Bio1B Evolution 2

Last lecture:

- Introduction to Craig & lecture outline
- Foundations
  - Pre-Darwinian background
  - Darwin: early influences, Beagle voyage
  - Wallace

Today

- Natural selection - principles, lines of evidence in the “Origin”
- Descent with modification
- Estimation & interpretation of phylogeny
- Some major insights about the “Tree of Life”
  - 3 kingdoms: Archaea, Bacteria, Eukarya
  - Assembling the eukaryote cell
  - Metazoan origins & relationships

On-line resources:

Understanding Evolution (UCMP): http://evolution.berkeley.edu/

Tree of life: www.tolweb.org/tree/

The Darwin-Wallace principle of Natural selection

- Individuals within a population vary for one or more characteristics (traits)
- Traits are (to some extent) inherited by offspring from their parents
- More offspring are produced than can survive

=> those with traits that improve survival/reproduction leave more offspring

=> these favorable traits will accumulate in the population over generations

Lines of evidence in the “Origin of the species by means of natural selection” (Darwin, 1859)

- Artificial selection as analogy to natural selection
- Biogeography: Nested geographic distributions
- Homology of traits modified for different purposes
- Population pressure

“It may be confidently asserted that the characters of the six breeds which have been figured are not in the least exaggerated.” - Charles Darwin, *Animals and Plants Under Domestication.*

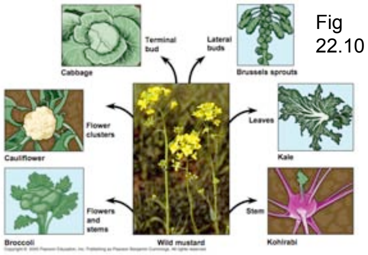


Fig 22.10

Homologous structures: variations on a structure present in a common ancestor

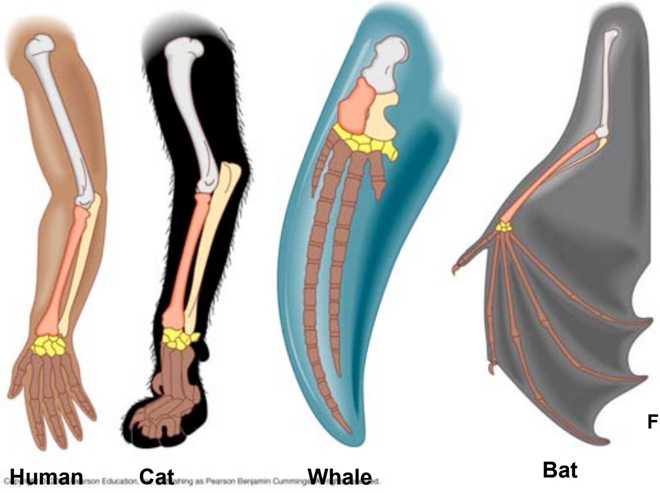
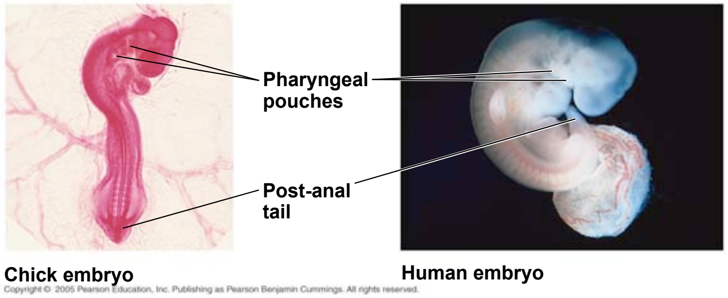


