FILOGEOGRAFIA

Avise 1987, 1994, 2000; Hillis *et al.* 1996

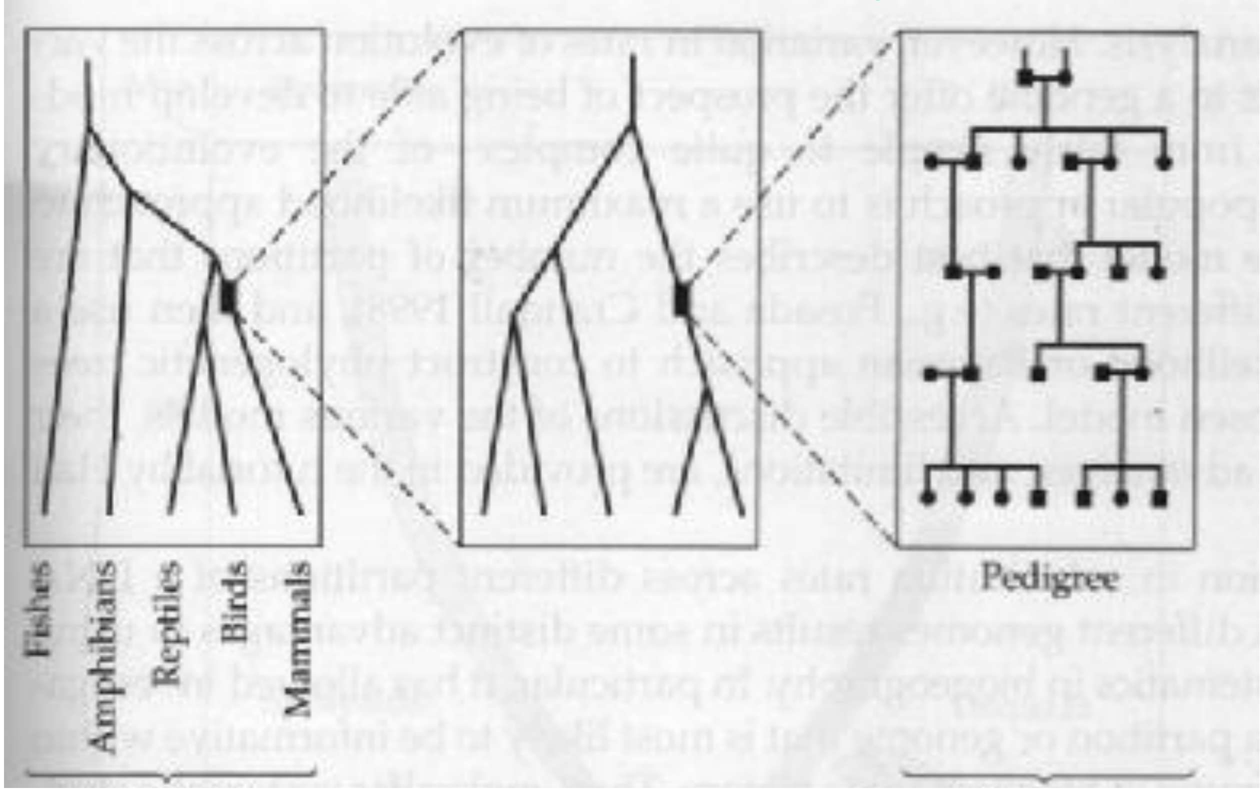
Estudo dos princípios e processos que governam a distribuição geográfica das linhagens genealógicas em nível intra-específico (ou entre espécies muito proximamente relacionadas).

Emprego de estudos genômicos para estudar a estrutura intra-específica de populações naturais.

FILOGEOGRAFIA

Avise 1987, 1994, 2000; Hillis *et al.* 1996

Natureza hierárquica da filogenia:



Macroescala → **microescala**

FILOGENIA

Contínuo de conectividade genética
da MACROESCALA à microescala

FILOGEOGRAFIA

Avise 1987, 1994, 2000; Hillis *et al.* 1996

Quantidade e distribuição da variação dentro e entre populações depende do tamanho das mesmas e da taxa de fluxo gênico.

A distribuição espacial das características nos organismos NÃO é regida apenas por pressões ecológicas contemporâneas;

Seleção natural NÃO é o único mecanismo capaz de gerar padrões geográficos em atributos genéticos, pois em pops delimitadas historicamente e que experimentaram pouco ou nenhum fluxo gênico por um período de tempo longo, a divergência genética ocorrerá inexoravelmente tanto em genes neutros como em genes sob seleção.
As frequências de alelos nas populações variam aleatoriamente = deriva genética – causa perda de variabilidade genética dentro da pop. e aumenta as diferenças entre pops.

FILOGEOGRAFIA

Avise 1987, 1994, 2000, ; Hillis *et al.* 1996

Estudos genômicos **para estudar a estrutura intra-específica de populações:**

- **sítios de restrição – AFLP (**amplified fragment lenght polymorphism)

- **microssatélites: SSRs** (Simple Sequence Repeats) e **STRs** (Short Tandem Repeats) – sequências repetidas de 1-6 pares de bases de DNA. Tipicamente neutros e codominantes; numerosas no genoma de animais e plantas; **alta taxa de mutação** .

- **seqüenciamento de nucleotídeos.**

- **mtDNA e cpDNA – herança materna, e não sofrem recombinação = transmitidos de modo clonal = compartilham um mesmo padrão histórico de descendência comum.**

FILOGEOGRAFIA

Avise 1987, 1994, 2000, ; Hillis *et al.* 1996

Características relevantes do mtDNA:

- taxa de evolução muito mais rápida que a do nDNA

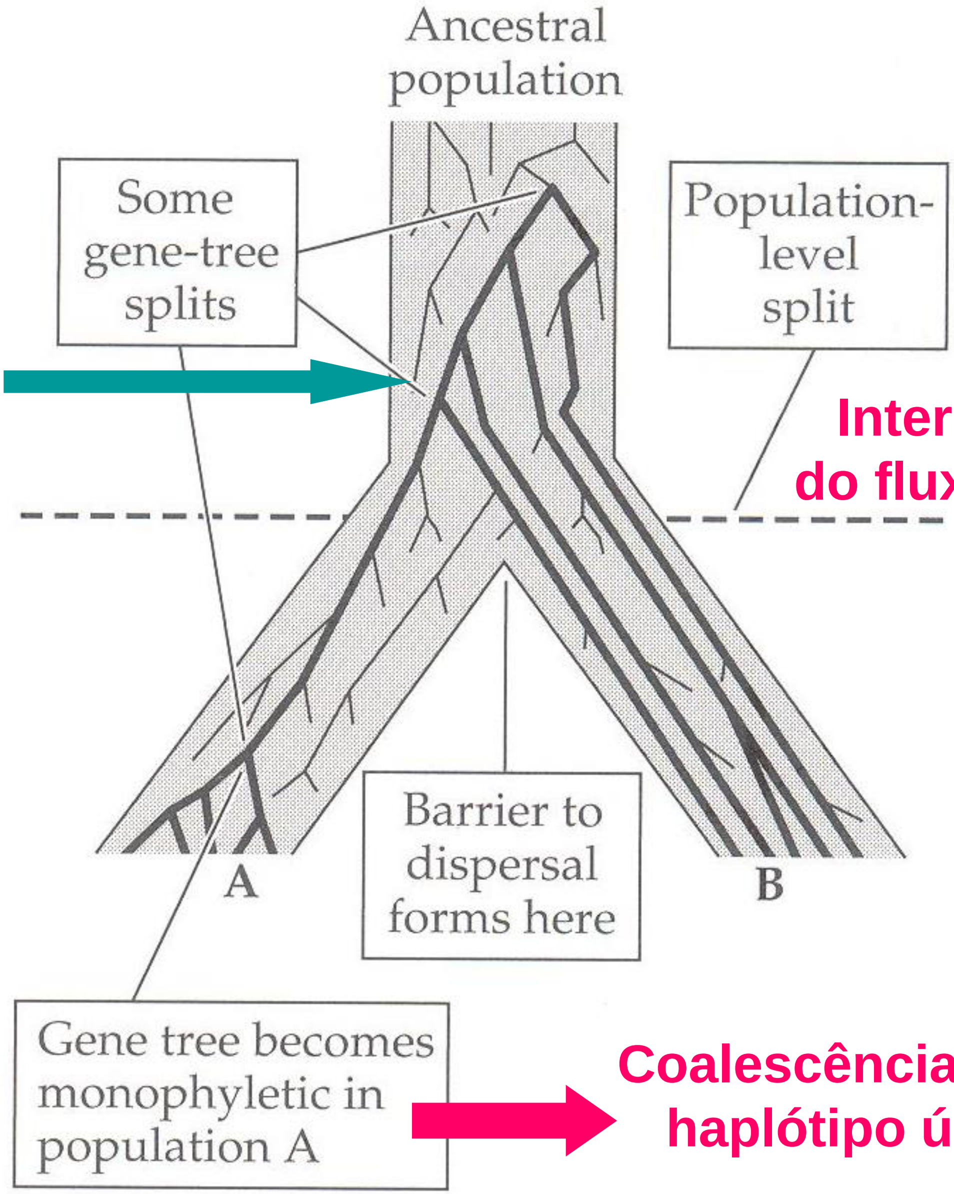
- herança materna permite que se trate o mtDNA todo (genes codificantes de proteínas, genes tRNA e rRNA, e sequências não-codificantes) como um único "locus";

- mtDNA é um genoma haplóide (não diplóide) = genótipos diferentes são denominados HAPLÓTIPOS;

- mtDNA é transmitido de uma geração a outra por intermédio de uma linhagem materna – linhagem matrilinear.

Árvores de genes – Linhagens

Extinção estocástica de linhagens haplotípicas ancestrais



Interrupção do fluxo gênico

Coalescência a um haplótipo único

Lomolino et al. 2006

FIGURE 11.10 Gene trees embedded within population trees. Note that the gene tree divergence between populations will not always be concordant with the time of population divergence, and that the rate of ancestral lineage sorting can occur at very different rates in different populations. In this case, the gene tree in population A is monophyletic with respect to population B, but did not become so until well after the time of the population split. Population B is still paraphyletic with respect to population A. At any point in time prior to the coalescence of the gene tree in population 1 to monophyly, populations A and B would have been polyphyletic. (After Avise 2000.)

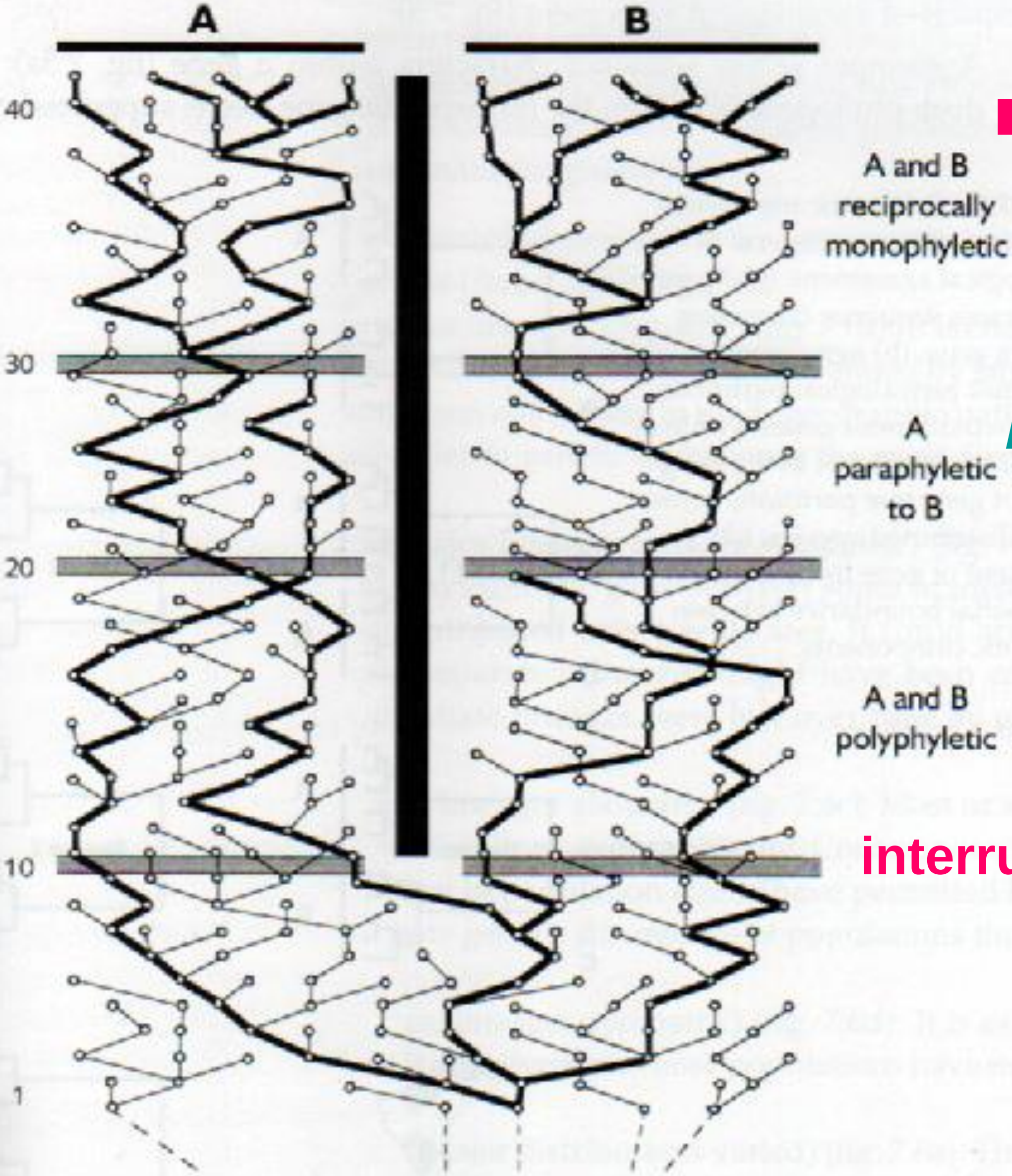


Figure 7.4 Schematic representation of the matrilineal sorting process of two sister pop
lations, along 40 generations, separated by a barrier to gene flow.

Coalescência a um haplótipo único de mtDNA ou cpDNA é <u>muito mais rápida do que a do nDNA</u>

2 pops isoladas passarão por estágios reciprocamente poli-, para- ou monofiléticos em relação às suas ascendências matriarcais

interrupção do fluxo gênico

Morrone 2009

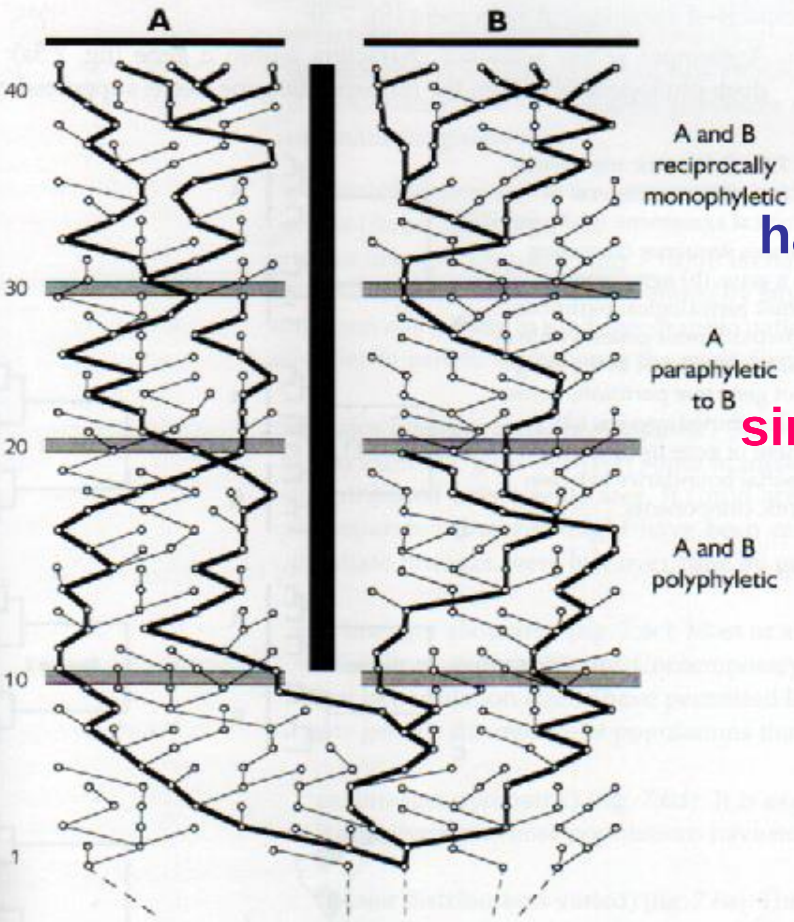


Figure 7.4 Schematic representation of the matrilineal sorting process of two sister pop
lations, along 40 generations, separated by a barrier to gene flow.

Morrone 2009

Alta taxa de mutação
gerando novos haplótipos rapidamente
+ rápida extinção de
haplótipos ancestrais numa população =

mtDNA desenvolve um
sinal de divergência (monofilia recíproca)
entre 2 pops isoladas
(coalescência em cada pop)
num lapso (depois do isolamento)
muito mais breve do que no <u>nDNA</u>

Plantas: cpDNA taxa de evolução mas baixa,
mas muitas regiões têm taxa rápida.

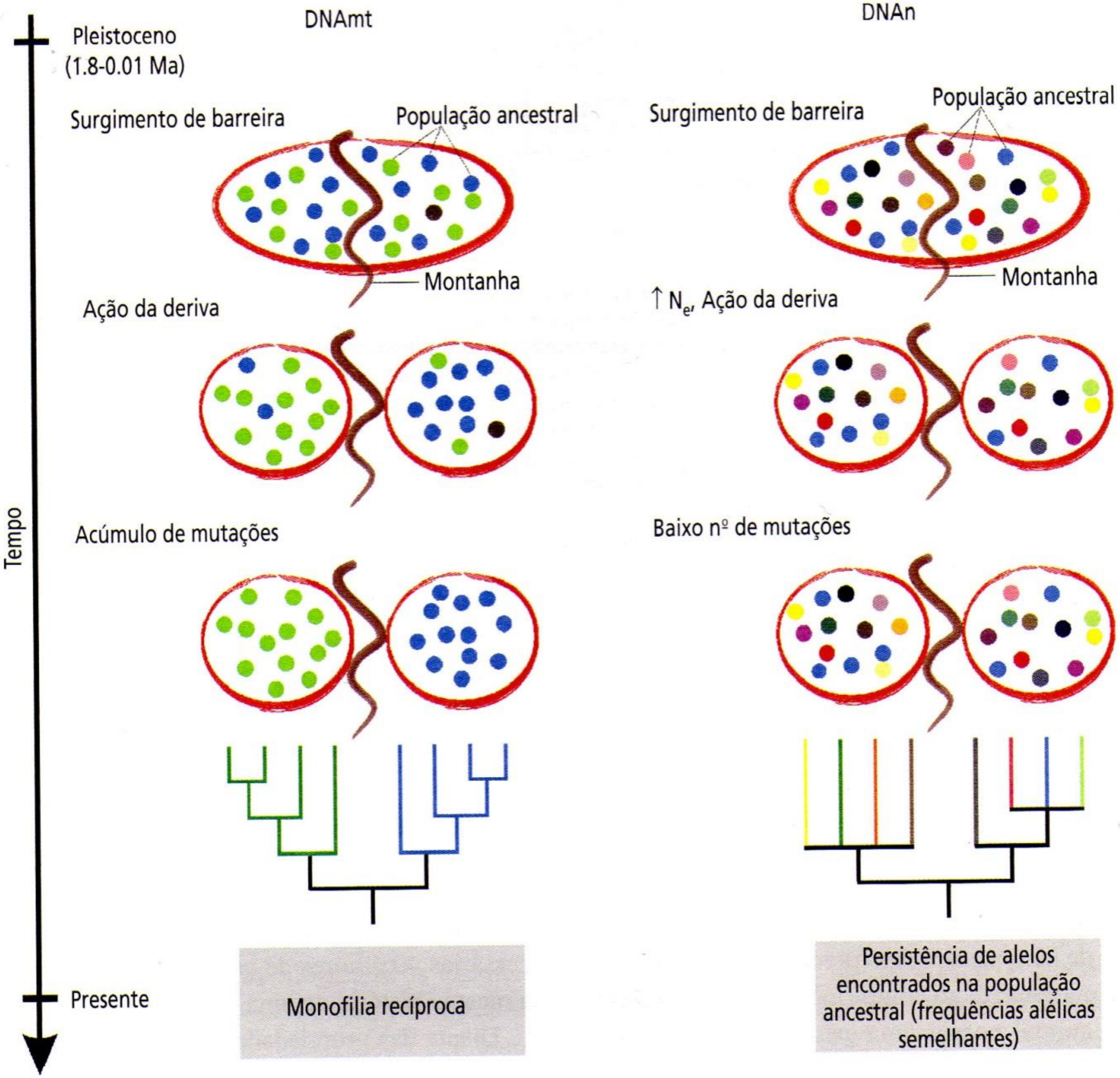


Figura 8.2 – Processo de deriva e sorteio de linhagens para um marcador mitocondrial (*esquerda*) e nuclear (*direita*), a partir de um evento recente que gerou uma barreira ao fluxo gênico. Em razão do menor número efetivo e maior taxa de mutação, o marcador mitocondrial recupera a verdadeira história das linhagens, enquanto o marcador nuclear não é capaz de recuperar a história das populações. DNAmt = ácido desoxirribonucleico mitocondrial; DNAn = ácido desoxirribonucleico nuclear; N_e = tamanho populacional efetivo.

Martins & Domingues in Carvalho & Almeida 2010

Exemplo de estudo:

10 sequências amostradas.

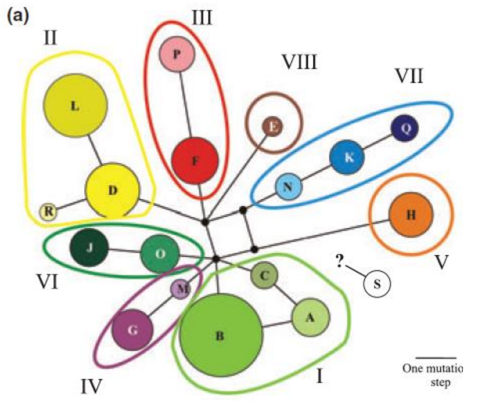
Variações entre elas **sublinhadas**.

Espécime 1	AAATGCGCTCAATGCGATTCCGCCCGTCGCTAAGAT
Espécime 2	AAATGCGCTCAATGCGATTCCGCCCGTCGCTAAGAT
Espécime 3	AAATGCGCTCAATGCGATTCCGCCCGTCGCTAAGAT
Espécime 4	AAATGCGCTCAATGCGATTCCGCCCGTCGCTAAGAT
Espécime 5	AAATGCGCTCAATGCGATTCCGCCCGTCGCTAAGAT
Espécime 6	AAATGCG**T**TCAATGCGATTCCGCCCGTCGCTAAGAT
Espécime 7	AAATGCGCT**G**AATGCGATTCCGCCCGTCGCTAAGAT
Espécime 8	AAATGCGCTCAA**C**GCGATTCCGCCCGTCGCTAAGAT
Espécime 9	AAATGCGCTCAATGCG**T**TTCCGCCCGTCGCTAAGAT
Espécime 10	AAATGCGCTCAATGCGATTCCGCCCGT**A**GCTAAGAT

Matriz de distâncias entre as sequências amostradas

	1	2	3	4	5	6	7	8	9	10
1	X									
2	0	X								
3	0	0	X							
4	0	0	0	X						
5	0	0	0	0	X					
6	1	1	1	1	1	X				
7	1	1	1	1	1	2	X			
8	1	1	1	1	1	2	2	X		
9	1	1	1	1	1	2	2	2	X	
10	1	1	1	1	1	2	2	2	2	X

Matriz de distâncias permite:
detectar **quantos haplótipos** existem na amostragem;
estimar a **frequência de cada um** desses haplótipos;
construir uma **rede de haplótipos** com as sequências:



Padrões Filogeográficos:
as 5 categorias possíveis

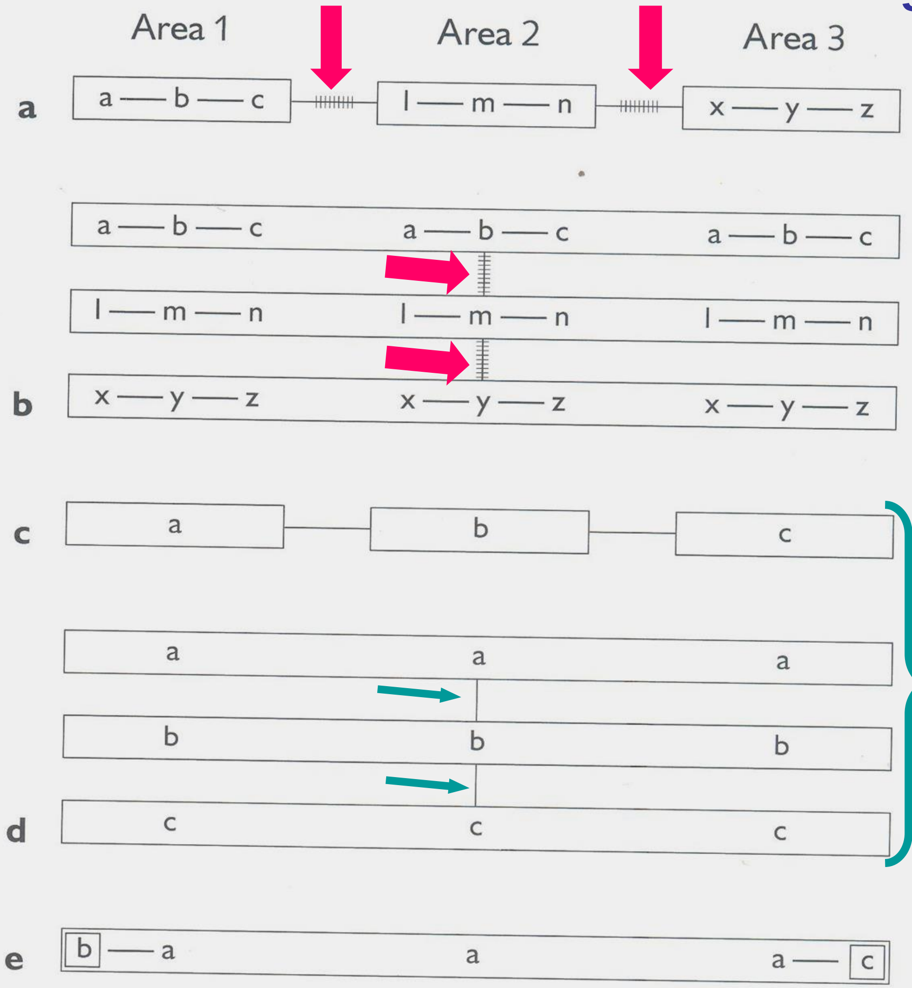
segundo Avise 2000

letras = haplótipos

**retângulos = grupos
de haplótipos
proximamente
relacionados**

Grandes lacunas genéticas (gaps)
-várias mutações

FILOGRUPOS



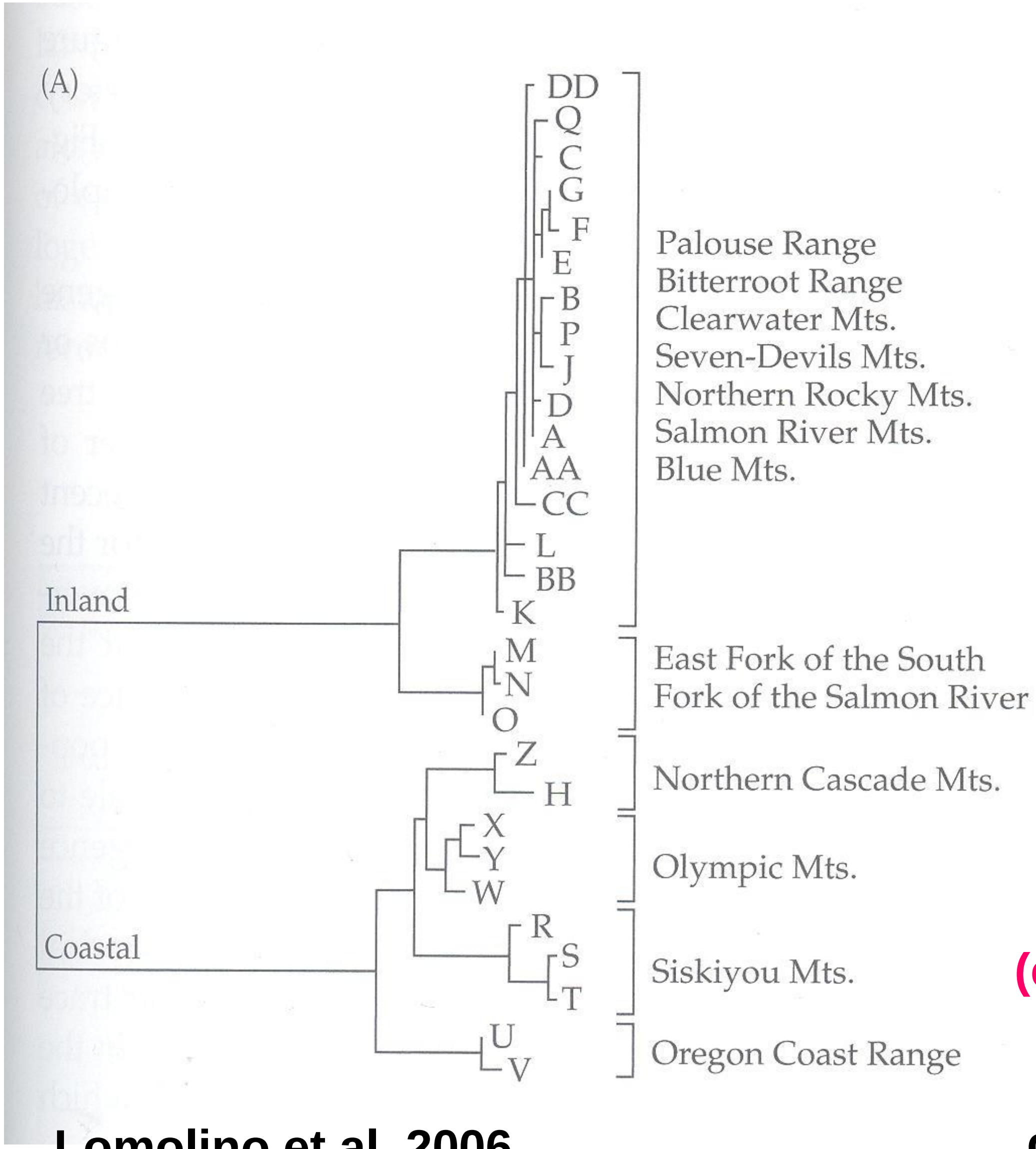
Sem grandes lacunas genéticas (gaps)
- uma mutação

padrões similares a a e b, porém mais recentes, resultantes de histórias de vida, não de atributos biogeográficos

sp com fluxo gênico contínuo entre pops

Figure 7.6 Different phylogeographic patterns for mtDNA gene cladograms. (a) Category I (deep gene tree, major lineages allopatric); (b) Category II (deep gene tree, major lineages broadly sympatric); (c) Category III (shallow gene tree, lineages allopatric); (d) Category IV (shallow gene tree, lineages sympatric); (e) Category V (shallow gene tree, major distributions varied).

(Morrone 2009)



Lomolino et al. 2006

Ascaphus truei

frog

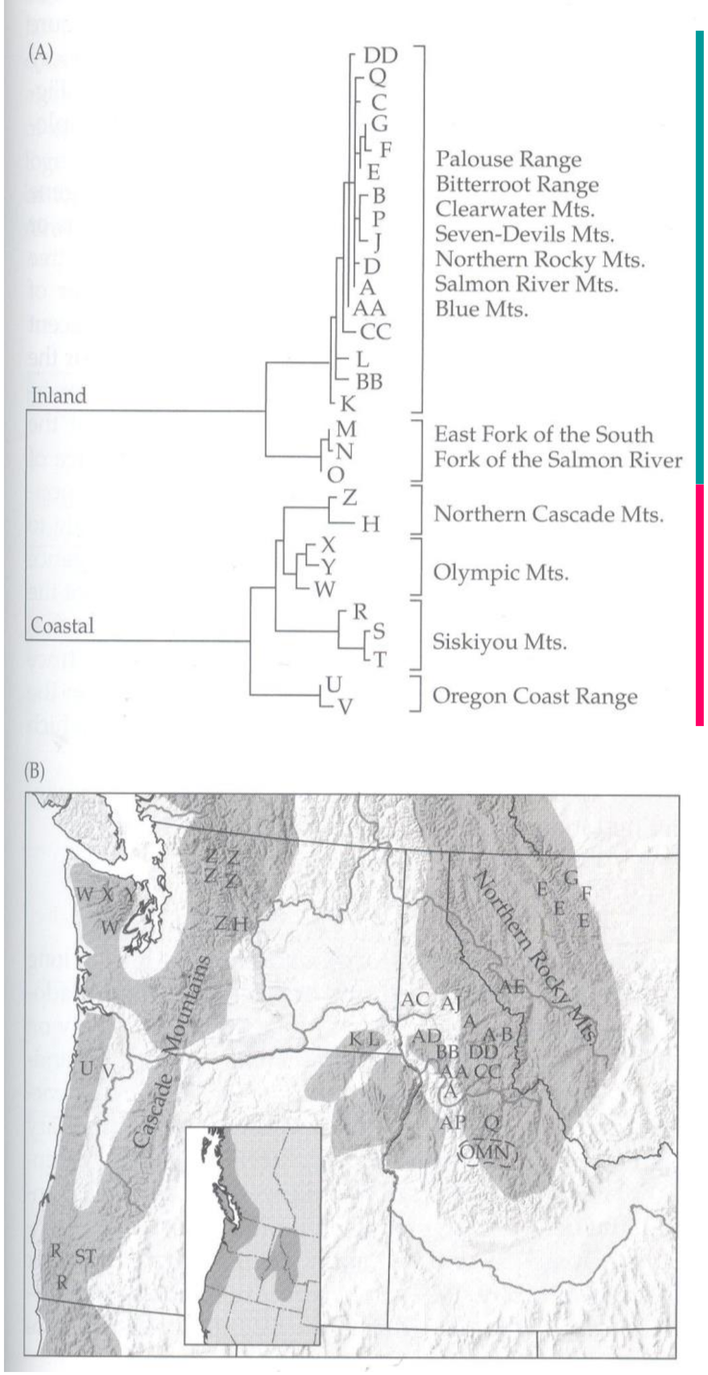
Costa Noroeste Pacífica
EUA

Padrões com FILOGRUPOS
(categorias a e b de Avise 2000)
são adequados a
análises filogenéticas:
cada haplótipo único é tratado
como uma OTU numa matriz de dados
submetida aos algoritmos usados
na reconstrução de filogenias.

