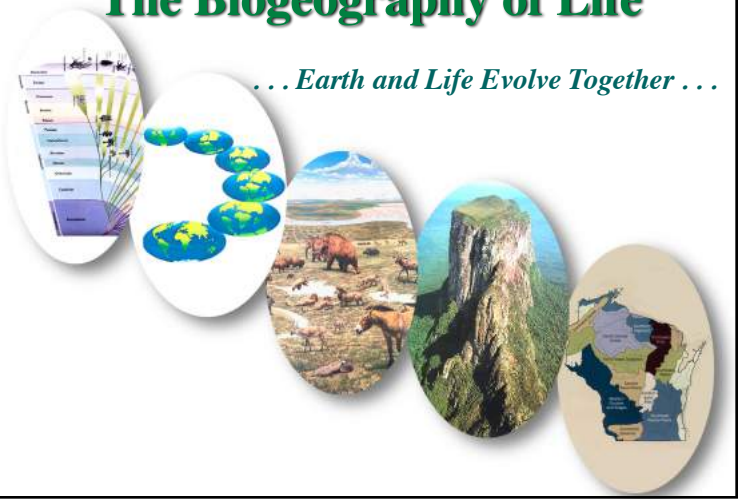
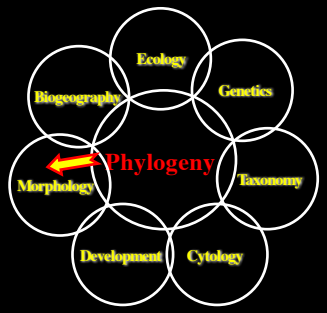
The Biogeography of Life

. . . Earth and Life Evolve Together . . .

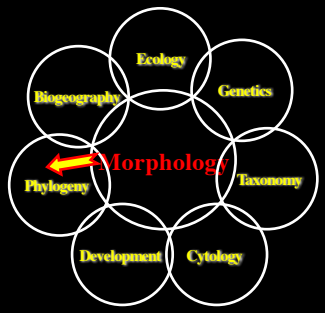


"Nothing in evolution makes sense except in the light of molecular phylogenetics?"

Yes, in part

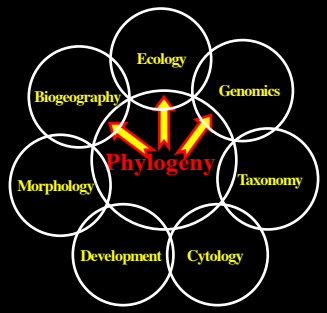


But, it is a two-way interaction



Future of Molecular Systematics

1. Biogeography
2. Ecology
3. Genomics



Future of Molecular Systematics

1. Biogeography
2. Ecology
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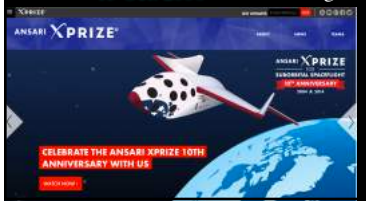
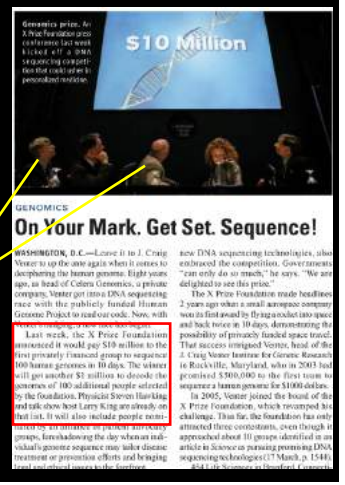
Science Magazine
13 Oct. 2006

Francis Collins
Craig Venter





Future of Molecular Systematics

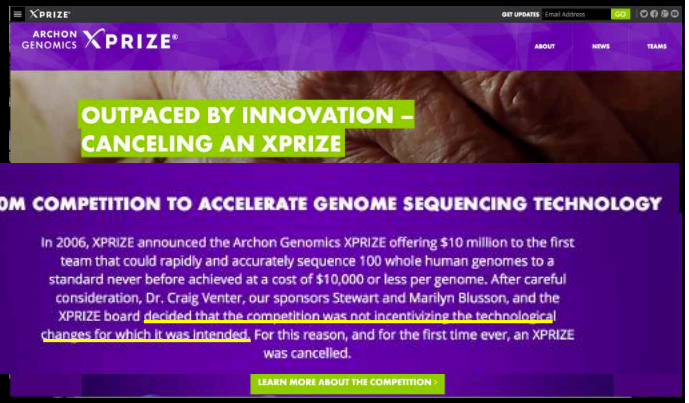
1. Biogeography
2. Ecology
3. Genomics

Nature Genetics
27 Oct. 2011

The Archon Genomics X Prize contest has been declared for January 2013. Larry Kedes and Grant Campany explain the selection of centenarian genomes for the contest and provide the rules by which the contestants will be judged.