Fig. 22-17

Fig. 22-18

Anatomical homologies of embryos

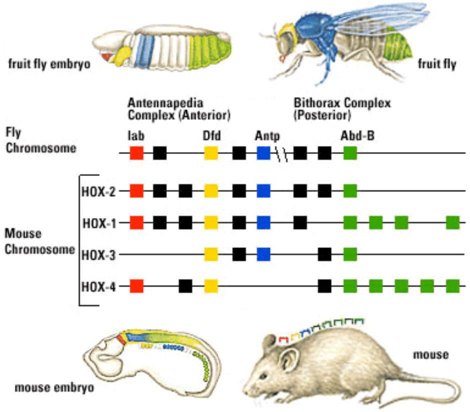


Pharangeal pouches → Fish - gills

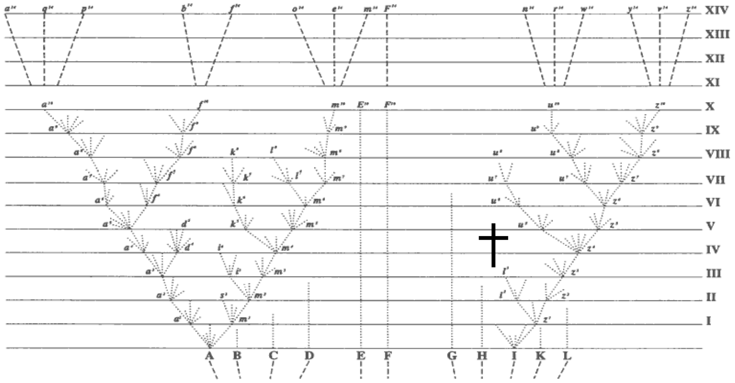
Pharangeal pouches → Mammals - ears, throat

Molecular homologies - new insights invisible to Darwin

- Genetic code
- Transcription & translation machinery
- Colinear segmentation (Hox) genes
- etc etc.



Descent with modification by natural selection + extinction

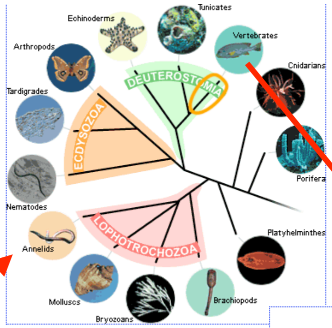


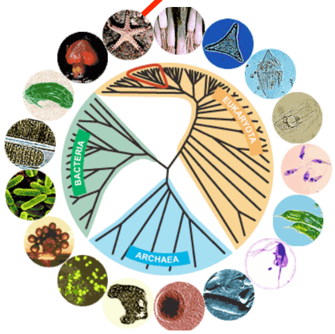
time

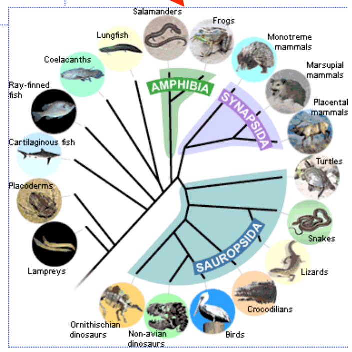
Phenotype

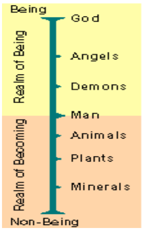
The current view of the phylogenetic hierarchy

(Understanding Evolution web site)



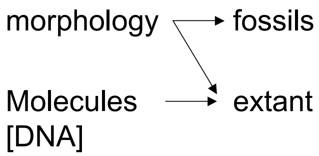






cf. Aristotle's scala naturae

What evidence do we use to estimate the tree of life?

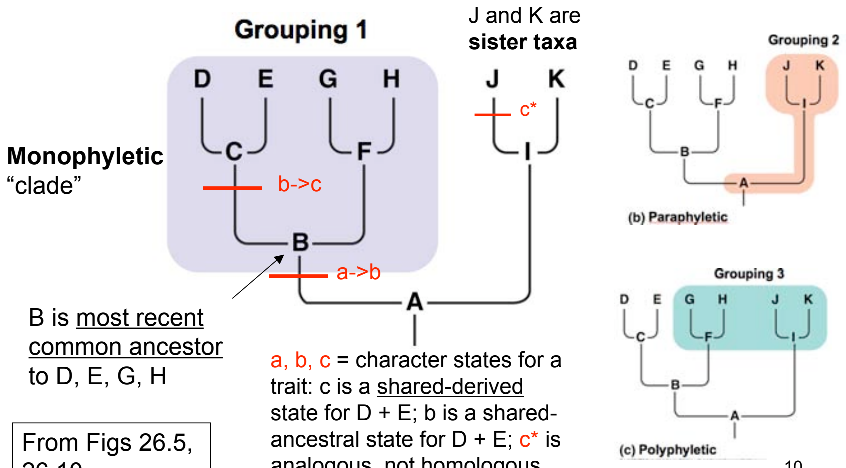


General principles:

Taxa (species, genera etc.) are grouped by shared-derived traits

Taxa should be monophyletic

Key concepts in tree thinking



Monophyletic "clade"

B is most recent common ancestor to D, E, G, H

From Figs 26.5, 26.10

a, b, c = character states for a trait: c is a shared-derived state for D + E; b is a shared-ancestral state for D + E; c* is analogous, not homologous

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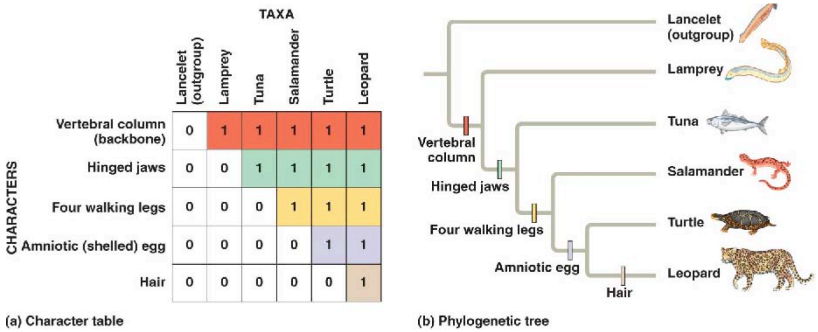
Examples of shared-derived traits that group major lineages of vertebrates



TAXA

CHARACTERS	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

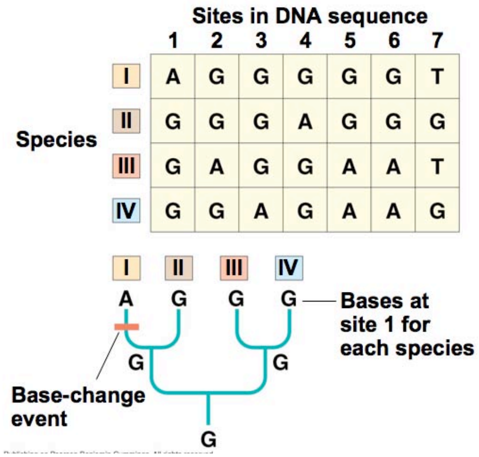
(b) Phylogenetic tree

Fig 26.11

DNA sequence variation

Fitting observed patterns of sequence variation at homologous (aligned) sites to a phylogenetic hypothesis

(see also Fig. 26.8)

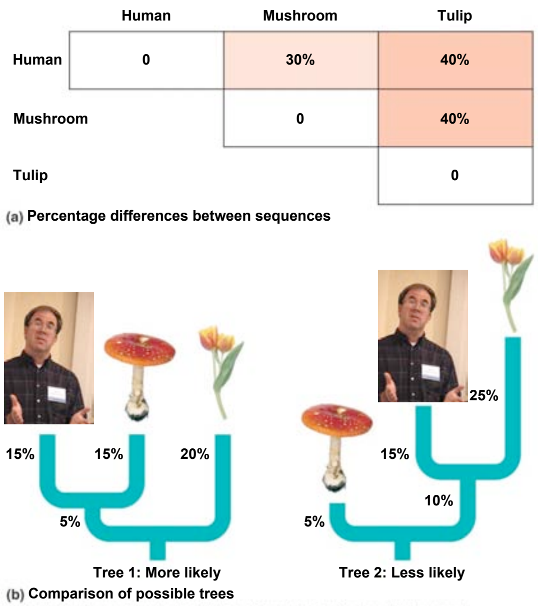


Sites in DNA sequence

Species	1	2	3	4	5	6	7
I	A	G	G	G	G	G	T
II	G	G	G	A	G	G	G
III	G	A	G	G	A	A	T
IV	G	G	A	G	A	A	G

Methods for estimating phylogeny from molecular data

- Parsimony - minimize #changes on tree
- Maximum likelihood, Bayesian (data + model of sequence evolution)
  - Find tree that is most probable given the data