Ascaphus truei

Costa Noroeste Pacífica
EUA

Haplotipos
formando 2 clados
profundamente divergentes,
reciprocamente monofiléticos
e alopátridos



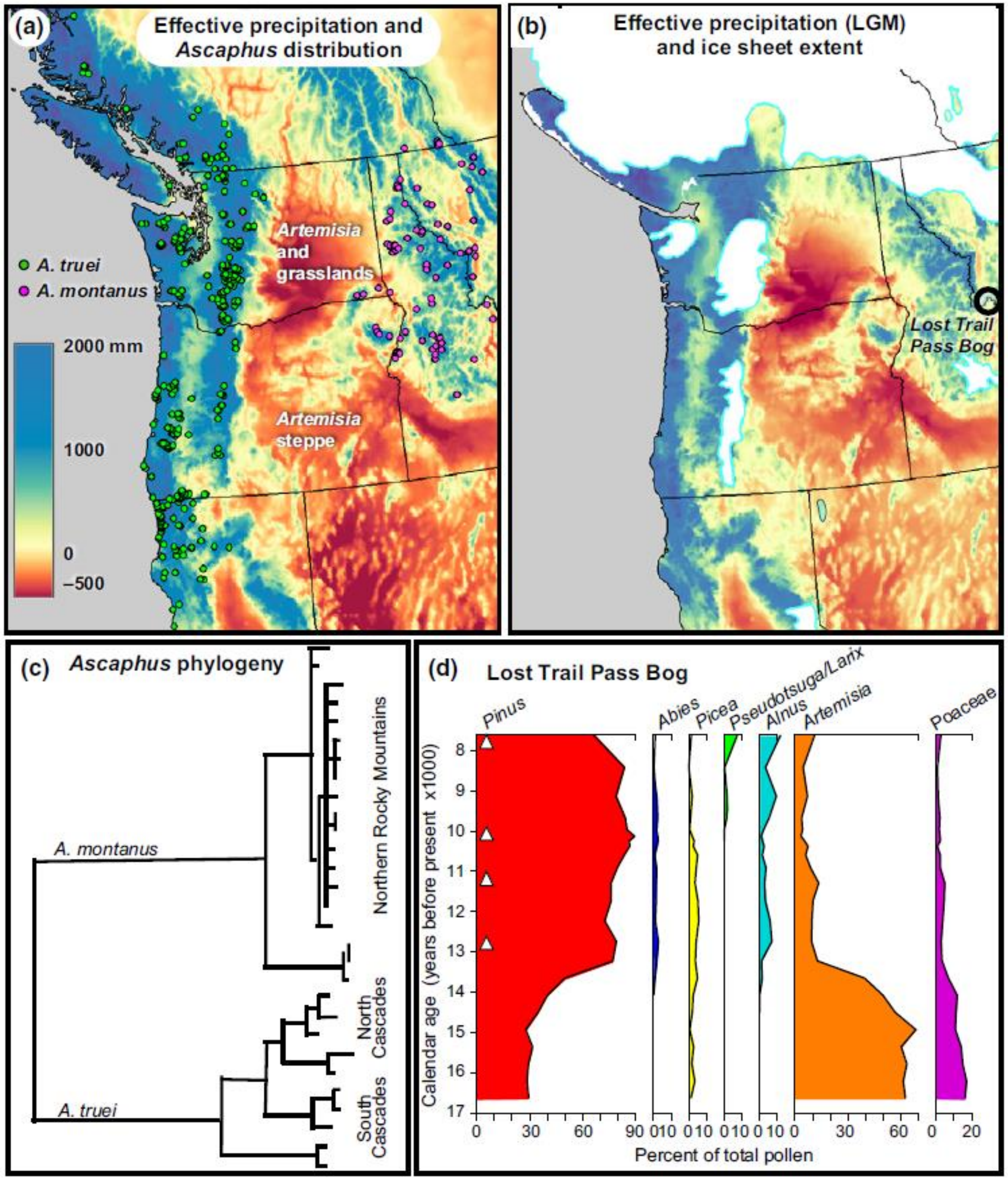
filogrupo continental

filogrupo costeiro
(pontos de coalescência
mais profundos
entre os subclados)

2 espécies crípticas?

FIGURE 11.13 (A) Mitochondrial DNA phylogenetic tree for mtDNA haplotypes (capital letters) drawn from populations of the Tailed frog, *Ascaphus truei*, from the Pacific Northwest, USA. Haplotypes form two deeply divergent, reciprocally monophyletic and geographically disjunct clades—an Inland group and a Coastal group (B). With exception of the split between haplotype group M + N + O and all other Inland haplotypes, the Coastal clade has generally deeper points of coalescence among subclades, suggesting older splits between populations from different mountain ranges than is shown for the Inland clade. This phylogeny was used to propose that the Inland and Coastal populations represent two separate, morphologically "cryptic" species. (From Nielson et al. 2001.)

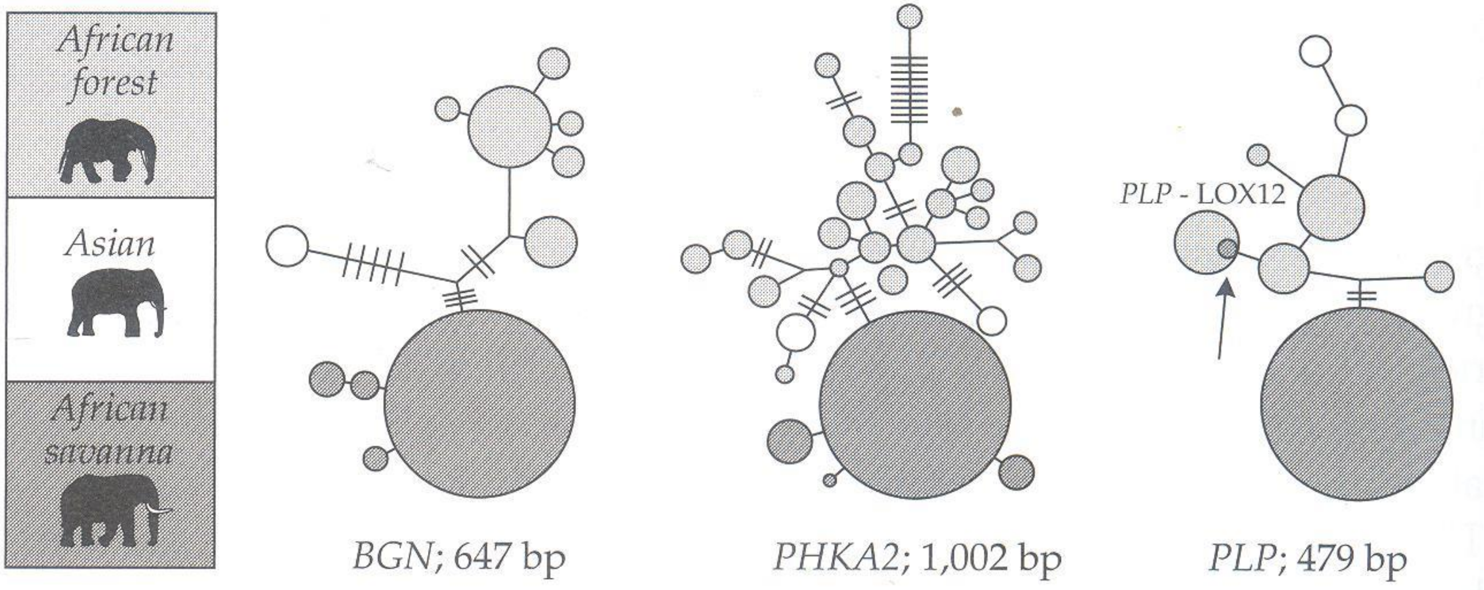
Nielson et al. 2001
apud
Lomolino
et al. 2006



Gavin et al. 2014

Reconstrução paleoclimática explicativa da especiação em *Ascaphus*

***Loxodonta* e *Elephas* - haplótipos não-enraizados (network)**



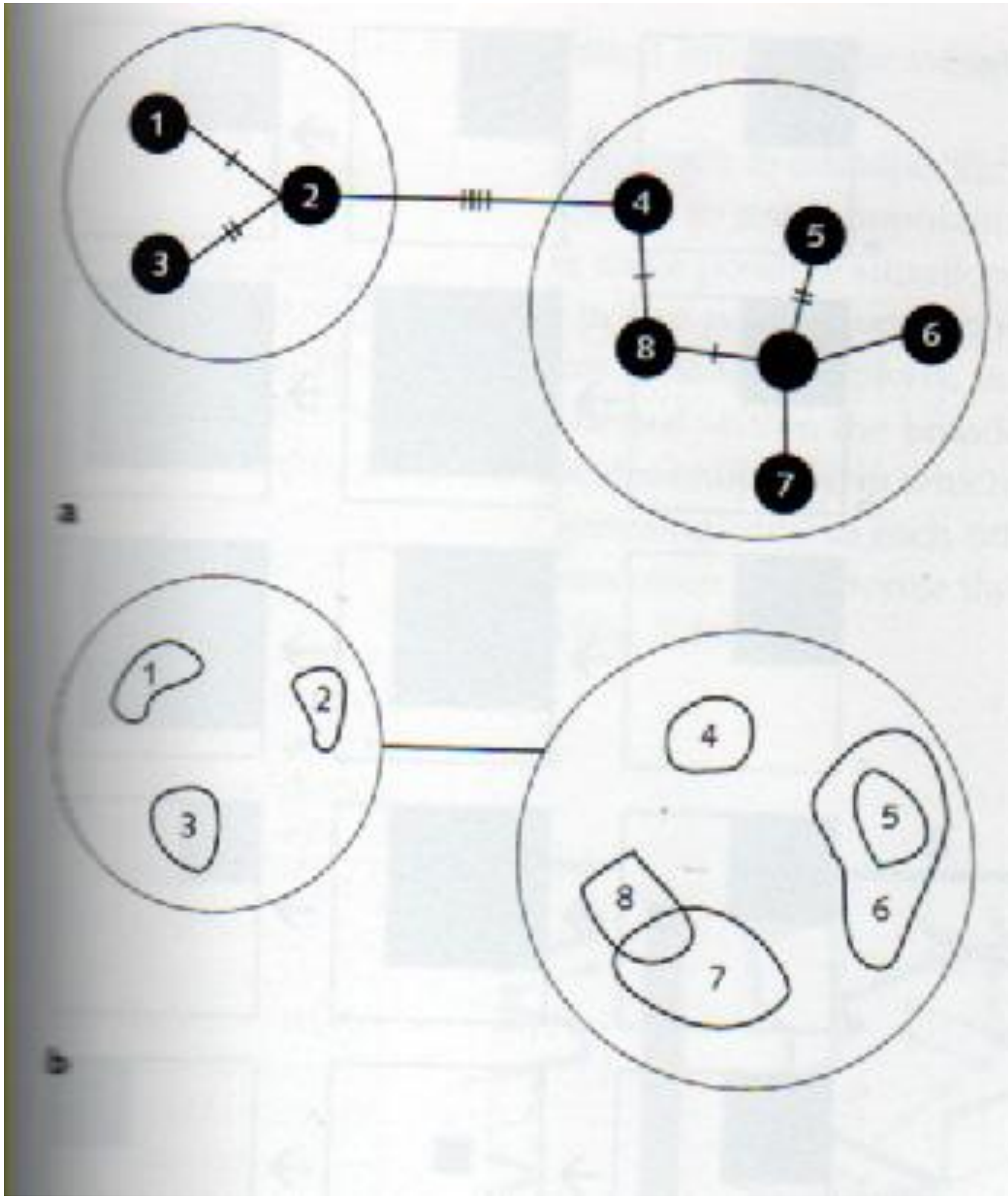
3 genes nucleares

FIGURE 11.14 Three unrooted haplotype networks within and among two species of African (genus *Loxodonta*) and one species of Asian (*Elephas*) elephant. Each network represents a separate gene from the nuclear DNA. The haplotypes from Asian elephants are shown as white circles, those from African savanna elephants are dark gray circles, and those from African forest elephants are light gray circles. Slashes across lines connecting haplotypes each represent a single mutational step (lines without a slash represent one mutational step between haplotypes). Note that haplotypes from each species cluster together in all cases except one (for *PLP*, the two savanna elephant individuals at the arrow carried a haplotype that was otherwise common in the forest species). The pattern of haplotype clustering provides evidence of genetic divergence between the three species. (After Roca et al. 2005.)

Padrões sem FILOGRUPOS
(categorias c, d, e de Avise 2000):
rede filogenética não-enraizada
sumariza as relações entre os haplotipos

Roca et al. 2005,
apud Lomolino et al. 2006

Hipótese filogeográfica



Rede parcimoniosa conectando haplótipos e 2 filogrupos

Distribuição geográfica dos haplótipos

Morrone 2009

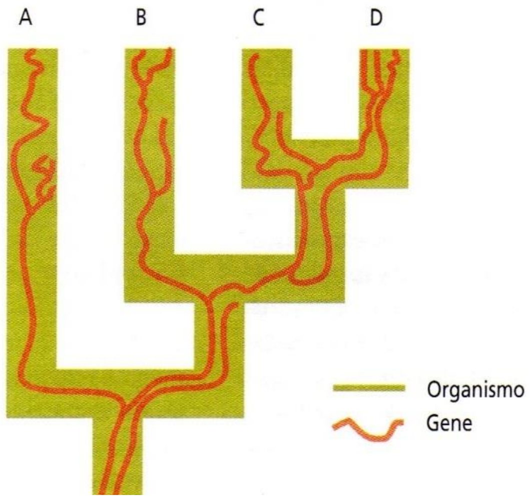
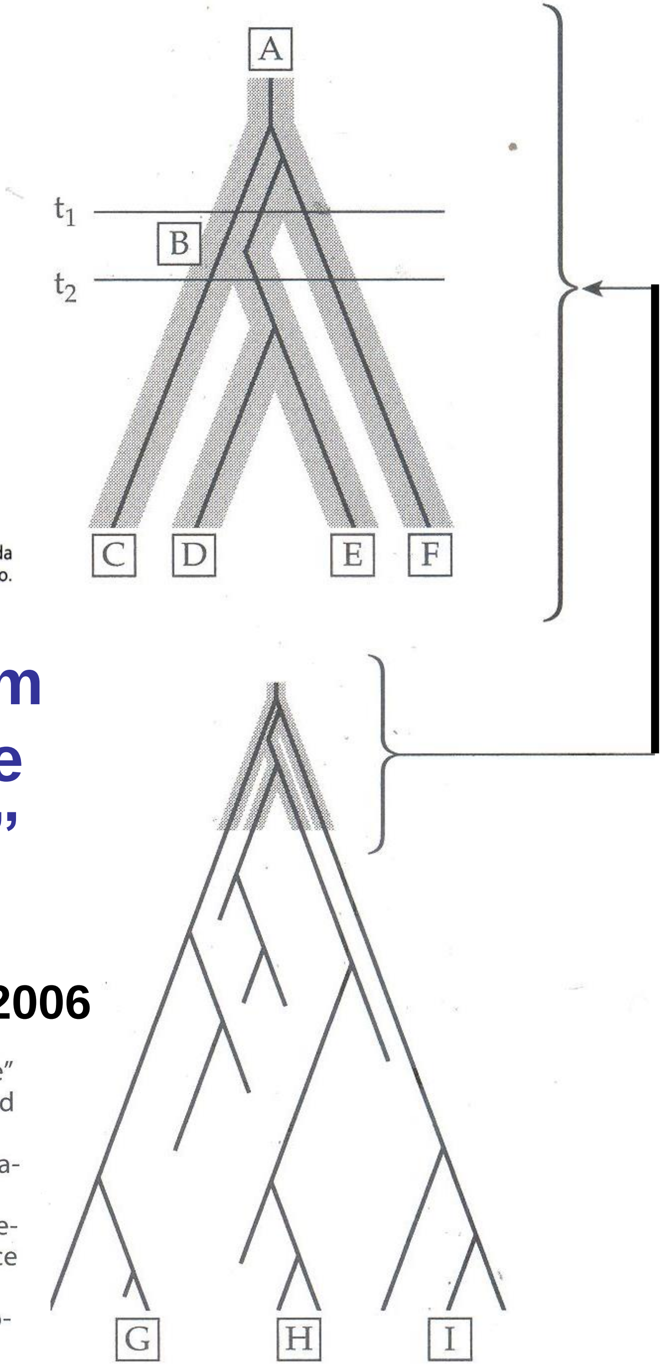


Figura 8.3 – Incongruência entre história filogenética de populações e de um marcador molecular hipotético decorrente da estocasticidade dos processos de mutação e deriva genética. Note que a população D não é monofilética para o gene estudado.

Martins & Domingues in
Carvalho & Almeida 2010



Árvore genética com topologia diferente da “filogenia real”

Avise 2002,
apud Lomolino et al. 2006

URE 11.15 An illustration of a gene tree that differs topologically from the “true” ogenetic relationships among species. In the top figure, species D and E are allied C, but the gene tree in D and E is allied with F. This is because population B re- s ancestral polymorphism between the time interval t_1 to t_2 and across the specia- event between C and D + E. As this interval becomes shorter (i.e., time between secutive branching events becomes reduced), the probability of a discordance be- en species and gene tree topologies increases. The bottom figure shows that once a discordance arises, it becomes permanently frozen into place, so must always onsidered a possible source of error when using gene trees to infer species histo- from sampling of extant lineages (G, H, and I). (After Avise 2002.)

FILOGEOGRAFIA

Avise 1987, 1994, 2000; Hillis *et al.* 1996

Estrutura genética das pops permite:
-estimar filogenia das populações

-investigar os padrões de biogeografia histórica (dispersão como migrações, colonizações, isolamento geográfico)

- comparar espécies simpátridas que não exibam padrões congruentes.

Ronquist (1997): filogeografia é uma aproximação da Biogeogr. Histórica a uma escala ecológica de tempo.

Hipóteses filogeográficas (Walker & Avise 1998):

1. **a maioria das espécies compõem-se de pops geográficas, as quais ocupam ramos distintos de uma árvore filogenética intra-específica.**

2.

3.

Hipóteses filogeográficas (Walker & Avise 1998):

1. **a maioria das espécies compõem-se de pops geográficas, as quais ocupam ramos distintos de uma árvore filogenética intra-específica.**

2. **as espécies que não exibem uma estrutura genealógica que evidencie sua distribuição geográfica devem ter ocupado habitats livres de barreiras ao fluxo gênico e devem ter sofrido dispersão entre suas pops.**

3.

Hipóteses filogeográficas (Walker & Avise 1998):

1. **a maioria das espécies compõem-se de pops geográficas, as quais ocupam ramos distintos de uma árvore filogenética intra-específica.**

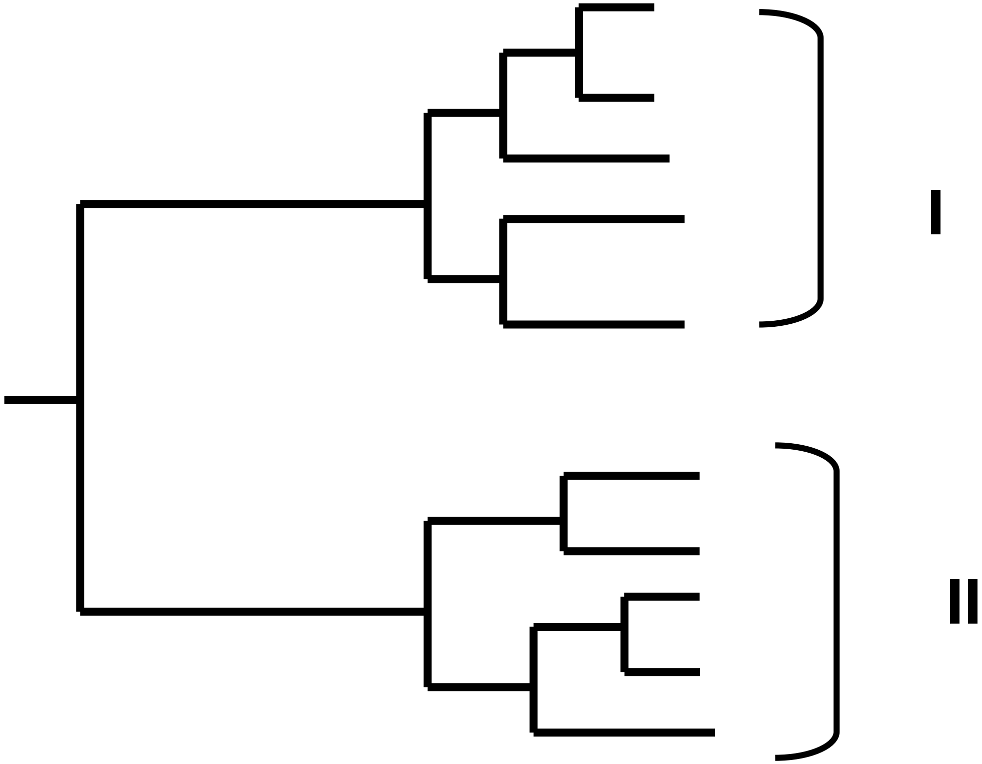
2. **as espécies que não exibem uma estrutura genealógica que evidencie sua distribuição geográfica devem ter ocupado habitats livres de barreiras ao fluxo gênico e devem ter sofrido dispersão entre suas pops.**

3. **os grupos monofiléticos intra-específicos que se distinguem por grandes separações filogenéticas devem ter-se originado devido à presença de barreiras extrínsecas (biogeográficas) de longa duração.**

Esta última hipótese inclui 4 corolários (4 aspectos da concordância genealógica):

Filogeografia - Corolário 1

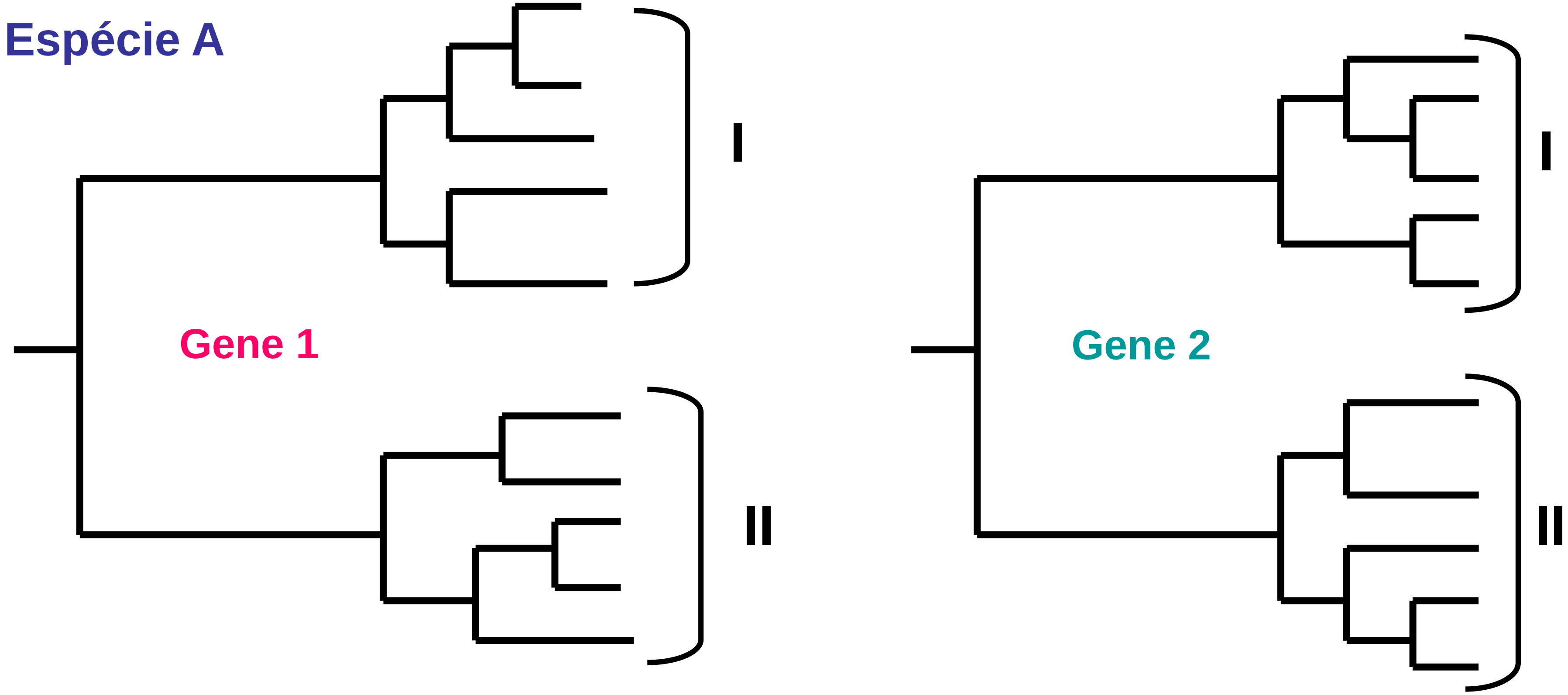
Concordância entre caracteres seqüenciais dentro de um gene



Espécie A
Gene 1

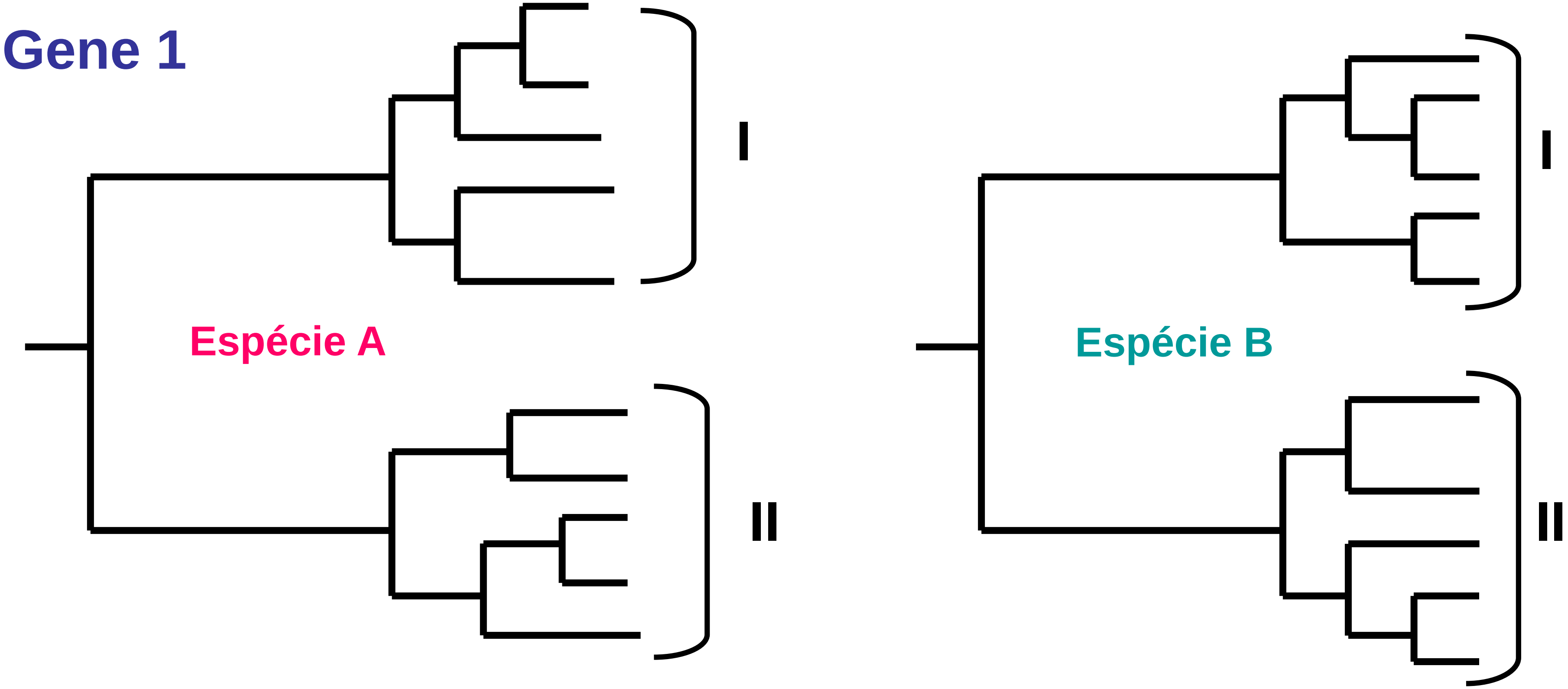
Filogeografia - Corolário 2

Concordância em parte significativa das partições genealógicas entre múltiplos genes dentro de uma espécie



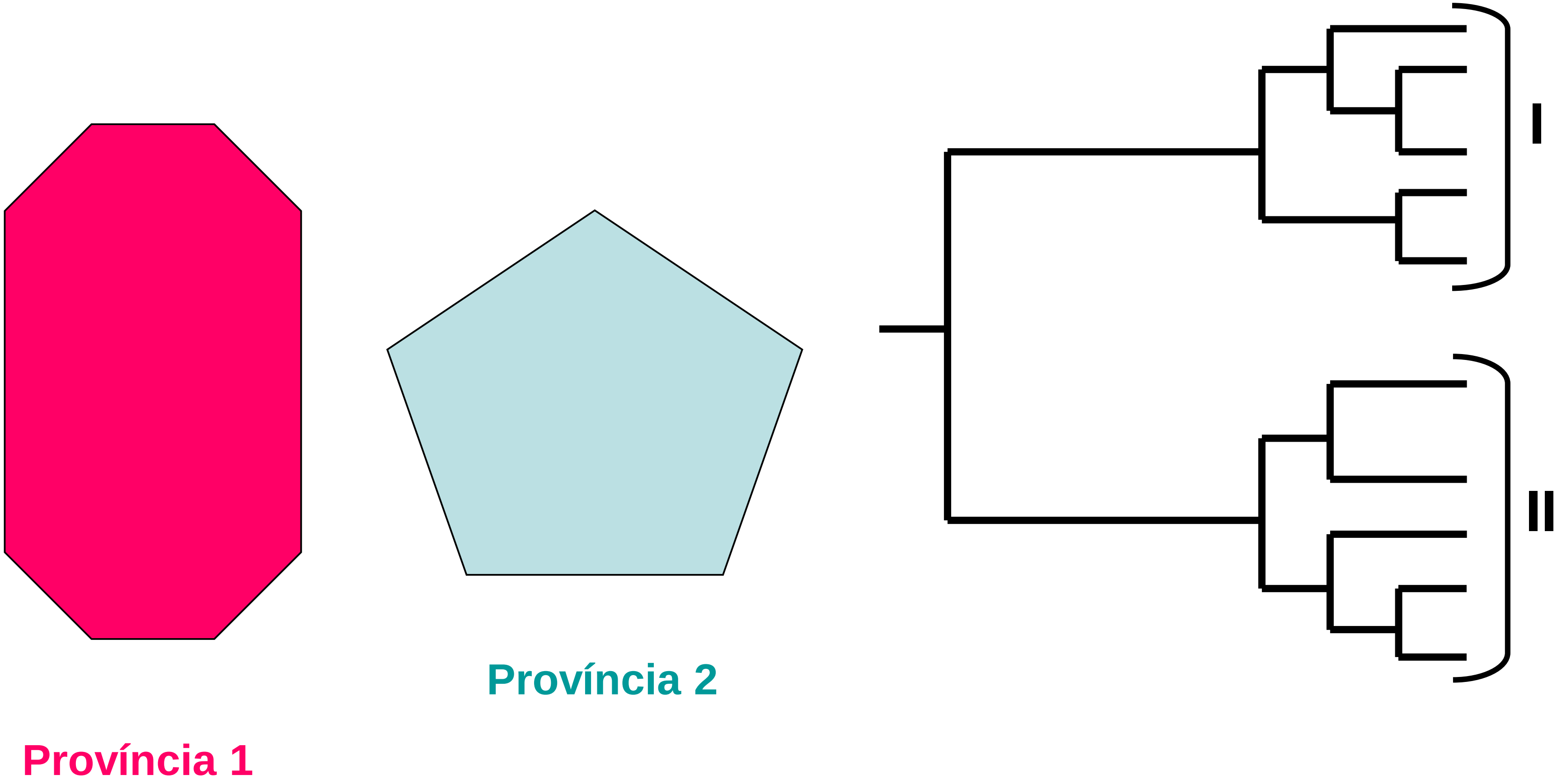
Filogeografia - Corolário 3

Concordância das partições da árvore de genes entre múltiplas espécies co-ocorrentes



Filogeografia
Corolário 4

Concordância das partições da árvore de genes com limites espaciais entre prov. biogeográficas tradicionais



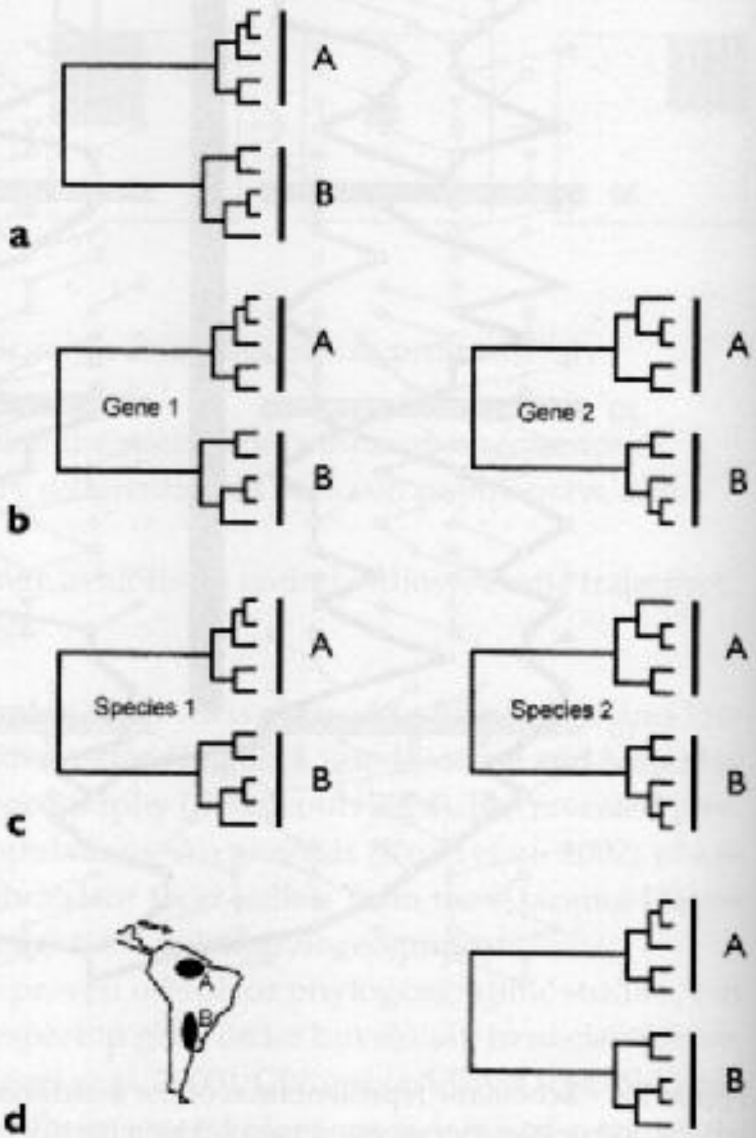


Figure 7.5 Schematic representation of four different aspects of genealogical agreement. (a) Agreement across sequence characters within a gene; (b) agreement in significant genealogical partitions across two different genes within a species; (c) agreement in the geography of gene tree partitions across two codistributed species; (d) agreement of gene tree partitions with spatial boundaries between two biotic components.

4 aspectos distintos de concordância genealógica

Morrone 2009

Padrões Filogeográficos:
as 5 categorias possíveis

segundo Avise 2000

letras = haplotipos

retângulos = grupos de haplotipos proximamente relacionados

Grandes lacunas genéticas (gaps)
-várias mutações

FILOGRUPOS

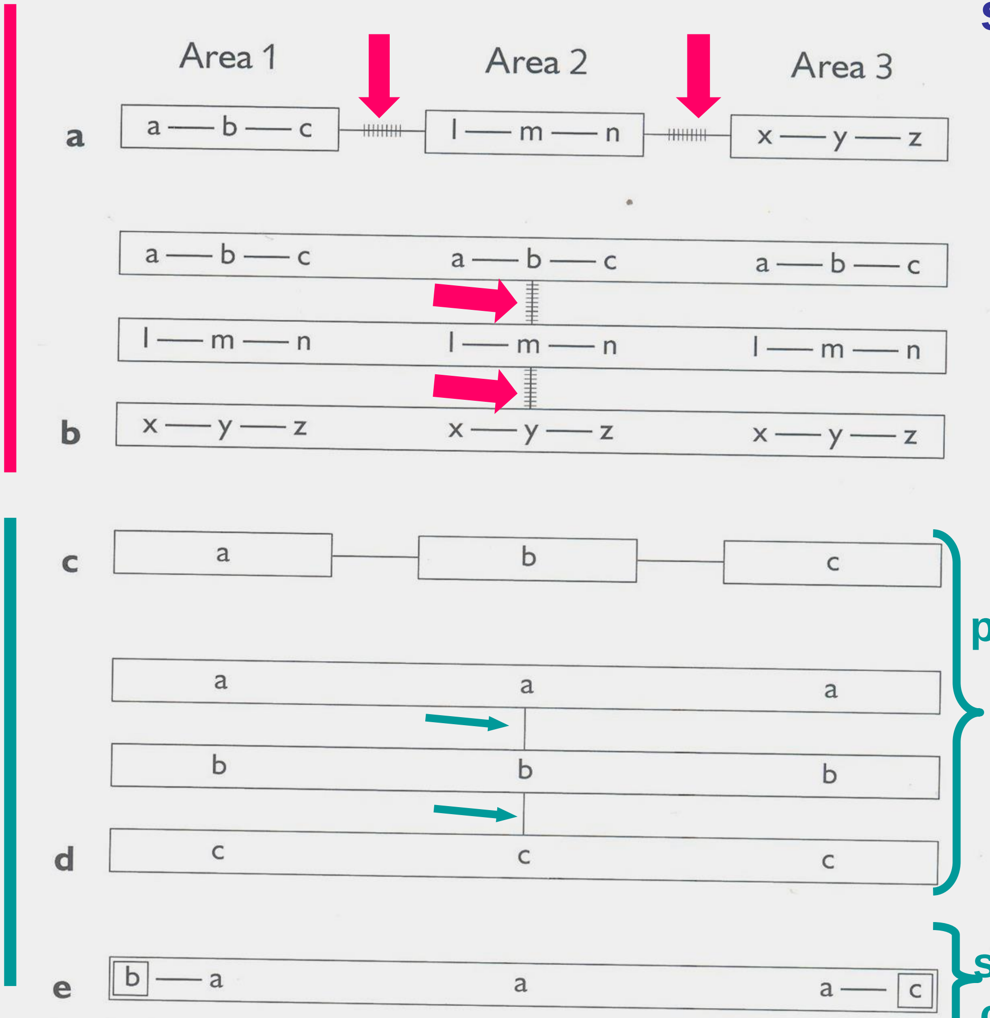


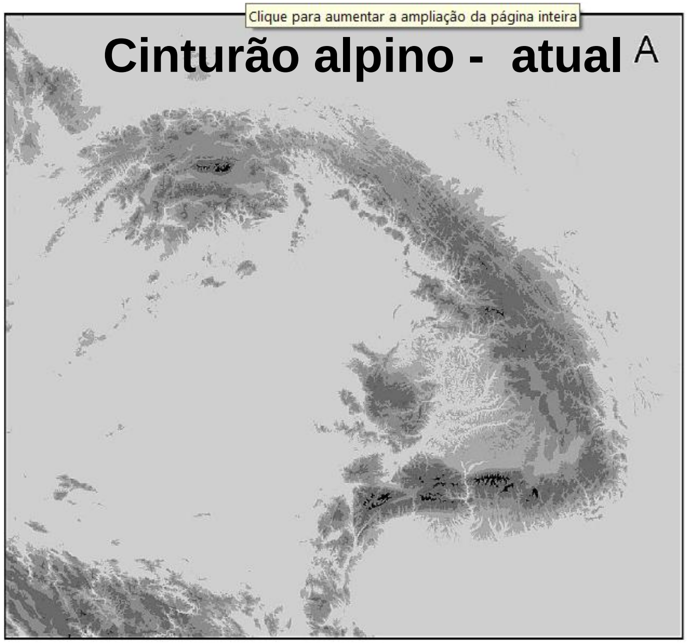
Figure 7.6 Different phylogeographic patterns for mtDNA gene cladograms. (a) Category I (deep gene tree, major lineages allopatric); (b) Category II (deep gene tree, major lineages broadly sympatric); (c) Category III (shallow gene tree, lineages allopatric); (d) Category IV (shallow gene tree, lineages sympatric); (e) Category V (shallow gene tree, major distributions varied).

