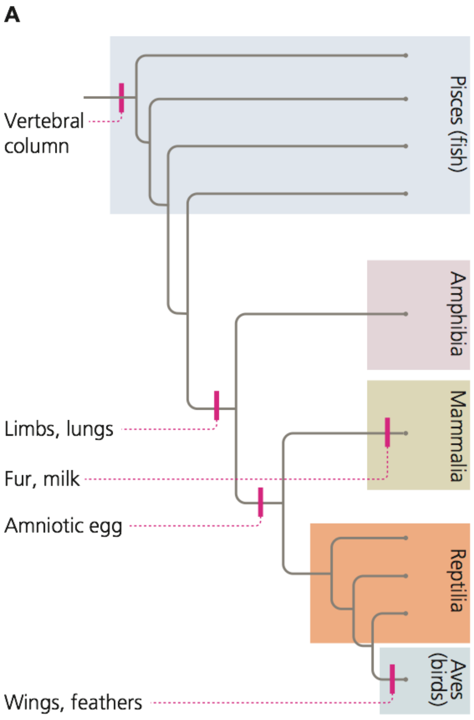
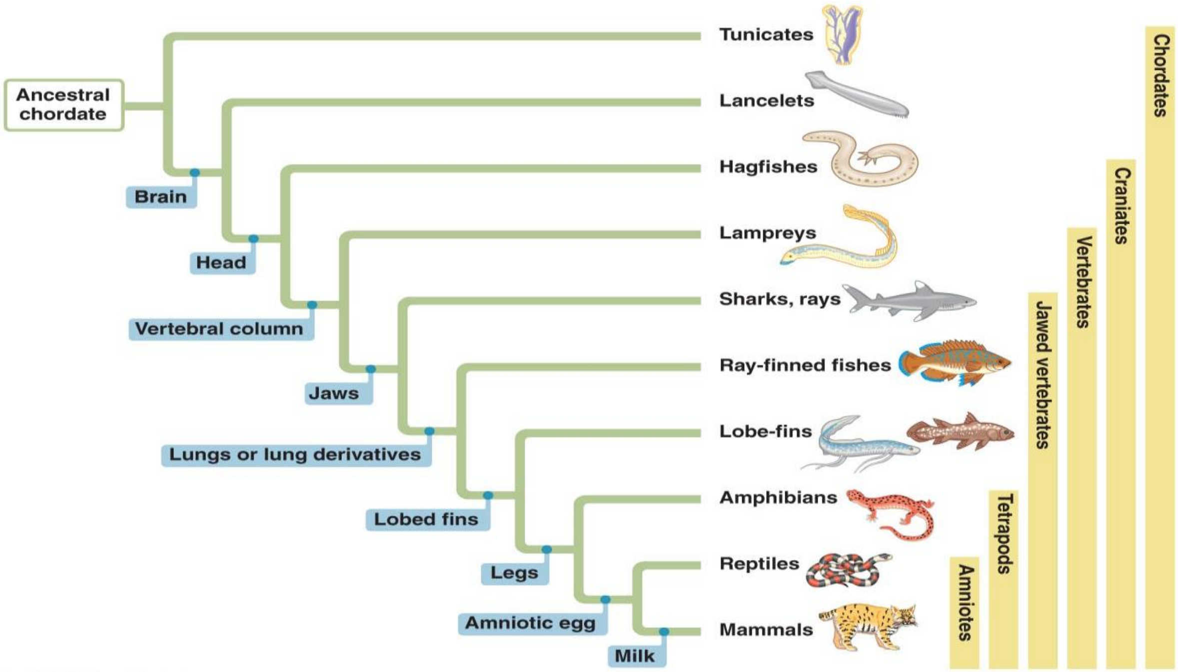
Chapter 8 The history in our genes

So originally we had morphological trees like these.

And then scientists began looking at molecular genetic data (the sequence of nucleotides or a.a.)!





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How do we make trees based on molecular genetic data?