A head-to-head competition will take place from 3 January to 3 February 2013. The $10 million grand prize will be awarded to the team(s) able to sequence 100 human genomes within 30 days to an accuracy of 1 error per 1,000,000 bases, with 98% completeness. Identification of insertions, deletions and rearrangements, and a complete haplotype, at an audited total cost of $1,000 per genome. The complete rules for the Archon Genomics X PRIZE presented by MEDCO are available as a supplement to this Commentary (Supplementary Note) and at the competition web site: http://genomics.xprize.org/.

ug 2013



Future of Molecular Systematics

1. Biogeography
2. Ecology
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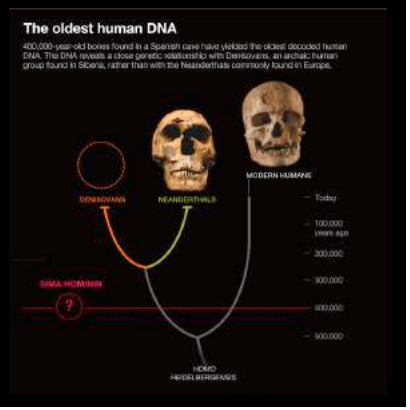
Entire Genome of Extinct Neandertal Decoded
7 Feb 2012

Svante Paabo – Max-Planck Institute

Future of Molecular Systematics

1. Biogeography
2. Ecology
3. Genomics

Nature
November 2013

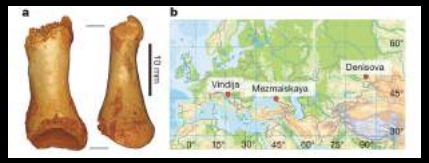


ARTICLE

The complete genome sequence of a Neanderthal from the Altai Mountains

Kay Prüfer[1], Fernando Racimo[2], Nick Patterson[3], Flora Jay[2], Sriram Sankararaman[3,4], Susanna Sawyer[1], Anja Heinze[1], Gabriel Renaud[1], Peter H. Sudmant[5], Cesare de Filippo[1], Heng Li[3], Swapan Mallick[3,4], Michael Dannemann[1], Qiaomei Fu[1,6], Martin Kircher[1,7], Martin Kuhlwilm[1], Michael Lachmann[1], Matthias Meyer[1], Matthias Ongyerth[1], Michael Siebauer[1], Christoph Theunert[1], Arti Tandon[3,8], Priya Moorjani[9], Joseph Pickrell[9], James C. Mullikin[10], Samuel H. Vohr[8], Richard E. Green[8], Ines Hellmann[11], Philip L. F. Johnson[12], Hélène Blanche[13], Howard Cann[13], Jacob O. Kitzman[14], Jay Shendure[14], Evan E. Eichler[15,16], Ed S. Lein[17], Trygve E. Bakken[17], Liubov V. Golovanova[18], Vladimir B. Doronichev[18], Michael V. Shunkov[19], Anatoli P. Derevianko[19], Bence Viola[20], Montgomery Slatkin[2], David Reich[3,4,21], Janet Kelso[1] & Svante Pääbo[1]

We present a high-quality genome sequence of a Neanderthal woman from Siberia. We show that her parents were related at the level of half-siblings and that mating among close relatives was common among her recent ancestors. We also sequenced the genome of a Neanderthal from the Caucasus to low coverage. An analysis of the relationships and population history of available archaic genomes and 25 present-day human genomes shows that several gene flow events occurred among Neanderthals, Denisovans and early modern humans, possibly including gene flow into Denisovans from an unknown archaic group. Thus, interbreeding, albeit of low magnitude, occurred among many hominin groups in the Late Pleistocene. In addition, the high-quality Neanderthal genome allows us to establish a definitive list of substitutions that became fixed in modern humans after their separation from the ancestors of Neanderthals and Denisovans.



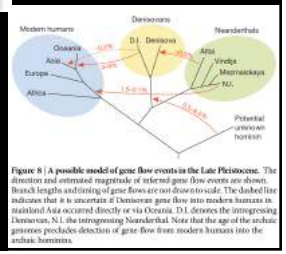


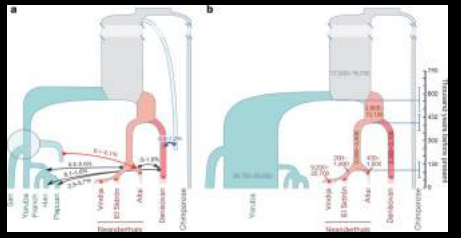
Figure 8 | A possible model of gene flow events in the Late Pleistocene. The direction and estimated magnitude of inferred gene flow events are shown. Branch lengths and timing of gene flows are not drawn to scale. The dashed line indicates that it is uncertain if Denisovan gene flow into modern humans in mainland Asia occurred directly or via Oceania. D.I. denotes the introgressing Denisovan, N.I. the introgressing Neanderthal. Note that the age of the archaic genomes precludes detection of gene flow from modern humans into the archaic hominins.

Nature
January 2014

Ancient gene flow from early modern humans into Eastern Neanderthals

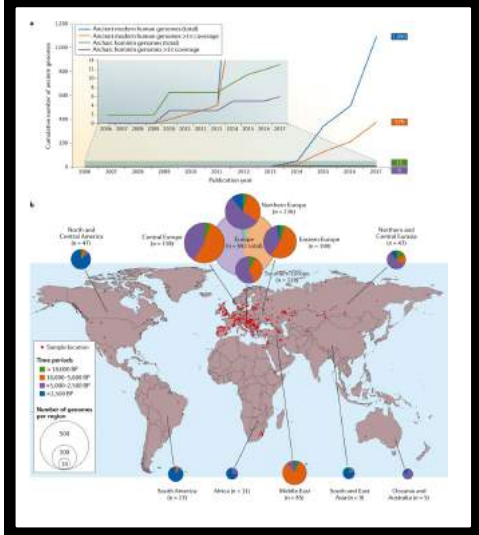
Martin Kuhlwilm[1*], Ilan Gronau[2*], Melissa J. Hubisz[3], Cesare de Filippo[1], Javier Prado-Martinez[4], Martin Kircher[1,5], Qiaomei Fu[1,6,7], Hernán A. Burbano[1,8], Carles Lalueza-Fox[9], Marco de la Rasilla[10], Antonio Rosas[10], Pavao Rudan[11], Dejana Rajkovic[12], Željko Kucan[11], Ivan Gušic[12], Tomas Marques-Bonet[4,13,14], Aida M. Andrés[3], Bence Viola[15,16], Svante Pääbo[1], Matthias Meyer[1], Adam Siepel[2,17] & Sergi Castellano[1]