Sem grandes lacunas genéticas (gaps)
- uma mutação

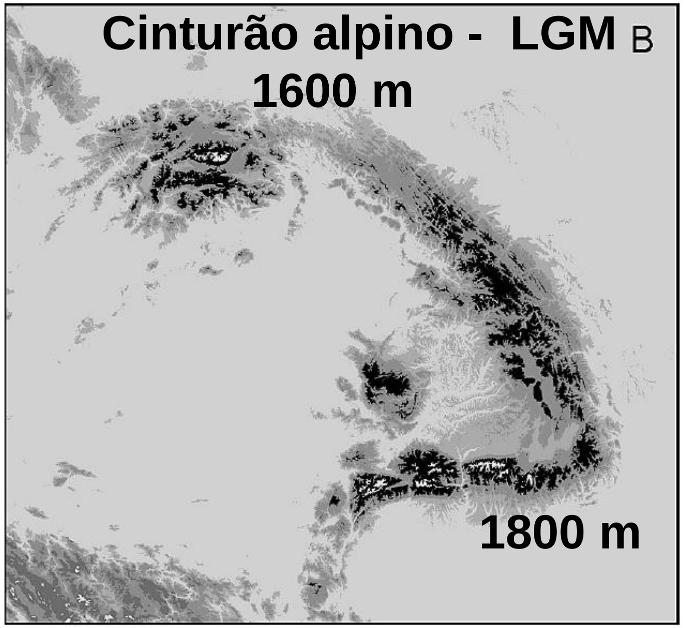
padrões similares a a e b, porém <u>mais recentes</u>, resultantes de histórias de vida, não de atributos biogeográficos

sp com fluxo gênico contínuo entre pops

(Morrone 2009)

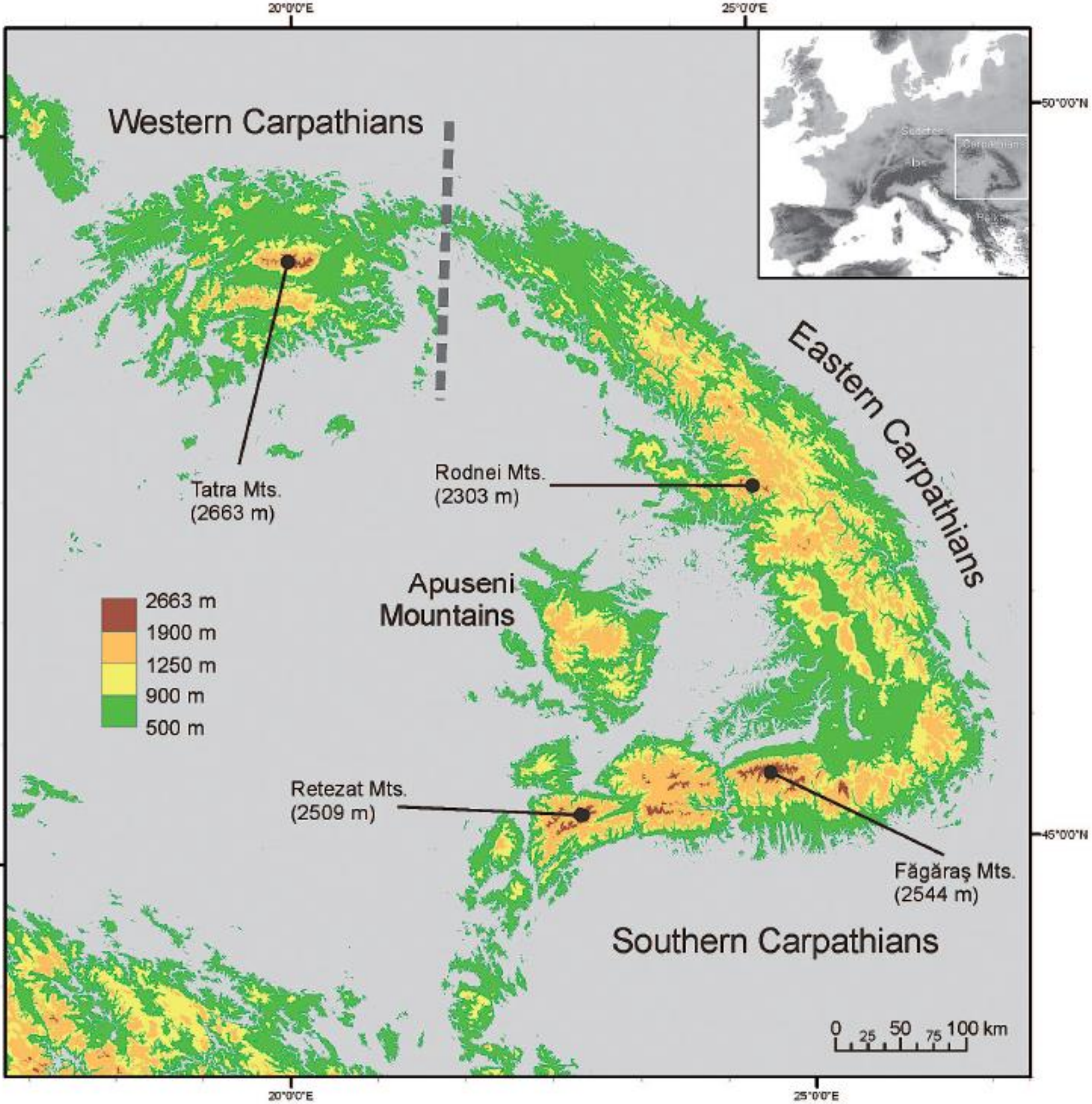


Cinturão alpino - atual



Cinturão alpino - LGM
1600 m

1800 m



Filogeografia nos Cárpatos

Ronikier 2011

Cárpatos

Ronikier 2011

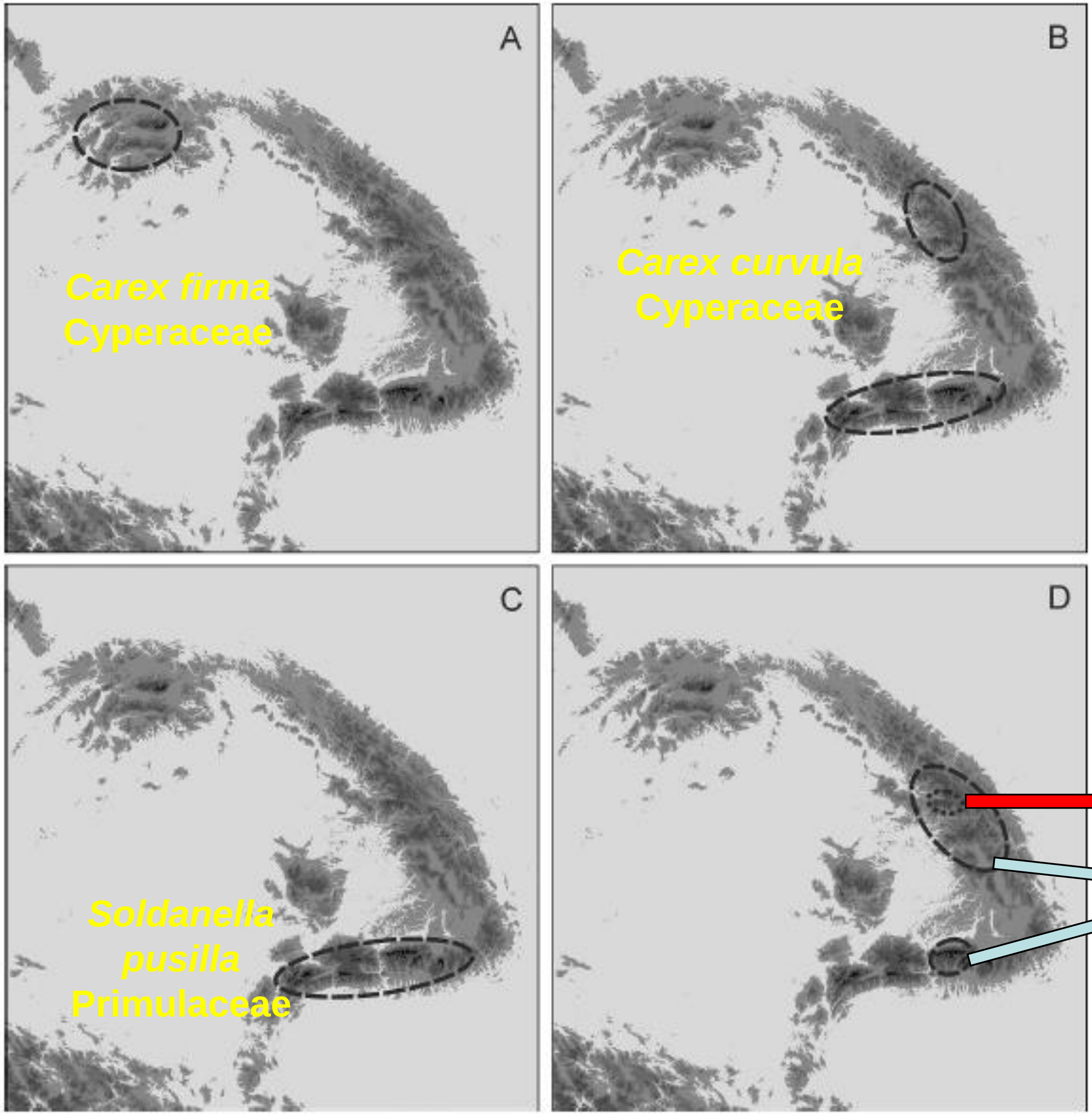


Fig. 3. Examples of floristic distributions shaping the phytogeographical divisions of the Carpathians (schematically outlined by dashed lines). **A,** Species limited in the Carpathians to the Western Carpathians: *Carex firma*; **B,** species limited in the Carpathians to the South-Eastern Carpathians: *Carex curvula*; **C,** species limited in the Carpathians to the Southern Carpathians: *Soldanella pusilla*; **D,** species endemic to the Eastern or South-Eastern Carpathians: *Silene* (*Lychnis*) *nivalis* (dotted line) and *Silene zawadzkii* (dashed line).

Silene nivalis

Silene zawadzkii

Caryophyllaceae

Cárpatos
Ronikier 2011

Campanula alpina
Campanulaceae

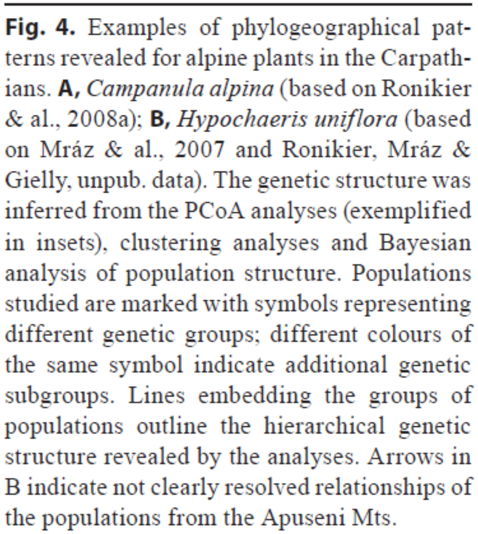
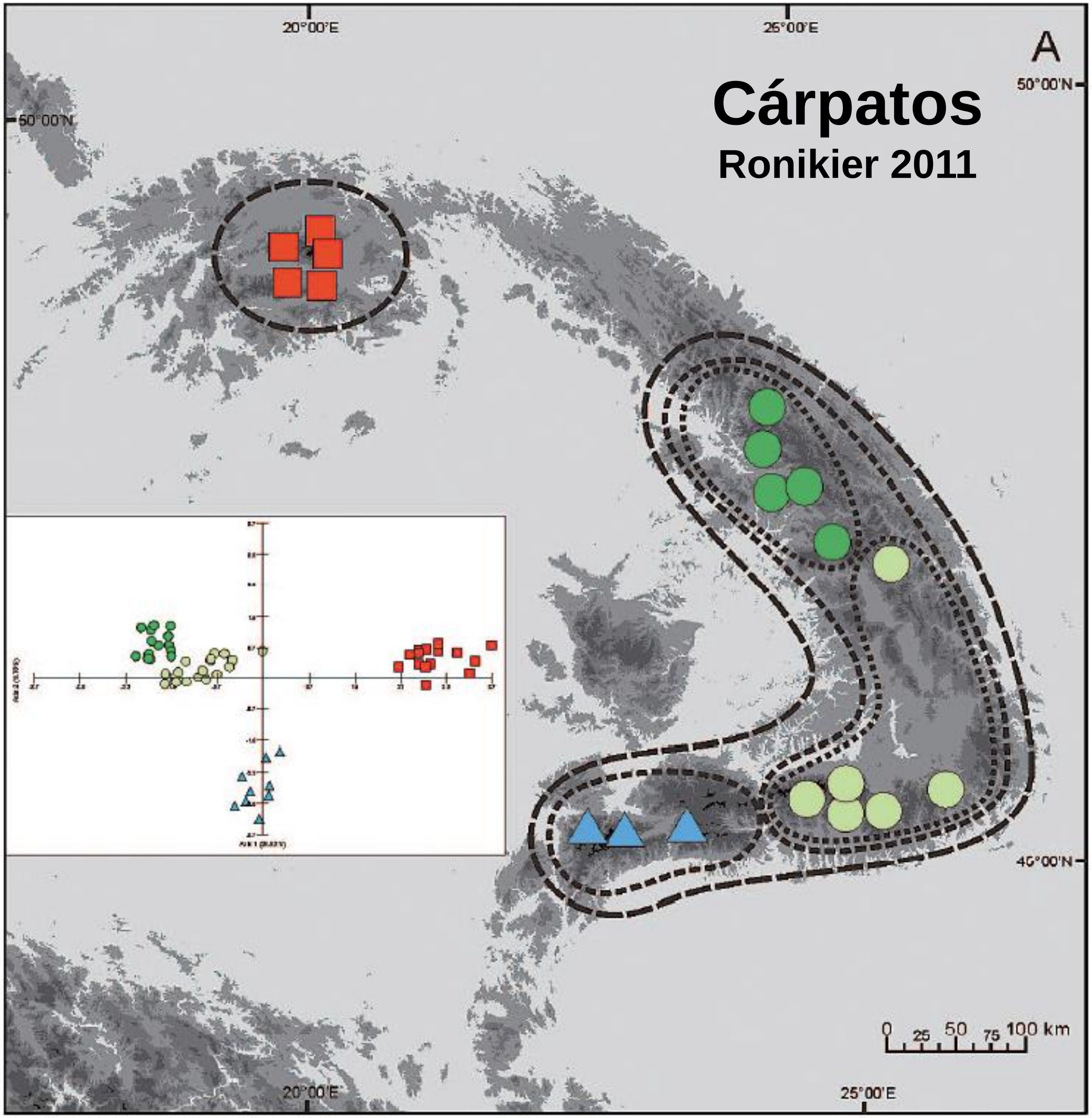


Fig. 4. Examples of phylogeographical patterns revealed for alpine plants in the Carpathians. **A,** *Campanula alpina* (based on Ronikier & al., 2008a); **B,** *Hypochaeris uniflora* (based on Mráz & al., 2007 and Ronikier, Mráz & Gielly, unpub. data). The genetic structure was inferred from the PCoA analyses (exemplified in insets), clustering analyses and Bayesian analysis of population structure. Populations studied are marked with symbols representing different genetic groups; different colours of the same symbol indicate additional genetic subgroups. Lines embedding the groups of populations outline the hierarchical genetic structure revealed by the analyses. Arrows in B indicate not clearly resolved relationships of the populations from the Apuseni Mts.



Cárpatos

Ronikier 2011

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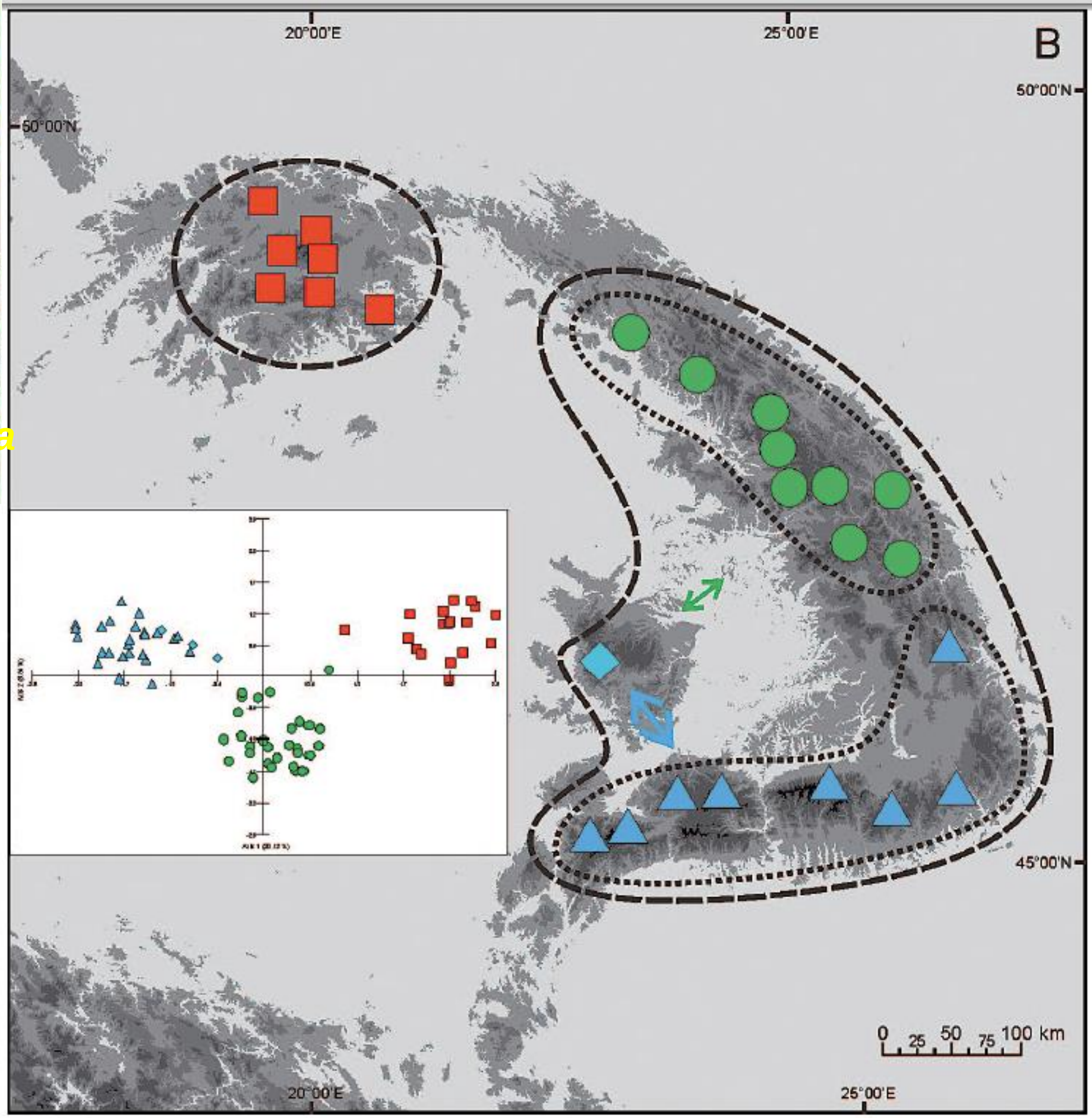

Cárpatos

Ronikier 2011

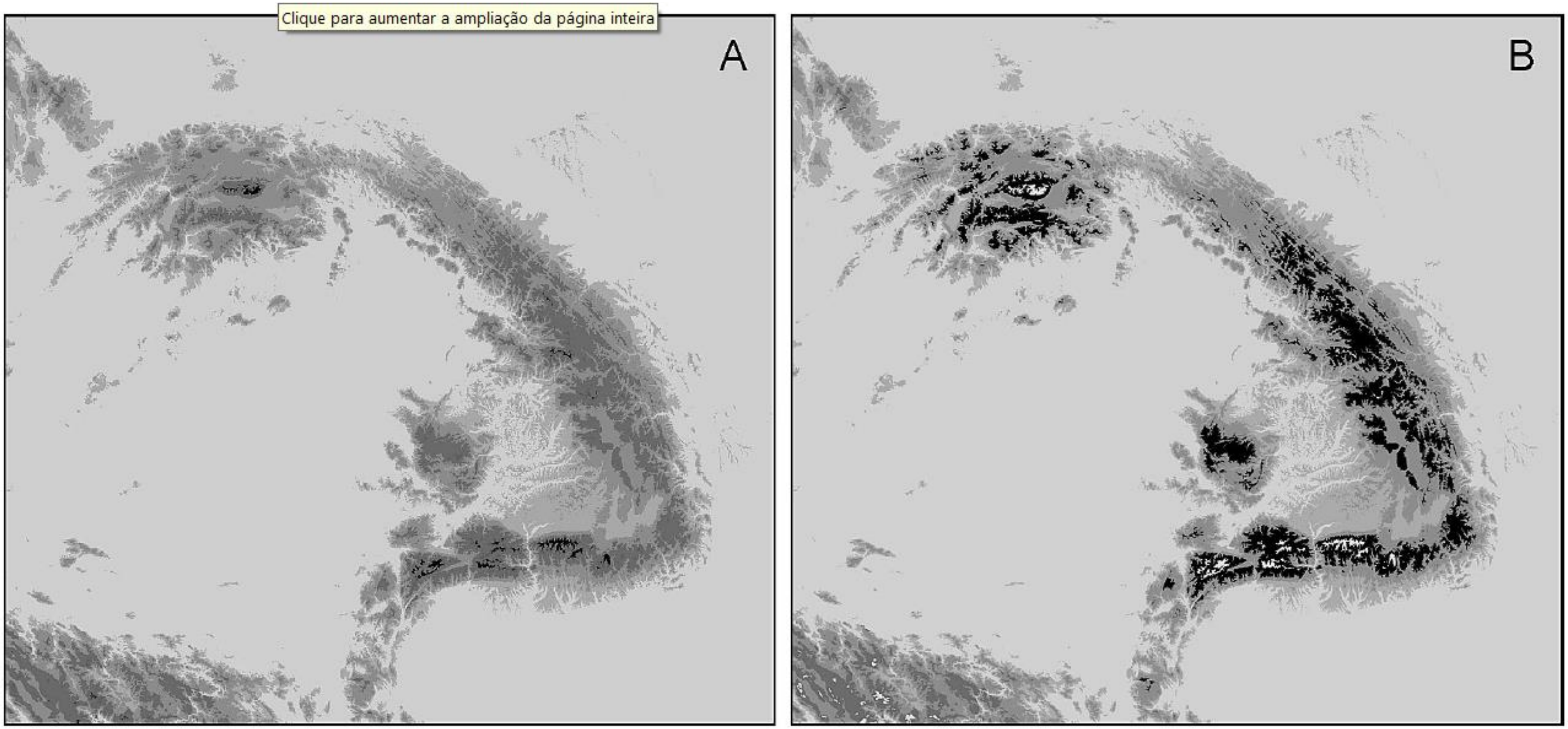

Fig. 2. Approximate extension of the alpine belt in the Carpathians. **A,** An altitudinal model of the contemporary alpine belt in the Carpathians (areas marked in black). **B,** A simplified model of the hypothetical extension of the alpine belt during the Last Glacial Maximum (LGM) in the Carpathians; in white, areas above the permanent snow line during LGM (1600 m for Western Carpathians and 1800 m for South-Eastern Carpathians); in black, extension of the alpine belt assuming a downward displacement of vegetation belts equivalent to the depression of the snowline (cf. Tribsch & Schönswetter, 2003). It should be noted that treeless areas extended over even larger areas and that in the highest massifs with permanent snow cover local glaciers were developed (see also text).

AFLPs, RAPDs, isozimas:

Proteopsis argentea, Asteraceae (isozimas) – Jesus et al. 2001
Cryptocarya aschersoniana, Lauraceae (isozimas) – Moares & Derbyshire 2003
Machaerium villosum, Leg.Pap. (isozimas) - Botrel & Carvalho 2004
Eschweilera ovata, Lecythidaceae (isozimas) – Gusson et al. 2005
Bromus auleticus, Poaceae (isozimas e RAPDs) - Yanaka et al. 2005

Microssatélites (SSRs) e sequenciamento de marcadores genômicos plastidiais (como íntron *trnL* e o espaçador intergênico *psbA-trnH*) e nucleares (espaçador não codificador *ITS* nrDNA):

Lychnophora ericoides, Asteraceae – Colevatti et al. 2009
Wunderlichia mirabilis, Asteraceae - Feres et al. 2009
Cedrela fissilis, Meliaceae - Garcia et al. 2011, Mangaravite et al. 2016
Callibrachoa spp. e *Petunia* spp., Solanaceae – Fregonezzi et al. 2012
Tabebuia impetiginosa, Bignoniaceae – Colevatti et al. 2012
Mauritia flexuosa, Arecaceae – Lima et al. 2014

Amostragens crescentes: 12 populações, 192 indivíduos (Collevati et al. 2009); 40 pops, 220 indivíduos (Novaes et al. 2010)

Network analysis, AMOVA (Analysis of Molecular Variance), testes de Mantel

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Network analysis, AMOVA (Analysis of Molecular Variance), testes de Mantel

Padrão comum em muitas espécies brasileiras:
variabilidade genética maior dentro das populações do que entre populações
+ ausência de correlação geográfica e genética

Molecular Ecology: INVITED REVIEW AND META-ANALYSES :

Phylogeographical patterns shed light on evolutionary process in South America

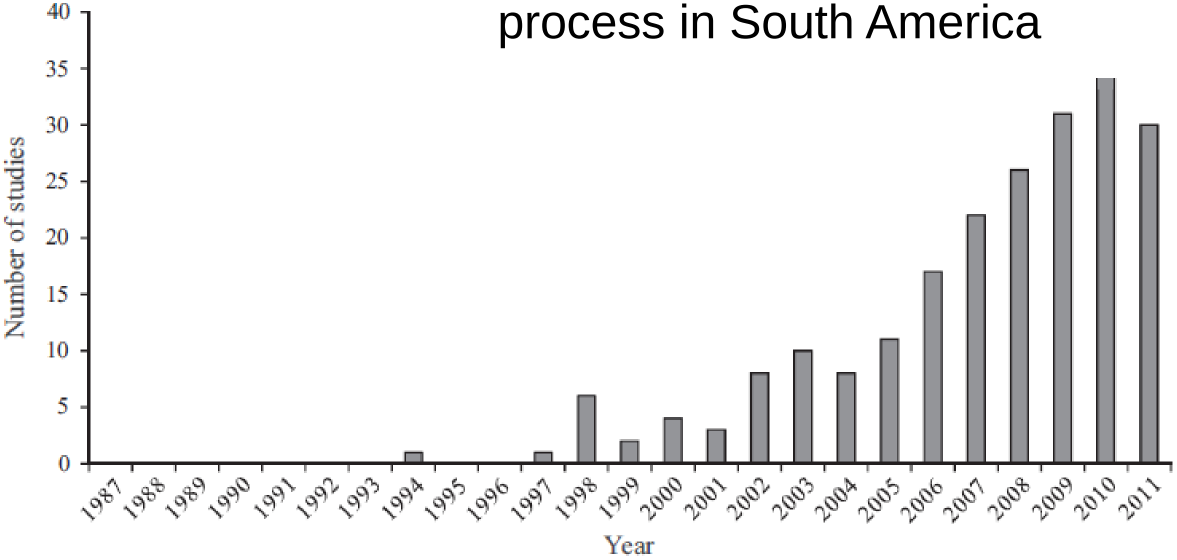

Fig. 2 Number of phylogeographical articles published between 1987 and 2011 in which organism distribution ranges encompass primarily the South American continent.

Turchetto-Zolet et al. 2012

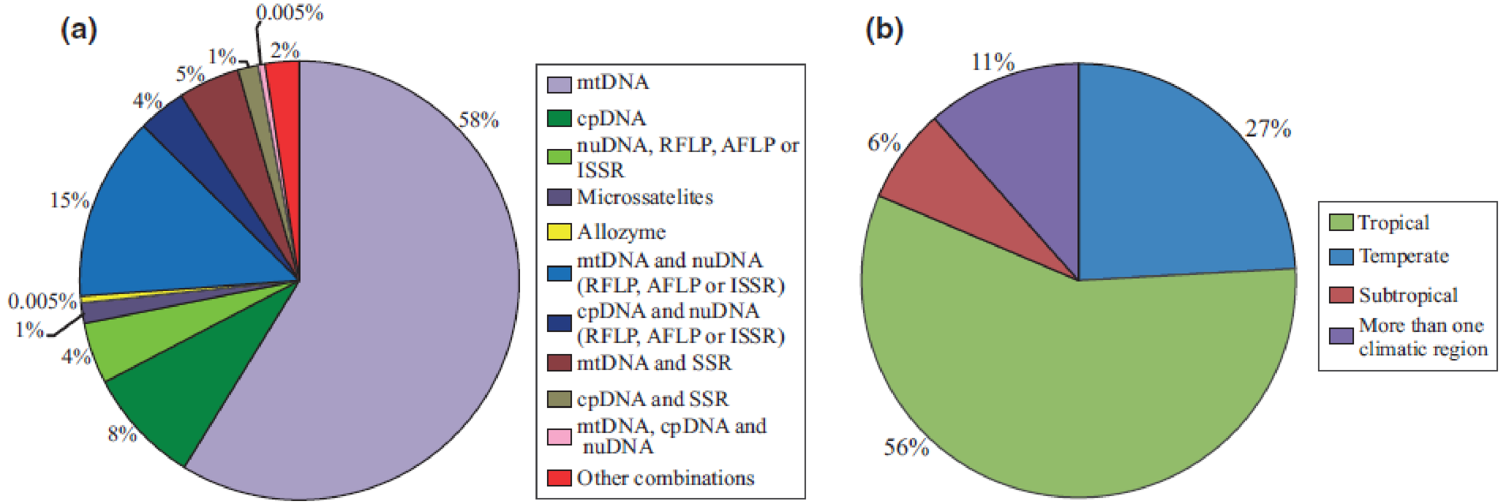

Fig. 3 Percentage of phylogeography articles published between 1987 and 2011 according to (a) classes of genetic marker or marker combinations used (categories are mutually exclusive) and (b) type of environment (see text for details).

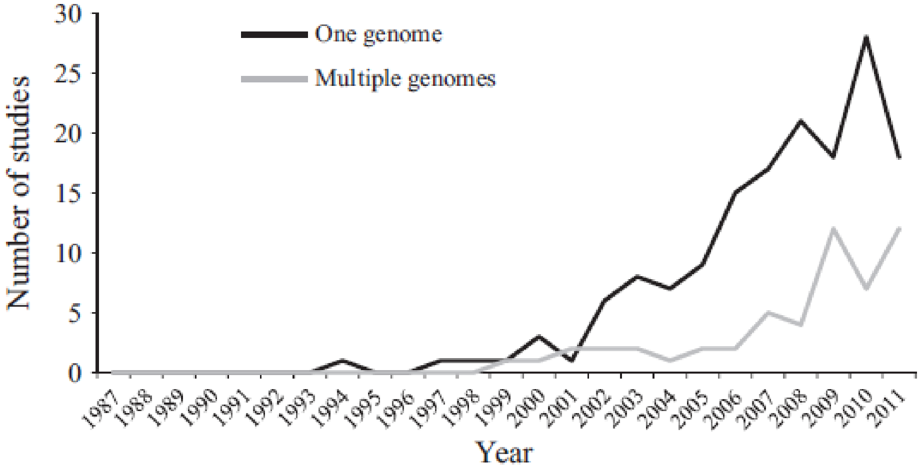

Fig. 4 Phylogeographical studies between 1987 and 2011 showing the proportion per year of those that used a single genome (black line) vs. multiple genomes (grey line).

Turchetto-Zolet et al. 2012

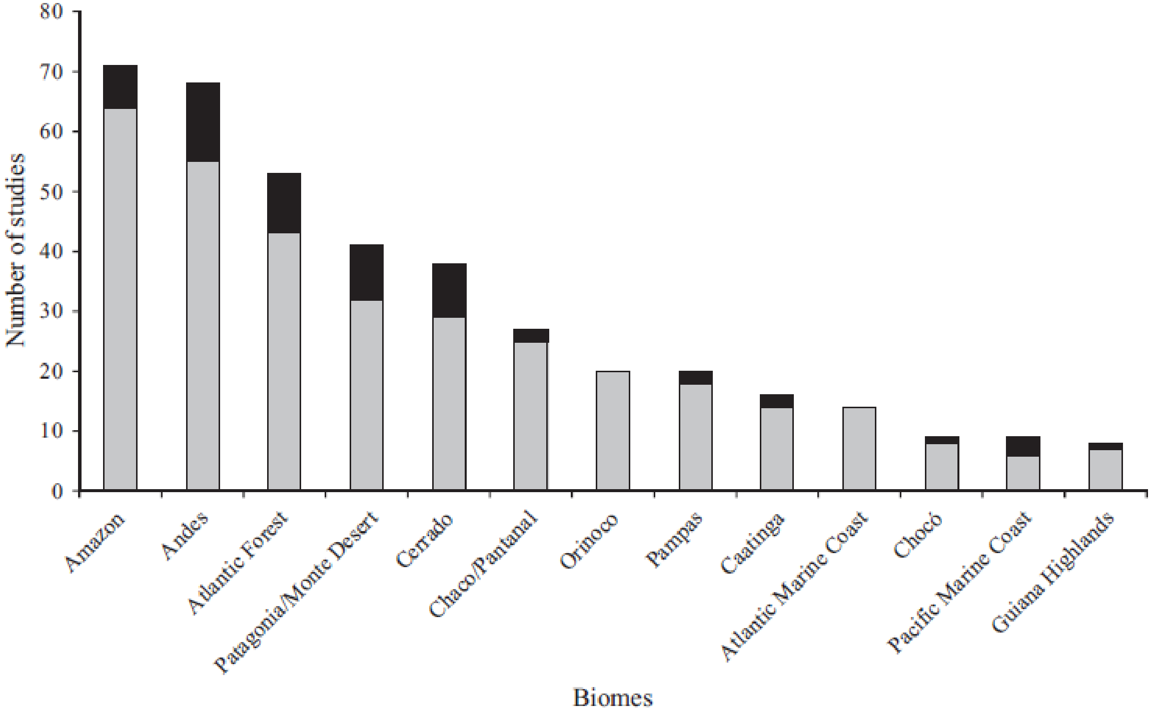

Fig. 5 Number of times that individual biomes/ecoregions were included in a phylogeographical study of South America published between 1987 and 2011 (categories are not exclusive to a certain paper, see the text for details). The corresponding numbers of times that animals (grey) and plants (black) were addressed in each biome/ecoregion are also indicated.

