

# **BIOGEOGRAFIA HISTÓRICA**

## **ENFOQUES FUNDAMENTAIS**

**Dispersalismo – Darwin 1859, Wallace 1876**

**Biogeografia filogenética – Hennig 1966, Brundin 1966**

**Áreas ancestrais – Bremer 1992, Ronquist 1994**

**Panbiogeografia – Croizat 1958, Craw 1988, Page 1987**

**Biogeografia cladística – Nelson 1974, D. Rosen 1976, Nelson & Platnick 1981**

**Análise de parcimônia de endemismos (PAE) - B. Rosen 1988, Craw 1988, Morrone 1988**

**Métodos baseados em eventos – Page 1994, Ronquist 1997**

**Filogeografia – *Avise et al.* 1987**

**Biogeografia experimental – Haydon, Tadtkey & Pianka 1994**

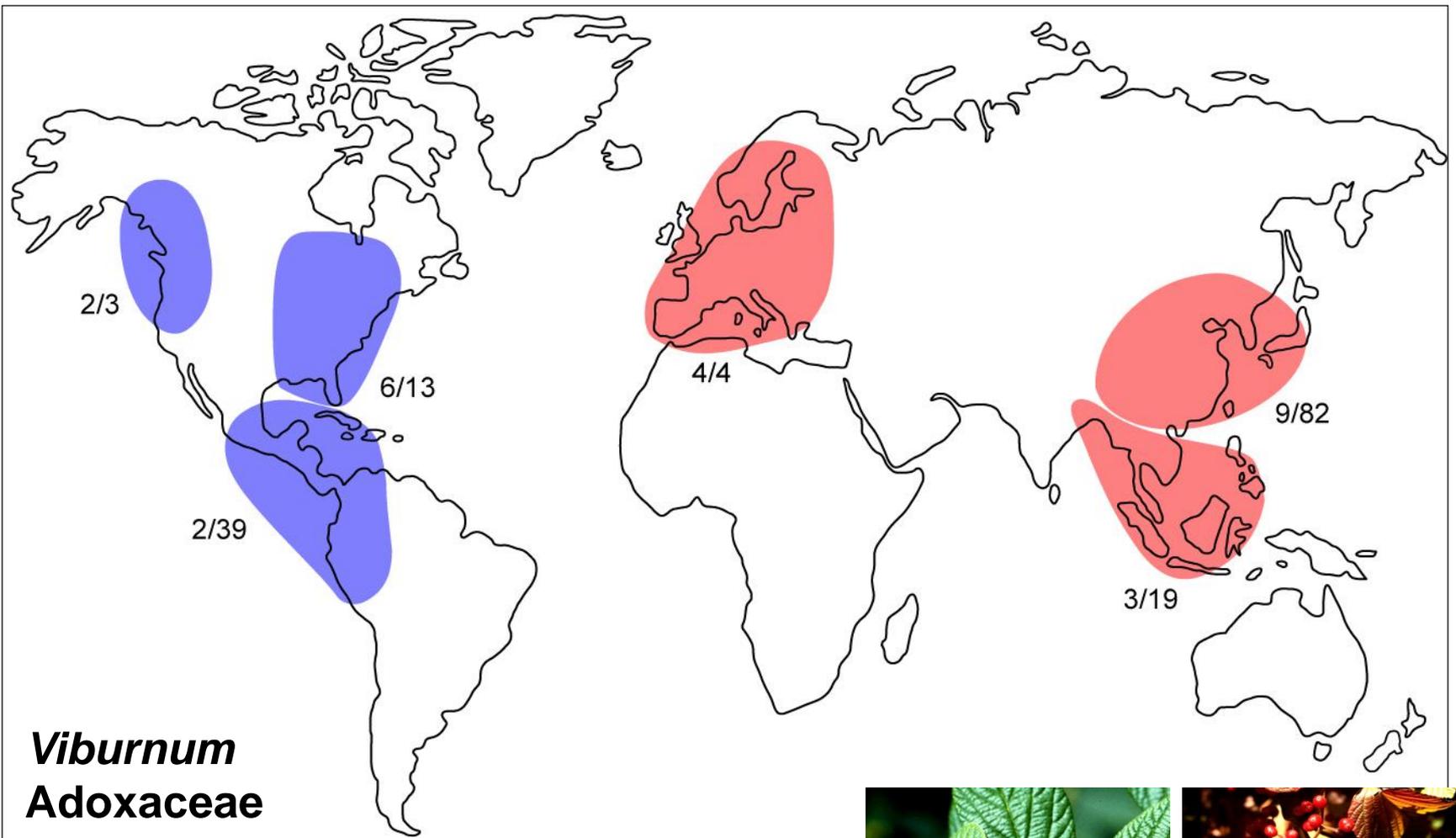
**Biogeografia Integrativa – Donoghue & Moore 2003**

# Métodos baseados em eventos

Page 1994, Ronquist 1997

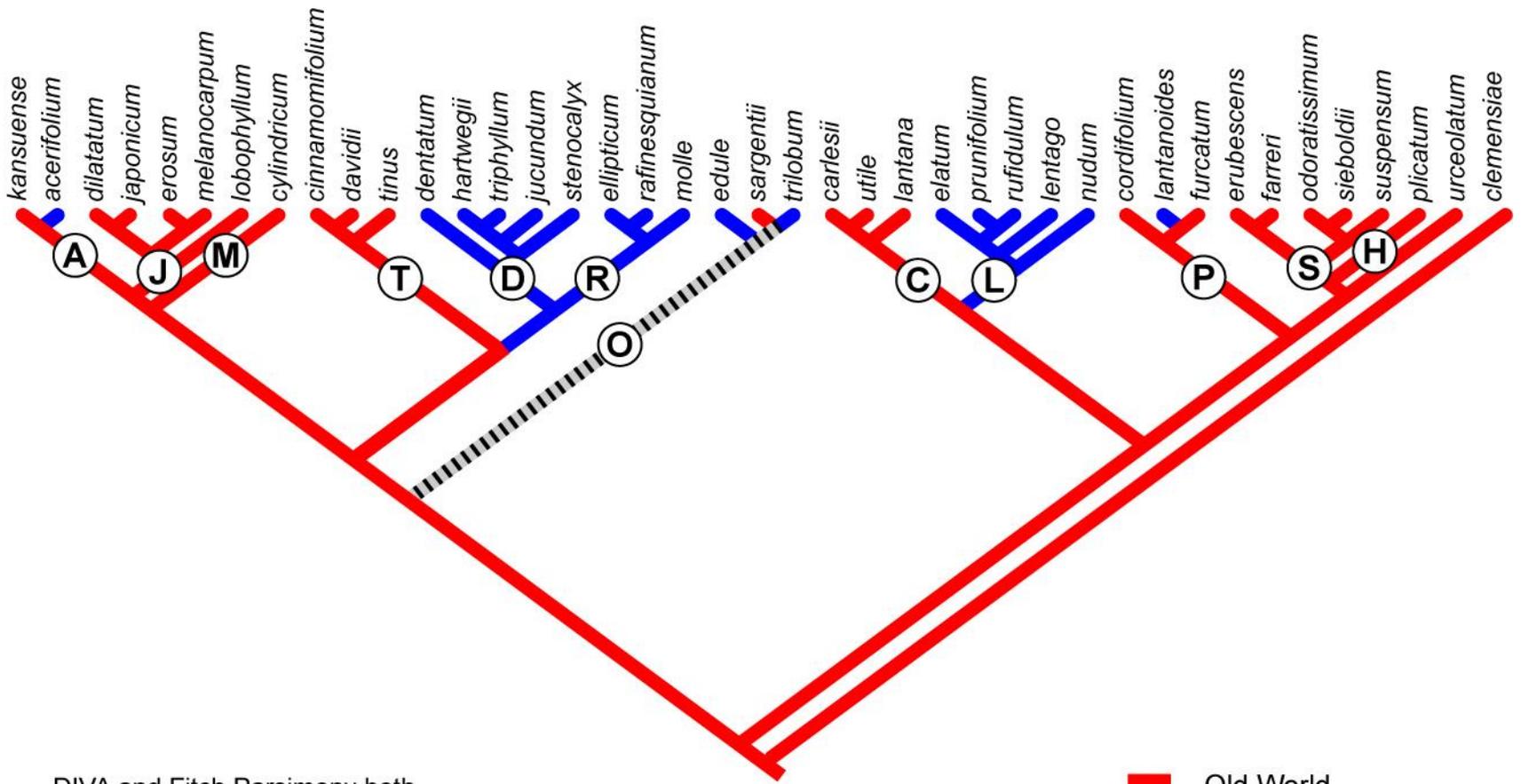
Diferentemente da maioria dos métodos da Biogeogr. Histórica, esses métodos postulam **modelos explícitos dos processos** que afetam a distr. geogr. dos organismos: **dispersão, extinção, paralogia geográfica ou duplicação e vicariância**

História da distr. de **um táxon** é inferida com base em informações filogenéticas aplicando-se critério explícito de máximo benefício e custo mínimo a todos ou só alguns dos processos (Page 1994)



***Viburnum***  
**Adoxaceae**





DIVA and Fitch Parsimony both reconstruct 4-6 Old World/New World transitions.

Modified from Winkworth & Donoghue (2005).

- █ Old World
- █ New World
- ▨ Equivocal

# Métodos baseados em eventos

## Análise de Dispersão e Vicariância (DIVA - Ronquist 1997)

DIVA reconstitui a distribuição pretérita de um grupo com base em um modelo biogeográfico simples; permite reconstrução de um **cenário biogeogr. que inclua possibilidade de reticulação entre áreas** (e não apenas relações hierárquicas, como nos métodos da Biogeogr. Cladística)

# Métodos baseados em eventos

## Análise de Dispersão e Vicariância (DIVA - Ronquist 1997)

DIVA reconstitui a distr. ancestral em cada nó interno do cladograma de um grupo por um **conjunto de critérios de otimização** para eventos de dispersão e extinção:

Eventos	Valores de custo
Vicariância	0
Duplicação	0
Extinção	1
Dispersão ao acaso	1
Dispersão predizível	não considerada

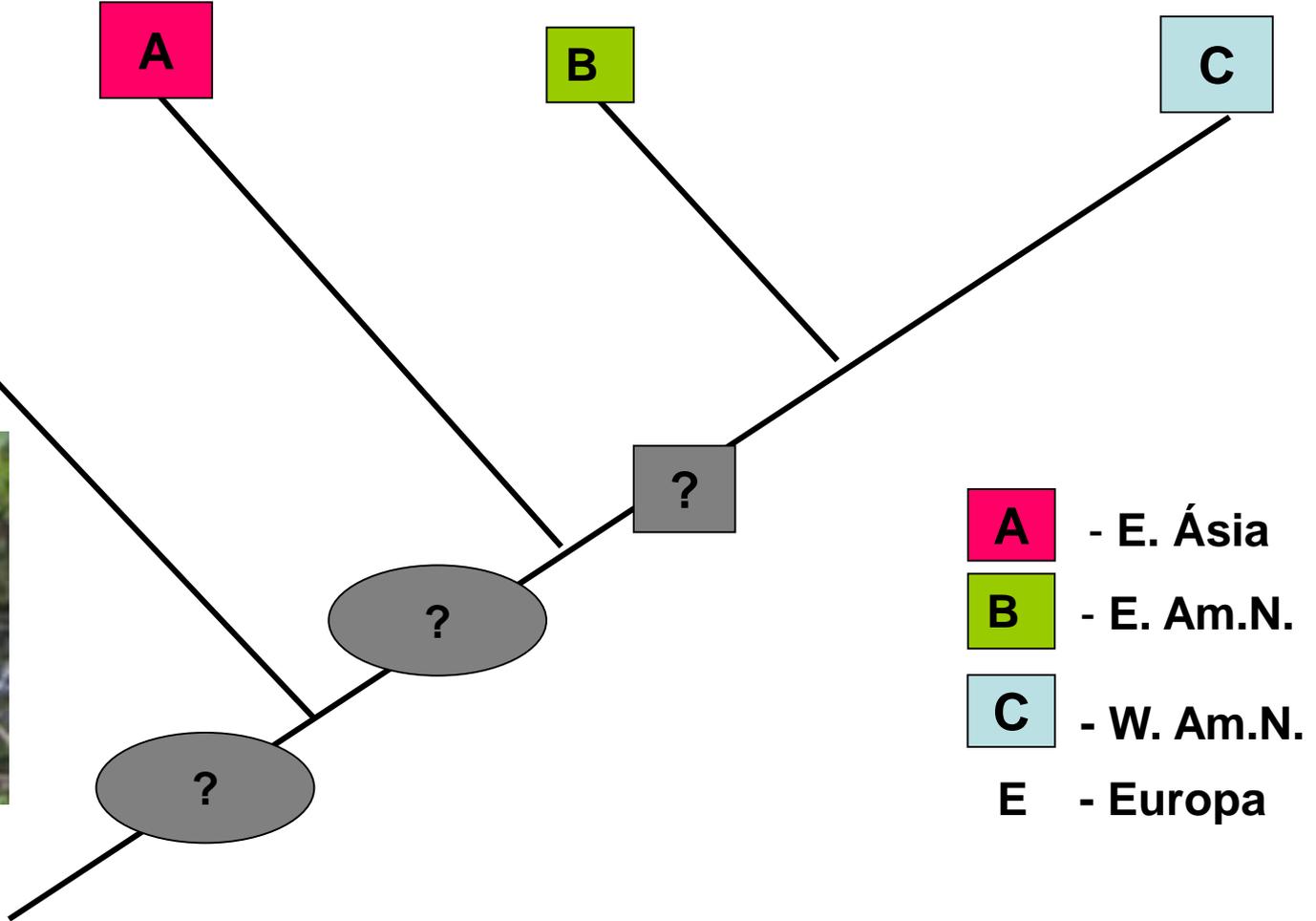
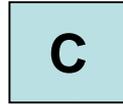
*Trautvetteria* (Ranunculaceae)

