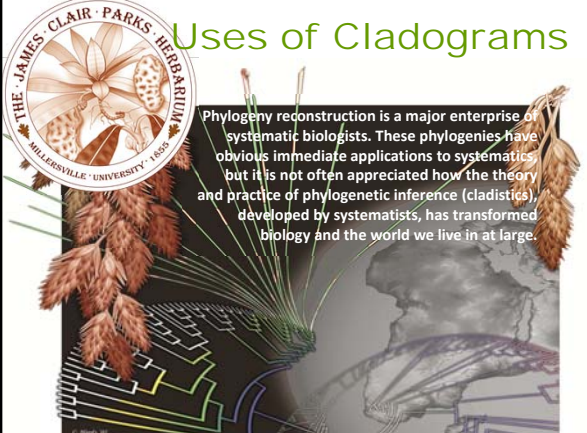


Uses of Cladograms

Phylogeny reconstruction is a major enterprise of systematic biologists. These phylogenies have obvious immediate applications to systematics, but it is not often appreciated how the theory and practice of phylogenetic inference (cladistics), developed by systematists, has transformed biology and the world we live in at large.

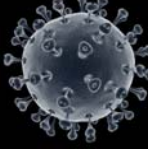


I. Disease Origins & Epidemiology



HIV Origins





HIV Origins






Table 1. A comparison of the two major families of Human Immunodeficiency Virus (HIV).

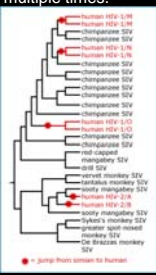
Species	Virulence	Transmissibility	Prevalence
HIV-1	High	High	Global
HIV-2	Lower	Low	West Africa



HIV Origins

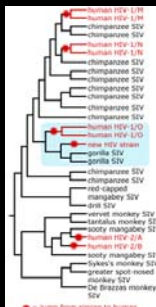
Cladograms show HIV derived from SIV multiple times.





2008


• = Jump from non-human to human



2015


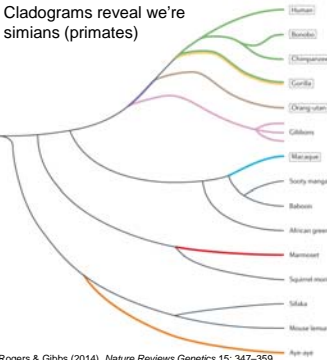
• = Jump from non-human to human

http://evolution.berkeley.edu/evolibrary/news/081101_hivorigins




HIV Origins

Cladograms reveal we're simians (primates)

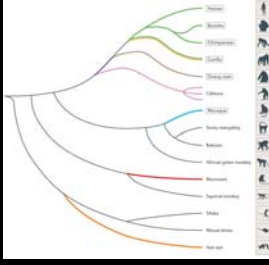
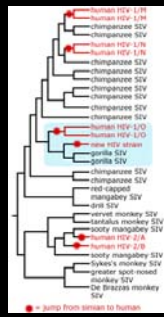



Rogers & Gibbs (2014). *Nature Reviews Genetics* 15: 347–359.



HIV Origins

Cladograms help explain why most widespread & virulent (HIV-1) came from chimp & gorilla SIV.



HIV Origins

But how?





HIV Origins

But how?

A Startling New Theory Attempts To Answer The Question 'Was It An Act Of God Or An Act Of Man?'

by Tom Curtis

Rolling Stone, Issue 626, 19 March 1992, pp. 54-59, 61, 106, 108, omitting photos and captions.

It was almost thirty years ago, but I clearly remember one event on that hot and humid day early in August 1962. Like communicants in some universal mass, my two brothers, my parents and I slowly moved to the head of a very long, snaking line composed of thousands of people - a significant part of the population of Galveston, Texas. All were awaiting admittance into the central hallway of Ball High School so we could approach a simple wooden table - a kind of altar of science - where a volunteer nurse handed each individual a tiny paper cup containing a sugar cube. I gazed intently at mine. One side had a faint yellow tinge and dark specks where the half-cubic-centimeter or so drop of liquid vaccine had landed. Though I was surprised that my cube was so dirty looking, I popped it in my mouth, chewed and swallowed. The rest of my family followed suit. Over the next two years, the same ritual was played out in towns and cities across America. These other patient believers, like me and my family, were seeking not life eternal but science's more secular but no less miraculous promise: everlasting immunity from the most dreaded scourge of the Forties and Fifties - paralytic poliomyelitis. Before the polio vaccines were introduced in the Fifties, the disease had struck about 22,000 people a year in the United States alone - often young children. The new, vibrant medium of television showed kids like us shackled by leg braces and crutches or imprisoned in iron lings - huge cylinders covering all but their heads. I had an even more terrifying image of the ravages of polio. A close friend of my parents, a vital young physician named Martin Schneider, had contracted the disease in 1948 and would spend the last two decades of his life paralyzed from the waist down and confined to a wheelchair.

