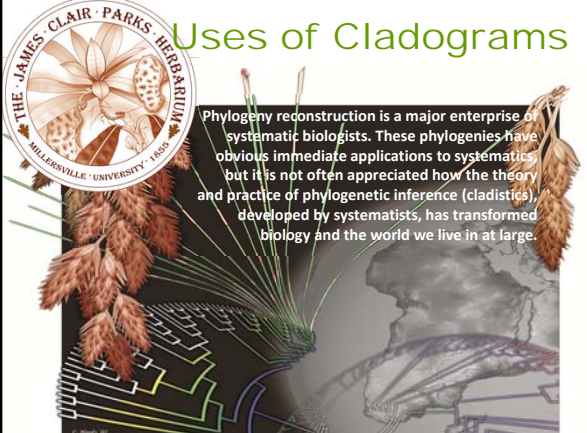


Uses of Cladograms

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.



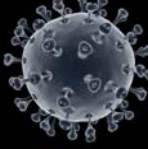
I. Disease Origins & Epidemiology





HIV Origins





HIV Origins





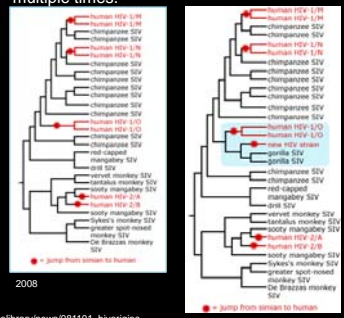
Table 1. A comparison of the two major families of Human Immunodeficiency Virus (HIV).

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.



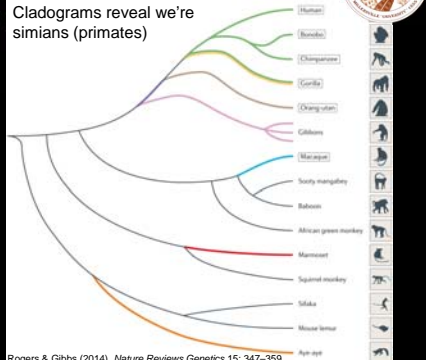
2008 2015

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

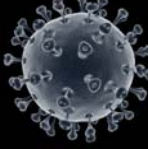
But how?

1992: *Rolling Stone*, Tom Curtis:
HIV-1 may have jumped into humans via OPV

- Chimps have related Simian IV (SIVcpz)
- Human HIV is clearly derived from SIVcpz
- Certain population of chimps in DR Congo were allegedly used to prepare OPV by Hilary Koprowski in the 1950's.
- Rolling stone retracts story.


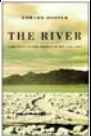


HIV Origins

But how?





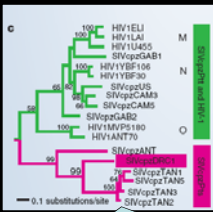
1999: *"The River: A Journey to the Source of HIV and AIDS"* by Edward Hooper.

- 7 yrs journalistic research.
- His conclusion: "Good" evidence for OPV-origin.
- <http://www.aidsorigins.com/>

HIV Origins

Worobey et al. (2004) *Nature* 428: 820.

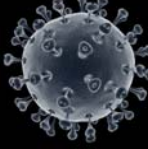
Map of chimp subspecies *Pan troglodytes troglodytes* (green) and *P. t. schweinfurthii* (red)

Cladogram showing phylogenetic relation of HIV-1 types to SIV found in Pit.

HIV Origins

Cladistic findings highlight the role of the bushmeat trade.




