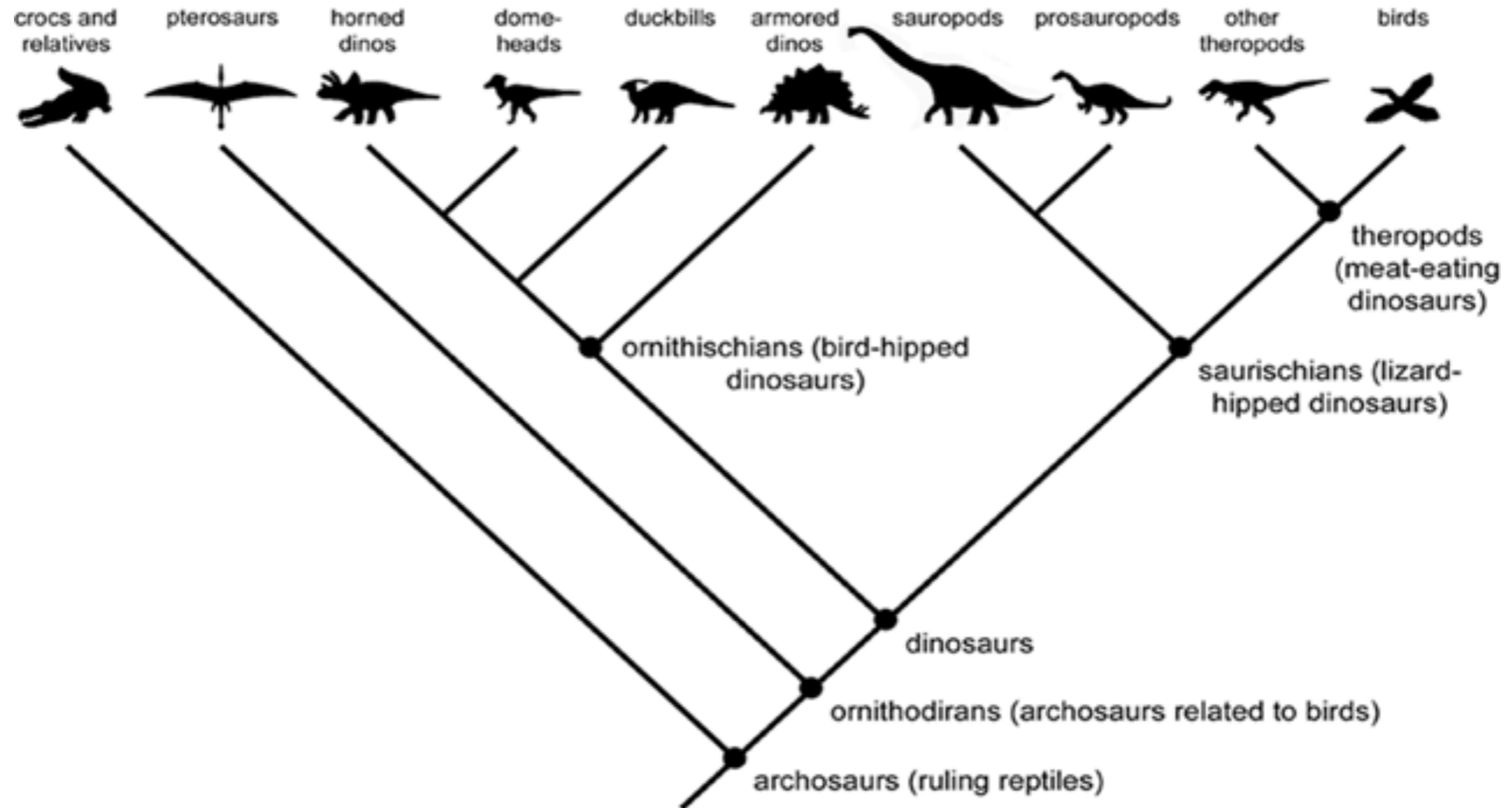


# CLADISTICS



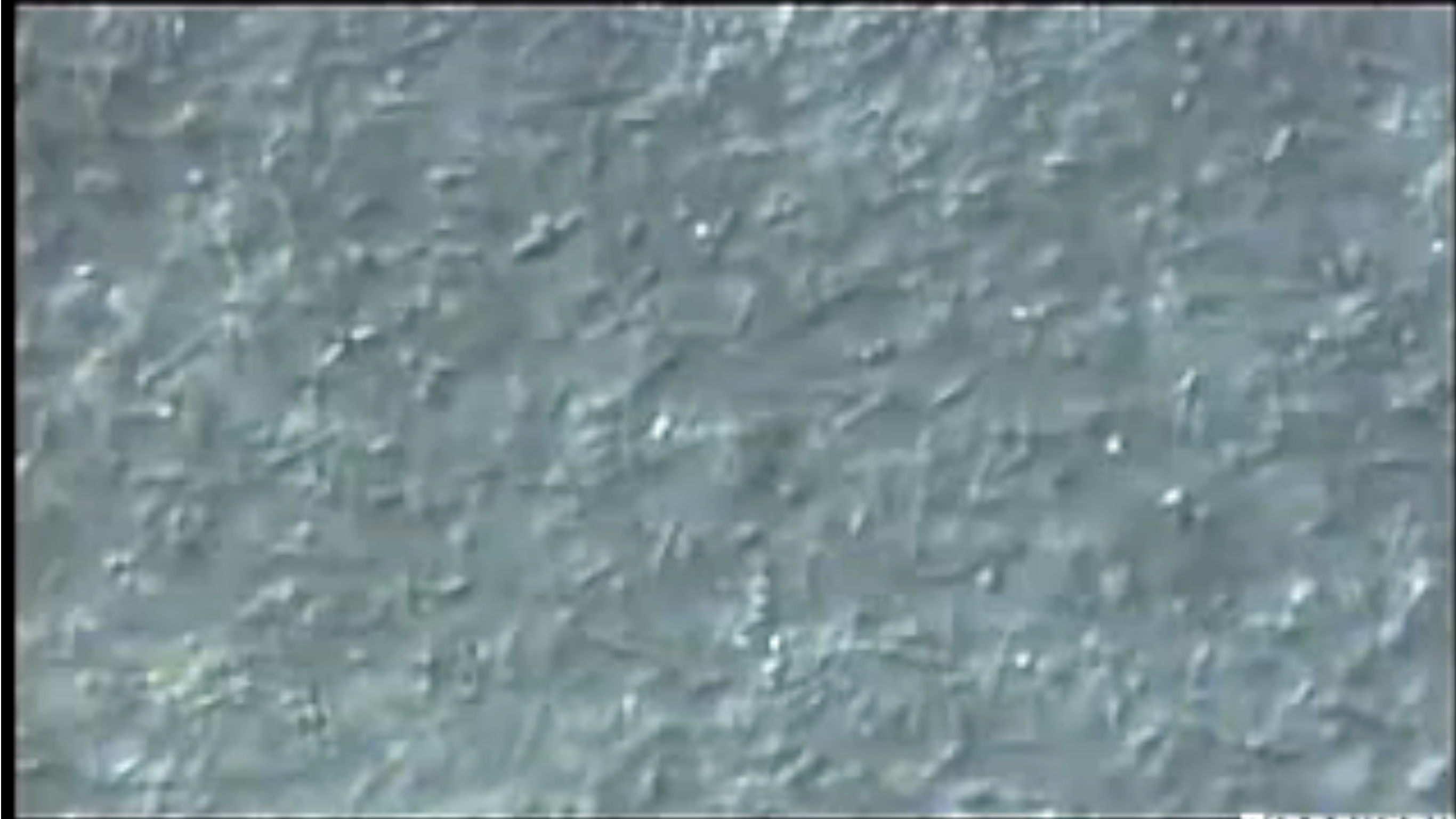


*Carl Woese made an amazing discovery in biology...  
Watch the short video clip as he relives his discovery.*

