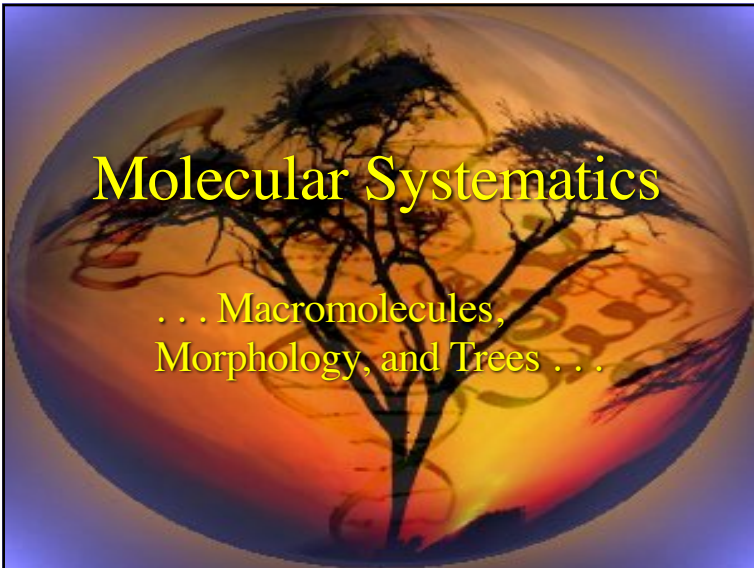


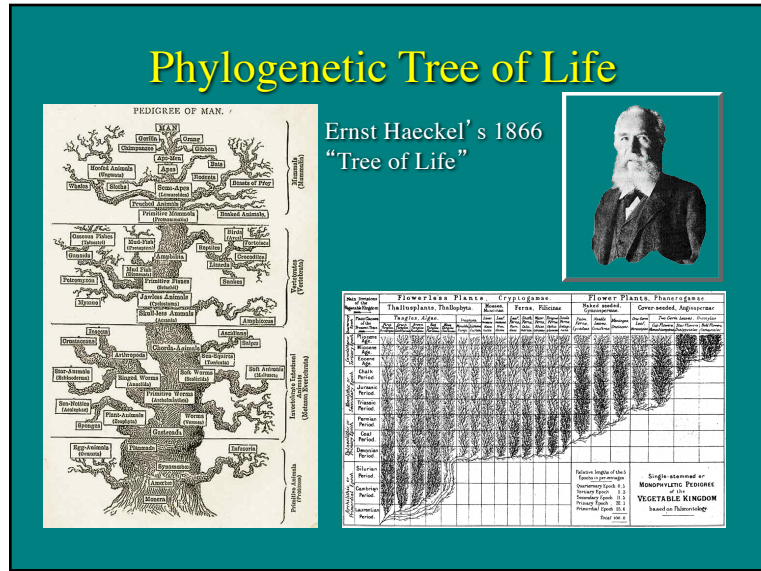
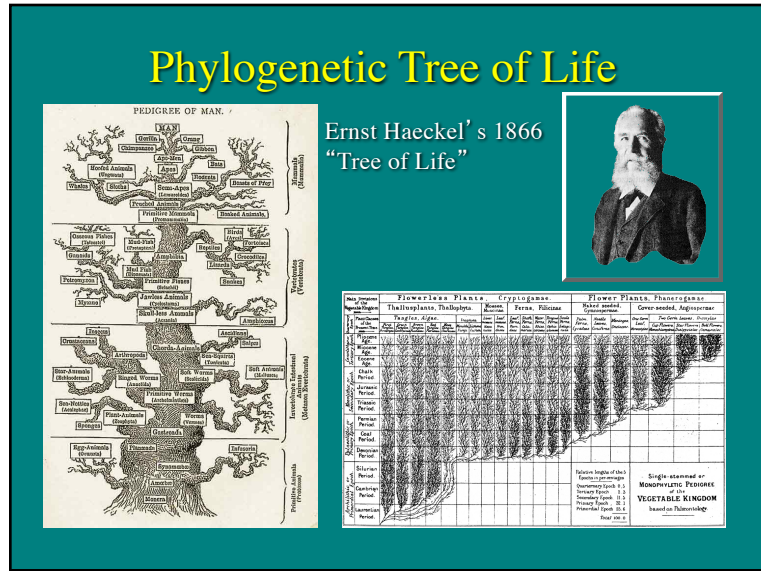
Molecular Systematics

... Macromolecules,
Morphology, and Trees ...



Molecular Systematics

... Macromolecules,
Morphology, and Trees ...

[illegible][illegible]

Tree of Life 150 Years Later?