Andrade et al. 2009

marcadores AFLP

12 populações de *Anthurium sinuatum* e *A. pentaphyllum*

100 I. M. ANDRADE *ET AL.*

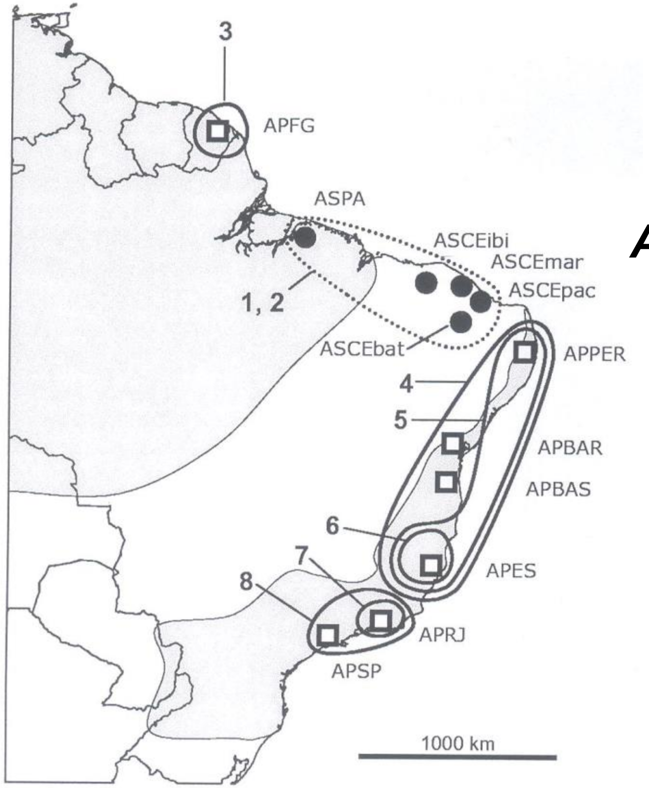

Figure 4. Genetic structure analysis of *Anthurium pentaphyllum* and *A. sinuatum* showing pure genetic clusters plotted geographically. Lines group the populations that contributed individuals to the numbered genetic clusters. The dotted line shows clusters (1, 2) consisting of *Anthurium sinuatum* individuals only. Full lines show clusters (3–8) composed of *A. pentaphyllum* individuals only. Filled circles are *A. sinuatum* populations; open squares are *A. pentaphyllum* populations. Approximate area of Amazon and Atlantic forests prior to European colonization shown by grey tone. Analysis performed with STRUCTURE version 2.1 (Pritchard *et al.*, 2000) based on AFLP molecular data. See Table 1 for population codes.

GENETIC VARIATION IN N.E. BRAZILIAN ANTHURIUM 97

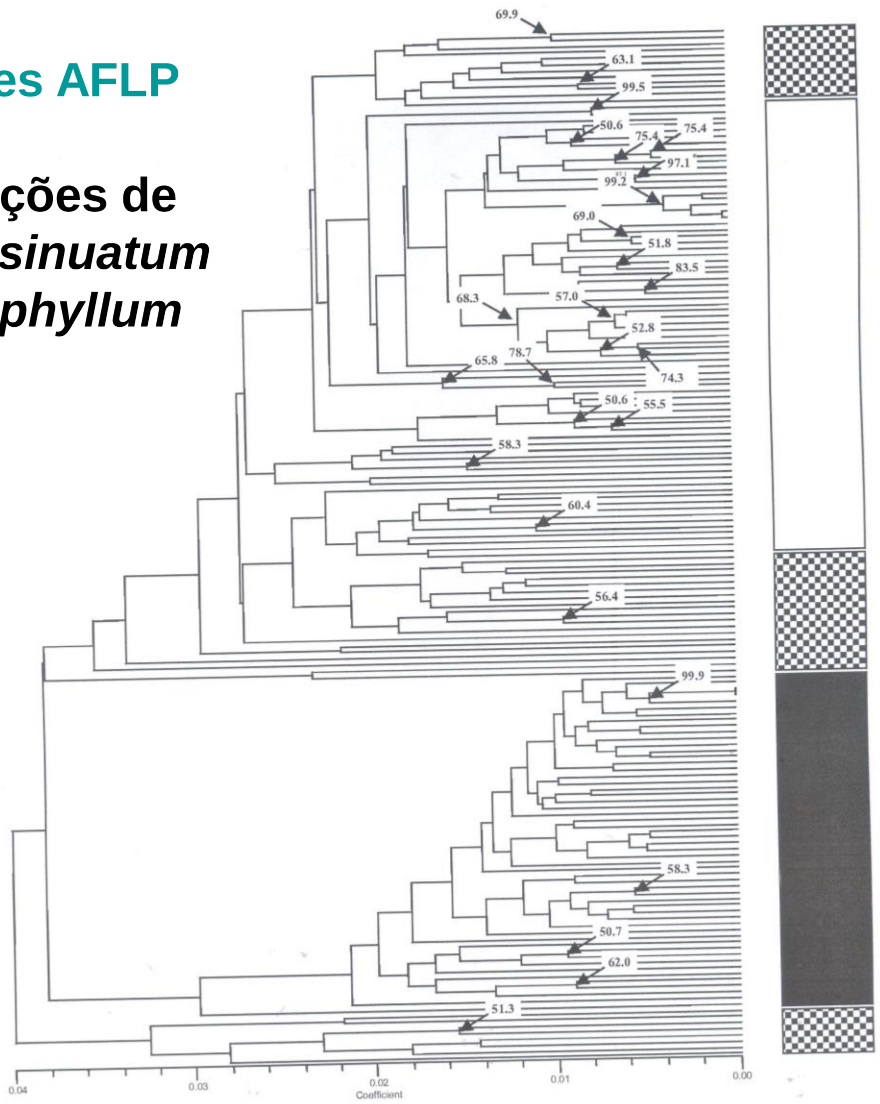

Figure 2. Unweighted pair group method with arithmetic averaging (UPGMA) cluster analysis of individuals of *Anthurium pentaphyllum* and *A. sinuatum*. Computed from AFLP molecular data with NTSYSpc version 2.2d (Rohlf, 2005) based on a distance matrix computed by RESTDIST module in PHYLIP version 3.66 (Felsenstein, 2006); bootstrap values (only those > 50% shown) derived from 1000 replicate bootstrap analysis computed in PHYLIP. Open bar, clusters containing individuals of *Anthurium pentaphyllum* only; filled bar, *Anthurium sinuatum* individuals only; chequered bars, clusters including individuals of both species.

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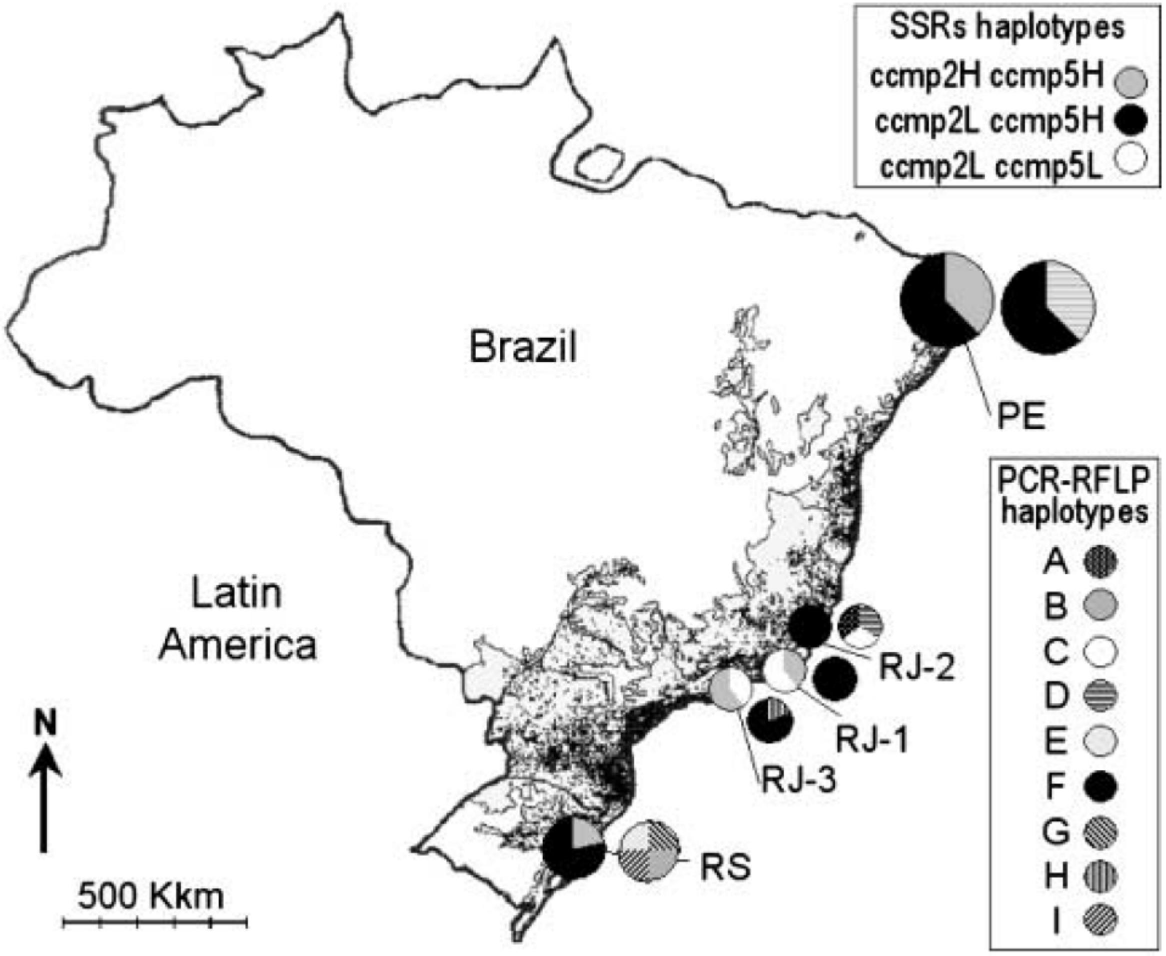
Eugenia uniflora (Myrtaceae)

- **AFLP** markers – moderate genetic variance among studied populations, with 78.9% of variability residing within populations.

Populations with a considerable genetic structure (nuclear and chloroplastic **DNA markers**).

- Data suggest the existence of different glacial refugia and a limited pollen and seed gene flow, mainly between the southern and the other regions enclosed in the Atlantic rain forest.

Population differentiation in *Eugenia uniflora*



Salgueiro *et al.* 2004

Figure 1 Location of five *E. uniflora* populations on the Brazilian Atlantic Coast: PE (Pernambuco), RJ1 (Macaé, Rio de Janeiro), RJ2 (Rio de Janeiro, Rio de Janeiro), RJ3 (Ilha Grande, Rio de Janeiro), RS (Gravataí and Capivari, Rio Grande do Sul). Each pair of circles represents the relative percentage of chloroplastic haplotype from microsatellites (circles at the left) or PCR-RFLP (circles at the right side) analyses in each population. Their sizes are function of the number of samples. The region corresponding to the Atlantic rain forest domain is drawn in light to dark-grey tonalities depending on the vegetation density.

Extreme long-distance dispersal of the lowland tropical rainforest tree *Ceiba pentandra* L. (Malvaceae) in Africa and the Neotropics

Fig. 1 *Ceiba pentandra* clockwise from left (1) emergent Amazon tree with a person beside the characteristic buttress trunk (photo credit R. Gribel); (2) dehiscing fruit with kapok (photo credit A. Gentry); (3) seed enveloped in kapok (photo credit C. Dick).

Dick et al. 2007

Rainforest form	Cultivated form	Savannah form
Trunk spiny (prickles)	Trunk usually spineless	Trunk spineless
Buttress large	Buttress small	Buttress none
Branches horizontal	Branches ascending	Branches strongly ascending
Trunk straight	Trunk straight	Trunk often forked
Reproduction superannual	Reproduction annual	Reproduction annual
Leaves narrow	Leaves broader	Leaves broadest
Fruit capsule dehiscent	Fruit capsule indehiscent	Fruit capsule dehiscent
Chromosomes $2n = 80, 88$	$2n = 72–80$ (variable)	$2n = 72$

Table 1 List of morphological and cytological character differences between three forms of *Ceiba pentandra*. Only the rainforest form (column 1) is found in Africa and Neotropics. The cultivated form, which shows intermediate features, is widely planted is Southeast Asia (modified from Table 1 in Baker 1965)

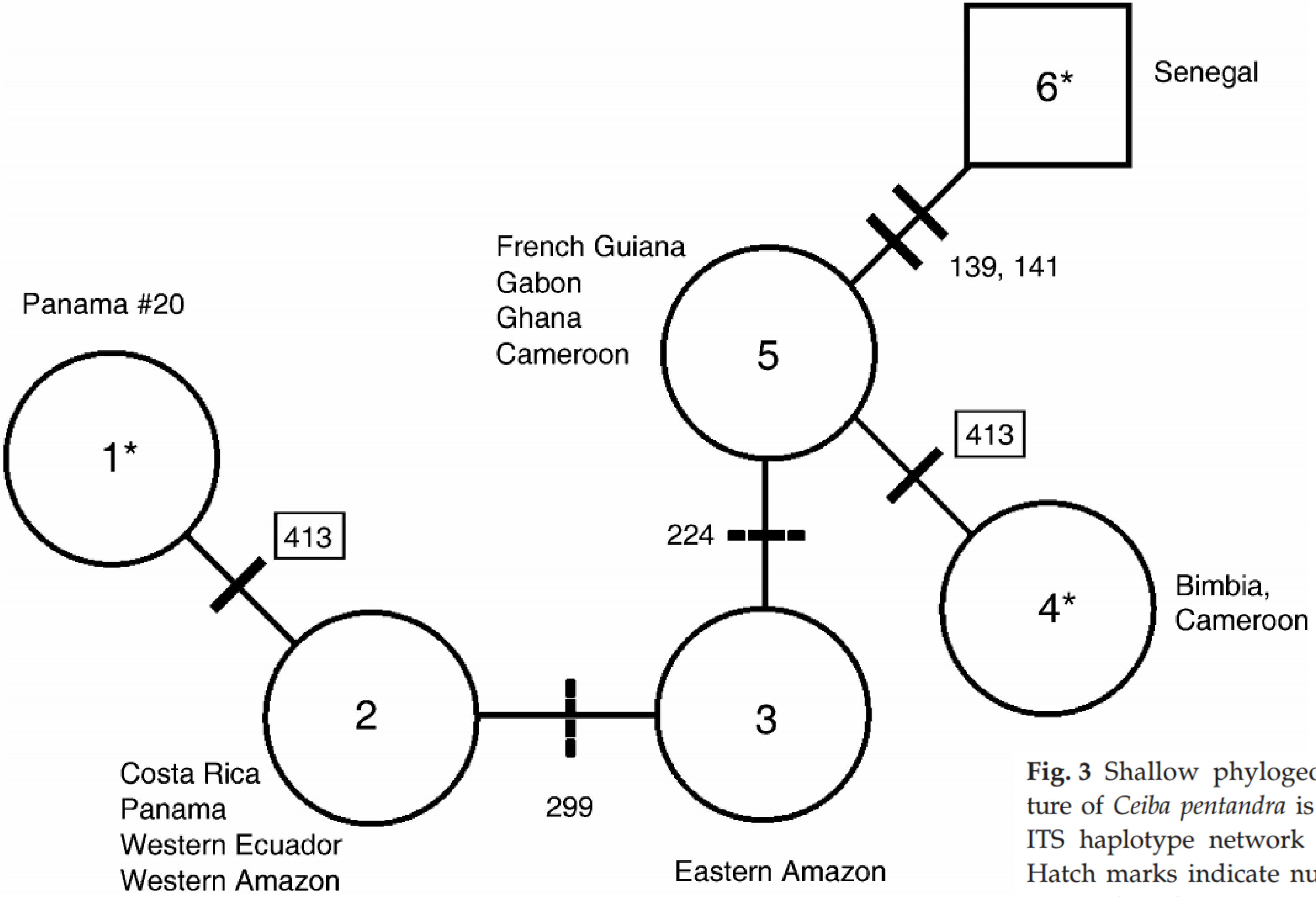


Fig. 3 Shallow phylogeographical structure of *Ceiba pentandra* is indicated by the ITS haplotype network (see also Fig. 2). Hatch marks indicate nucleotide changes at numbered positions in the consensus sequence. Sites 299 and 224, represented by dashed lines, were heterozygous in some individuals in Manaus. The substitution at site 413 is homoplasic in haplotypes 1 and 4 in this network. The squared haplotype is from the savanna form of *C. pentandra*. *represented by a single individual.

Dick et al. 2007

Extreme long-distance dispersal of the lowland tropical rainforest tree *Ceiba pentandra* L. (Malvaceae) in Africa and the Neotropics

Dick et al. 2007

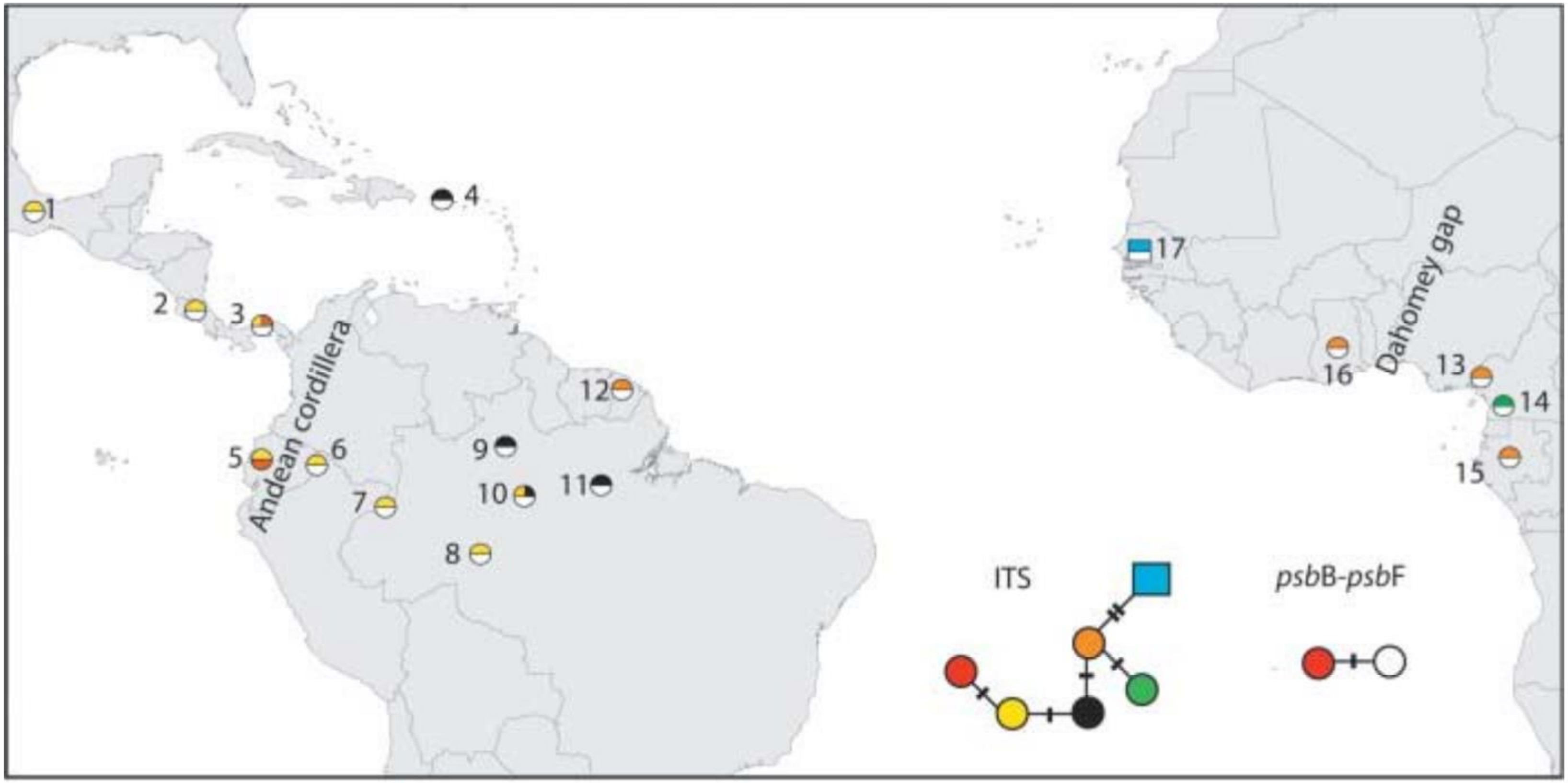


Fig. 2 Geographical distribution of ITS (upper semicircle) and *psb*B-*psb*F (lower semicircle) haplotypes sampled from Neotropical and Western African *Ceiba pentandra*. The square haplotype (site 17, Senegal) represents the savanna form. Numbered collection sites correspond to column one in Table 3. Hatches correspond to numbers of nucleotide substitutions in the haplotype networks. Identical *psb*B-*psb*F and ITS haplotypes across the Andes and between Africa and the Neotropics are evidence of long-distance dispersal.

Extreme long-distance dispersal of the lowland tropical rainforest tree *Ceiba pentandra* L. (Malvaceae) in Africa and the Neotropics

Dick et al. 2007

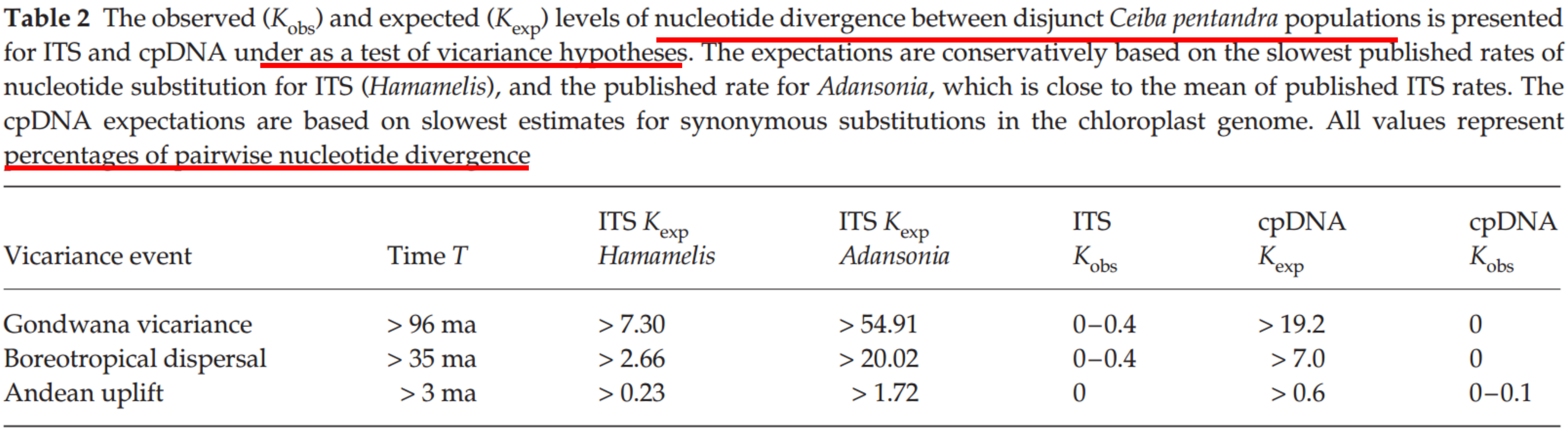
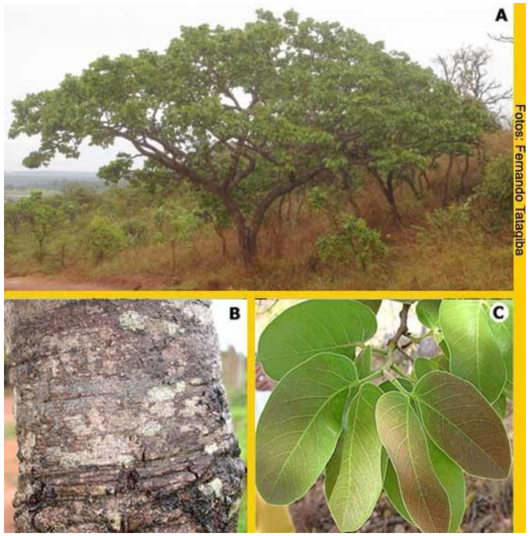


Table 2 The observed (K_{obs}) and expected (K_{exp}) levels of nucleotide divergence between disjunct *Ceiba pentandra* populations is presented for ITS and cpDNA under as a test of vicariance hypotheses. The expectations are conservatively based on the slowest published rates of nucleotide substitution for ITS (*Hamamelis*), and the published rate for *Adansonia*, which is close to the mean of published ITS rates. The cpDNA expectations are based on slowest estimates for synonymous substitutions in the chloroplast genome. All values represent percentages of pairwise nucleotide divergence

Vicariance event	Time T	ITS K_{exp} *Hamamelis*	ITS K_{exp} *Adansonia*	ITS K_{obs}	cpDNA K_{exp}	cpDNA K_{obs}
Gondwana vicariance	> 96 ma	> 7.30	> 54.91	0–0.4	> 19.2	0
Boreotropical dispersal	> 35 ma	> 2.66	> 20.02	0–0.4	> 7.0	0
Andean uplift	> 3 ma	> 0.23	> 1.72	0	> 0.6	0–0.1



Hymenaea stigonocarpa – Leg.Caes.

Ramos et al. 2007

Ramos et al. — *Phylogeography of* Hymenaea stigonocarpa 1221

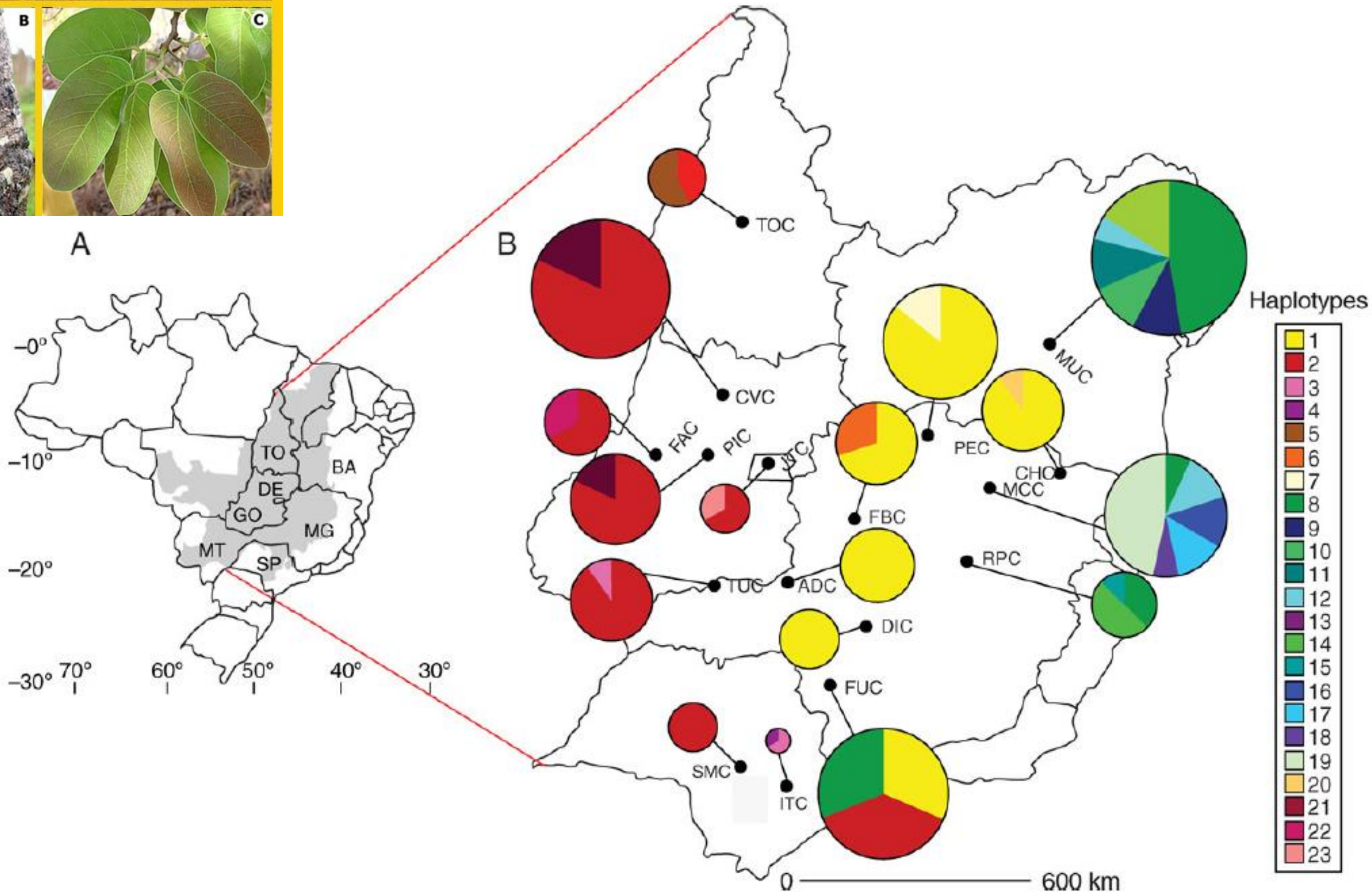


FIG. 1. (A) Map of Brazil and distribution of cerrado vegetation in grey. (B) Approximate geographic location and plastid DNA haplotype frequencies of the populations of *H. stigonocarpa* studied. Circle size is proportional to sample size and colours represent the different haplotypes as shown in the key.

Plathymenia reticulata (Leguminosae-Mimosoideae) - vinhático

41 pops **trnS-trnG e trnL-trnL-trnF** **cpDNA**

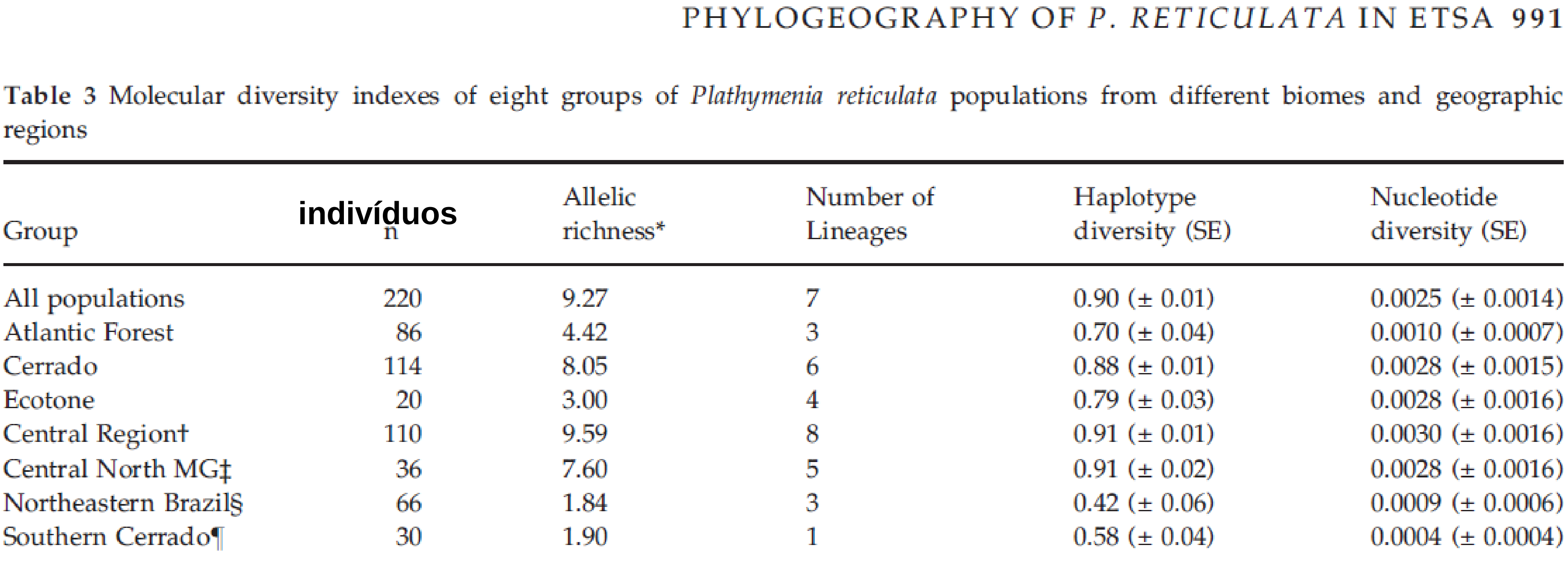


Table 3 Molecular diversity indexes of eight groups of *Plathymenia reticulata* populations from different biomes and geographic regions

Group	indivíduos n	Allelic richness*	Number of Lineages	Haplotype diversity (SE)	Nucleotide diversity (SE)
All populations	220	9.27	7	0.90 (± 0.01)	0.0025 (± 0.0014)
Atlantic Forest	86	4.42	3	0.70 (± 0.04)	0.0010 (± 0.0007)
Cerrado	114	8.05	6	0.88 (± 0.01)	0.0028 (± 0.0015)
Ecotone	20	3.00	4	0.79 (± 0.03)	0.0028 (± 0.0016)
Central Region†	110	9.59	8	0.91 (± 0.01)	0.0030 (± 0.0016)
Central North MG‡	36	7.60	5	0.91 (± 0.02)	0.0028 (± 0.0016)
Northeastern Brazil§	66	1.84	3	0.42 (± 0.06)	0.0009 (± 0.0006)
Southern Cerrado¶	30	1.90	1	0.58 (± 0.04)	0.0004 (± 0.0004)

*Allelic richness after rarefaction to 20.

†Populations from MG and GO states (see Table 1).

‡Populations delimited by the dashed rectangle in Fig. 2, i.e. CGC, GMC, IBC, JAC, J

§Populations from the Atlantic Forest to the north of the Rio Doce Valley, including t
ADE, APF, BOF, BPF, CRF, IPF, JDE, LEE, RUF, SBF and SOF.