Grupo-externo

*T. japonica*

*T. carolinensis*

*T. grandis*



- A** - E. Ásia
- B** - E. Am.N.
- C** - W. Am.N.
- E** - Europa

Passos Biogeográficos: vicariâncias?

dispersões? →

Xiang & Soltis 2001

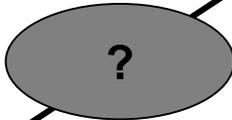
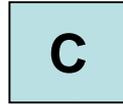
# *Trautvetteria* (Ranunculaceae)

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- W. Am.N.

E - Europa

Passos

Biogeográficos: vicariâncias?

dispersões?



Xiang &  
Soltis 2001

# *Trautvetteria* (Ranunculaceae)

Grupo-externo

*T. japonica*

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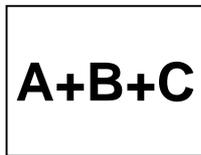
- E. Am.N.



- W. Am.N.

E - Europa

Passos biogeográficos: 2 vicariâncias, sem dispersão



V1

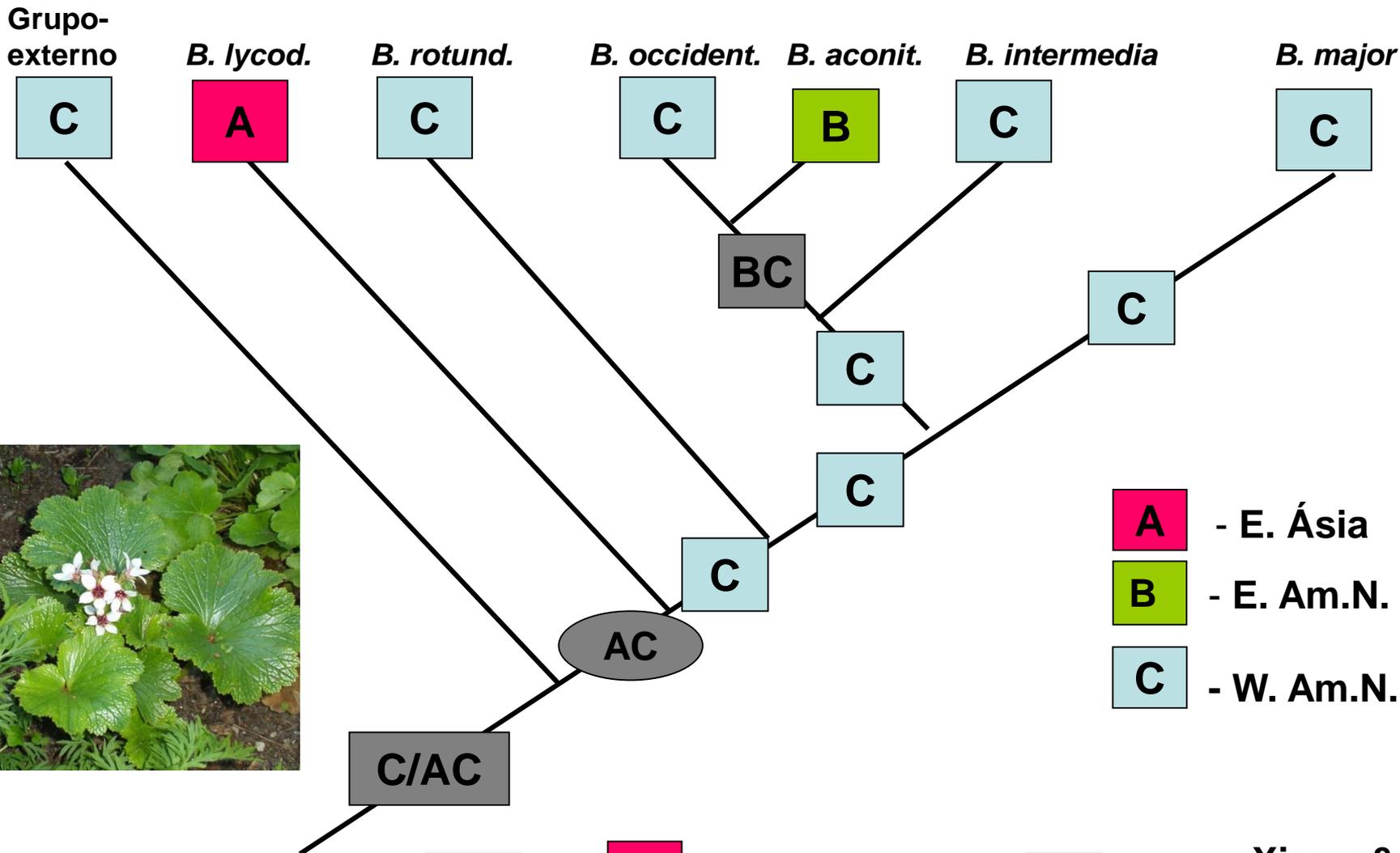


V2

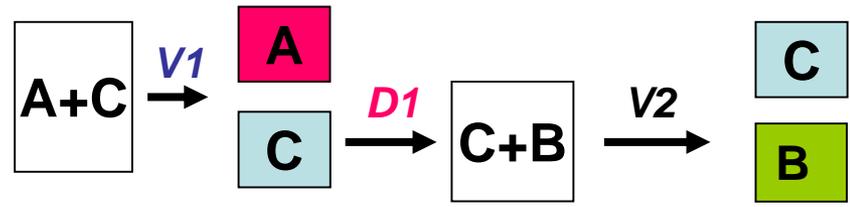


Xiang & Soltis 2001

# Boykinia (Saxifragaceae)



Passos biogeográficos:  
2 vicariâncias,  
1 dispersão



Xiang &  
Soltis 2001

## Xiang & Soltis 2001

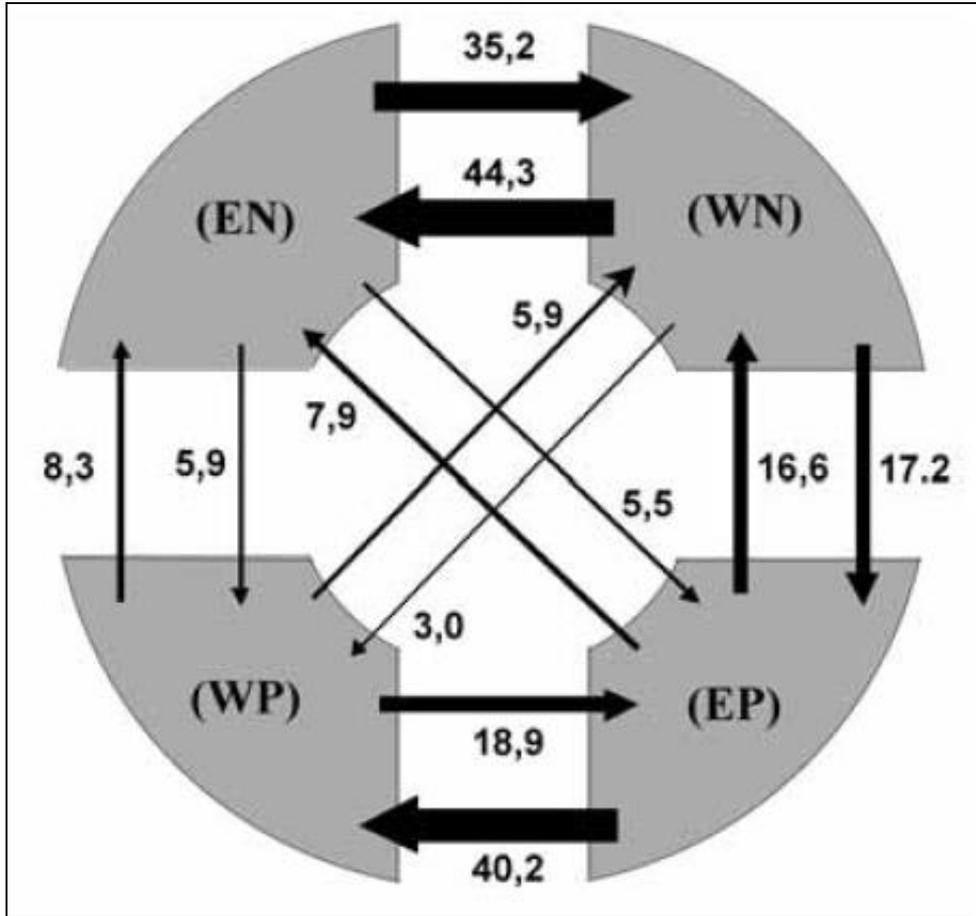
### Disjunções intercontinentais no Hemisfério Norte com uso de DIVA

#### 4 padrões:

1. Origem e especiação na E Ásia com subsequente expansão na Am.N e/ou Europa (*Aralia, Symplocarpus, Asarum, Aesculus e Chrysosplenium*)
2. Origem na E Ásia e W Am.N com subsequente migração na Am.N (*Calycanthus e Boyckinia*)
3. Origem disjunta na E Ásia e E Am.N com subsequente dispersão a partir da E Ásia para a E Am.N (*Panax*)
4. Origem ampla no Hem. Norte com subsequente fragmentação por vicariância intercontinental (*Cornus e Trautvetteria*)

Resultados indicam que as disjunções de linhagens de angiospermas no Hem. N **não podem ser explicadas com modelo simples de vicariância,** mas sim uma **história complexa:** haveria **pseudocongruência** entre linhagens nas relações filogenéticas e padrões de distribuição.

Maioria das linhagens teria estado ancestralmente restritas a uma ou 2 áreas adjacentes e teriam expandido secundariamente suas distribuições por dispersão.



