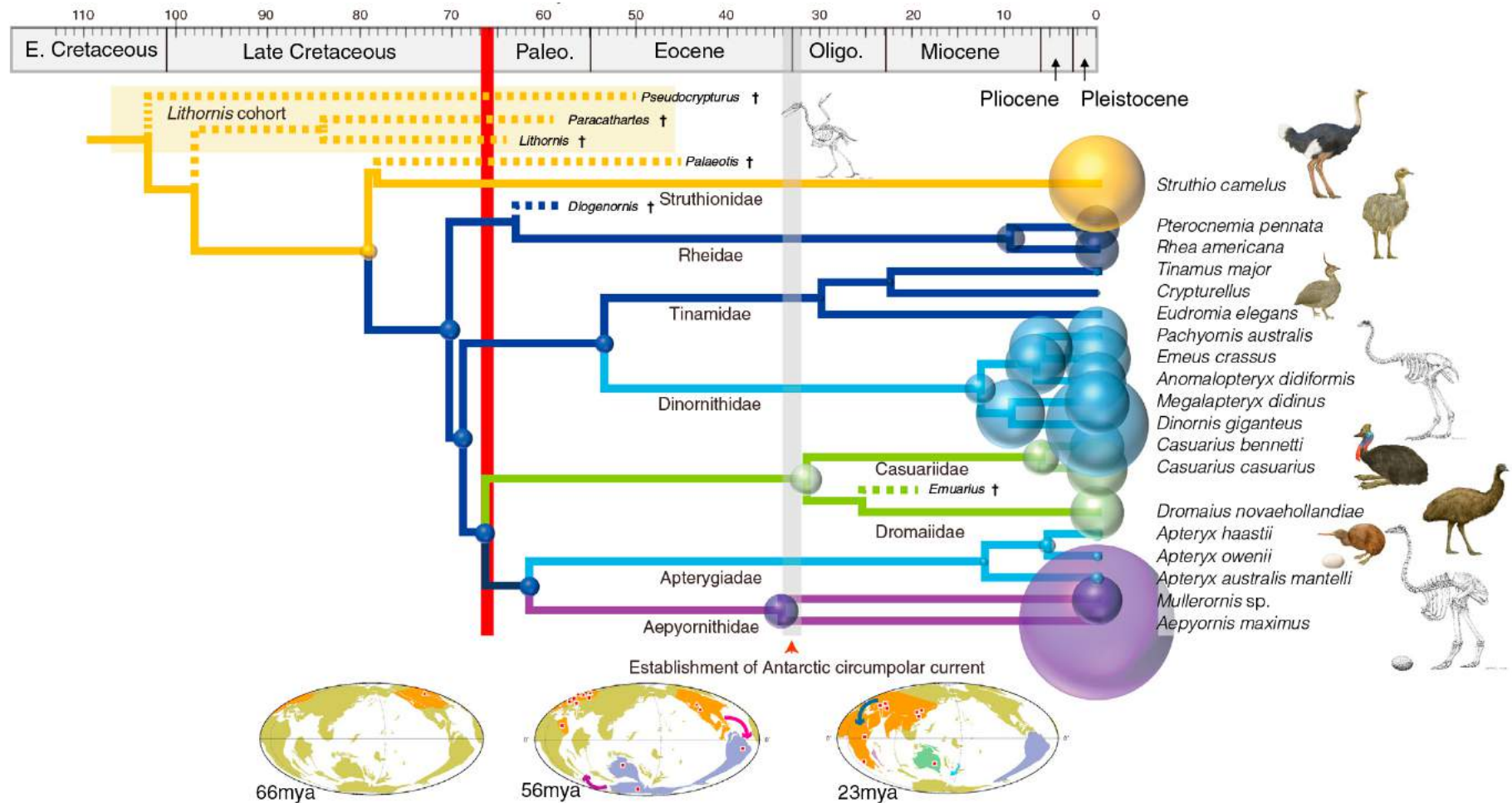
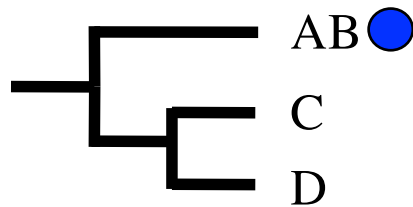


