

What does Universal Common Ancestry mean?

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Phil 2330

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Everybody alive
today is related

True of humans -
and true of every
other species too

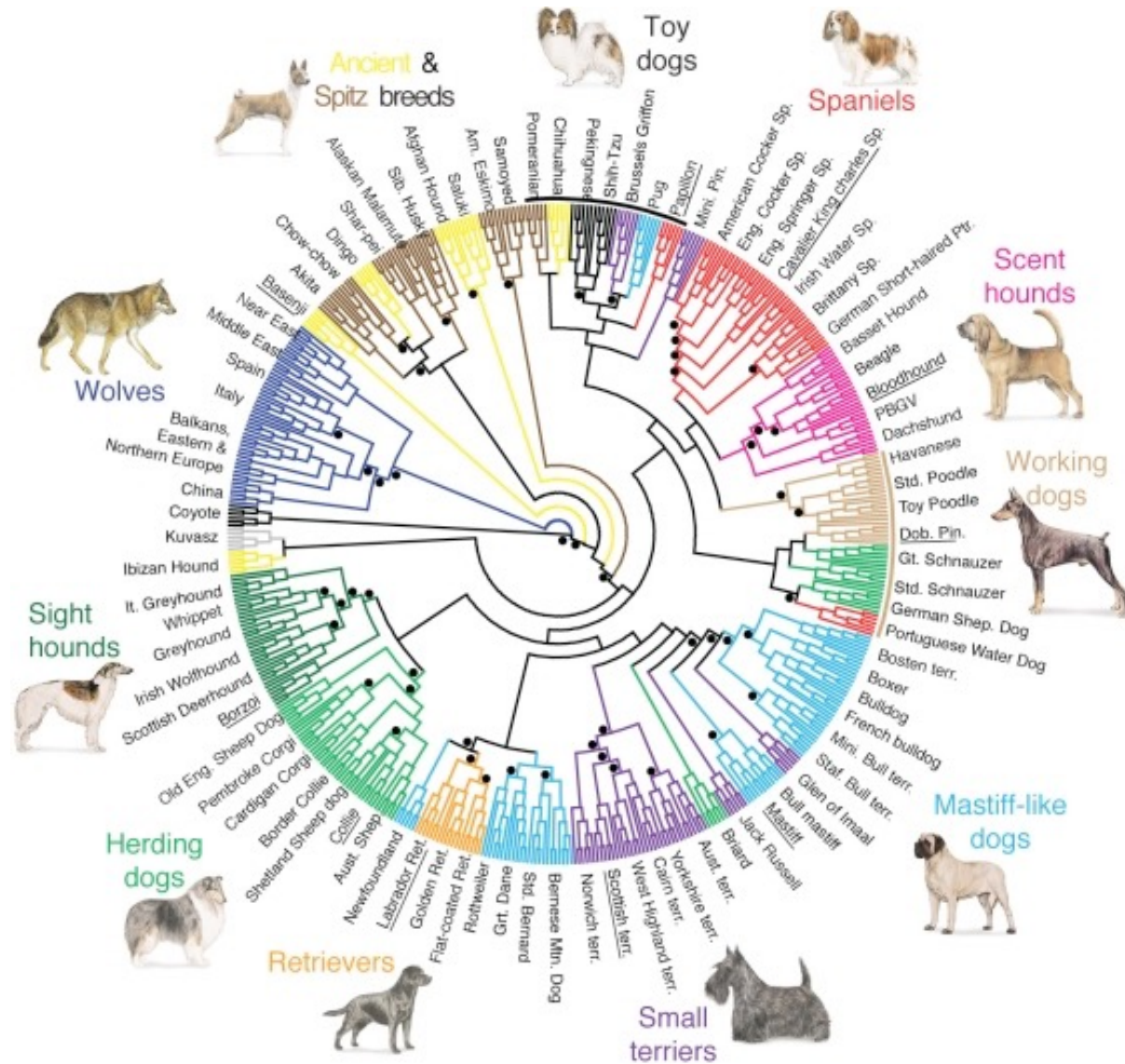


These dogs (like all dogs) are distant cousins. They shared a common ancestor (at most) 30,000 years ago.





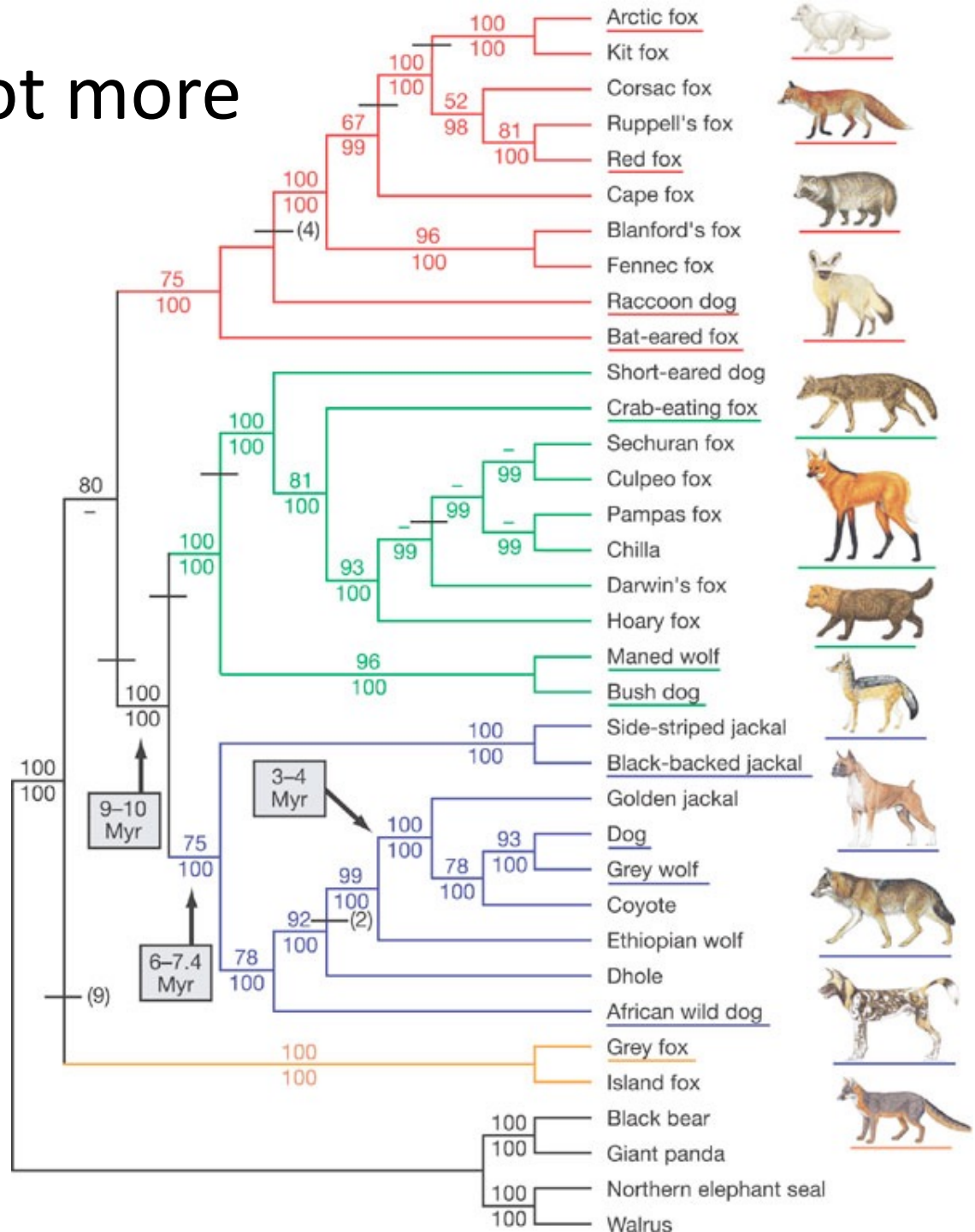
Just like humans, dogs have pedigrees and are related to other dogs. Trace back far enough...



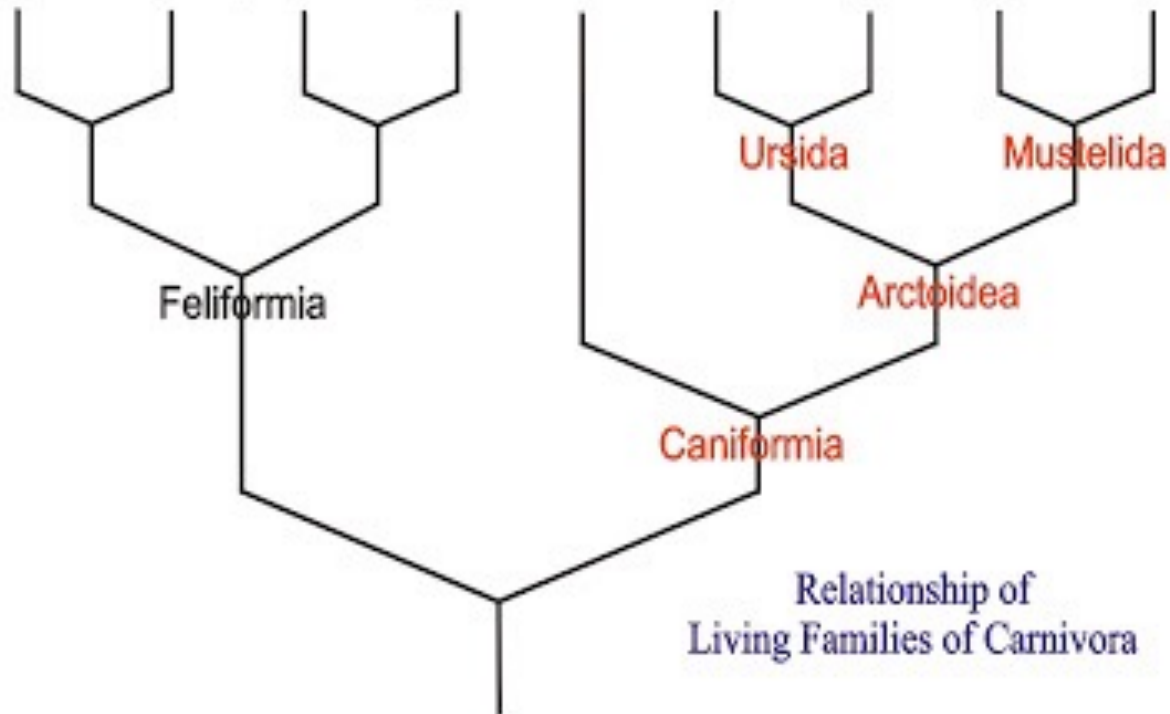
Phylogeny of 85 dog breeds (study using 900 dogs and 200 wolves - from Wayne et al. 2010, Nature)

But dogs have a lot more distant cousins...

Phylogeny of the canids (from Lindblad-Toh et al. 2005, Nature)