Broadly speaking we line up the same regions of the genomes of different **living** species (or extract from ancient bodies) and compare how many differences we see between them.

Remember we talked about comparing populations by choosing two individuals and comparing them? (bighorn sheep and others…)

- If they are **very different** at many nucleotide bases (or a.a.) we assume the lineages split from one another a long time ago.
- If they are **quite similar** to one another then we assume they split more recently.

Chapter 8 The history in our genes

- **Whale evolution** (connects to material earlier in semester)-Ex of morphological tree being fixed (and then we found some fossil support)
- **Mammals**… Ex of a tree still in process of being figured out (not in your book)
- ***So is one kind of tree "better"?***
  (Advantages and Disadvantages of different trees)
- **What regions of the genome do we look at?** (Rates of Evolution in different regions of genome)
- ~~**Molecular Clocks-Briefly cover**~~

Molecular vs Morphological Trees (2 examples)

Ex. Whale evolution

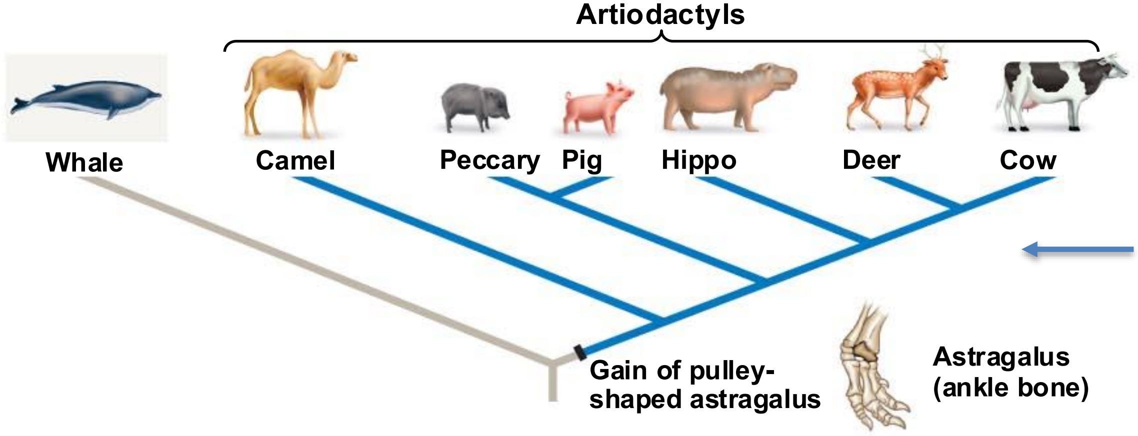
Remember this story ?

No astragalus, found cool fossils, realized lost astragalus and realized that they share a common ancestor with arteriodactyls (even toed ungulates) rather than carnivores (which was one early hypothesis)!

We now know molecular data supports this.

Warning.. example has a slightly different tree style

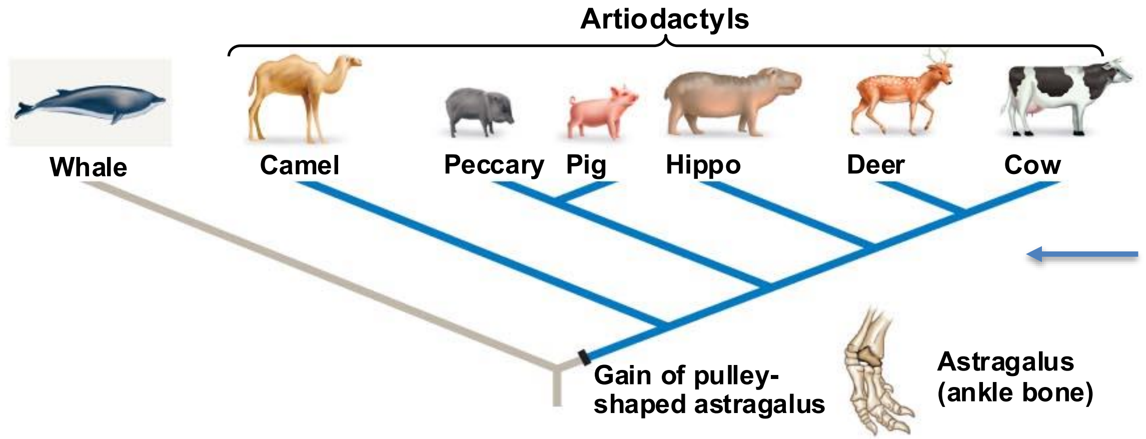
(a) The astragalus is a synapomorphy that identifies artiodactyls as a monophyletic group.