It has been shown that Neanderthals contributed genetically to modern humans outside Africa 47,000–65,000 years ago. Here we analyse the genomes of a Neanderthal and a Denisovan from the Altai Mountains in Siberia together with the sequences of chromosome 21 of two Neanderthals from Spain and Croatia. We find that a population that diverged early from other modern humans in Africa contributed genetically to the ancestors of Neanderthals from the Altai Mountains roughly 100,000 years ago. By contrast, we do not detect such a genetic contribution to the Denisovan or the two European Neanderthals. We conclude that in addition to later interbreeding events, the ancestors of Neanderthals from the Altai Mountains and early modern humans met and interbred, possibly in the Near East, many thousands of years earlier than previously thought.



Nature
February 2016

Refined demography of archaic and modern humans



Nature Reviews
November 2017

Together with evidence of adaptive introgression of genetic variants from archaic hominins to humans and emerging ancient genome data sets for domesticated animals and plants, these studies provide novel insights into human evolution and the evolutionary consequences of human behaviour

Future of Molecular Systematics

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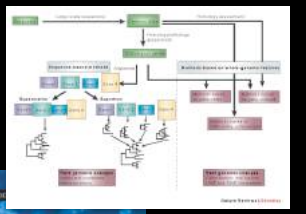
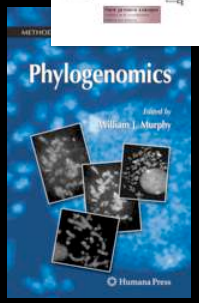
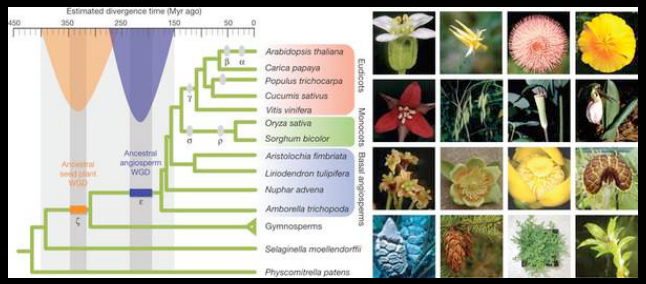




Explicit marriage between phylogenetics and genomics now — phylogenomics

Future of Molecular Systematics



Explicit marriage between phylogenetics and genomics now — phylogenomics

Ancestral polyploidy in seed plants and angiosperms

Yuannian Jiao, Norman J. Wickett, Saravanaraj Ayyampalayam, André S. Chanderbali, Lena Landherr, Paula E. Ralph, Lynn P. Tomsho, Yi Hu, Haiying Liang, Pamela S. Soltis, Douglas E. Soltis, Sandra W. Clifton, Scott E. Schlarbaum, Stephan C. Schuster, Hong Ma, Jim Leebens-Mack & Claude W. dePamphilis

Affiliations | Contributions | Corresponding author

Nature **473**, 97–100 (05 May 2011) | doi:10.1038/nature09916
Received 29 August 2010 | Accepted 10 February 2011 | Published online 10 April 2011

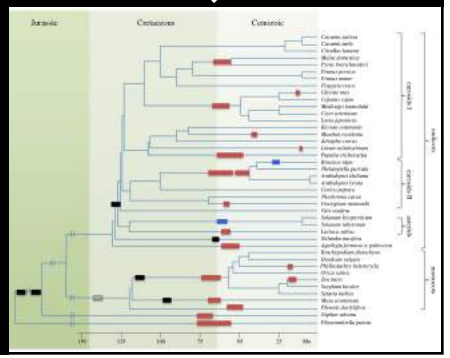
Future of Molecular Systematics

PHILOSOPHICAL TRANSACTIONS OF THE ROYAL SOCIETY B

Tangled up in two: a burst of genome duplications at the end of the Cretaceous and the consequences for plant evolution

2014

K-Pg event



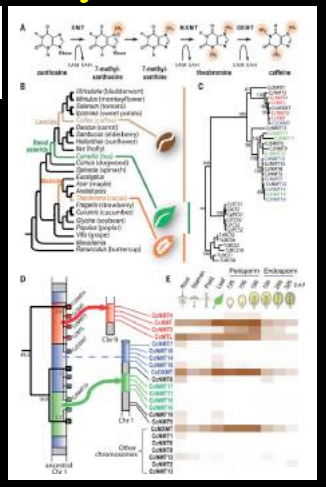
Future of Molecular Systematics

PLANT GENOMICS

The coffee genome provides insight into the convergent evolution of caffeine biosynthesis

Science, Sept 2014

Explicit marriage between phylogenetics and genomics now — phylogenomics



Future of Molecular Systematics

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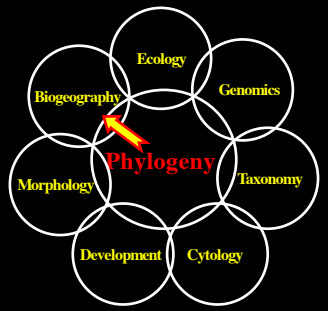


The Biogeography of Life

" . . . that grand subject, that almost keystone of the laws of creation, ***Geographical Distribution*** *"*

[Charles Darwin, 1845, in a letter to Joseph Dalton Hooker, later Director of the Royal Botanic Garden, Kew]

The Biogeography of Life

" . . . that grand subject, that almost keystone of the laws of creation, ***Geographical Distribution*** *"*

Darwin needed two chapters in the *Origin of Species* to cover his ideas on geographical distributions of organisms

"I am prepared to go to the stake, if requisite, in support of the chapters on the geological and geographical distribution of life."