¶Cerrado populations located at latitudes higher than 20° S, i.e. ASC, FUC, MGC, SM

G.P. Lewis

Novaes et al. 2010

Dados combinados de trnS-trnG e trnL-trnF revelaram 18 haplótipos estruturados geograficamente (8 linhagens)

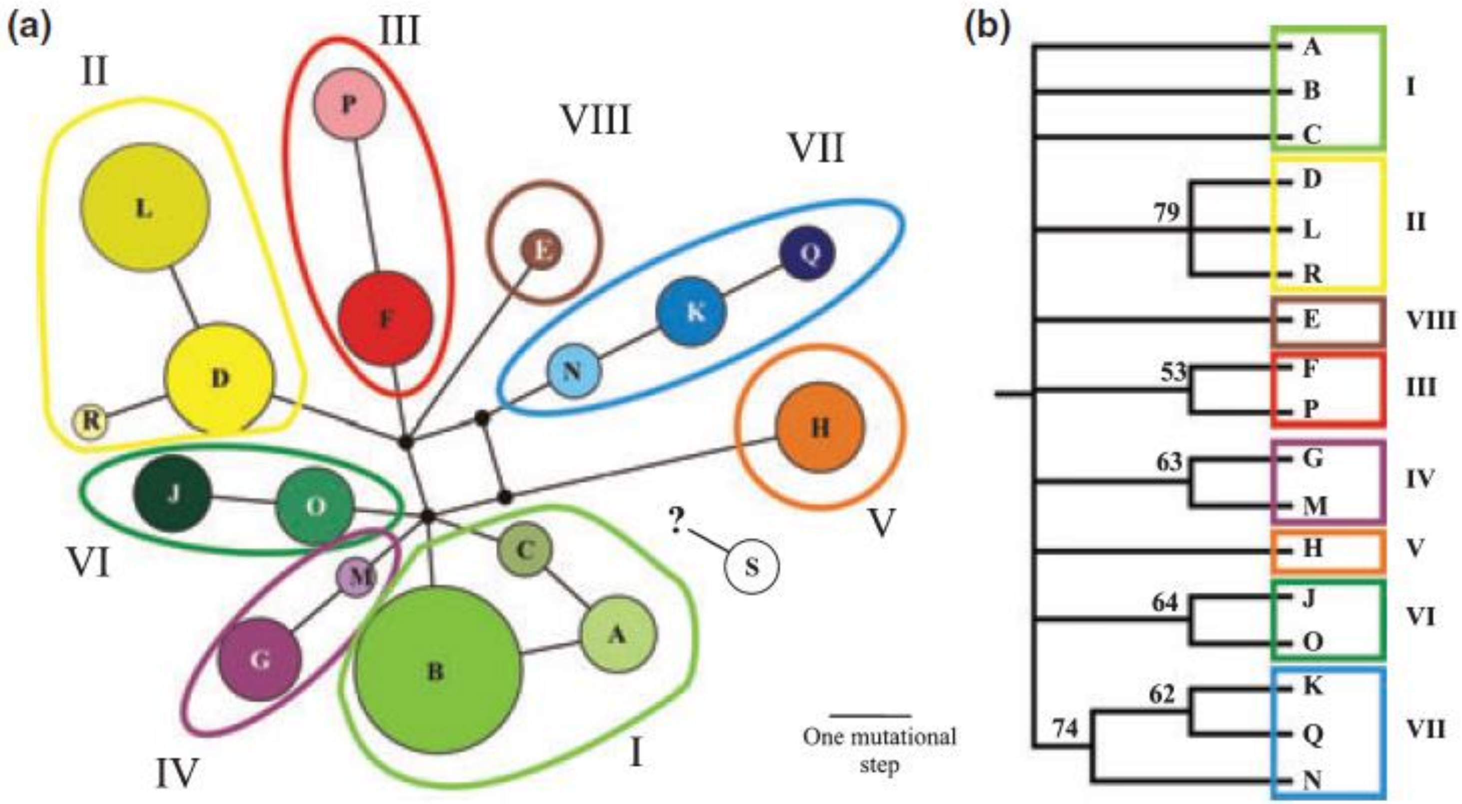
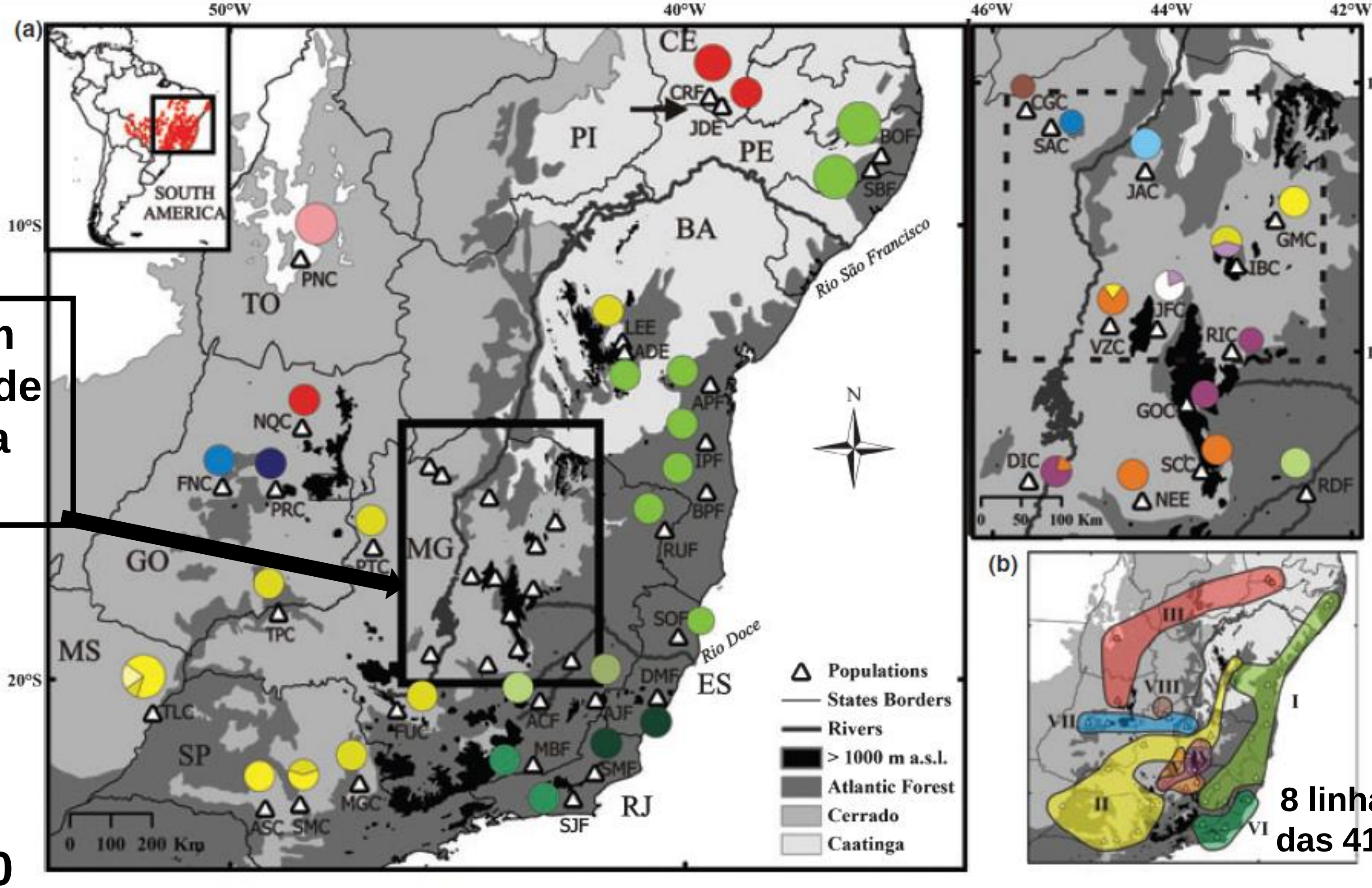


Fig. 1 Estimated relationships among the 18 cpDNA haplotypes of *Plathymenia reticulata.* (a) Statistical parsimony network and (b) maximum parsimony consensus tree with bootstrap values > 50. The haplotype and lineage codes correspond to those in Table 2 and Fig. 2. The empty circles (a) and rectangles (b) delimit the eight lineages; their colours are equivalent among them and to those in Fig. 2b. The full circles sizes (a) are proportional to the number of individuals.

Phylogeography of *Plathymenia reticulata* (Leguminosae) reveals patterns of **recent range expansion towards northeastern Brazil and southern Cerrados** in Eastern Tropical South America

Novaes et al. 2010

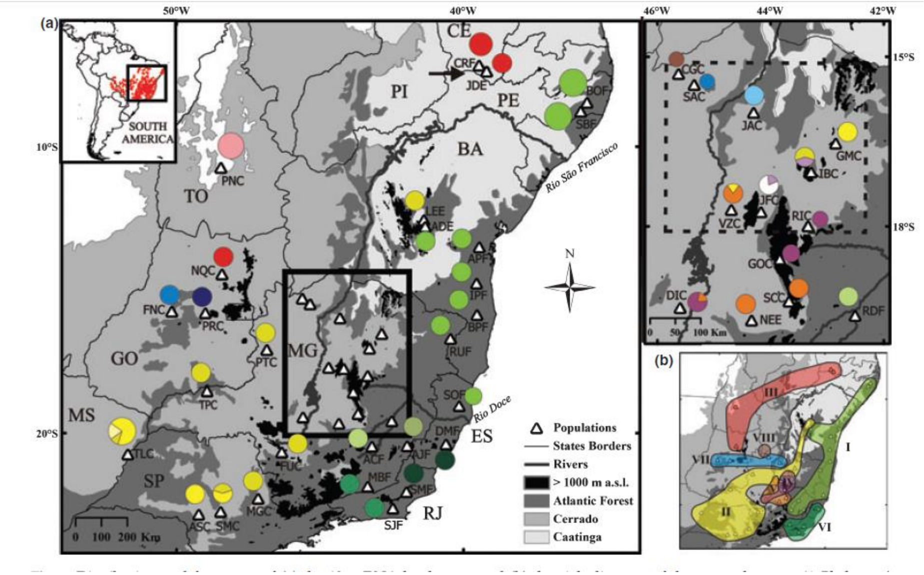
Área com diversidade genética maior

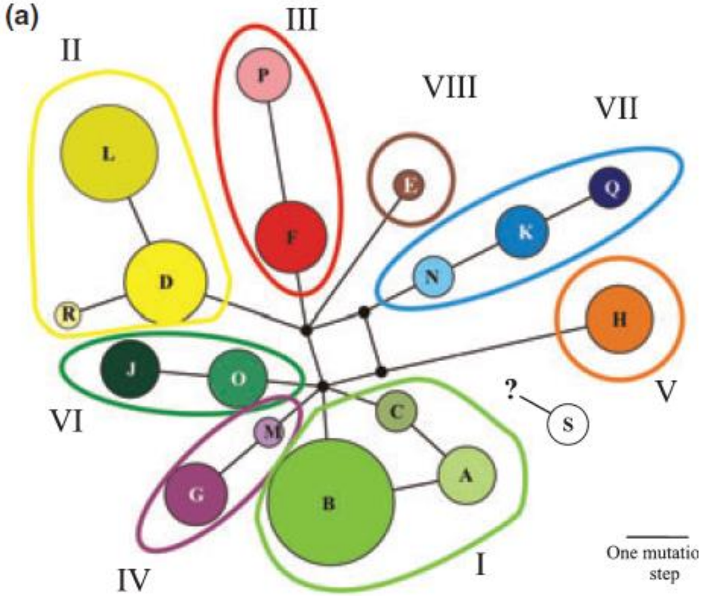


8 linhagens das 41 pops

Novaes et al. 2010

Fig. 2 Distribution and frequency of (a) the 18 cpDNA haplotypes and (b) the eight lineages of the network across 41 *Plathymenia reticulata* populations. In the South American map at the upper-left, the current distribution range of *P. reticulata* is represented in red. The distribution of ETSA biomes are in grey. The haplotype and lineage colours match those in Fig. 1. The circles sizes are proportional to the frequency of the haplotype. The dashed rectangle delimits the region in central-north MG with high genetic diversity (see text). The two-letter abbreviations correspond to Brazilian states; the three-letter abbreviations correspond to the population codes in Table 1 and their third letters represent the biome of origin of the population; C, Cerrado; E, Ecotone; F, Atlantic Forest. a.s.l., above sea level. The arrow points to forest enclaves in the northeastern Caatinga. The Brazilian states are: BA, Bahia; CE, Ceará; ES, Espírito Santo; GO, Goiás; MG, Minas Gerais; MS, Mato Grosso do Sul; PE, Pernambuco; PI, Piauí; RJ, Rio de Janeiro; SP, São Paulo; TO, Tocantins.





8 linhagens

Padrões filogeográficos:

maior diversidade genética na área central

+

poucos haplótipos das periferias são comuns aos da área central

+

"long-branched star-like network"

Padrões sugerem expansão recente da distribuição de *Plathymenia reticulata* a partir das fontes da região central.

Origem recente das espécies (Pleistocene inferior) ou extinção de algumas pops devido a climas mais secos ou mais frios no LGM ?

Novaes et al. 2010

Tibouchina papyrus (Melastomataceae) - árvore-do-papel

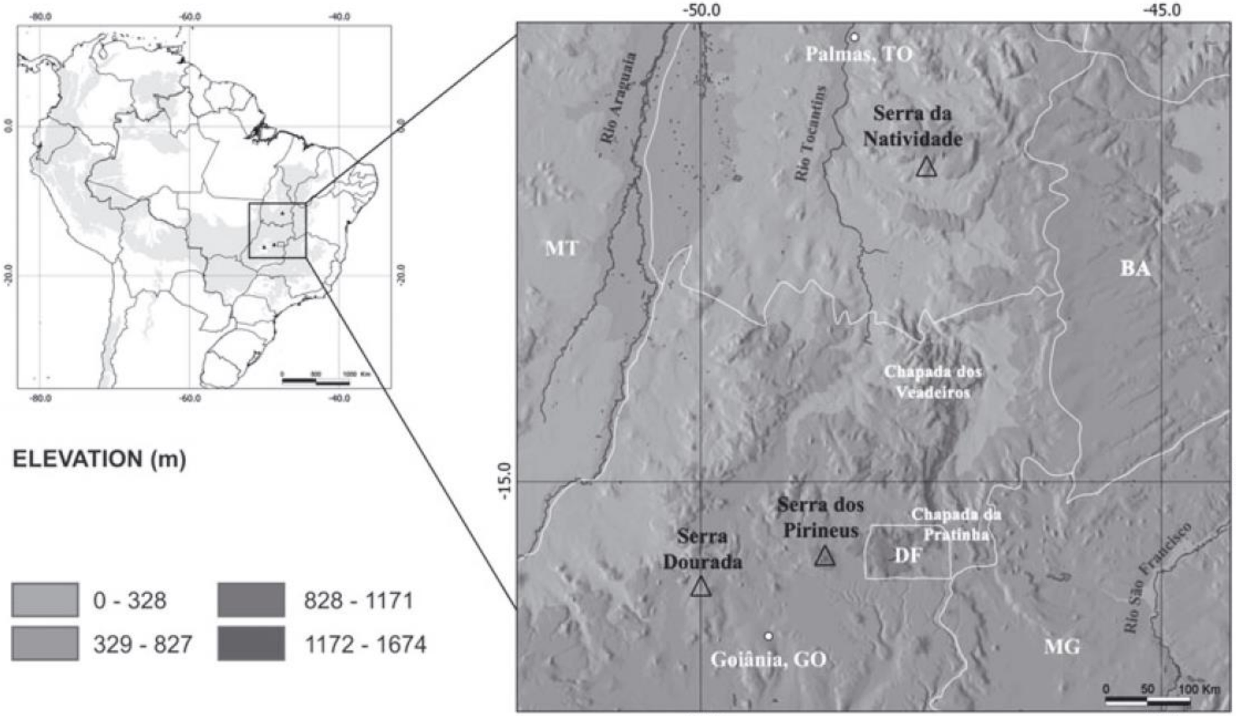


Figure 1. The sample sites of *Tibouchina papyrus* populations in Central Brazil. NAT, Serra da Natividade, Natividade, TO; PIR, Serra dos Pirineus (PIR), Pirenópolis, GO; SDO, Serra Dourada, Cidade de Goiás, GO. White lines are the state divisions. Black lines are the main rivers in the studied region.

474 indivíduos das 3 localidades:
Serra dos Pirineus, Serra Dourada, Serra de Natividade.
Polimorfismos no cpDNA e nos loci de microssatélites nucleares

Colevatti et al. 2012

Filogeografia de *Tibouchina papyrus* (Melastomataceae)

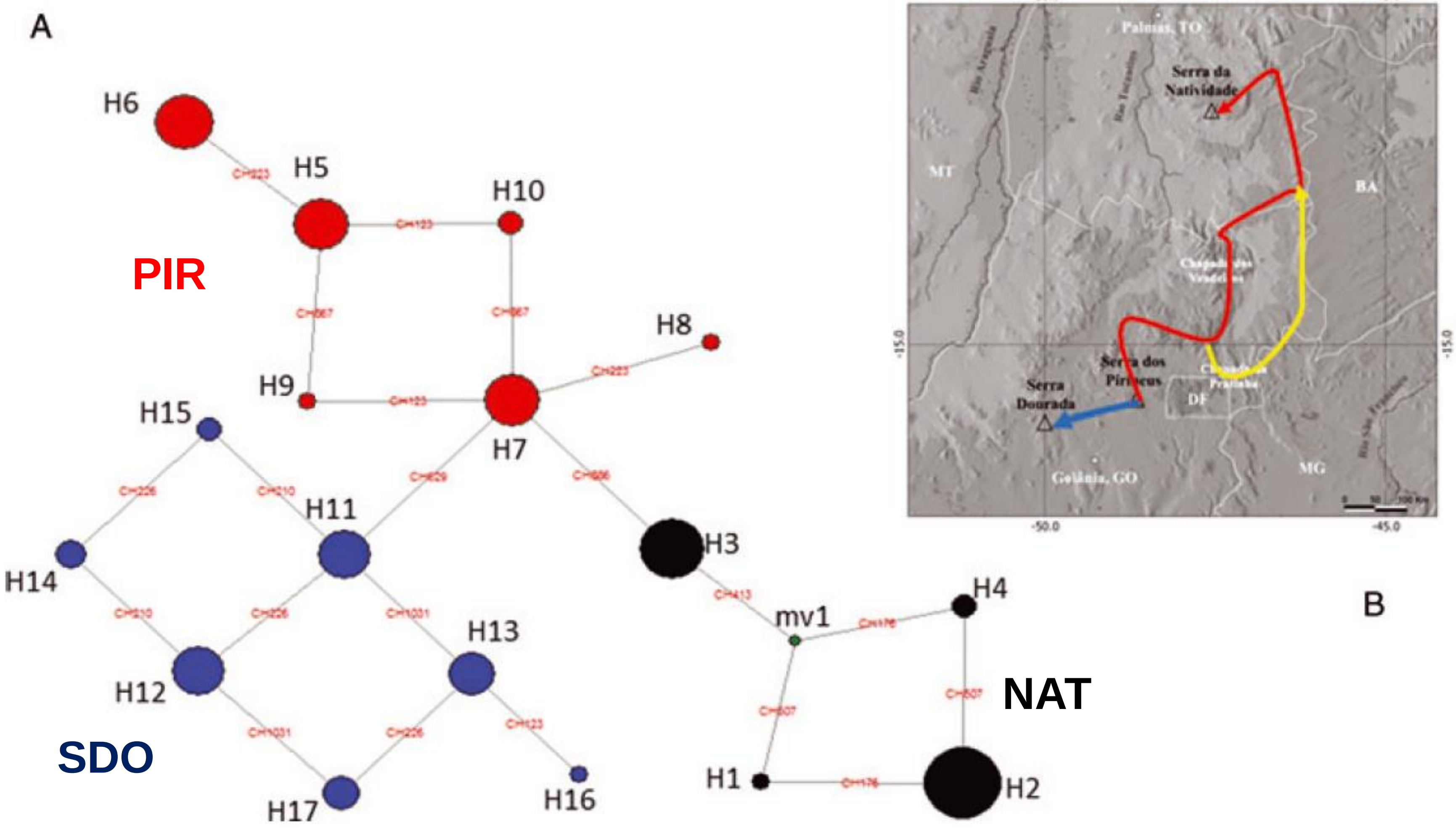


Figure 2. (A) Median-joining network based on the sequences of chloroplast noncoding regions from 96 individuals of *Tibouchina papyrus* from three localities in Central Brazil. Circumference size is proportional to the haplotype frequency. Haplotypes corresponds to those described in S1. All mutations are shown in the network, mv1, median vector. Different colors were assigned for each population: NAT, black; PIR, red; SDO, blue. (B) The model of bidirectional expansion of ancestral population from PIR to SDO and NAT. The arrows show the possible paths following the hills with two possible paths from PIR to NAT.

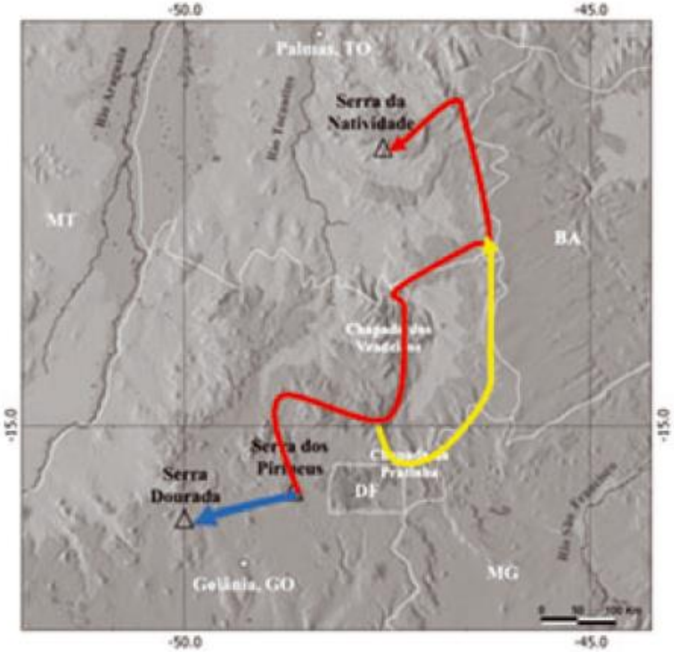
Colevatti et al. 2012

Filogeografia de *Tibouchina papyrus* (Melastomataceae)

Análise de coalescência: estimativa de tempo de divergência desde o ancestral comum mais recente (TMRCA).

Fluxo gênico entre pops das 3 áreas quase ausente + genoma plastidial com tempo de coalescência antigo: TMRCA datou de ~836.491 ± 107.515 kyr BP

distribution disjunta atual pode constituir relicto climático*:*
Expansão bidirectional da distr. geogr. original favorecida pelas condições mais secas e frias que prevaleceram em larga extensão do Brazil durante a Glaciação Pre-Illinioiana, seguida de retração à medida que o clima ficou mais quente e úmido.

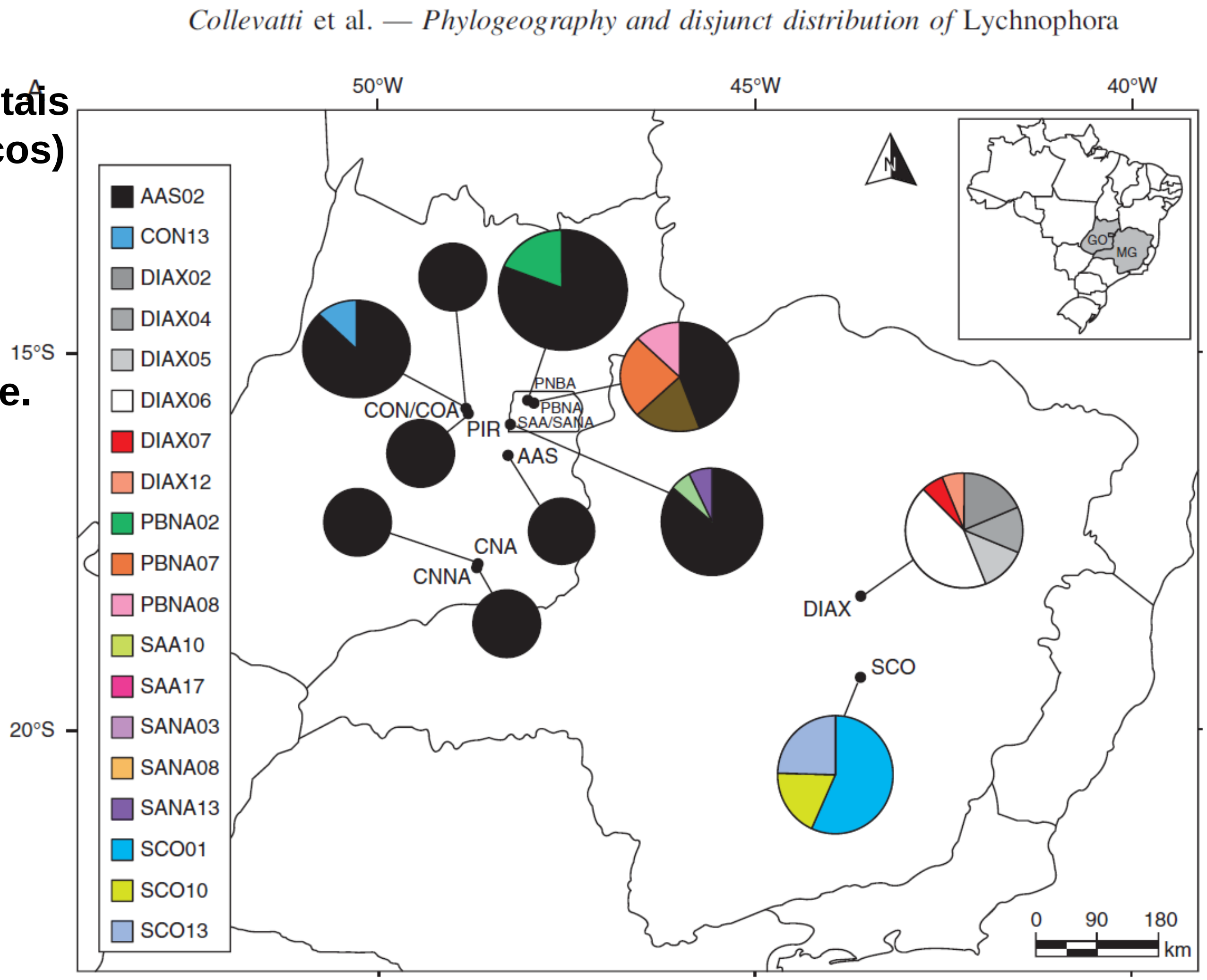


Colevatti et al. 2012

FILOGEOGRAFIA: processos genéticos demográficos

***Lychnophora ericoides*, Asteraceae** **Collevatti *et al.* 2009**

No âmbito populacional, marcas de eventos ambientais (por exemplo paleoclimáticos) podem ser notados na estruturação genética (distribuição de alelos) e distribuição espacial de populações de uma espécie.



Análises filogeográficas disponíveis permitem avaliar (corroborando ou não) hipóteses de eventos ambientais pretéritos como causadores de isolamento espacial e interrupção de fluxo gênico entre populações levando a aumento de divergência genética interpopulacional e diversificação.

***Epidendrum cinnabarinum* (A)**
***E. secundum* (B)**
Orchidaceae

Pinheiro *et al.* 2014

Rock outcrop orchids reveal the genetic connectivity and diversity of inselbergs of northeastern Brazil

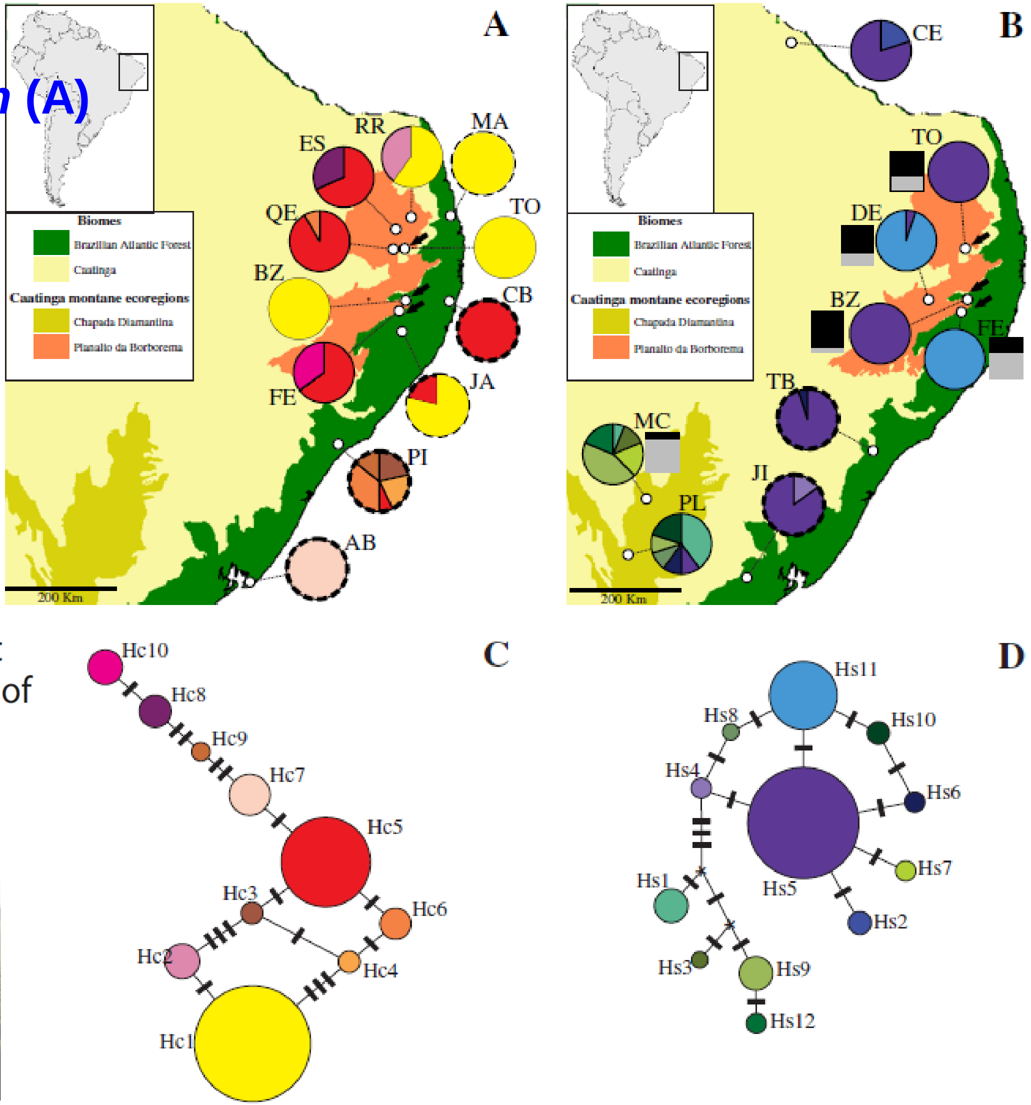


Figure 1 Geographic distribution of sampled populations. Maps showing sampled populations of *Epidendrum cinnabarinum* **(A)** and *E. secundum* **(B)**, and respective plastid DNA networks for each species **(C and D)**. Pie charts reflect the frequency of occurrence of each haplotype in each population. Haplotype colours correspond to those shown in networks. Pie charts with solid and broken outlines indicate Caatinga and Brazilian Atlantic Forest populations, respectively. Nuclear genetic groups are indicated for *E. secundum* (Nuclear cluster 1 – black; Nuclear cluster 2 – grey). In the statistical parsimony networks **(C and D)**, the haplotype frequencies are proportional to circle sizes. The number of mutations required to explain transitions among haplotypes is indicated along the lines connecting the haplotypes by cross hatches.

Genetic Structure Is Associated with Phenotypic Divergence in Floral Traits and Reproductive Investment in a High-Altitude Orchid from the Iron Quadrangle, Southeastern Brazil

Leles et al. 2015

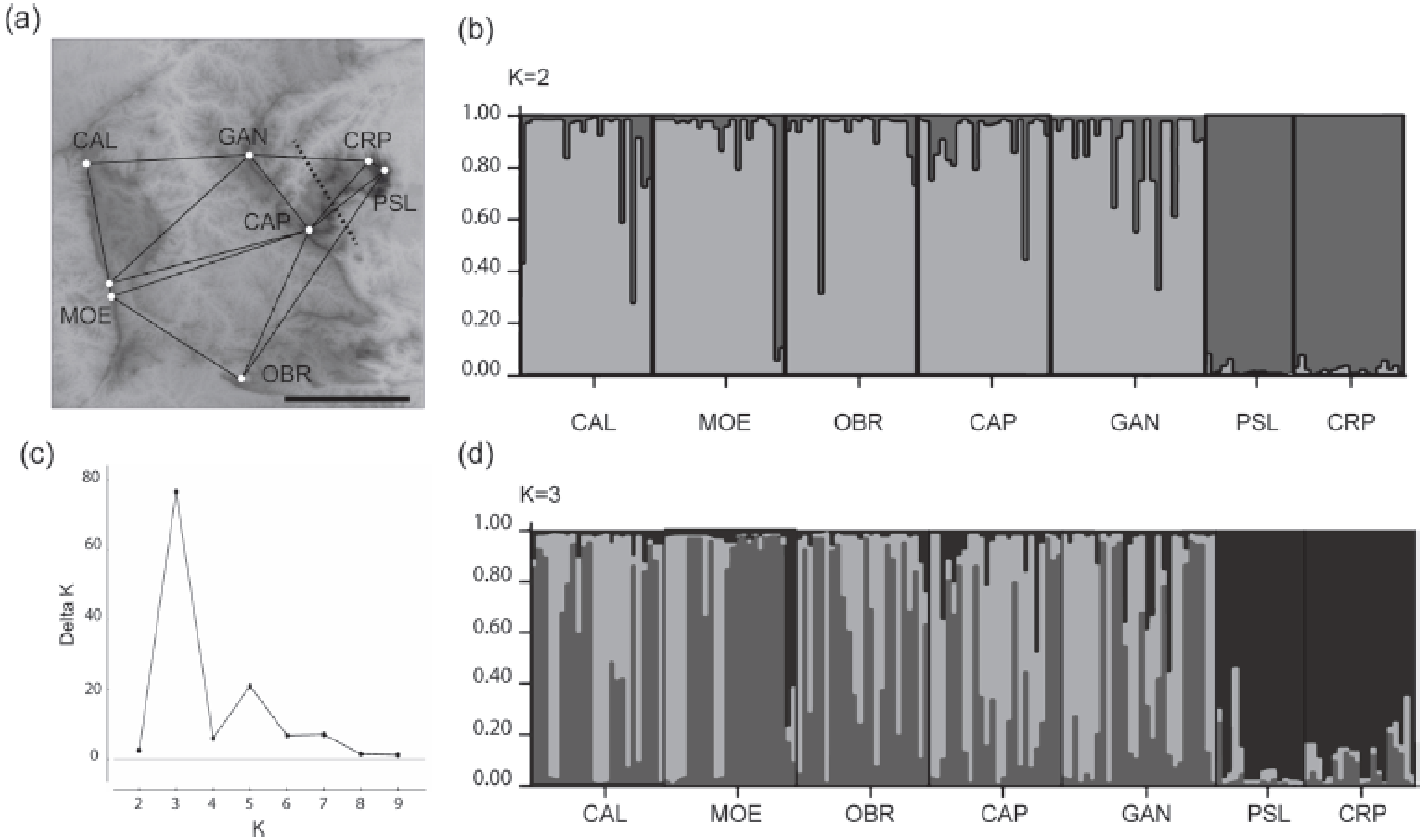


Fig 3. Genetic structure of *Cattleya liliputana* populations. (a) Genetic barrier (dotted line) estimated by Monmonier´s maximum difference algorithm. (b) Representation of Bayesian clustering analysis of seven populations of *Cattleya liliputana* based on seven microsatellite loci for *K* = 2. (c) Delta *K* graphic of the average likelihood for each *K* based on ten runs. (d) Representation of Bayesian clustering analysis of seven populations of *Cattleya liliputana* for *K* = 3. Different colours represent different genetic clusters. Populations are separated by vertical bars. For population names see Table 1.

