

Classification and Phylogeny (Feb 13th)

Name:

26.1 – 26.6 Reference (yellow book) ----- Each species has two _____.
These are used together to give a precise reference to this species. _____ is
given first and is always written with an _____ case letter. e.g. Homo.
_____ epithet follows the genus and is written in lower case e.g. sapiens

Therefore the species name for humans is *Homo sapiens*

Rules of writing Binomial nomenclature:

- If written by hand the name should also be underlined
- If typed the name should really be in italics but this convention is often ignored
- Often the name will be followed by another name in brackets e.g. (Dickson) which refers to the first person to scientifically identify the species.

	Ex. 1:	Ex. 2:
Kingdom		
Phylum		
Class		
Order		
Family		
Genus		
Species		

Terms to define:

Phylogeny:

Molecular systematics:

Convergent evolution:

Cladogram:

Homologous structures:

Clade:

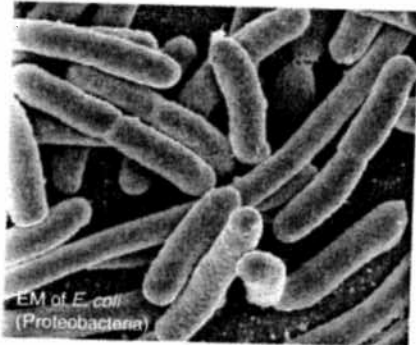
Taxonomy:

Binomial nomenclature

Descent and Common Ancestry

Our knowledge of how organisms are related has grown rapidly in recent decades. Traditional schemes for classifying the living world, which were based primarily on morphological comparisons, have been considerably revised in the light of new techniques in **molecular phylogenetics**. Such techniques compare the DNA, RNA, and proteins of organisms to establish evolutionary

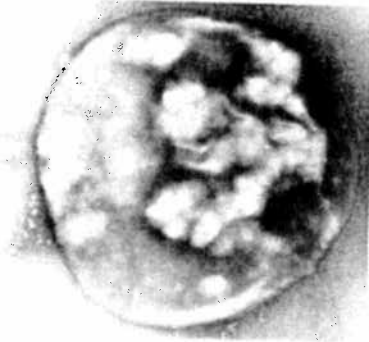
relationships. Molecular phylogenetics has enabled scientists to clarify the very earliest origins of eukaryotes and to recognize two prokaryote domains (rather than a single prokaryote superkingdom). Powerful evidence for the common ancestry of all life comes from the commonality in the genetic code, and from the similarities in the molecular machinery of all cells.



Rocky Mountain Laboratories, NIAID, NIH

DOMAIN BACTERIA

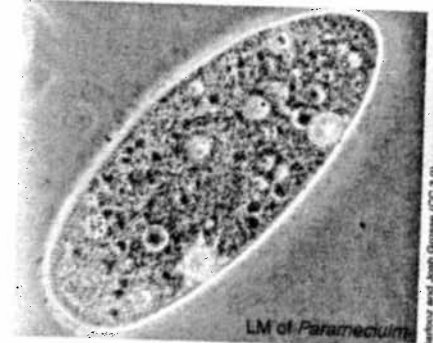
Lack a distinct nucleus and cell organelles. Generally prefer less extreme environments than Archaea. Includes well-known pathogens, many harmless and beneficial species, and the cyanobacteria (photosynthetic bacteria containing the pigments chlorophyll a and phycocyanin). Endosymbiosis of ancestral bacteria during evolution gave rise to the eukaryotic organelles mitochondria and chloroplasts.



Xiangyux (PD)