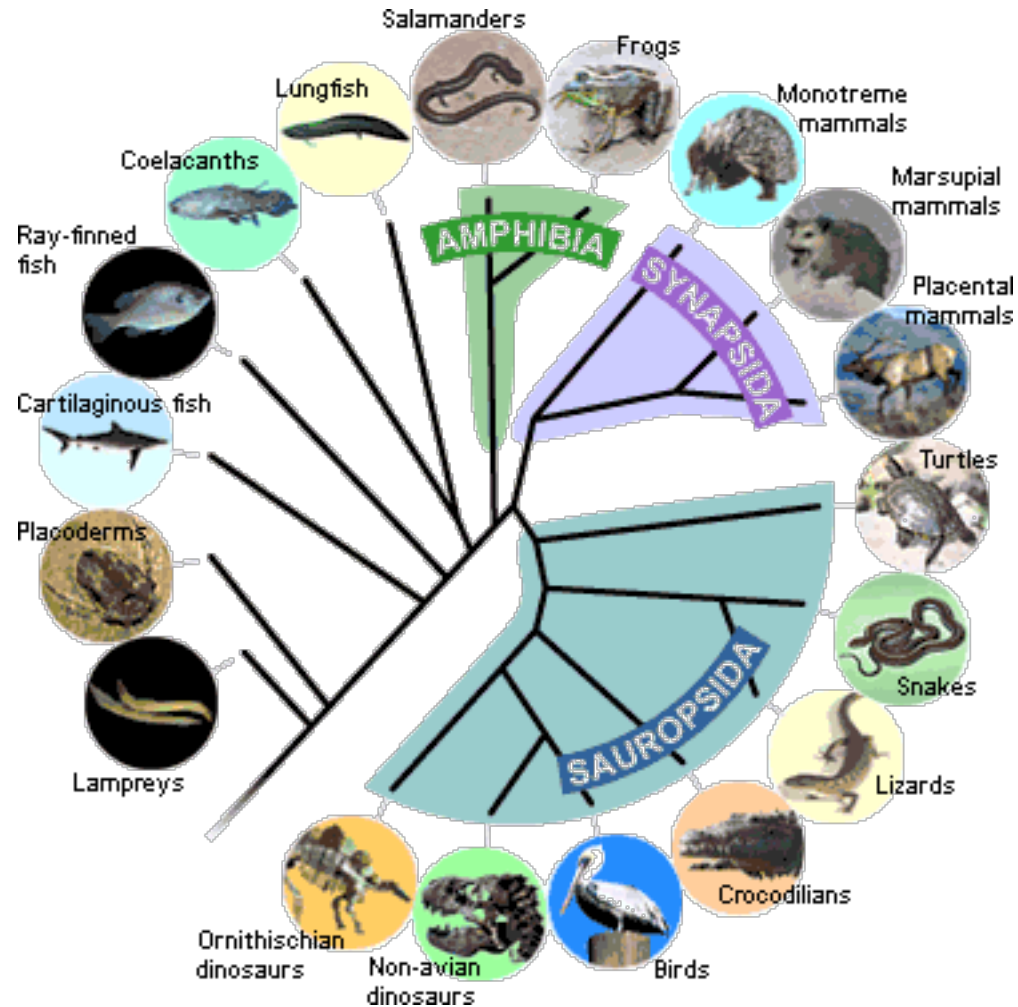


All the carnivores are related

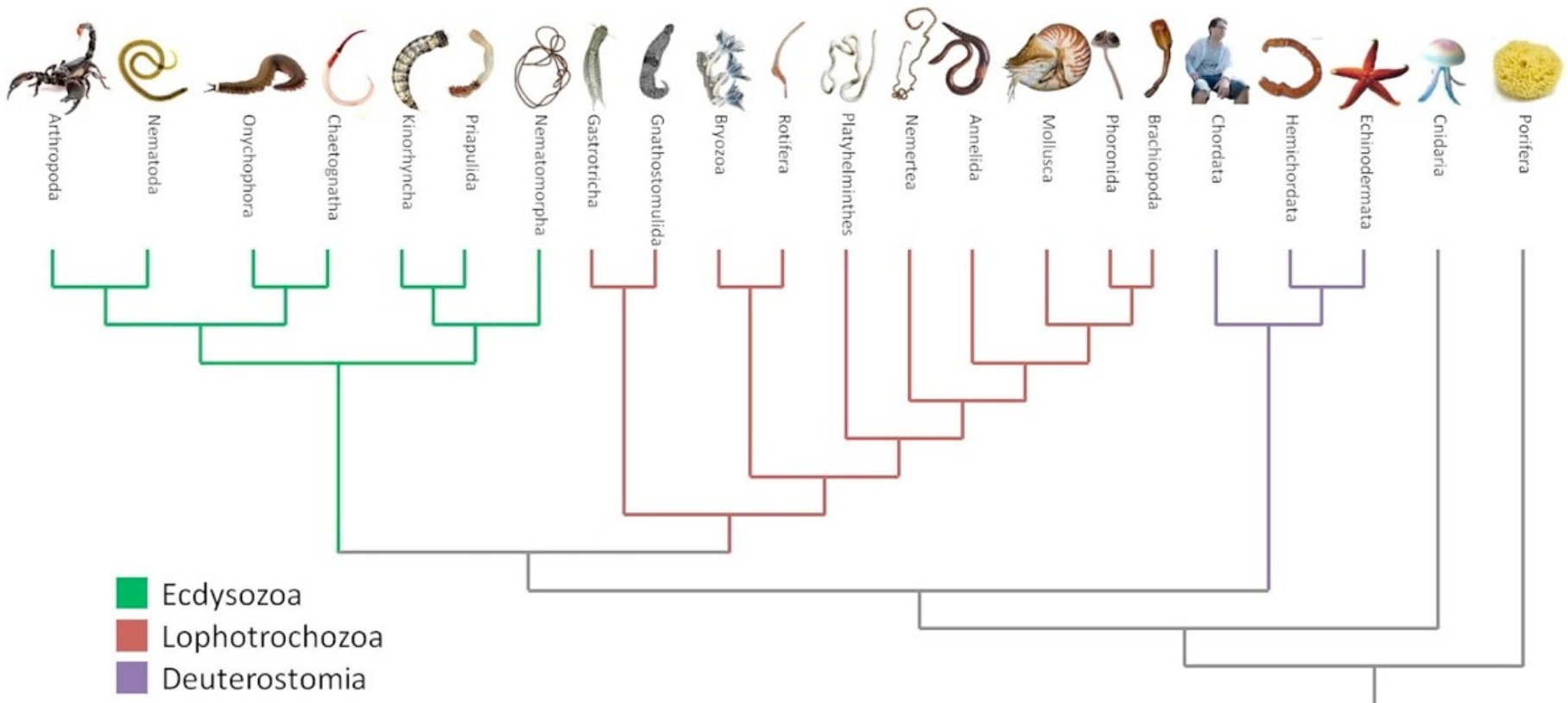


Relationship of Living Families of Carnivora

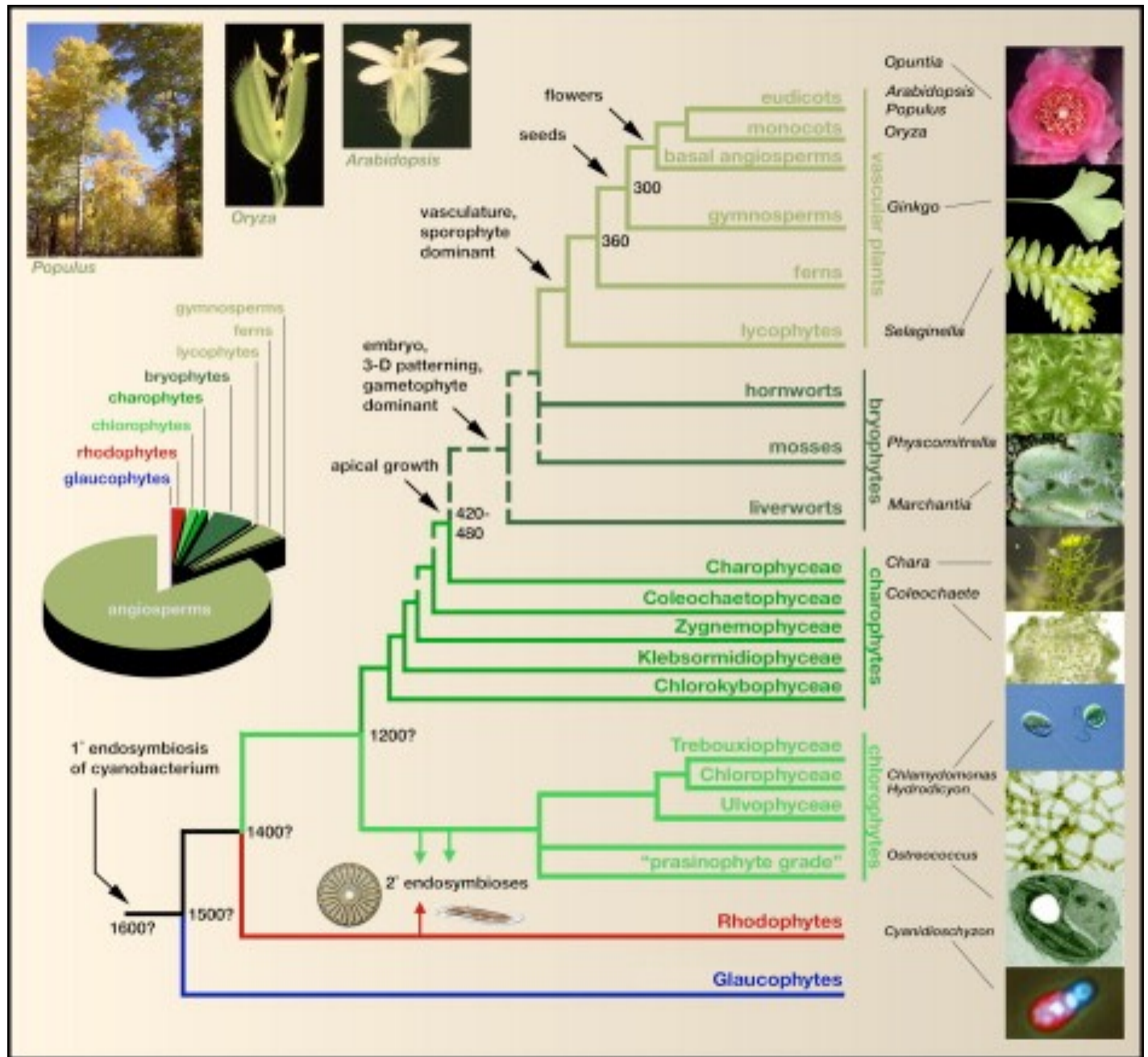
And the vertebrates



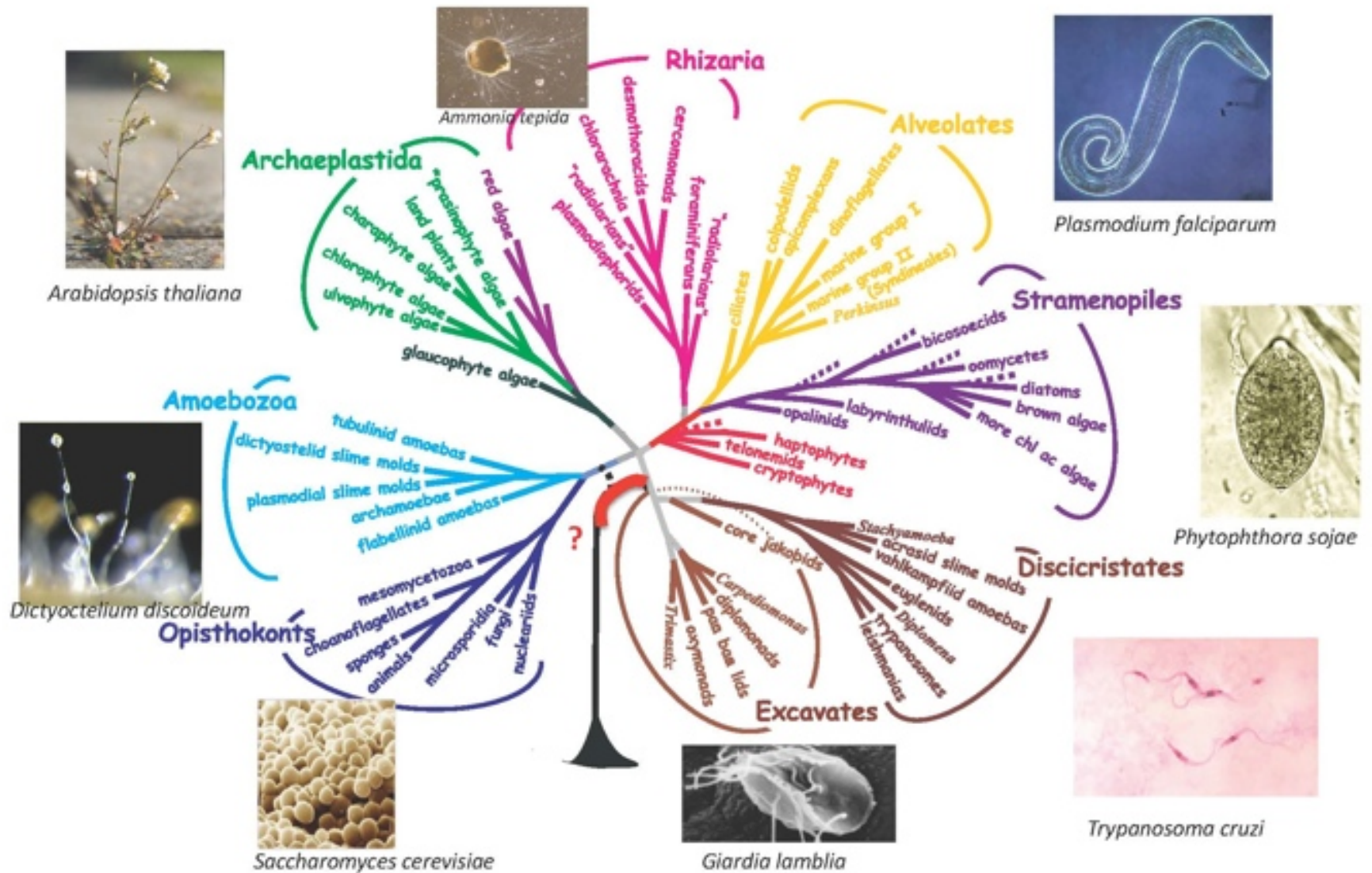
And all the animals

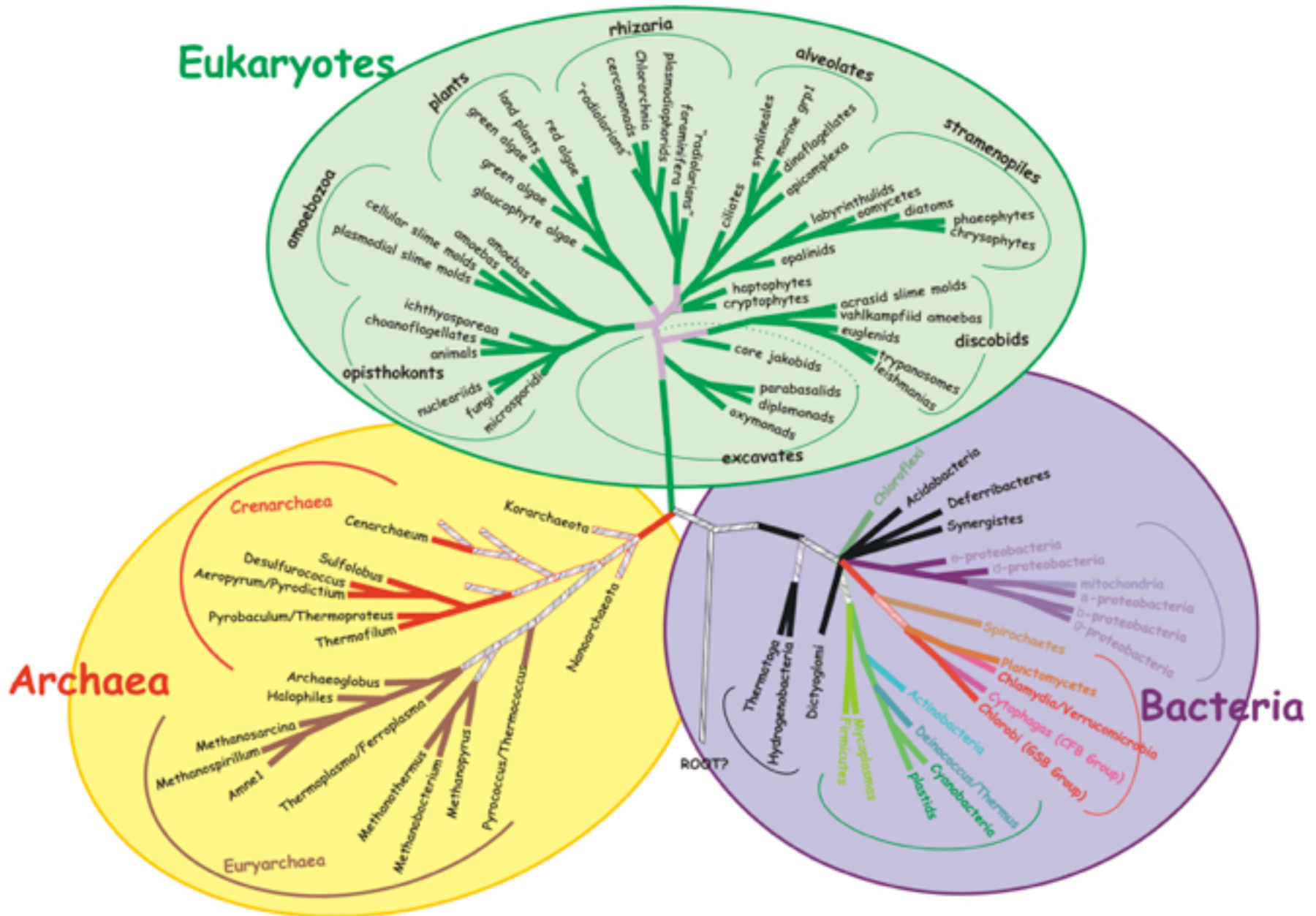


And
the
plants!



Eukaryotic Tree of Life





Current Tree of Life from Barton et al. *Evolution*

How do we know that
Common Ancestry is true?

Theodosius Dobzhansky (1900-1975)

committed Russian
Orthodox Christian

1974 - “Nothing in Biology
Makes Sense Except in
the Light of Evolution”

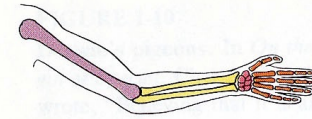


What is the evidence for common ancestry?

- **Homology**
 - “Unexpected” similarities among organisms
- **Classification**
 - Hierarchical nesting of taxa within taxa
- **Biogeography**
 - Similar species occur near one another
- **The fossil record**
 - Transitional forms in temporal sequence
 - The “fossil record” inside us (genetics)

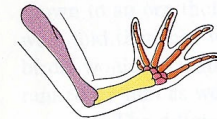
Deep Homology

- Distantly related organisms share structural similarities
- Function varies
- Explicable by common ancestry



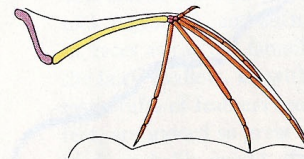
Human

grasping



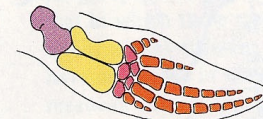
Frog

leaping



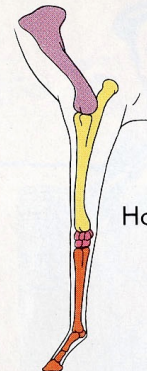
Bat

flying



Porpoise

swimming



Horse

running

Whales have hands!