*As you watch:*

*1. Make note of why his discovery was so  
important.*

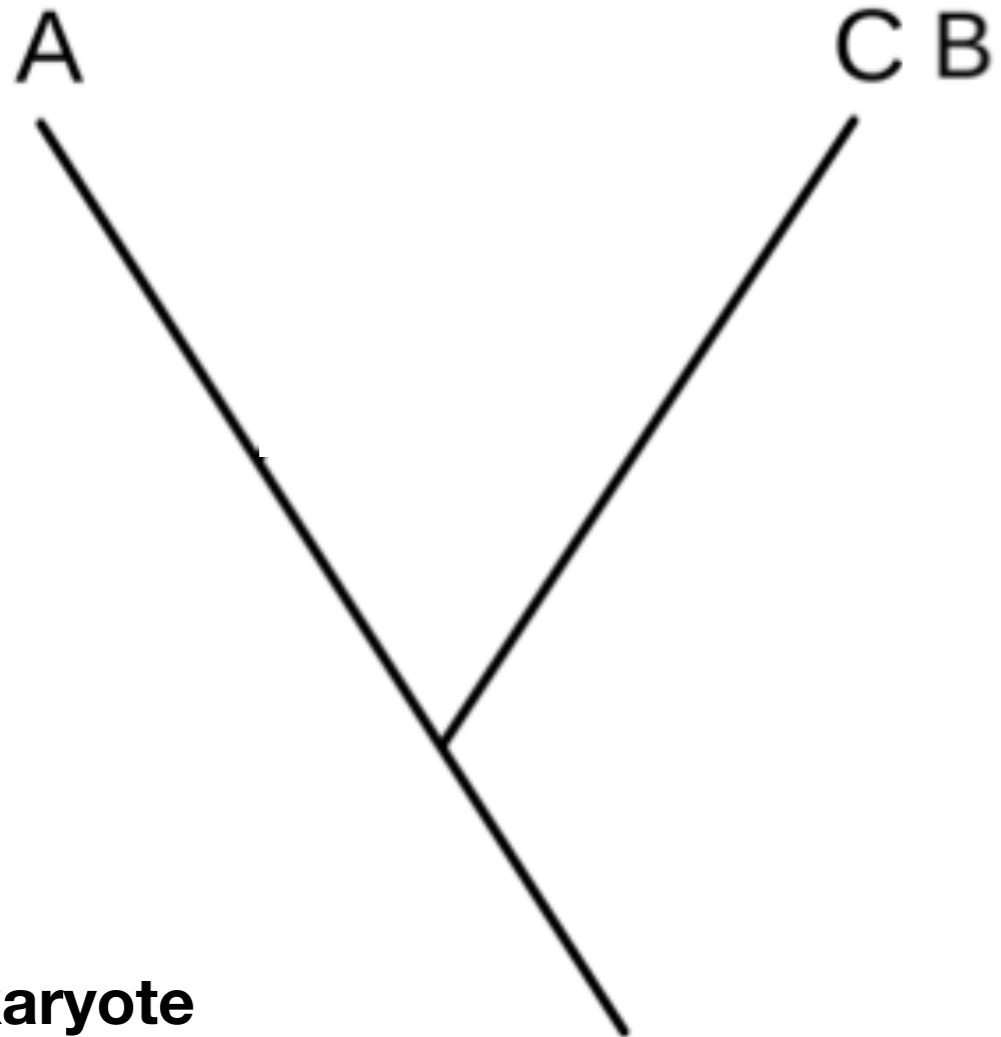
*2. How are archaea fundamentally different  
from other cells.*



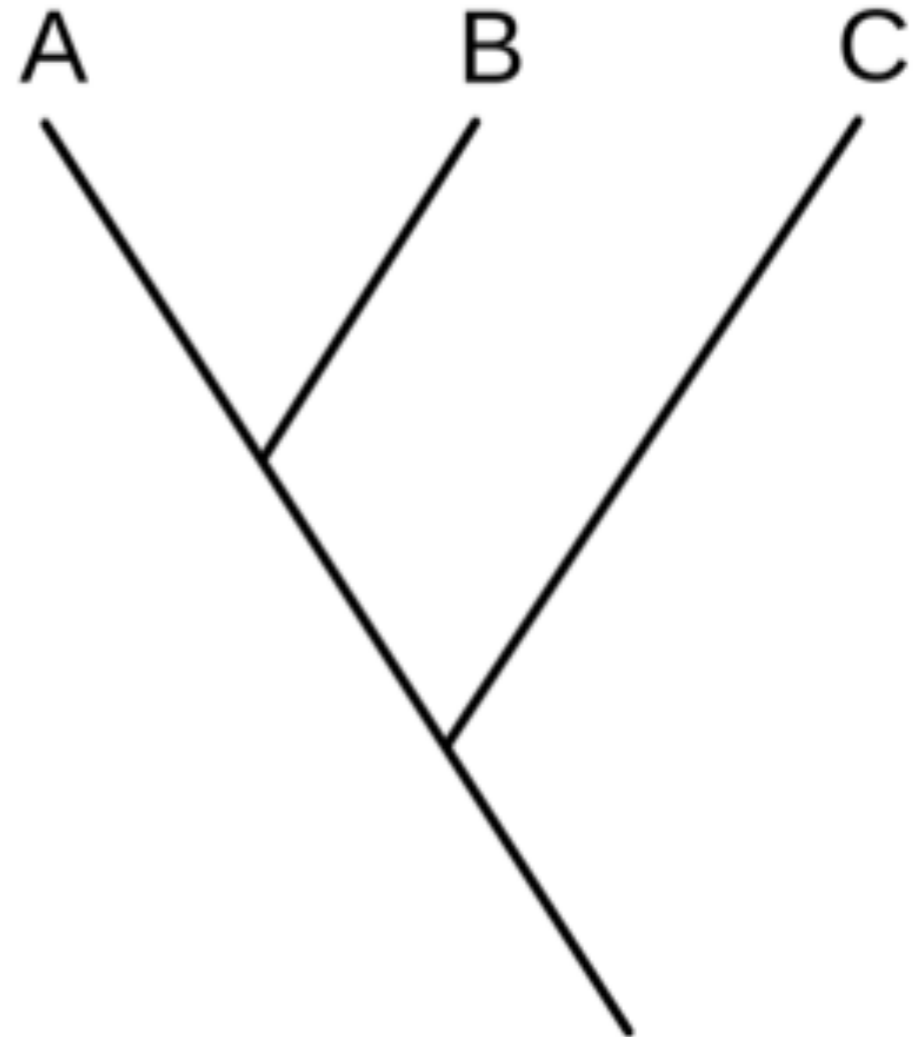


- 1. Make note of why his discovery was so important.*
- 2. How are archaea fundamentally different from other cells.*