DOMAIN ARCHAEA

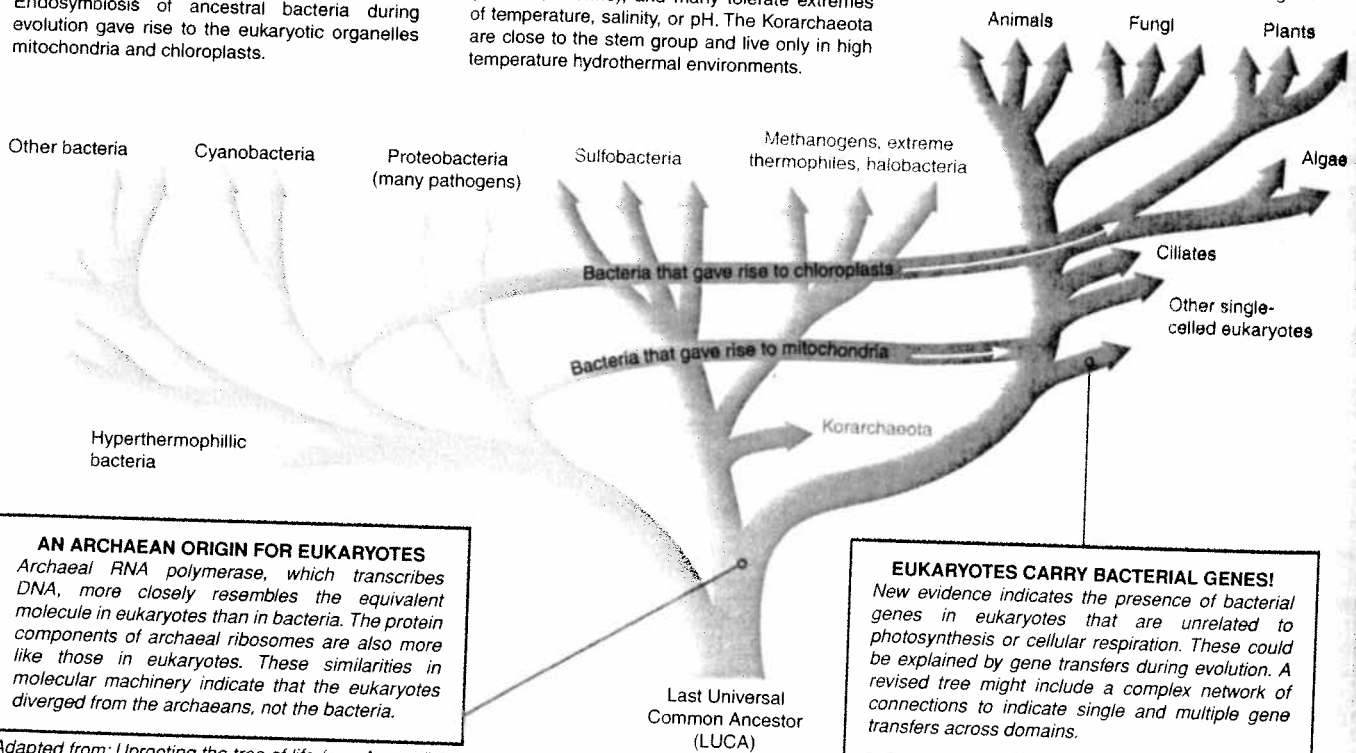
Closely resemble eubacteria in many ways but membrane and cell wall composition and aspects of metabolism are very different. Live in extreme environments similar to those on primeval Earth. They may utilize sulfur, methane, or halogens (chlorine, fluorine), and many tolerate extremes of temperature, salinity, or pH. The Korarchaeota are close to the stem group and live only in high temperature hydrothermal environments.



Rehner and Josh Grasse (CC 3.0)

DOMAIN EUKARYA

Complex cells with organelles and a membrane-bound nucleus. This domain contains four of the kingdoms recognized under a traditional scheme. Note that Kingdom Protista is separated into distinct taxa, recognizing their diverse origins.



AN ARCHAEAN ORIGIN FOR EUKARYOTES
 Archaeal RNA polymerase, which transcribes DNA, more closely resembles the equivalent molecule in eukaryotes than in bacteria. The protein components of archaeal ribosomes are also more like those in eukaryotes. These similarities in molecular machinery indicate that the eukaryotes diverged from the archaeans, not the bacteria.

EUKARYOTES CARRY BACTERIAL GENES!
 New evidence indicates the presence of bacterial genes in eukaryotes that are unrelated to photosynthesis or cellular respiration. These could be explained by gene transfers during evolution. A revised tree might include a complex network of connections to indicate single and multiple gene transfers across domains.

Adapted from: Uprooting the tree of life (see Appendix)

1. Explain the role of molecular phylogenetics in revising the traditional classification schemes (pre-1980):

2. Describe the evidence for the archaean origin of eukaryotic cells:

3. What evidence is there for a Last Universal Common Ancestor?

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Cladograms and Phylogenetic Trees

Phylogenetic systematics is a science in which the fields of taxonomy (the study of naming organisms) and phylogenetics (the study of evolutionary history) overlap. Traditional methods for establishing **phylogenetic trees** have emphasized morphological similarities in order to group species into genera and other higher level taxa. In contrast, **cladistics** is a methodology that relies on **shared derived characteristics (synapomorphies)** and ignores features that are not the result of shared ancestry. A cladogram is a phylogenetic tree constructed using cladistics.

Although cladistics has traditionally relied on morphological data, molecular data are increasingly being used to construct cladograms. Traditional and cladistic trees do not necessarily conflict, but there have been reclassifications of some taxa (notably primates, reptiles, and fish). Popular classifications will probably continue to reflect similarities and differences in appearance, rather than a strict evolutionary history. In this respect, they are a compromise between phylogeny and the need for a convenient filing system for species diversity.

Constructing a Simple Cladogram

A table listing the features for comparison allows us to identify where we should make branches in the **cladogram**. An outgroup (one which is known to have no or little relationship to the other organisms) is used as a basis for comparison.