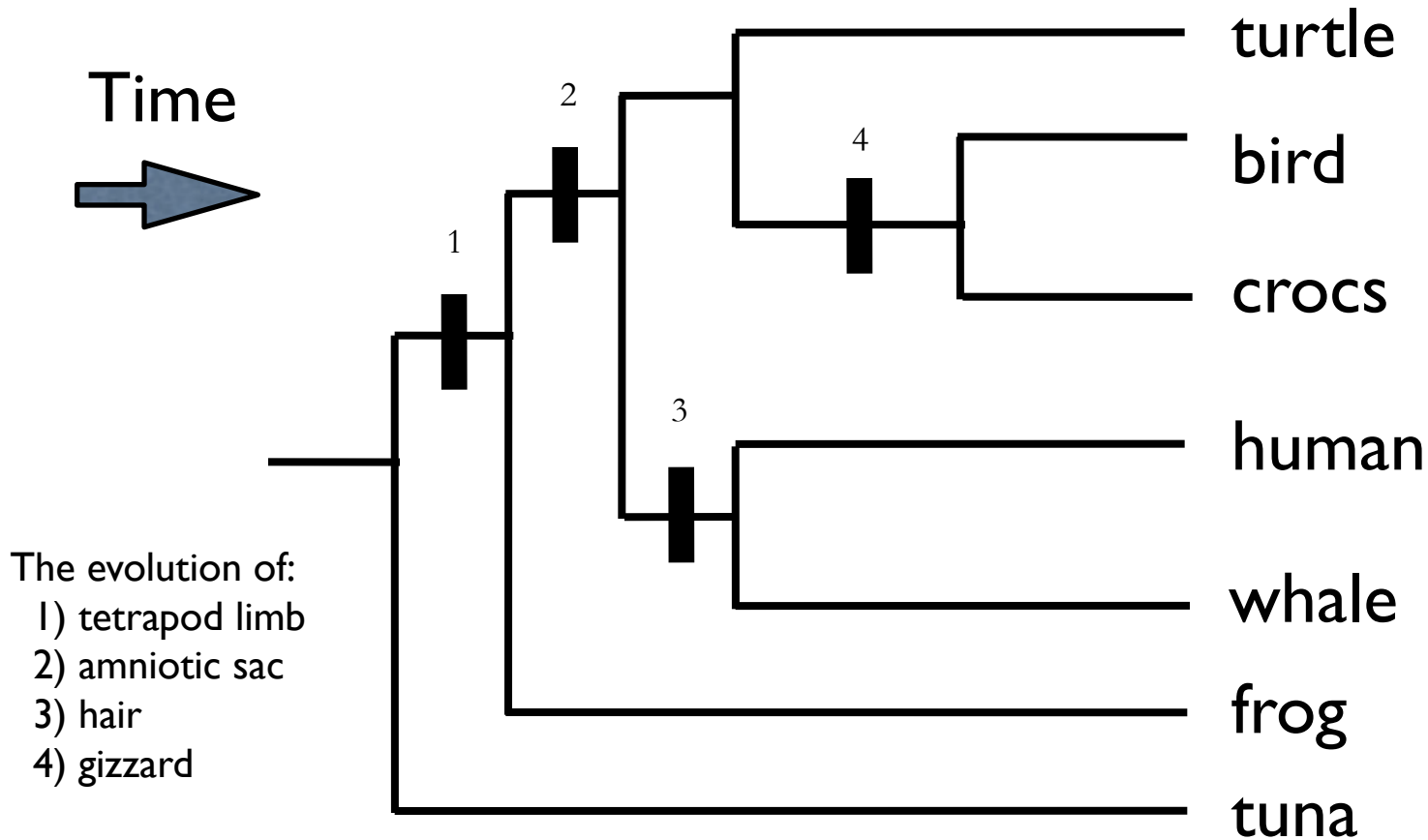
Homology

- Also true of molecular data

The screenshot displays the BioEdit Sequence Alignment Editor interface. The window title is "BioEdit Sequence Alignment Editor". The menu bar includes "File", "Edit", "Sequence", "Alignment", "View", "Accessory Application", "RNA", "World Wide Web", "Options", "Window", and "Help". The main window shows a multiple sequence alignment of 9 sequences, all identified as "cox2". The sequences are: KK01, KK02-cox2, KK03-cox2, KK04-cox2, KK05-cox2, KK06-cox2, KK07-cox2, KK08-cox2, and KK09-cox2. The alignment is displayed in a grid format with a ruler at the top indicating positions from 10 to 120. The sequences are highly conserved, with most positions containing the same nucleotide across all species. The alignment is shown in a color-coded format where different nucleotides are represented by different colors: Adenine (A) is green, Guanine (G) is red, Cytosine (C) is blue, and Thymine (T) is black. Gaps are represented by dashes. The alignment shows a high degree of similarity between the sequences, particularly in the regions around positions 10-120.

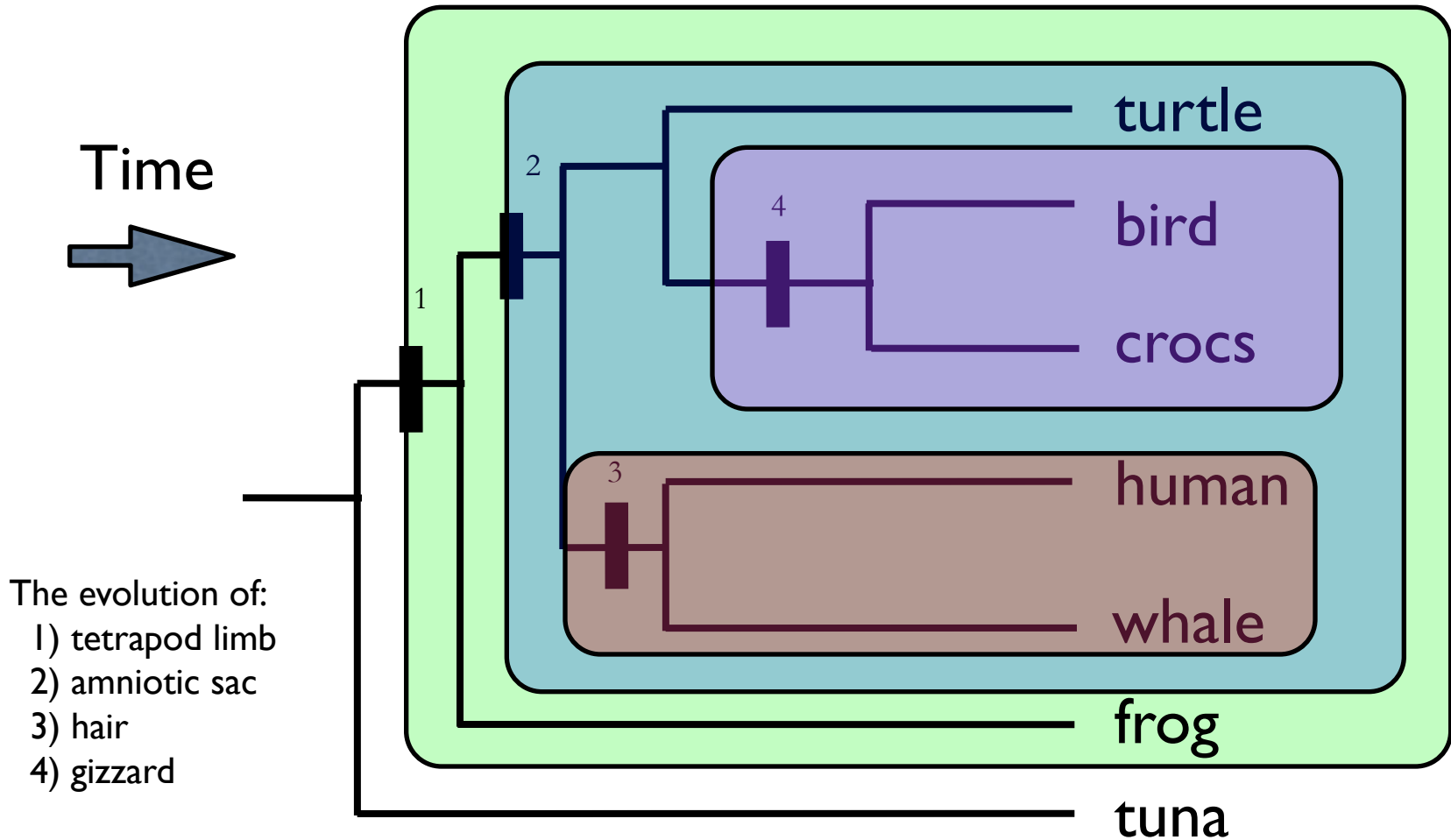
Nested hierarchical structure

“groups within groups”



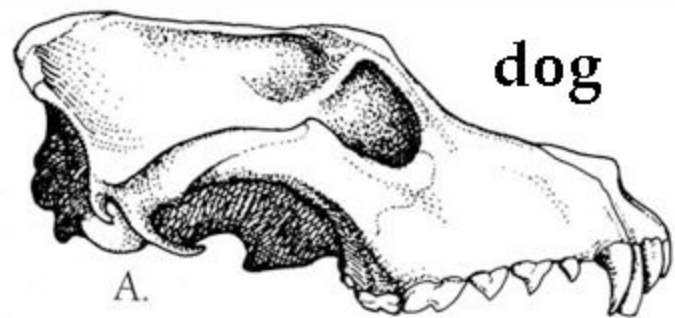
Nested hierarchical structure

“groups within groups”

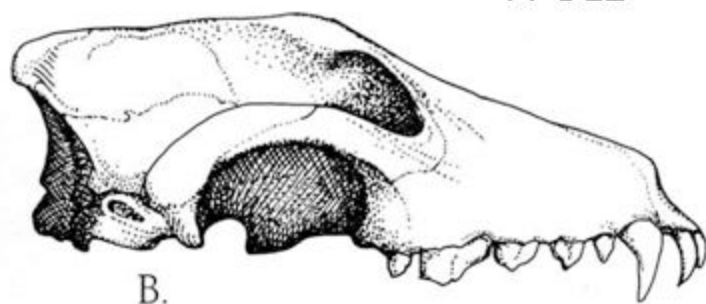


Why do we predict nested hierarchical structure?

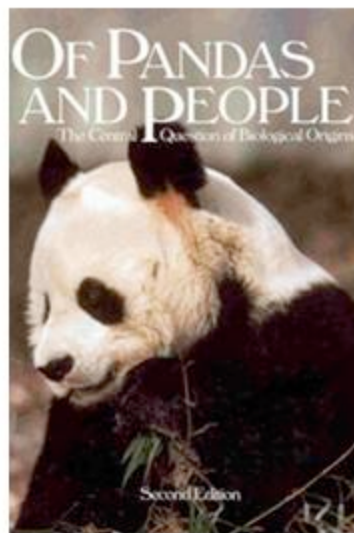
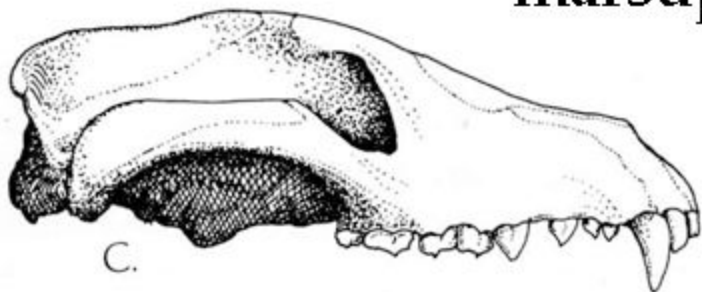
- Only branching evolutionary processes are capable of generating nested hierarchical structure.
- For example, human languages, which have common ancestors and are derived by descent with modification, can be classified in **objective** nested hierarchies.
- Library books cannot be classified in this way (traits like subject matter, author, date written, etc. overlap.)



wolf



marsupial "wolf"



(*Pandas*, p. 117)

Figure 5-2. The skulls of a dog (A), a North American wolf (B), and a Tasmanian wolf (C). Notice that the skull of the North American wolf is somewhat similar to the dog's, which is said to be related to it, but nearly identical to the Tasmanian wolf, which is allegedly only distantly related to it.

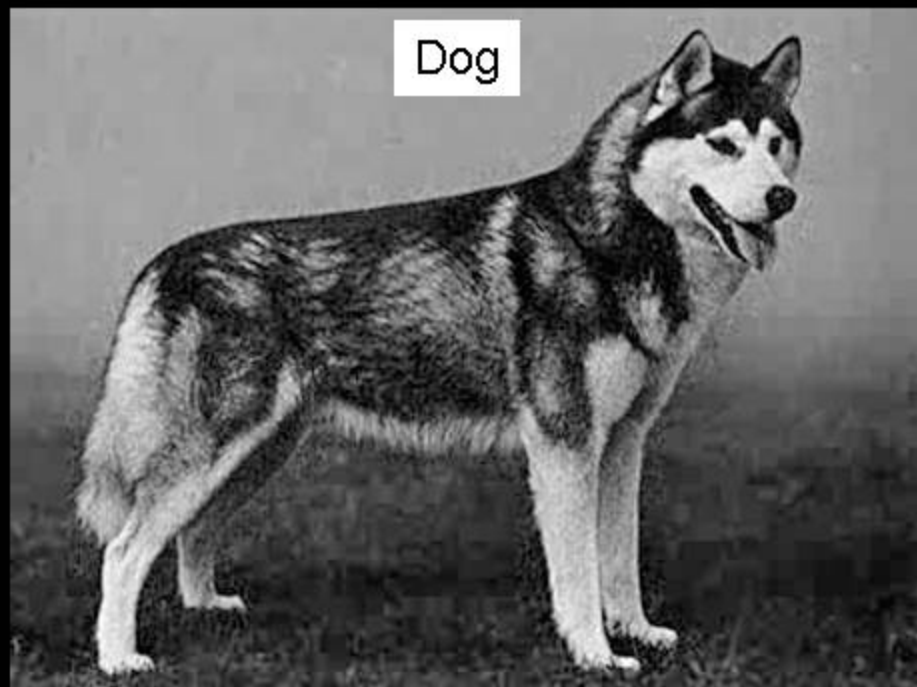
Of Pandas and People:

“Notice the skull of the North American wolf is somewhat similar to the dog's, which is said to be related to it, but nearly identical to the Tasmanian wolf, which is allegedly only distantly related to it.”

Tasmanian wolf



Dog



North American wolf



N. Am. wolf

NO

Para-occipital process present

NO

4 premolars

2 molars

Ear bulla present

YES

Carnassial tooth

Cheek bone & jaw joint

Tasmanian wolf

YES

Tooth formula

YES

4 molars

3 premolars

Lacrimal bone visible from side

NO



Dog



NO

Para-occipital process present

4 premolars

NO

2 molars

Ear bulla present

43

YES

Carnassial tooth

Cheek bone & jaw joint

N.Am. wolf

NO

Tooth formula

4 premolars

NO

2 molars

YES

Carnassial tooth

Lacrimal bone visible from side



Kangaroo

YES



Para-occipital process present

YES

4 molars

Ear bulla present

NO

Cheek bone & jaw joint

Tasmanian wolf

YES

YES

4 molars

3 premolars

Tooth formula

NO

Lacrimal bone visible from side



Kangaroo

YES



Para-occipital process present

YES

4 molars

Ear bulla present

NO

Cheek bone & jaw joint

Tasmanian wolf

YES

YES

4 molars

3 premolars

Tooth formula

NO

Lacrimal bone visible from side



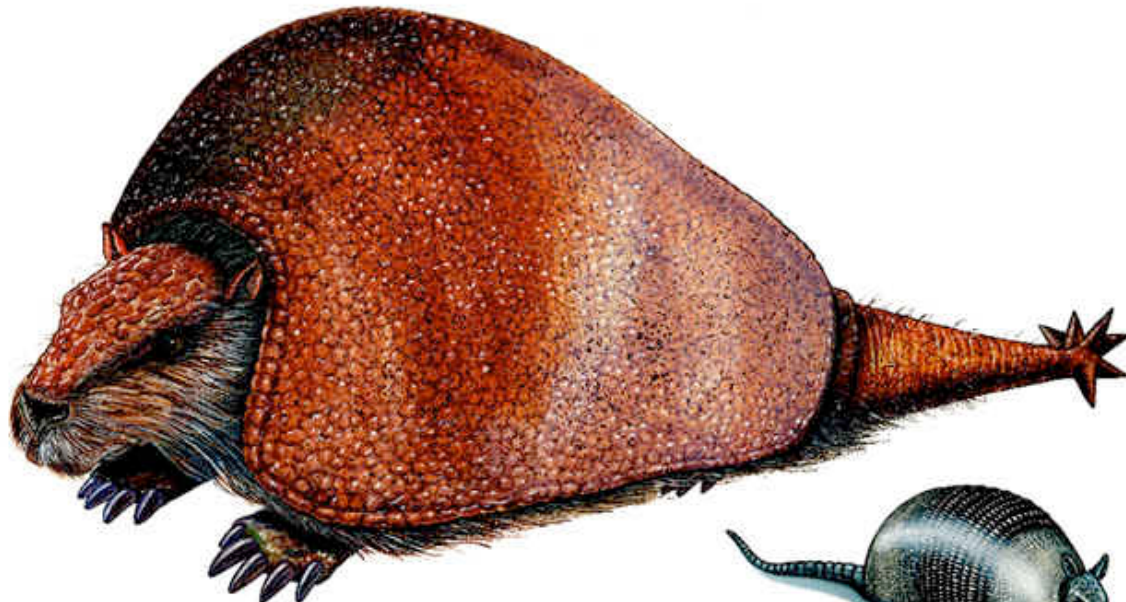
Not just the pouch

Similar traits among the Tasmanian wolf and other marsupials:

- Para-occipital process
- Do not have ear bulla
- Cheek bone meets jaw joint
- General tooth formula
- Lacrimal is visible from the side
- Wide nasal bones
- Holes in palatal bones
- Reflected lamina
- Nuclear DNA
- Mitochondrial DNA
- Ribosomal genes

Biogeography

- Species (living and fossil) tend to live near their closest relatives



Glyptodont

Armadillo

Biogeography: closely related species live near each other

Charles Darwin wrote of the Galapagos finches: “Seeing this gradation and diversity of structure in one small, intimately related group of birds, one might really fancy that from an original paucity of birds in this archipelago, one species has been taken and modified for different ends.” (C. Darwin, 1859)