In one of the greatest triumphs of twentieth-century medicine, the promise to deliver us from that crippling contagion was kept. The one-two punch of the "polio shots" developed by Dr. Jonas Salk and the oral






HIV Origins


Cladistic findings highlight the role of the bushmeat trade.



HIV Epidemiology

Ou et al. (1992) *Science* 256: 1165 (and others)

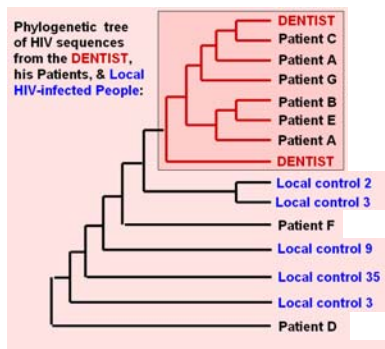


1990s, small Florida town:

- Young patient with no apparent risk factors comes down with and dies of AIDS.
- CDC investigates and finds other infected persons
- Many shared dentist who was HIV positive.

- Did these infections stem from the dentist?

Phylogenetic tree of HIV sequences from the **DENTIST**, his Patients, & Local HIV-infected People:



Which patients were infected by dentist, which were not?

From Ou et al. (1992) and Page & Holmes (1998)

II. Character Evolution



A. Homology Assessment

1. 1° homology assessment during character coding & scoring

e.g.,
PETAL COLOR:
0 = red; 1 = blue

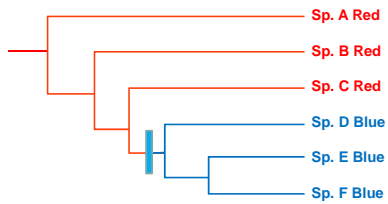
Position 4 in *rbcL*
A; G; C; or T

II. Character Evolution



A. Homology Assessment

2. 2° homology assessment read from cladogram using optimization methods

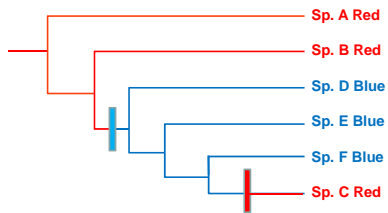


II. Character Evolution



A. Homology Assessment

2. 2° homology assessment read from cladogram using optimization methods



II. Character Evolution



B. Testing Adaptational Hypotheses e.g., succulence

Observation:
Cactaceae are succulent and grow in xeric envs

Hypothesis:
Succulence is an adaptation to xeric envs



Cereus (Cactaceae)

II. Character Evolution

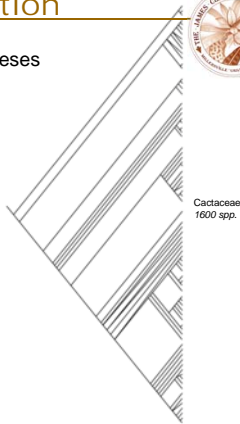


B. Testing Adaptational Hypotheses e.g., succulence

Observation:
Cactaceae are succulent and grow in xeric envs

Hypothesis:
Succulence is an adaptation to xeric envs

Test:
Do nearly 1600 obs of succulence & xeric envs support this?



II. Character Evolution



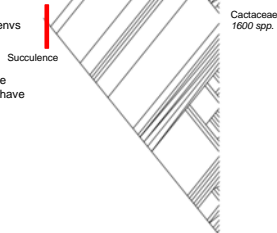
B. Testing Adaptational Hypotheses e.g., succulence

Observation:
Cactaceae are succulent and grow in xeric envs

Hypothesis:
Succulence is an adaptation to xeric envs

Test:
Do nearly 1600 obs of succulence & xeric envs support this?

Answer:
No. You have one occurrence of succulence evolving with a xeric habitat. 1600 species have simply inherited these traits.



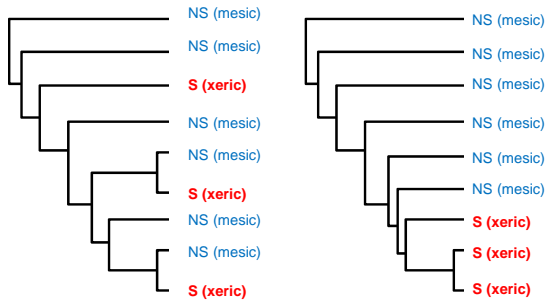
II. Character Evolution



B. Testing Adaptational Hypotheses

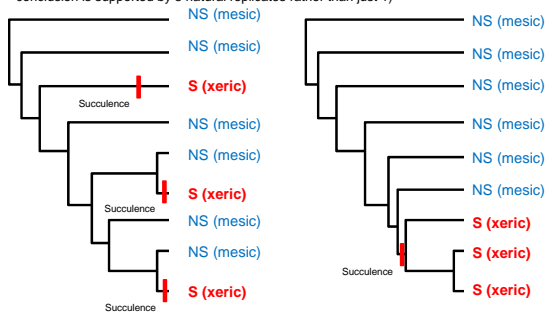


Which cladogram(s) provides evidence for succulence as an adaptation to desert (xeric) environments?