Figure 4. Palaeognathae Genomic Time Tree and Body Size

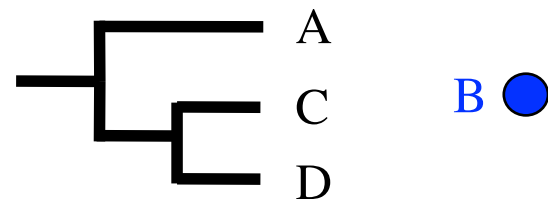
# Cladistic Biogeography

Issue #3 — taxa / area inconsistencies:

- *Widespread taxa*: Taxa present in more than one area
- *Missing areas*: Some of the areas are missing from one of the compared cladograms
- *Redundant distributions*: Areas that harbor more than one taxon

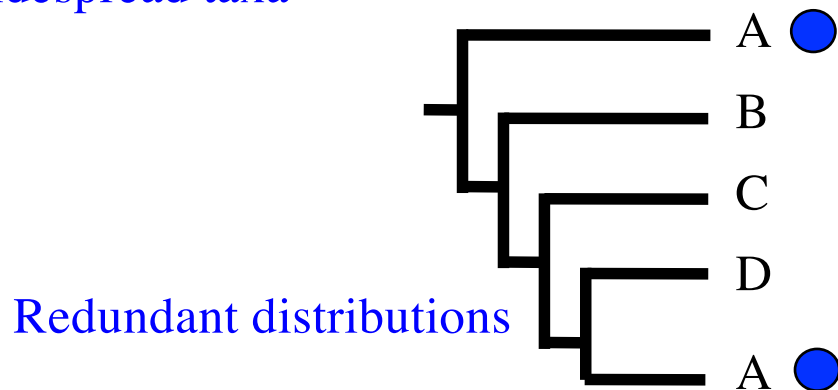


Area cladograms  
[areas A,B,C,D]