Biogeography: closely related species live near each other



Hummingbirds: New World not Old World



Penguins: Antarctica not the Arctic



Cactus: New World
~1,750 species

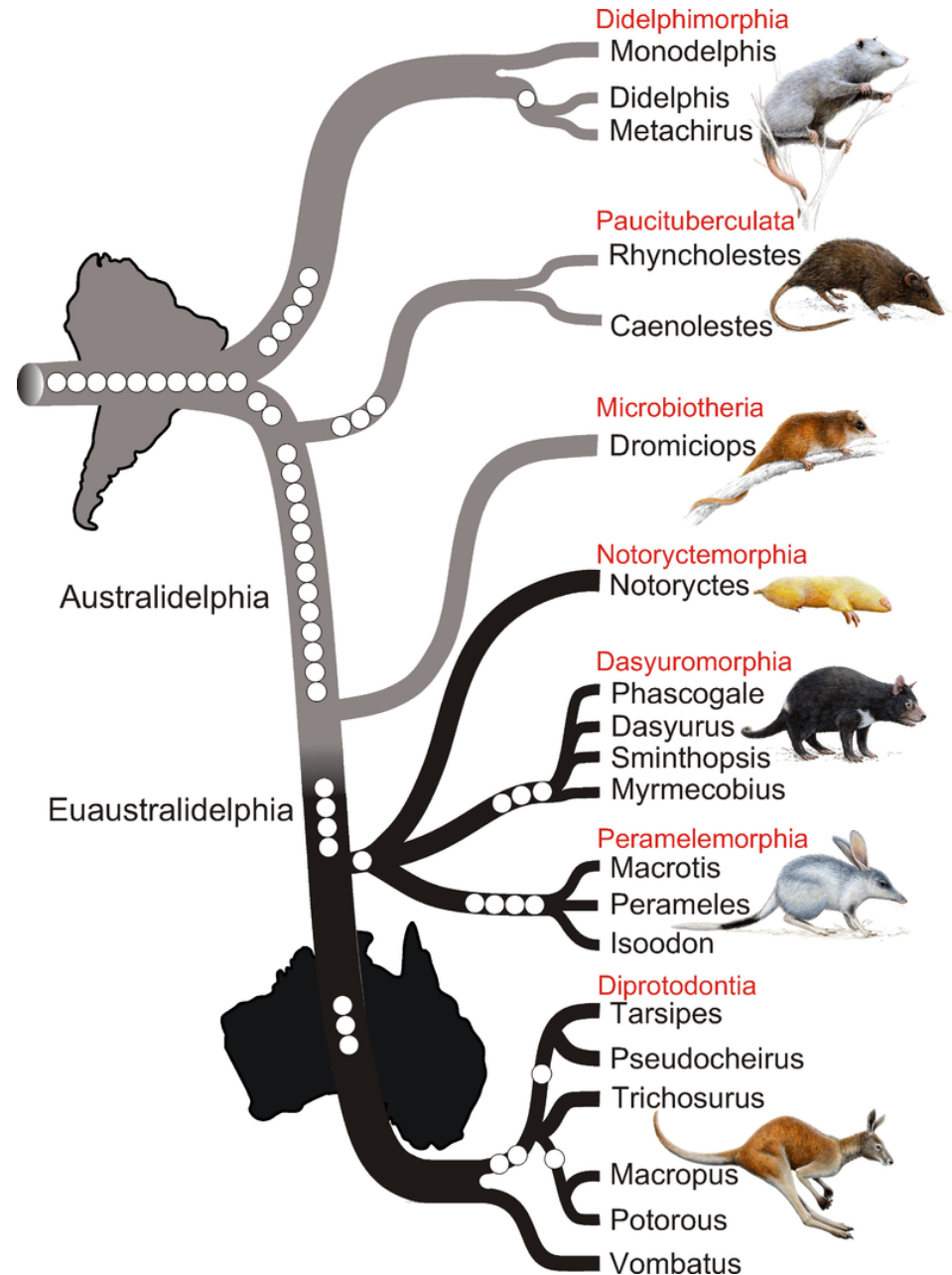
Euphorb: Old World
~7,500 species

Marsupials



History of Marsupials

— All Australian species evolved from one species ~50 million years ago which came from South America



Biogeography

- Facts about the distribution of fossils
- Facts about the distribution of types of organisms (cactus, hummingbirds, penguins, etc.)
- Facts about the distribution of native life on islands (continental vs. oceanic)

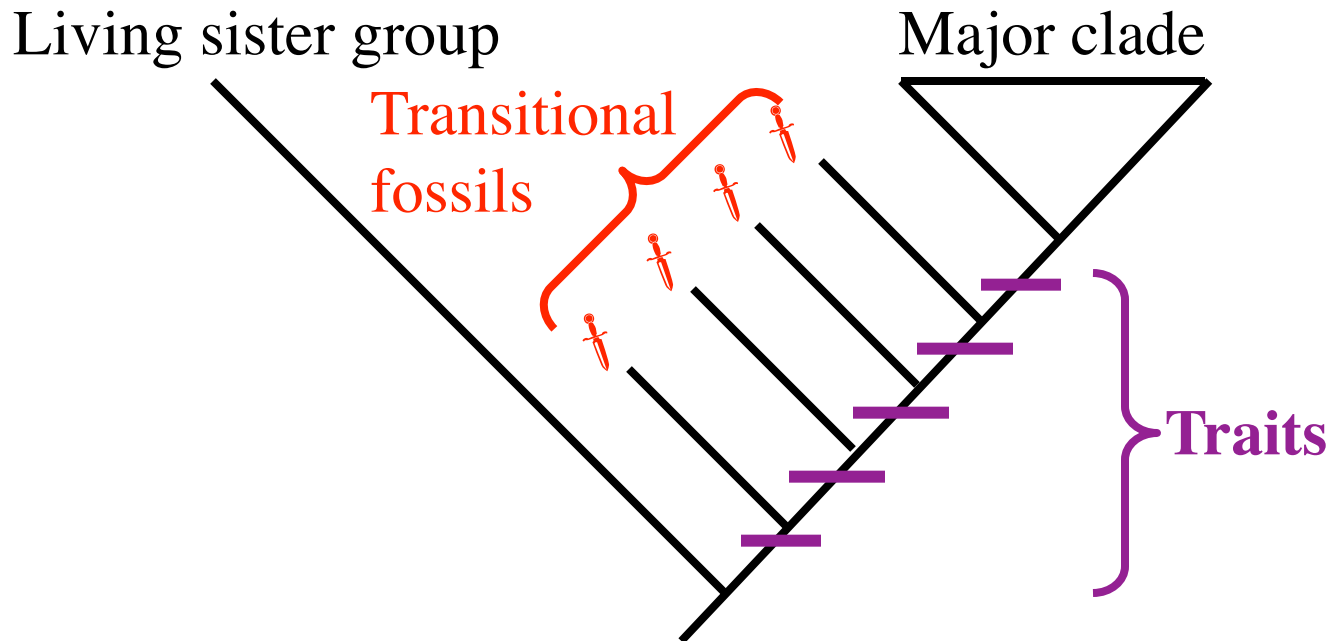
The predictions of common ancestry and descent with modification are borne out again and again. No other theory can explain so well

Fossils



Evidence for common ancestry

- Fossil record
 - Transitional fossils (sometimes in temporal sequence): consistent with the existence of real common ancestors



Origin of Tetrapods (4-limbed)

New tetrapod traits include:

- Limbs and digits
- Interlocking vertebrae - (connecting ribs)
- Ears
- Lungs instead of gills

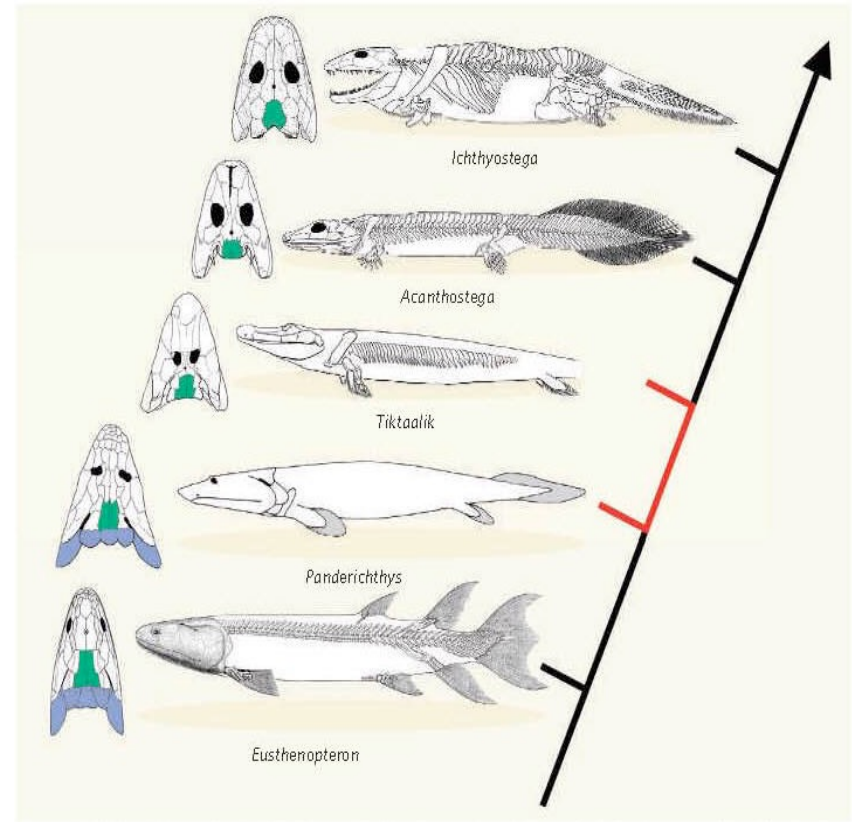
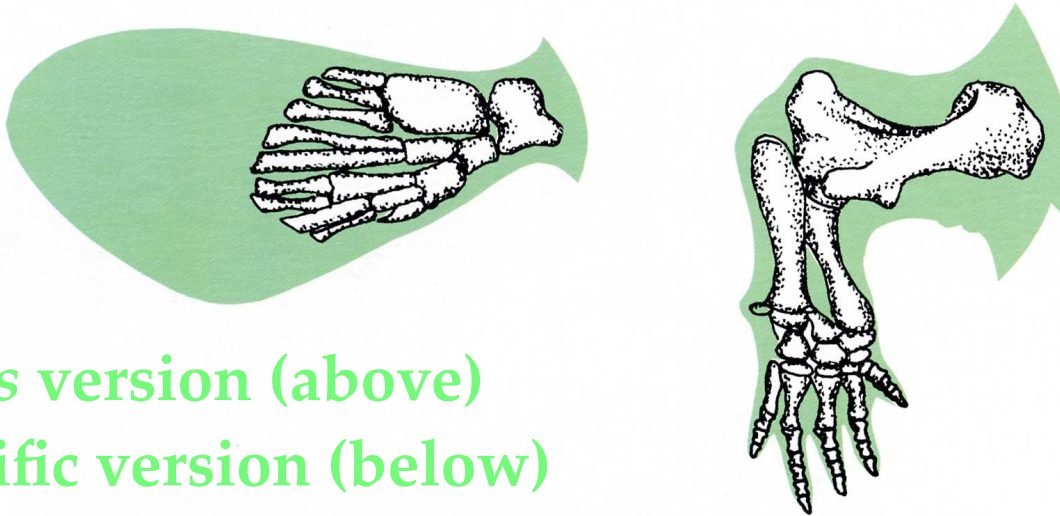


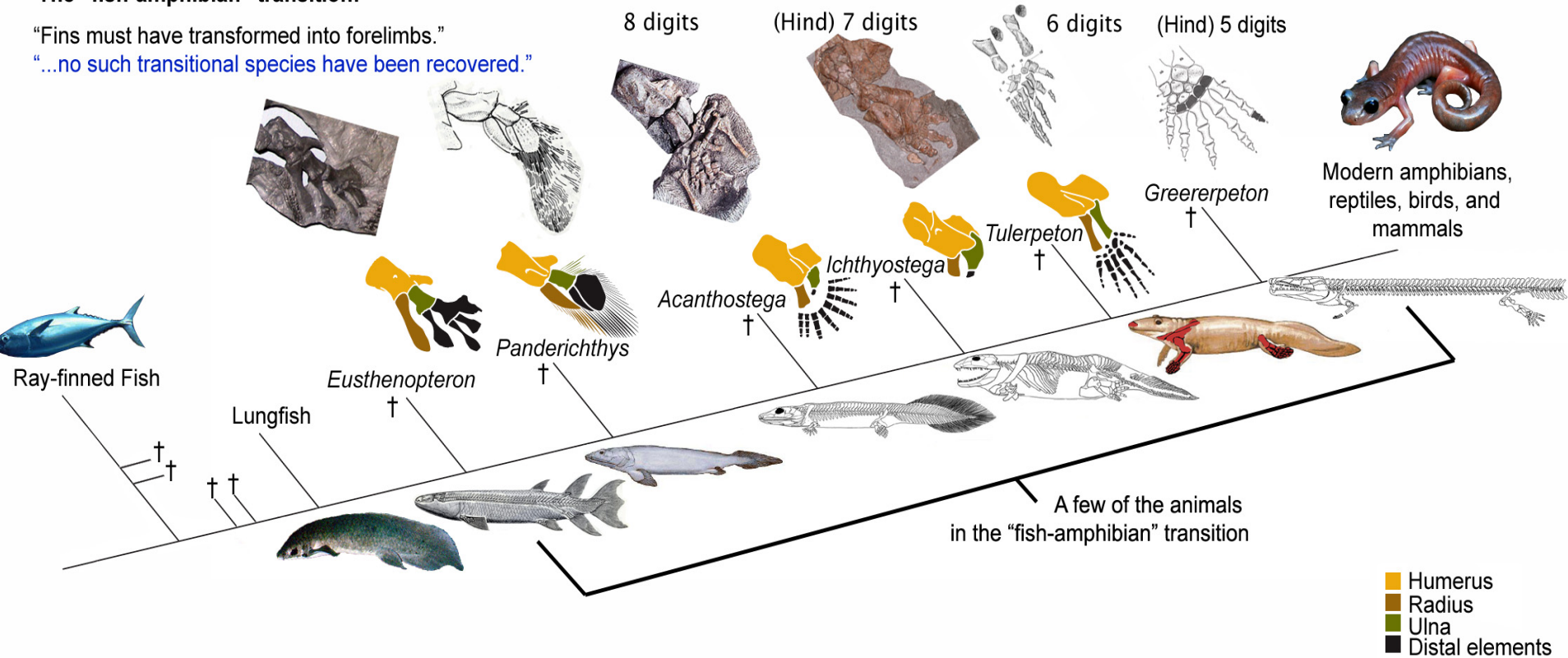
Figure 4-9. The bones of a crossopterygian fin compared to the bones of an ichthyostegid forelimb.



Pandas version (above)
 Scientific version (below)

The “fish-amphibian” transition:

“Fins must have transformed into forelimbs.”
 “...no such transitional species have been recovered.”

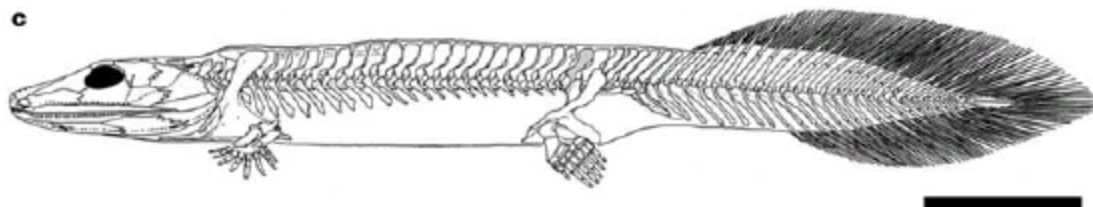


Acanthostega (~360 mya)

Found in 1952, eastern Greenland

- Limbs: no ankles, paddle-like, 8 digits
- Skeleton: ribs too short to support weight out of the water
- Lungs: present, internal gills

First fossil evidence that feet did not evolve for walking!