**Disjunções do Hemisfério Norte**  
 Sanmartín and Ronquist (2001)  
 Xiang et al. (2001)  
 Donoghue and Smith (2004)

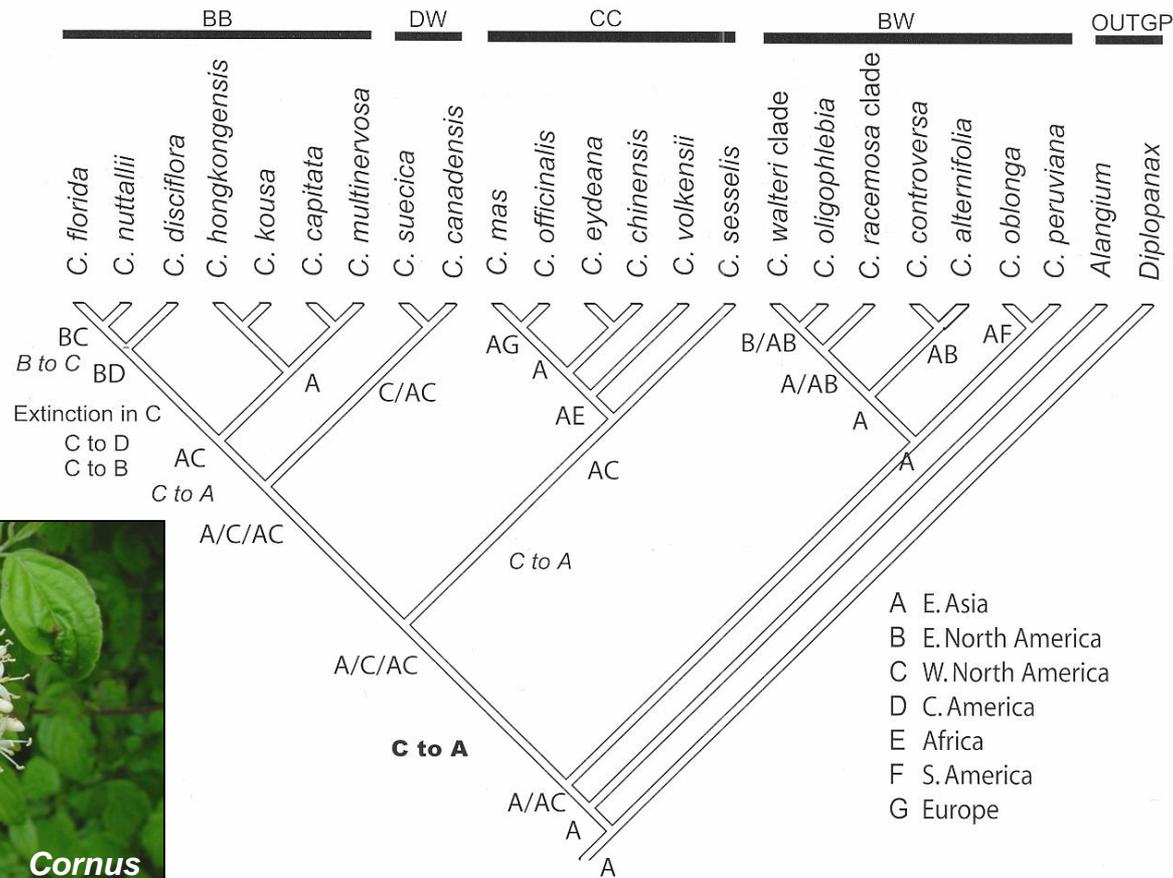
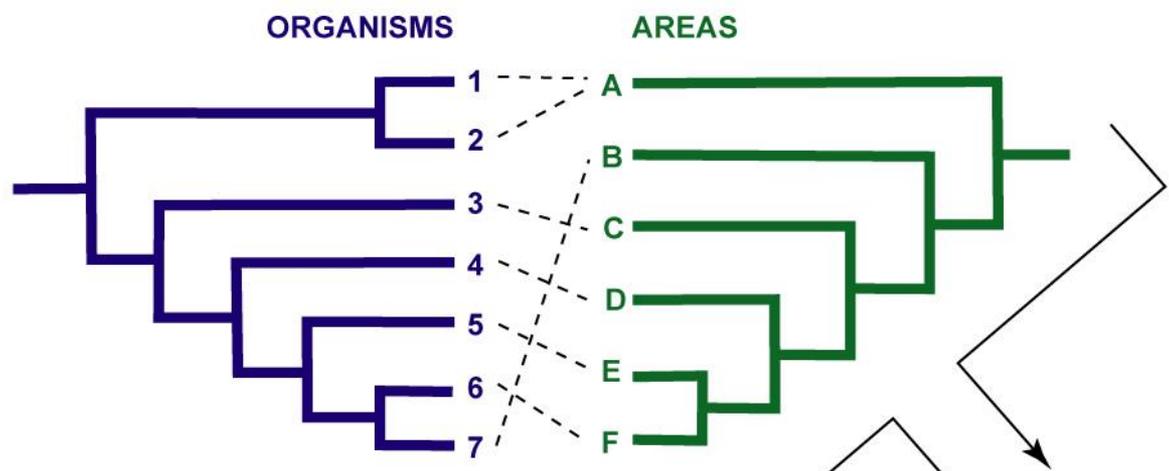


Fig. 8. Results of ancestral area reconstruction using dispersal-vicariant analysis (DIVA) based on the total evidence phylogeny and distribution of extant species. The optimization was conducted with a constraint of maximum areas of two.

## *Cornus*, Cornaceae

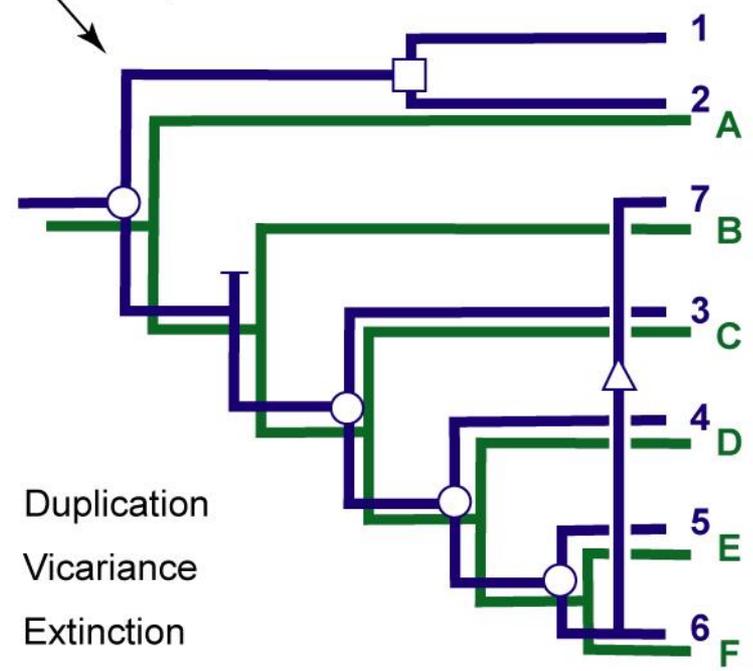
Xiang *et al.* 2006

Modificado de Sanmartín & Ronquist 2004



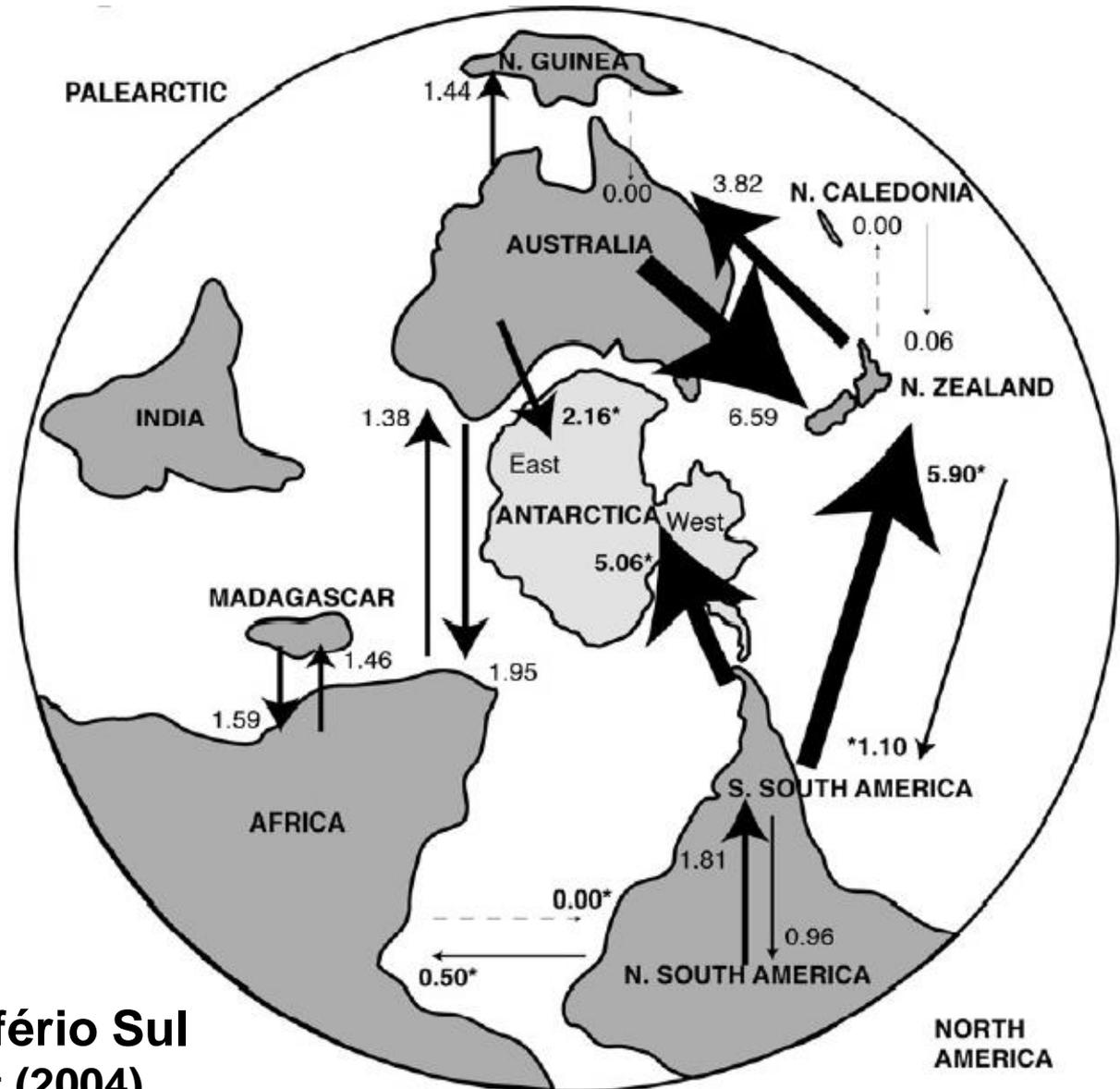
Parsimony-based Tree Fitting  
Page (1995)

- Duplication
- Vicariance
- ┼ Extinction
- △ Dispersal



## 19 filogenias de plantas e fungos

Uso de Parsimony-based tree-fitting para analisar padrões biogeográficos no Hemisfério Sul, evidenciando papel relevante de dispersão.



**Disjunções no Hemisfério Sul**  
Sanmartín & Ronquist (2004)

# Importante!

Esses métodos têm sido muito úteis para o aprimoramento de nosso conhecimento em Biogeografia Histórica,

**MAS** têm a limitação crítica de basear-se exclusivamente em **TOPOLOGIA**,  
i. e. padrão evolutivo.

A complexidade dos processos envolvidos requer incorporação de muitas outras fontes de dados: **tempo**,  
**eventos geológico/climáticos**,  
**ecologia**.

Sem isso fica difícil interpretar os resultados, sobretudo de métodos cladísticos baseados em busca de **consenso**.

# Spatial evolutionary and ecological vicariance analysis (SEEVA), a novel approach to biogeography and speciation research, with an example from Brazilian Gentianaceae

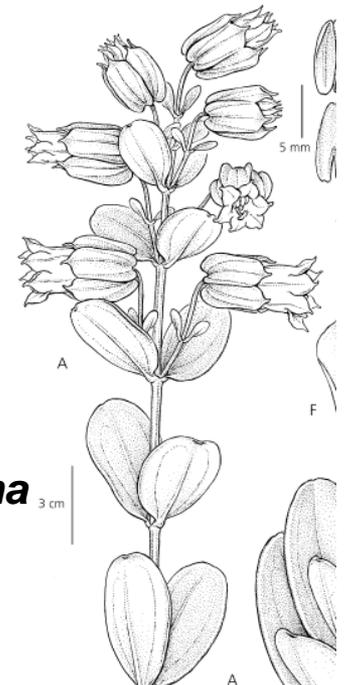
Lena Struwe<sup>1,2\*</sup>, Peter E. Smouse<sup>1</sup>, Einar Heiberg<sup>3</sup>, Scott Haag<sup>4</sup> and Richard G. Lathrop<sup>1,4</sup>