Thomas Huxley after reading the *Origin of Species*

What is Biogeography?

1. *How* are organisms and their attributes distributed over the surface of the earth, and over the history of the earth?

2. *Why* do organisms and their attributes show these patterns of distribution?

Argyroxiphium sandwicense - Haleakala silversword

Approaches to Biogeography

• Biogeography is a broad field - requires information from:

ecology, systematics, evolutionary biology, population biology, genetics, cytology, morphology and anatomy, physiology, paleobiology, the geosciences, and natural history

Argyroxiphium sandwicense - Haleakala silversword

Approaches to Biogeography

• Biogeography is a broad field - requires information from:

ecology, systematics, evolutionary biology, population biology, genetics, cytology, morphology and anatomy, physiology, paleobiology, the geosciences, and natural history

• 3 main flavors of biogeography

Argyroxiphium sandwicense - Haleakala silversword

Floristic (or Faunistic) Biogeography

— Where various *taxa* are distributed

Where are members of the Cactaceae (cactus family) found?

Ecological Biogeography

Koompassia (Fabaceae)

— Distributions of *attributes* of organisms without concern to their classification

Why do rainforests occur where they do?

The plants that dominate the rain forests of southeast Asia are taxonomically distinct from those of South America, but forests are physiognomically similar (e.g. giant buttress-rooted emergent trees)

Vegetation looks the same, but the floras are different (Alexander von Humboldt!)

Historical Biogeography

— Combines organismal history with geological events to explain past and present distributions

"Earth and Life Evolve Together"

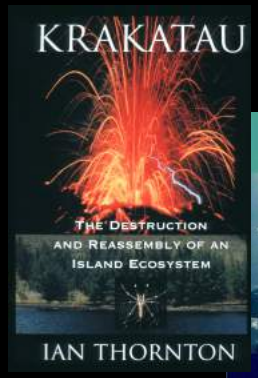
Requires information from previous two branches of biogeography plus phylogenetics and earth history

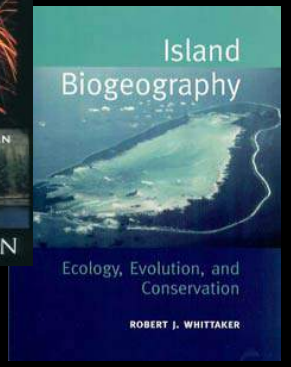
Historical Biogeography

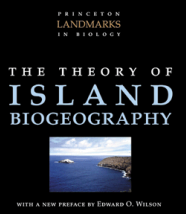
— Combines organismal history with geological events to explain past and present distributions

The interplay of geological and biological evolution is critical in understanding why the Haleakala silversword is found in Maui, when and where it or its ancestors came from, and why it is has specific features of morphology, chromosome number, and physiology.

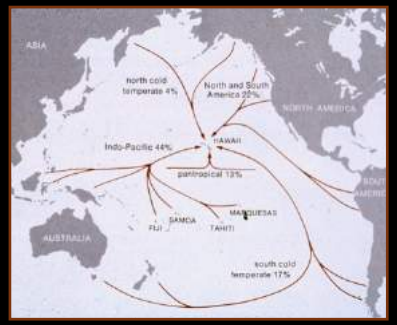
Biogeography includes . . . island biogeography







Biogeography includes . . . dispersal biogeography

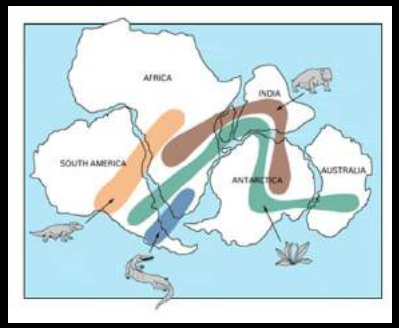


Biogeography includes . . . plate tectonics

Biogeography includes . . . plate tectonics

Alfred Wegener (1920) described both plant and animal fossil examples supporting his theory — he believed that this biogeographic data was the strongest evidence for his theory

- geological strata continuous between continents
- fossil disjunct distributions between continents



Glossopteris - Permian "fern"

Mesosaurus - Permian freshwater reptile

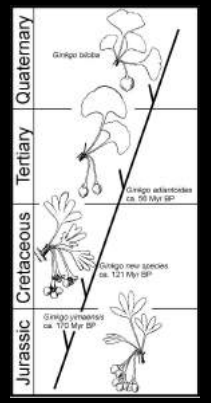
Cynognathus - Triassic land reptile

Lystrosaurus - Triassic land reptile

Biogeography includes . . . paleobiogeography

Jurassic Period (208 - 146 mya)

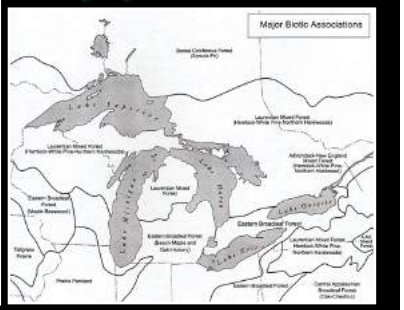
"Modern" genera are first seen for *Ginkgo*



Biogeography includes . . . glacial history

Pleistocene

The final shaping of North American (and Great Lakes) flora and vegetation occurs during the Recent Epoch (Holocene) following the glaciation of the Pleistocene

