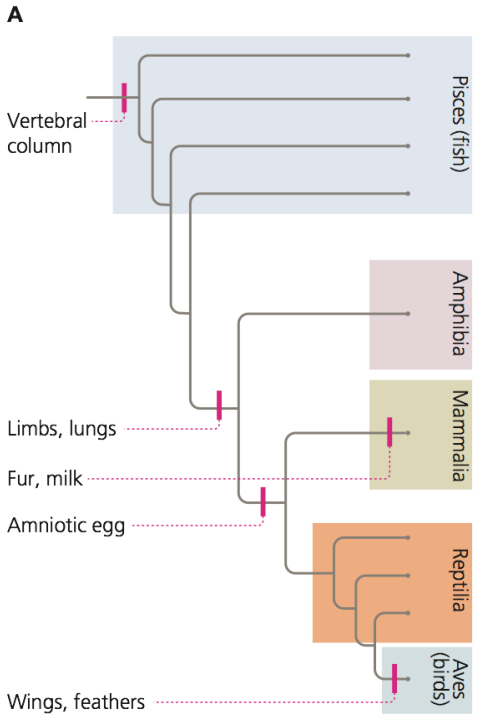
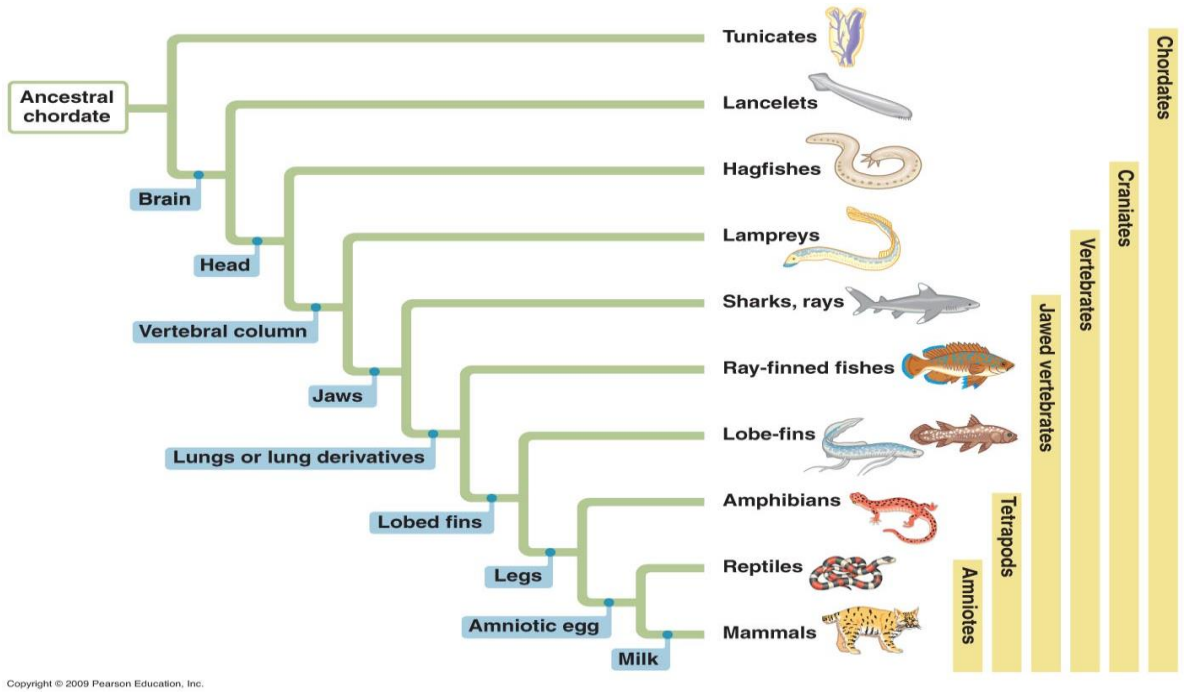
Chapter 8 The history in our genes

So originally we had morphological trees like these.

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





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

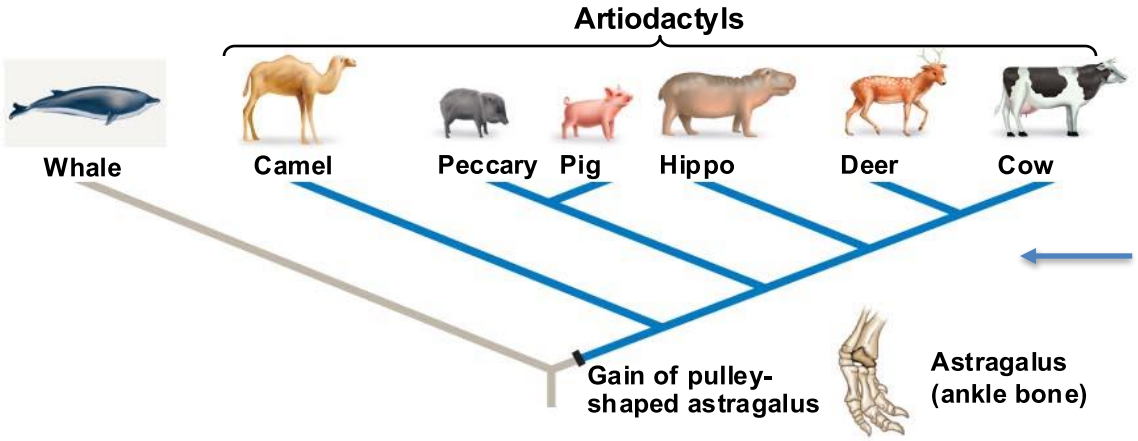
Remember this story ?

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.

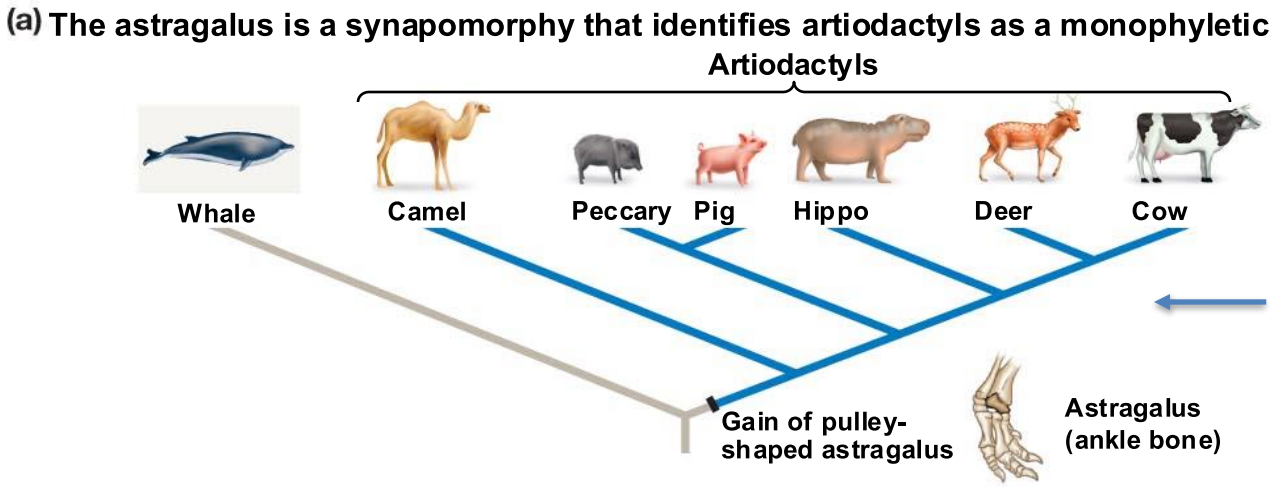
Warning.. example has a slightly different tree style