HIV Epidemiology

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

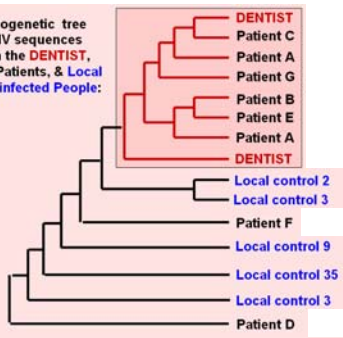
1990s, small Florida town:

- 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

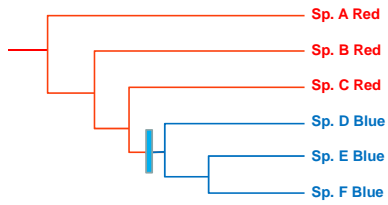


II. Character Evolution



A. Homology Assessment

2. 2^o homology assessment read from cladogram using optimization methods

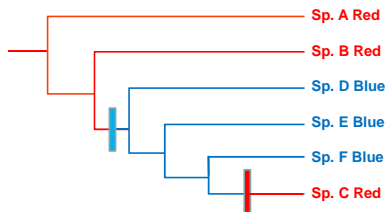


II. Character Evolution



A. Homology Assessment

2. 2^o 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)

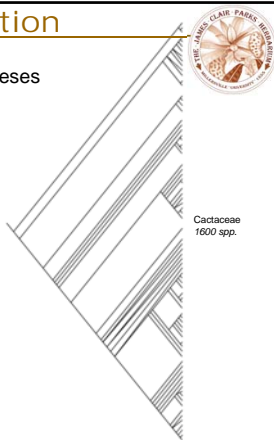
II. Character Evolution

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

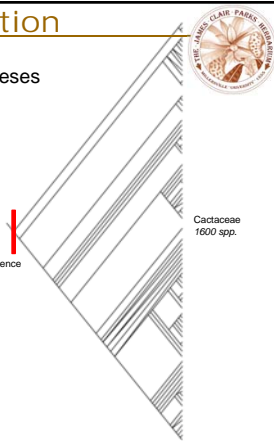
B. Testing Adaptational Hypotheses e.g., succulence

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.

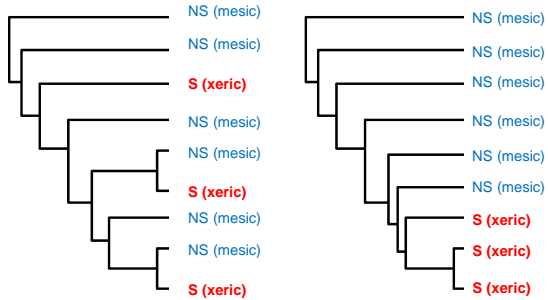


II. Character Evolution

B. Testing Adaptational Hypotheses

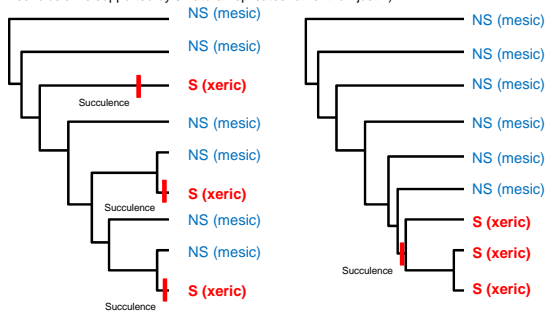


Which cladogram(s) provides evidence for succulence as an adaptation to desert (xeric) environments?



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

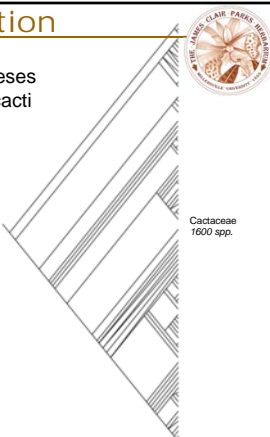
B. Testing Adaptational Hypotheses e.g., origin of epiphytism in cacti

Observation 2

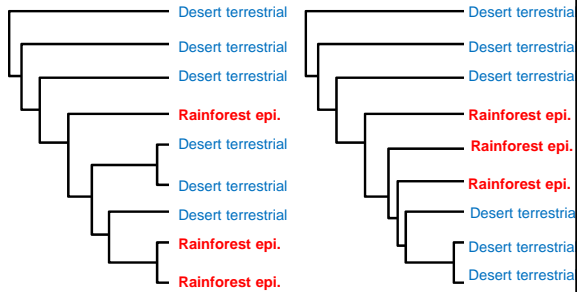
1. While many Cactaceae occur in deserts, some occur as epiphytes in Neotropical rainforests.
2. Epiphytism requires water-use efficiency.