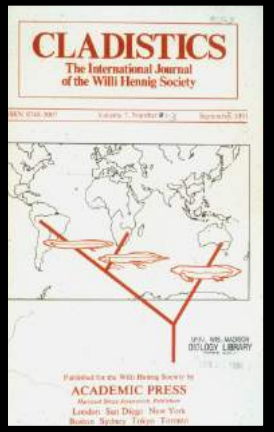


Holocene

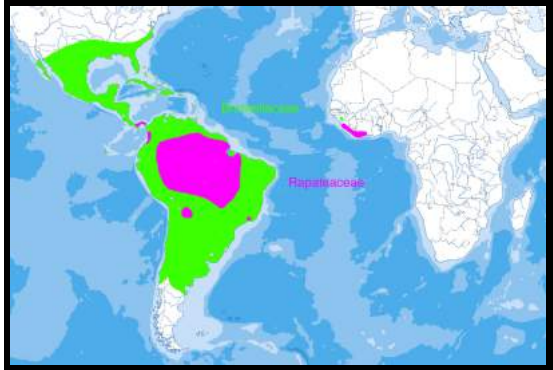
Biogeography + Phylogenetics

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

Phylogenetics and historical biogeography are now intimately intertwined . . .



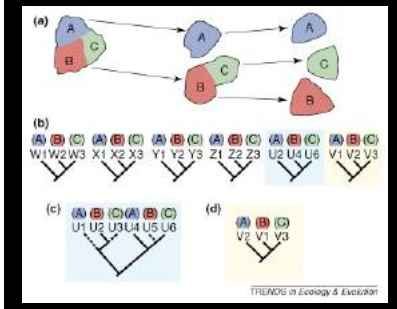
Disjunctions: how are these distribution patterns explained?

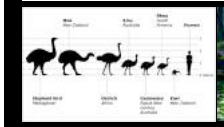


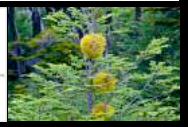
Two main ideas:

- geological events separate once continuous biota (vicariance)
- dispersal events over geological barriers (dispersalism)

Disjunctions: how are these distribution patterns explained?







Vicariance paradigm:

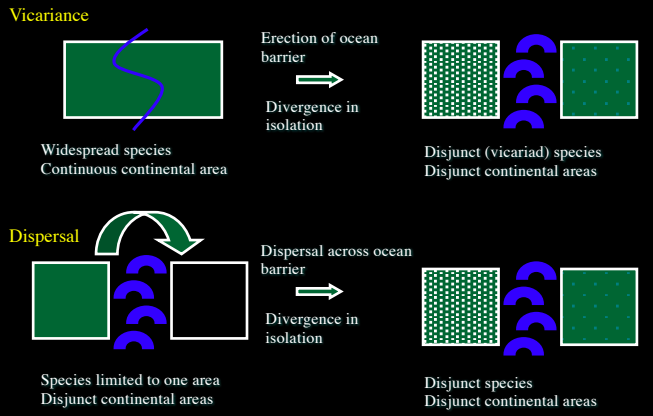
- unrelated sets of species show repeated pattern of area relationships via geological events (e.g., rafting of continents)

Disjunctions: how are these distribution patterns explained?

Dispersalist paradigm:

- species move independently via long distance dispersal over pre-existing geological barriers

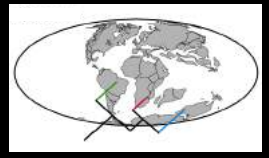
Vicariance vs. Dispersal similar pattern, different process



Vicariance vs. Dispersal how do you decide?

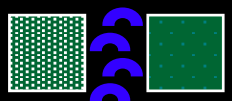
Historical Biogeography has relied on two sources of information

1. Phylogenetic trees - clades
2. Knowledge of splitting events of areas - continents, mountain erection, etc.



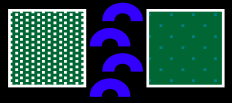
If multiple groups of organisms show congruence in the pattern - then vicariance is assumed

Vicariance



Disjunct (vicariad) species
Disjunct continental areas

Dispersal



Disjunct species
Disjunct continental areas

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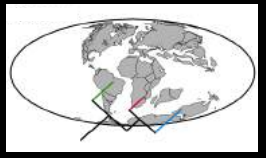
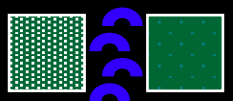


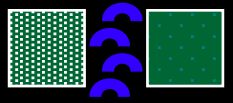
Dispersal is often relegated to "geographical noise", *ad hoc*, untestable, and thus even non-scientific

Vicariance



Disjunct (vicariad) species
Disjunct continental areas

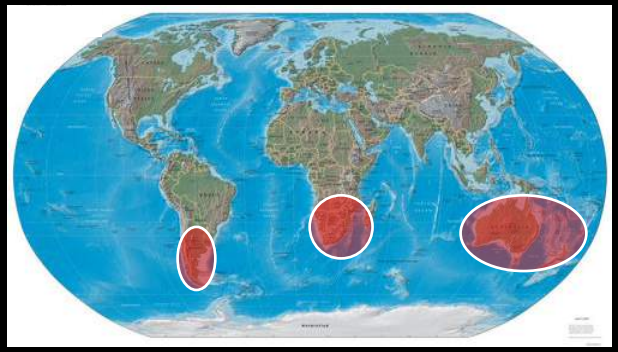
Dispersal



Disjunct species
Disjunct continental areas

Southern Hemisphere Temperate Flora

• Southern Hemisphere temperate plants, animal, and fungi are classic in vicariance vs. dispersal arguments