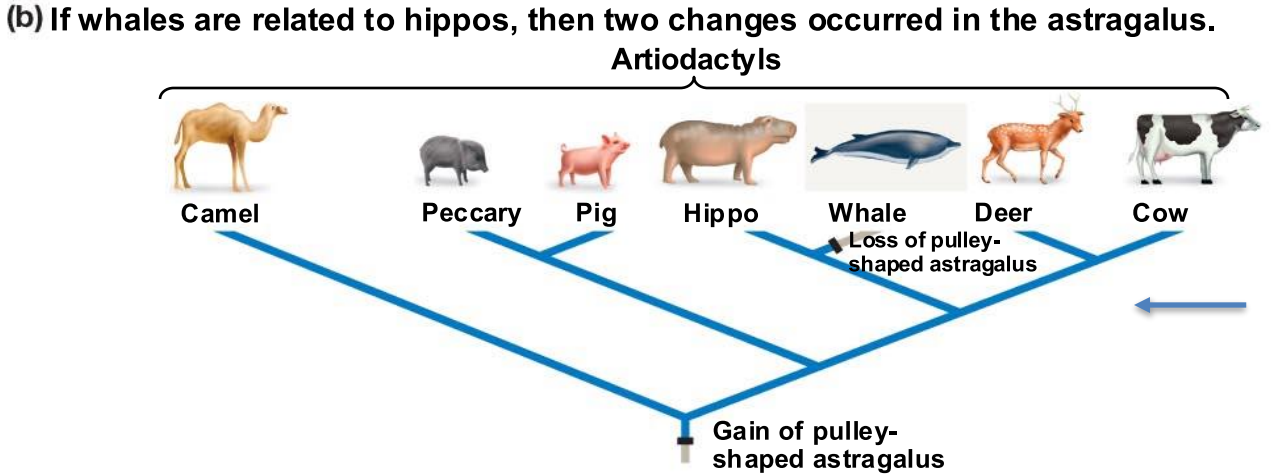
(a) The astragalus is a synapomorphy that identifies artiodactyls as a monophyletic group.



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

Most **parsimonious morphological tree**!



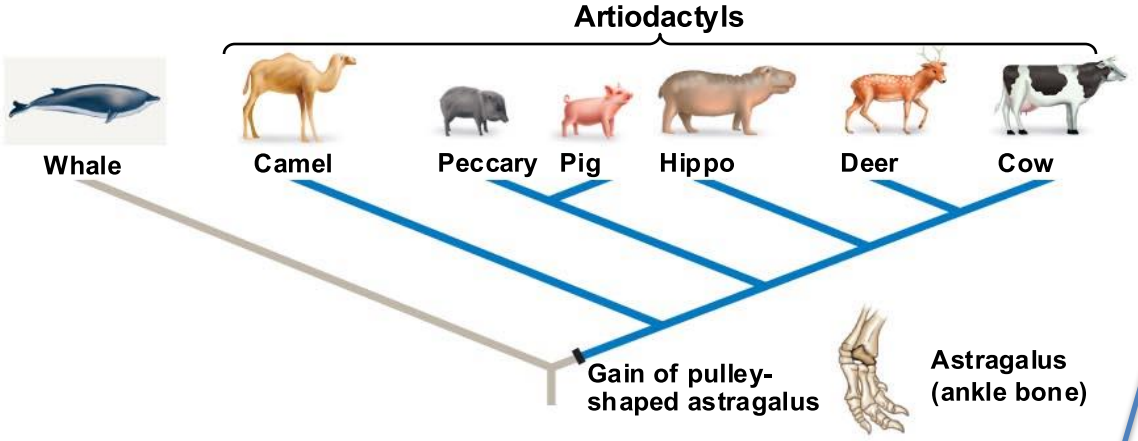


Morphological tree based on fact that they don't have an astragalus.

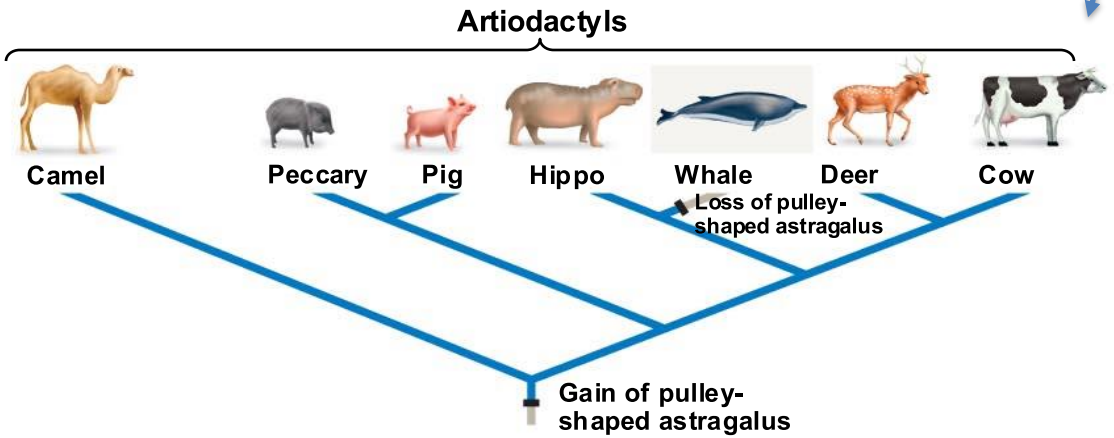
(it is the most **parsimonious morphological tree**!)

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).

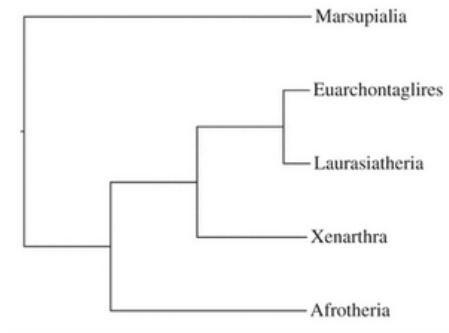
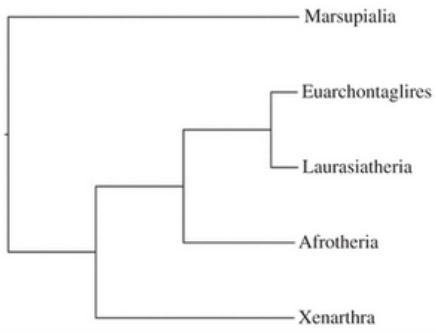
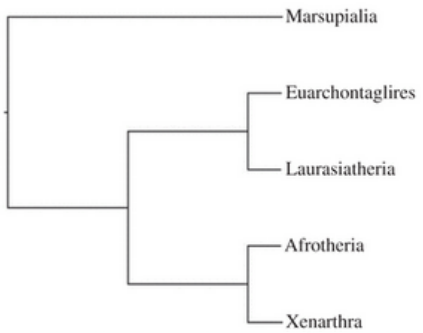
Ex. Mammals

Morphological trees and molecular trees sometimes yield very different patterns!
Science at work!