**1975**



**Carl Woese  
1977**

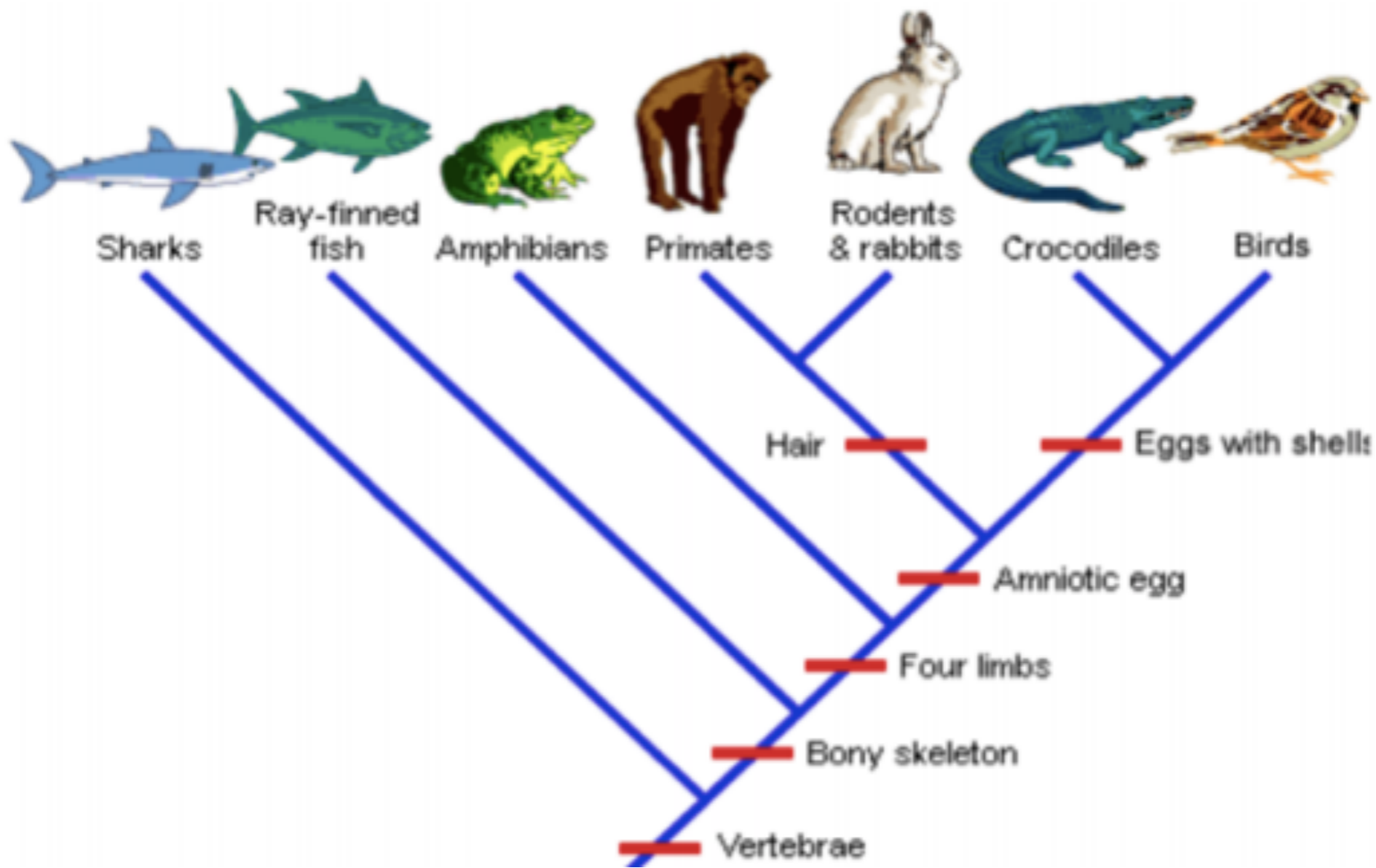


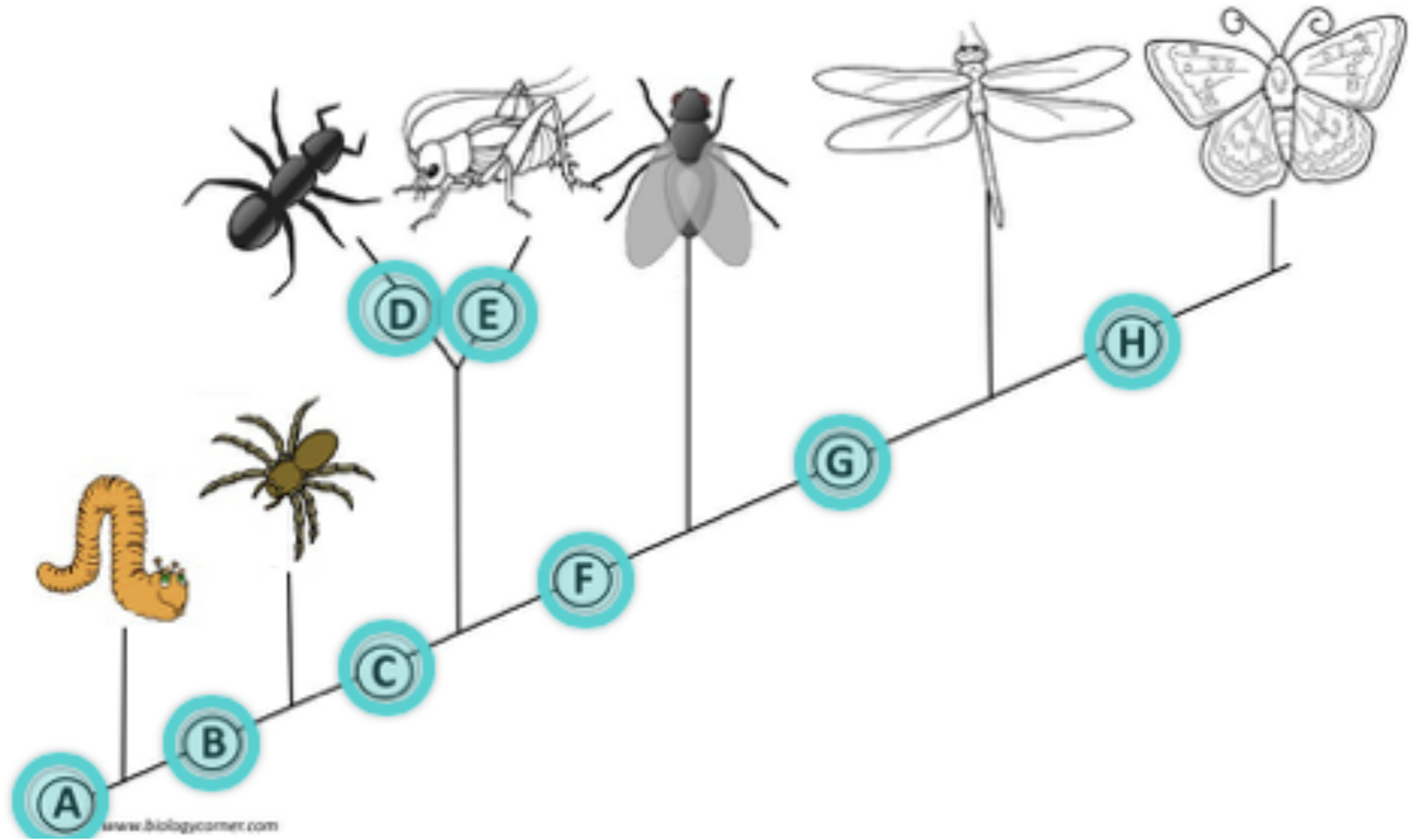
**A- Eukaryote  
B- Archaea  
C- Prokaryotes**

# Let's compare species



	Symmetry	Segmented	Legs	Antenna	Wings	Eyltron
Worm						
Spider						
Jelly fish						
Beetle						
Sponge						
Butterfly						
Ant						