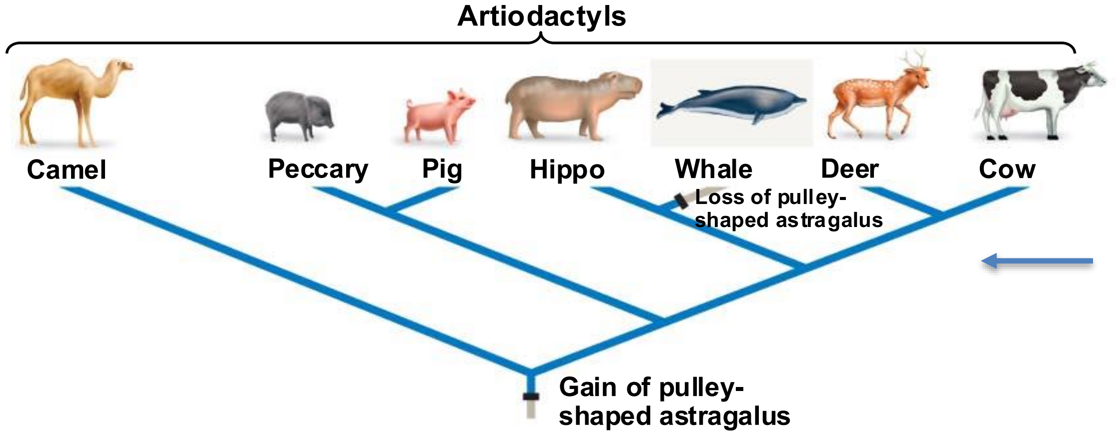
Morphological tree based on fact that they don’t have an astragalus.

Most **parsimonious morphological tree**!

(a) The astragalus is a synapomorphy that identifies artiodactyls as a monophyletic group.



(b) If whales are related to hippos, then two changes occurred in the astragalus.

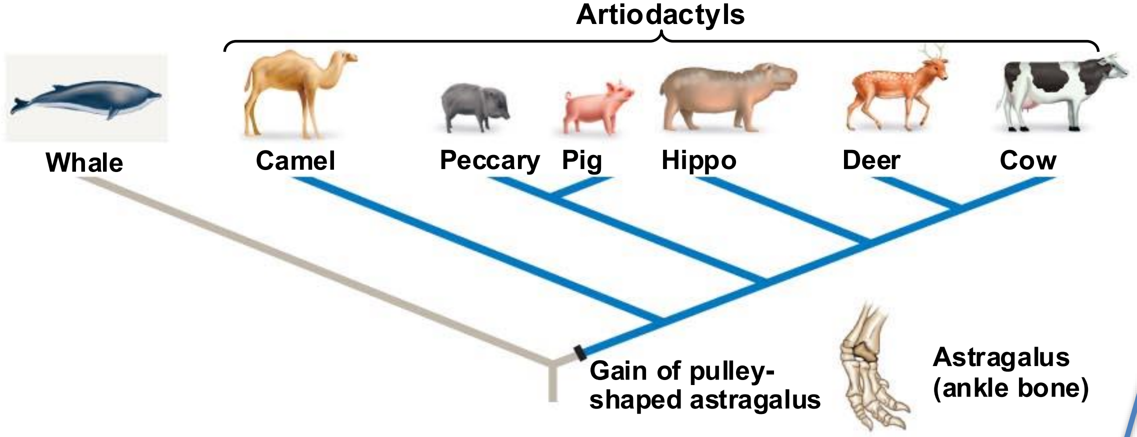


Morphological tree based on fact that they don't have an astragalus.