Cattleya liliputana, Orchidaceae
Iron Quadrangle, Southeastern Brazil

Leles et al. 2015

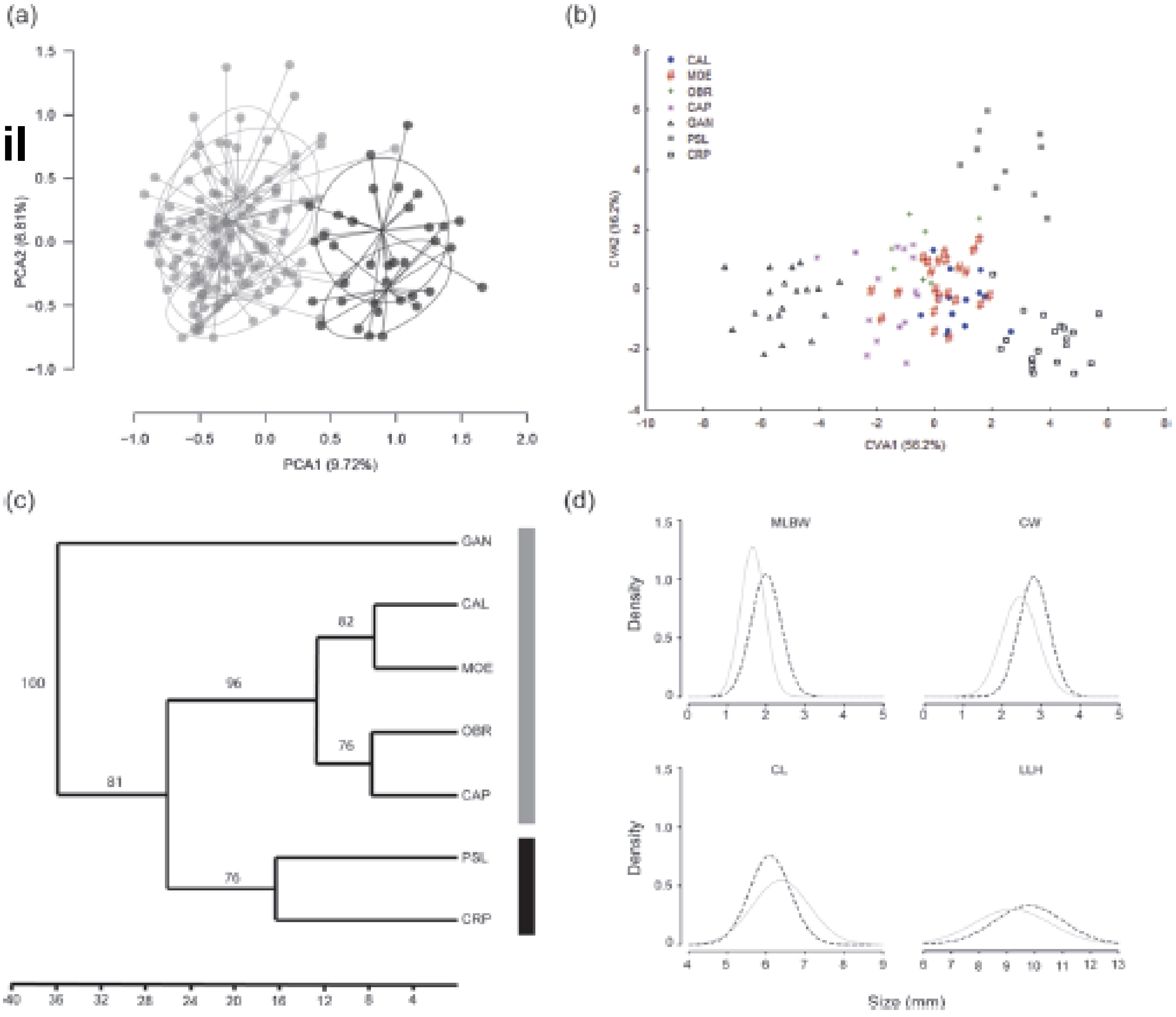


Fig 4. Morphological and genetic divergence of *Cattleya liliputana* populations. (a) Principal component analysis for microsatellite markers of Serra do Caraça (black) and core IQ (grey) individuals. (b) Representation of the scores of first and second canonical axes of CVA using 18 floral and eight vegetative continuous traits. (c) Dendrogram of morphological relationships constructed using Mahalanobis generalized distance clustered with paired group and Manhattan similarity algorithm. Bootstrap support was obtained by 1,000 replicates. Cophenetic correlation = 0.9703. (d) Phenotypic divergence in floral traits for Serra do Caraça (black dashed line) and core IQ (grey solid line). MLBL, medium lobe base width; LLH, lateral lobe high; CW, column width; CL, column length. These characters correspond to numbers 3, 7, 26 and 25,

Cattleya liliputana, Orchidaceae, Iron Quadrangle, Southeastern Brazil

Leles et al. 2015

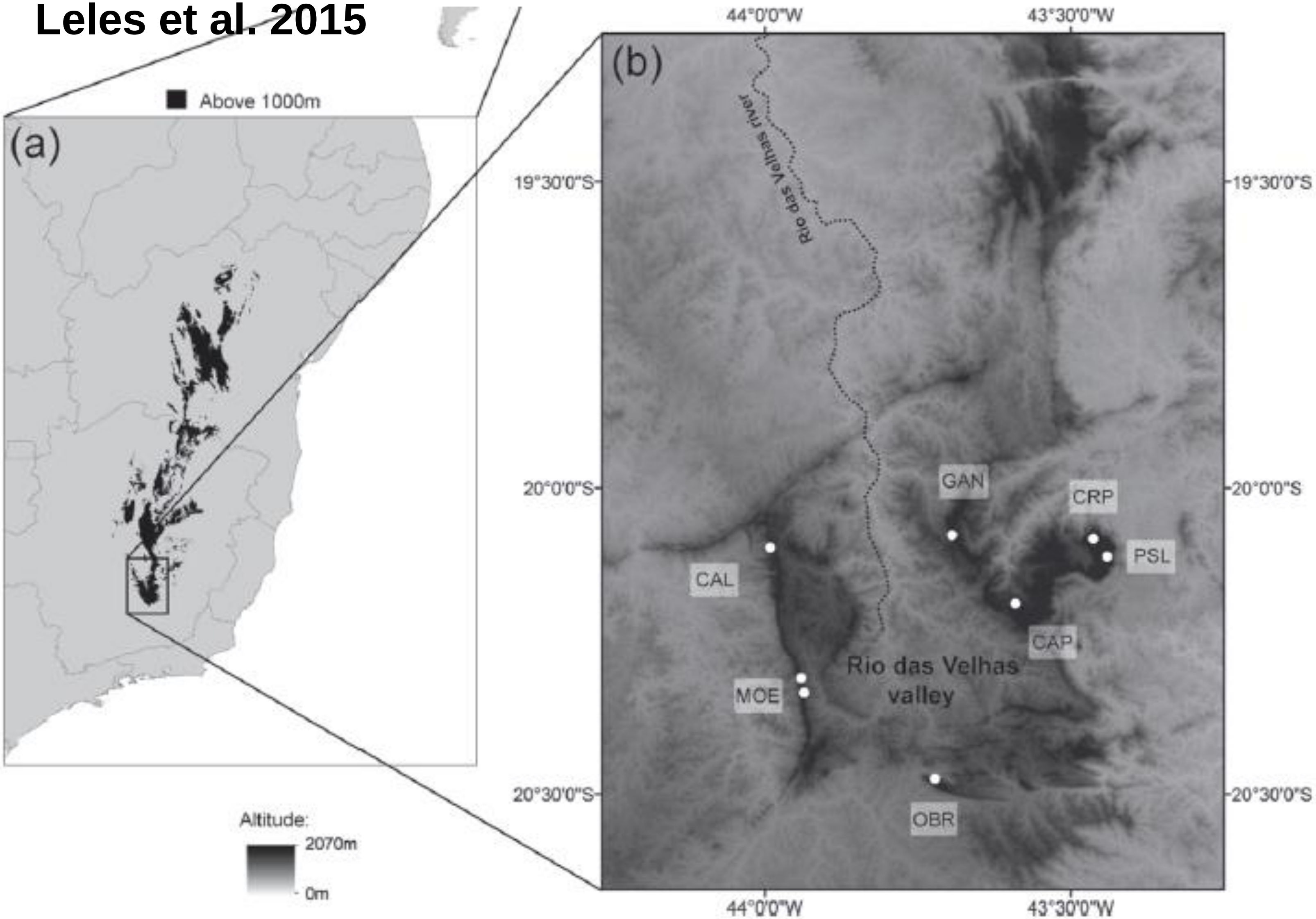


Fig 1. Sampled populations of *Cattleya liliputana* occurring in the Iron Quadrangle. (a) Espinhaço Range Region above 1,000 m a.s.l. in eastern tropical South America. (b) Altitude map of the Iron Quadrangle showing the *Cattleya liliputana* populations analysed in the study.

Cattleya liliputana, Orchidaceae
Iron Quadrangle, Southeastern Brazil

Leles et al. 2015

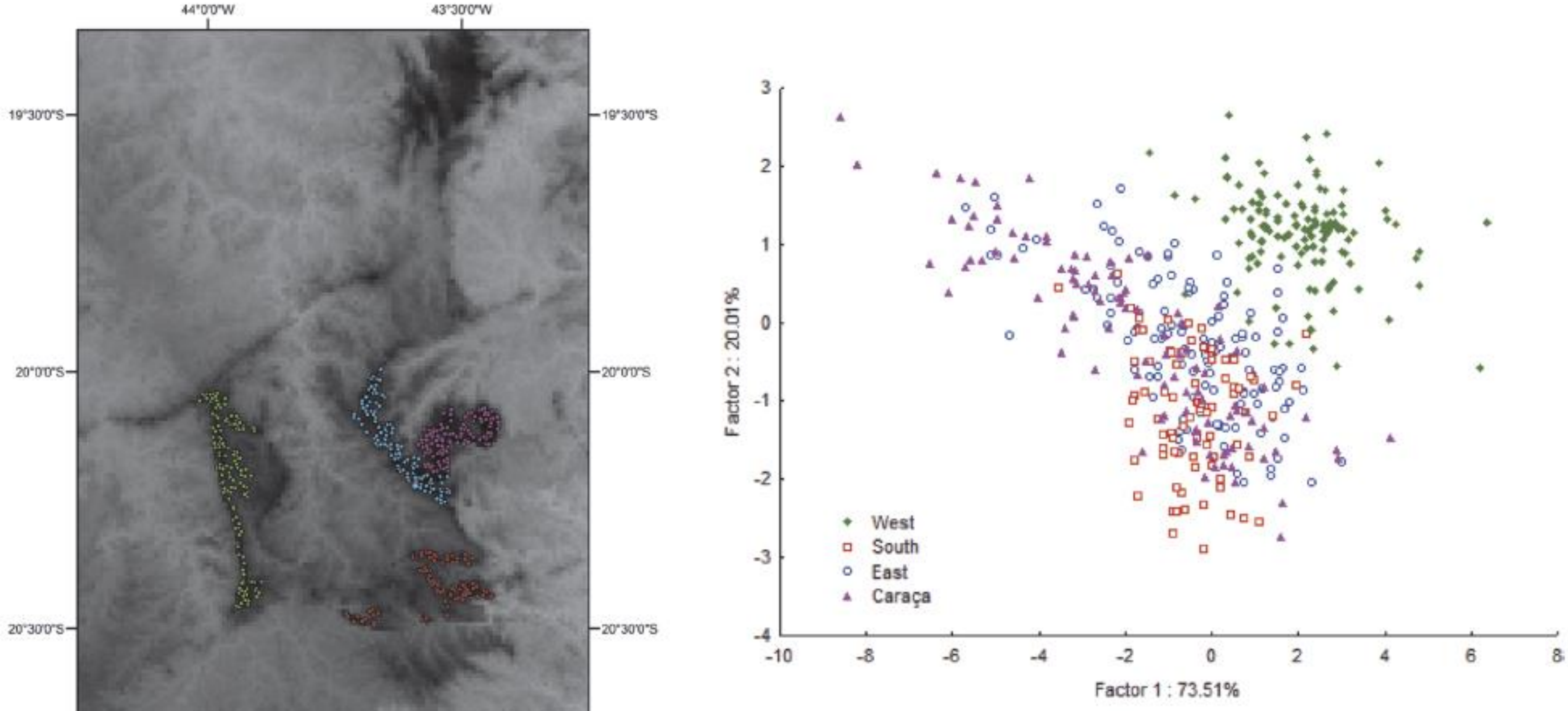


Fig 6. Climatic structure of mountain areas above 1,300 m a.s.l. in the Iron Quadrangle, Brazil. (a) Random points sampled for climatic variables are coloured according to geographic region; Green, west region; Red, south region; Blue, east region; Pink, Serra do Caraça region. (b) Principal component analysis of sampled points according to annual mean precipitation; annual mean temperature; mean diurnal temperature range; minimum temperature of th coldest month; predicted evapotranspiration; vegetation index at July and altitude.

Genetic Consequences of Range Expansions

Excoffier et al. 2009

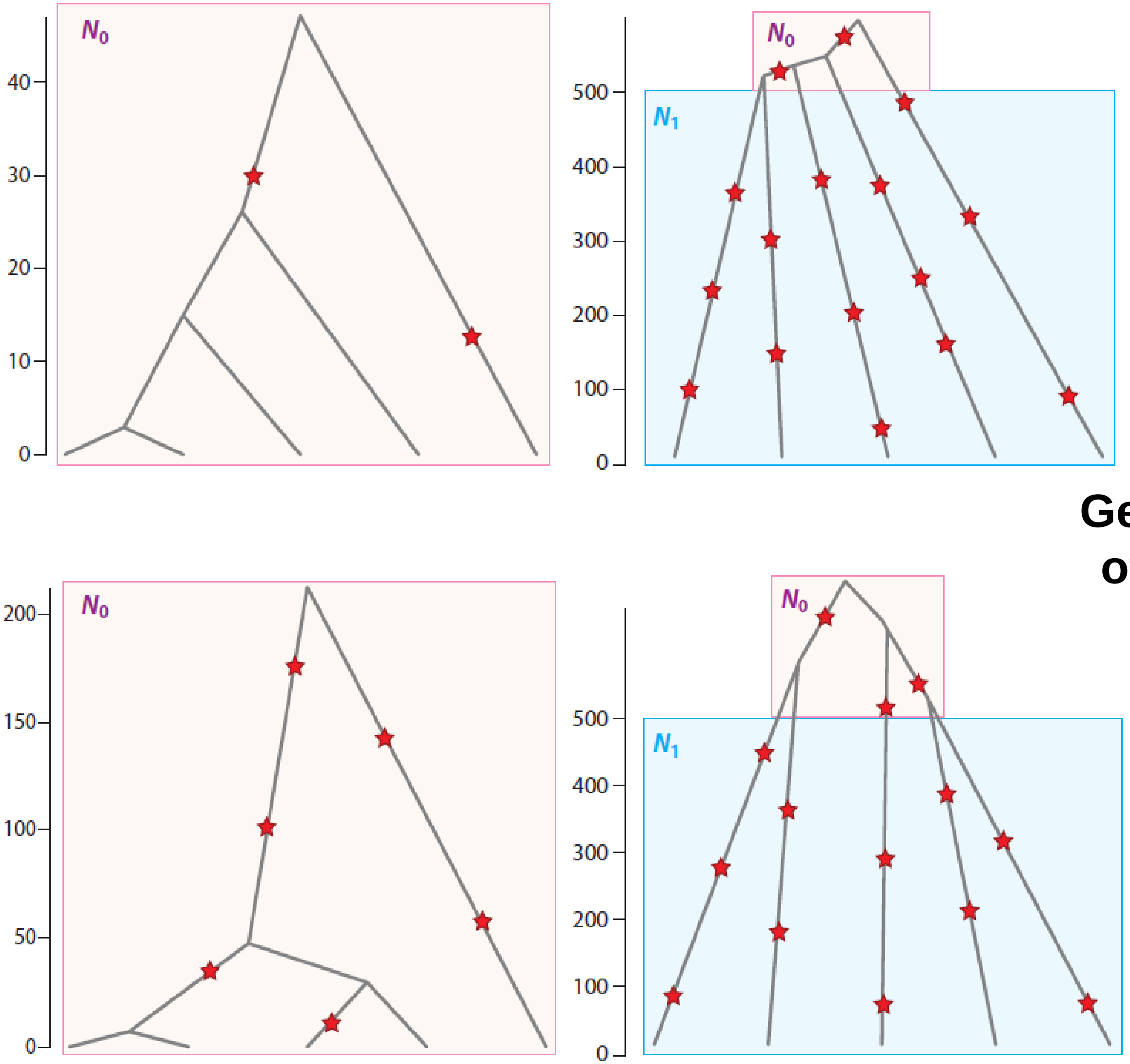


Figure 1

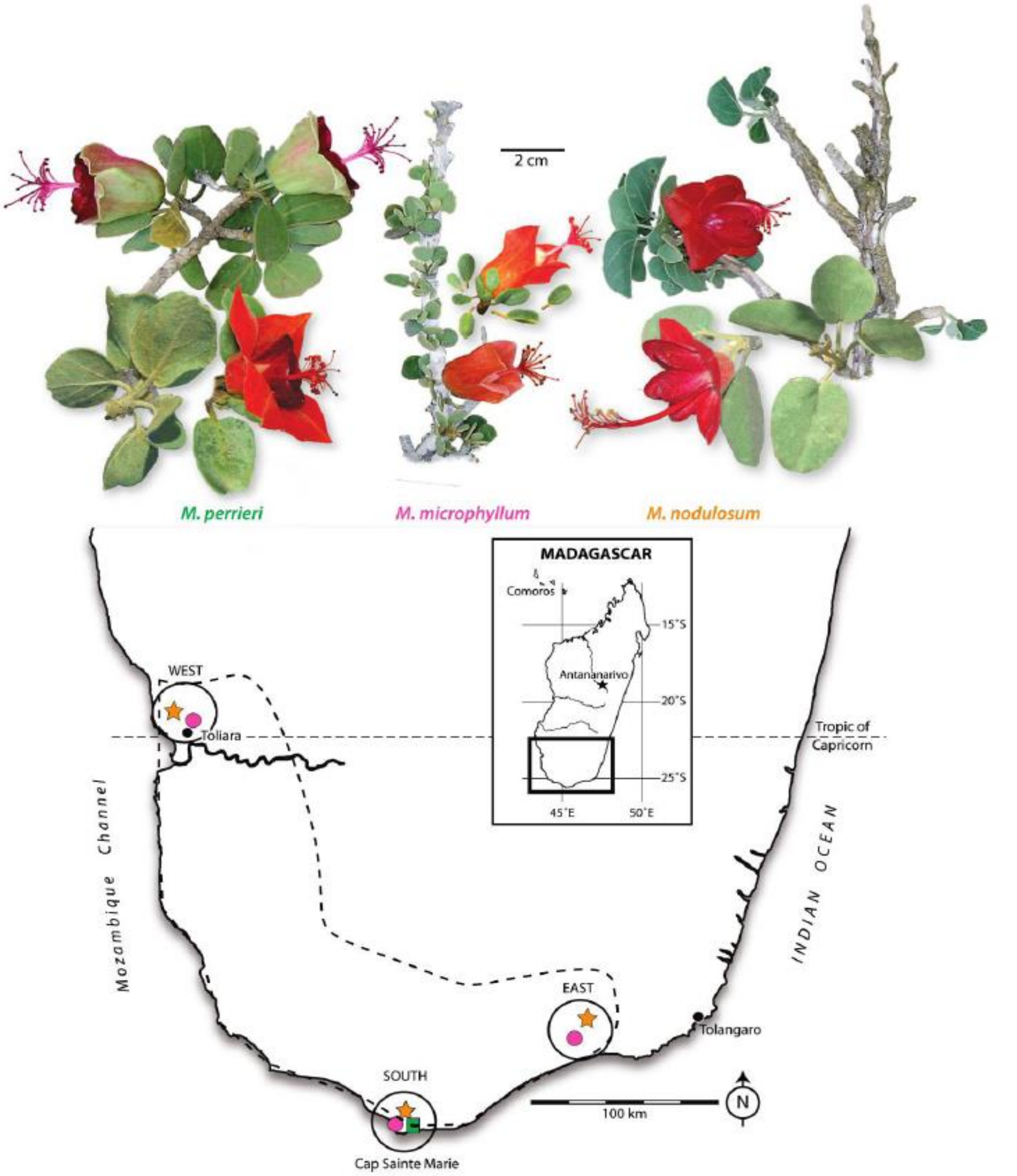
Random genealogies of five gene copies drawn from a stationary population (*left panels*) or from a population having gone through an instantaneous demographic expansion that occurred 500 generations ago (*right panels*). In our simulations, $N_0 = 100$ and $N_1 = 10{,}000$. Note that the timescales are in number of generations and that they are different for each genealogy. Red stars represent mutation events happening randomly along the genealogy according to a Poisson process.

ISOLATING NUCLEAR GENES AND IDENTIFYING LINEAGES WITHOUT MONOPHYLY: AN EXAMPLE OF CLOSELY RELATED SPECIES FROM SOUTHERN MADAGASCAR

Megistostegium
(endêmico de Madagascar)
Malvaceae

Koopman & Baum 2010

KOOPMAN & BAUM—ISOLATE AND IDENTIFY LINEAGES WITHOUT MONOPHYLY 763



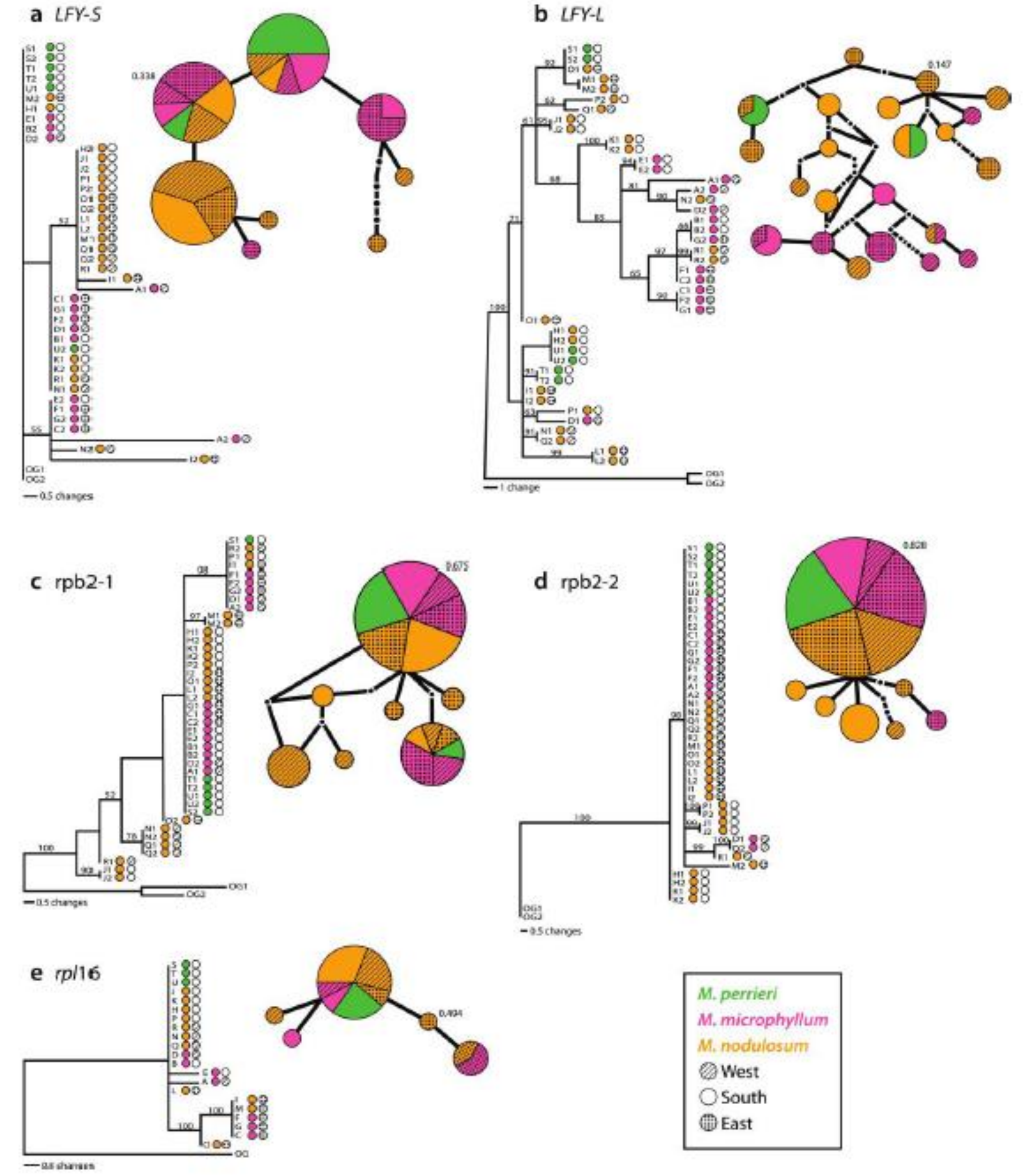
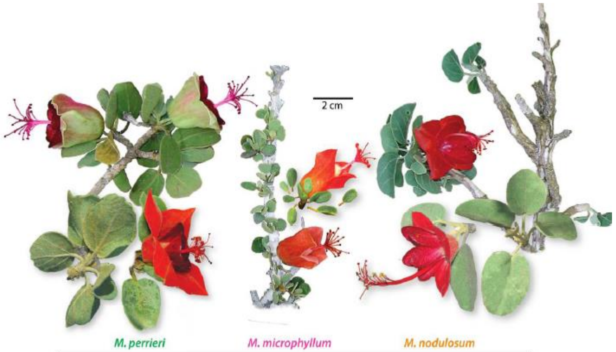


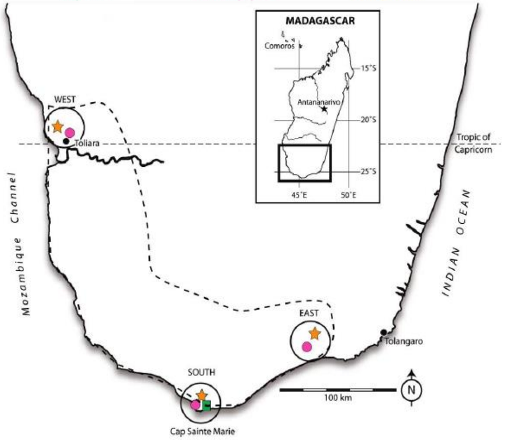
Fig. 2 Maximum likelihood trees and haplotype networks for each locus. Bootstrap support values are indicated above branches. Green, *Megistostegium perrieri*; orange, *Megistostegium nodulosum*; pink, *Megistostegium microphyllum*. Solid shading, southern population; striped, western population; checked, eastern population.

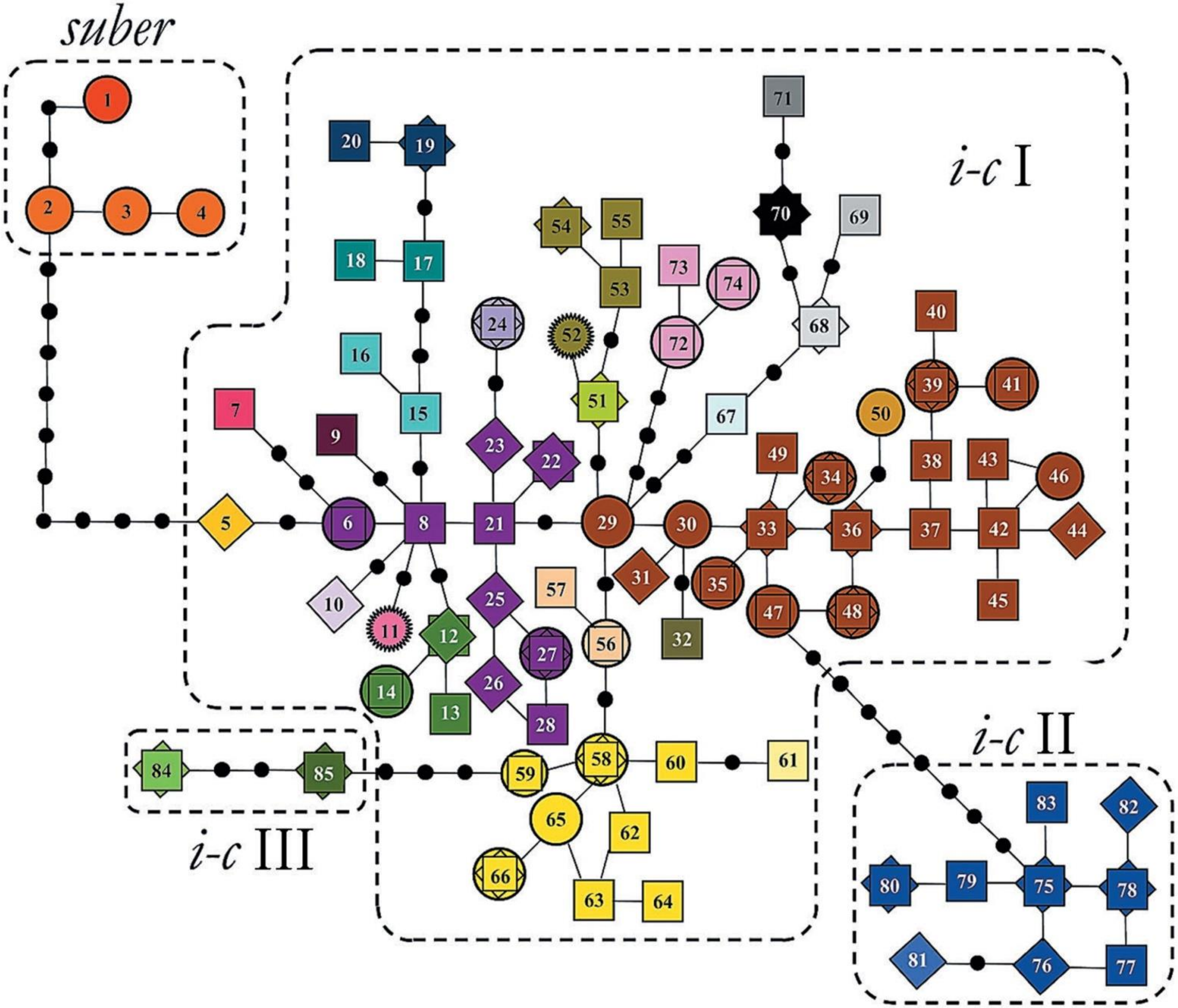
CLOSELY RELATED SPECIES FROM SOUTHERN MADAGASCAR

Megistostegium
(endêmico de Madagascar)
Malvaceae

Koopman & Baum 2010



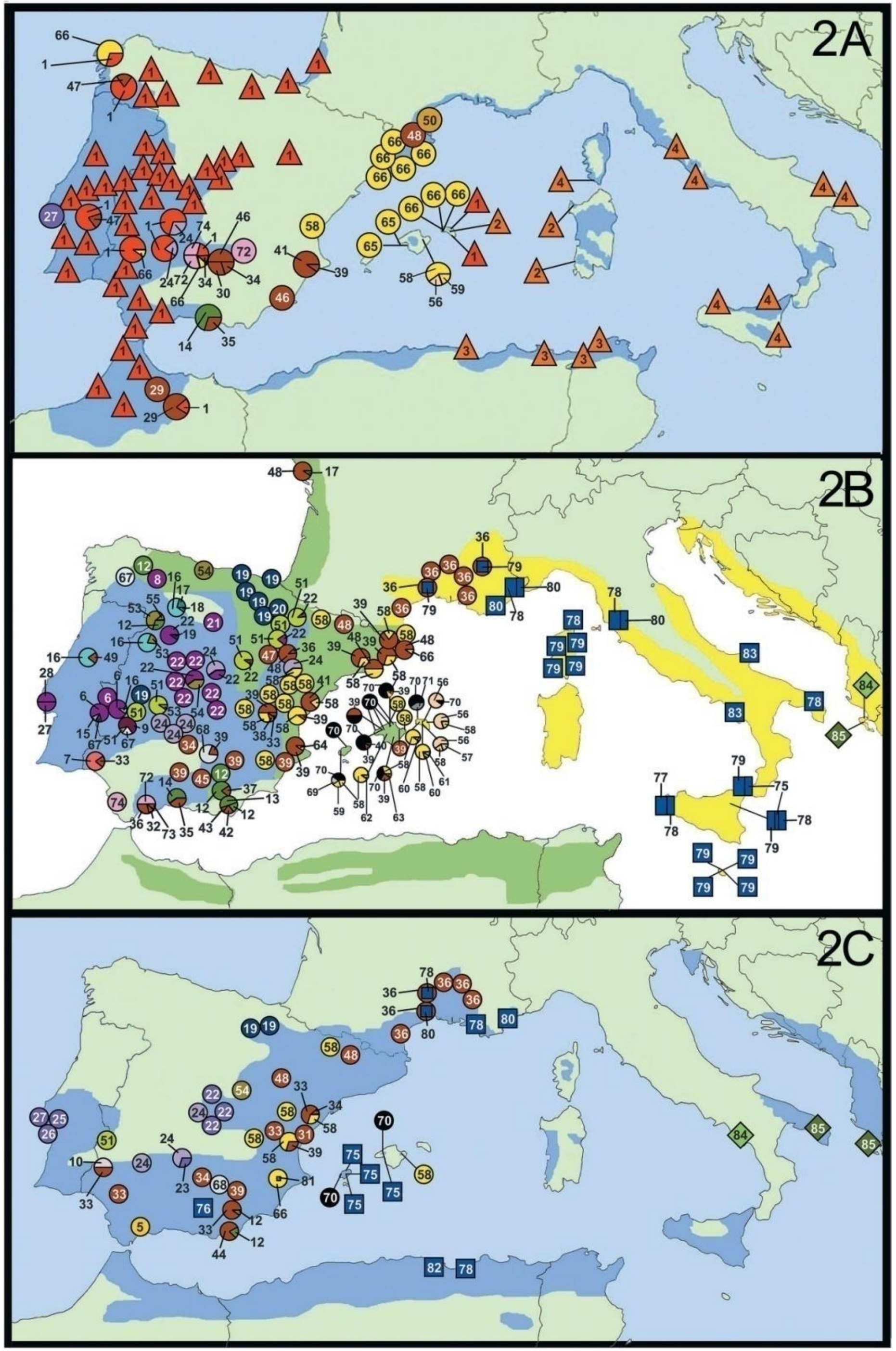




Quercus 3 spp.
FAGACEAE

Marcadores
nucleares
(AFLPs + ITSs)
e
cpDNA

López de Heredia
et al. 2007



Quercus 3 spp.

Marcadores nucleares (AFLPs + ITSs) e cpDNA

López de Heredia et al. 2007

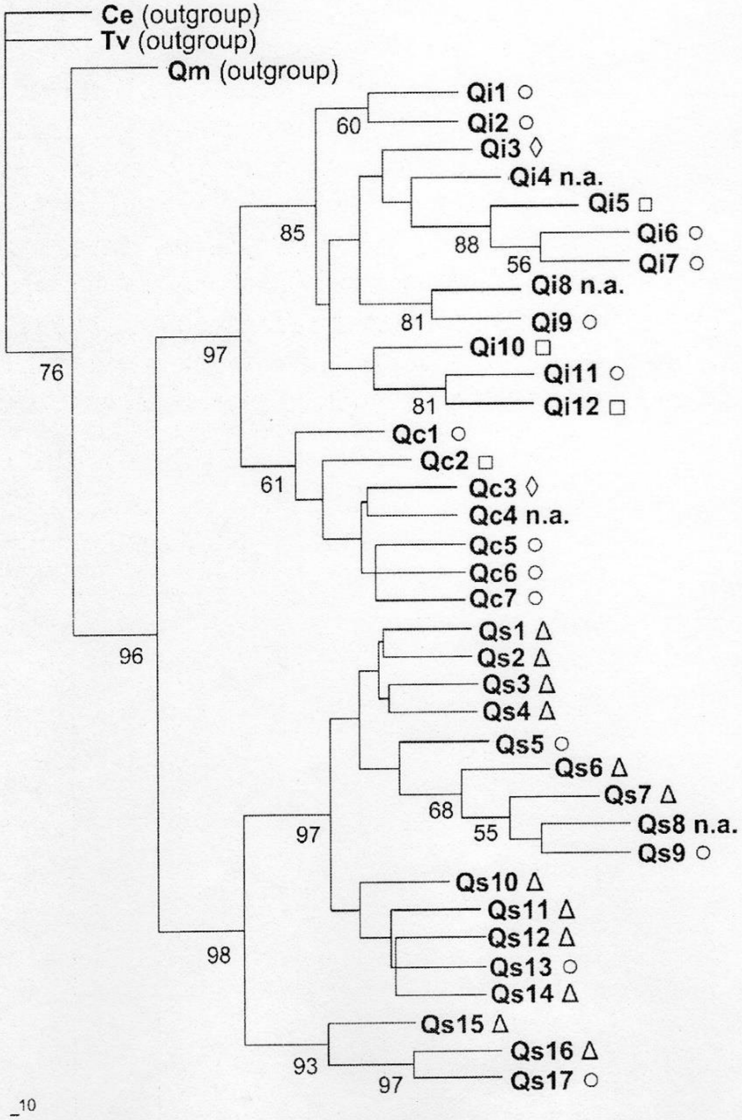


Fig. 3. ITS consensus parsimony tree after 100 bootstrap resampling. Only bootstrap values higher than 50% are indicated. Codes like in Appendix 1. Chloroplast DNA lineage of the accession is indicated. ○, *i-c* I; □, *i-c* II; ◇, *i-c* III; Δ: *suber*, n.a.: no cpDNA analysis.

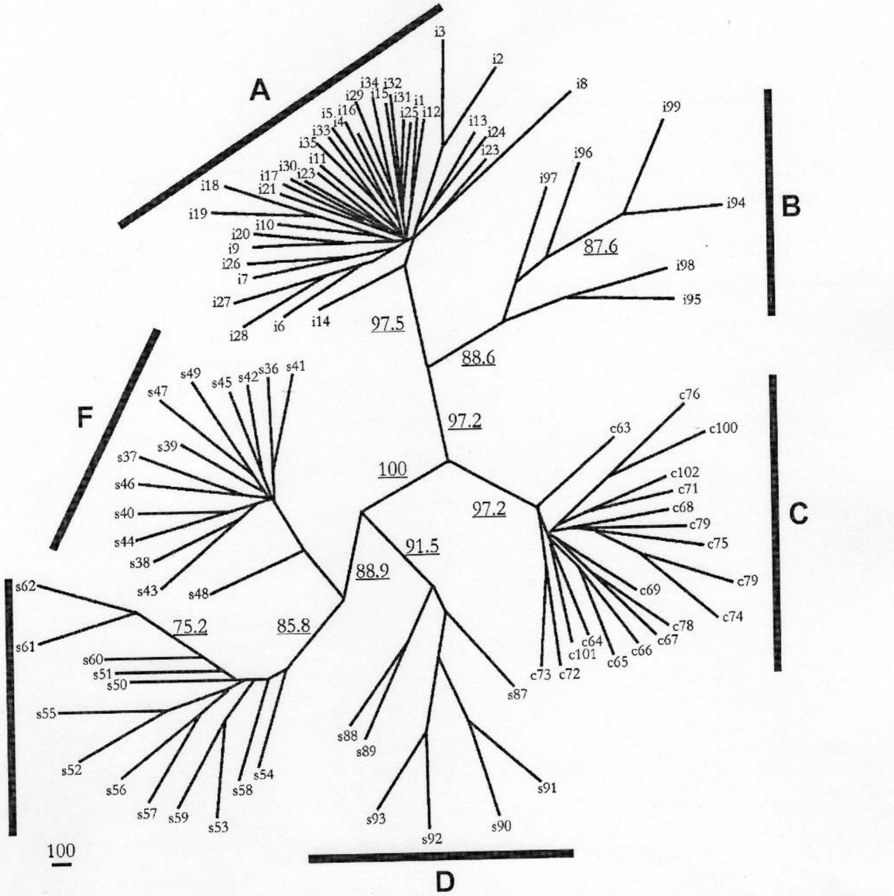


Fig. 4. Consensus unrooted dendrogram of *Q. ilex*, *Q. coccifera* and *Q. suber* accessions constructed from AFLP fragment similarities (Dice coefficient) with the UPGMA clustering method. Bootstrap values of the branches > 75 % are indicated (after 1,000 replications). A, *Q. ilex* (lineage *i-c* I); B, *Q. ilex* (lineage *i-c* II); C, *Q. coccifera*; D, *Q. suber* (lineage *suber*: Tyrrhenian accessions); E, *Q. suber* (lineage *suber*: Iberian accessions); F, *Q. suber* (lineage *i-c* I).