Which cladogram(s) provides evidence for succulence as an adaptation to desert (xeric) environments?

- Left has succulence evolving with xeric 3x's rather than 1x.
- Repeated evolution of 1 trait with 1 particular selective agent provides stronger evidence (i.e. conclusion is supported by 3 natural replicates rather than just 1)



II. Character Evolution

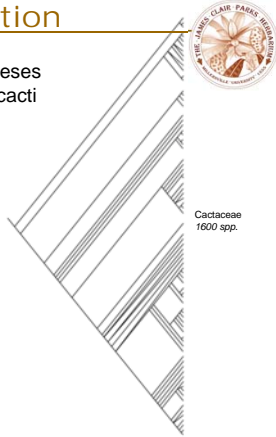
B. Testing Adaptational Hypotheses e.g., origin of epiphytism in cacti

Observation 2

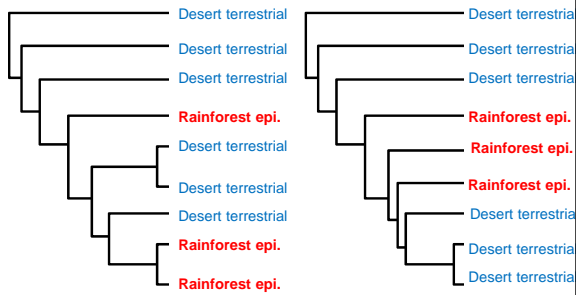
1. While many Cactaceae occur in deserts, some occur as epiphytes in Neotropical rainforests.
2. Epiphytism requires water-use efficiency.

Hypotheses:

Adaptation of terrestrial cacti to deserts may have allowed them to invade rainforest canopies as epiphytes.

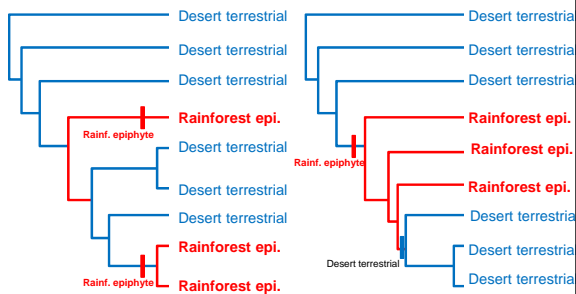


Which cladogram(s) support this?

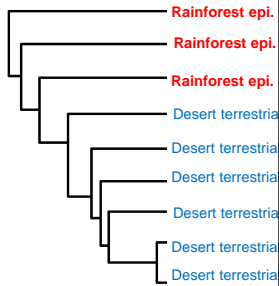


Which cladogram(s) support this?

- Both show rainforest epiphytism evolving from a desert terrestrial habit.

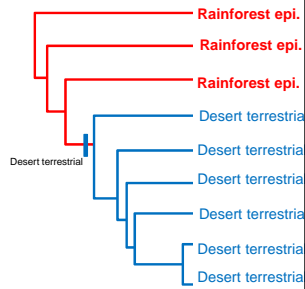


What does this cladogram suggest?



What does this cladogram suggest?

- This one shows the inverse of our hyp: that desert terrestrials evolved from rainforest epiphytes.

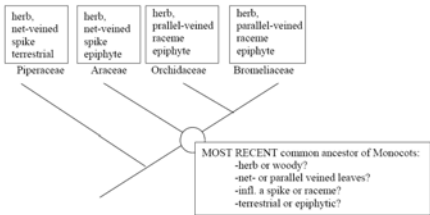


II. Character Evolution



C. Ancestor Reconstruction

34. Based on the following cladogram and the principle of parsimony, infer the morphology of the MOST RECENT common ancestor of monocots.



- an epiphytic shrub with net-veined leaves and a raceme for an inflorescence.
- an epiphytic herb with net-veined leaves and spike inflorescences.
- a terrestrial herb with net-veined leaves and raceme inflorescences.

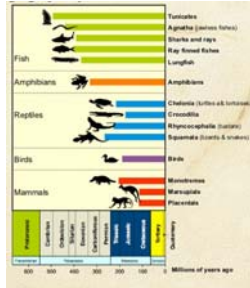
II. Character Evolution



C. Ancestor Reconstruction Tetrapod origins / evolution

Observation:
Fish fossils date back more than 450 mya
Tetrapod fossils date no more than 350 mya

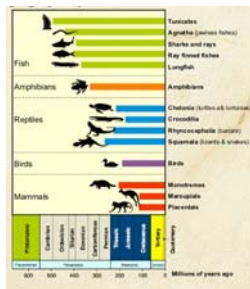
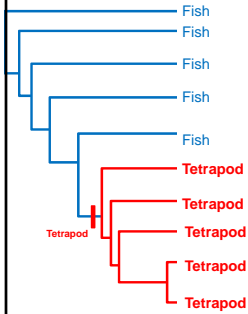
Hypothesis:
Tetrapod verts evolved from fish.