Hypotheses:

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

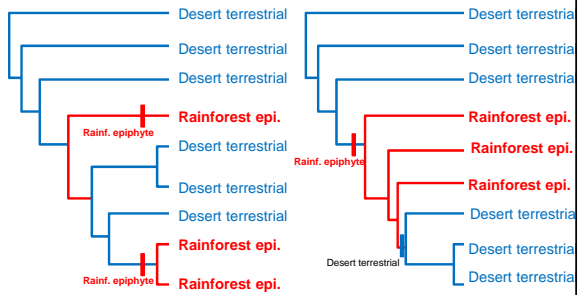


Which cladogram(s) support this?

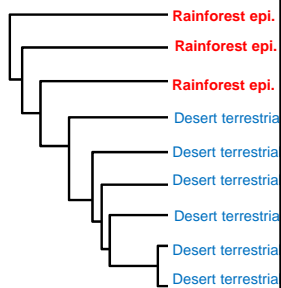


Which cladogram(s) support this?

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

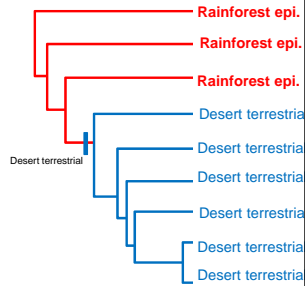


What does this cladogram suggest?



What does this cladogram suggest?

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

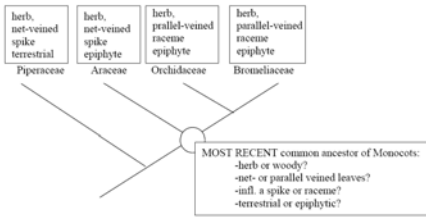


II. Character Evolution



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.

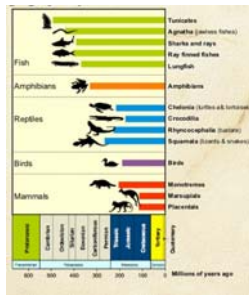
II. Character Evolution



C. Ancestor Reconstruction Tetrapod origins / evolution

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

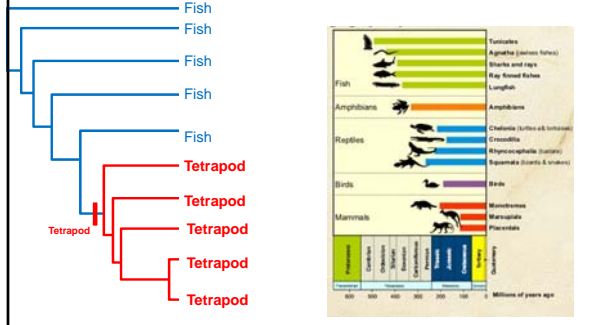
Hypothesis:
Tetrapod verts evolved from fish.



II. Character Evolution



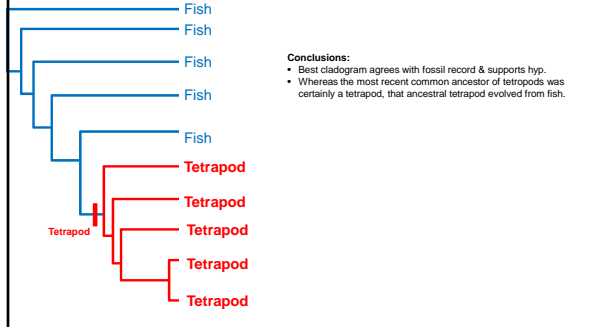
C. Ancestor Reconstruction Tetrapod origins / evolution