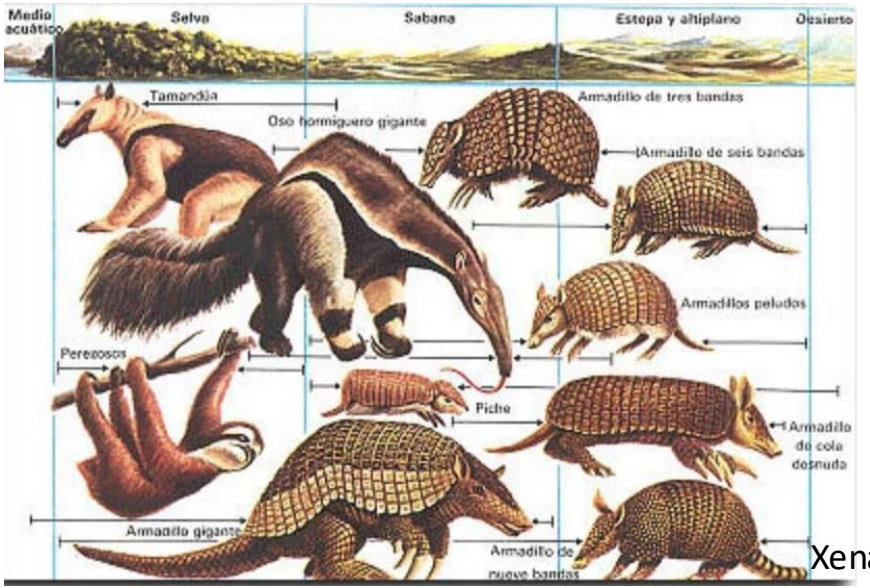
Morph Trees		Molec Trees
Novacek [24]	O'Leary *et al.* [8]	references [4–6,13–16,26–29]
Edentata	'insectivore group'	Xenarthra
Cingulata, Pilosa,	*Eulipotyphla, Afrosoricida,*	*Cingulata, Pilosa*
Pholidota	*Macroscelidea*	Afrotheria
other placental mammals	other placental mammals	*Macroscelidea, Afroscoricida, 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.

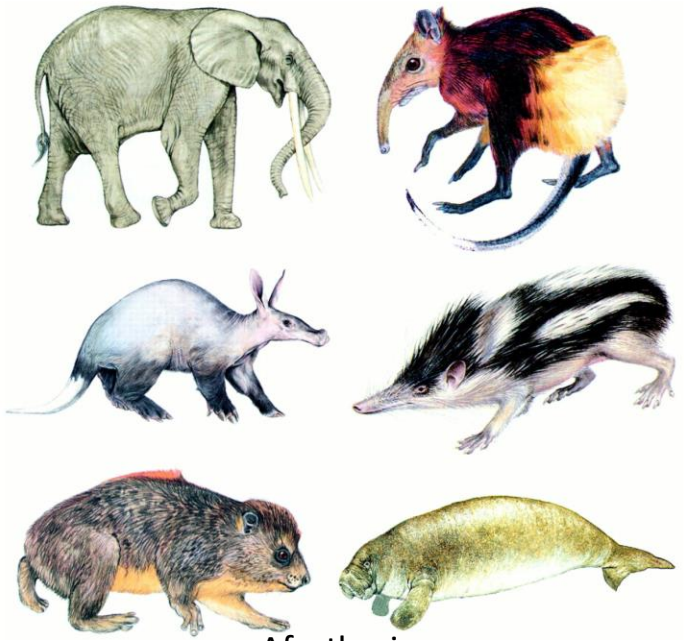
Exafroplacentalia	Epitheria	Atlantogenata
		
supported by: [4,13,15,16,21,26,28,29,42,44–51]	supported by: [8,41,42,47,50,51]	supported by: [4,6,7,15,27,42,47,50–63]

What are the problem groups here?



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

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



Xenartha

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.

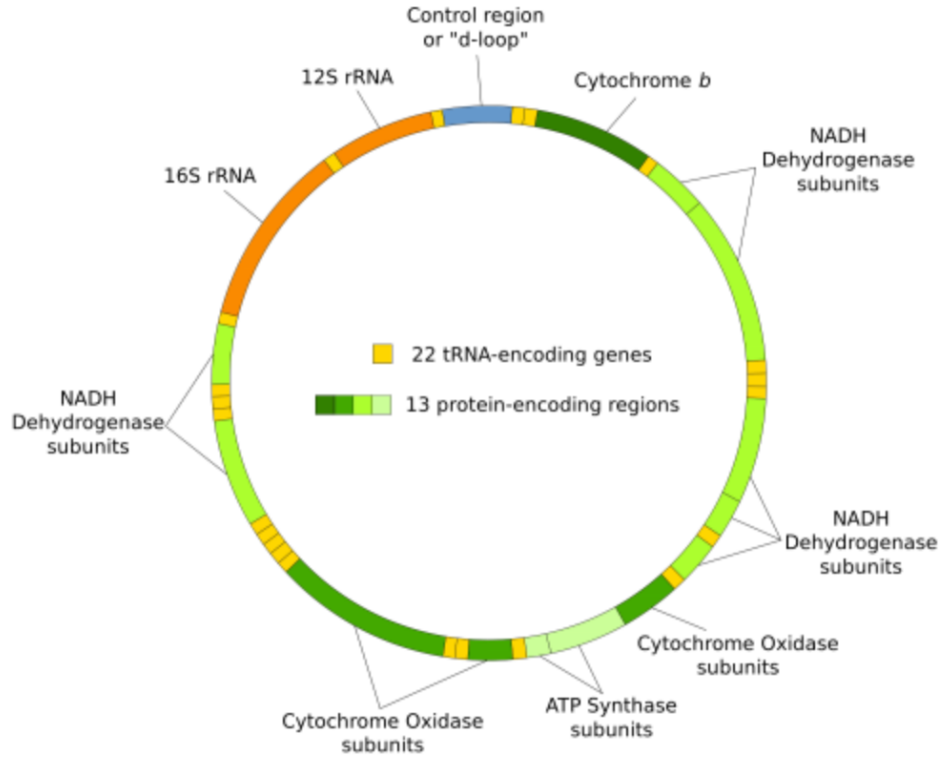
- Whale evolution (connects to material earlier in semester)-Ex of morphological tree being fixed
- Mammals… Ex of a tree still in process of being figured out (not in your book)
- *So is one kind of tree "better"? (Advantages and Disadvantages of different trees)*
- **What regions of the genome do we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