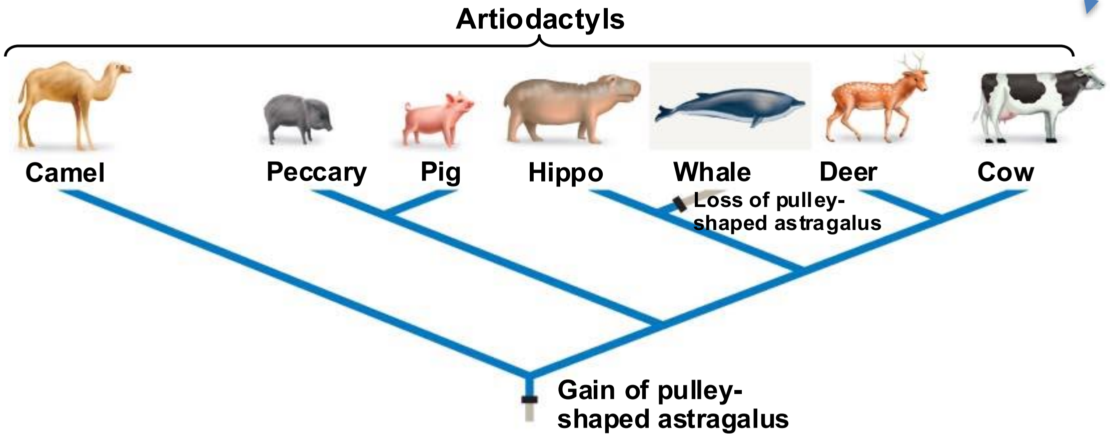
(it is the most **parsimonious morphological tree**!)

Fossils told us a more complete story since we found some that had an astragalus, so we revised our tree - to one that was less parsimonious!

(a) The astragalus is a synapomorphy that identifies artiodactyls as a monophyletic group.



(b) If whales are related to hippos, then two changes occurred in the astragalus.



Molecular data (SINE genes) confirmed that fossil based tree.

FYI: SINE genes are non-coding and there are lots of copies of them in our genomes-this shows which copies are present in which species

(c) Data on the presence and absence of SINE genes support the close relationship between whales and hippos.

Locus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Cow	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	0
Deer	0	0	0	0	0	0	0	1	?	1	1	1	1	1	1	?	1	1	0	0
Whale	1	1	1	1	1	1	1	0	?	1	0	1	1	0	0	0	?	1	0	0
Hippo	0	?	0	1	1	1	1	0	1	1	0	1	1	0	0	0	?	1	0	0
Pig	0	0	0	?	0	0	0	0	?	0	0	0	?	?	0	0	0	1	1	1
Peccary	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	1	1
Camel	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

1 = gene present
0 = gene absent
? = still undetermined

Whales and hippos share four *unique* SINE genes (4, 5, 6, and 7)

Mammal madness: is the mammal tree of life not yet resolved?

Nicole M. Foley, Mark S. Springer, Emma C. Teeling

Published 20 June 2016. DOI: 10.1098/rstb.2015.0140

Table 1.

Higher-level relationships of placental mammal orders based on morphology *versus* molecules. Orders (italics) are coloured by their superordinal membership according to molecular studies. The majority of superordinal groups based on morphology are polyphyletic and reflect ecomorphological convergence (e.g. 'ant and termite eating group' includes representatives from Xenarthra, Afrotheria, and Laurasiatheria).