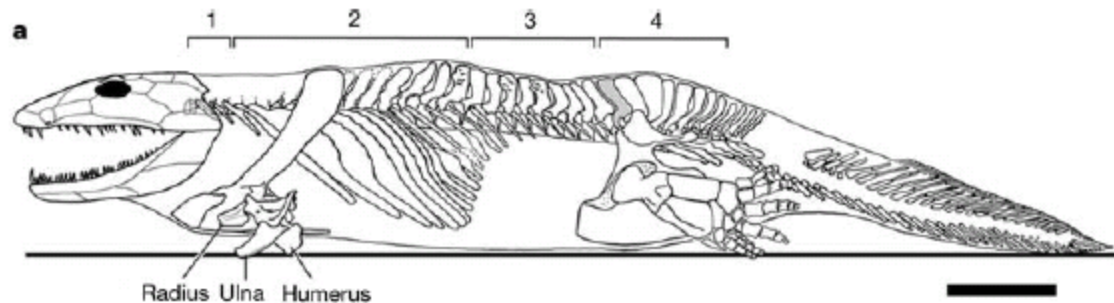
Ahlberg *et al.* (2005)
Nature

Ichthyostega (~363 mya)

Found in 1955, eastern Greenland

- Limbs: strong enough to support itself, hind limbs were 'flipper-like', 7 digits
- Skeleton: able to support organs out of water, but no lateral movement
- Lungs: present/gills

First fossil evidence for non-aquatic limb use!



Ahlberg *et al.*
(2005) *Nature*

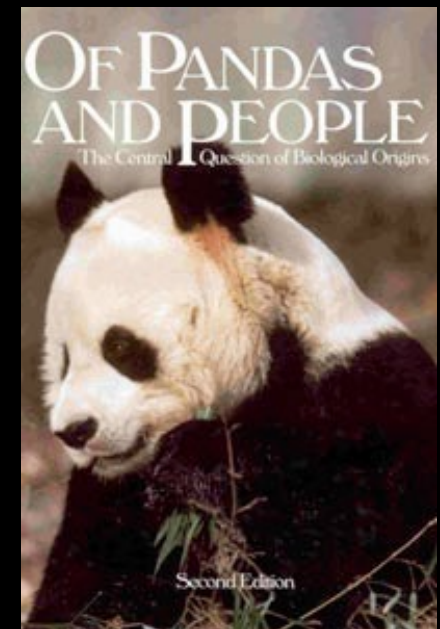
- *Tiktaalik roseae* ~375 mya (unveiled in 2006)
- has fish gills/scales/fins
- has “fishapod” limbs, joints, ear
- has tetrapod ribs, neck, lungs



3 skeletons discovered in Ellesmere Island, Nunavut, Canada. Team led by Neil Shubin (Chicago) and Ted Daeschler (UPenn) found it right where they expected

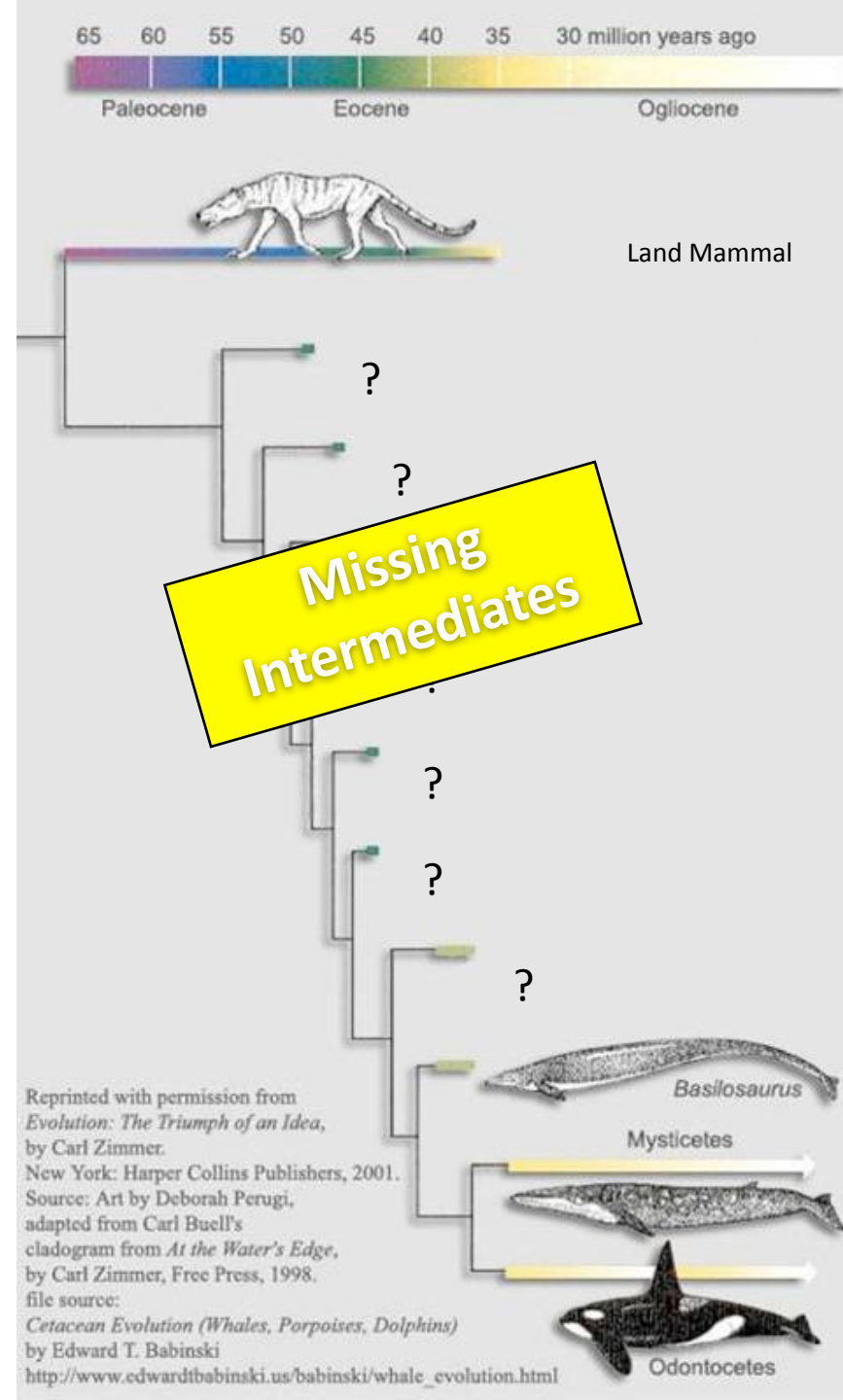
The origin of whales

The absence of unambiguous transitional fossils is illustrated by the fossil record of whales. The earliest forms of whales occur in rocks of Eocene age, dated some 50 million years ago, but little is known of their possible ancestors. By and large, Darwinists believe that whales evolved from a land mammal. The problem is that there are no clear transitional fossils linking land mammals to whales. If whales did have land-dwelling ancestors, it is reasonable to expect to find some transitional fossils.

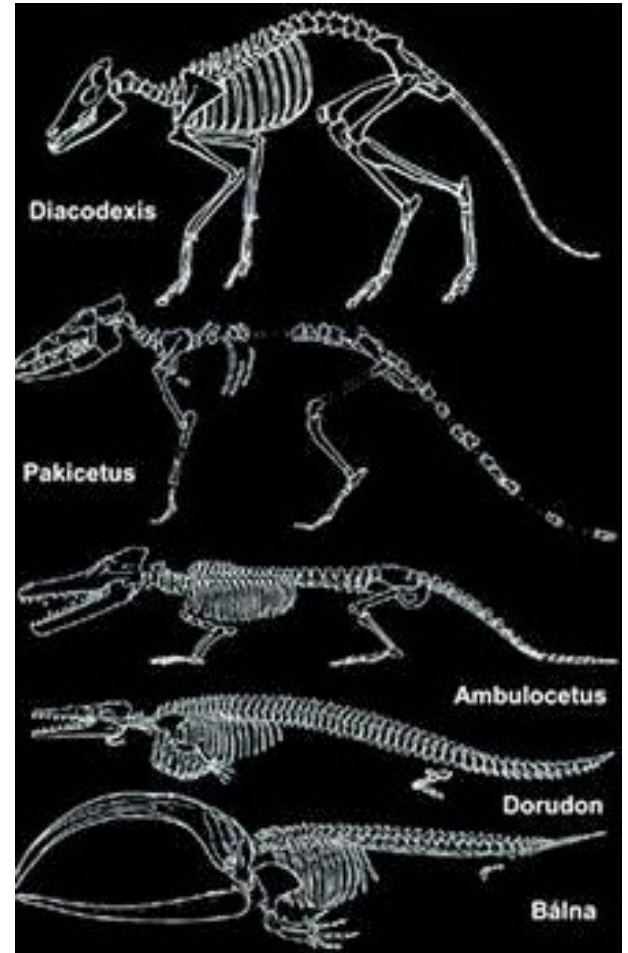
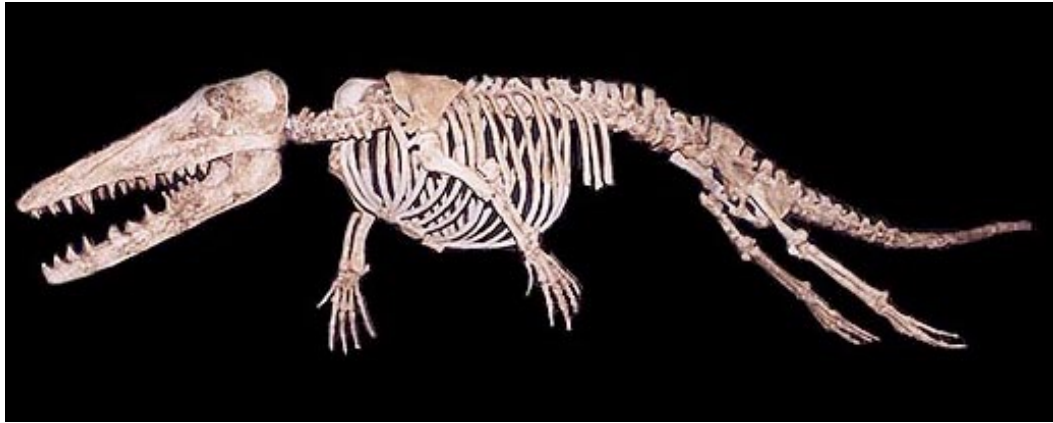


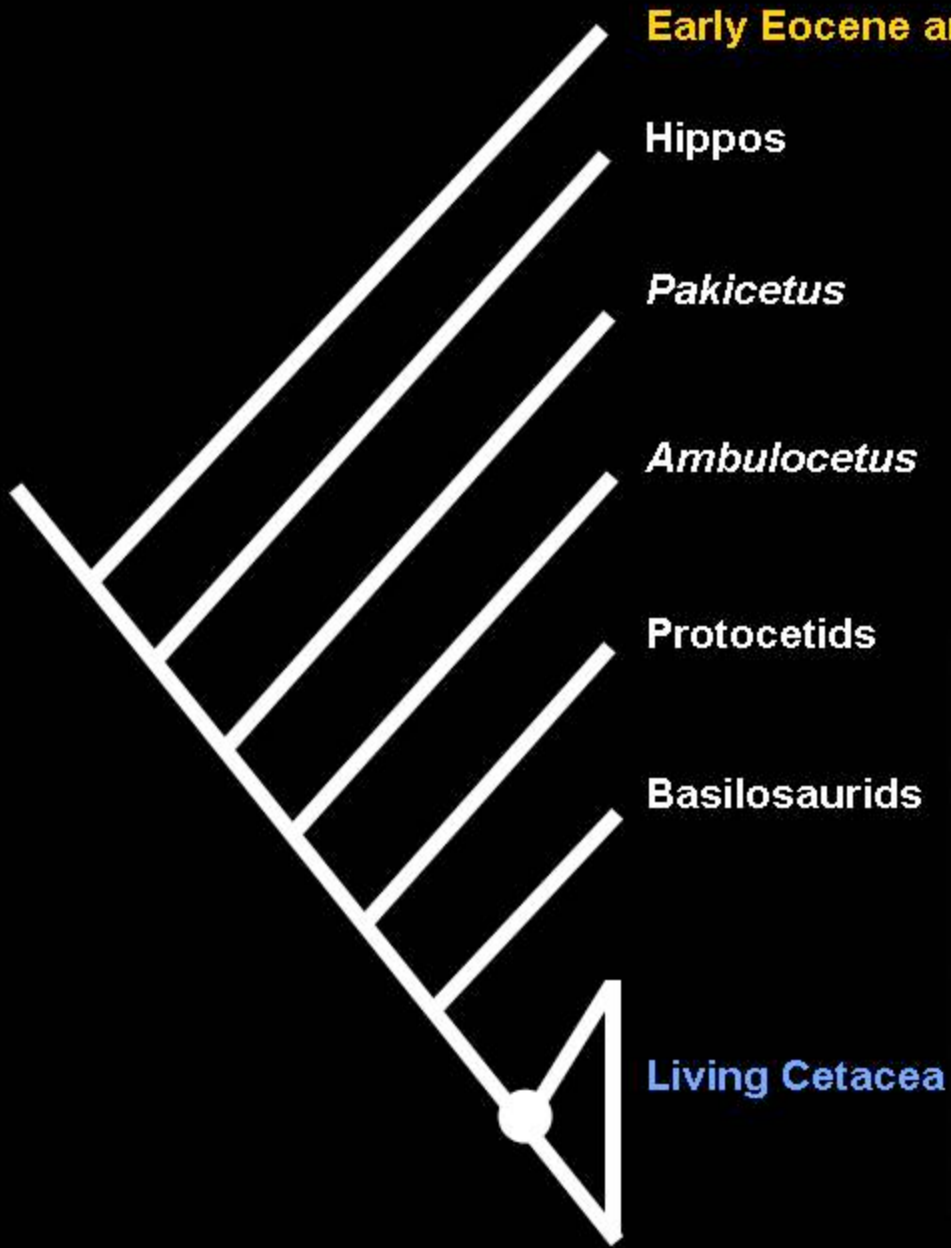
(Pandas, pp.

Is there a big problem here? How could you get from a land animal to a whale (or dolphin or porpoise)?