	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

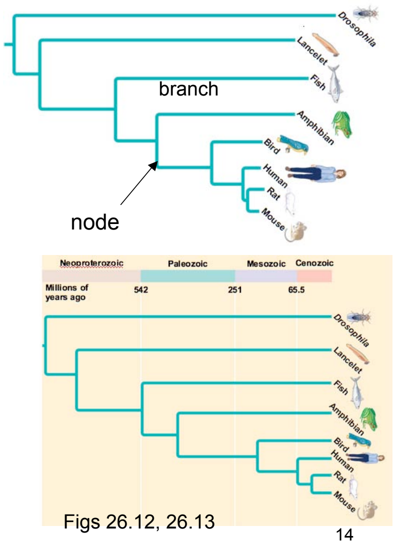
(a) Percentage differences between sequences

(b) Comparison of possible trees

John Huelsenbeck, IB & MVZ "curator of trees"

Estimating divergence times from a phylogeny

- Branch lengths are proportional to amount of change (Fig 29.19)
- **Molecular clock:**
  - Zuckerkandle & Pauling 1960s
  - Some genes evolve at approx constant rate
  - Absolute rate can be estimated from fossils at (or near) nodes
  - This calibration can be used to estimate other divergence times in tree
  - See text for caveats!



Figs 26.12, 26.13

Surprise 1: 3 Domains of life

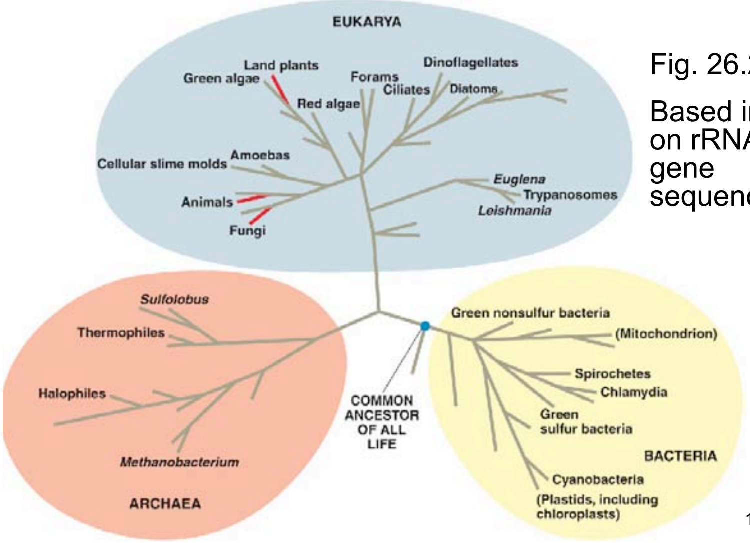
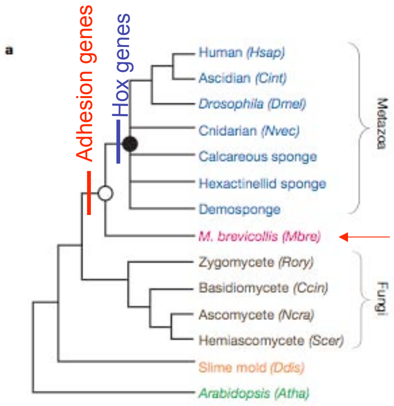
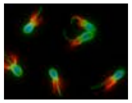


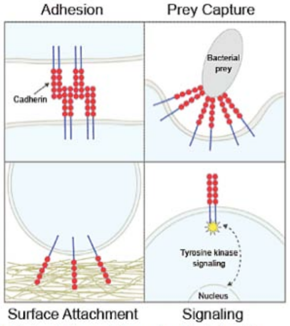
Fig. 26.21

Based initially on rRNA gene sequences

Cool stuff - understanding metazoan origins (Nicole King, MCB)







Cadherin proteins were discovered in animals, where they mediate cell-cell adhesion and signaling. Researchers have since found them in one-celled choanoflagellates, where their role is unknown. Choanoflagellates cadherins may play analogous roles, however, ranging from the capture of bacterial prey (a form of cell adhesion) or attachment to surfaces in the environment, to the detection of environmental cues that trigger cellular responses (cell signaling). *(Nicole King lab/UC Berkeley)*

See also Fig. 32.3

Surprise 2

Eukaryotic cells were assemble via endosymbiosis - mitochondrial & chloroplasts are modified symbiotic bacteria

Each has a (small) genome separate from the nucleus