II. Character Evolution



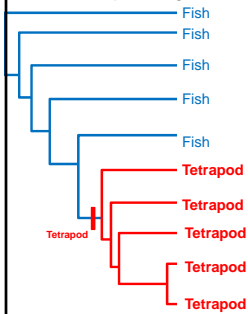
C. Ancestor Reconstruction Tetrapod origins / evolution



II. Character Evolution



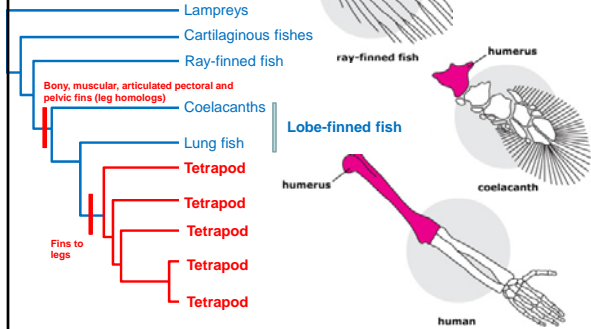
C. Ancestor Reconstruction Tetrapod origins / evolution



Conclusions:
- Best cladogram agrees with fossil record & supports hyp.
• Whereas the most recent common ancestor of tetrapods was certainly a tetrapod, that ancestral tetrapod evolved from fish.

II. Character Evolution

Higher resolution of the sister clades to tetrapods provide the roadmap to understanding the evolution of legs and other tetrapod traits



III. Conservation Planning

A. Prioritizing Species

Botany American Journal of Botany 99(3): 1408–1414, 2012.

BRIEF COMMUNICATION

EVIDENCE FOR THE PERSISTENCE OF WILD *GINKGO BILoba* (GINKGOACEAE) POPULATIONS IN THE DALOU MOUNTAINS, SOUTHWESTERN CHINA

CINDY Q. TANG^{1,2}, YONGCHUAN YANG^{3,2}, MASAMIKO OHMURA³, SH-RONG YU⁴, AKIYA MORIBARA⁵, WEN-HUA SU⁶, HUAN-CHENG WANG⁶, ZHI-YING ZHANG⁷, MING-CHEN PENG⁷, and ZHAO-LE WU²

¹Institute of Ecology and Geobotany, Yunnan University, Kunming 650091, China; ²Faculty of Urban Construction and Environmental Engineering, Chongqing University, Chongqing 400045, China; ³Institute of Medicinal Plant Cultivation of Chongqing, Nanchnan 400410, China; ⁴Graduate School of Horticulture, Chiba University, 666 Matsudo, Chiba 270-8501, Japan; and ⁵Institute of Plant Science, Yunnan University, Kunming 650091, China

• *Purpose of the study:* The possible persistence of wild *Ginkgo biloba* populations in China has long been debated but never scientifically confirmed. We test our hypothesis that the extant *Ginkgo* populations in the Dalou Mountains (SW China) represent fragments of the original natural *Ginkgo* range and offer a range of perspective on the living fossil *Ginkgo*'s history, phylogeny, ecology, and place in human culture—all important aspects of this highly valued species.

• *Methods:* We analyzed the vegetation of the study area, determined the population age structure of *Ginkgo*, and compared it to existing fossil records. For supporting material, we also examined records of the lack of human presence before the mid-17th century in the area, the local people's beliefs regarding provenance of the forests and existing genetic studies.

• *Key results:* Current species composition of *Ginkgo* forests in the Dalou Mountains agrees closely with Holoceic assemblages from fossil records bearing *G. biloba*. Current populations are found in habitats similar to those of fossil *Ginkgo*, which, in habitat, featured such corridors. Results we made indicate an 8.9–10.0-million-year time span of that forest shows that it did not arise recently.

III. Conservation Planning

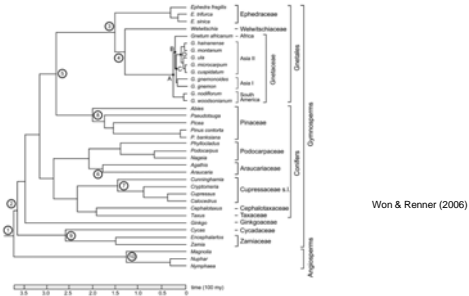


III. Conservation Planning

A. Prioritizing Species

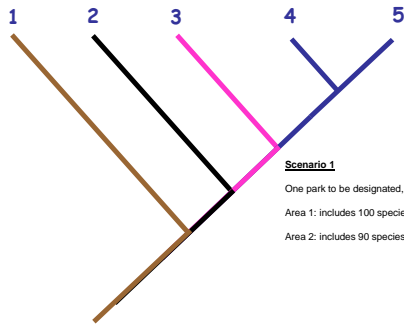
What arguments can be made for preserving this habitat?

- *Ginkgo* otherwise extinct in the wild.
- *Ginkgo* is the most phylogenetically isolated sp.