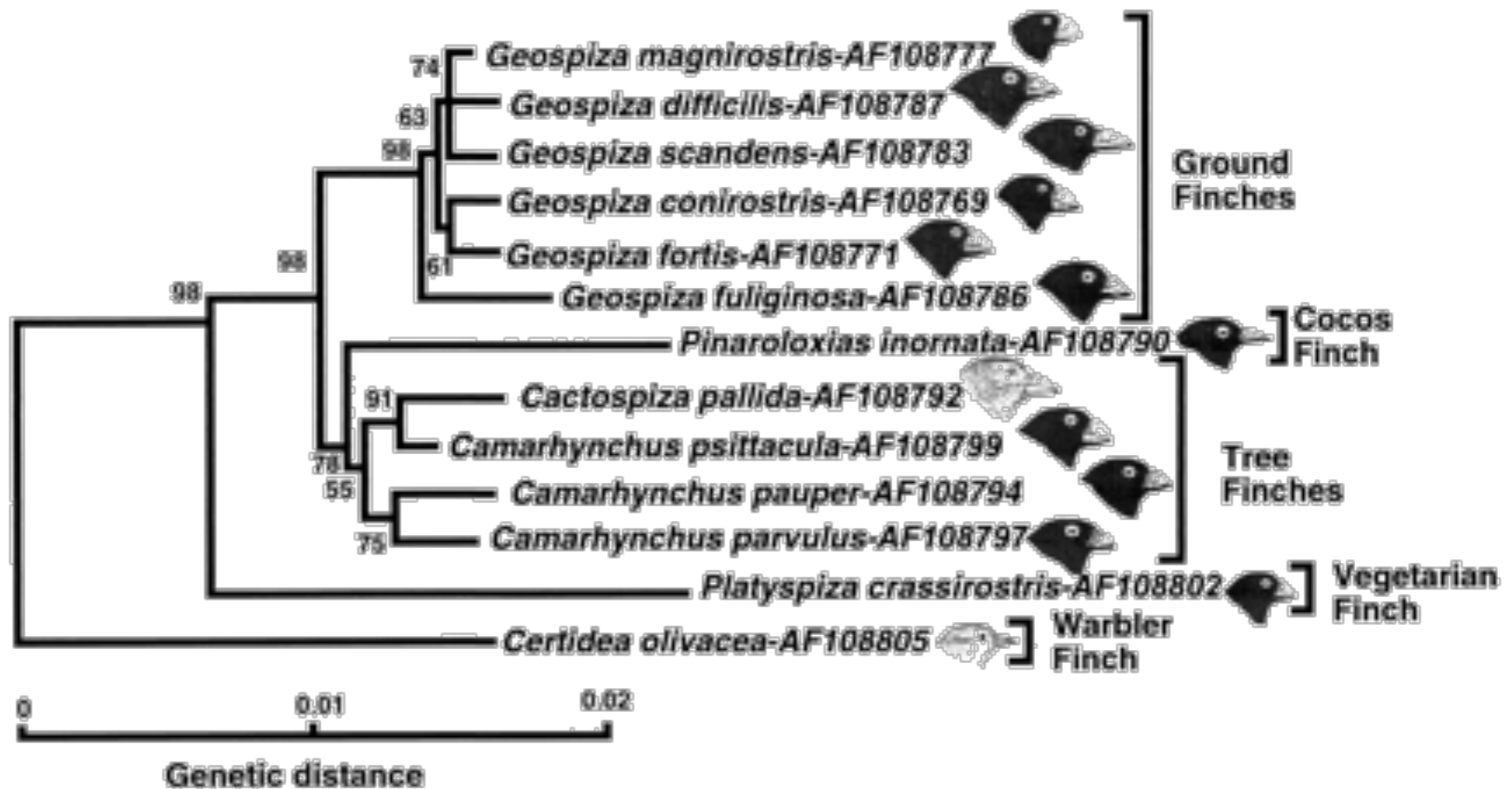


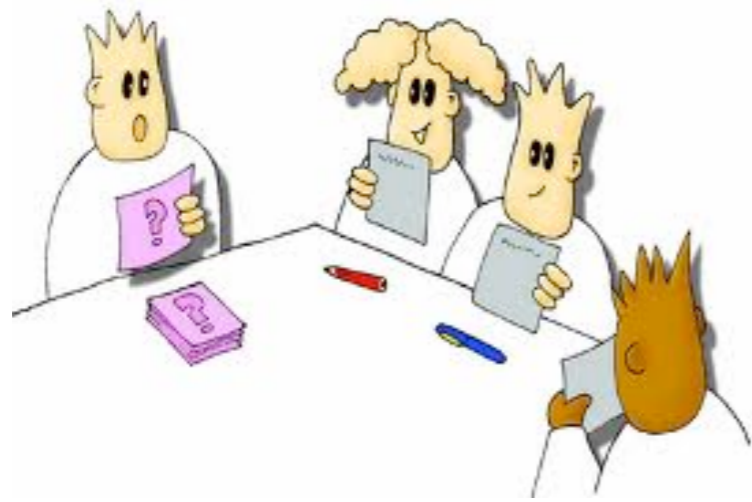


# Clades

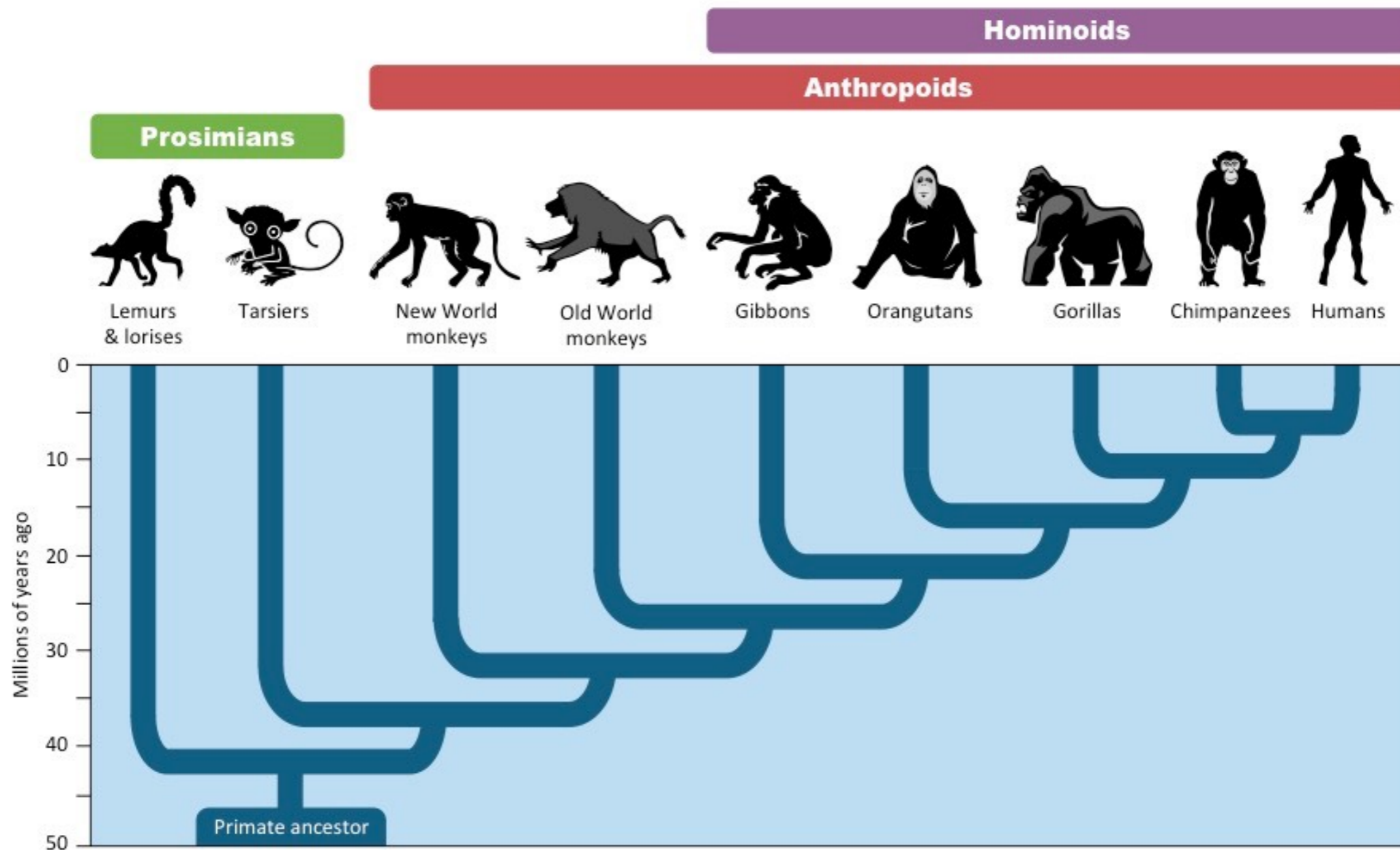
Clades are a group of organisms that have evolved from a common ancestor. This would include