Evolution of the whale





Early Eocene artiodactyls

Hippos

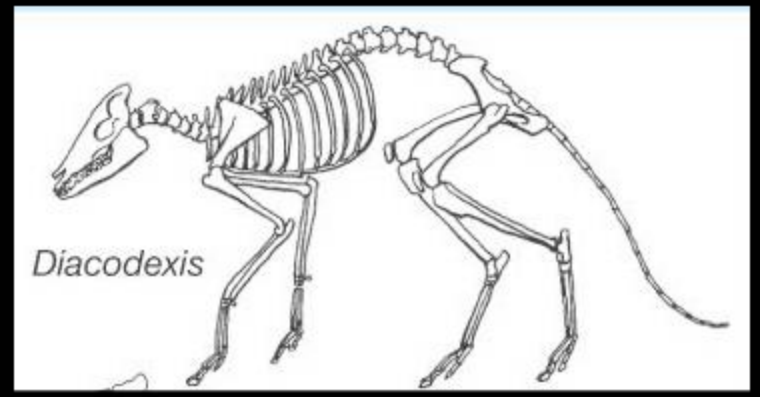
Pakicetus

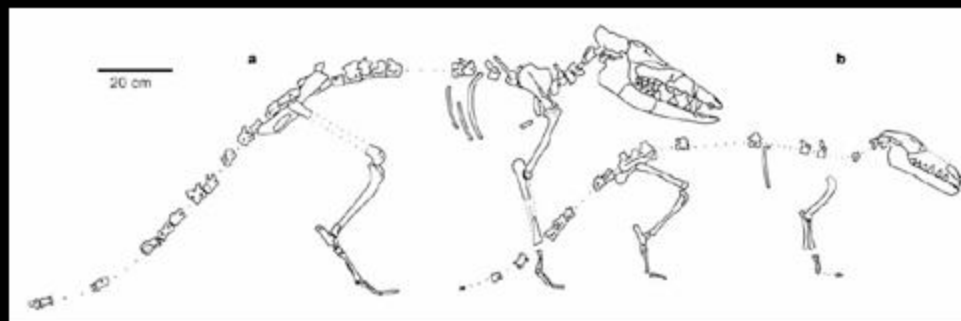
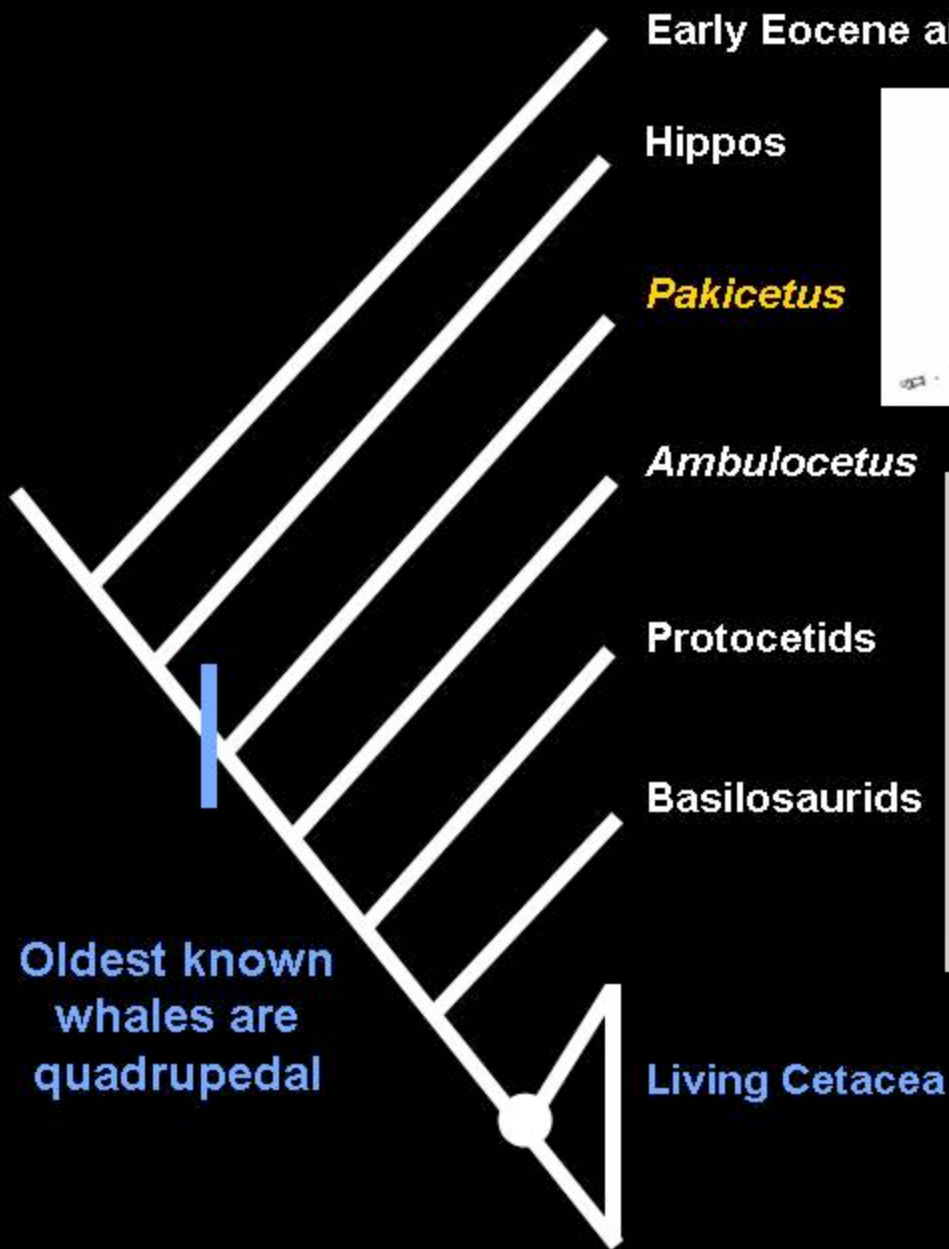
Ambulocetus

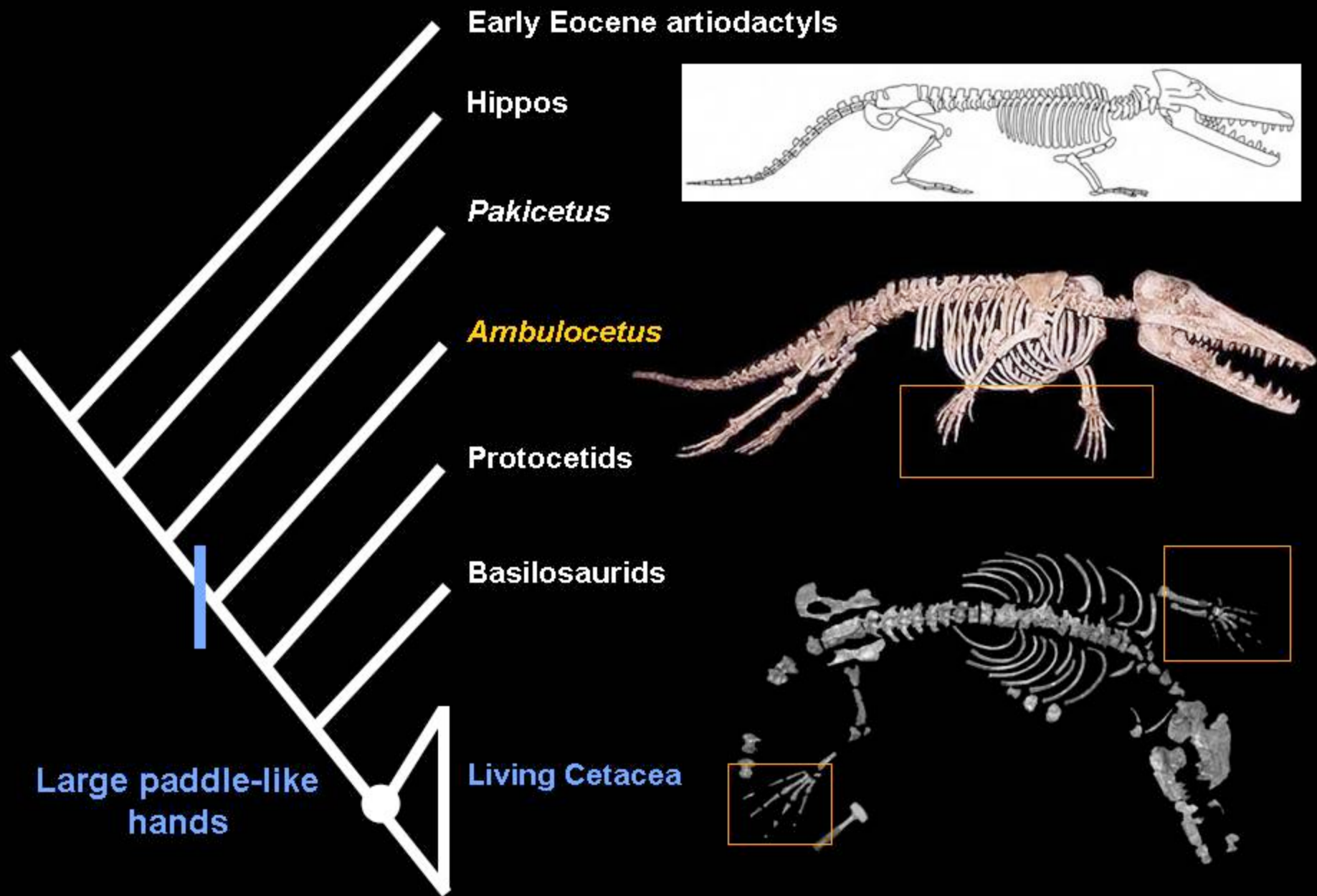
Protocetids

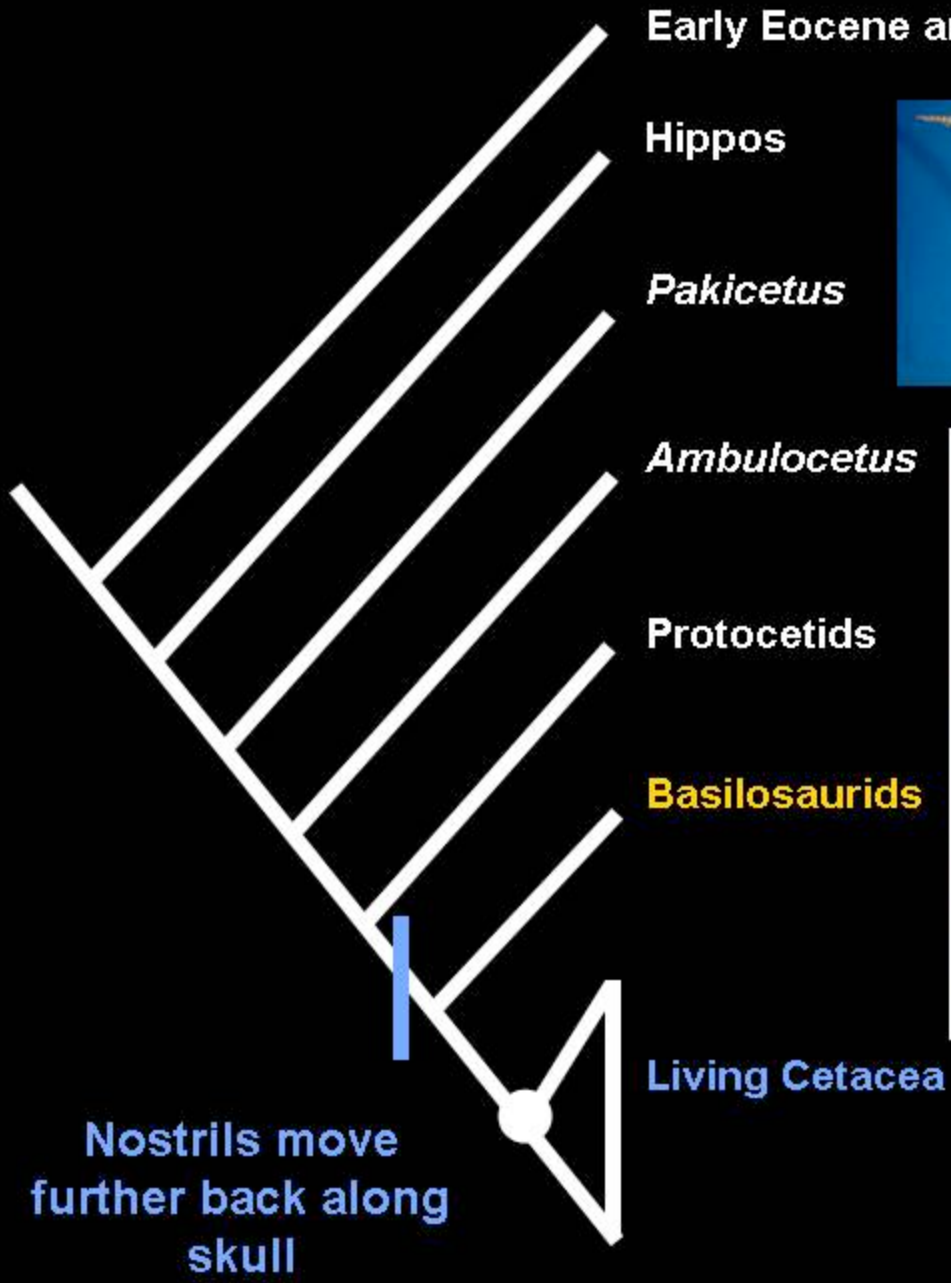
Basilosaurids

Living Cetacea



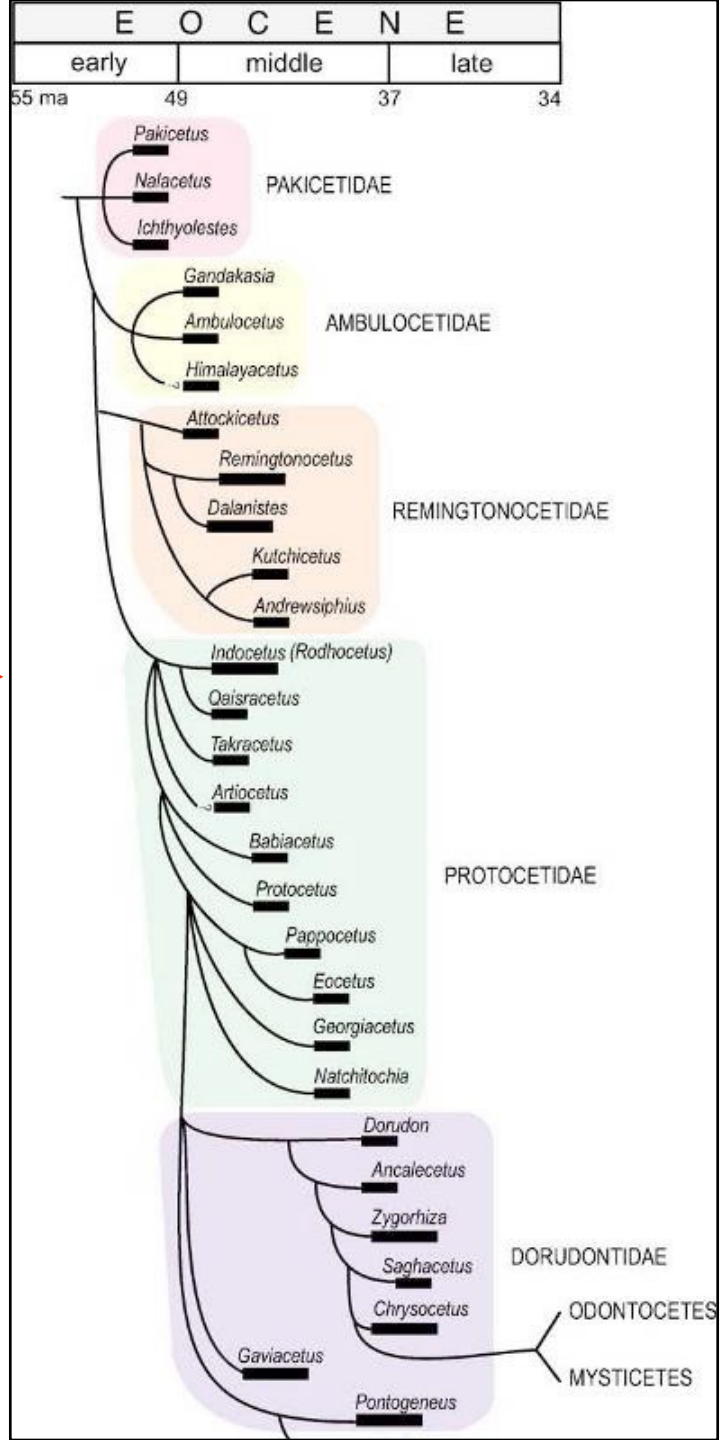
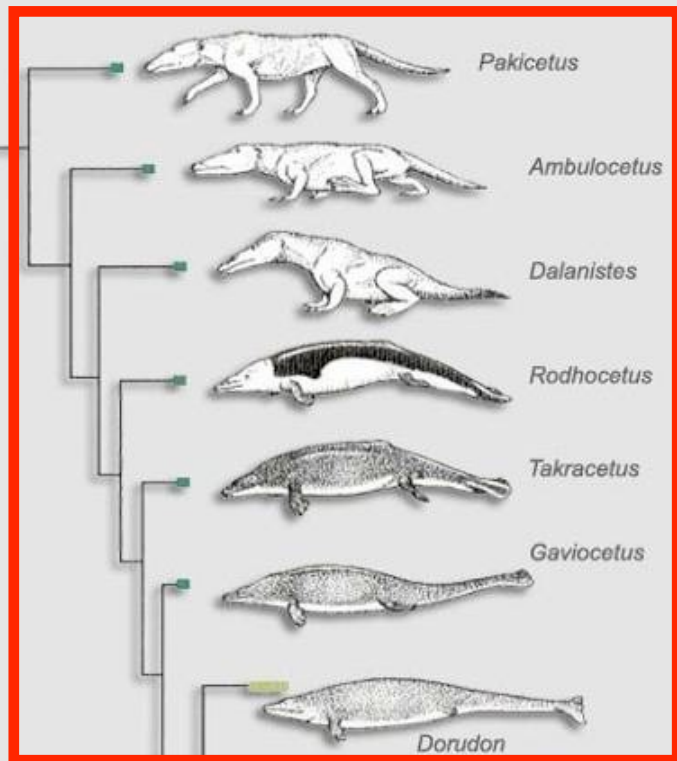