Quercus 3 spp.

López de Heredia et al. 2007

Neogene origins and implied warmth tolerance of Amazon tree species

Dick et al. 2012

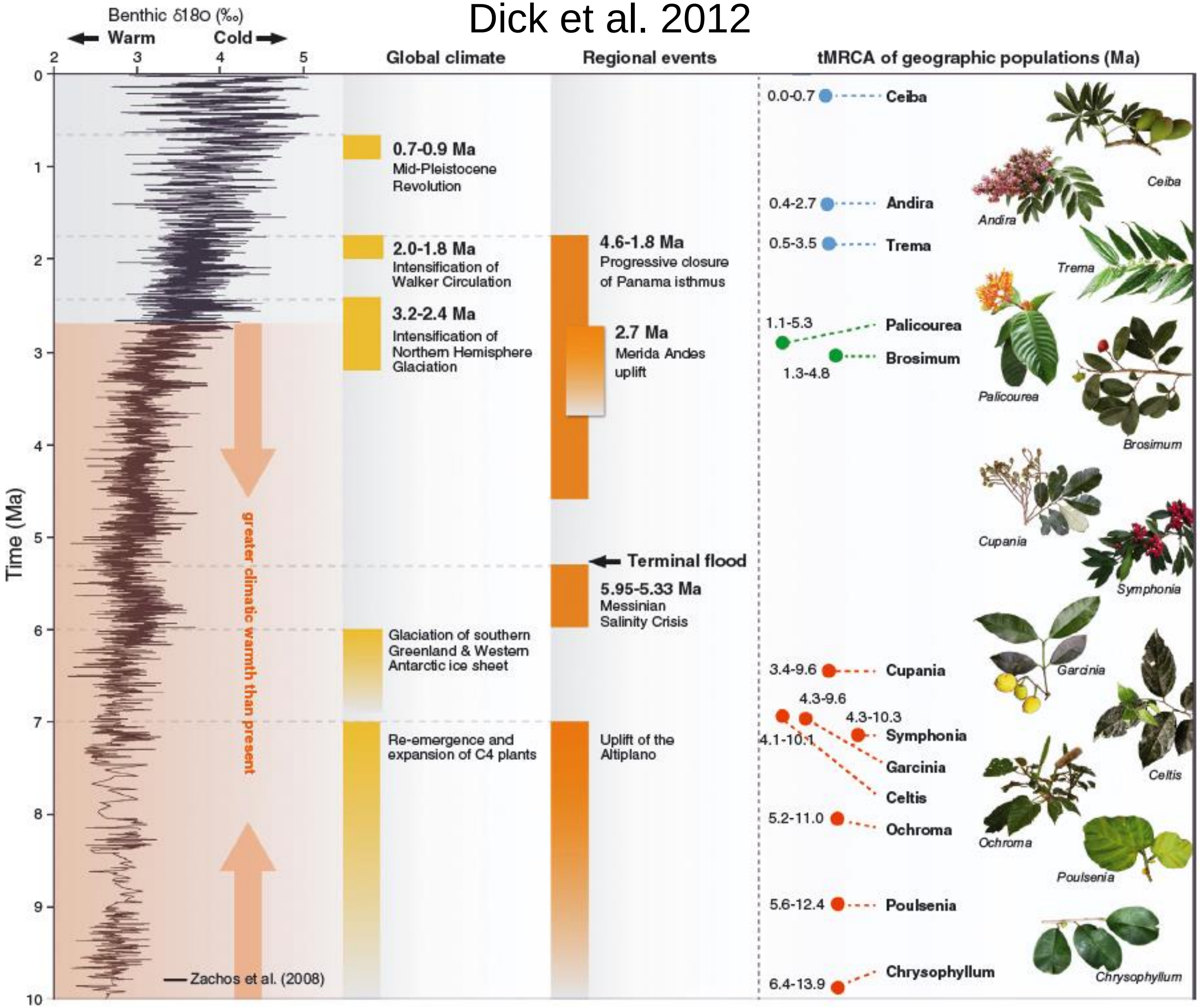


Figure 3. tMRCA of geographic lineages and relevant corresponding surface air temperatures (Zachos et al. 2008) and climatic and geological events. Mean tMRCA estimates are shown in colored circles (Pleistocene blue, Pliocene green, Miocene red) accompanied by upper and lower 95% HPD intervals. Large vertical arrows indicate period in which average surface air temperatures were warmer than present. Tree photographs were provided by Center for Tropical Forest Sciences.

Neogene origins and implied warmth tolerance of Amazon tree species
Dick et al. 2012

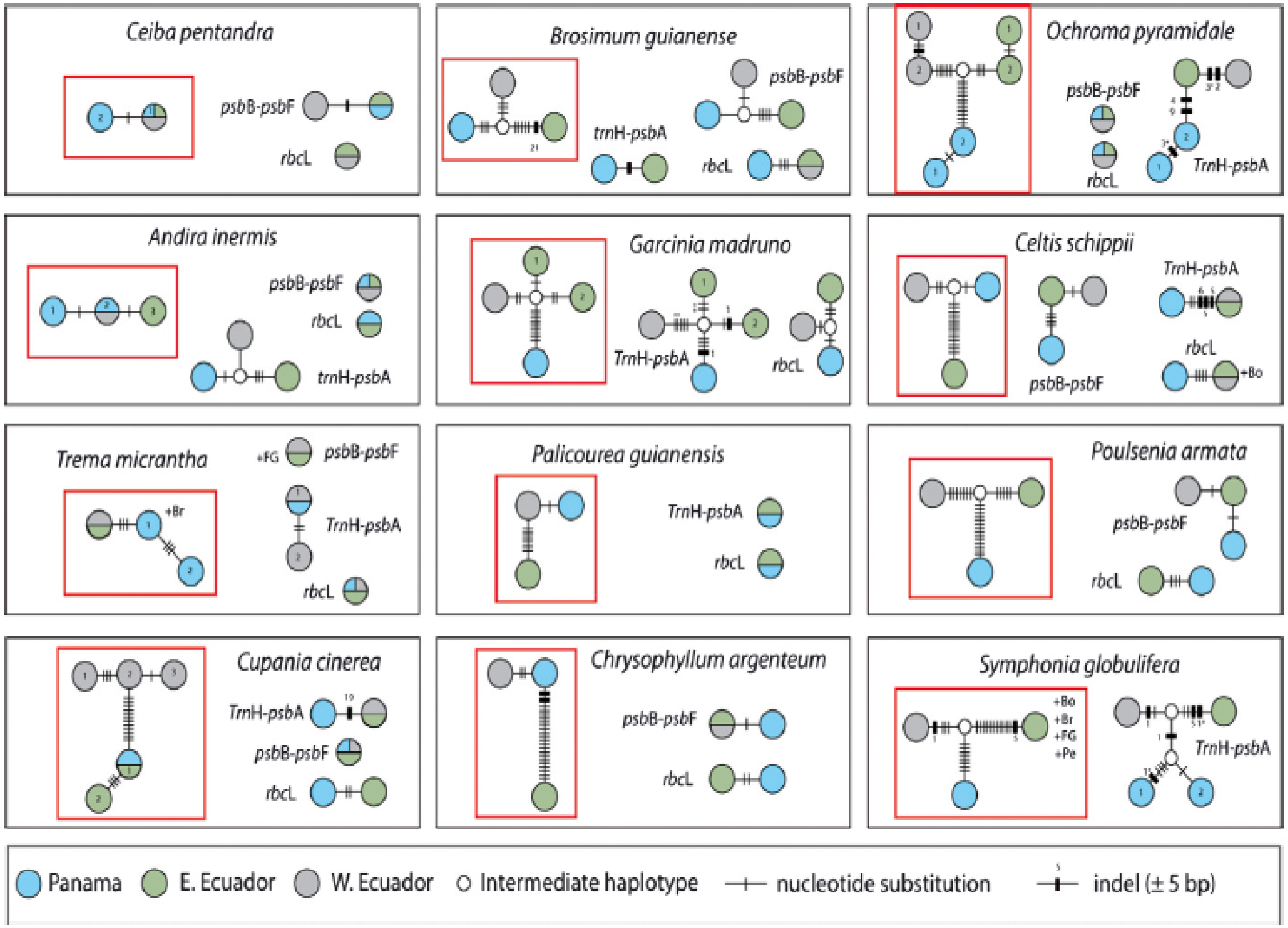


Figure 2. Haplotype networks for nuclear ITS and chloroplast DNA sequence data. Circles represent haplotypes, colors are geographic locations; hatch marks represent mutational steps. ITS haplotypes are bounded by red rectangles. Additional geographic representation of some haplotypes is indicated by country abbreviations: Bolivia (Bo), Brazil (Br), French Guiana (FG), and Peru (Pe).

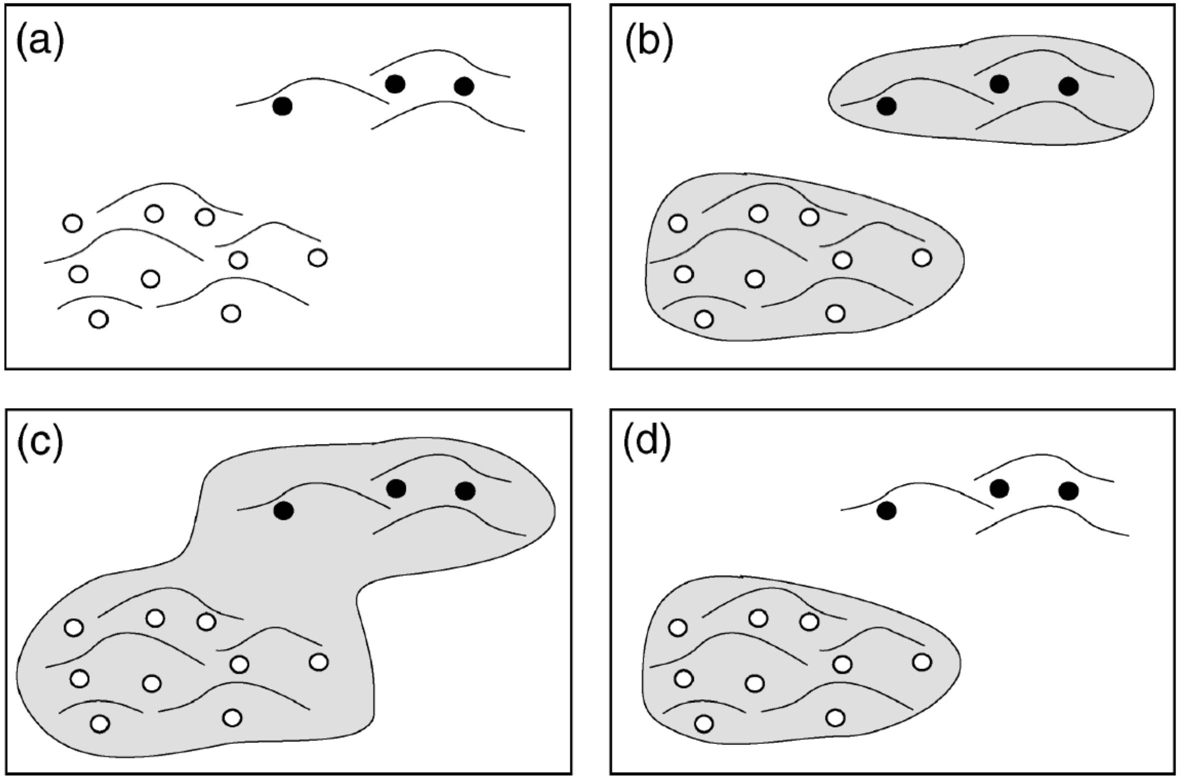


Figure 1 Hypothetical example illustrating niche conservatism, ecological niche modeling, and species delimitation. (a) Two sets of allopatric populations occur in two geographically separate montane regions. One set (*open circles*) is a previously described species, the other set (*closed circles*) is of unknown taxonomic status. (*b*) Ecological niche modeling shows that the two sets of populations share a similar climatic niche envelope (*shown in gray*). The intervening lowland areas between the montane regions are outside the envelope of acceptable environmental conditions, which suggests that niche conservatism may prevent gene flow between these two sets of populations and supports the hypothesis that they are distinct species. (c) The two sets of populations share a similar climatic niche envelope, but this niche envelope also includes the areas between them. This result suggests that niche conservatism is not important in isolating them and that there may be ongoing dispersal and gene flow between them (if no other barriers are present). This pattern would not add support to the hypothesis that they are distinct species. (d) The two sets of populations have dissimilar climatic niche envelopes (illustrated here by the restricted niche envelope of the known species). This result suggests that past niche evolution (and current niche conservatism) maintains the geographic separation of these populations and supports the hypothesis that they are distinct species.

Conservantismo de nicho

+

Modelagem de nicho +

Delimitação de espécies

Wiens & Graham 2005

Padrões esperados em consequência de Conservantismo de nicho

X padrões que rejeitam o modelo

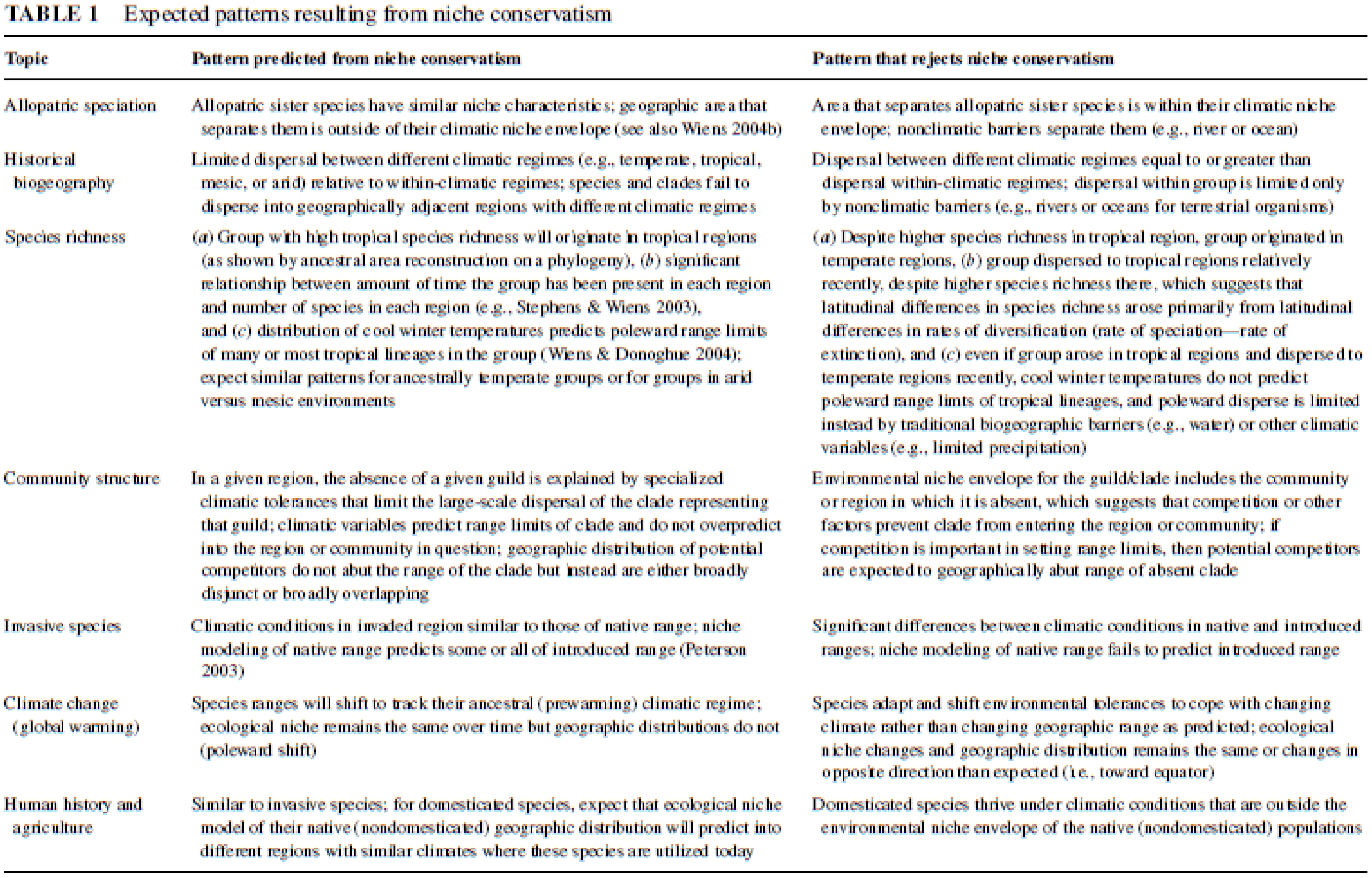


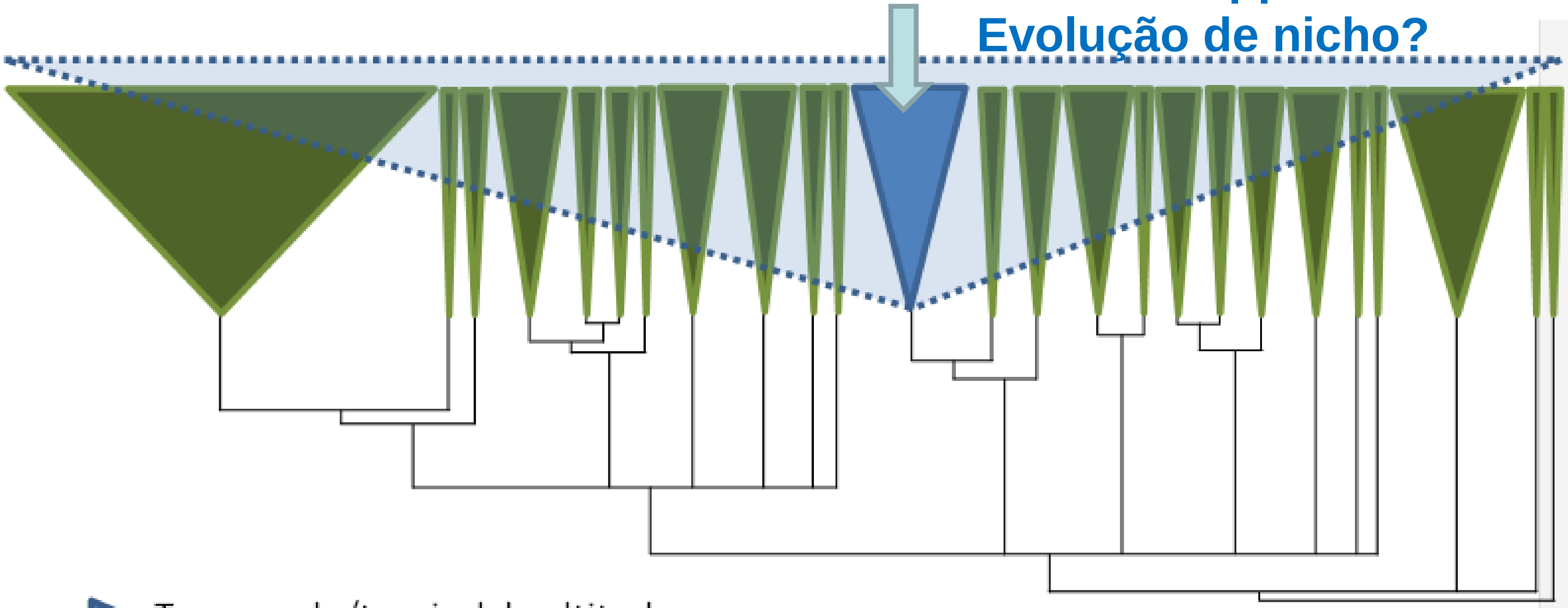
TABLE 1 Expected patterns resulting from niche conservatism

Topic	Pattern predicted from niche conservatism	Pattern that rejects niche conservatism
Allopatric speciation	Allopatric sister species have similar niche characteristics; geographic area that separates them is outside of their climatic niche envelope (see also Wiens 2004b)	Area that separates allopatric sister species is within their climatic niche envelope; nonclimatic barriers separate them (e.g., river or ocean)
Historical biogeography	Limited dispersal between different climatic regimes (e.g., temperate, tropical, mesic, or arid) relative to within-climatic regimes; species and clades fail to disperse into geographically adjacent regions with different climatic regimes	Dispersal between different climatic regimes equal to or greater than dispersal within-climatic regimes; dispersal within group is limited only by nonclimatic barriers (e.g., rivers or oceans for terrestrial organisms)
Species richness	(*a*) Group with high tropical species richness will originate in tropical regions (as shown by ancestral area reconstruction on a phylogeny), (*b*) significant relationship between amount of time the group has been present in each region and number of species in each region (e.g., Stephens & Wiens 2003), and (*c*) distribution of cool winter temperatures predicts poleward range limits of many or most tropical lineages in the group (Wiens & Donoghue 2004); expect similar patterns for ancestrally temperate groups or for groups in arid versus mesic environments	(*a*) Despite higher species richness in tropical region, group originated in temperate regions, (*b*) group dispersed to tropical regions relatively recently, despite higher species richness there, which suggests that latitudinal differences in species richness arose primarily from latitudinal differences in rates of diversification (rate of speciation—rate of extinction), and (*c*) even if group arose in tropical regions and dispersed to temperate regions recently, cool winter temperatures do not predict poleward range limits of tropical lineages, and poleward disperse is limited instead by traditional biogeographic barriers (e.g., water) or other climatic variables (e.g., limited precipitation)
Community structure	In a given region, the absence of a given guild is explained by specialized climatic tolerances that limit the large-scale dispersal of the clade representing that guild; climatic variables predict range limits of clade and do not overpredict into the region or community in question; geographic distribution of potential competitors do not abut the range of the clade but instead are either broadly disjunct or broadly overlapping	Environmental niche envelope for the guild/clade includes the community or region in which it is absent, which suggests that competition or other factors prevent clade from entering the region or community; if competition is important in setting range limits, then potential competitors are expected to geographically abut range of absent clade
Invasive species	Climatic conditions in invaded region similar to those of native range; niche modeling of native range predicts some or all of introduced range (Peterson 2003)	Significant differences between climatic conditions in native and introduced ranges; niche modeling of native range fails to predict introduced range
Climate change (global warming)	Species ranges will shift to track their ancestral (prewarming) climatic regime; ecological niche remains the same over time but geographic distributions do not (poleward shift)	Species adapt and shift environmental tolerances to cope with changing climate rather than changing geographic range as predicted; ecological niche changes and geographic distribution remains the same or changes in opposite direction than expected (i.e., toward equator)
Human history and agriculture	Similar to invasive species; for domesticated species, expect that ecological niche model of their native (nondomesticated) geographic distribution will predict into different regions with similar climates where these species are utilized today	Domesticated species thrive under climatic conditions that are outside the environmental niche envelope of the native (nondomesticated) populations

Wiens & Graham 2005

VIOLACEAE

***Viola* - ½ das spp da família**
Evolução de nicho?



- ▶ Temperado/tropical de altitude
- ▶ Tropical
- ▶ Projeção do número de espécies do clado

23 gêneros tropicais

Anchietea

Hybanthopsis

consenso estrito máxima parcimônia
***trn*L-F de 97 táxons**

Paula-Souza & Pirani *em prep.*

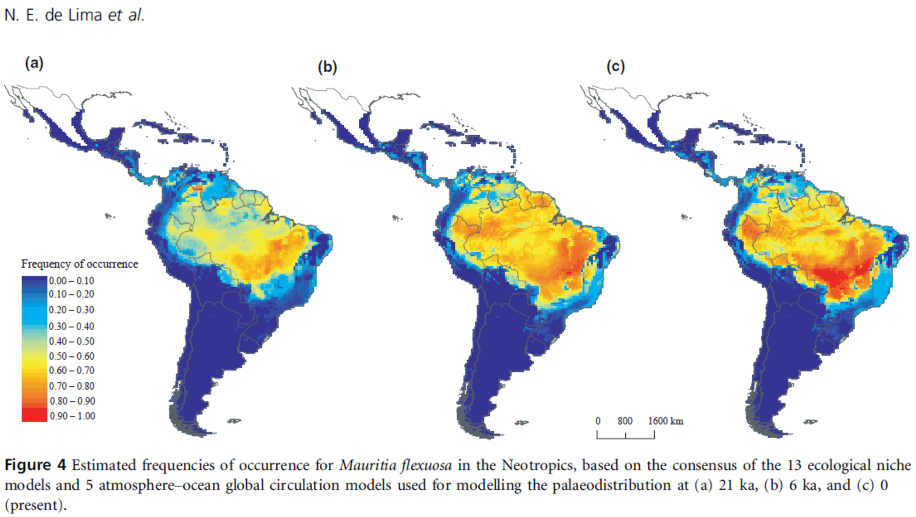
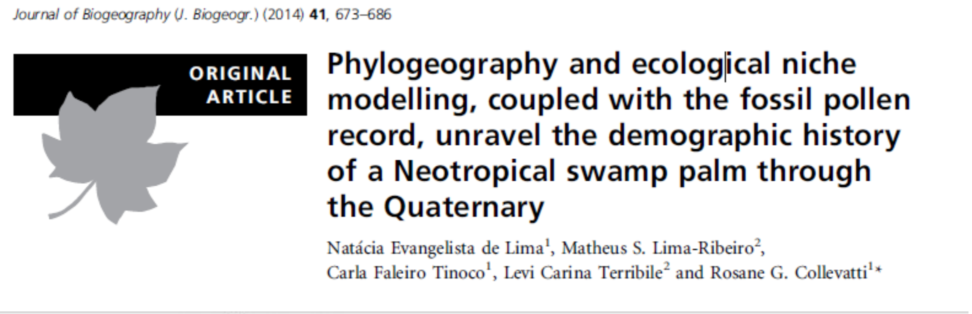

N. E. de Lima *et al.*

Figure 4 Estimated frequencies of occurrence for *Mauritia flexuosa* in the Neotropics, based on the consensus of the 13 ecological niche models and 5 atmosphere–ocean global circulation models used for modelling the palaeodistribution at (a) 21 ka, (b) 6 ka, and (c) 0 (present).


Journal of Biogeography (*J. Biogeogr.*) (2014) **41**, 673–686

ORIGINAL ARTICLE

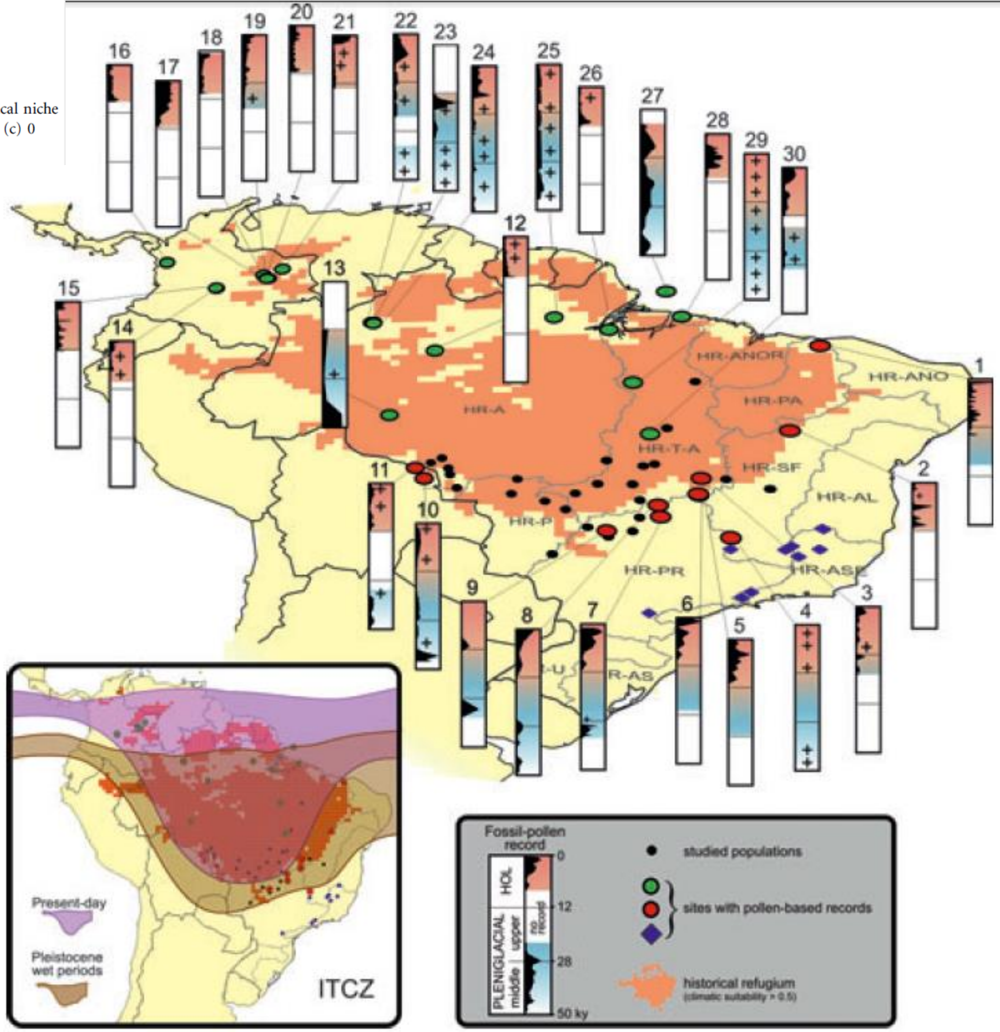
Phylogeography and ecological niche modelling, coupled with the fossil pollen record, unravel the demographic history of a Neotropical swamp palm through the Quaternary

Natácia Evangelista de Lima[1], Matheus S. Lima-Ribeiro[2],
Carla Faleiro Tinoco[1], Levi Carina Terribile[2] and Rosane G. Collevatti[1]*

Filogeografia + modelagem de nicho ecológico: História demográfica no Quaternário

Mauritia flexuosa
Arecaceae

Lima *et al.* 2014

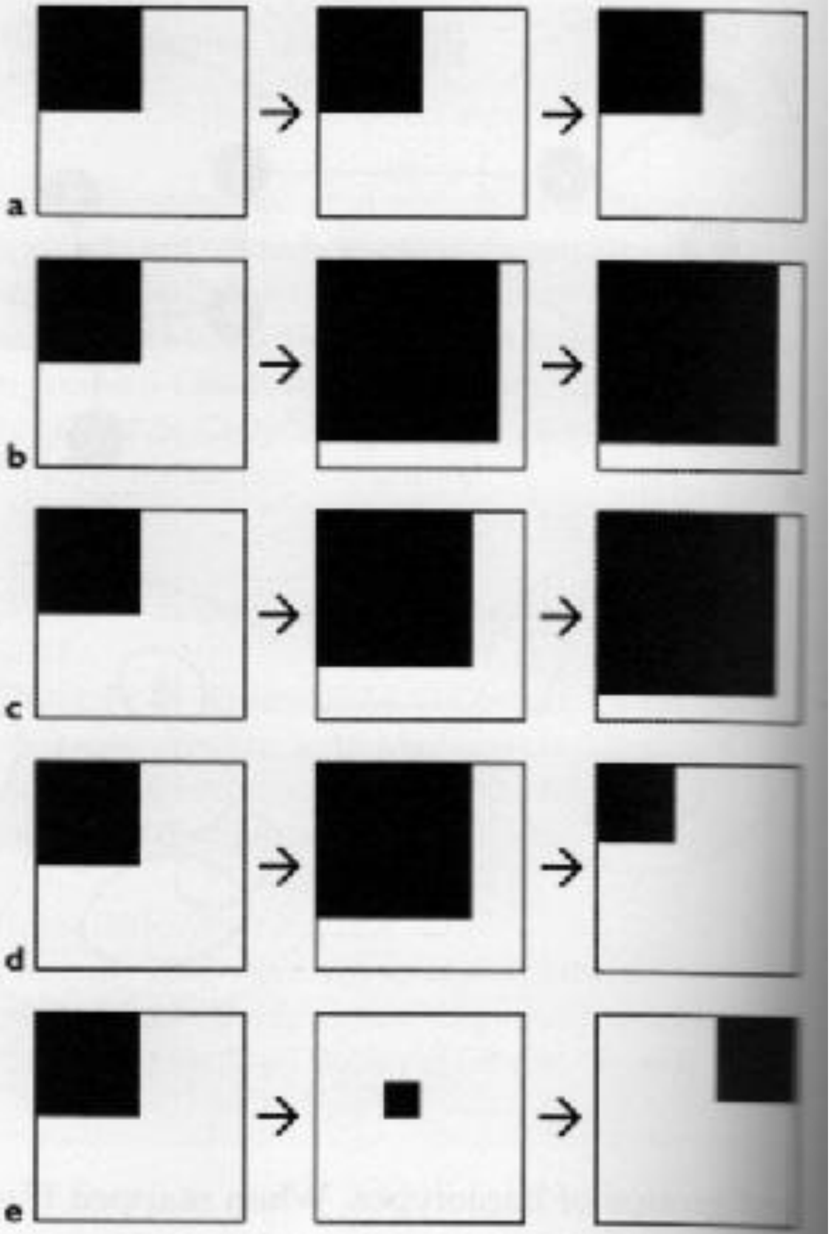


Filogeografia e Biogeografia Ecológica:

Filogeografia ajuda a identificar qual das classes de dinâmica de distribuição corresponde a uma dada espécie analisada (Gaston 2003)

PALEOFILOGEOGRAFIA
(Betancourt 2004)

Figure 7.3 Types of species range dynamics. (a) Stasis; (b) stasis postexpansion; (c) age and area; (d) cyclic; (e) idiosyncratic.



Morrone 2009

BIOGEOGRAFIA HISTÓRICA

“What biogeography is: a place for process”.

‘Vicariância e dispersão são atributos das distribuições bióticas. A Filogeografia tem grande potencial em ajudar a determinar qual desses processos gerou os padrões observados’.

R. M. McDowall 2004

J. Biogeogr. 31.

SÍNTESE EMERGENTE NA BIOGEOGRAFIA ?

Methodology for creating geophylogenies

Geophlogenies can be generated in Keyhole Markup Language (KML) format from a phylogenetic tree and

1. Modelos de Biogeografia Ecológica incorporando Filogenias e Filogeografia (Wiens & Donoghue 2004, Hawkins et al. 2006, Riddle & Hafner 2006)

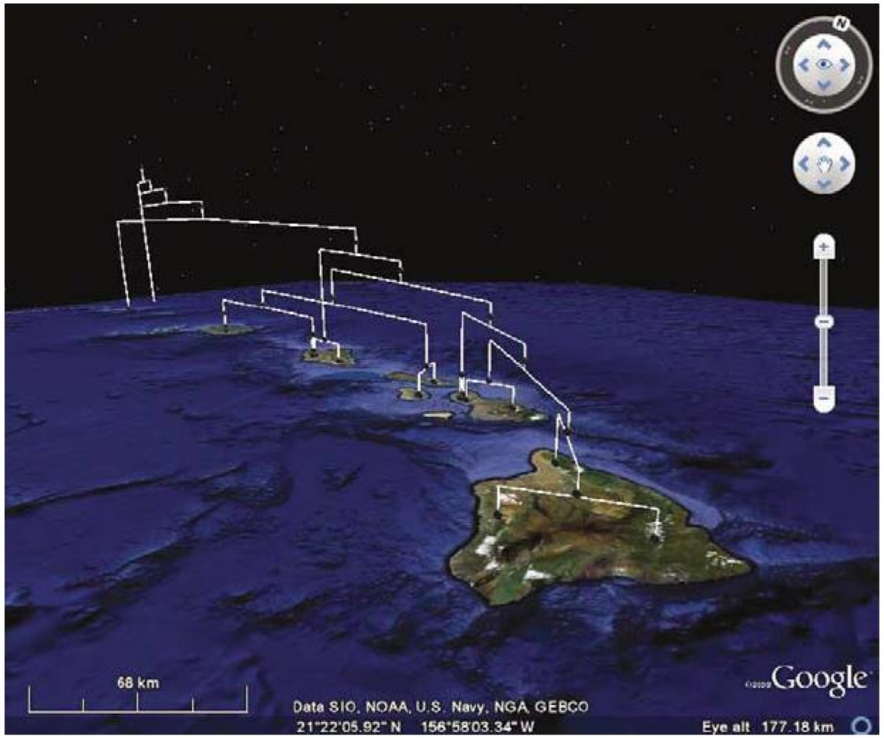


Figure 1. The phylogeny of *Banza* as reported in Shapiro et al. (2006) here presented as a geophylogeny similar to that of Page (2008) but built using the automated services of the GeoPhylo Engine. See the "Examples" section of the GeoPhylo Engine website for details on this geophylogeny.