## ABSTRACT

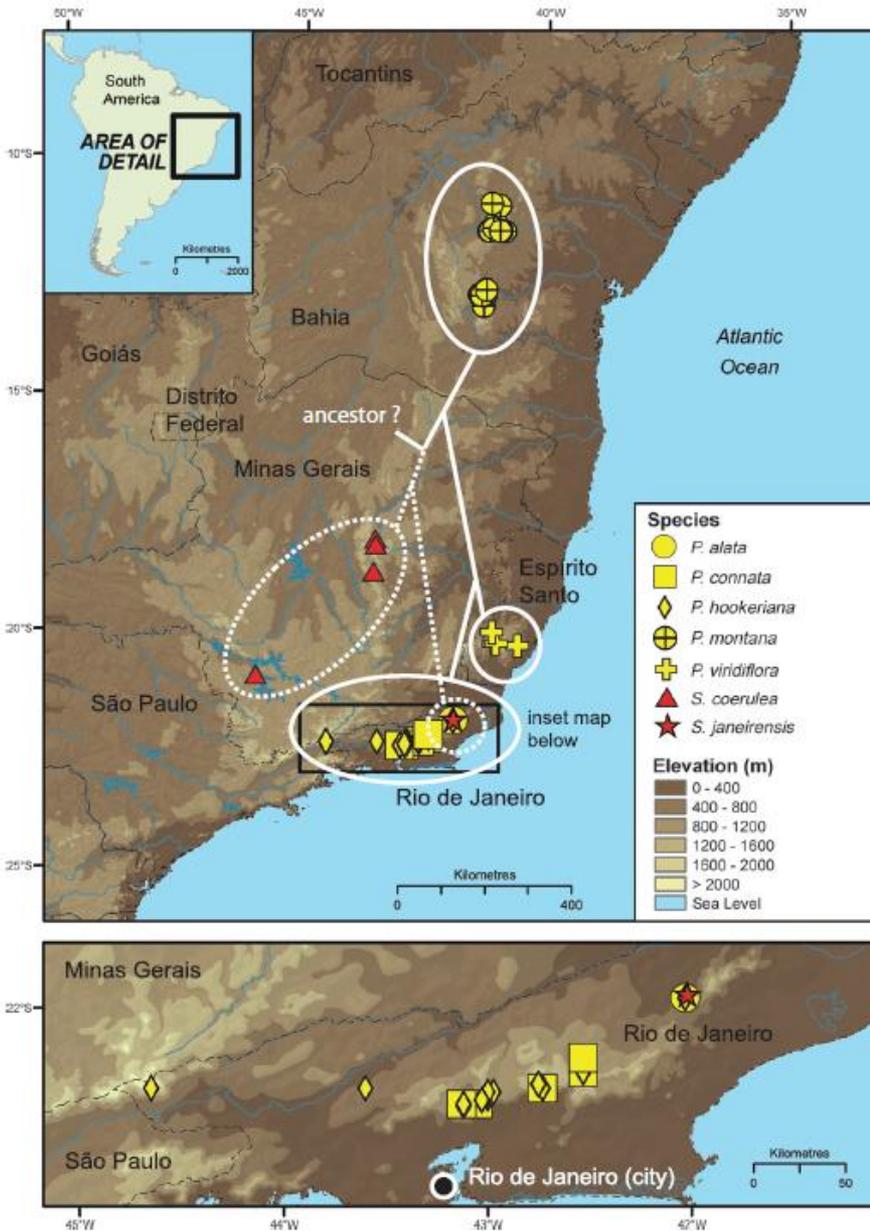
**Aim** Spatial evolutionary and ecological vicariance analysis (SEEVA) is a simple analytical method that evaluates environmental or ecological divergence associated with evolutionary splits. It integrates evolutionary hypotheses, phylogenetic data, and spatial, temporal, environmental and geographical information to elucidate patterns. Using a phylogeny of *Prepusa* Mart. and *Senaea* Taub. (Angiospermae: Gentianaceae), SEEVA is used to describe the radiation and ecological patterns of this basal gentian group across south-eastern Brazil.

# SEEVA

## Struwe et al. (2011)



*Prepusa montana*



**Figure 1** Distribution map of *Prepusa* and *Senaea* in south-eastern Brazil, showing geolocated collections of the seven species. The phylogenetic relationships are superimposed as white lines; note that the ancestor's location is hypothetical. The bottom inset map is a close-up of the coastal mountains near Rio de Janeiro, home to four of the seven species.

# GENTIANACEAE - Heleiae

Calió 2009

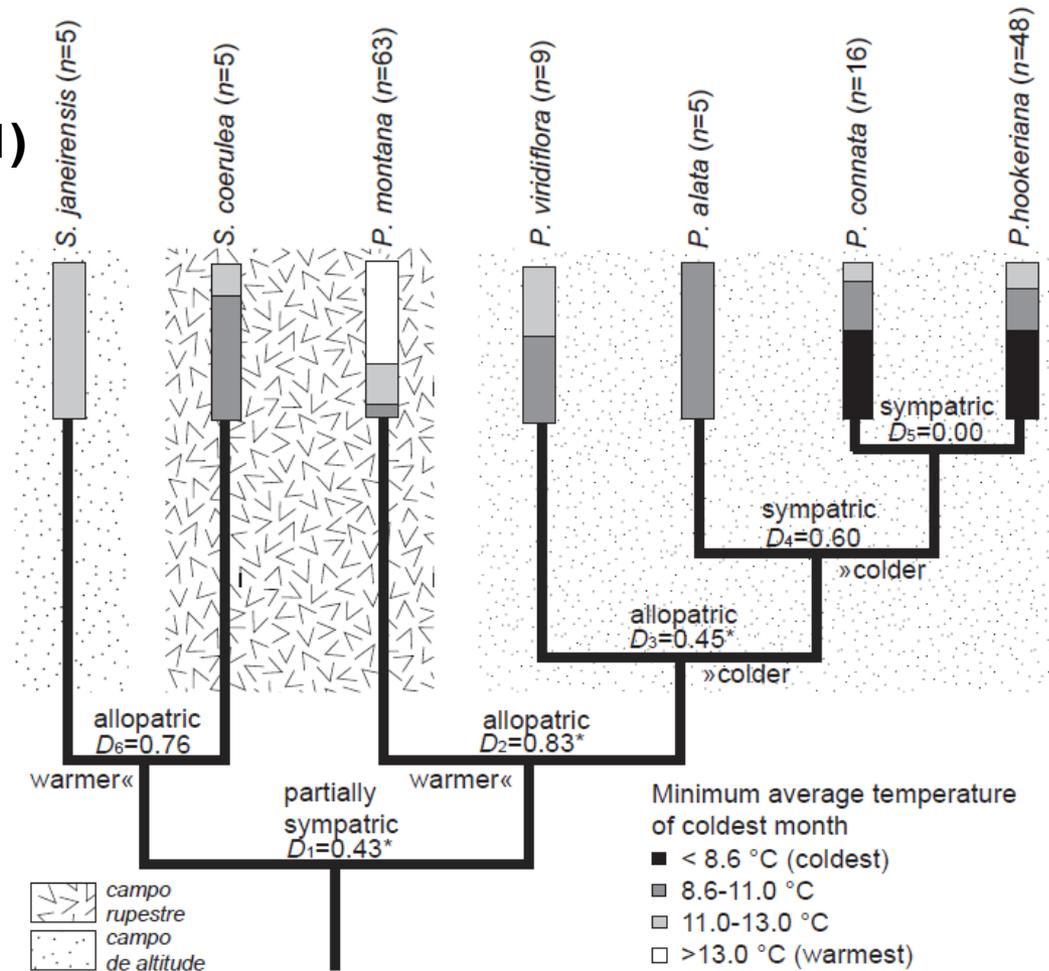


**A. *Senaea janeirensis***  
**B-C. *Prepusa viridiflora***

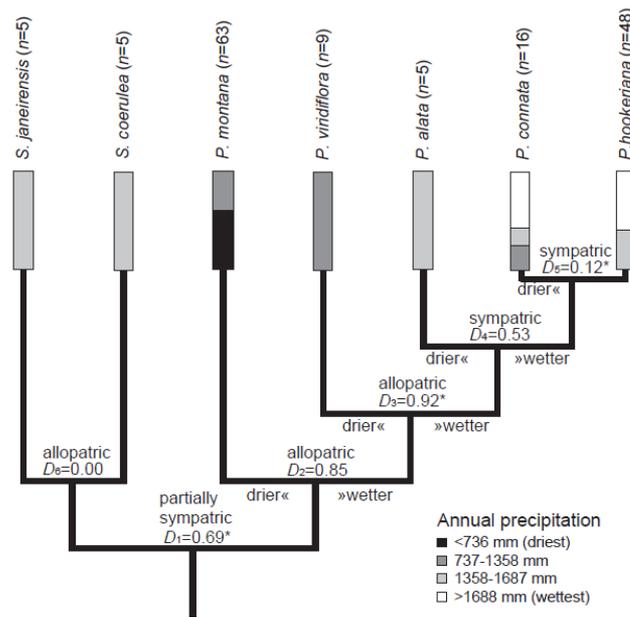
**A-C. *Prepusa connata*, D-E. *P. hookeriana***

Struwe et al. (2011)

# Habitat e temperatura



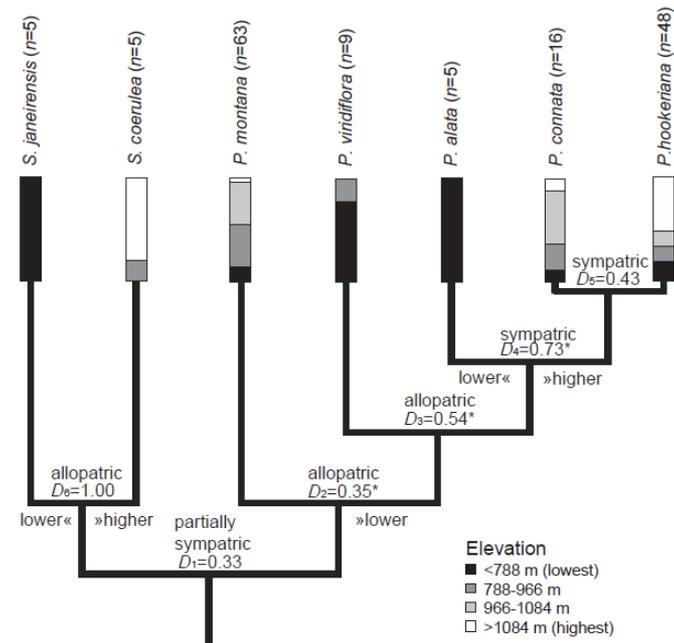
**Figure 2** Phylogenetic hypothesis for *Prepusa* and *Senaea* from south-eastern Brazil, based on Calió *et al.* (2008; outgroups excluded). Numbered nodes correspond to nodes in the spatial evolutionary and ecological vicariance analysis (SEEVA), and geographic sympatry/allopatry is indicated at each node. The SEEVA results for the variable 'minimum average temperature of the coldest month' (coded as four qualitative states, using SEEVA software) are shown as histograms for each species. Total height of each histogram bar equals 100% of observations for each species; number of observations ( $n$ ) is indicated after each species name; greyscale colours of histograms represent the four different states. Divergence indices are provided for each node;  $*P \leq 0.0085$  (significant difference between clades after Bonferroni correction).



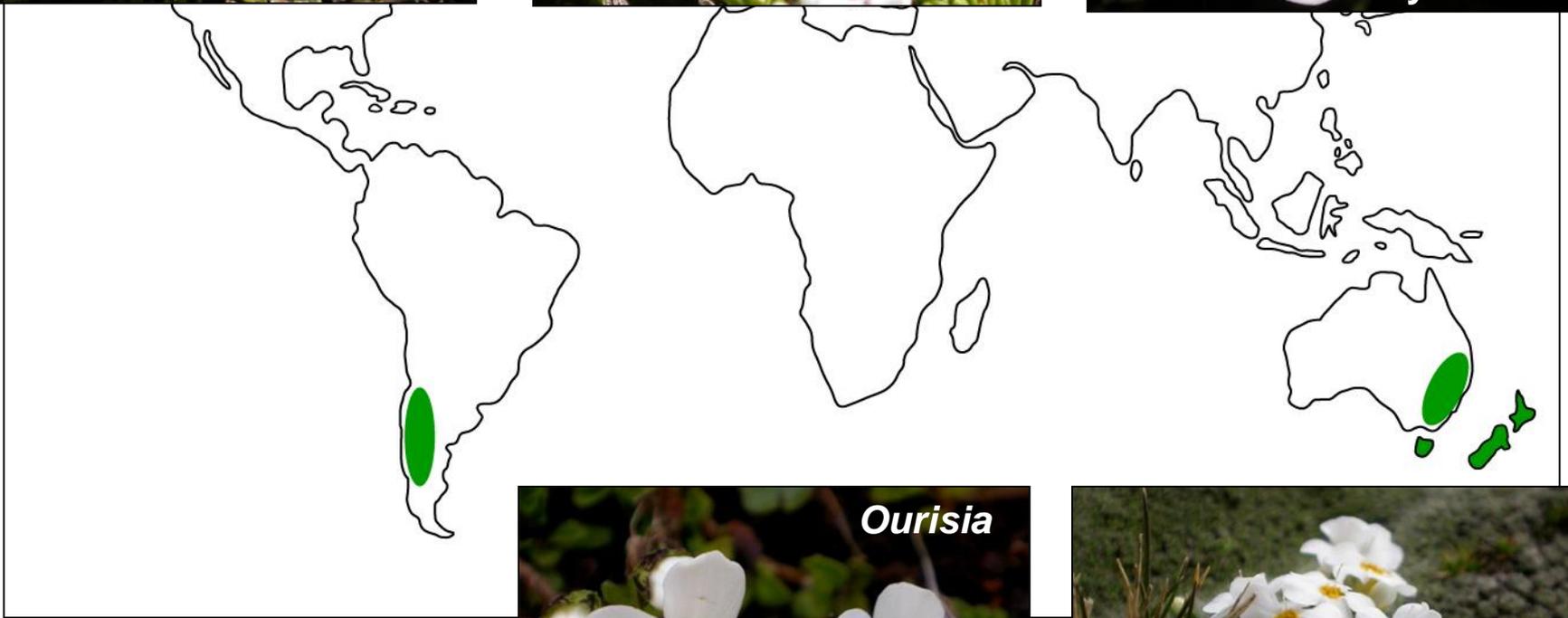
**Figure 3** Spatial evolutionary and ecological vicariance analysis (SEEVA) results for the variable 'annual precipitation' coded as four qualitative states, using SEEVA software. Total height of each histogram bar equals 100% of observations for each *Prepusa* and *Senaea* species from south-eastern Brazil, with number of observations (*n*) indicated after each species name; greyscale colours of histograms represent the four different states. Divergence indices are noted for each node; \* $P \leq 0.0085$  (significant difference between clades after Bonferroni correction).