Widespread taxa

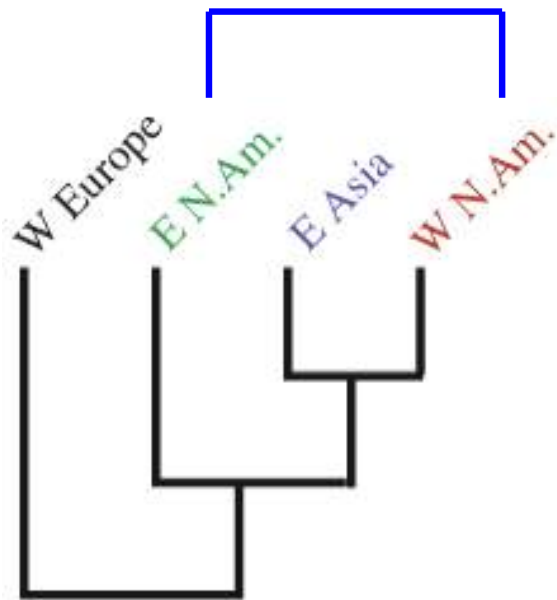
Missing areas



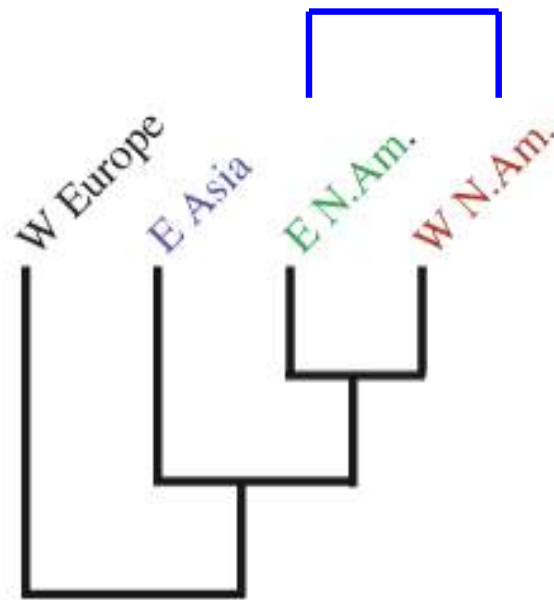
Redundant distributions

# Cladistic Biogeography

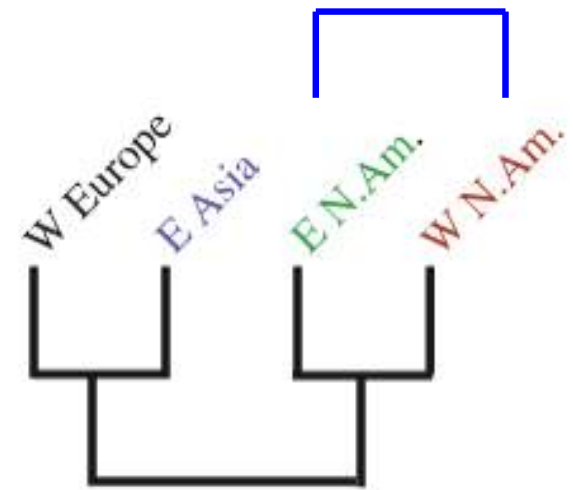
Issue #4 — **incongruent cladograms**: different groups give different area relationships