- All living species
- Common ancestral species (extinct)



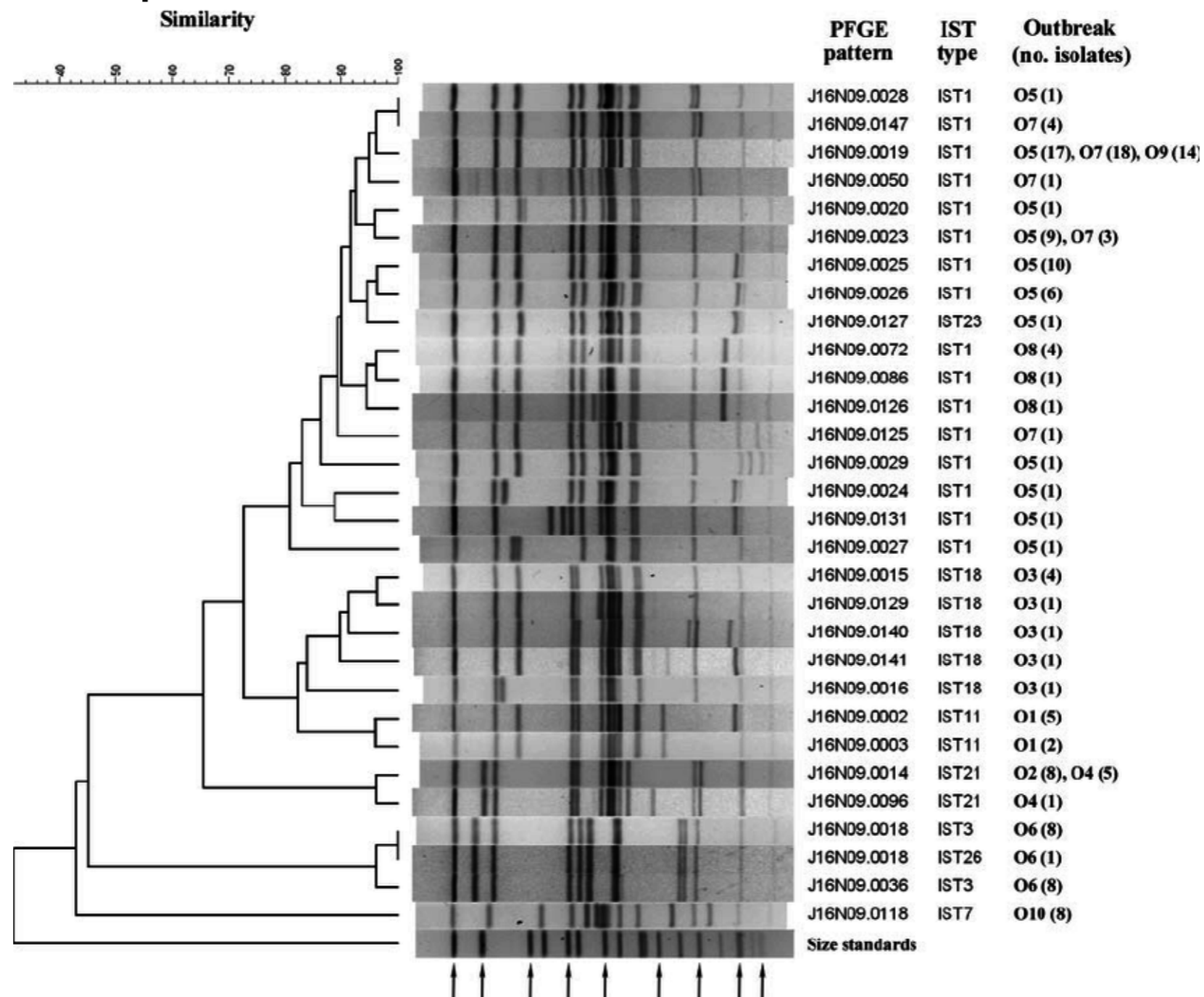


Which of these species would you not include in a unifying clade?



# Clades

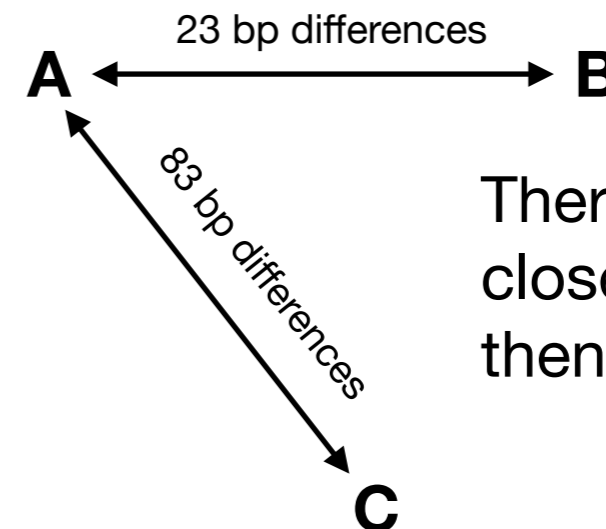
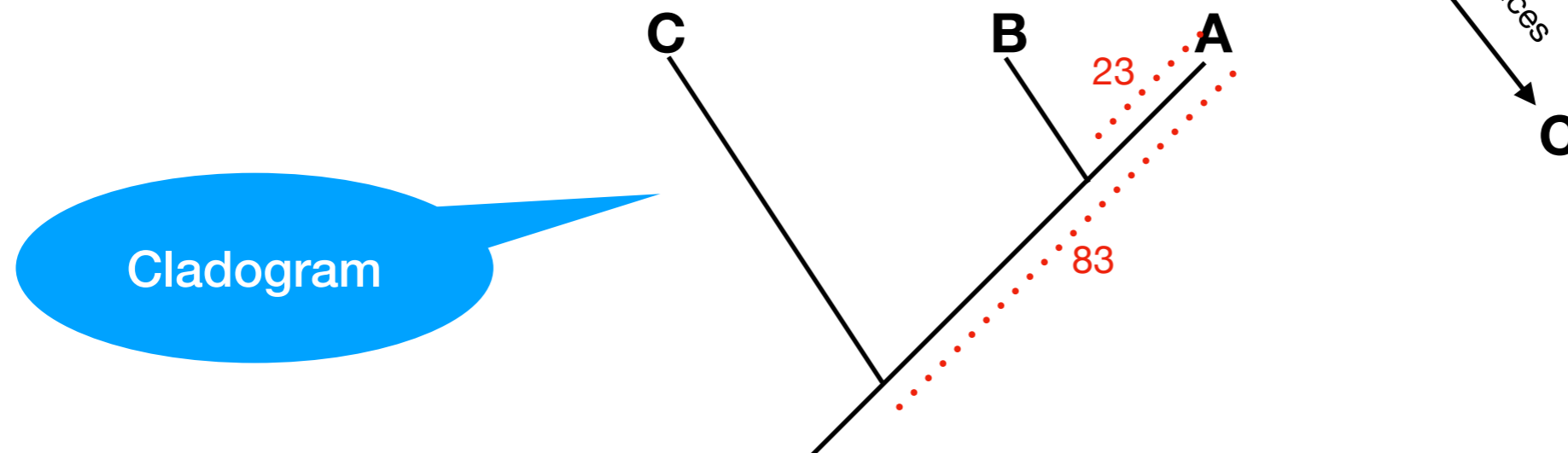
Clades generally would usually include species that show a strong gene DNA sequence or amino acid sequence of a protein relationship