The Tree of Life

Archaea

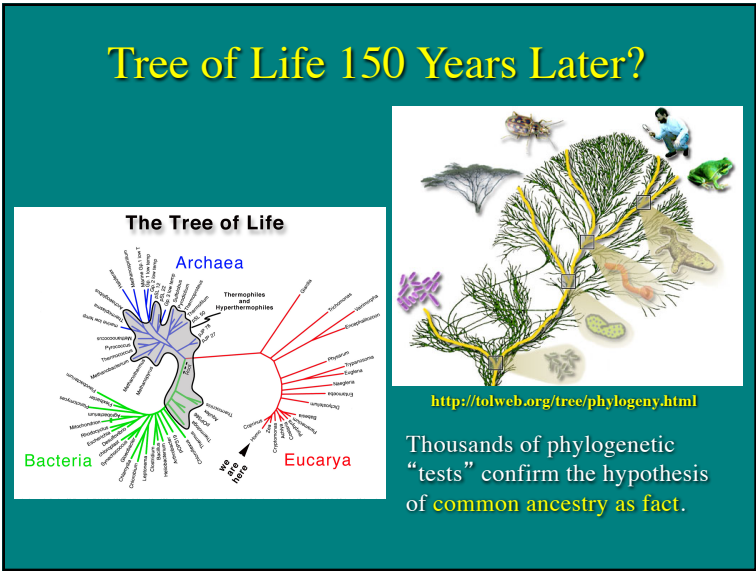
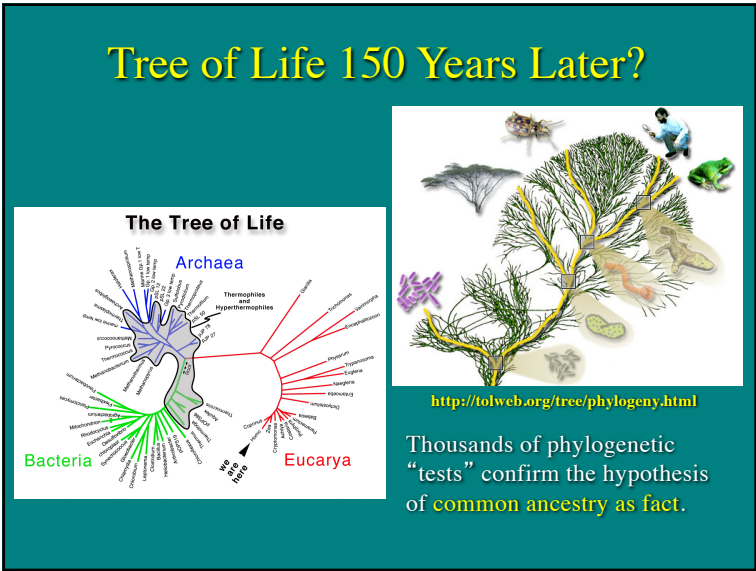
Bacteria

Eucarya

The Tree of Life

<http://tolweb.org/tree/phylogeny.html>

Thousands of phylogenetic “tests” confirm the hypothesis of common ancestry as fact.



Tree of Life 150 Years Later?

The Tree of Life

Archaea

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Thousands of phylogenetic “tests” confirm the hypothesis of common ancestry as fact.

Tree of Life 150 Years Later?

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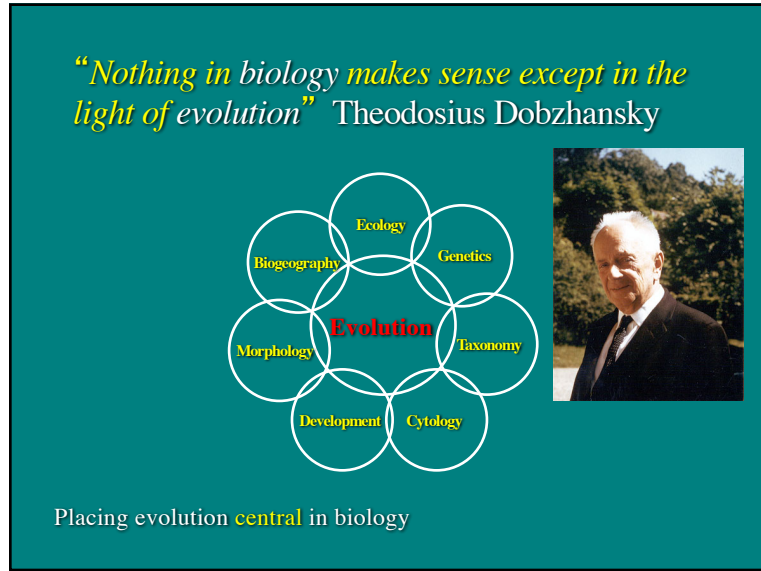
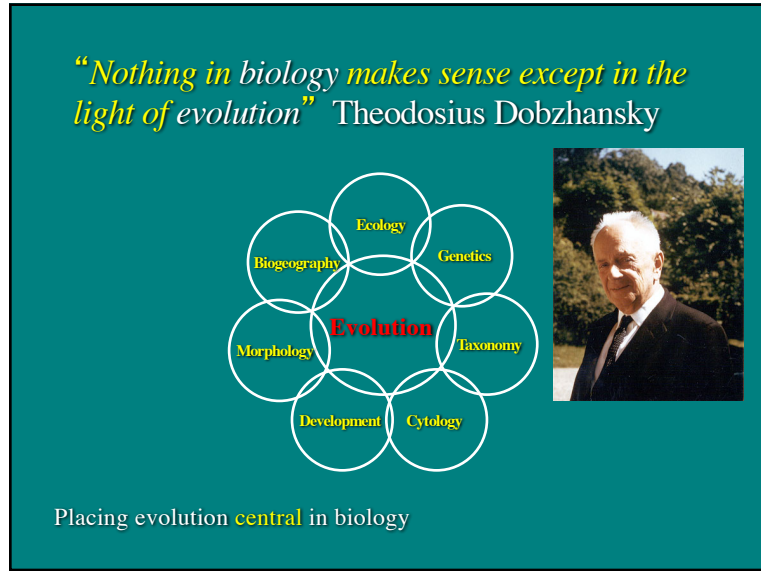
Thousands of phylogenetic “tests” confirm the hypothesis of common ancestry as fact.