**oaks**



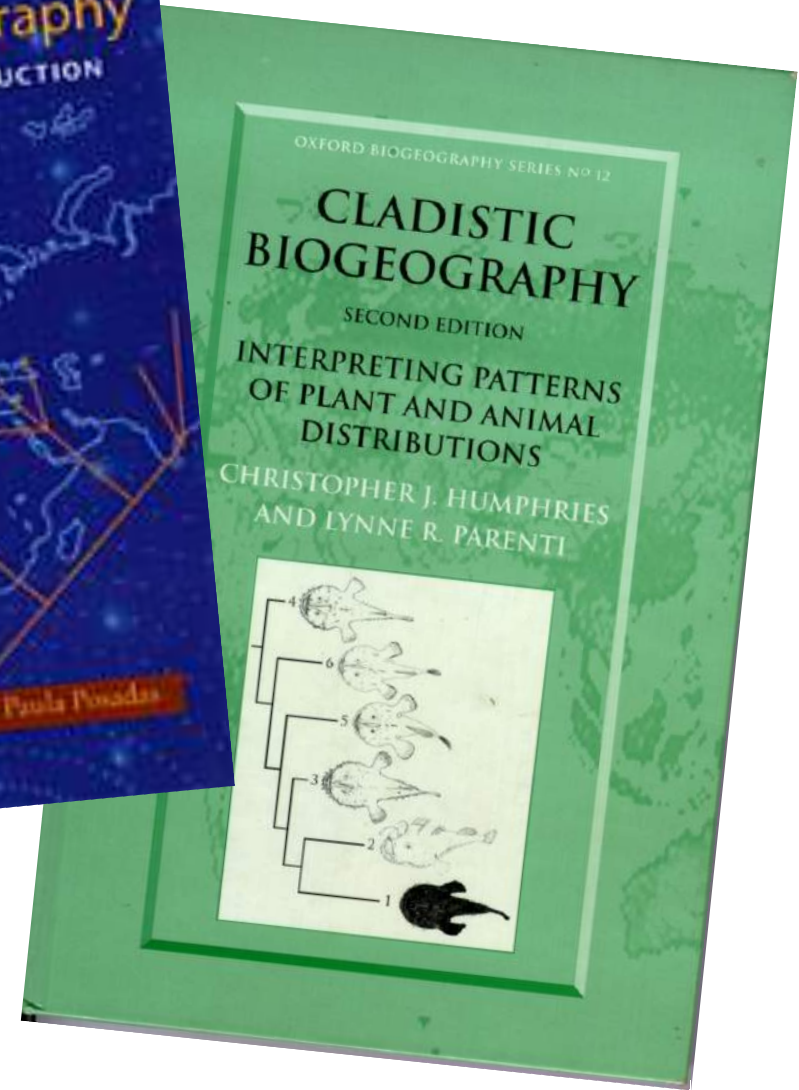
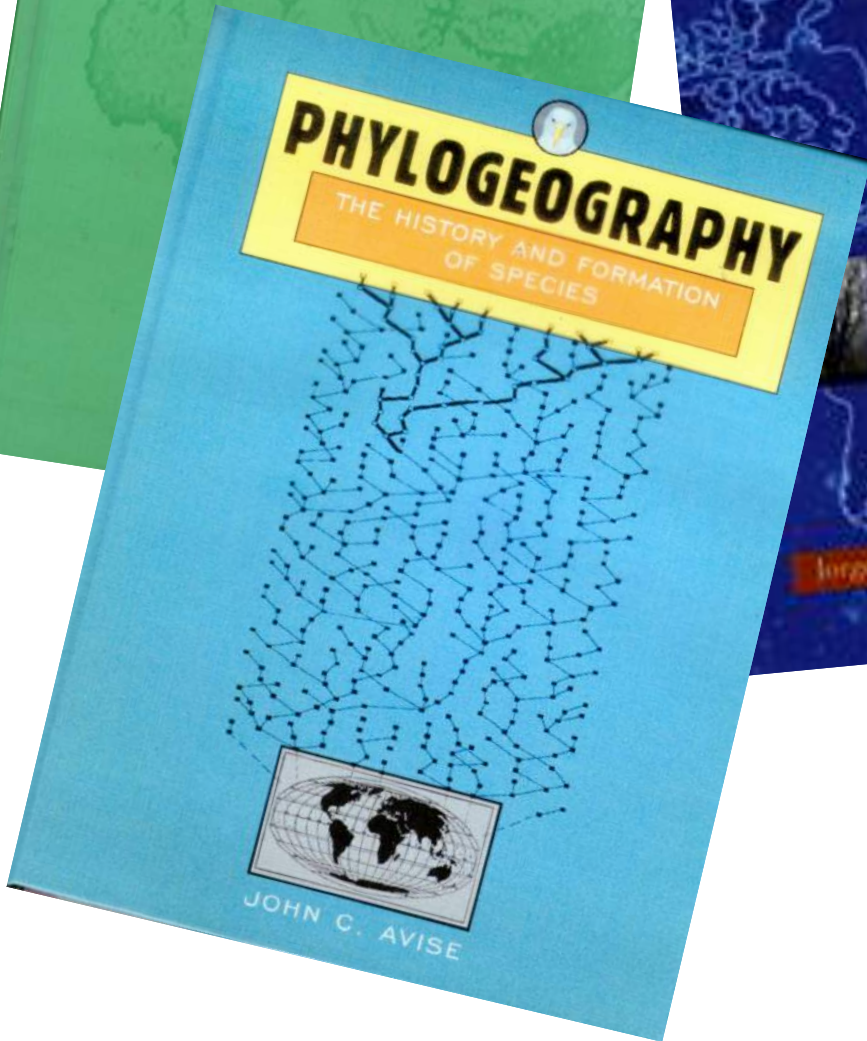