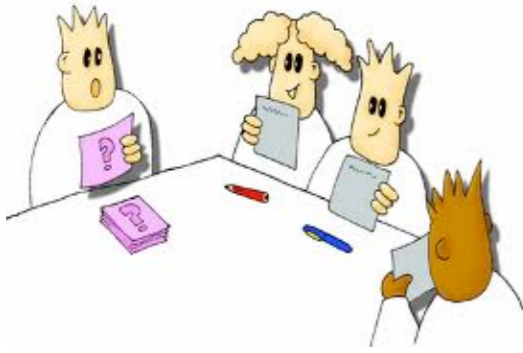
# Cladograms include a molecular clock

- **Mutation** occur randomly and these changes in DNA and genes will be gradual over time.
- Changes could allow estimates of how far back two species are related...

eg Species A,B,C

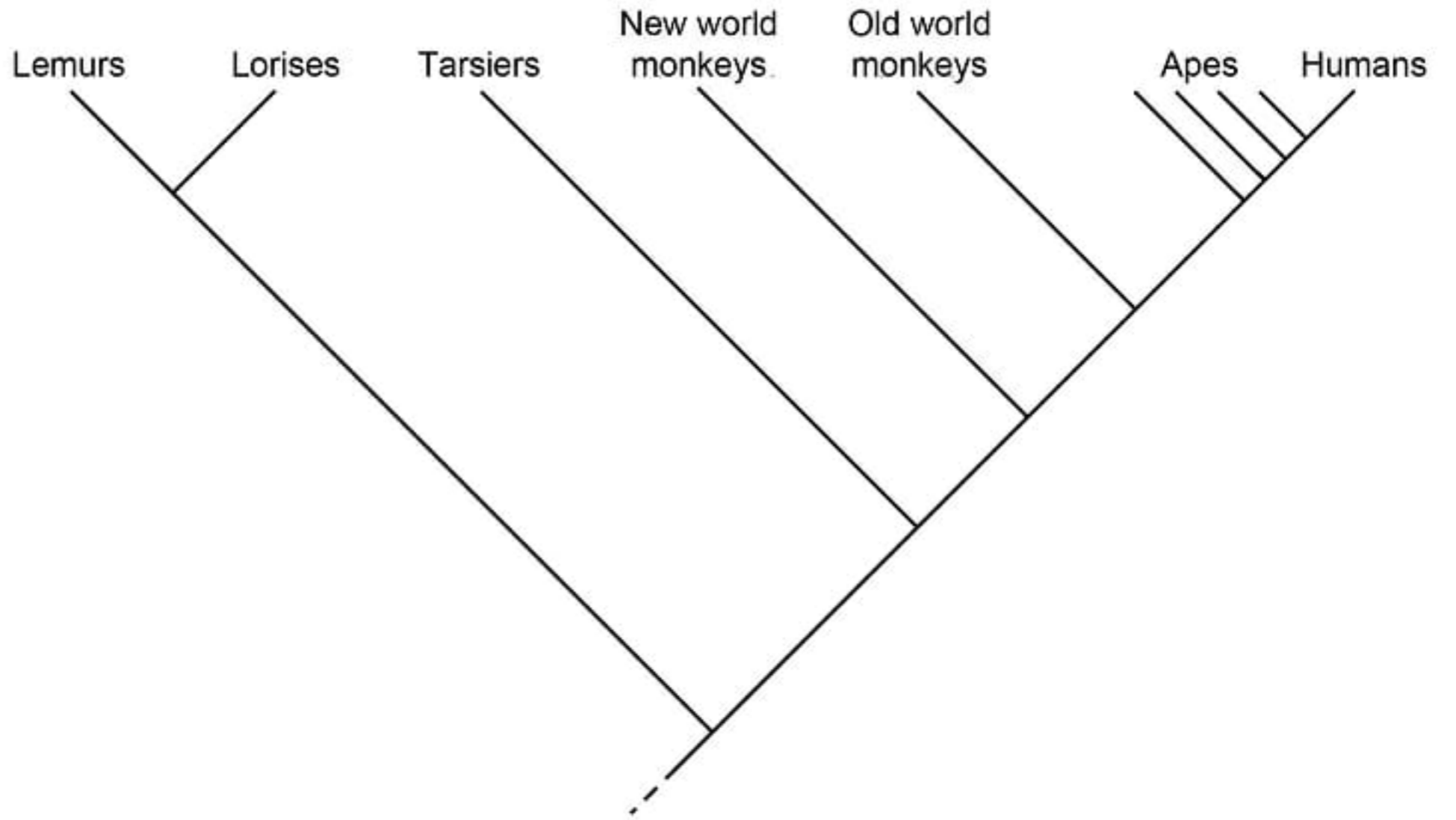
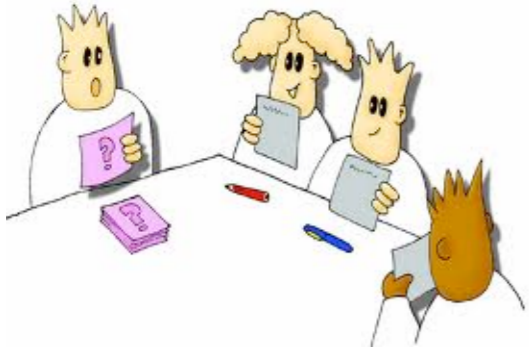


Therefore A is more closely related to B than A to C



Which of these species the closest related?  
 Which species is the farthest related to the others?  
 Can you construct a cladogram of this?