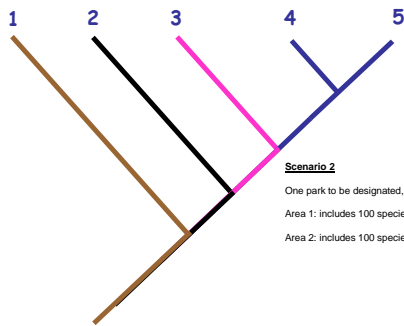


III. Conservation Planning

B. Prioritizing Areas



III. Conservation Planning



IV. Taxonomies



A. Revision of Existing Classification Schemes

Procedure:

1. Conduct cladistic analysis to test monophyly of existing named ingroup taxa.
2. Revise classification as necessary to ensure monophyly of ingroup taxa

IV. Taxonomies

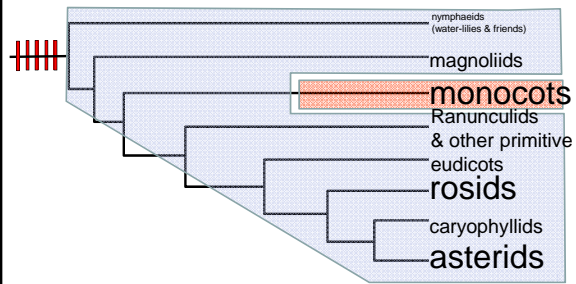


A. Revision of Existing Classification Schemes

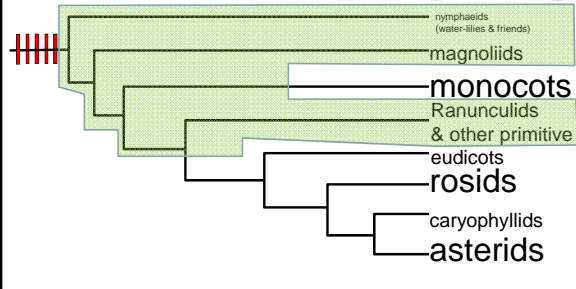
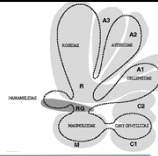
(e.g., angiosperms)

Cronquist divided the angiosperms into 2 classes.

Magnoliophyta (angiosperms)
Magnoliopsida (dicots)
Liliopsida (monocots)



More:
Cronquist's Magnoliidae included water-lilies,
magnolias, and buttercups



Chase et al. (1993)
(Or should we call it Chase et al?)

**PHYLOGENETICS OF SEED
PLANTS: AN ANALYSIS OF
NUCLEOTIDE SEQUENCES
FROM THE PLASTID
GENE *rbcL***

Mark W. Chase,¹ Douglas E. Soltis,²
Richard G. Olmstead,³ David Morgan,⁴
Donald H. Lee,⁵ Brent D. Mishler,⁶
Melvin R. Duvall,⁷ Robert A. Price,⁸
Harold G. Hills,⁹ Yun-Long Qiu,¹⁰
Kathleen A. Kron,¹¹ Jeffrey H. Remy,¹²
Elisa Cava,¹³ Jeffrey D. Palmer,¹⁴
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Helen J. Michaels,¹⁷ W. John Krause,¹⁸
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Glenn R. Furness,²⁷ Steven H. Strauss,²⁸
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Edward Golenberg,³⁷
Gerald H. Lemm, Jr.,³⁸ Susan W. Graham,³⁹
Sigmund C. H. Barrett,⁴⁰
Selvadurai Deyanandan,⁴¹ and
Victor A. Albert

ABSTRACT
We present the results of two exploratory parsimony analyses of DNA sequences from 475 and 699 species of seed plants, respectively, representing all major taxonomic groups. The data sets exclusively from the chloroplast gene *rbcL*, which codes for the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) or RbcL gene. We used two different analysis combinations, maximum parsimony in the one site of *rbcL* and maximum likelihood in the two sites of *rbcL*.

Angiosperm Phylogeny Group (2009)

**An update of the Angiosperm Phylogeny Group
classification for the orders and families of flowering
plants: APG III**

THE ANGIOSPERM PHYLOGENY GROUP¹

¹Biocentennial citation: APG III (2009). This paper was compiled by Brigitte Bremer, Kjerfve Bremer, Mark W. Chase, Michael P. Fay, James L. Hamrick, Douglas E. Soltis, Pamela S. Soltis and Peter F. Stevens, who were equally responsible and listed here in alphabetical order only, with contributions from Arne A. Andersson, Michael A. Moore, Richard G. Olmstead, Paul A. Raub, Kenneth J. Sytsma, David C. Rank, Kenneth Wurdack, Jimmy Q.-Y. Xiang and four Emeriti in alphabetical order. Address: B. Bremer, The Bergius Foundation of the Royal Swedish Academy of Sciences, PO Box 50017, SE-104 05 Stockholm, Sweden; K. Bremer, Vasa Chemicolab, Stockholm University, SE-200 81 Stockholm, Sweden; M. W. Chase, M. P. Fay, J. Hamrick, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3BG, UK; J. L. Hamrick, L. J. Bailey Herbarium, Department of Plant Biology, 412 Mann Building, Cornell University, Ithaca, NY 14853-4501, USA; D. E. Soltis, Department of Botany, University of Florida, Gainesville, Florida 32611-8525, USA; P. S. Soltis, Florida Museum of Natural History, University of Florida, Gainesville, Florida, 32611-7800, USA; and P. F. Stevens, Department of Biology, University of Missouri-St. Louis and Missouri Botanical Garden, PO Box 200, St. Louis, Missouri 63103-0200, USA.