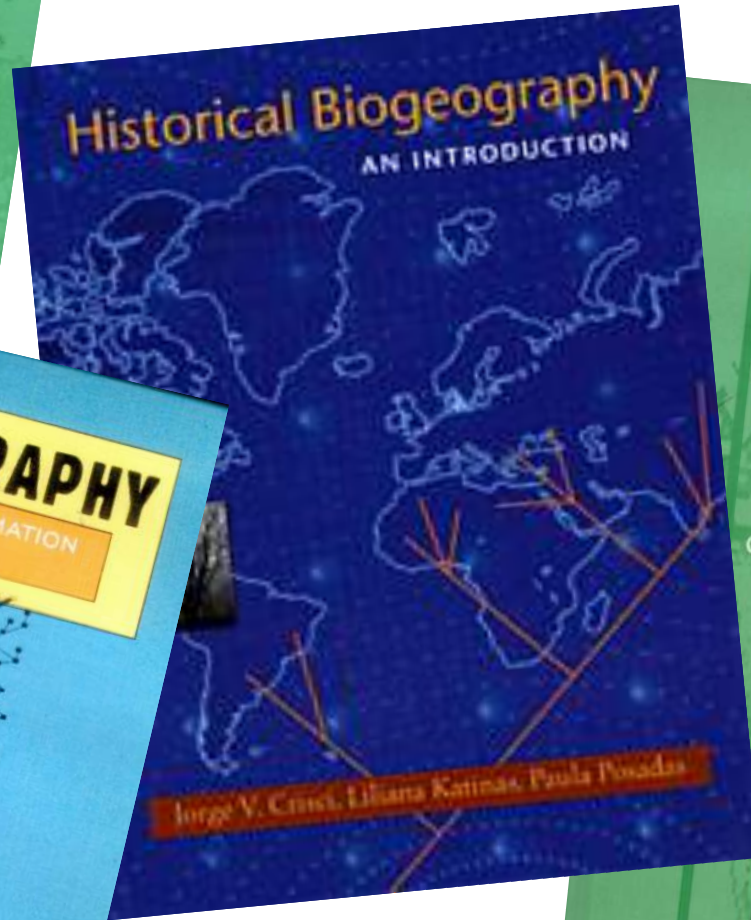
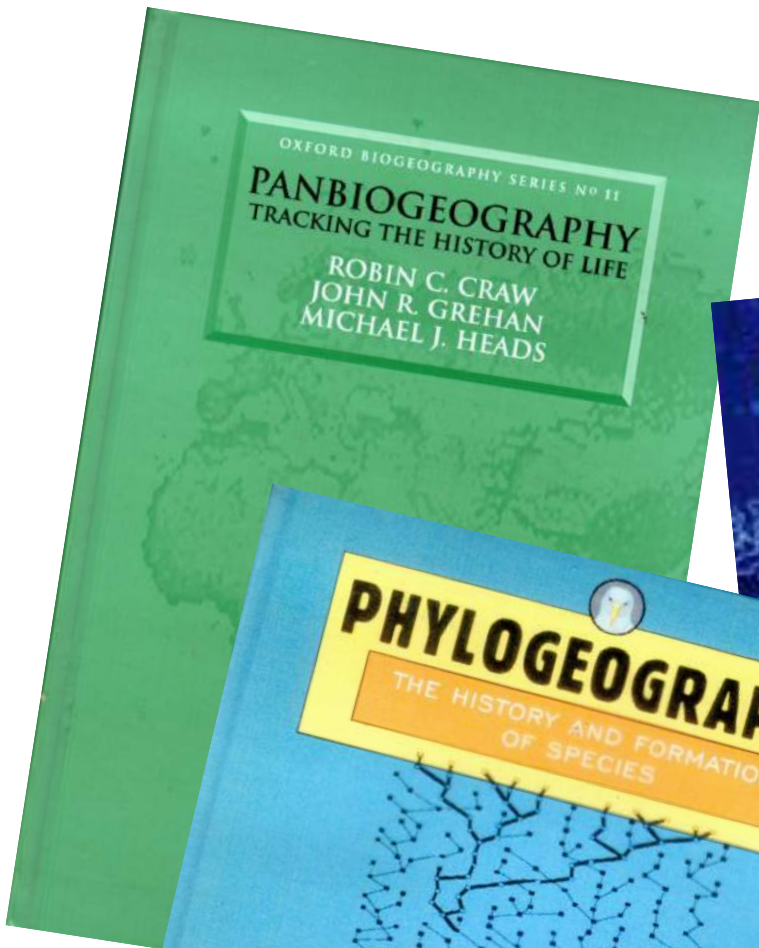
**sycamores**