II. Character Evolution



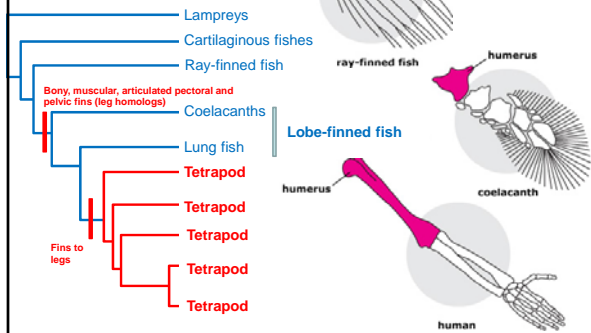
C. Ancestor Reconstruction Tetrapod origins / evolution



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. Targeting Single 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

CHEN Q. TANG^{1,2}, YONGCIUAN YANG^{1,2}, MAAMING OHLONG¹, SHI-RONG YU¹, ARATA MORIHARA³, WEN-HUA SU², HUAN-CHANG WANG², ZHANG-YANG ZHANG³, MING-CHEN PENG³, AND ZHAO-LI WU²

¹Institute of Ecology and Geobotany, Yunnan University, Kunming 650091, China; ²School of Urban Construction and Environmental Engineering, Chengde University, Chengde 666045, China; ³Institute of Medicinal Plants, Cultivation of Chengde, Nanban 816031, China; ⁴Yunnan School of Herpetology, China University of Aeronautics and Astronautics, 121, 8100, 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 (DM) China represent fragments of the original natural *Ginkgo* range and offer a range of pertinent perspectives on the living fossil *Ginkgo*'s history, phylogeny, ecology, and place in human culture—of 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 preservation of the forests and existing genetic studies.
- Key results:** Current genetic composition of *Ginkgo* forests in the Dalou Mountains agrees closely with findings available from fossil records bearing *G. biloba*. Current populations are found in habitats similar to those of fossil *Ginkgo*, which, as noted, featured such a structure. Results in this study raise an S.V. Extinction event has occurred in the Dalou since the last ice retreat.

III. Conservation Planning



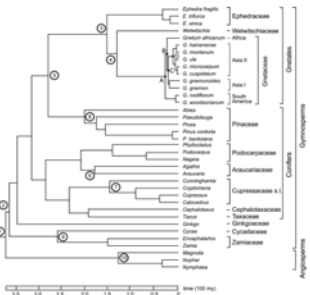
© Cindy Q. Tang - Yunnan University, Kunming, China

III. Conservation Planning

A. Targeting Single Species

What arguments can be made for preserving this habitat?

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



Won & Renner (2006)

III. Conservation Planning

B. Prioritizing Conservation Areas

Scenario 1
 One park to be designated, two possible locations of equal area:
 Area 1: includes 100 species from lineages 4 and 5
 Area 2: includes 90 species from lineages 1 and 4.

III. Conservation Planning

Scenario 2
 One park to be designated, two possible locations of equal area:
 Area 1: includes 100 species from lineages 1 and 2
 Area 2: includes 100 species from lineages 3 and 5.

IV. Taxonomies

A. Revision of Existing Classification Schemes

It's about testing monophyly of existing taxa, discovering clades & revising as necessary.

IV. Taxonomies

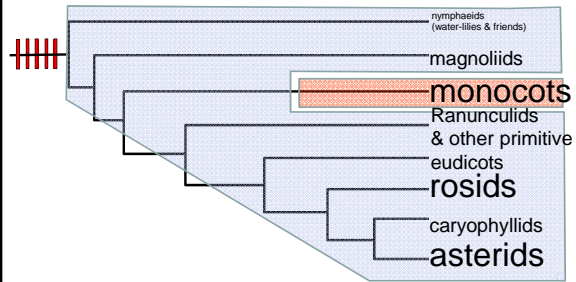


A. Revision of Existing Classification Schemes

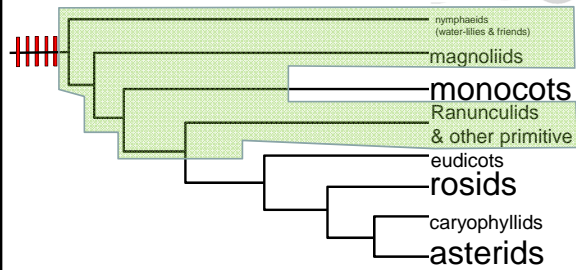
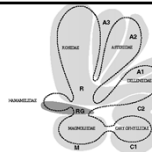
(e.g., angiosperms)