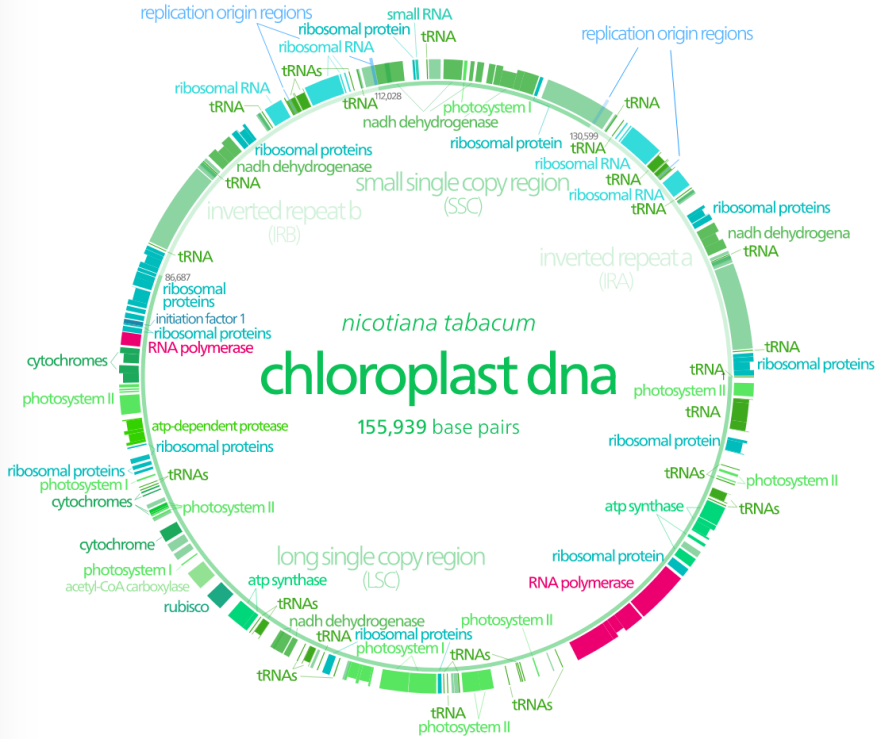
- Autosomes
- Sex chromosomes (Y)
- Mitochondria
- Chloroplasts

Which do not experience recombination?
Which give you the most “holistic” information?
Which give specific types of information?

Why are mitochondrial and chloroplast genomes circular?



Mitochondrial DNA. Credit: en.wikipedia.org



https://link.springer.com/article/10.1023%2FA%3A1007564209282?LI=true

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

- Autosomes
- Sex chromosomes (Y)
- Mitochondria
- Chloroplasts

Then we may choose to use…

- One gene
- Or a set of genes…

Phylogenetic relationships are often constructed by weighing evidence from **multiple genes because that is probably more accurate than looking at one gene or region!**

Then we also have to be aware that….

Different parts of the genome differ in their **rate of evolution** and therefore their utility in building trees.

If you were exploring the phylogenetic (evolutionary) relationships in protists during the Precambrian, would you select a slowly or rapidly evolving region?

If you were exploring the phylogenetic relationships between different subpopulations of big horn sheep would you select a slowly or rapidly evolving region?

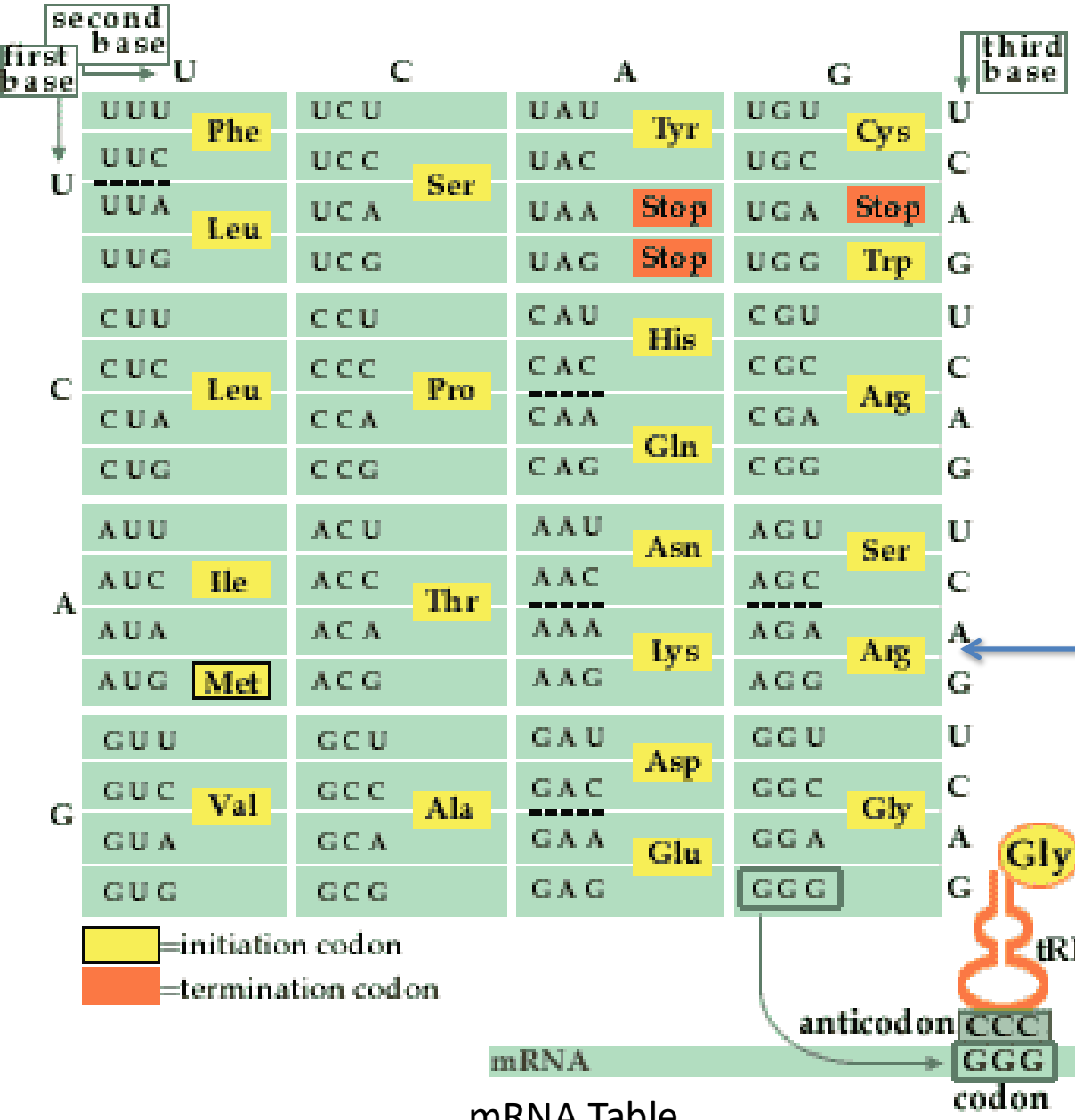
Which of the following would be more useful in determining the relationships between **very ancient lineages.**

- Nucleotides (DNA) or Amino Acid Sequences (proteins)?
- Functioning/Important Genes or Pseudogenes?
- Functioning/Important Genes or Mobile genetic elements (repetitive sequences)?
- Non-coding regions or coding regions?
- Introns or Exons?
- Synonymous mutations or Non-synonymous mutations?