## Precipitação anual

## Altitude



**Figure 4** Spatial evolutionary and ecological vicariance analysis (SEEVA) results for the variable elevation coded as four qualitative states, using SEEVA software. Total height of each histogram bar equals 100% of observations for each species, and number of observations (*n*) is indicated after each *Prepusa* or *Senaea* species from south-eastern Brazil; greyscale colours of histograms represent the four different states. Divergence indices are noted for each node; \* $P \leq 0.0085$  (significant difference between clades after Bonferroni correction).



**Interpretação geral da Biogeografia Cladística:**

**SIMILARIDADES RESULTAM DE HERANÇA COMUM ANTIGA:**

**Essas linhagens eram parte de uma **antiga flora Gonduânica comum** que foi subdividida pela fragmentação desse supercontinente.**

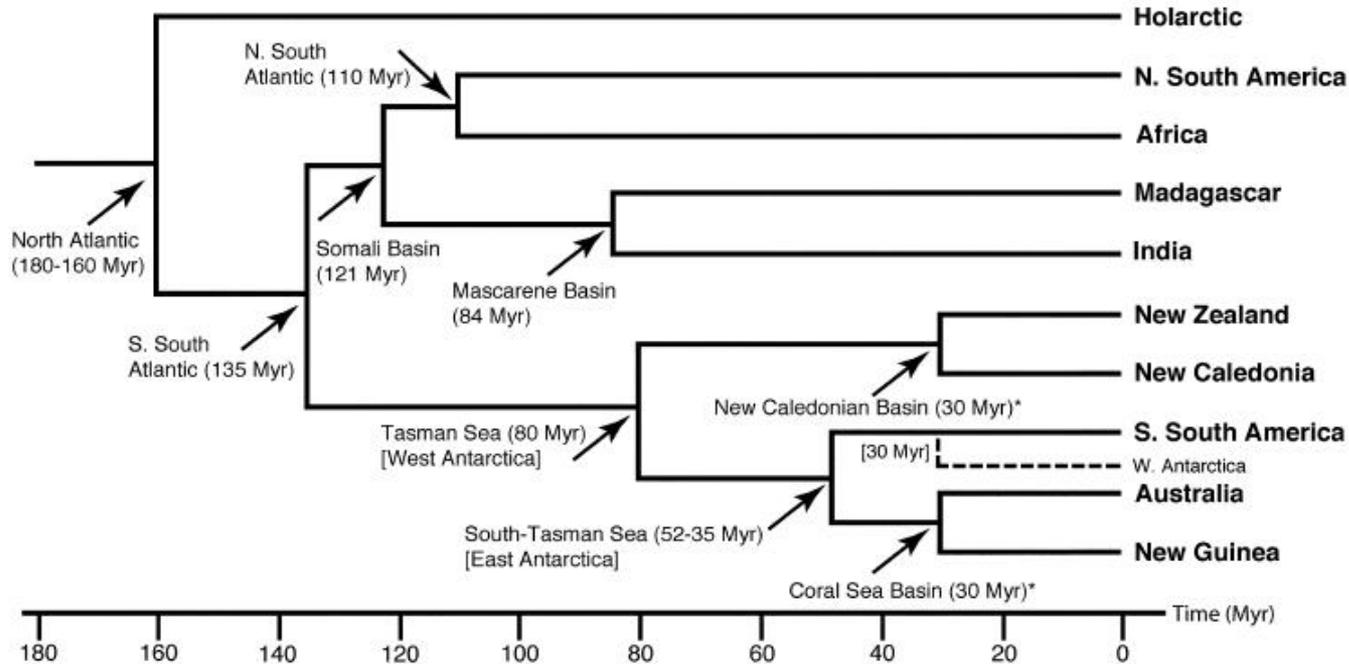
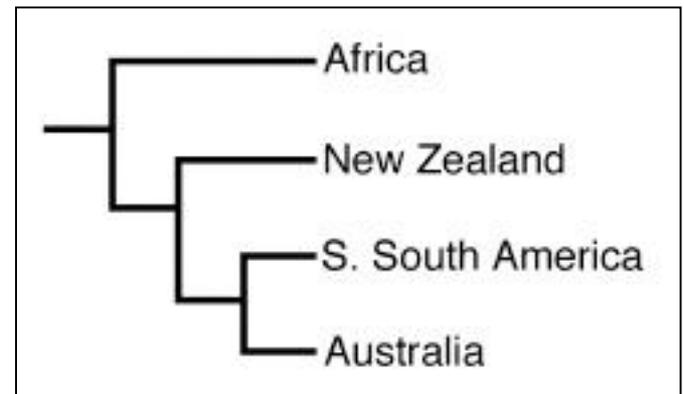
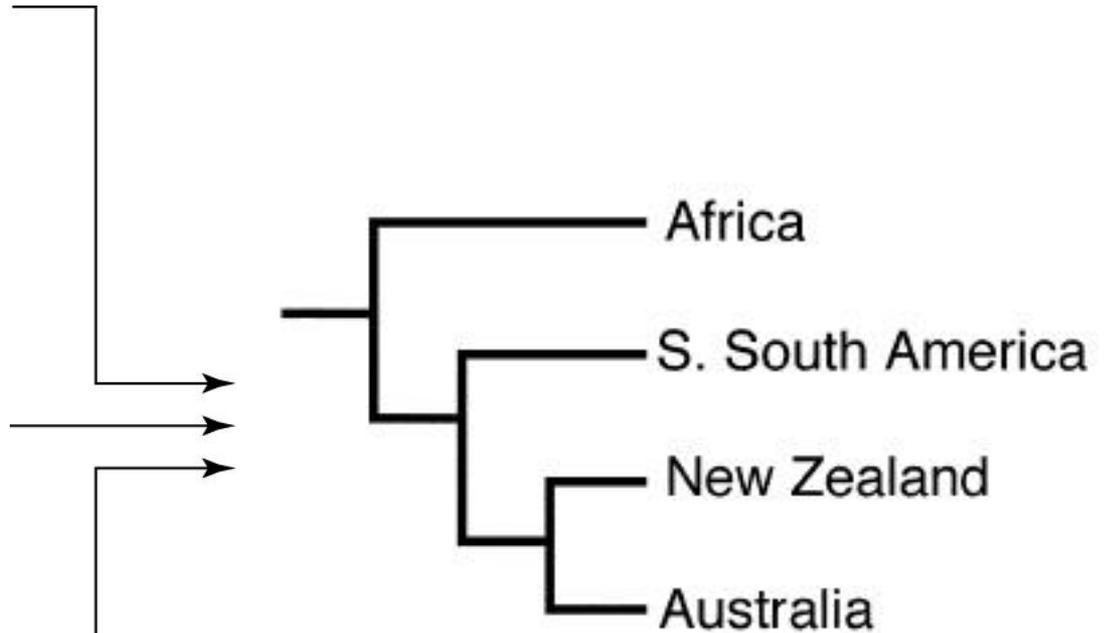


FIGURE 1. Geological area cladogram representing the relationships among the Southern Hemisphere landmasses based on paleogeographic evidence (from several sources). The time of vicariance is the assumed primary fragmentation, (\*) dated as 70–60 MYA (MYA) in alternative reconstructions.