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,¹ Richard G. Olmstead,² David Morgan,³ Donald H. Les,⁴ Brent D. Mishler,⁵ Melissa R. Donnell,⁶ Robert A. Price,⁷ Harold G. Hills,⁸ Yin-Lang Qiu,⁹ Kathleen A. Kron,¹⁰ Jeffrey H. Remy,¹¹ Elvira Casas,¹² Jeffrey D. Palmer,¹³ James R. Manhart,¹⁴ Kenneth J. Sytsma,¹⁵ Helen J. Michaels,¹⁶ W. John Kress,¹⁷ Kenneth G. Karol,¹⁸ W. Dennis Clark,¹⁹ Mikael Holmström,²⁰ Brandon S. Gaut,²¹ Robert K. Jansen,²² Kijoung Kim,²³ Charles F. Wimpers,²⁴ James F. Smith,²⁵ Glenn R. Farnsworth,²⁶ Steven H. Strauss,²⁷ Qiu-Yan Liang,²⁸ Gregory M. Plunkett,²⁹ Pamela S. Soltis,³⁰ Susan M. Swenson,³¹ Stephen R. Williams,³² Paul A. Gauthier,³³ Christopher J. Quinn,³⁴ Luis E. Escobar,³⁵ Edward Galsberg,³⁶ Gerald H. Lemm, Jr.,³⁷ Sean W. Graham,³⁸ Spencer C. H. Barrett,³⁹ Sridharan Dayanandan,⁴⁰ and Victor A. Albert⁴¹

ABSTRACT
We present the results of two exploratory parsimony analyses of DNA sequences from 475 and 499 species of seed plants, respectively, representing all major taxonomic groups. The data are exclusively from the chloroplast gene *rbcL*, which codes for the large subunit of ribulose 1,5-bisphosphate carboxylase/oxygenase (RuBisCO or RuBisCar). We used two different parsimony optimization routines in two sets of analyses. The results indicate that

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

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

¹Blomensated citation: APG III (2009). This paper was compiled by Brigitte Bremer, Kjerfve Bremer, Mark W. Chase, Michael P. Cox, James L. Bernal, 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. Andersberg, Michael A. Moore, Richard G. Olmstead, Paul A. Gauthier, Kenneth J. Sytsma, David C. Baskin, Kenneth Wurdack, Jiny-Qi Xiang and four Emeritus (in alphabetical order): Adolfsson B. Bremer, The Bergius Foundation of the Royal Swedish Academy of Sciences, PO Box 50017, SE-104 05 Stockholm, Sweden; K. Bremer, Vasa Christofer, Stockholm University, SE-200 81 Stockholm, Sweden; M. W. Chase, M. P. Cox, J. B. Fay, Juhlil Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3EQ, UK; J. L. Bernal, 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 32611-0325, 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, P.O. Box 200, St. Louis, Missouri 63102-0200, 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

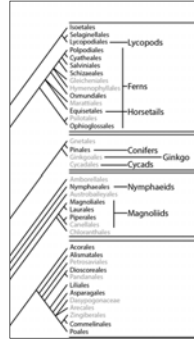
Angiosperm Phylogeny Group (2009)

... have generally recognized to include various taxa in a single sequence of the largely unaltered tree in Hickey et al. (2000). While useful, the sequence of families is alphabetical. Families "new" family plants, rarely recognized earlier for the APC system, have family circumscriptions described in the text. Families that represent the broader circumscription of orders available in APC II and beyond have circumscriptions that were in scope for APC II. The narrower circumscriptions followed here. The list reflects a starting date for all flowering plant family names as 1 August 1980 (James, *Green plants*). Full citations are available elsewhere (Shaw, 2009 - internet). A conventional phylogenetic tree representing the relationships among the major groups recognized here is presented in Figure 1.