<b>Species A</b>	Amino Acid Sequence: ISO-SER-ASP-GLN-PHE-ILE-LEU-GLN-SER-ARG-LEU-LEU-HIS DNA Sequence: ATTAGCGACCAGTTTATCCTACAATCCCGTCTACTTCAT
<b>Species B</b>	Amino Acid Sequence: LEU-ISO-PRO-PRO-PHE-ILE-LEU-LEU-SER-HIS-LEU-LEU-SER DNA Sequence: CTAATCCCCCGTTTATCCTACTTTCCCATCTACTAAGT
<b>Species C</b>	Amino Acid Sequence: LEU-ISO-ASP-PRO-PHE-ILE-LEU-HIS-SER-ARG-LEU-LEU-ARG DNA Sequence: CTTATCGACCCGTTTATCCTACATTCCCGTCTACCTTCGT
<b>Species D</b>	Amino Acid Sequence: LEU-ISO-PRO-PRO-PHE-ILE-LEU-LEU-SER-HIS-LEU-LEU-SER DNA Sequence: TTAATCCCCCGTTTATCCTACTTTCCCATCTACTAAGT
<b>Species E</b>	Amino Acid Sequence: LEU-ISO-PRO-PRO-PHE-ILE-LEU-LEU-SER-ARG-LEU-LEU-ARG DNA Sequence: CTTATCCCCCGTTTATCCTACTTTCCCGTCTACTTCGT



Cladogram of Primates

# Cladograms

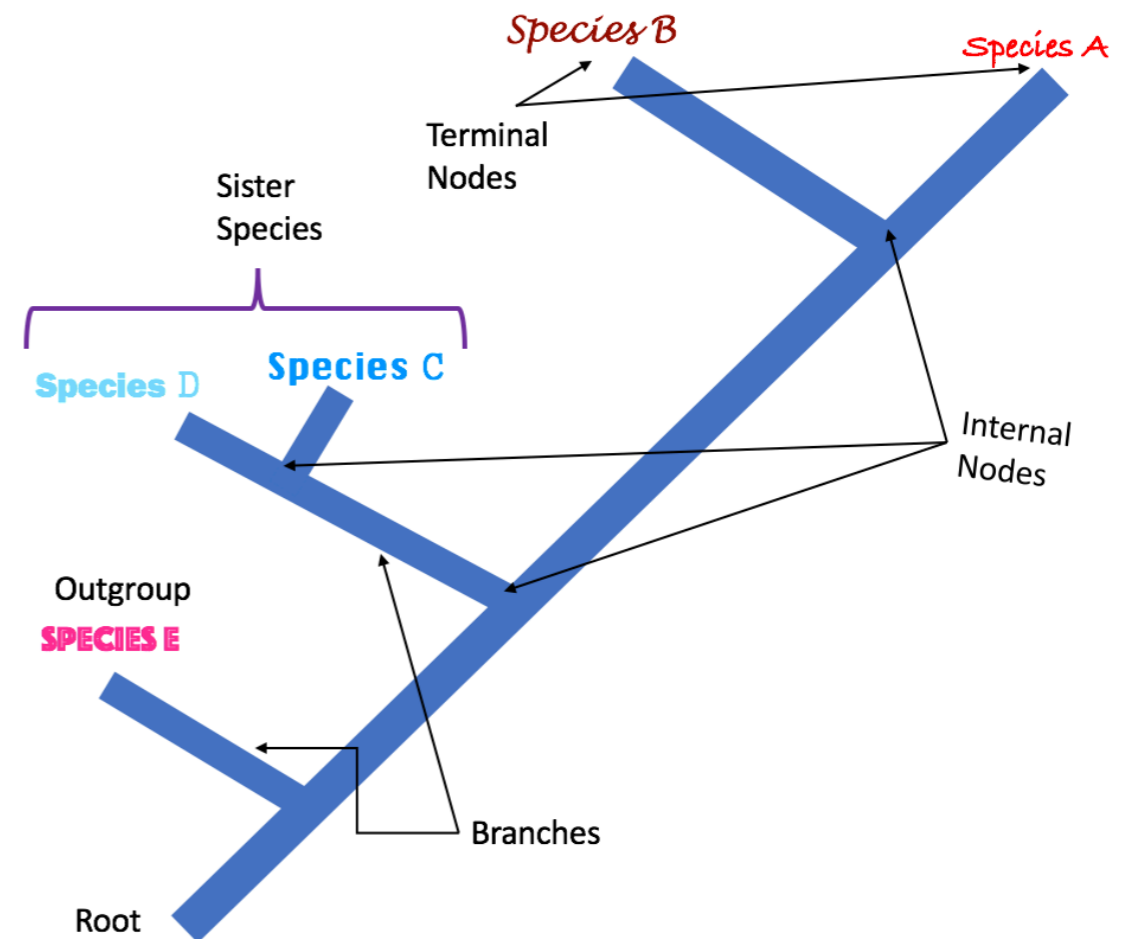
**Cladograms** show the most probable sequence of divergence in clades

- usually based on Amino acid sequence of proteins
- computer generated
- assumes that change is based on the simplest and most likely (principle of parsimony)

Branches are called **nodes**- hypothetical species split

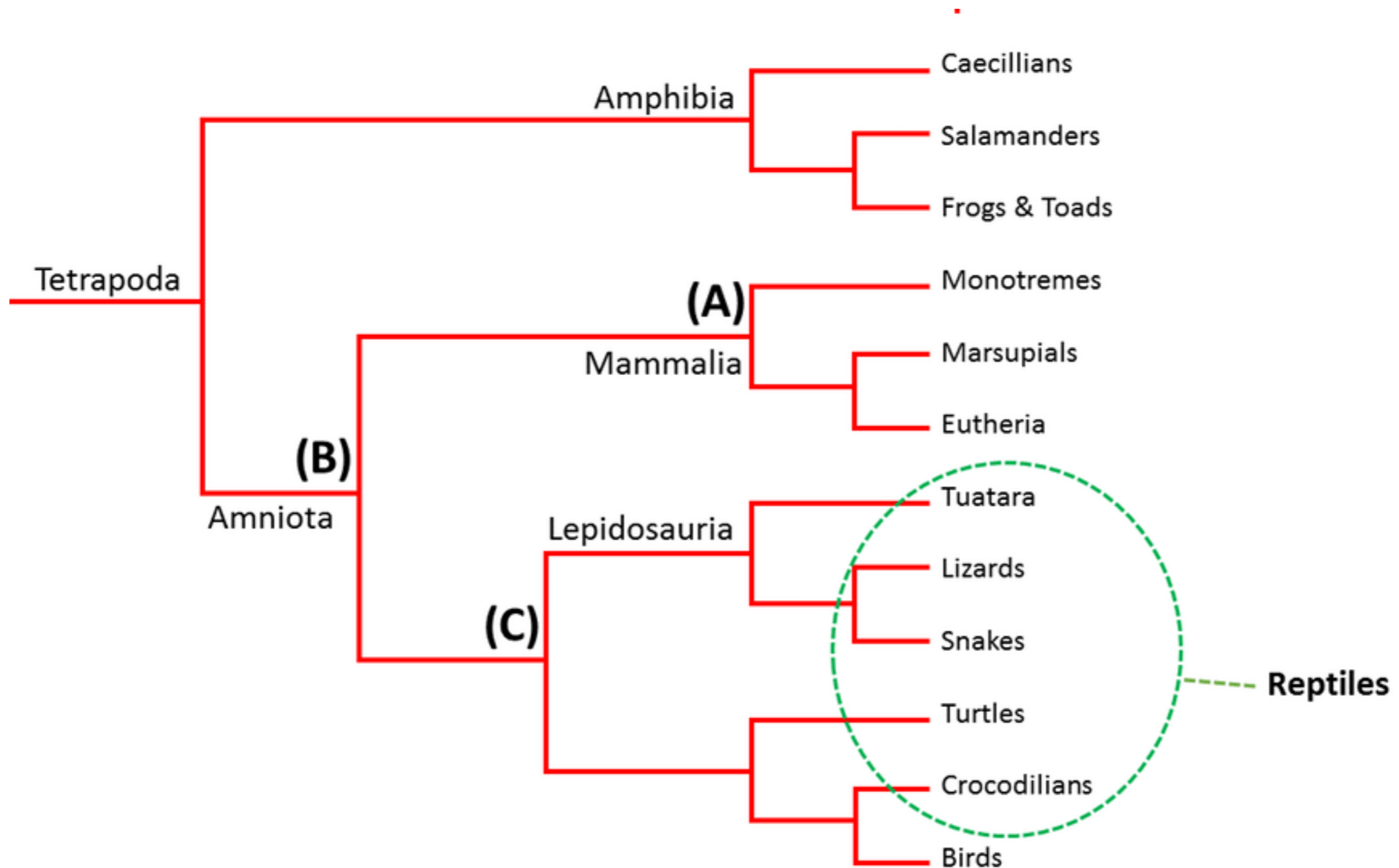
**Sister species**- are closest in a clade