"Nothing in biology makes sense except in the light of evolution" Theodosius Dobzhansky

A diagram consisting of seven overlapping white circles arranged in a circular pattern. The word "Evolution" is written in red, bold, serif font in the center, overlapping all seven circles. The other circles contain the following labels in yellow, sans-serif font: "Ecology" (top), "Genetics" (top-right), "Taxonomy" (right), "Cytology" (bottom-right), "Development" (bottom), "Morphology" (bottom-left), and "Biogeography" (left).

A color photograph of Theodosius Dobzhansky, an elderly man with white hair, wearing a dark suit, white shirt, and patterned tie. He is smiling slightly and looking towards the camera. The background is a blurred outdoor scene with green trees.

Placing evolution **central** in biology



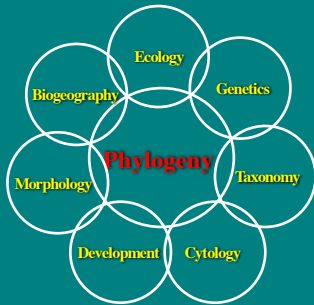
"Nothing in biology makes sense except in the light of evolution" Theodosius Dobzhansky

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Placing evolution **central** in biology

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



Placing molecular phylogenetics **central** in biology?

Molecules **vs.** Morphology?

How do you best "estimate" this tree of life?



Morphology, field studies, herbarium?

Zea mays - maize *Tripsacum* - teosinte

Hugh Iltis – emeritus Director of Herbarium and maize specialist

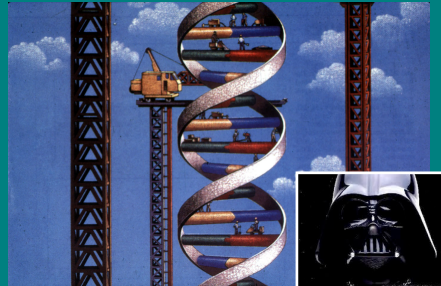
Molecules **vs.** Morphology?

How do you best "estimate" this tree of life?



Morphology, field studies, herbarium?

Hugh Iltis – emeritus Director of Herbarium and maize specialist



Macromolecules – DNA sequencing, genomics?

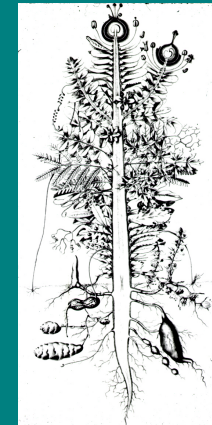
John Doebley – Iltis grad, Genetics faculty member and maize specialist

Molecules **vs.** Morphology?

Is the use of morphology suspect?

CA 4 CO 4 A 4,8 G (4)

5 merous *Oenothera* mutant



Modular plasticity in plants

Molecules *vs.* Morphology?

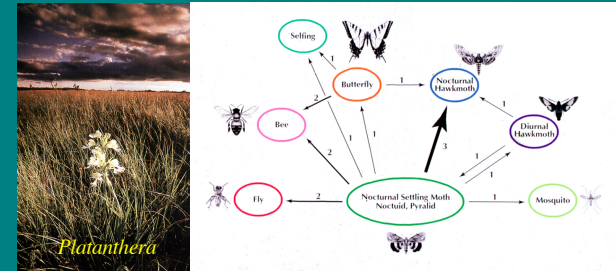
Is the use of morphology suspect?



- convergence of unrelated species under similar selection pressure

Molecules *vs.* Morphology?

Is the use of morphology suspect?