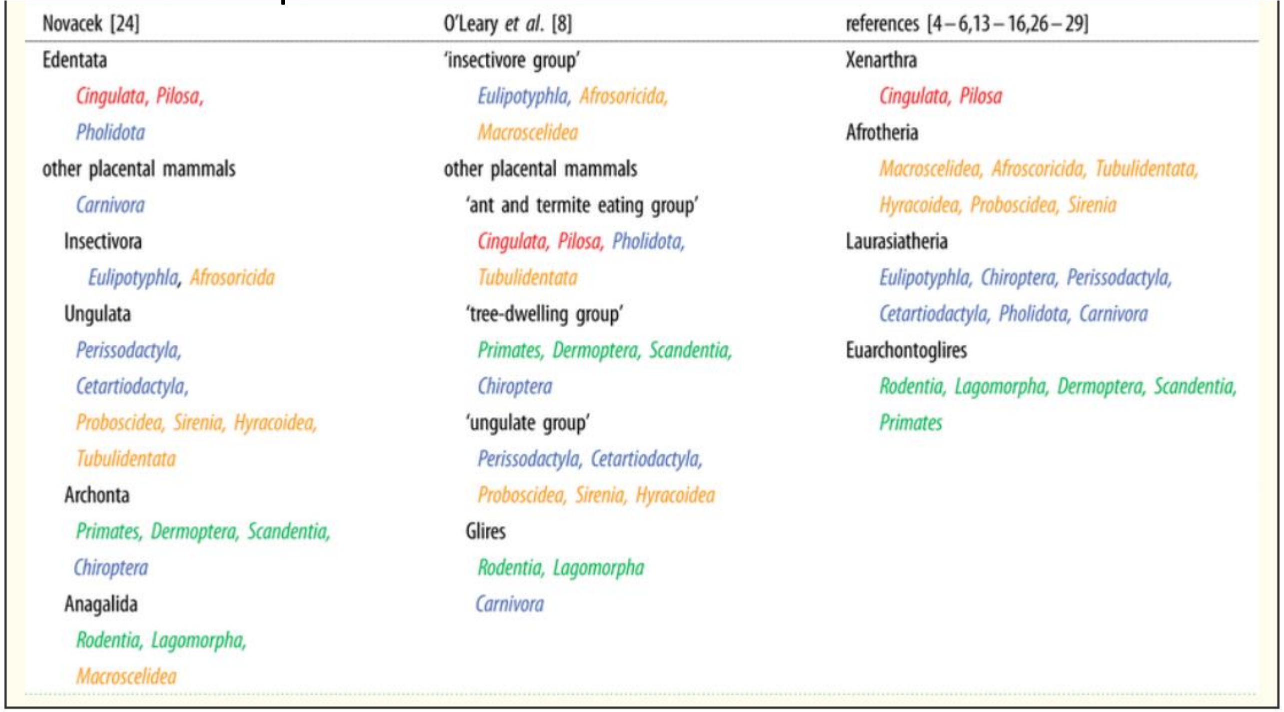
Ex. Mammals

Morphological trees and molecular trees sometimes yield very different patterns!

Science at work!