Synonymous *do not alter the amino acid sequence of the protein and are often* ***selectively neutral***

Non-synonymous *mutation DO alter the amino acid sequence of the protein more likely to be subject to selection*

What are some synonymous substitutions here?



mRNA Table

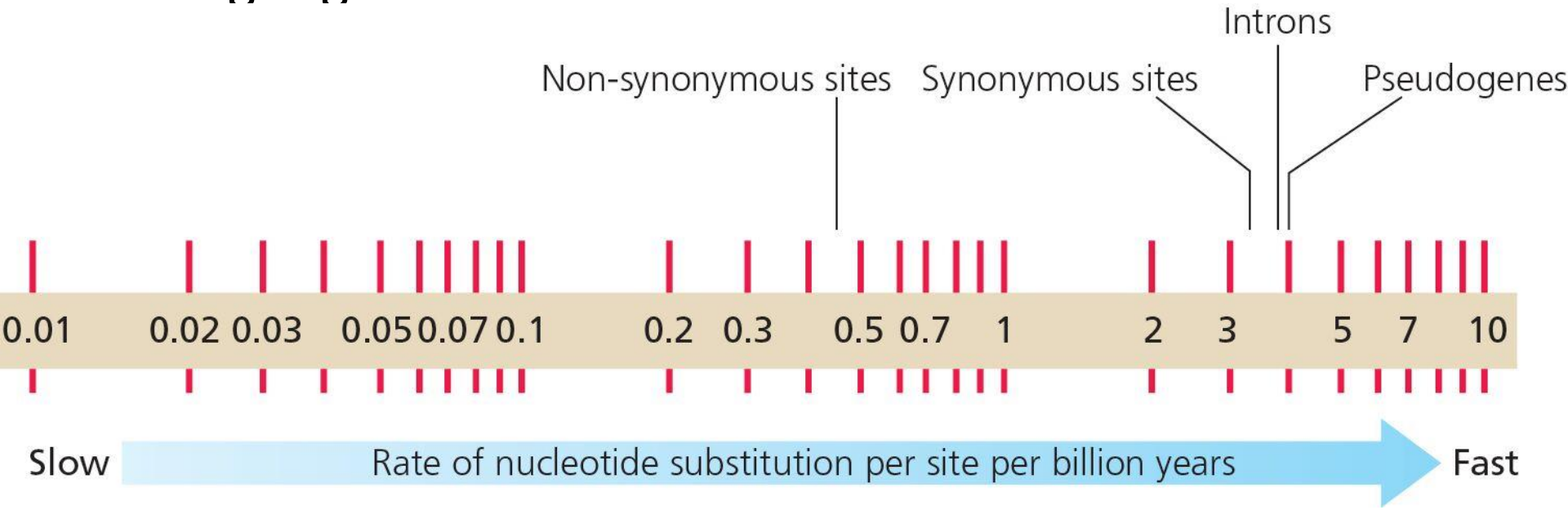
Mutation of A-> G in the third base of the codon here would both yield Arg so that would be a synonymous mutation- does NOT change the structure of the protein.

GGU, GGC, GGA will also match to Glycine

To summarize…Different parts of the genome differ in their rate of evolution and therefore their utility in building trees.

You would want to choose the right region to consider.

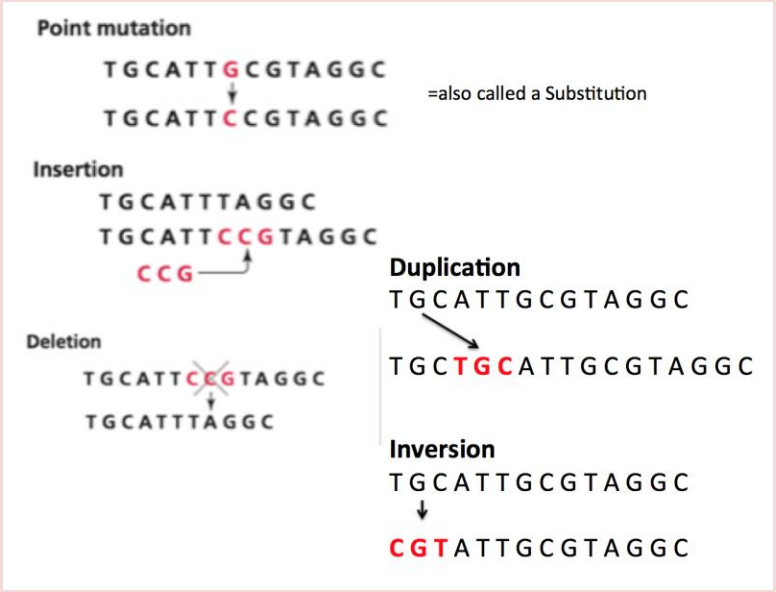
If your Q is about a **recent divergence**-choose fast evolving regions.
If your Q is about **ancient divergence**-choose slowly evolving regions.