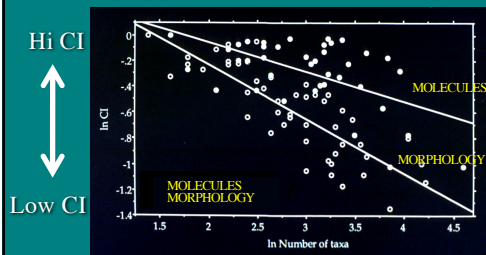


- convergence of unrelated species under similar selection pressure
- divergence of related species under different selection pressure

Molecules *and* Morphology

Both approaches have issues and problems!

Assumptions and issues with molecular data more easily seen



Consistency index (CI) of molecular data is higher than that of morphological data

(Givnish & Sytsma, 1997a)

Homoplasy increases with more species sampled

Molecules *and* Morphology

Both approaches have issues and problems!

Assumptions and issues with molecular data more easily seen

Likelihood of correct phylogenetic estimate

		Likelihood of correct phylogenetic estimate	
		< 0.7	CI 0.7 - 1.0
Number of characters	few	Low	Moderate
	many	Moderate	High
		most morphological	most molecular

Likelihood of correct estimate from molecular data is higher than that from morphological data

(Givnish & Sytsma, 1997b)

Molecules *and* Morphology

Molecular classifications as the backbone

- Angiosperm Phylogeny Group classification

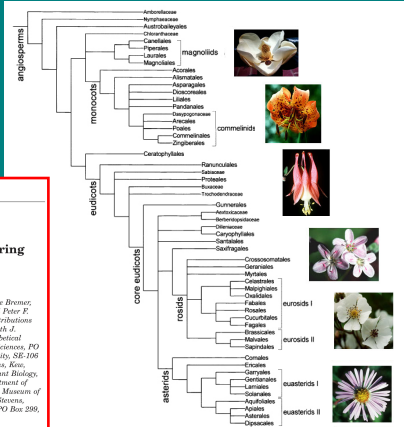
Botanical Journal of the Linnean Society, 2000, 101, 103–121. With 1 figure

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

THE ANGIOSPERM PHYLOGENY GROUP¹

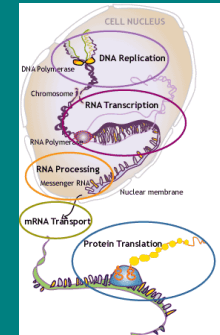
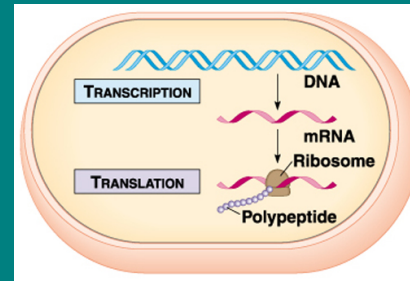
Recommended citation: APG III (2009). This paper was compiled by Birgitta Bremer, Kåre Bremer, Mark W. Chase, Michael P. Fay, James L. Reveal, Douglas E. Soltis, Pamela S. Soltis and Peter F. Stevens, who were equally responsible and listed here in alphabetical order only, with contributions from Arne A. Anderberg, Michael J. Moore, Richard G. Olmstead, Paula J. Rudall, Kenneth J. Sytsma, David C. Tank, Kenneth Wurdack, Jany Q.-Y. Xiang and Sue Zeng (in alphabetical order). Address: B. Bremer: The Regener Foundation at the Royal Swedish Academy of Sciences, PO Box 50017, SE-104 05 Stockholm, Sweden; K. Bremer: Vasa Chansellor, Stockholm University, SE-106 91 Stockholm, Sweden; M. W. Chase, M. P. Fay: Juddell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3ER, UK; J. L. Reveal, L.H. Bailey Hortorium, Department of Plant Biology, 112 Moore Building, Cornell University, Ithaca, NY 14853-0301, USA; D. E. Soltis, Department of Biology, University of Florida, Gainesville, Florida 32611-8025, USA; P. S. Soltis, Florida Museum of Natural History, University of Florida, Gainesville, Florida, 32611-7990, USA and P. F. Stevens, Department of Biology, University of Missouri-St. Louis and Missouri Botanical Garden, PO Box 299, St. Louis, Missouri 63106-0299, USA

Received 12 August 2009; accepted for publication 18 August 2009



Issues in Molecular Systematics

1. Loss of information as you move away from DNA . . .



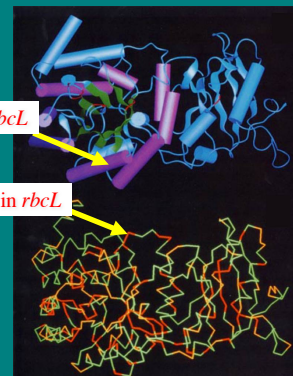
Issues in Molecular Systematics

1. . . and redundancy of genetic code, convergence not seen, selection not at DNA level