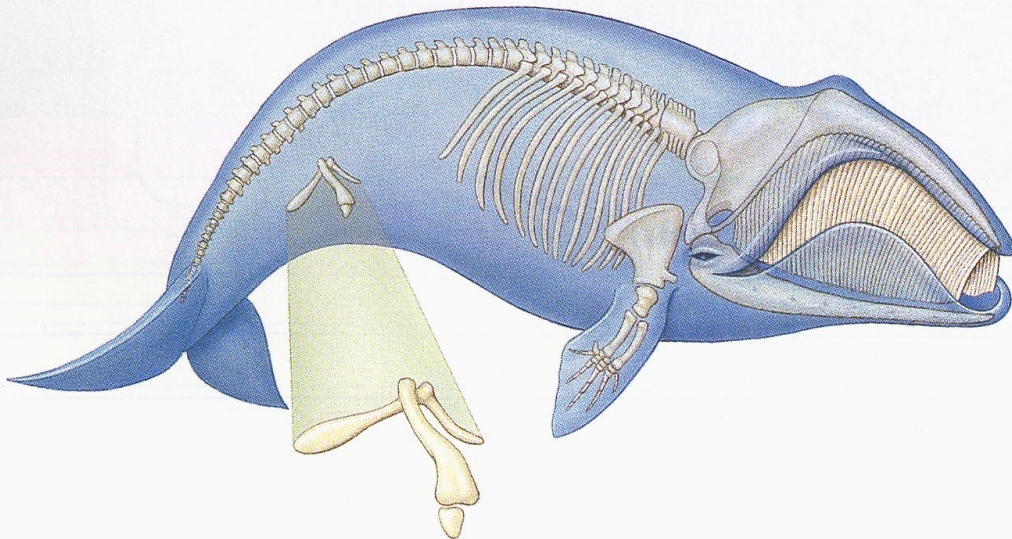
Mesonychids



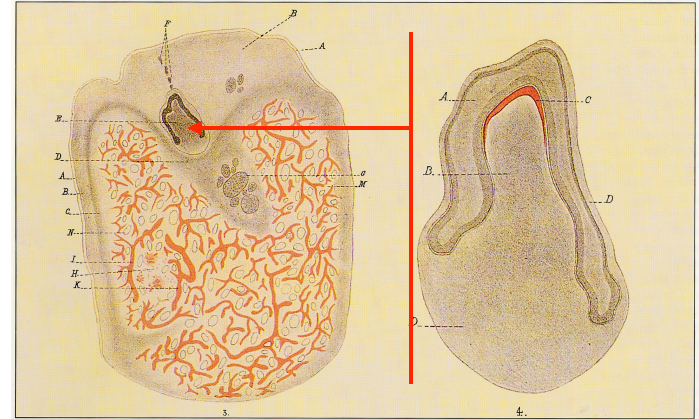
Reprinted with permission from *Evolution: The Triumph of an Idea*, by Carl Zimmer. New York: Harper Collins Publishers, 2001. Source: Art by Deborah Perugi, adapted from Carl Buell's cladogram from *At the Water's Edge*, by Carl Zimmer, Free Press, 1998. file source: *Cetacean Evolution (Whales, Porpoises, Dolphins)* by Edward T. Babinski http://www.edwardtbabinski.us/babinski/whale_evolution.html

Vestigial Structures in Whales

Evolution would also predict that species occupying very distinct environments from that of a common ancestor might show **vestigial** structures — structures obtained from a common ancestor but no longer needed for the original adaptive function.

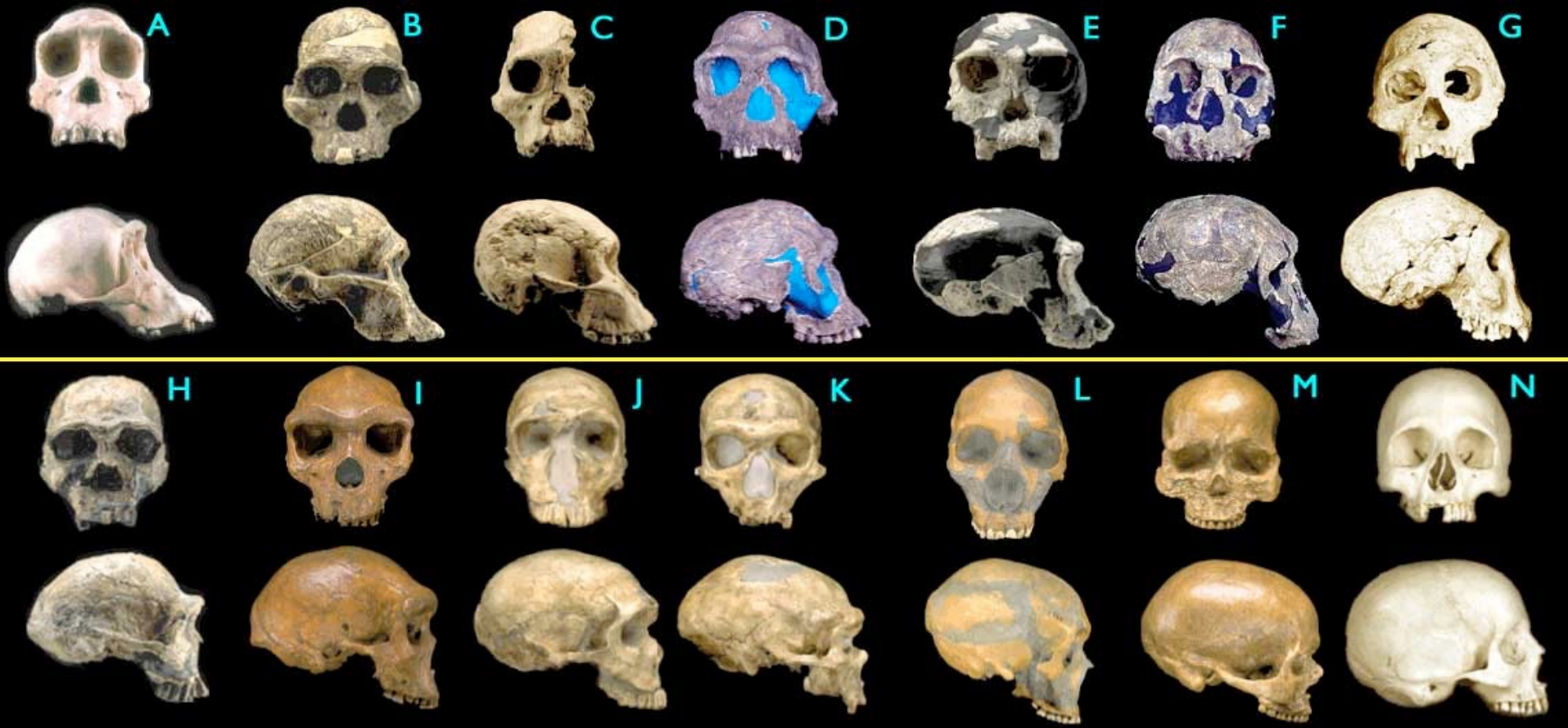


Sources: top - Young, 1992; lower - <http://www.lclark.edu/~seavey/genetics04/home.html>



Rudimentary tooth in lower jaw of a baleen whale

The **pelvic girdle** seen in reptiles and mammals as an adaptation for support in tetrapods, is vestigial in whales — it is a **“fossil” footprint** of their ancestry and serving no function today in swimming descendants of tetrapods.



- * (A) *Pan troglodytes*, chimpanzee, modern
- * (B) *Australopithecus africanus*, STS 5, 2.6 My
- * (C) *Australopithecus africanus*, STS 71, 2.5 My
- * (D) *Homo habilis*, KNM-ER 1813, 1.9 My
- * (E) *Homo habilis*, OH24, 1.8 My
- * (F) *Homo rudolfensis*, KNM-ER 1470, 1.8 My
- * (G) *Homo erectus*, Dmanisi cranium D2700, 1.75 My
- * (H) *Homo ergaster* (early *H. erectus*), KNM-ER 3733, 1.75 My
- * (I) *Homo heidelbergensis*, "Rhodesia man," 300,000 - 125,000 y
- * (J) *Homo sapiens neanderthalensis*, La Ferrassie 1, 70,000 y
- * (K) *Homo sapiens neanderthalensis*, La Chappelle-aux-Saints, 60,000 y
- * (L) *Homo sapiens neanderthalensis*, Le Moustier, 45,000 y
- * (M) *Homo sapiens sapiens*, Cro-Magnon I, 30,000 y
- * (N) *Homo sapiens sapiens*, modern

Brain size over time:

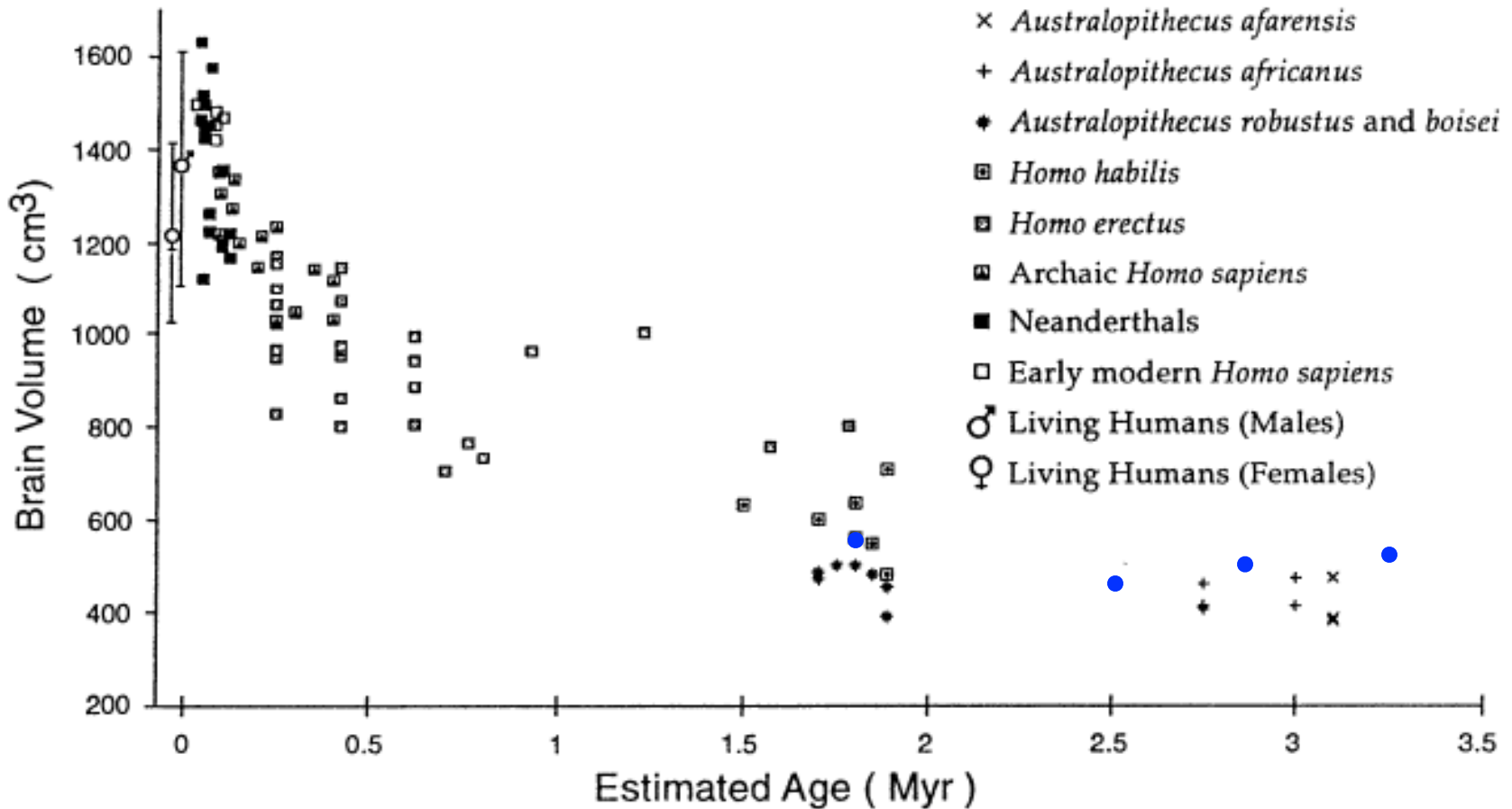


FIG. 4. Brain size (in cm^3) plotted against time (Myr) for specimens attributed to Hominidae.

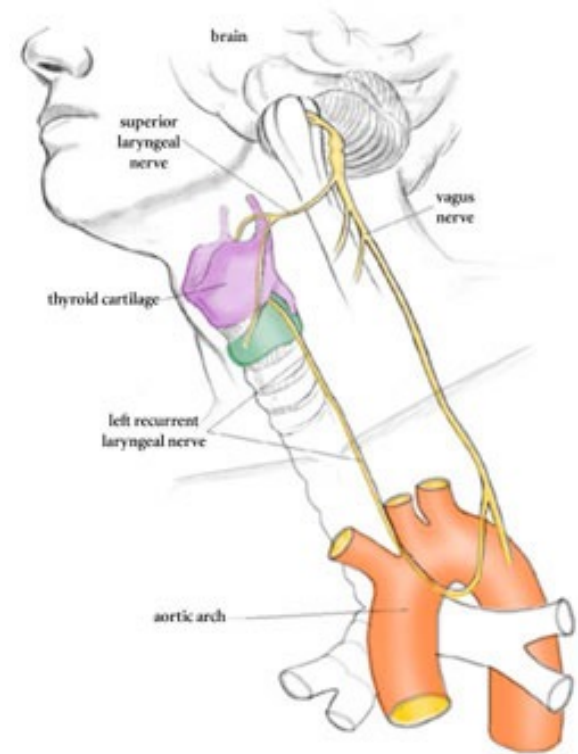
H. M. McHenry (1994). "Tempo and mode in human evolution." *Proceedings of the National Academy of Sciences*. 91(15), pp. 6780–6786. July 19, 1994. **New data** from McHenry (2002). "Introduction to the fossil record of human ancestry." Ch. 23 of: *The Primate Fossil Record*. Edited by W. C. Hartwig. pp. 401-405.