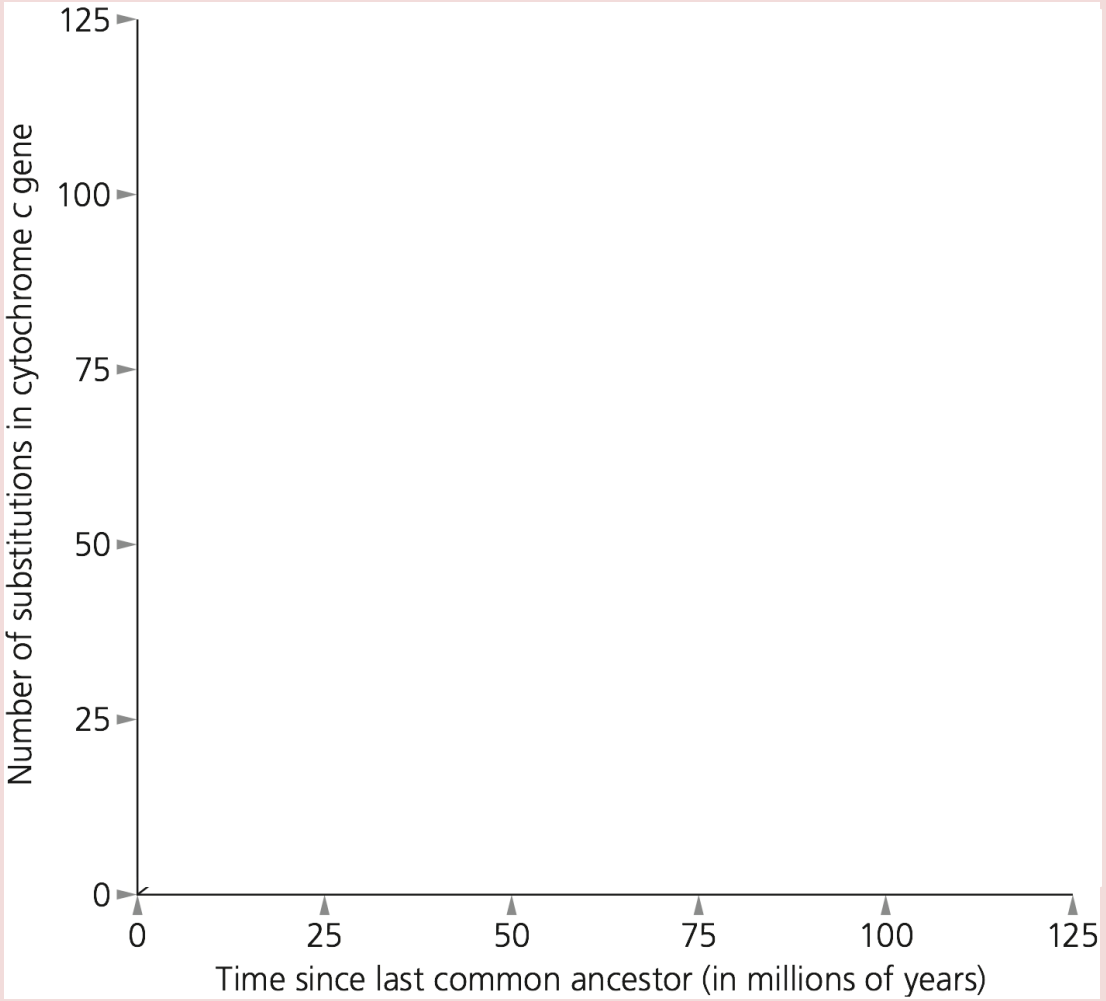


Molecular Clock

When we compare two species, would lineages that diverged a long time ago have a **greater** number or **smaller** number of substitutions (point mutations)?

These pink slides are optional!!



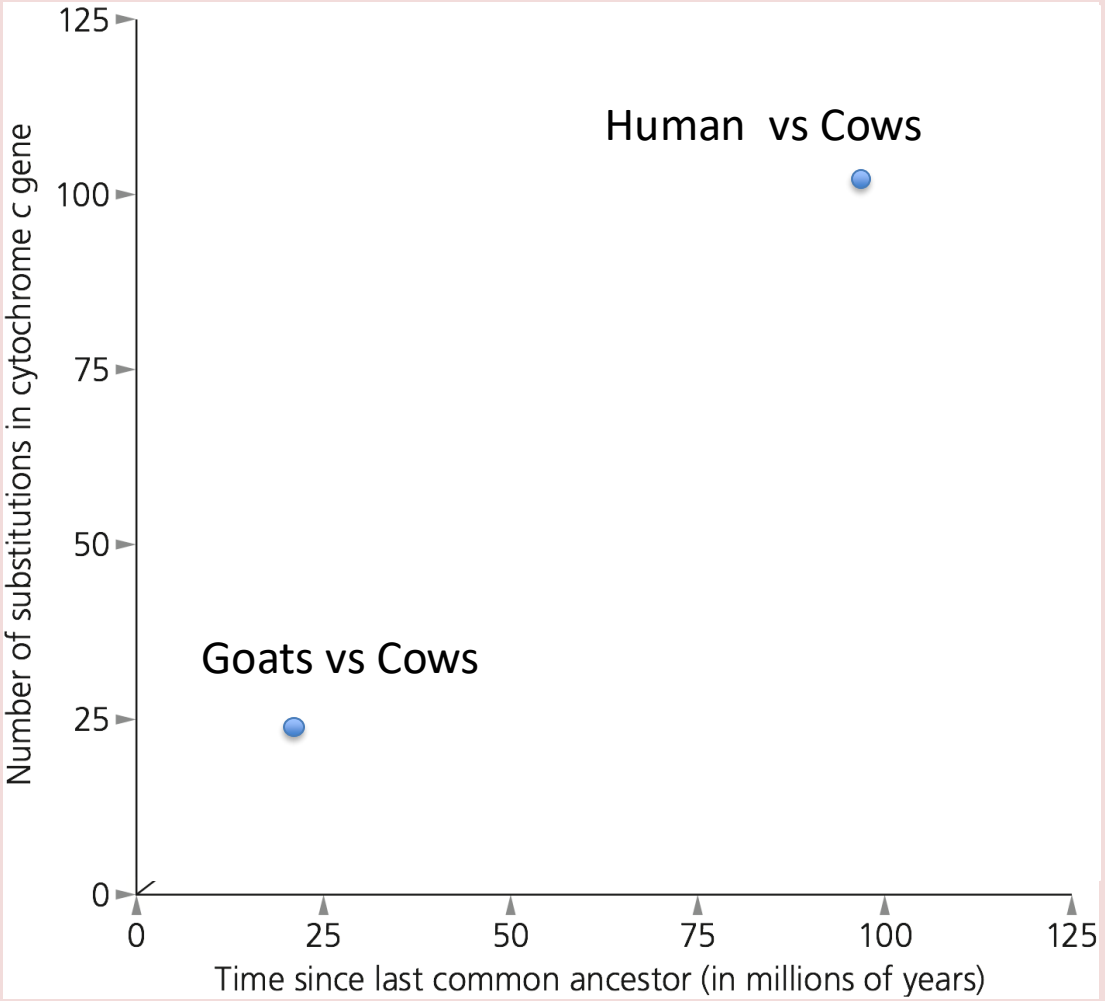


Molecular Clock

Goats vs Cows?