Southern Hemisphere Temperate Flora

Nothofagaceae - 35 species of trees and shrubs, evergreen and deciduous, restricted to South America, New Zealand, Australia, Tasmania, New Caledonia, New Guinea, and fossilized in Antarctica

Absent from Africa! — "odd continent out"

Southern Hemisphere Temperate Flora

Connections between South America and Australasia pronounced:

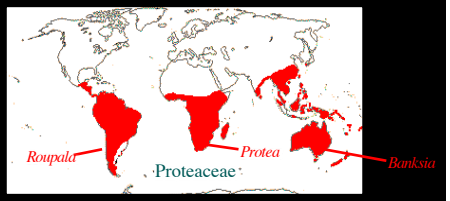
- Subg. *Nothofagus* — South America
- Subg. *Fuscospora* — S. Am., N. Zeal., Tasmania
- Subg. *Lophozonia* — S. Am., N. Zeal., Tasmania, Austr.
- Subg. *Brassospora* — New Caledonia, New Guinea

Southern Hemisphere Temperate Flora

Proteaceae comprise 1700 species of woody plants placed in 79 genera predominantly of the southern hemisphere. Unlike Nothofagaceae, occurs in south Africa and Madagascar, and extends into southern China.

The 16 genera from Africa are endemic and comprise only 3 lineages. In comparison, South America and Australasia share roughly half of the genera in common. All tribes within the latter two areas are shared.

Africa — "odd continent out"!



Southern Hemisphere Temperate Flora

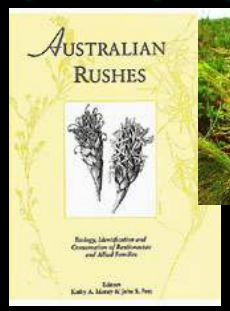
Restionaceae comprise 520 species of grass-like plants placed in 58 genera predominantly of the southern hemisphere.

Askidiosperma — Restionaceae
Cape Region

Southern Hemisphere Temperate Flora

Restionaceae comprise 520 species of grass-like plants placed in 58 genera predominantly of the southern hemisphere.

The 350 species from Africa are unique and belong only to 11 genera of the *Restio* group. In contrast, South America and Australasia share many genera including some species. Africa — "odd continent out"!



Fynbos, S. Africa
— Restionaceae

Southern Hemisphere Temperate Flora

Why is Africa the "odd continent out" when it comes to the *temperate* southern hemisphere flora?

Three reasons:

Proteaceae

Restionaceae

Nothofagaceae

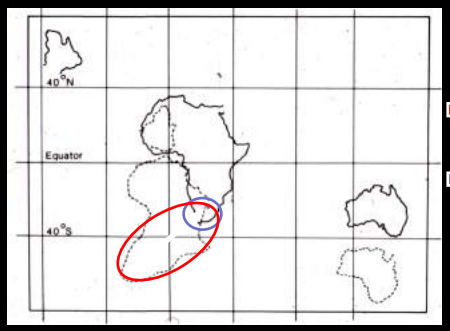
Southern Hemisphere Temperate Flora

1. All three continents separated from Gondwana at about 100-110 mya in the early Cretaceous, but South America and Australia linked with temperate Antarctica until about 50 mya (and via small water passages until 27 mya)

Estimates in millions of years BP when migration routes between land masses were broken or made.

Southern Hemisphere Temperate Flora

2. Africa drifted further north and experienced greater climatic change through this latitudinal journey. Greater extinction of temperate biota in Africa; which is now restricted to small area of south Africa.



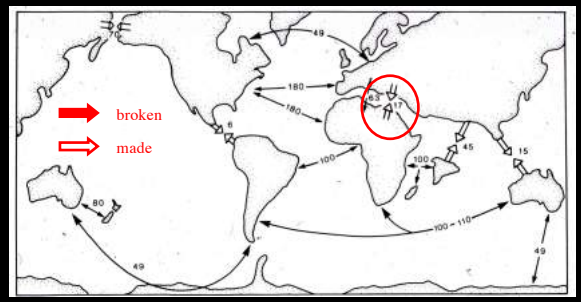
Temperate flora Triassic

Temperate flora Present

Positions of Labrador, Africa, and Australia in the Triassic (200 mya) and at the present

Southern Hemisphere Temperate Flora

3. Africa made secondary contact with temperate Eurasia around 17 mya; long contact further differentiated the temperate flora of Africa relative to South America and Australia



Estimates in millions of years BP when migration routes between land masses were broken or made.

Southern Hemisphere Temperate Flora

Bromeliaceae

Rapateaceae

Are all these southern hemisphere disjunct patterns best explained by vicariance (i.e., continental drift)?

We can get information about continents, the relationships of organisms or clades, but we still have little knowledge about timing of events or a clock.

Vicariance vs. Dispersal how do you decide?

Historical Biogeography has relied on two sources of information

1. Phylogenetic trees - clades
2. Knowledge of splitting events of areas - continents, mountain erection, etc.

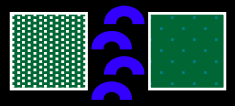
What is missing?