Morph Trees

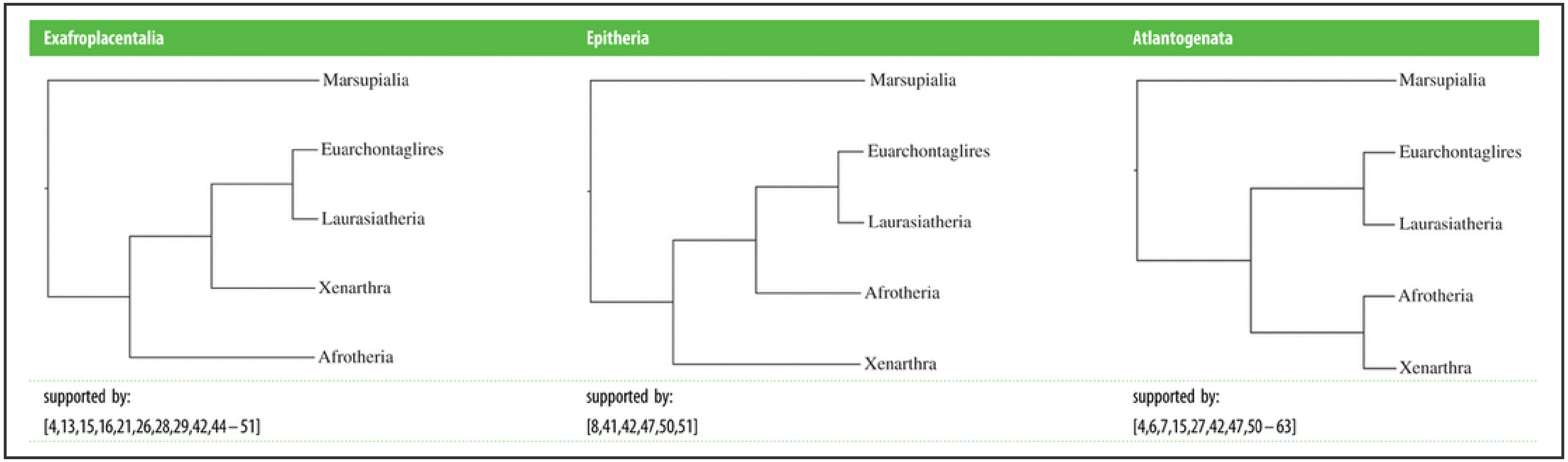
Molec Trees



Novacek [24]	O'Leary *et al.* [8]	references [4–6,13–16,26–29]
Edentata	'insectivore group'	Xenarthra
Cingulata, Pilosa,	*Eulipotyphla, Afrosoricida,*	*Cingulata, Pilosa*
Pholidota	*Macroscelidea*	Afrotheria
other placental mammals	other placental mammals	*Macroscelidea, Afroscoricida, Tubulidentata,*
Carnivora	'ant and termite eating group'	*Hyracoidea, Proboscidea, Sirenia*
Insectivora	*Cingulata, Pilosa, Pholidota,*	Laurasiatheria
Eulipotyphla, Afrosoricida	*Tubulidentata*	*Eulipotyphla, Chiroptera, Perissodactyla,*
Ungulata	'tree-dwelling group'	*Cetartiodactyla, Pholidota, Carnivora*
Perissodactyla,	*Primates, Dermoptera, Scandentia,*	Euarchontoglires
Cetartiodactyla,	*Chiroptera*	*Rodentia, Lagomorpha, Dermoptera, Scandentia,*
Proboscidea, Sirenia, Hyracoidea,	'ungulate group'	*Primates*
Tubulidentata	*Perissodactyla, Cetartiodactyla,*	
Archonta	*Proboscidea, Sirenia, Hyracoidea*	
Primates, Dermoptera, Scandentia,	Glires	
Chiroptera	*Rodentia, Lagomorpha*	
Anagalida	*Carnivora*	
Rodentia, Lagomorpha,		
Macroscelidea		

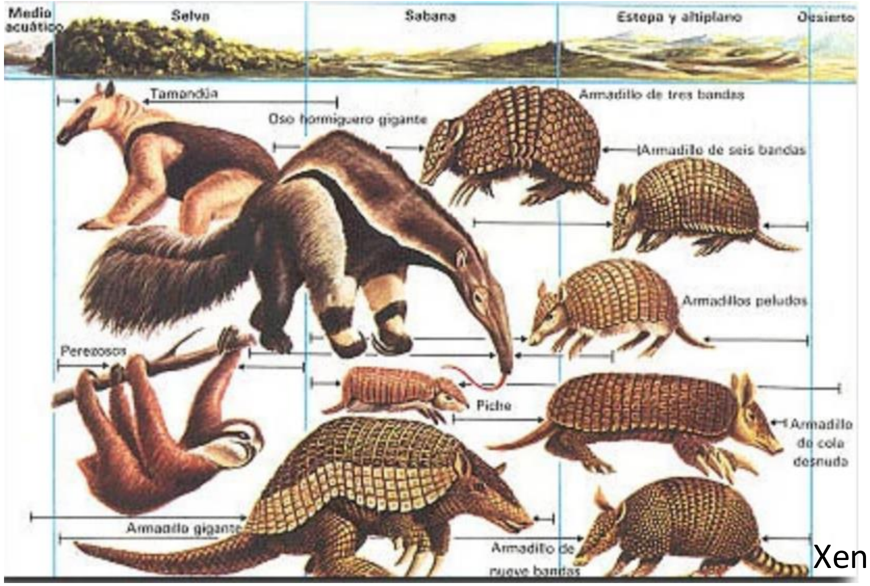
Table 2.