Second base	U	C	A	G	Third base
U	UUU Phe	UUC	UAU Tyr	UGU Cys	U
U	UUA	UUA Ser	UAC	UGA Stop	A
U	UUG	UUG	UAG Stop	UGG Trp	G
C	CUU	CCU	CAU	CGU	U
C	CUA	CCC	CAC	CGC	C
C	CUA	CCA	CAA	CGA	A
C	CUG	CCG	CAG	CGG	G
A	AUU	ACU	AUA	AGU Ser	U
A	AUC	ACC	AAC	AGC	C
A	AUA	ACA	AAA	AGA	A
A	AUG Met	ACG	AAG	AGG	G
G	GUU	GUU	GAU	GGU	U
G	GUC	GCC	GAC	GGC	C
G	GUA	GCA	GAA	GGA	A
G	GUG	GCG	GAG	GGG	G

Active sites in *rbcL*

Conserved sites in *rbcL*



Issues in Molecular Systematics

2. What macromolecule, what genome, what technique, what analysis?

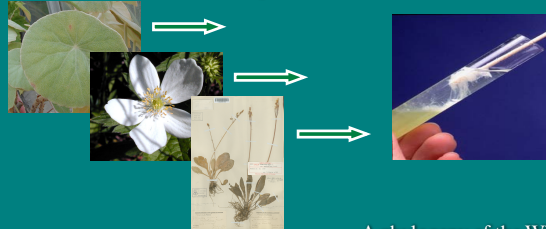
- Protein Genes
 - AA sequencing
 - Serology
 - Duplications
- DNA
 - DNA:DNA hybridization
 - Restriction enzyme digestions
 - DNA sequencing
 - Genome rearrangements
 - Genome sequencing

Table 3. Evolutionary properties different genomes and lineages^a

Genome	Lineage	Inheritance	Relative Mutation Rate or Amount of Variation		
			Point mutations	Size range (kb)	Rearrangements
mtDNA	Animals	Maternal	High	14–26	Very rare
mtDNA	Plants	Maternal	Very low	200–2500	Very frequent
mtDNA	Fungi	Allo	Low	20–200	Frequent
cpDNA	Plants	Allo	Low	120–217	Rare
nDNA	Animals	Biparental	Variable	1–1000 x 10 ⁵	Frequent
nDNA	Plants	Biparental	Variable	1–1000 x 10 ⁵	Frequent
nDNA	Fungi	Biparental	Not known	0.1–10 x 10 ⁵	Frequent

Molecular Systematics - in brief

Extract DNA from plant tissue



A phylogeny of the Wisconsin vascular flora **based on herbarium specimen**

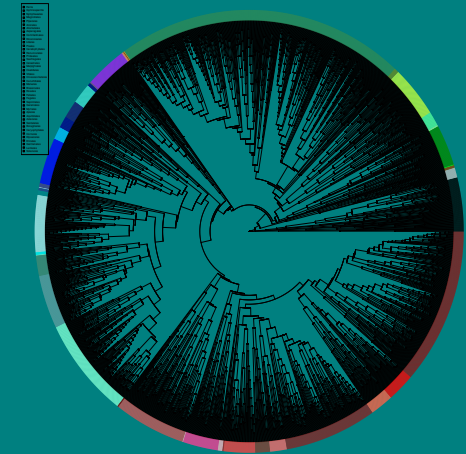


Molecular Systematics - in brief



Marissa Barrett
(graduated Botany major)
“CSI: On Wisconsin”

A phylogeny of the Wisconsin vascular flora **based on herbarium specimen DNA!**



Molecular Systematics - in brief

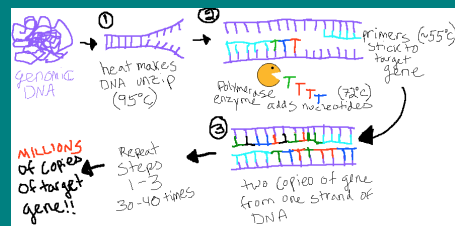
Polymerase chain reaction (PCR) to amplify DNA segment

total DNA



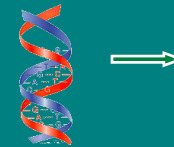
millions of copies of target region

“The Ghetto Guide to Genetics”

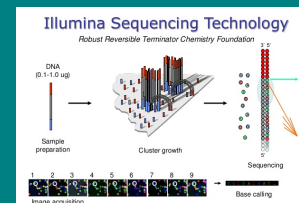


Molecular Systematics - in brief

Sequencing of DNA PCR product



...ACGGTCCA...