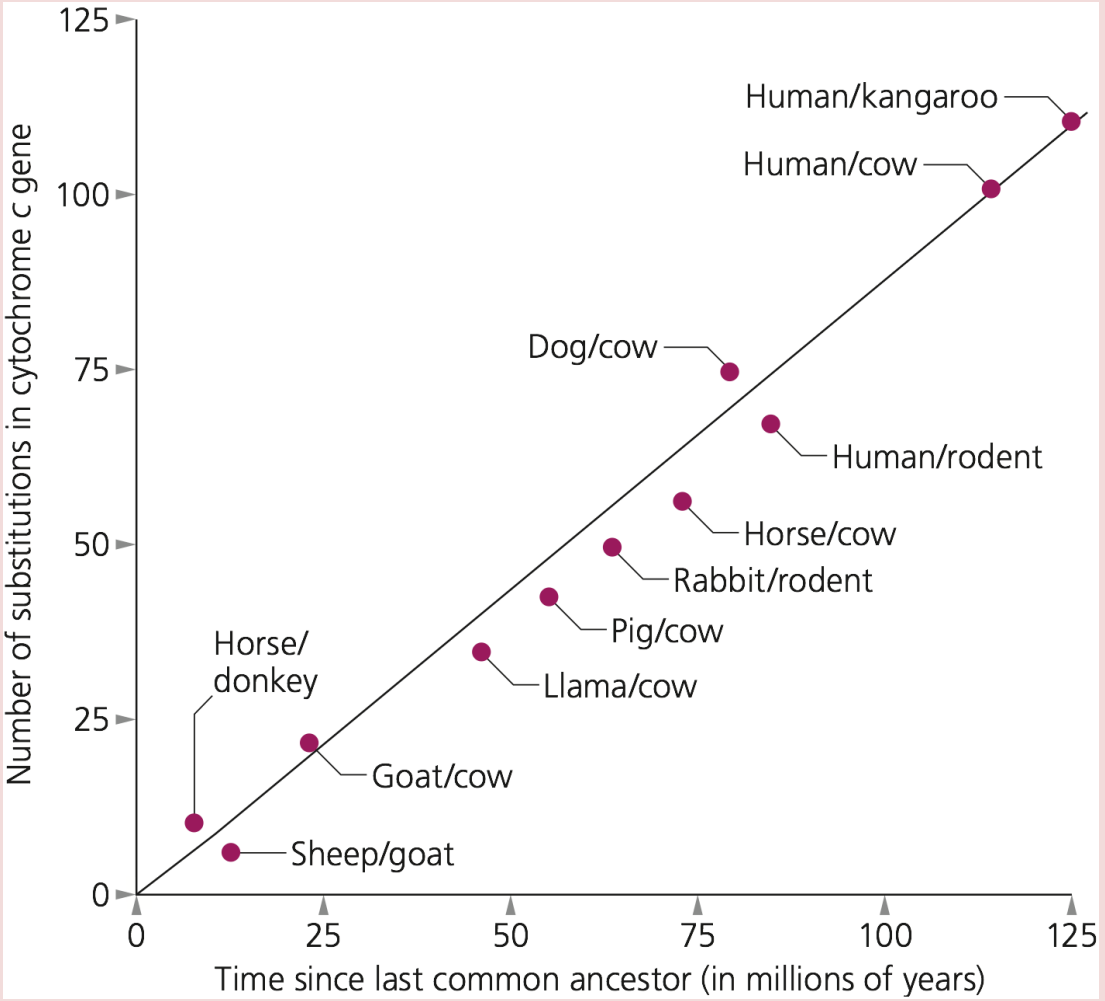
Humans vs Cows?

How do we know “Time since last common ancestor“?



Molecular Clock

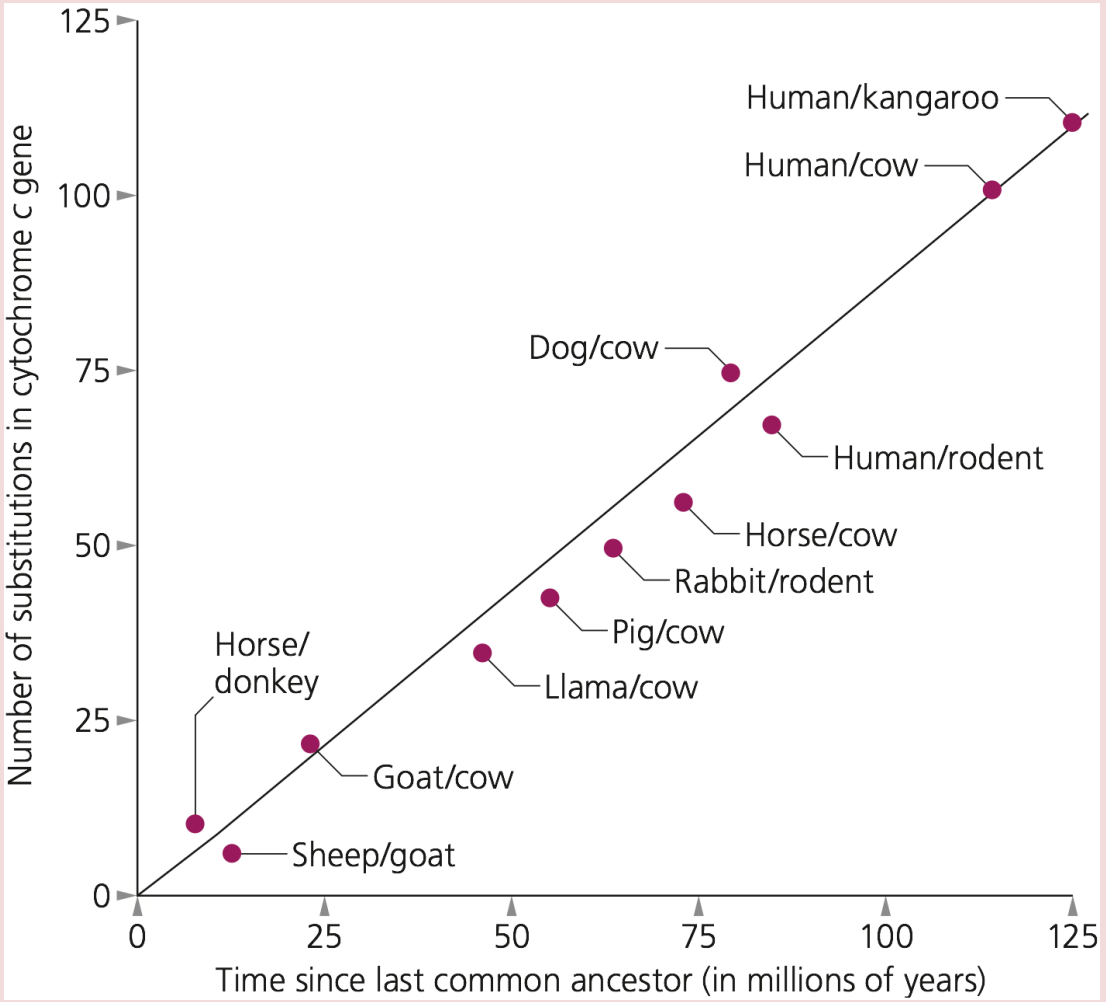
Remember to look back many millions of years you want a slowly or rapidly evolving region!