Received 12 August 2009; accepted for publication 18 August 2009

A revised and updated classification for the families of flowering plants is provided. Many recent studies have yielded increasingly detailed evidence for the positions of formerly unplaced families, resulting in a number of

Angiosperm Phylogeny Group (2009)

A new generic monophyletic group is created to accommodate the eight species of the largely isolated tree in Johnston et al. (2006). Within orders, the sequence of families is alphabetical. Families "new" family placement, newly recognized order for the APG system, have family circumscriptions described in the text. Families that represent the broader circumscriptions of orders available in APG II and beyond have circumscriptions that were in effect in APG I. The taxonomic circumscriptions followed here. The list reflects a starting date for all flowering plant family names as 1 August 1980 (James, *Generic plantations*). Full citations are available elsewhere (Stevens, 2001 – current). A conventional phylogenetic tree representing the relationships among the major groups suggested here is presented in Figure 1.

CLASSIFICATION OF FLOWERING PLANTS

Madhousha Madhousha, A.V. Babbar & Euphonia 1980

Andreasen-Petersen 1980, non. nom.

The evidence that Subfamily is an order to all other angiosperms is clear (e.g. Bremer et al., 2007; Johnston et al., 2005; Moore et al., 2005). However, even if they were sister to Nymphaeales (e.g. Gornall, 2004; York & Holmgren, 2006), they should be kept separate as their inclusion in Nymphaeales would result in a name without characters.

Magnoliaceae Link. ex Benth. & J. Presl (1820)

APG circumscription Link. ex Benth. (1820), non. nom.

Hydrocharitaceae U. Hohenstein (1976)

1876 Nymphaeales Link. (1820), non. nom.

There seems to be a general preference for keeping Calceolariales and Nymphaeales separate, although both are small in terms of genera. The two families are easily distinguished. The division of Hydrocharitaceae into two genera, *Hydrocharis* and *Hydrocharitella*, is a well supported morphological and molecularly supported division (e.g. 2007; Frodin, 2006; Judd et al., 2006).

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MAGNOLIIID

Caustophanes (1871)

Winterschnee E. B. ex Link. (1820), non. nom.

Pteris Benth. & J. Presl (1820)

Polypodiaceae Juss. (1789), non. nom.

Polypodiaceae C. Benth. (1821), non. nom.

Lauraceae Engelm. (1846), non. nom.

Polypodiaceae Benth. (1821), non. nom.

Polypodiaceae F. Vahl (1811), non. nom.

The relationships of Hydrocharitaceae are unclear within Pteridales.

Lauraceae Juss. ex Benth. & J. Presl (1820)

Almondeniaceae E. B. (1814)

Calceolariales Link. (1820), non. nom.

Calceolariales Benth. (1820), non. nom.

Hydrocharitaceae Benth. (1820), non. nom.

Hydrocharitaceae Juss. (1789), non. nom.

Hydrocharitaceae Juss. (1789), non. nom.

Hydrocharitaceae Juss. (1789), non. nom.

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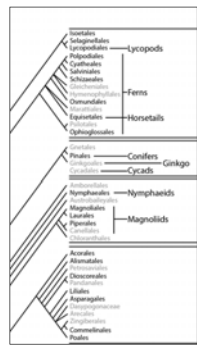
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Hydrocharitaceae Juss. (1789), non. nom.

Hydrocharitaceae Juss. (1789), non. nom.

Hydrocharitaceae Juss. (1789), non. nom.



IV. Taxonomies

B. New classifications

e.g., cycads (Stevenson 1992)



The Queen Sago cycad (*Cycas circinalis*). An endangered endemic of Southern India & Sri Lanka.

The Cycad Pages

Cycad Identification

The cycads are members of an ancient and very distinct natural group traditionally known as the Cycadophytes or Cycadales. This group has been divided into three families and 11 genera. A key distinguishing families and genera is at the top of this page, and each family and genus has its separate home page. Each genus page has links for all accepted species in that genus and keys to identify them. Evolution and distribution are discussed on other separate pages. You can also search the World List of Cycads for any cycad name.

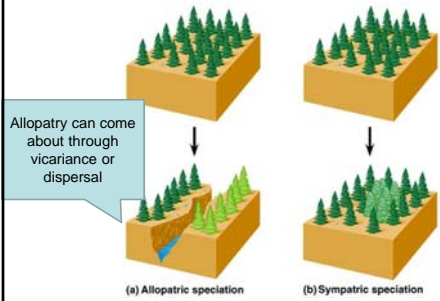
Cycad classification

The following detailed classification from Stevenson 1992 aims to accurately reflect inferred evolutionary relationships among the living cycads.