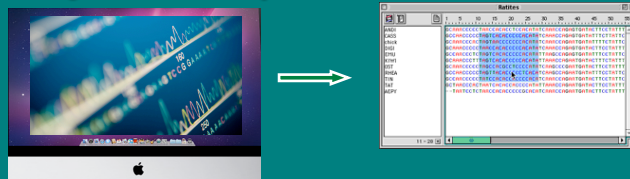
now . . . Next Generation Sequencing

Molecular Systematics - in brief

Sequencing of DNA PCR product

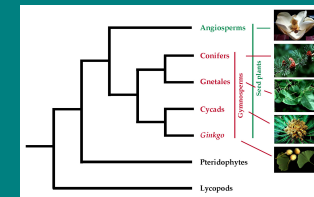
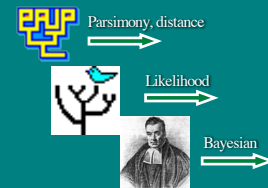


Alignment of DNA sequence

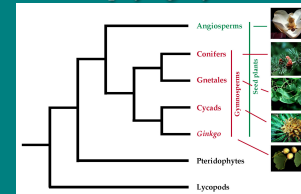


Molecular Systematics - in brief

Phylogenetic analysis



Use of phylogeny



Classification

Character evolution

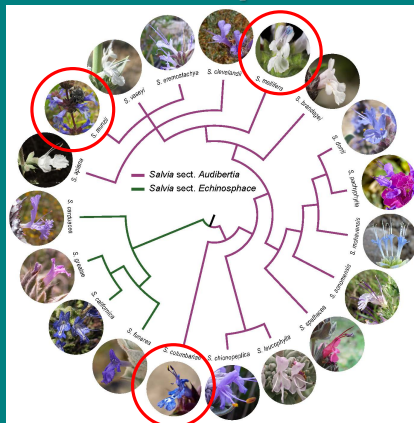
Biogeography

Diversification analysis

Community assembly

Issues in Molecular Systematics

3. "Gene trees" \neq "Species trees" all the time (hybridization issue)

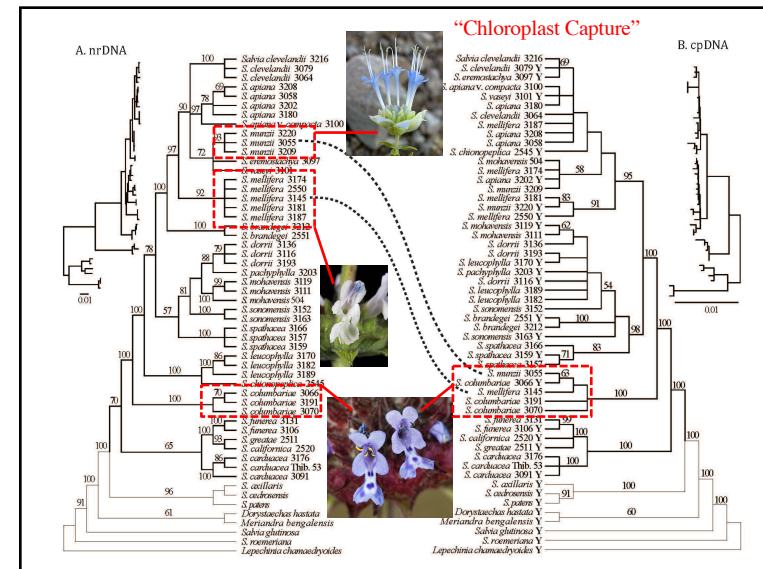


Salvia (sage mints) in California



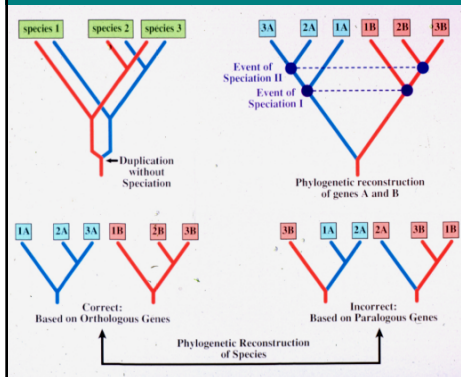
Jay Walker

Bryan Drew



Issues in Molecular Systematics

4. "Gene trees" \neq "Species trees" all the time (homology issue)



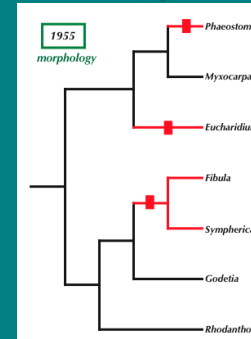
•compare "orthologous" gene copies, not "paralogous" copies

• big issue in molecular systematics of all organisms

Issues in Molecular Systematics

4. "Gene trees" \neq "Species trees" all the time (homology issue)

Sectional relationships of *Clarkia*



Lewis

Red sections exhibit a gene duplication of *pgi*

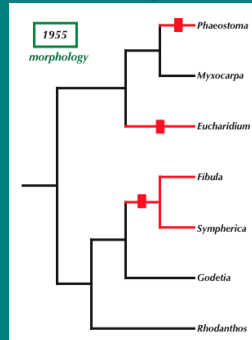
Clarkia



Issues in Molecular Systematics

4. "Gene trees" \neq "Species trees" all the time (homology issue)