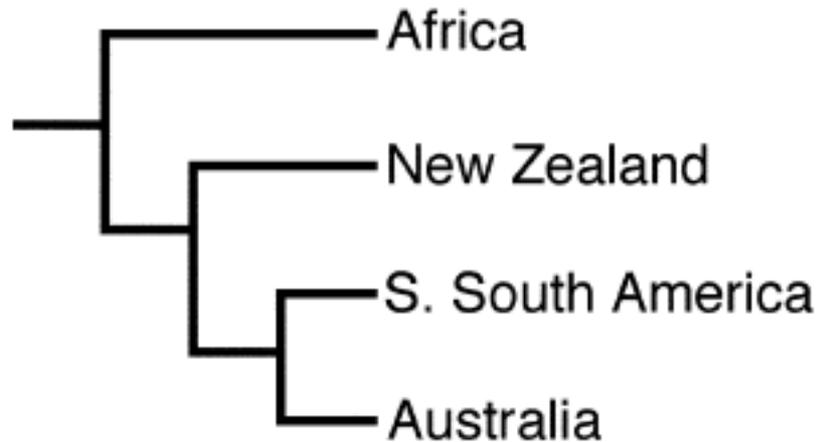
Sanmartín & Ronquist 2004



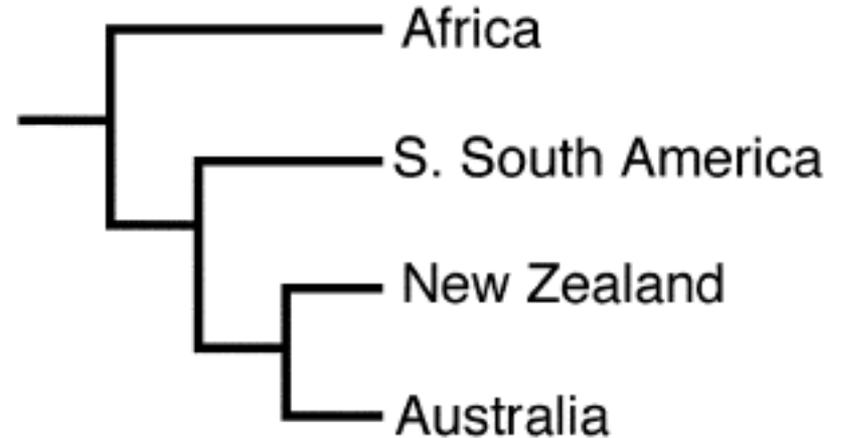


**Linder and Crisp (1995)**  
– 14 linhagens de plantas e fungos

**Sanmartín & Ronquist (2004)**  
– 19 linhagens de plantas e fungos



**GEOLOGIA**

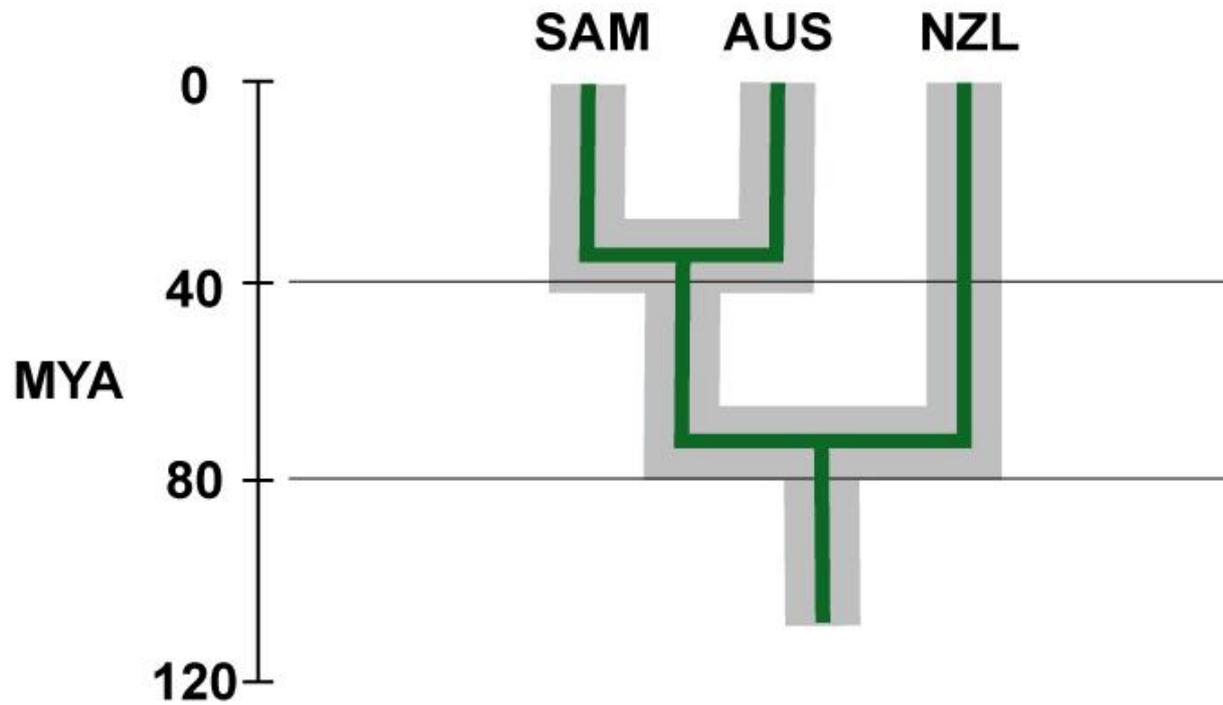


**ORGANISMOS**

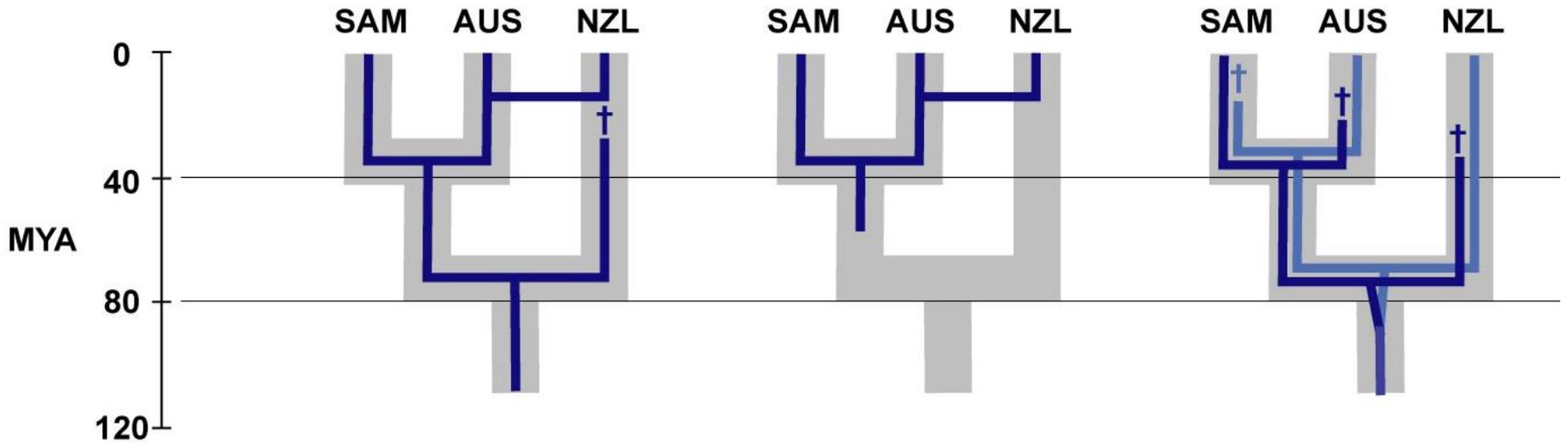
Como reconciliar as duas hipóteses?

**“dispersal is an unlikely explanation for this pattern, ... the solution might be found in alternative geological hypotheses”**

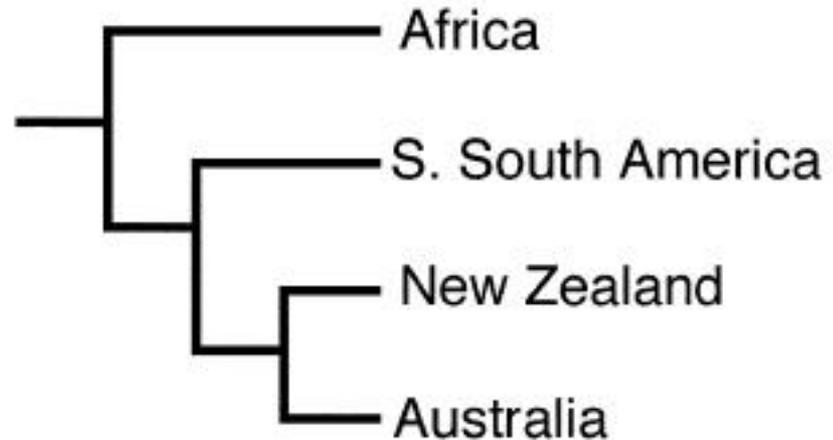
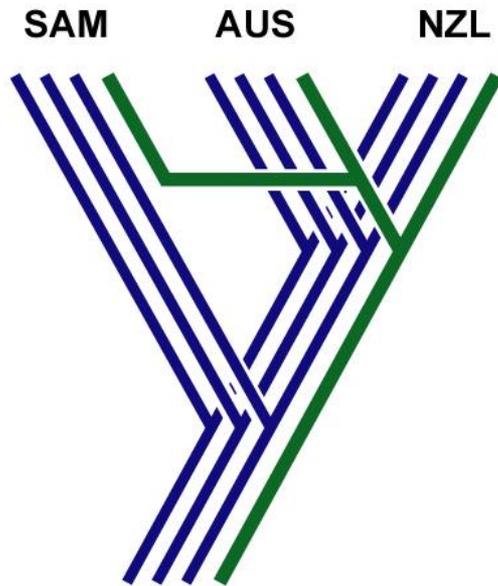
**Linder and Crisp (1995)**



Donoghue & Moore 2003



**Donoghue & Moore 2003**



“dispersal is an unlikely explanation for this pattern, ... the solution might be found in **alternative geological hypotheses**”

Linder and Crisp (1995)

X

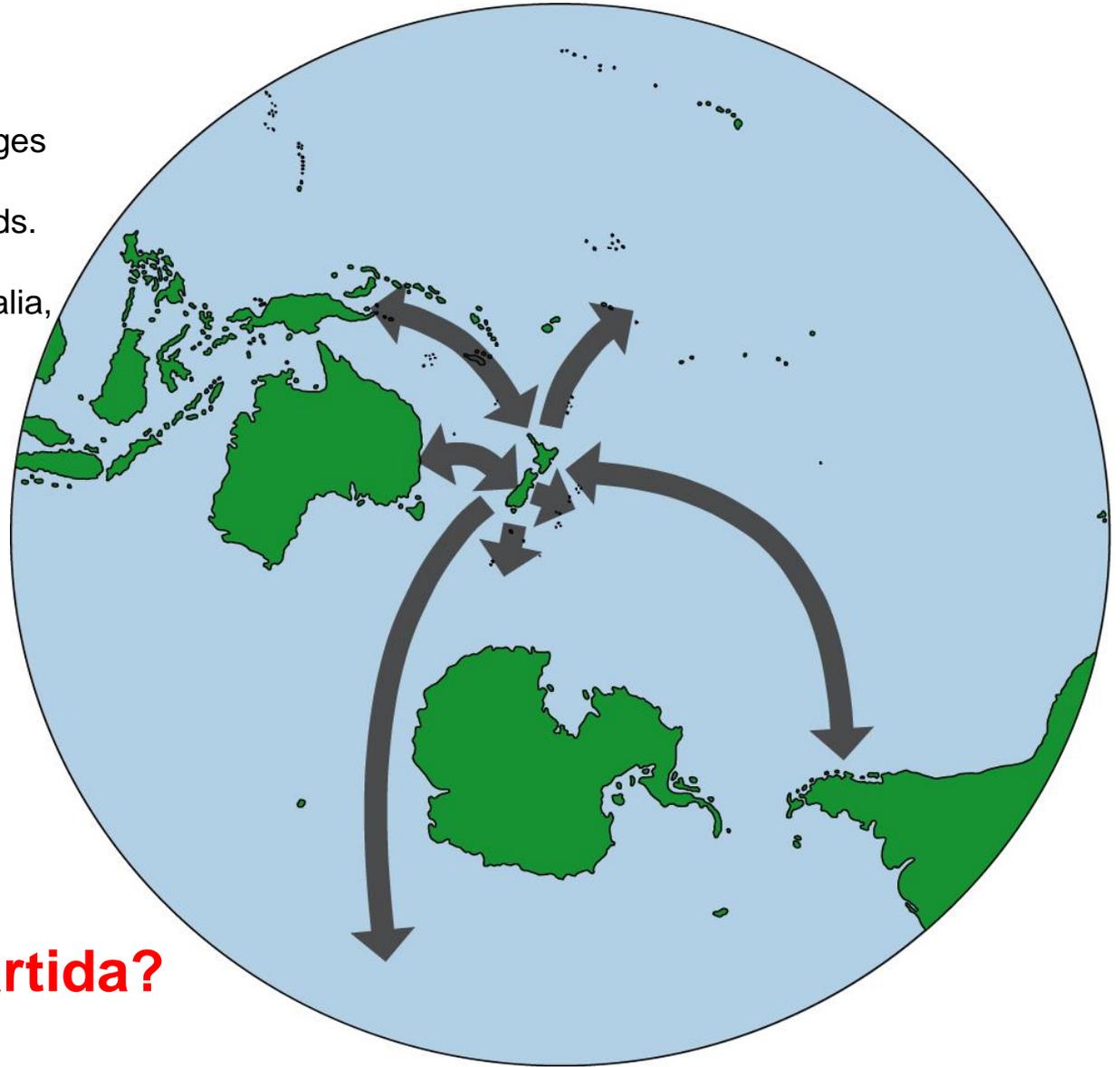
“rather than the pattern of relationships expected from a gondwanan breakup scenario (i.e. Australia and South America are sister) these analyses suggest a closer relationship between New Zealand and Australia ..... a relationship that may reflect dispersal – **the relative proximity of these two landmasses makes dispersal more likely**, c.f. dispersal from either of these two areas to South America

Winkworth *et al.* (2002)