**orchids**



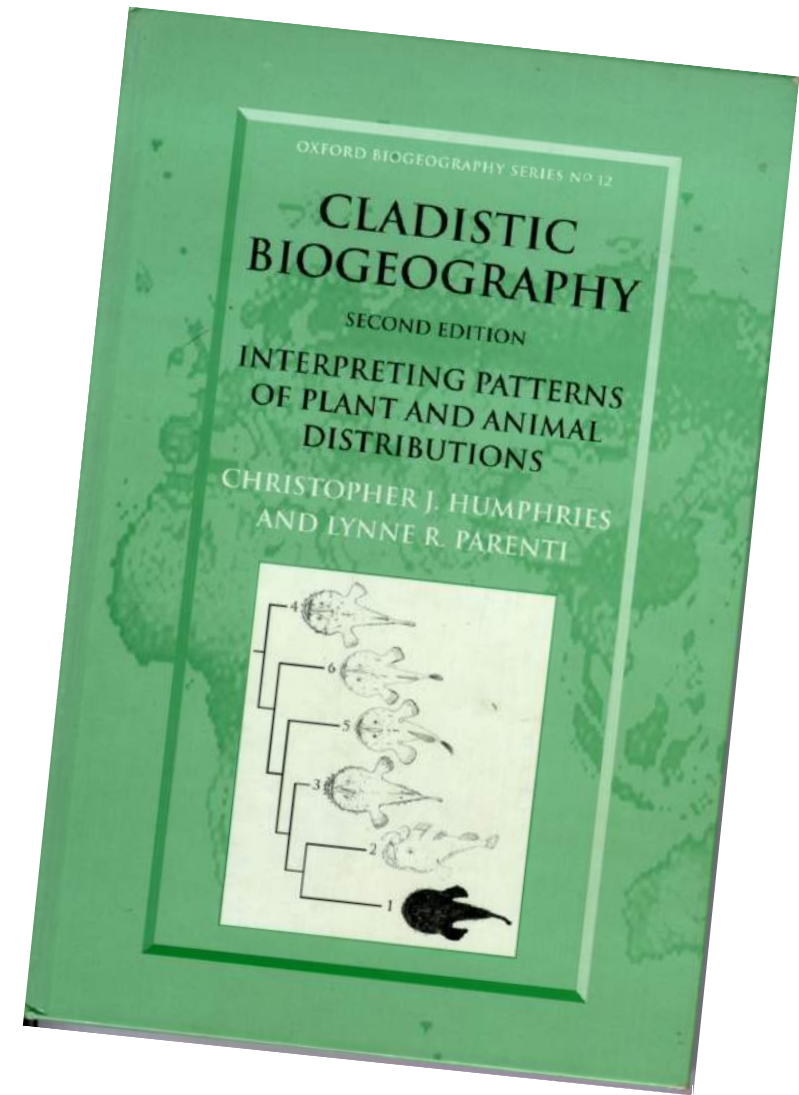
now a plethora of approaches



now a plethora of approaches



*Donn Rosen, Gareth Nelson, Norm Platnick 1983*



Vicariance OR dispersalism alone is **not** warranted



	DISPERSAL or VICARIANCE	DISPERSAL and VICARIANCE
Center of origin and dispersal		
Panbiogeography		
Phylogenetic biogeography		
Ancestral areas		
Cladistic biogeography		
Phylogeography		
DIVA		
DEC, <a href="#">BioGeoBEARS</a> (DECj)		