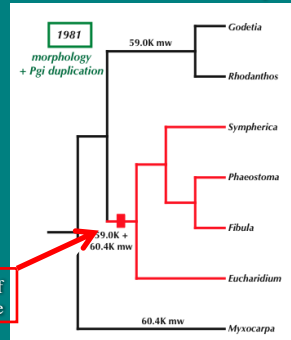
Sectional relationships of *Clarkia*



Lewis

Single origin of duplicated gene

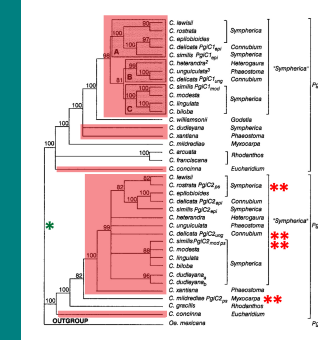
Modified sectional relationships



Issues in Molecular Systematics

4. "Gene trees" \neq "Species trees" all the time (homology issue)

Clarkia sections based on DNA sequencing of *Pgi* genes



DNA sequencing says no!

Gene copy 1 * Ancient duplication: all sections originally had two genes

Two gene trees that mirror each other

** Note pseudogenes for gene copy 2 in some species

Issues in Molecular Systematics

4. “Gene trees” \neq “Species trees” all the time (homology issue)

Phylogenetics

Advance Access publication September 21, 2010

BUCKY: Gene tree/species tree reconciliation with Bayesian concordance analysis

Bret R. Larget^{1,2}, Satish K. Kotha³, Colin N. Dewey^{3,4} and Cécile Ané^{1,2,*}

¹Department of Statistics, ²Department of Botany, ³Department of Computer Sciences and ⁴Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison, WI 53706, USA

Associate Editor: David Posada

Bret Larget



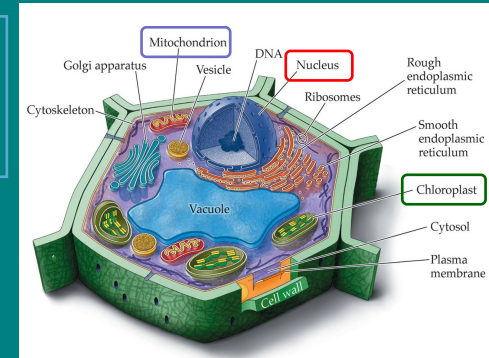
Cecile Ané

As sequencing costs continue to drop and multiple orthologous genes become easily available for a given set of individuals, phylogenetic trees are now commonly inferred from multiple loci at once. However, trees inferred from different loci are very often incongruent with each other. While some of this discordance might be explained by stochastic and technical errors (undetected paralogy or model misspecification), it has become obvious that biological processes are often at the heart of the discordance, including incomplete lineage sorting (ILS), whole genome duplications, horizontal gene transfers or hybridization.

Issues in Molecular Systematics

5. Horizontal gene transfer - endosymbiosis

Eukaryotes contain a “fossil” history of 2-3 or even more distinct lineages - a mosaic or chimaera

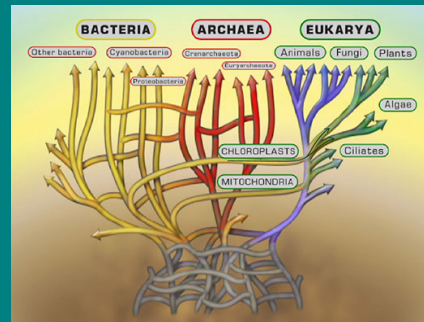


Issues in Molecular Systematics

5. Horizontal gene transfer - endosymbiosis

“mitochondria” transfer - 2,000 mya

“chloroplast” transfer - 1,600 mya



Issues in Molecular Systematics

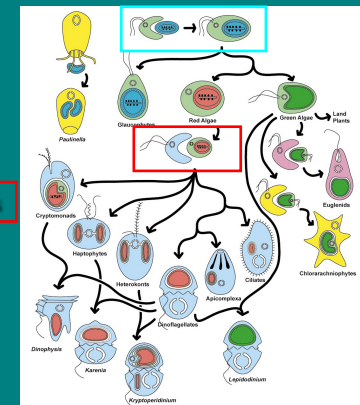
5. Horizontal gene transfer - fusion evolution