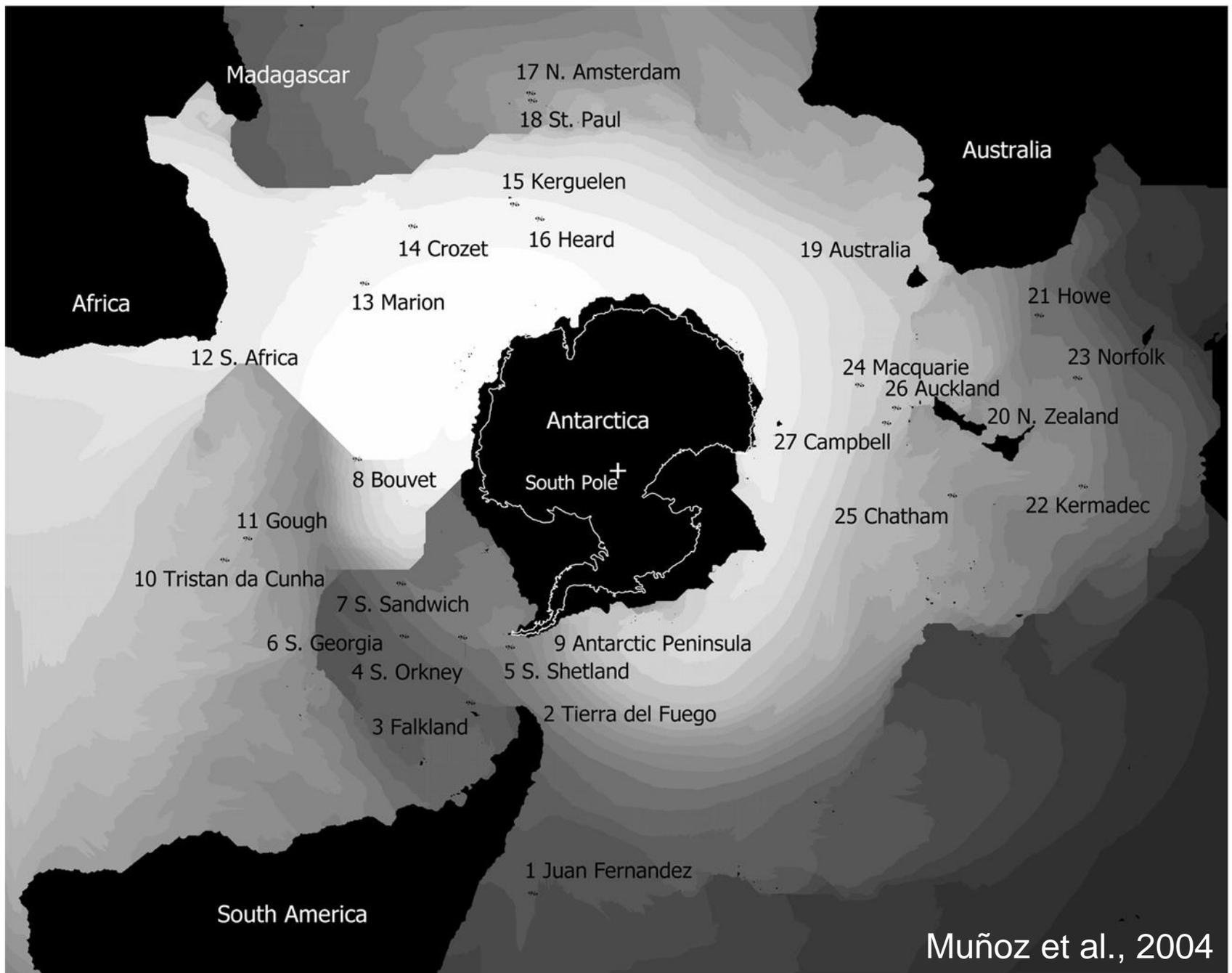


**New Zealand flora:**

seems to have both acquired lineages and acted as a source for lineages in other Southern Hemisphere lands. New Zealand plant species have links to South America, Australia, New Guinea, and several Pacific and Sub-Antarctic Islands.



**E o papel da Antártida?**





**Fig. 1.13** Illustration of the biotic assemblage from the limit Jurassic/Cretaceous (145.5 mya) of the Southern Cone. Theropod dinosaur on a swamp surrounded by ginkgos, araucarias, and arborescent ferns (original illustration by Sergio Elórtogui Francioli)

**Cone Sul da América do Sul**  
**Limite Jurássico-Cretáceo (145 m.a.)**

**Moreira-Muñoz 2011**

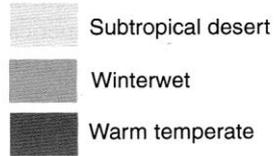
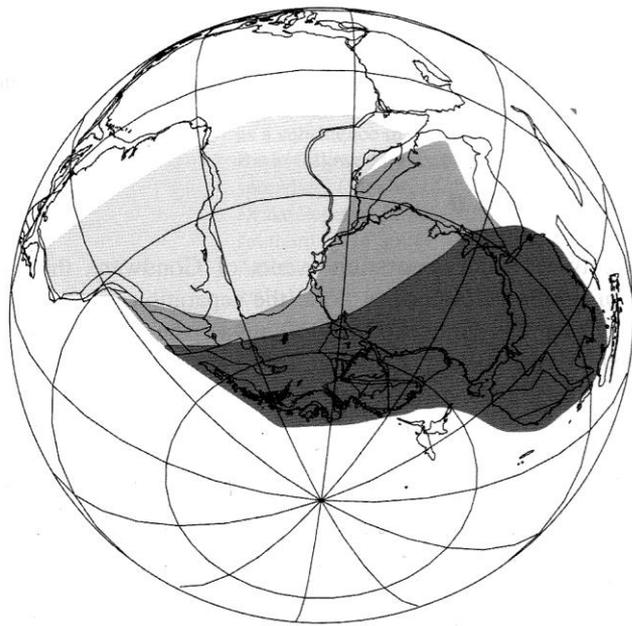


Fig. 1.11 Early Jurassic biomes (adapted from Willis and McElwain (2002) on a TimeTrek 4.2.5 model, Cambridge Paleomap Services)

## Jurássico Inferior (190 m.a.)

Moreira-Muñoz 2011

## Biomass

## Cretáceo Superior (55 m.a.)

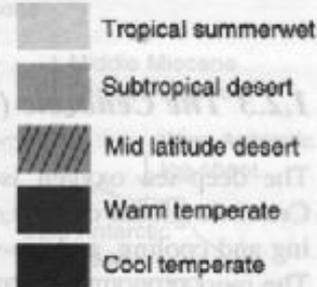
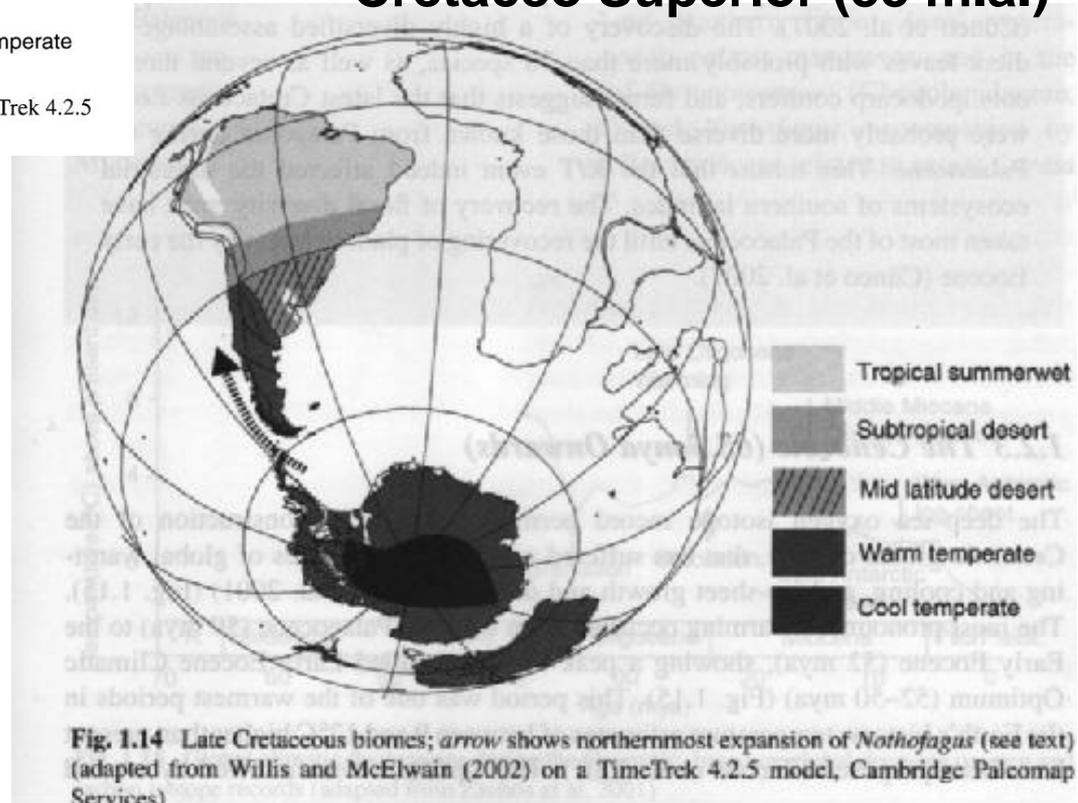
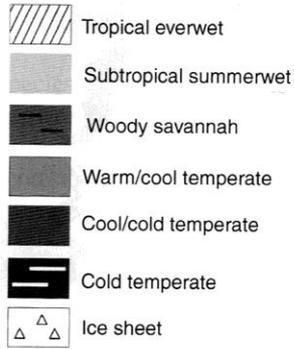


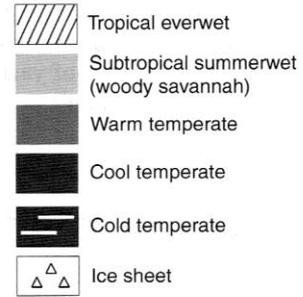
Fig. 1.14 Late Cretaceous biomes; arrow shows northernmost expansion of *Nothofagus* (see text) (adapted from Willis and McElwain (2002) on a TimeTrek 4.2.5 model, Cambridge Paleomap Services)

# Biomass



**Fig. 1.17** Early Oligocene biomes; arrows show mixture of tropical and austral floras (adapted from Willis and McElwain (2002) on a TimeTrek 4.2.5 model, Cambridge Paleomap Services)

## Oligoceno (34 m.a.)

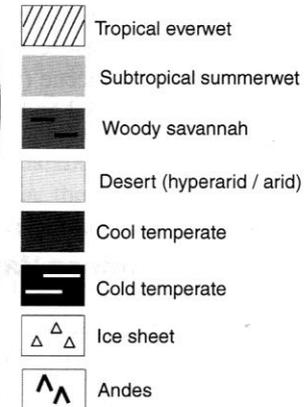
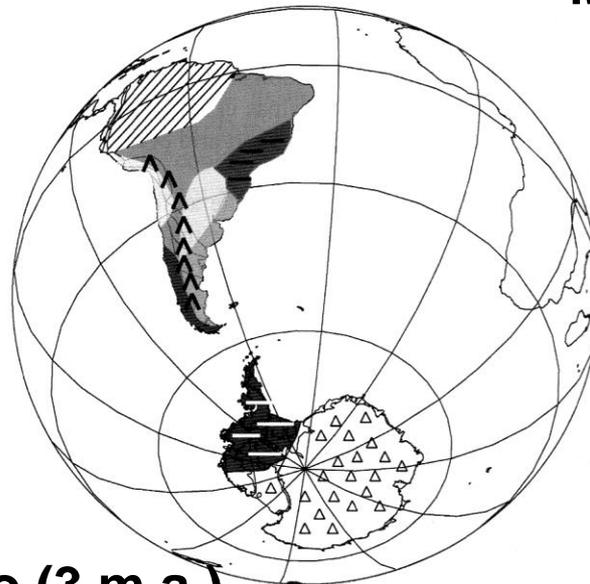


**Fig. 1.18** Miocene biomes (adapted from Willis and McElwain (2002) on a TimeTrek 4.2.5 model, Cambridge Paleomap Services)

## Mioceno (20-8 m.a.)

CENOZOIC		Age Ma	Modern World		
Quat.	Holocene	0.0115			
	Pleistocene	1.806			
Neogene	Miocene	Pliocene			
		Upper		Messinian	5.3
				Tortonian	7.25
		Middle		Serravallian	11.01
				Langhian	13.85
		Lower		Burdigalian	16.97
				Aquitanian	20.43
		Paleogene	Oligocene	Chatthian	23.03
				Rupelian	28.4
			Eocene		33.9
Paleocene				55.8	
			65.5		

After Gradstein et al. (2004, Fig 21.1)