Molecular Clock

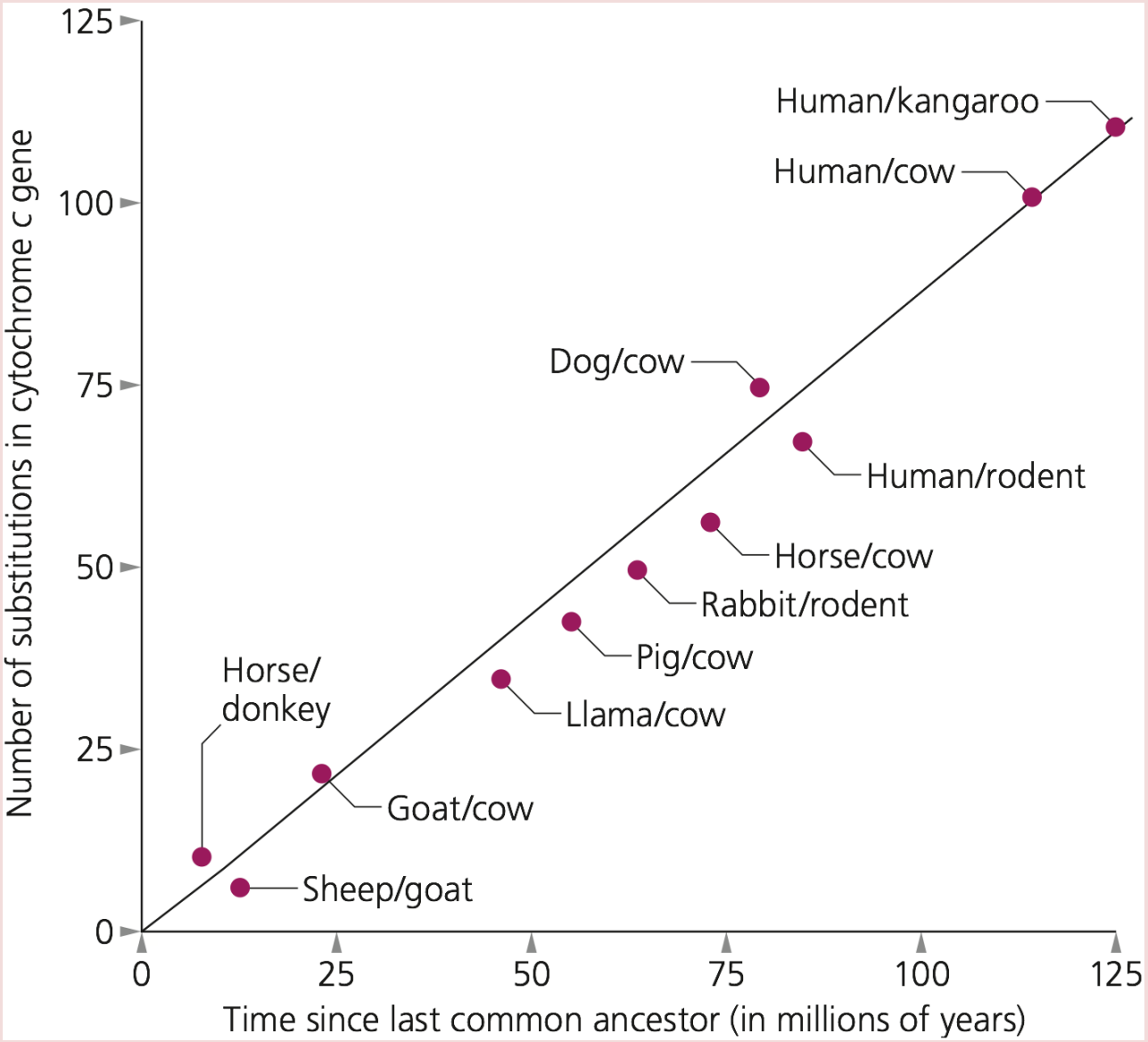
Once we have "calibrated the clock for mammals" by fitting a line to these data points…how can we use this information?

We can use it to extrapolate divergence dates for other mammals **without** a good fossil record.



So lets say we do not have a good fossil record of **manatees**, but we count 40 substitutions between them and cows and estimate their diverence rate to be...?

Can we use a mammal clock to look at reptile divergence dates?

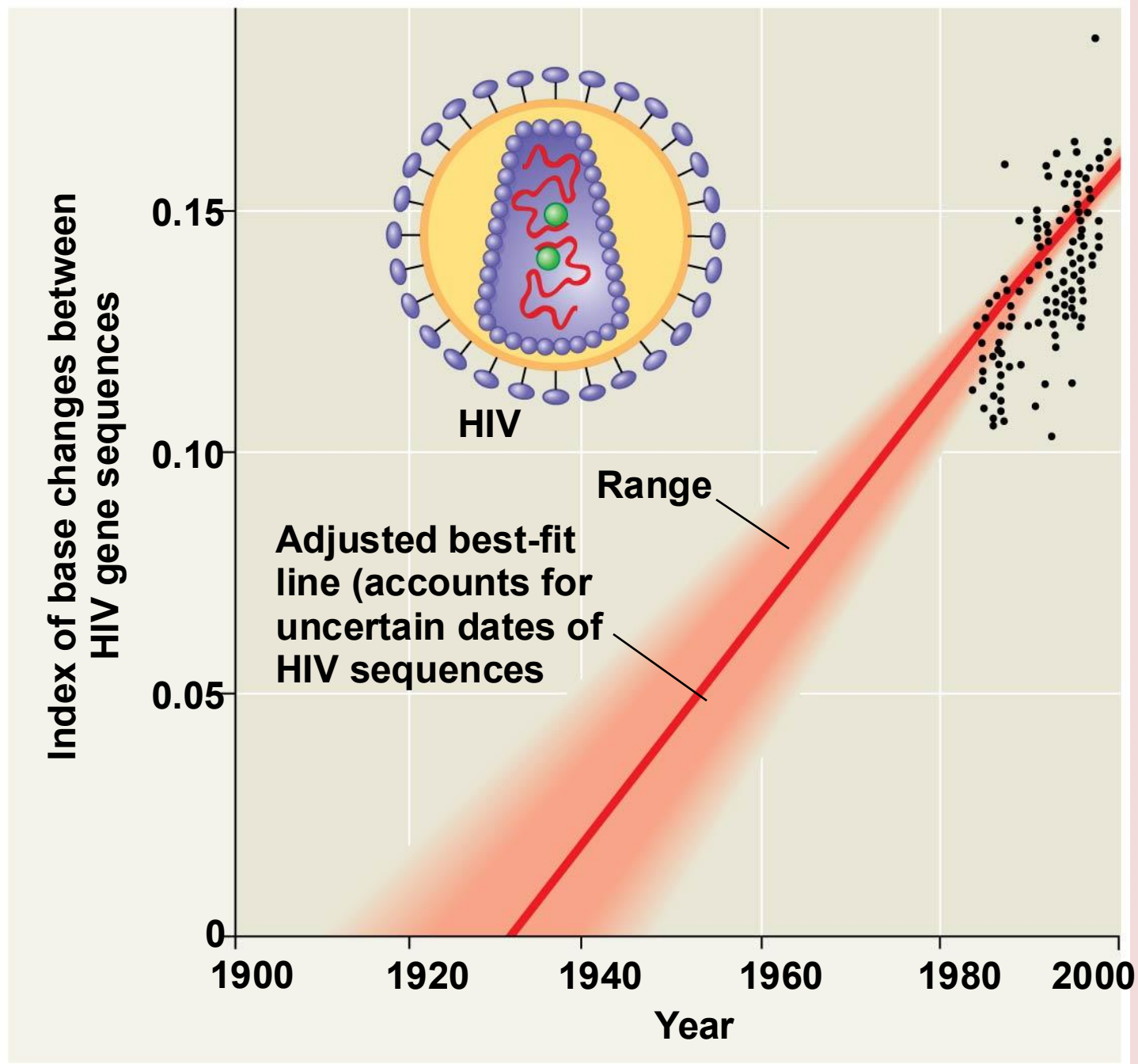


How do they use molecular clocks to establish origination dates of HIV virus?

With no fossil record, how was this clock calibrated?

(Imagine a freezer filled with samples labeled with the year they were collected…)

Longer ago samples collected, the more similar they are



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