“Fossil traits” of humans

- Arrector pili muscles (goose bumps)
- Muscles to wiggle ears
- Coccyx (sometimes with attached muscle to wiggle your non-existent tail)
- Embryos have a lanugo (coat of hair)
 - Yolk sacs
 - Branchial arches (become gills in fish)

Recurrent Laryngeal Nerve

- Originates from the vagal nerve, then extends down the neck into the chest, and then back up to the neck again (brain to larynx)
- In fish, this nerve follows a straight line (brain to gills)

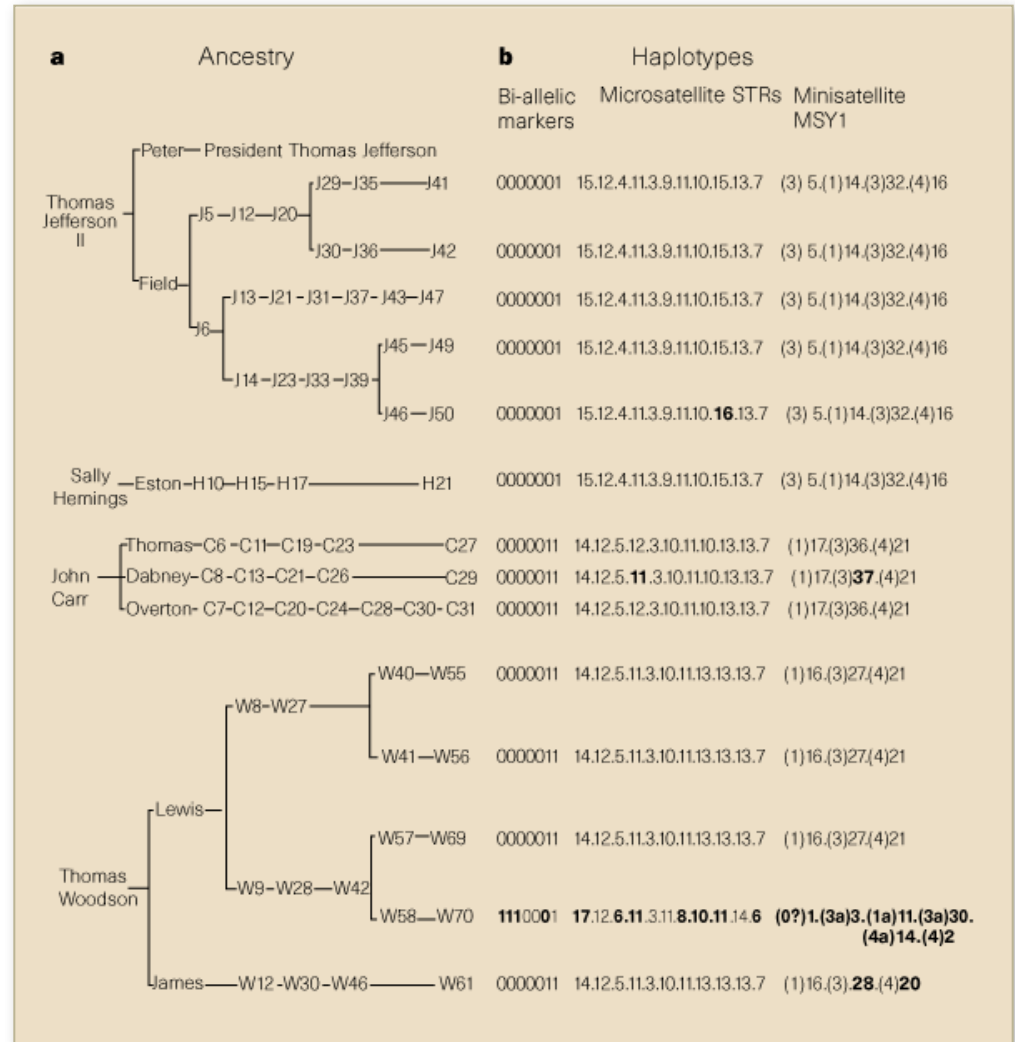


Fossil genes are even more impressive

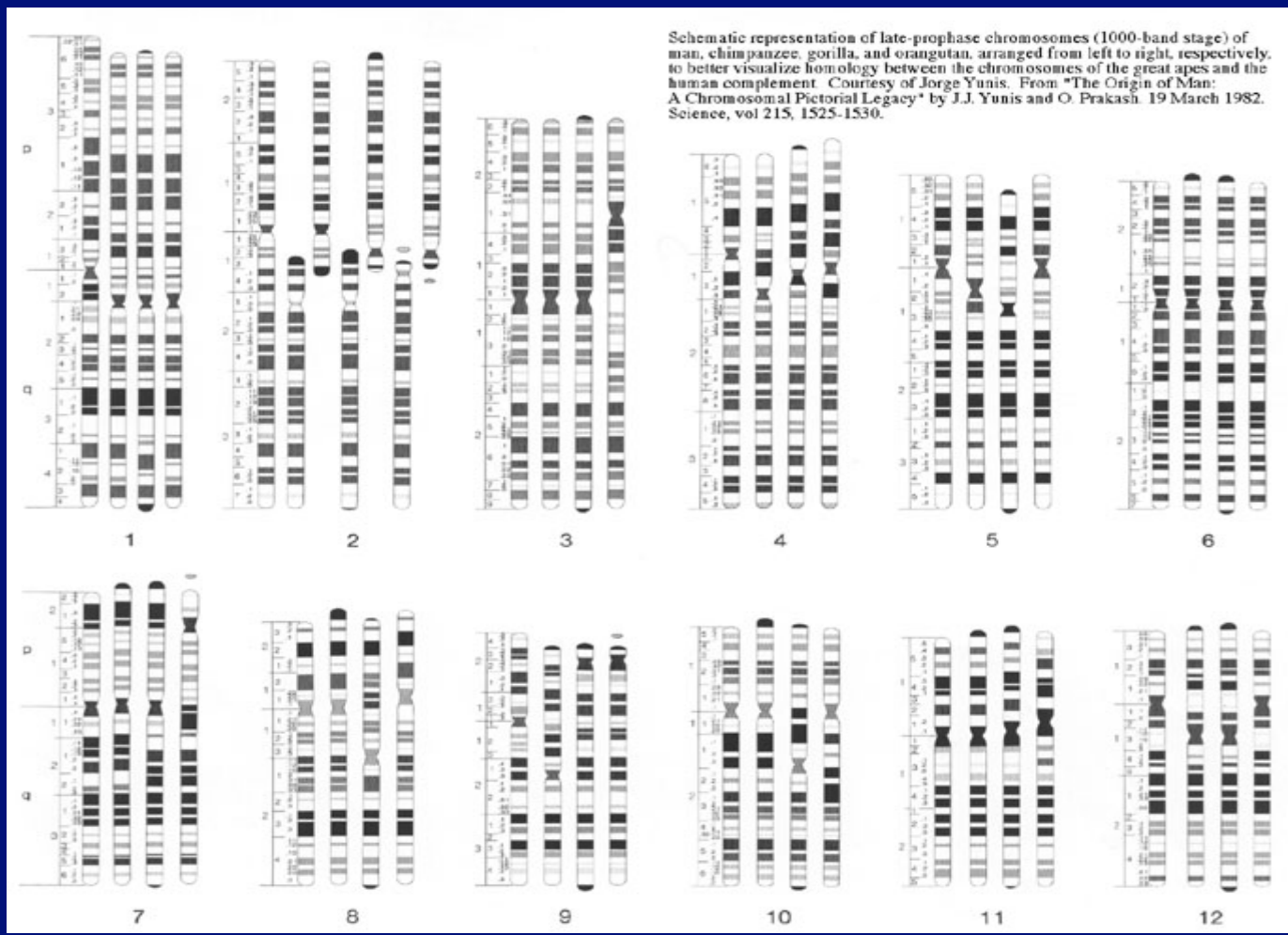
- We don't smell well since hundreds of our genes for olfactory receptors are broken (but there...)
- Primates (and fruit bats) have genes for metabolizing vitamin C, but they don't work anymore
- We have hundreds of molecular markers shared only with chimps, other shared with chimps and gorillas, others with all great apes, etc.

Forensics in humans uses molecular markers

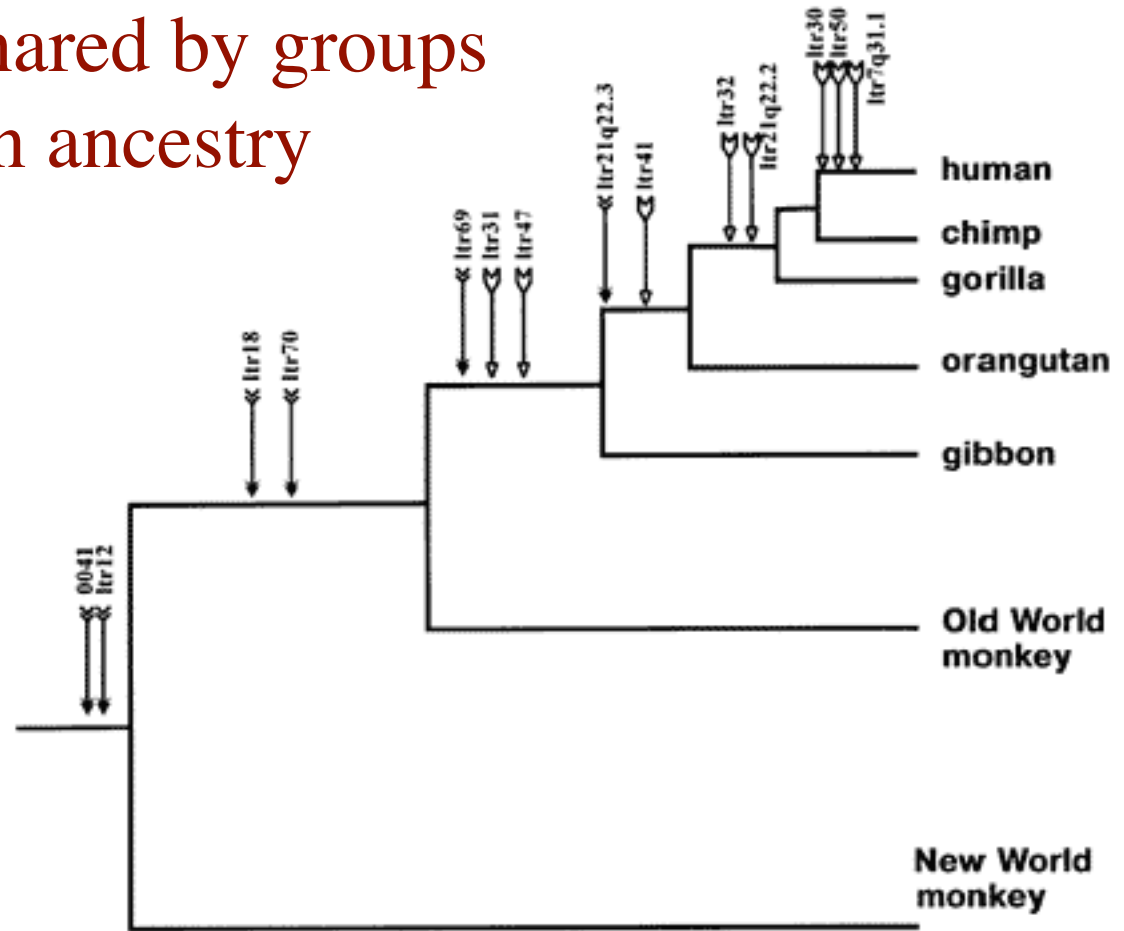
- Thomas Jefferson fathered Sally Hemings' last child (at least) - Nature, 1998



These same forsenic techniques can be used to detect our shared ancestry with the other great apes



Like other traits, endogenous retroviruses are shared by groups united by common ancestry



Comparative Genomic Evidence was Decisive



Chimp genetic code opens human frontiers Genome comparison reveals many similarities — and crucial differences

By Alan Boyle

Science editor
MSNBC

Updated: 4:20 p.m. ET Sept. 1, 2005

Scientists unleashed a torrent of new data comparing the DNA sequences of humans and chimpanzees on Sept. 1. The results appear to contain clues to how humans and their relatives in the animal kingdom evolved.

"We're really looking at an incredible discovery," said University of Washington geneticist Robert Waterston, senior author of a study in the journal Nature presenting the draft of the chimpanzee genome.

*"More than a century ago Darwin and Huxley posited that humans share recent common ancestors with the African great apes. **Modern molecular studies have spectacularly confirmed this prediction** and have refined the relationships, showing that the common chimpanzee (*Pan troglodytes*) and bonobo (*Pan paniscus*) are our closest living evolutionary relatives."*

Testing the Evolutionary Hypothesis of Common Ancestry

Chromosome numbers in the great apes:

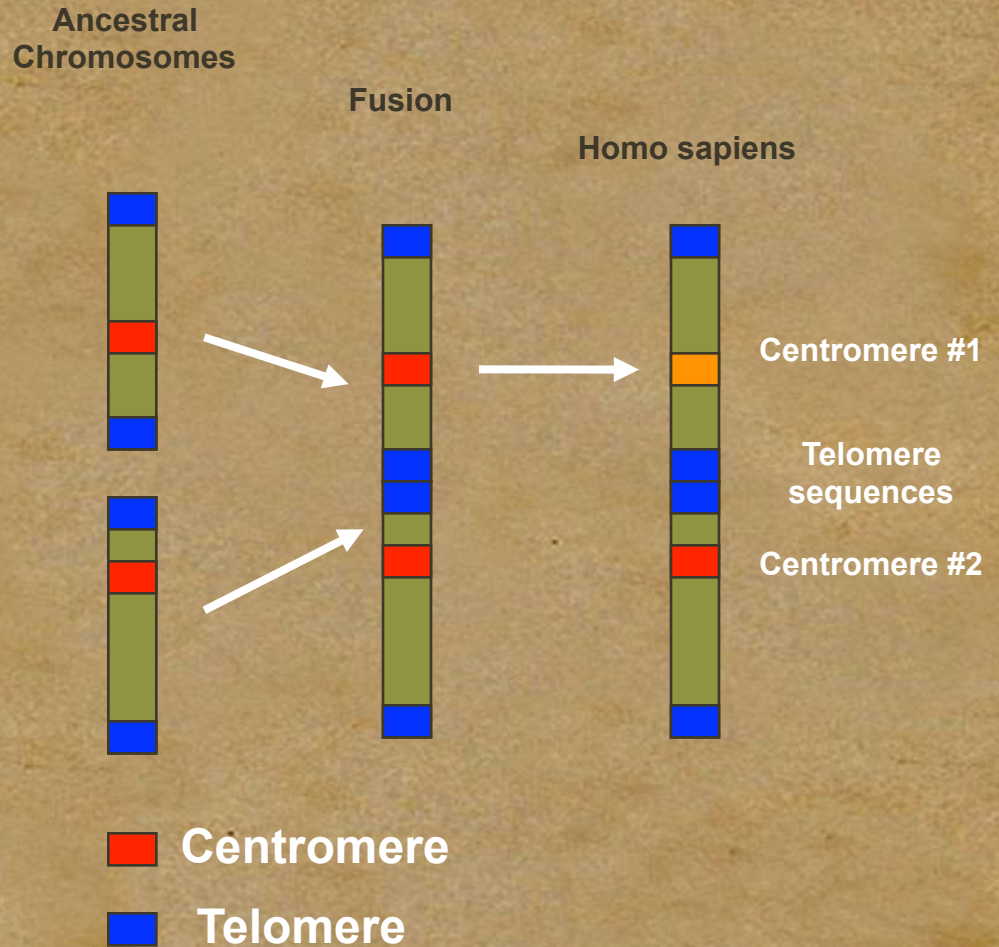
human (<i>Homo</i>)	46
chimpanzee (<i>Pan</i>)	48
gorilla (<i>Gorilla</i>)	48
orangutan (<i>Pongo</i>)	48



Testable prediction: If these organisms share common ancestry, the human genome must contain a fused chromosome.

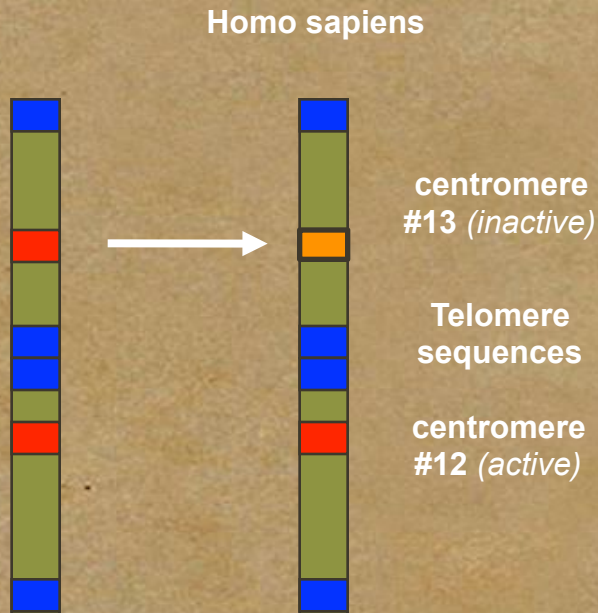
Chromosome numbers in the great apes (Hominidae):

human (Homo)	46
chimpanzee (Pan)	48
gorilla (Gorilla)	48
orangutan (Pongo)	48



Testable prediction: The marks of that fusion must appear in one of the human chromosomes.

Human Chromosome #2 shows the exact point at which this fusion took place



“Chromosome 2 is unique to the human lineage of evolution, having emerged as a result of head-to-head fusion of two acrocentric chromosomes that remained separate in other primates. The precise fusion site has been located in 2q13–2q14.1 (ref. 2; hg 16:114455823 – 114455838), where our analysis confirmed the presence of multiple subtelomeric duplications to chromosomes 1, 5, 8, 9, 10, 12, 19, 21 and 22 (Fig. 3; Supplementary Fig. 3a, region A). During the formation of human chromosome 2, one of the two centromeres became inactivated (2q21, which corresponds to the centromere from chimp chromosome 13) and the centromeric structure quickly deteriorated (42).”

Hillier *et al* (2005) “Generation and Annotation of the DNA sequences of human chromosomes 2 and 4,” *Nature* 434: 724-731.

Molecular similarities show a single origin for all living things

- DNA/RNA - same 4 nucleotides
- Proteins - same 20 L-amino acids
- Genetic code
- Ribosomes
- Similar membrane structures
- Shared metabolic pathways (ATP)
- Shared genes (many)