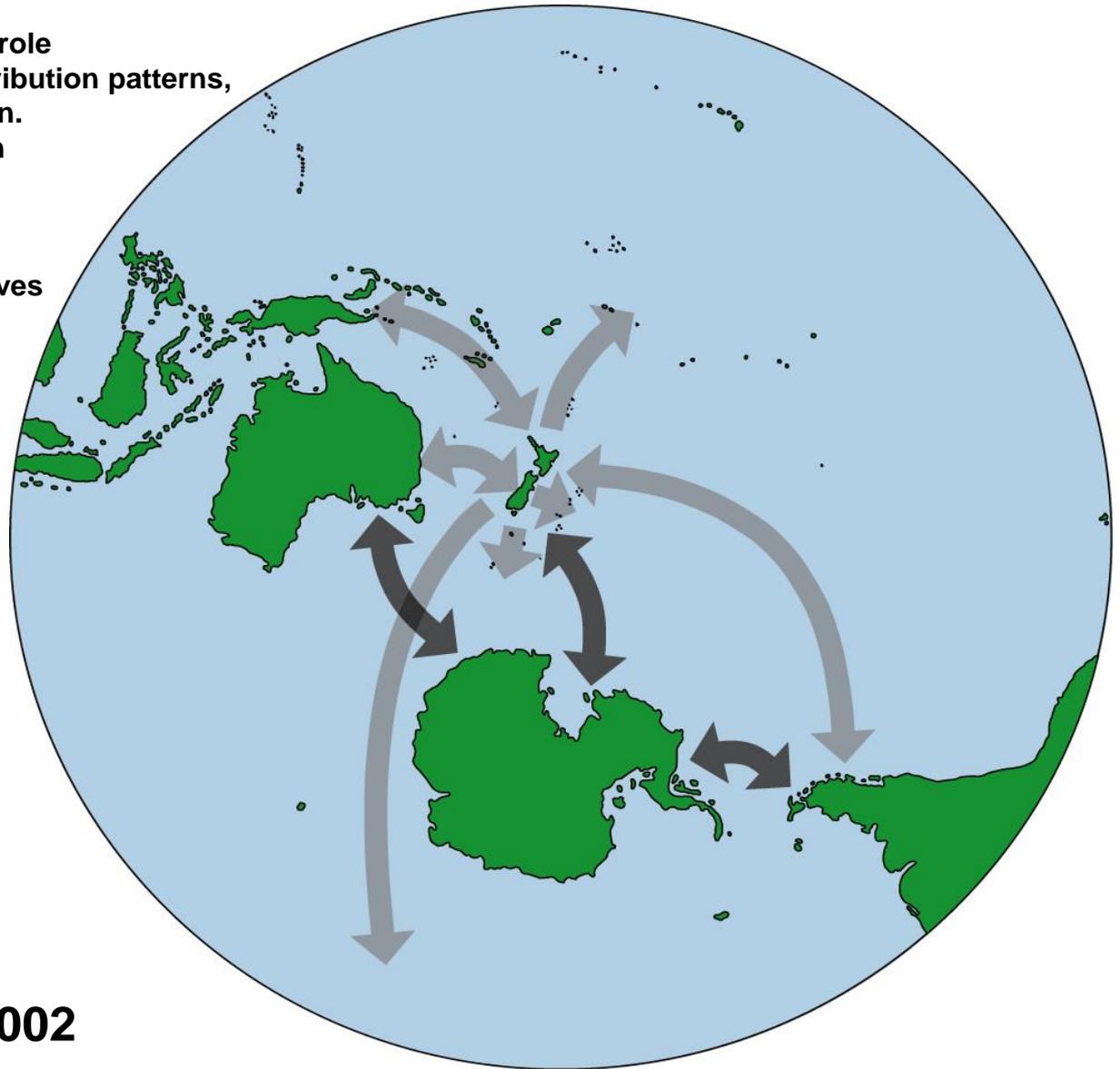
## Plioceno (3 m.a.)

**Fig. 1.19** Pliocene biomes (adapted from Dowsett et al. (1999) and Haywood et al. (2002), on a TimeTrek 4.2.5 model, Cambridge Paleomap Services)

## Moreira-Muñoz 2011

Dispersal may have had an important role in shaping Southern Hemisphere distribution patterns, but the routes involved are less certain. In particular, we have little information about the role of Antarctica in movements between Australia, New Zealand and South America. Since there are no extant representatives we cannot differentiate between direct dispersal or stepping stone models.

Fossil records indicate that many plant lineages may have survived in Antarctica until relatively recently (perhaps 3 MYA ), which hints at a role for Antarctica in shaping distribution patterns. However, limited preservation and taxonomic resolution make it difficult to test these hypotheses.



**Winkworth et al. 2002**

## Donoghue & Moore 2003

Métodos da Biogeografia Cladística são fundamentalmente **baseados em topologia** = padrões gerais são delineados com base em comparação ou combinação somente das topologias dos cladogramas de táxons e áreas.

Necessidade de **incorporação de datação absoluta** (temporalidade) da diversificação das linhagens componentes:

**“ Biogeografia Integrativa ”**

# Teste de tempo na Biogeografia Histórica

Donoghue & Moore 2003

Coincidência temporal

Sim

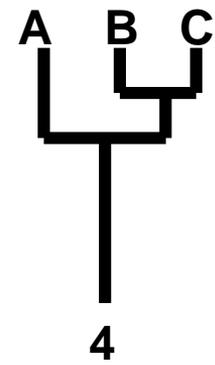
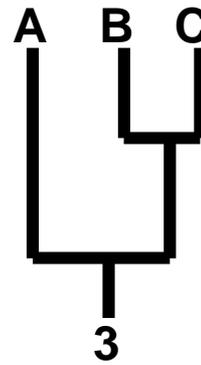
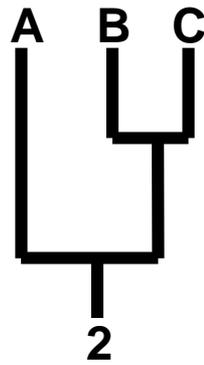
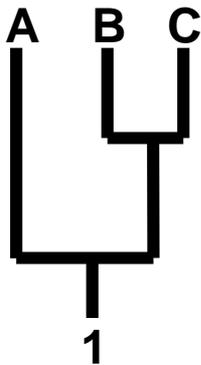
Congruência

Não

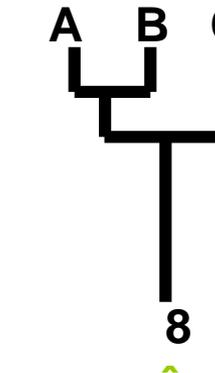
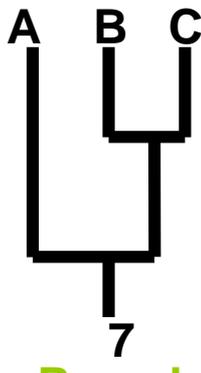
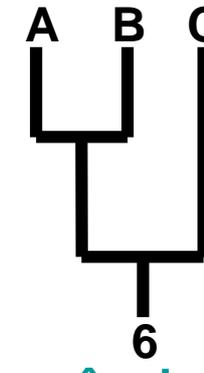
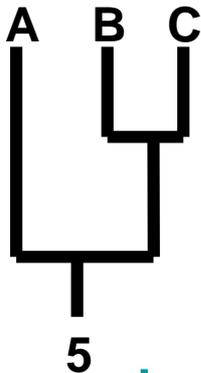
Pseudo-congruência

Coincidência topológica

Sim



Não



Incongruência

Pseudo-incongruência

# “**BIOGEOGRAFIA MOLECULAR**”

**Caccone *et al.* 1994, Lavin *et al.* 2000**

**Reconstrução da **história biogeográfica de 1 táxon**  
sob 2 perspectivas:**

- 1. Uso de **filogenia molecular como dado bruto**  
de métodos da Biogeografia Histórica**
- 2. Aplicação de **relógio molecular para incorporar tempo**  
nos métodos da Biogeografia Histórica**

# “Paradigma cronobiogeográfico”

Hunn & Upchurch 2000

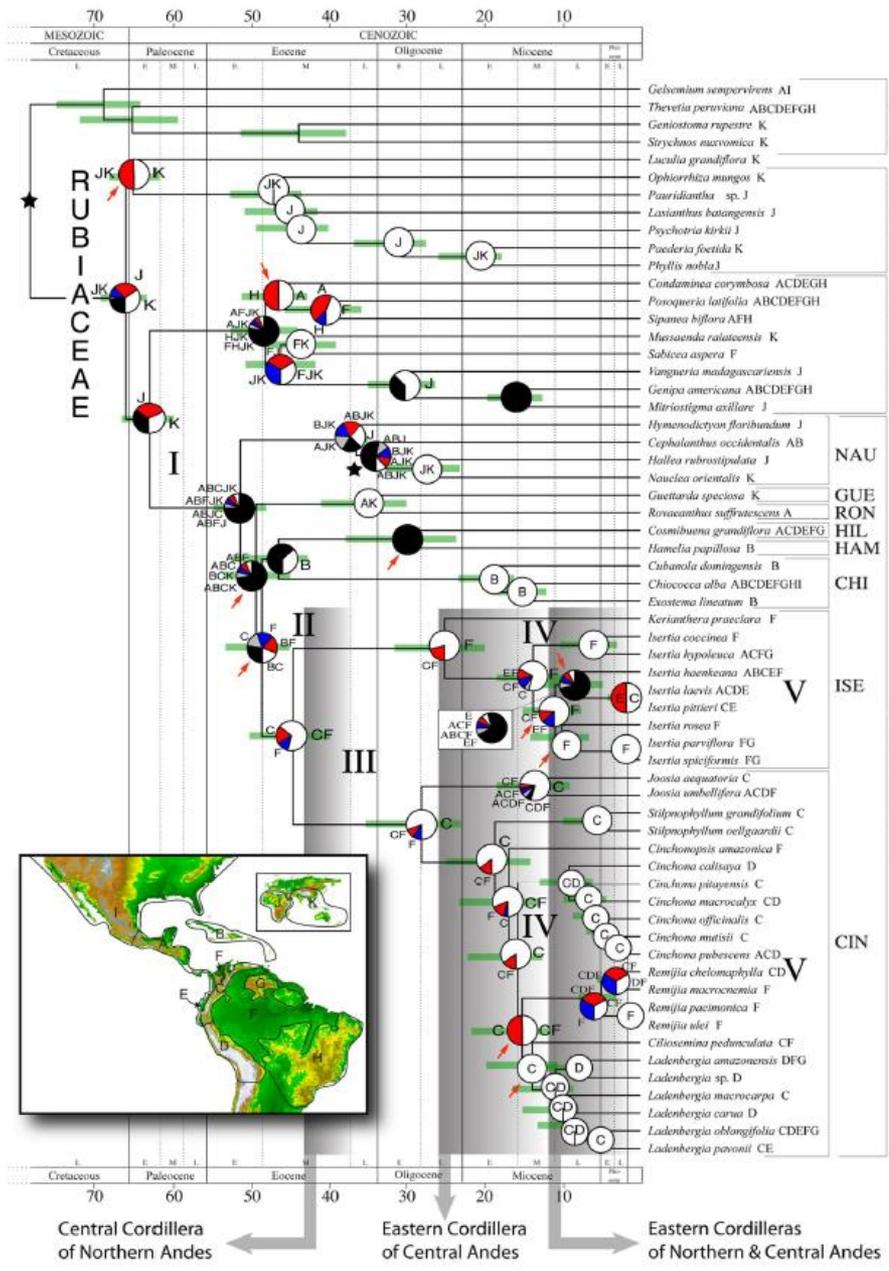
Elaboração lógica e não uma substituição do paradigma atual.

Requer métodos que permitam atribuir  
**valores de tempo a táxons**,  
i.e., tempo de origem e tempo de cada  
evento cladogenético numa filogenia.

Os dados de distribuição temporal dos organismos poderão prover  
reforço ou rejeição de hipóteses sobre a  
causalidade dos eventos filogenéticos.

# “Biogeografia Integrativa”

Donoghue & Moore 2003



# Cronograma combinado com análise biogeográfica das RUBIACEAE neotropicais

Antonelli et al. 2009

62 spp.  
5.894 caracteres derivados de *matK*, *rbcL*, *ITS1-5.8S-ITS2*, *trnL-F*, *rps16*

DIVA 1.1.  
(Ronquist 1996, 1997)

Fig. 1. Combined chronogram and biogeographic analysis of Neotropical Rubiaceae. The tree is the 50% majority-rule consensus (with compatible groups added) from the Bayesian analysis, with branches proportional to absolute ages (in millions of years) calculated from mean branch lengths of 6,000 Bayesian trees. Green bars indicate 95% confidence intervals of node ages estimated from 1,000 trees randomly sampled from the Bayesian stationary distribution. Node charts show the relative probabilities of alternative ancestral distributions obtained by integrating dispersal-variance analysis (DIVA) optimizations over the 1,000 Bayesian trees; the first 4 areas with highest probability are colored according to their relative probability in the following order: white > red > blue > gray; any remaining areas (usually frequencies <0.01) are collectively given with black color. Stars indicate calibration points. Red arrows indicate clades with a posterior probability <0.90. Present ranges for each species are given after the species name. Brackets identify subfamilies and tribes: CHI, Chiococceae; CIN, Cinchonoideae; GUE, Guettardeae; HAM, Hamelleae; HIL, Hillieae; ISE, Isertheae; NAU, Naucleae; RON, Rondeletieae. Shaded boxes indicate approximate periods of Andean uplift phases. The biogeographic interpretation of events I-V is summarized in Fig. 2. (Inset) Areas used in the biogeographic analysis. A, Central America; B, West Indies; C, Northern Andes; D, Central Andes; E, Chocó; F, Amazonia; G, The Guiana Shield; H, Southeastern South America; I, Temperate North America; J, Africa; K, Australasia. Topographic map from the National Geophysical Data Center ([www.ngdc.noaa.gov](http://www.ngdc.noaa.gov)).