Primary plastid endosymbiosis

- green algae
- red algae
- glaucophytes

Secondary plastid endosymbiosis

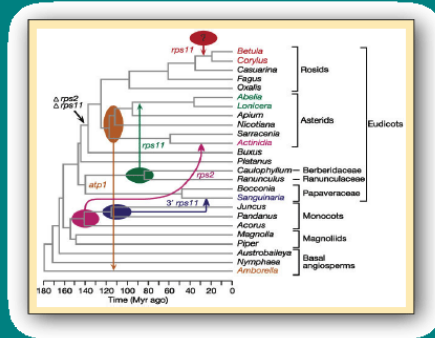
- cryptomonads
- dinoflagellates
- haptophytes, heterokonts
- ciliates



Issues in Molecular Systematics

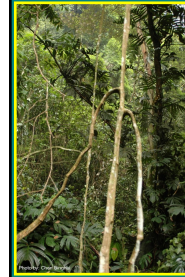
5. Horizontal gene transfer - parts of genomes

- evidence is mounting that bits and pieces of genomes (e.g., single gene) have and are still being transferred across species lines

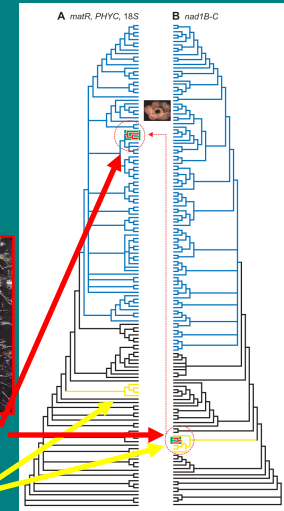


Unusual horizontal gene transfer between parasite and host

- Rafflesia* is imbedded in Malpighiales with most genes (A)
- Rafflesia* is imbedded in host Vitaceae for one mtDNA gene (B)



Parasite: *Rafflesia*
Host: *Tetrastigma* (Vitaceae)



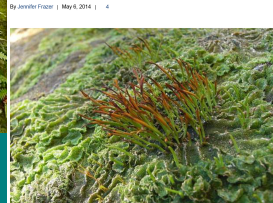
Davis & Wurdack, 2004 - Science

Unusual horizontal gene transfer between bryophyte and early fern

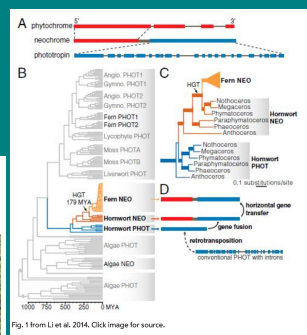
- Neochrome gene – for living in low light conditions



In Darkened Forests, Ferns Stole Gene From an Unlikely Source – and Then From Each Other



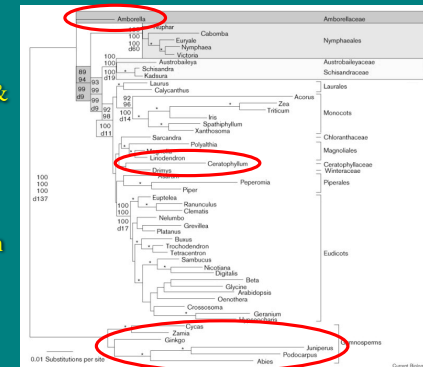
Li et al, 2014 - PNAS



Issues in Molecular Systematics

6. Sampling issues

- gene sampling too little: high levels of homoplasy & lack of resolution
- taxa sampling too little: placeholder issues
- isolated taxa: long branch attraction



1999 study of 50 seed plants, five genes, and three genomes

Issues in Molecular Systematics

6. Sampling issues

- gene sampling too little:
high levels of homoplasy & lack of resolution
- taxa sampling too little:
placeholder issues
- isolated taxa: long branch attraction
- all have been issues in seed plant phylogenetics

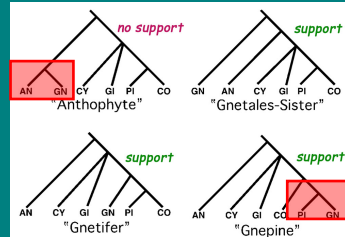


Fig. 1. Four major hypotheses of relationships among extant seed plant lineages. AN = angiosperms; CY = cycads; GI = Ginkgo; GN = Gnetales; PI = Pinaceae; CO = non-Pinaceae conifers.

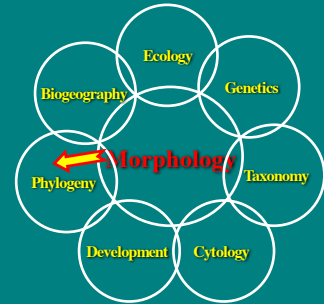
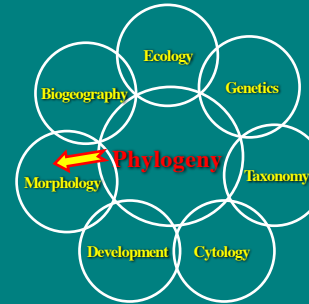
Welwitschia
(Gnetophyte)



"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. Genomics
2. Biogeography
3. Ecology