GeoPhylo: **an online tool for developing visualizations of phylogenetic trees in geographic space**

Hill & Guralnick 2010
Ecography

A step-wise approach to integrating phylogeographic and phylogenetic biogeographic perspectives on the history of a core North American warm deserts biota

Riddle & Hafner 2006

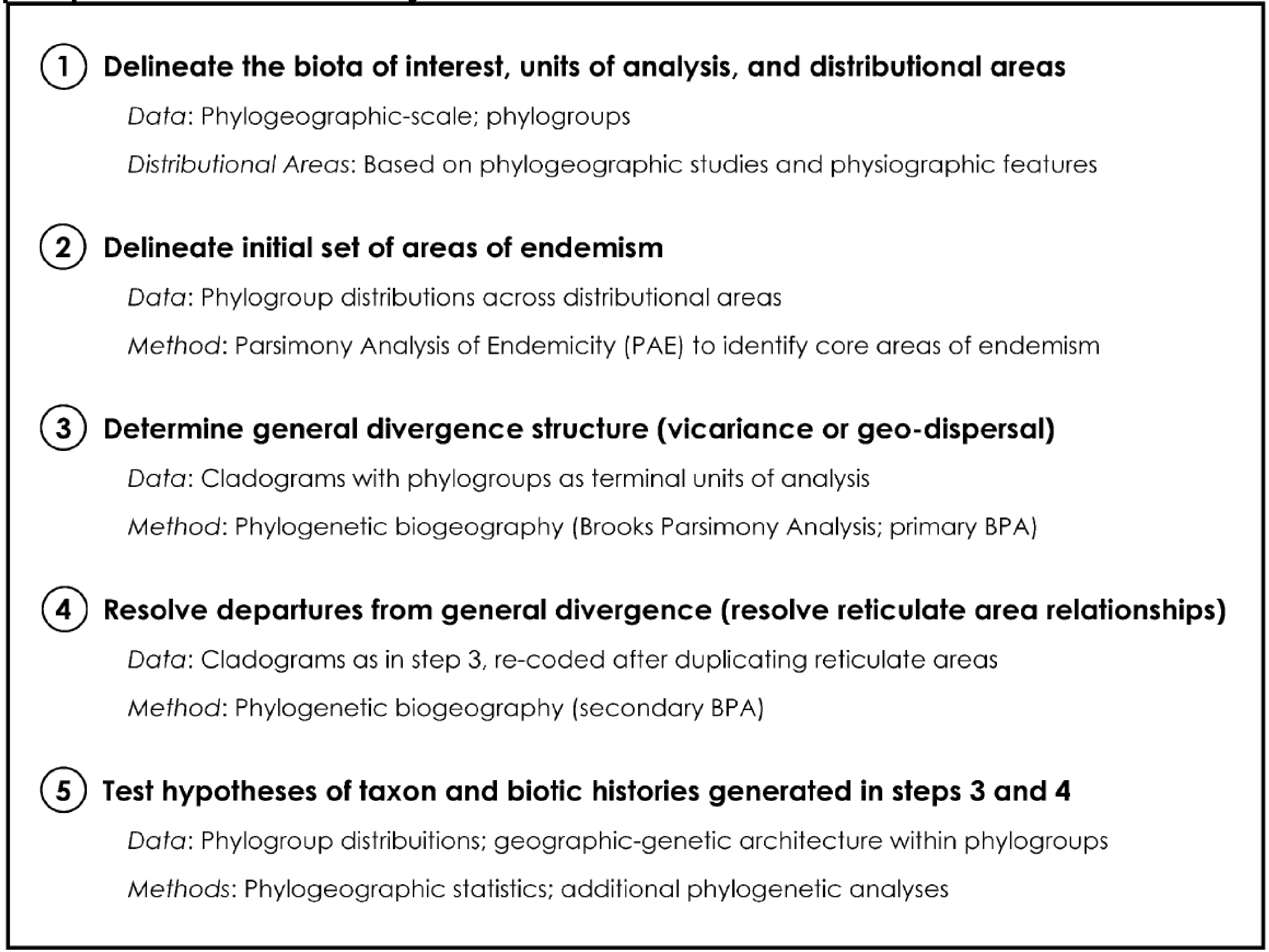
Development of a **five-step approach for analysis of historical relationships among areas of endemism using a set of 22 clades (9 mammal, 7 bird, 4 reptile, 1 amphibian, and 1 cactus)** drawn from the warm deserts biota of western North America:

Biota with a complex biogeographic history, but with substantial support for the influence of several major vicariant events in the diversification and assembly of the aridlands biota.

Discuss and demonstrate the reciprocal strengths (and weaknesses) of phylogeography and phylogenetic biogeography for defining **areas of endemism**, analysing **vicariance and dispersal**, and dealing with **temporal and spatial pseudo-congruence.**

5 steps approach to integrating phylogeographic and phylogenetic biogeographic perspectives on the history of a core biota

Riddle & Hafner 2006



① **Delineate the biota of interest, units of analysis, and distributional areas**

Data: Phylogeographic-scale; phylogroups

Distributional Areas: Based on phylogeographic studies and physiographic features

② **Delineate initial set of areas of endemism**

Data: Phylogroup distributions across distributional areas

Method: Parsimony Analysis of Endemicity (PAE) to identify core areas of endemism

③ **Determine general divergence structure (vicariance or geo-dispersal)**

Data: Cladograms with phylogroups as terminal units of analysis

Method: Phylogenetic biogeography (Brooks Parsimony Analysis; primary BPA)

④ **Resolve departures from general divergence (resolve reticulate area relationships)**

Data: Cladograms as in step 3, re-coded after duplicating reticulate areas

Method: Phylogenetic biogeography (secondary BPA)

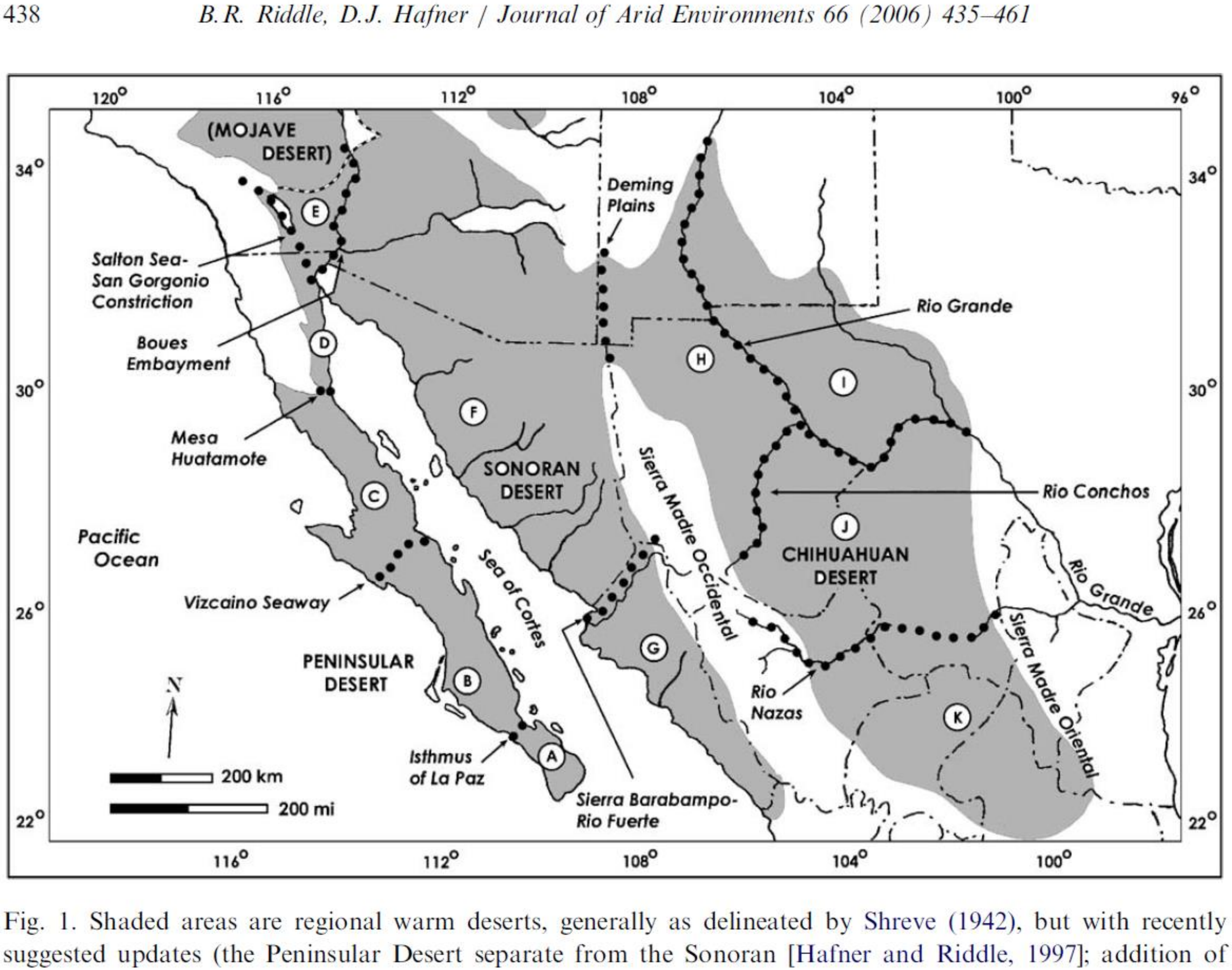
⑤ **Test hypotheses of taxon and biotic histories generated in steps 3 and 4**

Data: Phylogroup distribuitions; geographic-genetic architecture within phylogroups

Methods: Phylogeographic statistics; additional phylogenetic analyses

uso de PAE como etapa de estudo filogeográfico nos desertos da América do Norte

Riddle & Hafner 2006



438 B.R. Riddle, D.J. Hafner / Journal of Arid Environments 66 (2006) 435–461

Fig. 1. Shaded areas are regional warm deserts, generally as delineated by Shreve (1942), but with recently suggested updates (the Peninsular Desert separate from the Sonoran [Hafner and Riddle, 1997]; addition of

Analysis of historical relationships among areas of endemism using a set of 22 clades (9 mammal, 7 bird, 4 reptile, 1 amphibian, and 1 cactus)

-estudo filogeográfico
nos desertos da América do Norte

Riddle & Hafner 2006

B.R. Riddle, D.J. Hafner / Journal of Arid Environments 66 (2006) 435–461 441

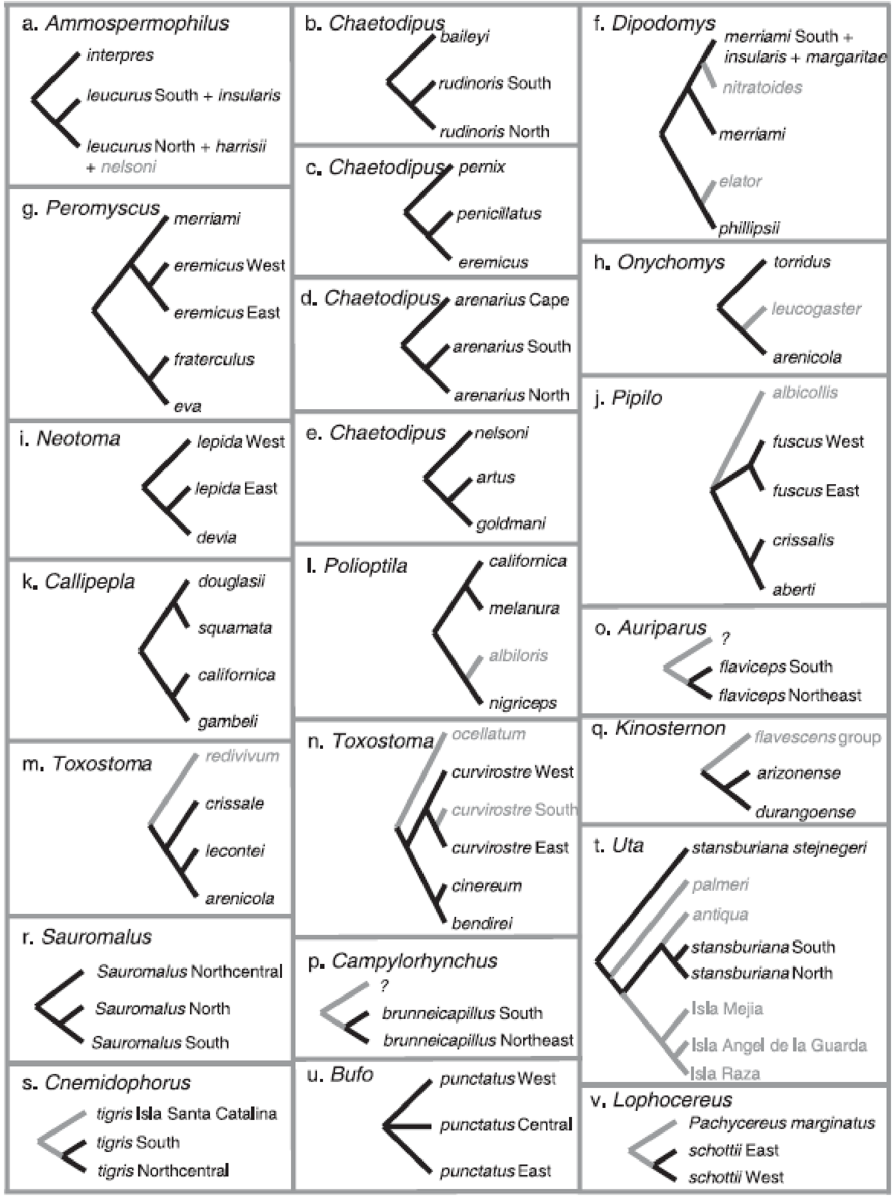


Fig. 2. Taxonomic cladograms used in this study (source literature in Table 1). Gray-shaded lineages—and so their biogeographic distributions—were trimmed prior to BPA analyses (see text for discussion). Question marks on cladograms o and p indicate uncertainty about sister-group relationships beyond the sister-taxa depicted. Original sources given in legend of Table 1.

uso de PAE como etapa inicial de estudo filogeográfico nos desertos da América do Norte

Riddle & Hafner 2006

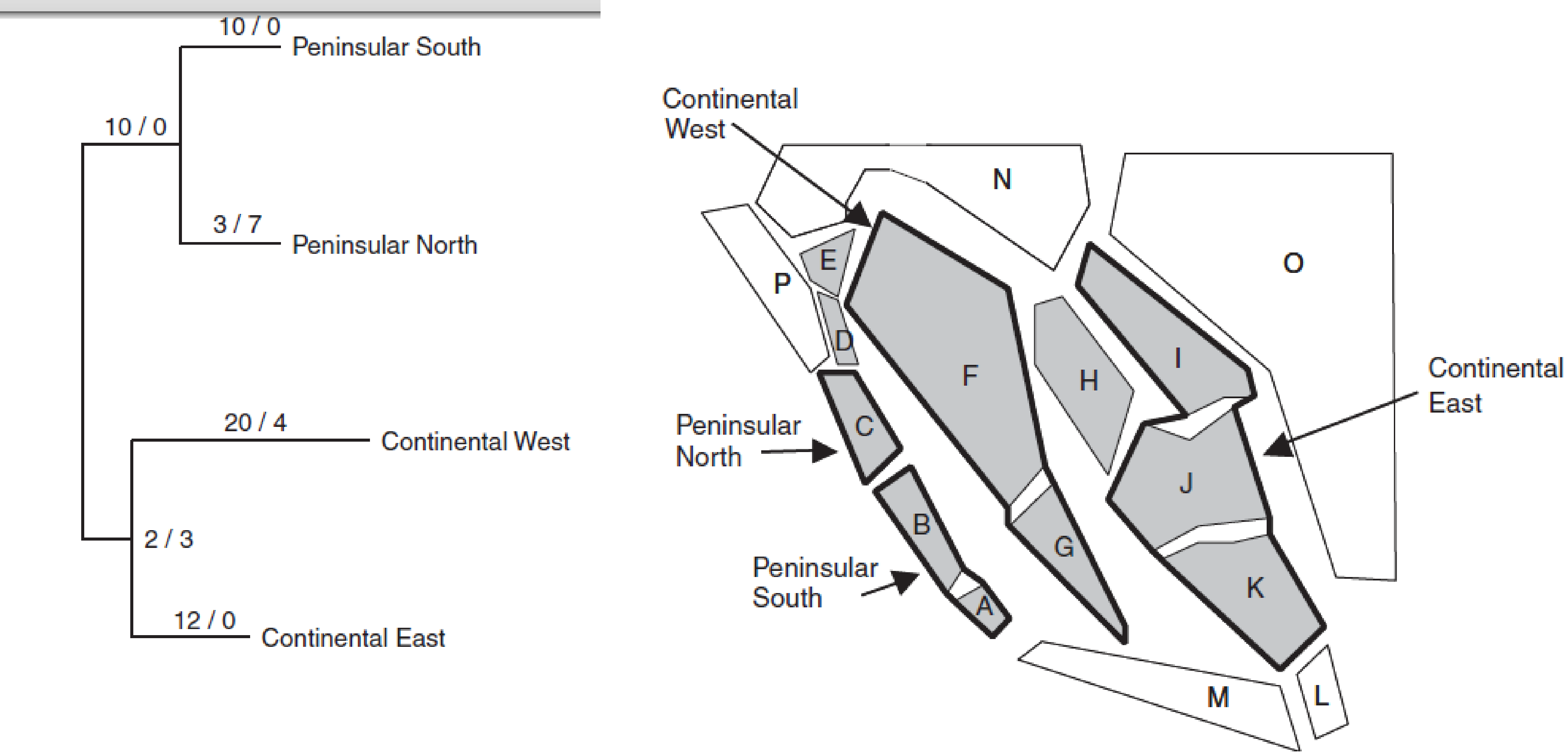
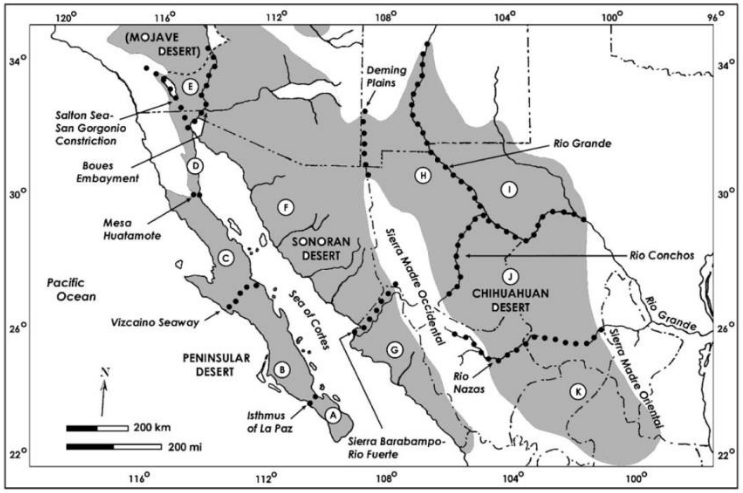


Fig. 5. Final PAE parsimony tree (top) and postulated areas of endemism comprised of one or more distributional areas (bottom). Numbers indicate endemic/widespread taxa.

estudo filogeográfico nos desertos da América do Norte

Riddle & Hafner 2006



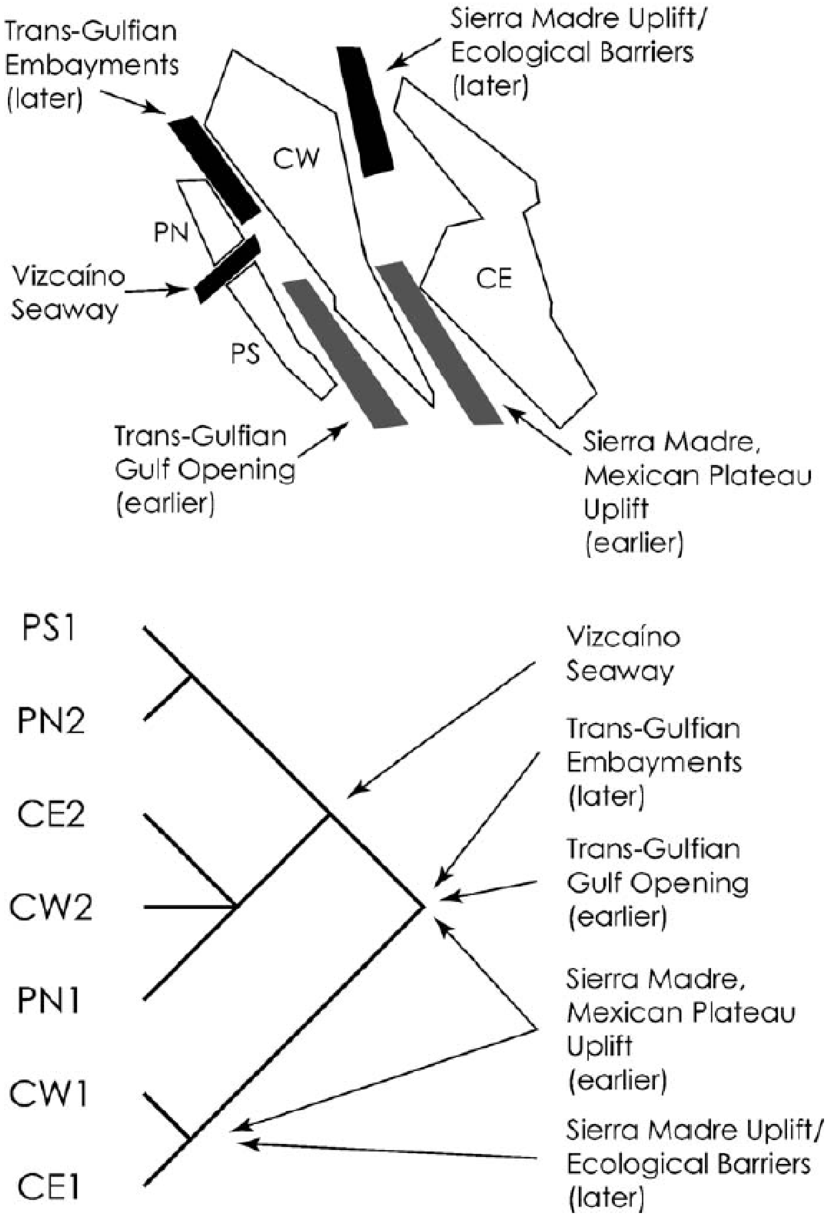


Fig. 8. Depiction of postulated vicariant events (top) among four areas of endemism, and a model of historical vicariance as the events are associated with the secondary BPA tree (Fig. 7).

SÍNTESE EMERGENTE NA BIOGEOGRAFIA ?

1. Modelos de Biogeografia Ecológica incorporando Filogenias e Filogeografia (Wiens & Donoghue 2004, Hawkins et al. 2006, Riddle & Hafner 2006, Hill & Guralnick 2010)

2. Paleobiogeógrafos empregando métodos filogenéticos modernos (Kuch et al. 2002, Lieberman 2003, Doyle 2008)

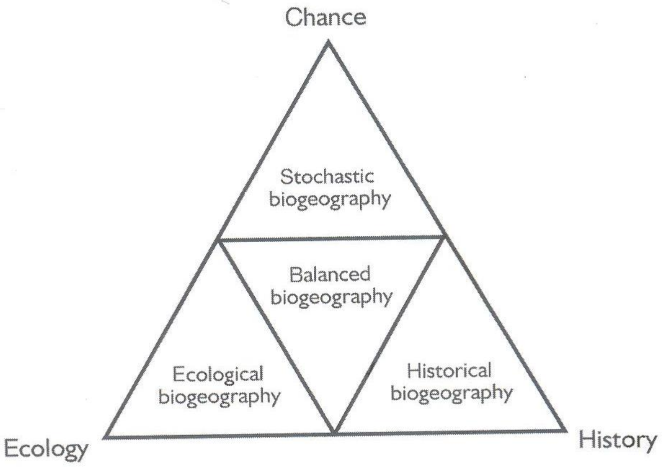
3. Estimativas mais refinadas de tempo de divergência (relógios moleculares relaxados) serão consistentes com registro fóssil (Renner 2005, Won & Renner 2006, De Baets et al. 2016).

4. Filogeografia aproximando as perspectivas modernas e paleoecológicas – biotas do Neógeno superior (Riddle & Hafner 2004, Betancourt 2004, Swenson 2008)

Lomolino et al. 2006

Baker et al. 2014:

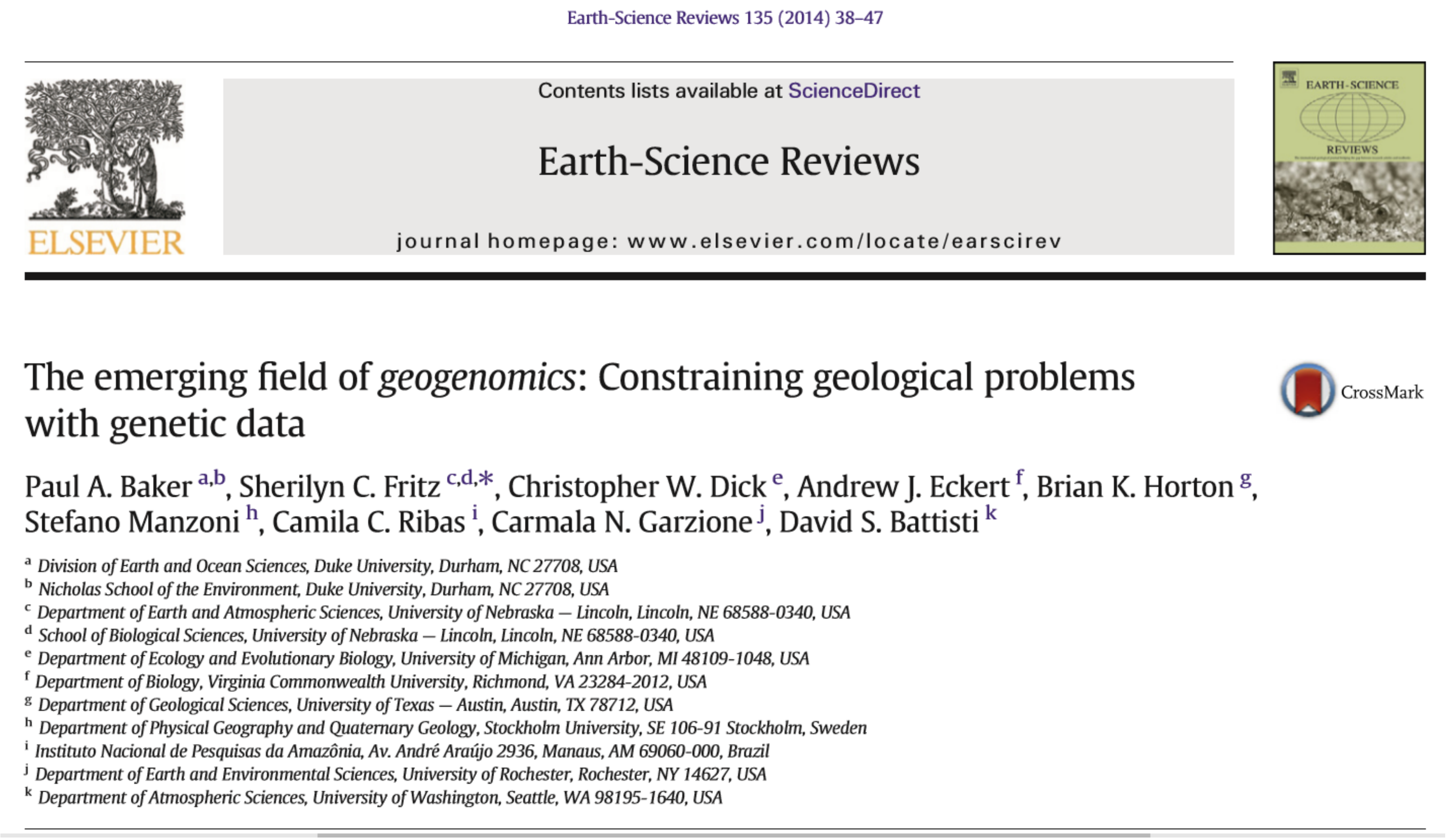
5. Geogenômica – testes de hipóteses geológicas por meio de dados bióticos evolutivos.



Morrone 2009

GEOGENÔMICA

Baker et al. 2014



Earth-Science Reviews 135 (2014) 38–47

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journal homepage: www.elsevier.com/locate/earscirev

The emerging field of *geogenomics*: Constraining geological problems with genetic data

Paul A. Baker [a,b], Sherilyn C. Fritz [c,d,*], Christopher W. Dick [e], Andrew J. Eckert [f], Brian K. Horton [g], Stefano Manzoni [h], Camila C. Ribas [i], Carmala N. Garzione [j], David S. Battisti [k]

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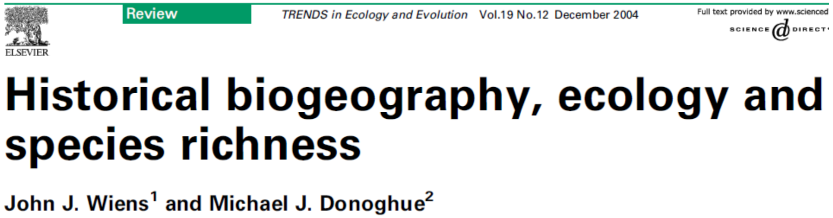
Modelo de Biogeografia Integrativa que discutiremos em classe



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Review

TRENDS in Ecology and Evolution Vol.19 No.12 December 2004

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Historical biogeography, ecology and species richness

John J. Wiens[1] and Michael J. Donoghue[2]

Wiens & Donoghue 2004

ecology
+ filogenia
+ microevolução

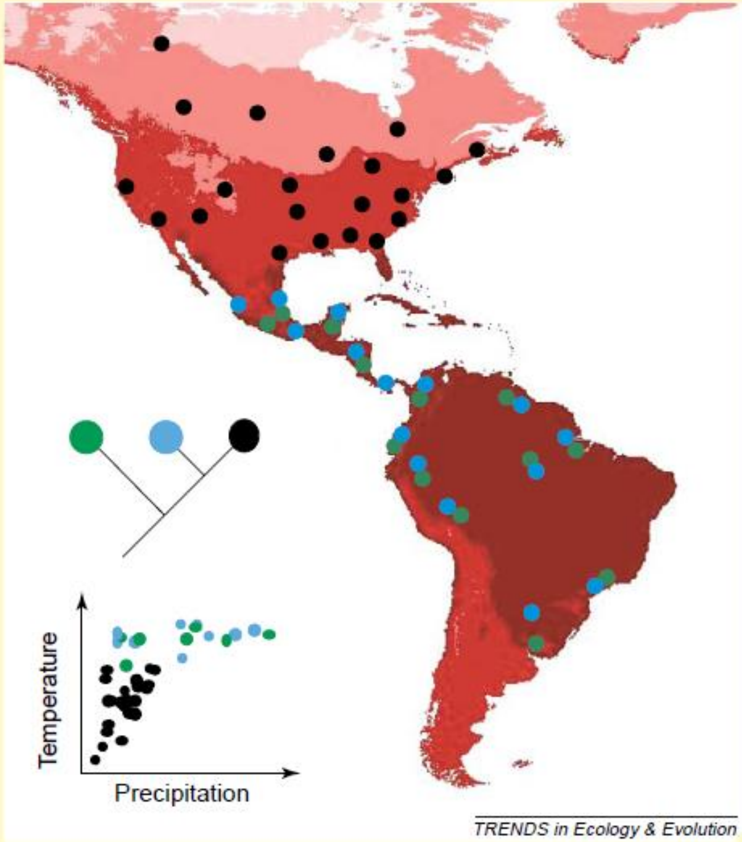

Figure I. Hypothetical example illustrating niche conservatism and niche evolution. Different colored dots on the map and graph indicate localities for members of three clades. Lighter shades of red indicate colder yearly minimum temperatures. Two of the clades (blue and green) exhibit niche conservatism. Species in these clades are confined to tropical climates and fail to invade cooler regions in North America, southern South America, and high elevations, despite their geographical proximity to these areas (we assume that their spread into these regions is not limited by competition). The third clade (black dots) exhibits niche evolution relative to the other two. This clade has invaded temperate regions (presumably by evolving tolerance to freezing winter temperatures) and no longer occurs in the ancestral tropical climatic regime.

Hubble 2001

The Unified Neutral Theory of Biodiversity and Biogeography

a general neutral theory to explain the origin, maintenance,
and loss of biodiversity in a biogeographic context.

Although neutral, Hubbell's theory is nevertheless able to generate many nonobvious, testable, and remarkably accurate quantitative predictions about biodiversity and biogeography.

In many ways Hubbell's theory is the ecological analog to the neutral theory of genetic drift in genetics.

The unified neutral theory of biogeography and biodiversity should stimulate research in new theoretical and empirical directions by ecologists, evolutionary biologists, and biogeographers.

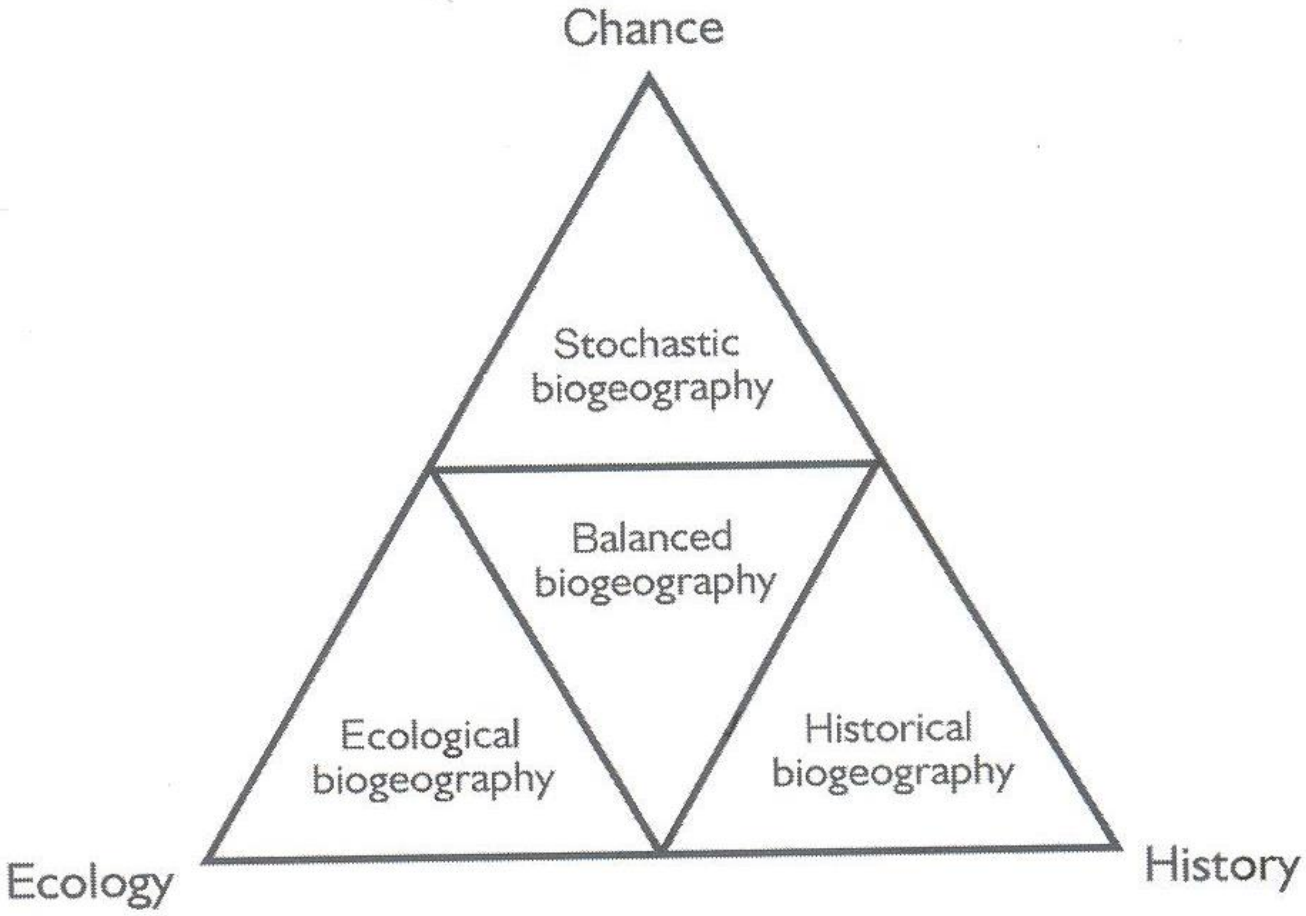

Figure 2.3 Balanced biogeography, as envisioned by Haydon et al. (1994), based on the complementary roles of ecology, history, and chance.

Morrone 2009