Summary of the various papers supporting one of the three hypotheses for the root node of eutherian mammals: Exafroplacentalia, Epitheria or Atlantogenata.



Exafroplacentalia	Epitheria	Atlantogenata
supported by: [4,13,15,16,21,26,28,29,42,44–51]	supported by: [8,41,42,47,50,51]	supported by: [4,6,7,15,27,42,47,50–63]

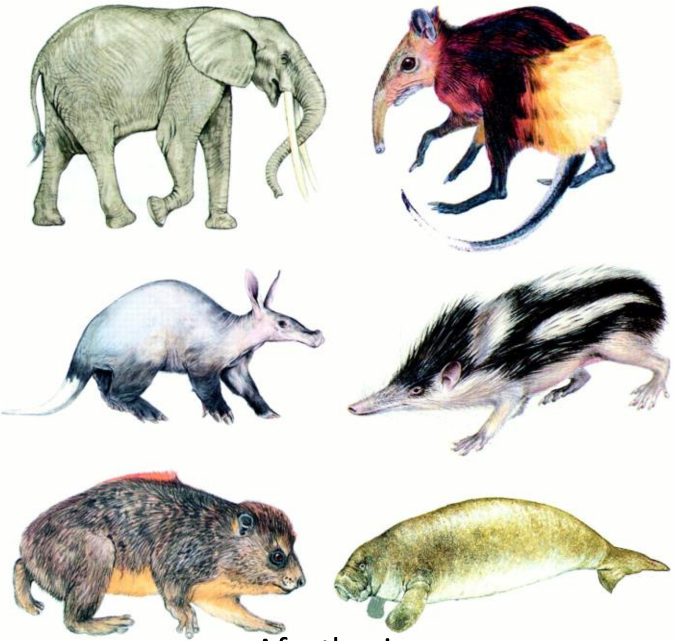
What are the problem groups here?



Xenartha

https://www.pnas.org/content/98/1/1

https://lifeform.fandom.com/wiki/Xenarthra_(Taxonomy)?file=Xenarthra.jpg



Afrotheria

Is it the case that one kind of tree is always better?

Advantages and Disadvantages of Morphological and Molecular Trees …

1. Morphological trees are great because…

2. Challenges of morphological trees...

3. Molecular trees are great because...

4. Challenges of molecular trees....

Take away is that…..
We usually use both and the two together might be thought of as a kind of conversation!

Even when we are making molecular trees….
We try not to rely on just one gene or region of genome.

- Whale evolution (connects to material earlier in semester)-Ex of morphological tree being fixed
- Mammals… Ex of a tree still in process of being figured out (not in your book)
- *So is one kind of tree "better"?*
  (Advantages and Disadvantages of different trees)
- **What regions of the genome do we look at?**
- ~~**Molecular Clocks-Briefly cover**~~

What regions do we use to build a phylogeny with genetic data? (What different kinds of DNA are there?)

- Autosomes
- Sex chromosomes (X and Y in mammals)
- Mitochondria
- Chloroplasts

Which do not experience recombination?

Chloroplasts, Mitochondria=no recombination and Sex chromosomes-not much recombination

Which give you the most "holistic" information?

Autosomes probably since can look at lots of different regions on whole genome.

Which give specific types of information?

Mitochondria are maternally inherited so give you info on that line of inheritance.

Y is inherited through sperm only so paternally inherited.