CLASSIFICATION OF FLOWERING PLANTS

Magnoliaceae Mikiyasu, A.V. Nelson & Epler (1999)
 Annonaceae Polak (1999), non sens.
 The evidence that Annonaceae are sister to all other angiosperms is clear (e.g. Bremer et al., 2007; James et al., 2007; Moore et al., 2007). However, even if they were sister to Trapa-like (e.g. Gerny et al., 2004; Hickey, 2009), they should be kept separate as their inclusion in Nymphaeales would result in a name without characters.
 Nymphaeaceae Ralsk. & Benth. & J. Presl (1820)
 Nymphaeaceae Ralsk. & Benth. (1820), non sens.
 Nymphaeaceae U. Holmskov (1976)
 Nymphaeaceae Ralsk. (1982), non sens.

There seems to be a general preference for keeping Calceolariaceae and Nymphaeaceae separate, although both are small in terms of genera. The two families are easily distinguished. The division of Heliconiaceae into several genera included in Poinsettia has not been accepted, but it is well supported morphologically and molecularly (Shaw et al., 2007; Frodin et al., 2006; Hall et al., 2006).



IV. Taxonomies

B. New classifications

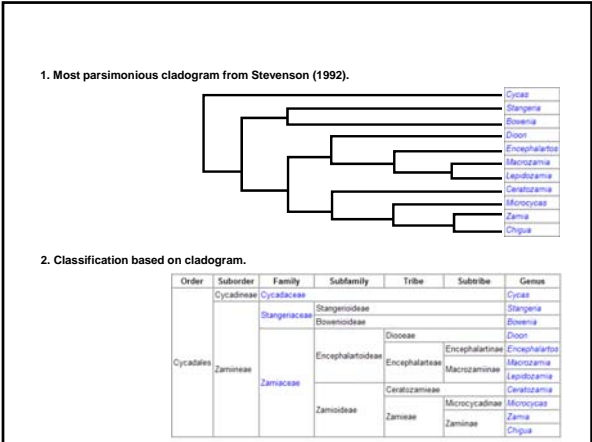
e.g., cycads
 (Stevenson 1992)



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

The screenshot shows the Cycad Pages website. It features a title "The Cycad Pages" and "Cycad Identification". Below the title is a paragraph of text explaining the website's purpose. To the right is a photograph of a cycad. Below the text is a classification table:

Order	Suborder	Family	Subfamily	Tribe	Subtribe	Genus		
Cycadales	Cycadaceae	Cycadaceae				<i>Cycas</i>		
						<i>Stangeria</i>		
						<i>Dioon</i>		
	Zamiaceae	Zamiaceae	Zamiaceae	Encephalartaceae	Encephalartaceae	Encephalartaceae	<i>Encephalartos</i>	
							<i>Microtaxia</i>	
		Zamiaceae	Zamiaceae	Zamiaceae	Zamiaceae	Zamiaceae	Zamiaceae	<i>Leontodermis</i>
								<i>Chelypteris</i>
								<i>Microcyclops</i>
								<i>Zamia</i>
								<i>Chigua</i>



IV. Taxonomies

B. New classifications

e.g., *Plowmanianthus* (Hardy & Faden 2004)

- 5 undescribed spp.
- Related to *Commelina* (dayflower) & *Tradescantia* (spiderwort)
- Do they comprise a new genus or belong to an existing genus?

IV. Taxonomies

Evans (2000). Cladistic analysis of the Commelinaceae

- Sister group relationship between these and *Cochlospermum*
- But sampled only a single species of both genera.