**Outgroup**- a more distantly related group of organisms that serves as a reference group when determining the evolutionary relationships



# Cladograms

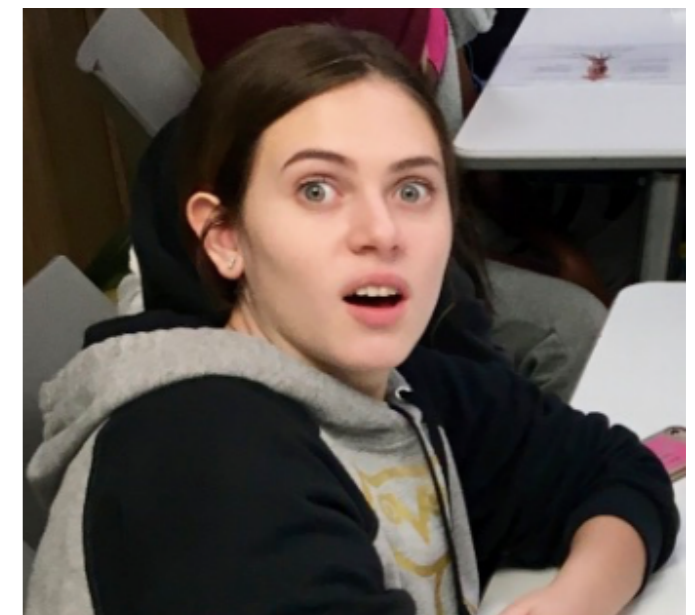
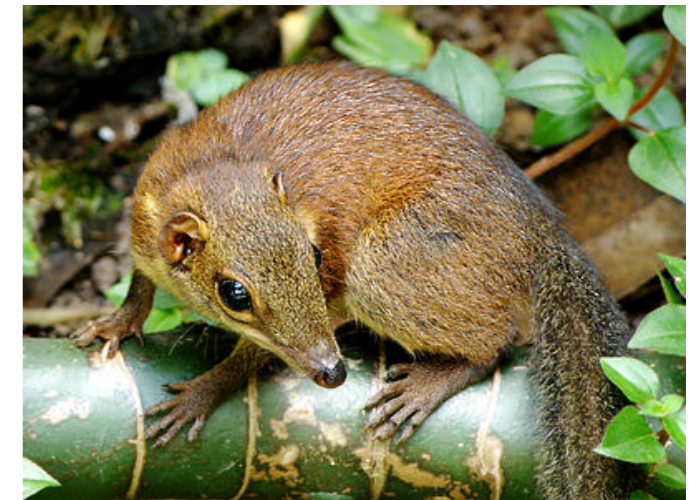
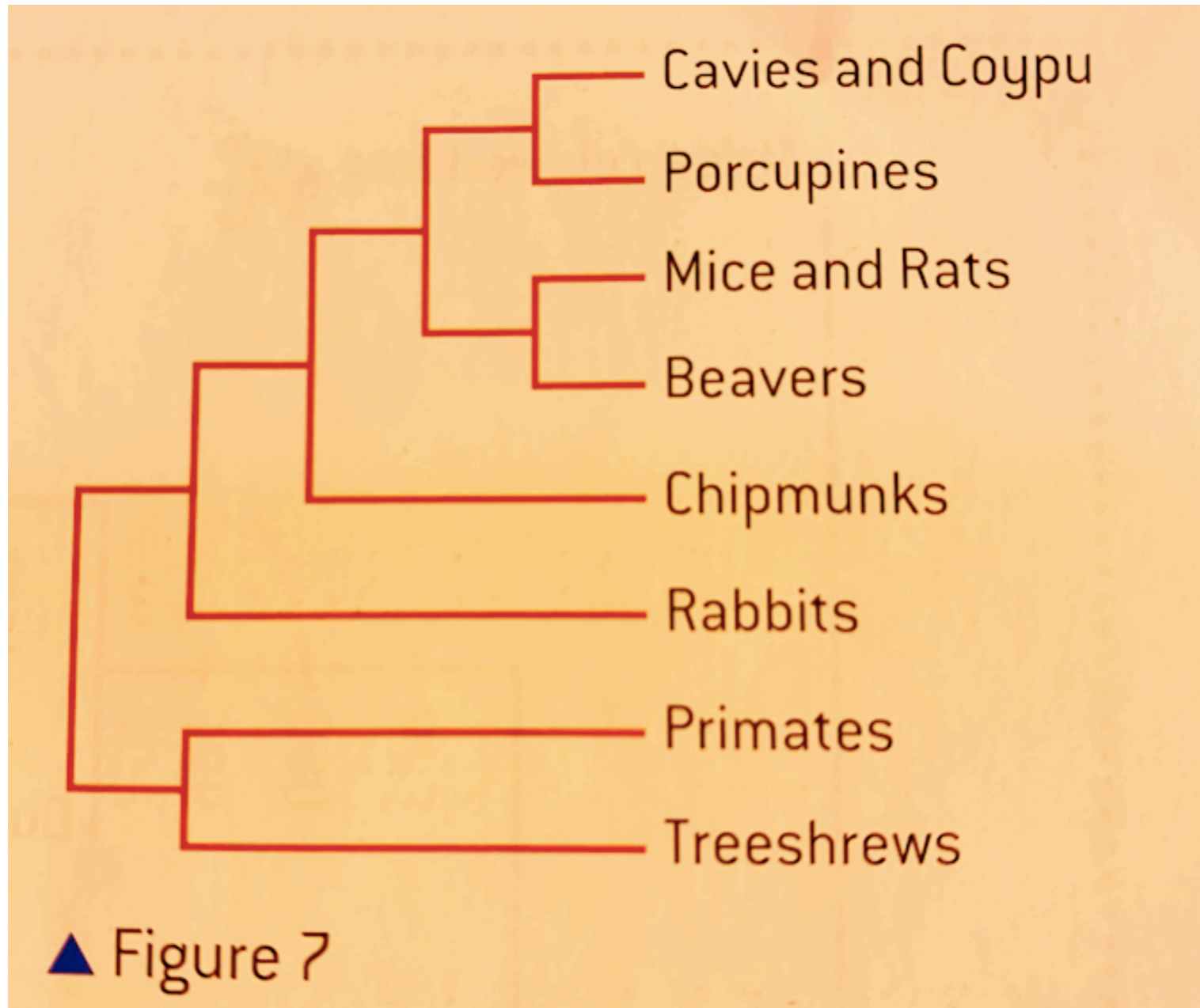
This cladogram was constructed based on amino acid sequence





# Cladograms

This cladogram was constructed based on amino acid sequence



# Cladograms and Classification

- **evidence from cladograms** has shown that classifications of groups based on structure did not correspond with the evolutionary origins of a group of species

- Each cladogram is a working hypothesis, and may be incorrect

- Every new discovery of a characteristic can change clades

**eg.** birds were on their own clade, but now they are more like reptiles

**eg.** Scrophulariaceae, a one time plants family was created based on morphology (anatomy), clades based on DNA have reclassified into different and new families

**eg.** Carl Woese discovery archaea redistributed clades at the domain level