Order	Suborder	Family	Subfamily	Tribe	Subtribe	Genus	
Cycadales	Cycadaceae	Zamiaceae	Zamiaceae	Zamiaceae	Zamiaceae	Cycas	
						Stangeriaceae	Stangeriaceae
			Zamiaceae	Zamiaceae	Zamiaceae	Stangeriaceae	Stangeriaceae
						Zamiaceae	Zamiaceae

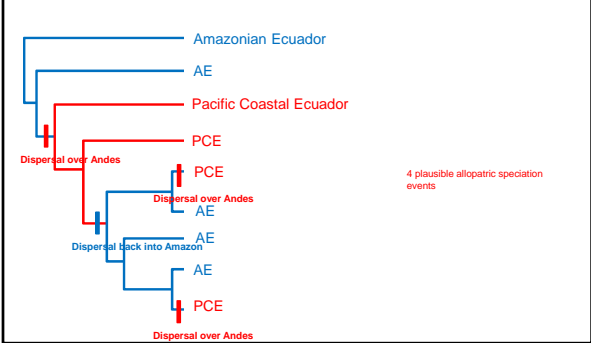
VI. Speciation

A. Allopatric vs. Sympatric or Parapatric Speciation



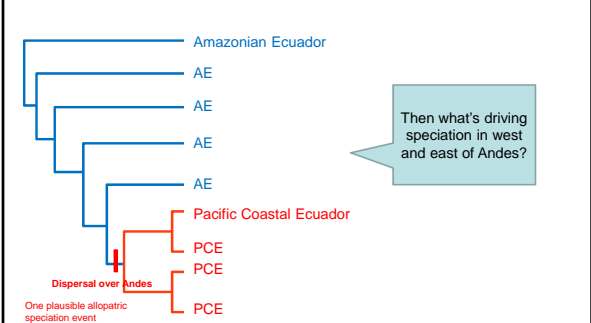
VI. Speciation

A. Allopatric vs. Sympatric or Parapatric Speciation



VI. Speciation

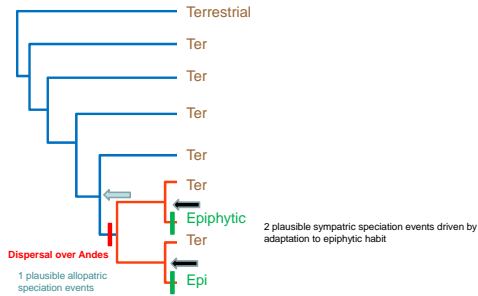
A. Allopatric vs. Sympatric or Parapatric Speciation



VI. Speciation



A. Allopatric vs. Sympatric or Parapatric Speciation

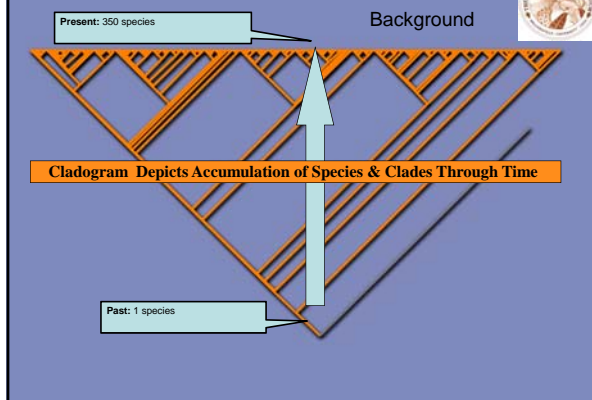


VI. Speciation



B. Key Innovation (skip)

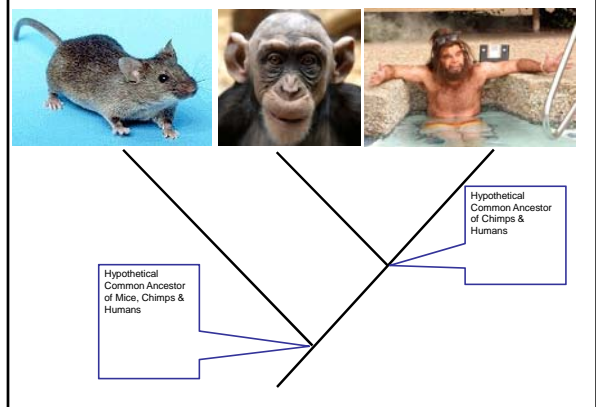
VII. Molecular Dating



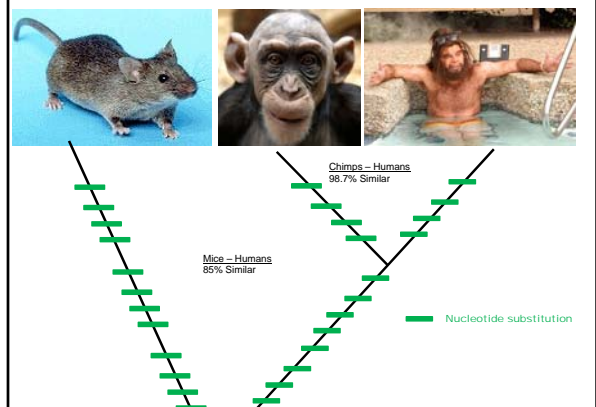
Converting Relative Time into Absolute Time:

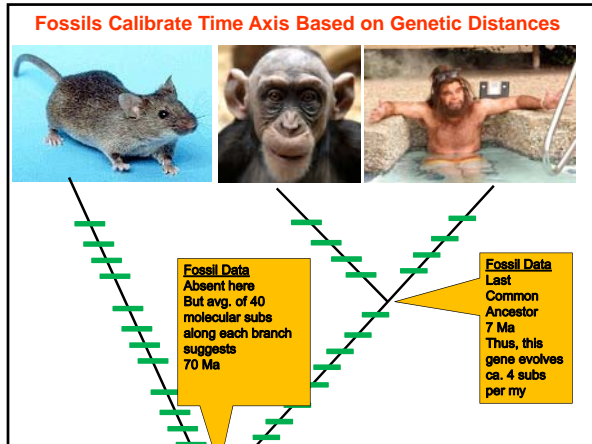
An Overview

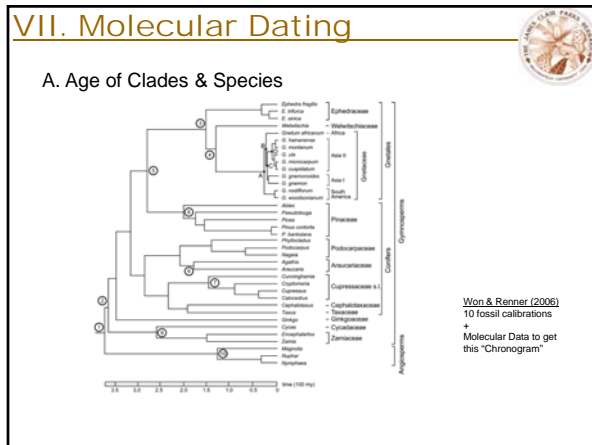
Ancestors are Represented in Phylogenetic Trees

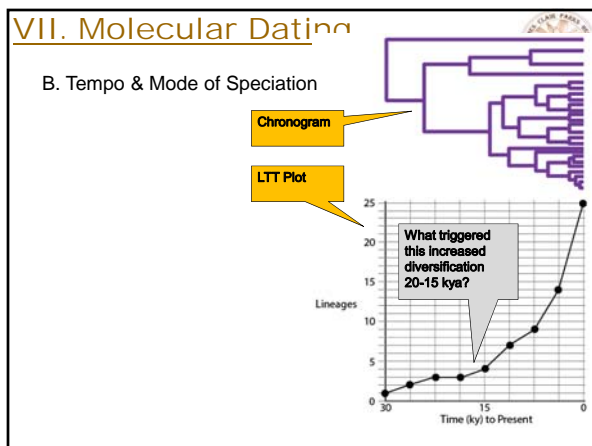


Genetic Distance Increases with Time Since Divergence





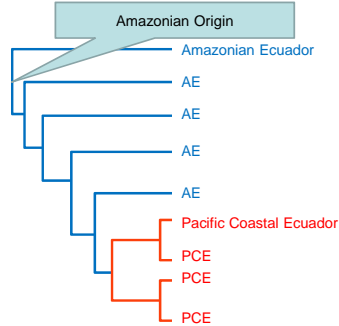




VIII. Biogeography



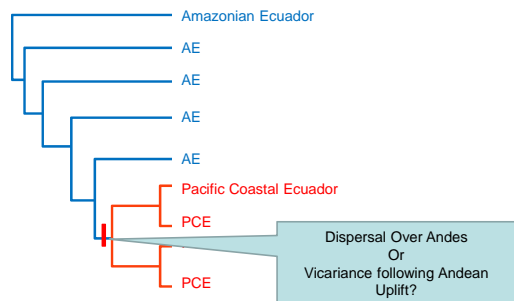
A. Geographic origins



VIII. Biogeography



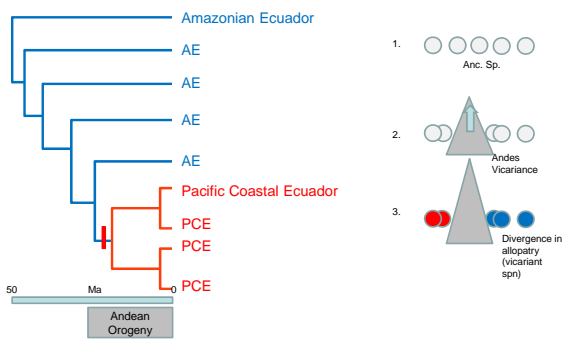
B. Vicariance or Dispersal?



VIII. Biogeography



B. Vicariance or Dispersal?



VIII. Biogeography



Clade age makes a difference in your interpretation