3. Times for branching events of clades - "clocks" !

Vicariance

Disjunct (vicariad) species
Disjunct continental areas

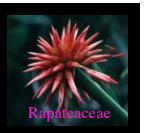
Dispersal



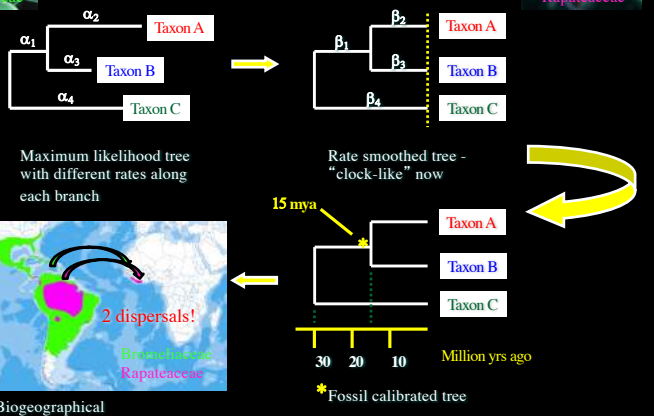
Disjunct species
Disjunct continental areas

Continents, Clades, and Clocks

Bromeliaceae

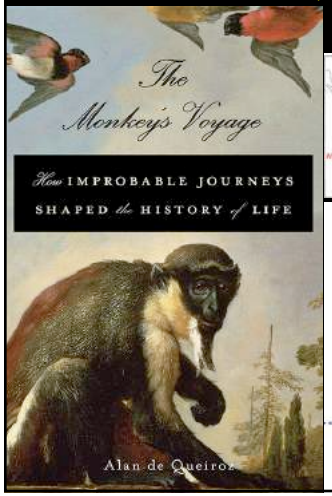


Rapateaceae

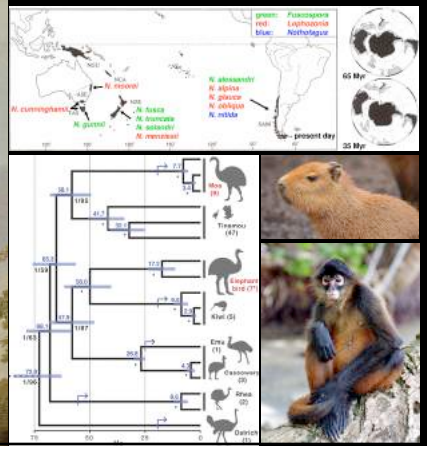


Biogeographical interpretation

Continents, Clades, and Clocks



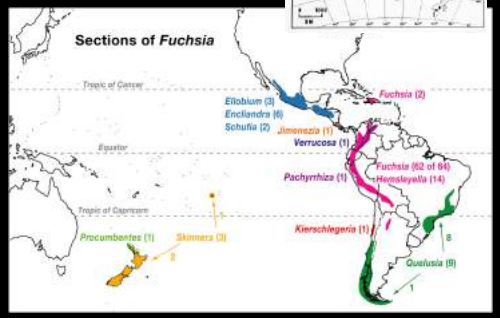
Re-thinking the "classic" vicariance stories . . .

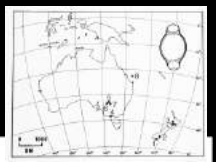


Earth and Life Evolve Together

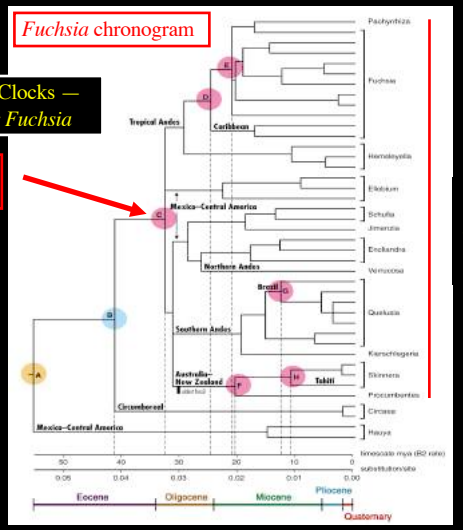
Continents, Clades, and Clocks — Putting it all together for *Fuchsia*

25-30 mya *Diporites* (*Fuchsia*) pollen fossils





Fuchsia chronogram

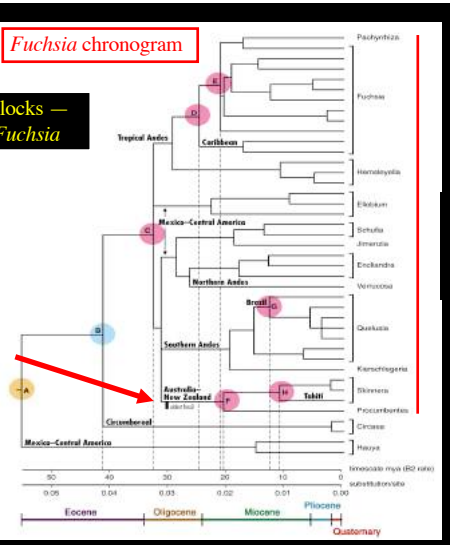


Continents, Clades, and Clocks — Putting it all together for *Fuchsia*

Fuchsia diversifies at 32 my in South America

Fuchsia

Fuchsia chronogram



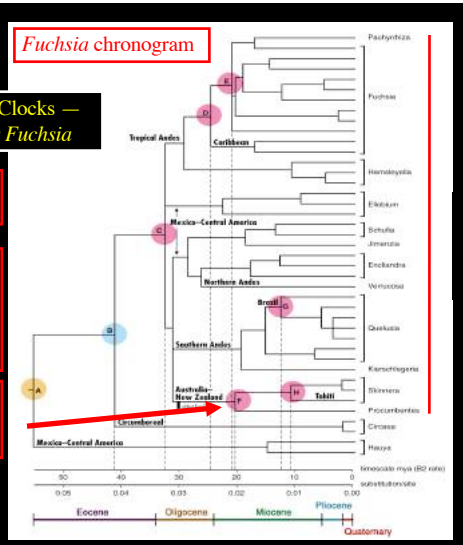
Continents, Clades, and Clocks — Putting it all together for *Fuchsia*

Fuchsia diversifies at 32 my in South America

Old world *Fuchsia* divergence dated at 30 my, consistent with oldest Australian fossils (25-30 my)

Fuchsia

Fuchsia chronogram



Continents, Clades, and Clocks — Putting it all together for *Fuchsia*

Fuchsia diversifies at 32 my in South America

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Long-distance Dispersal to New Zealand dated at 20 my

Fuchsia

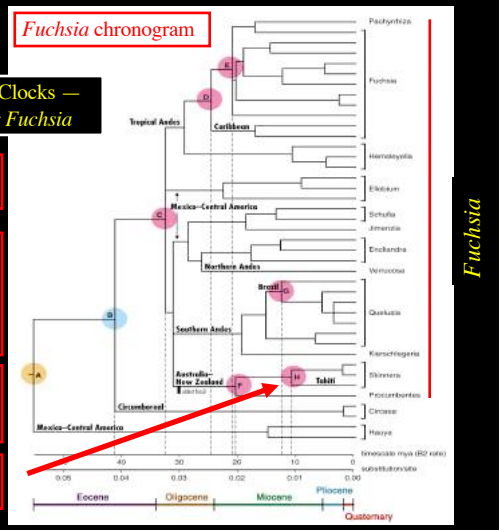
Continents, Clades, and Clocks — Putting it all together for *Fuchsia*

Fuchsia diversifies at 32 my in South America

Old world *Fuchsia* divergence dated at 30 my, consistent with oldest Australian fossils (25-30 my)

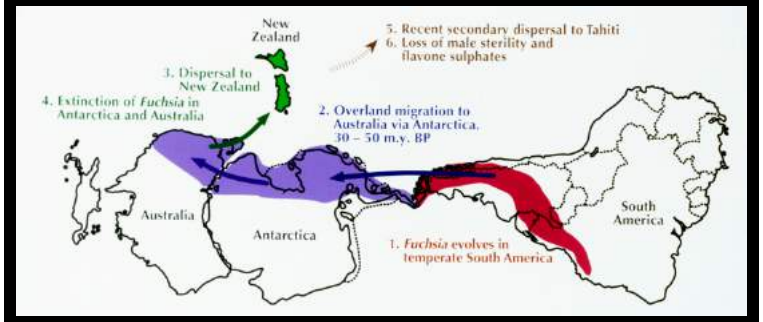
Long-distance Dispersal to New Zealand dated at 20 my

Long-distance Dispersal to Tahiti at 10 my



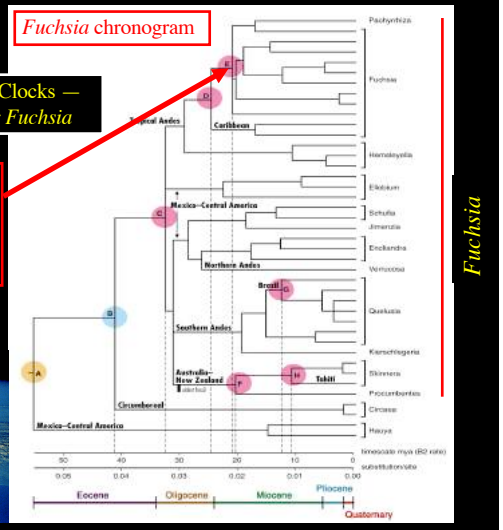
Continents, Clades, and Clocks — Putting it all together for *Fuchsia*

Species relationships and timing indicate Gondwanan break-up (vicariance) followed by dispersal events to New Zealand and later Tahiti



Continents, Clades, and Clocks — Putting it all together for *Fuchsia*

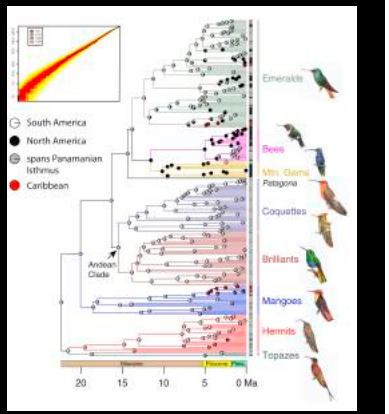
Explosive radiation of sect. *Fuchsia* dated at 20 my, consistent with initial orogeny of the Andean mountains . . .



Earth and Life Evolve Together

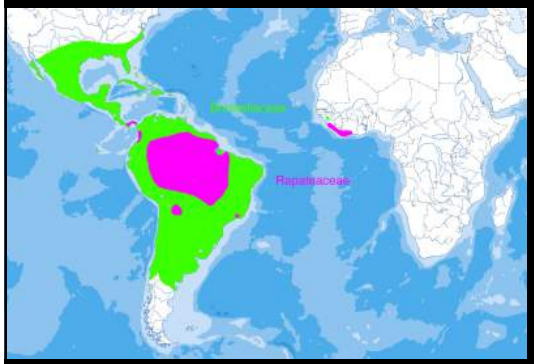
Continents, Clades, and Clocks — Putting it all together for *Fuchsia*

. . . and of their pollinators



Rapid radiation of hummingbirds – McGuire et al. 2015

Disjunctions: how are these distribution patterns explained?



Synthesis:

- vicariance explains some but not all disjunct patterns
- dispersalism requires numerous (but likely!) events
- many disjunctions are complex and involve both

" . . . *that grand subject, that almost keystone of the laws of creation, Geographical Distribution*"

If you are still around:
Botany 422 – *Biogeography*
Spring 2017