Comparative features	Taxa					
	Jawless fish (outgroup)	Bony fish	Amphibians	Lizards	Birds	Mammals
Vertebral column	✓	✓	✓	✓	✓	✓
Jaws	x	✓	✓	✓	✓	✓
Four supporting limbs	x	x	✓	✓	✓	✓
Amniotic egg	x	x	x	✓	✓	✓
Diapsid skull	x	x	x	✓	✓	x
Feathers	x	x	x	x	✓	x
Hair	x	x	x	x	x	✓

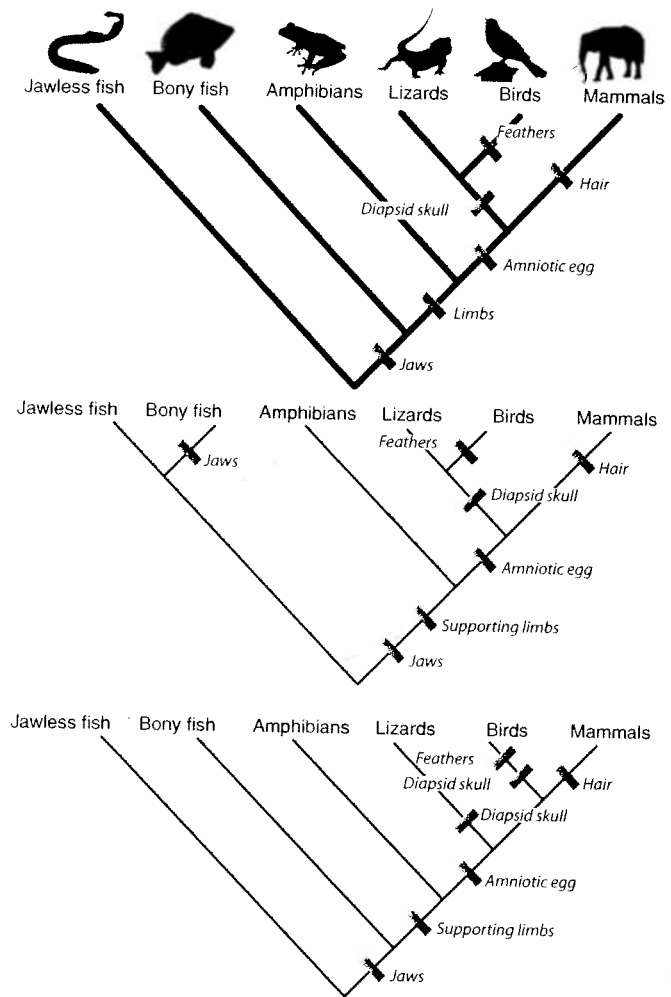
The table above lists features shared by selected taxa. The outgroup (jawless fish) shares just one feature (vertebral column), so it gives a reference for comparison and the first branch of the cladogram (tree).

As the number of taxa in the table increases, the number of possible trees that could be drawn increases exponentially. To determine the most likely relationships, the rule of **parsimony** is used. This assumes that the tree with the least number of evolutionary events is most likely to show the correct evolutionary relationship.

Three possible cladograms are shown on the right. The top cladogram requires six events while the other two require seven events. Applying the rule of parsimony, the top cladogram must be taken as correct.

Parsimony can lead to some confusion. Some evolutionary events have occurred multiple times. An example is the evolution of the four chambered heart, which occurred separately in both birds and mammals. The use of fossil evidence and DNA analysis can help to solve problems like this.

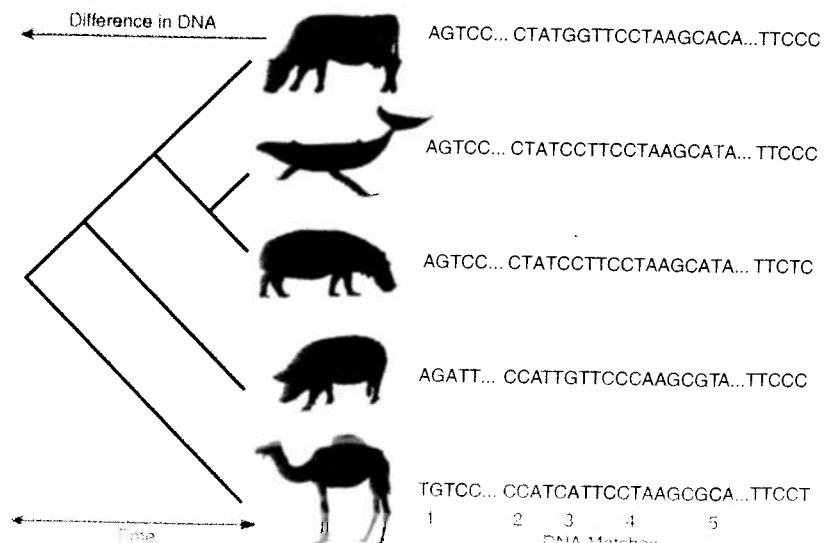
Possible Cladograms



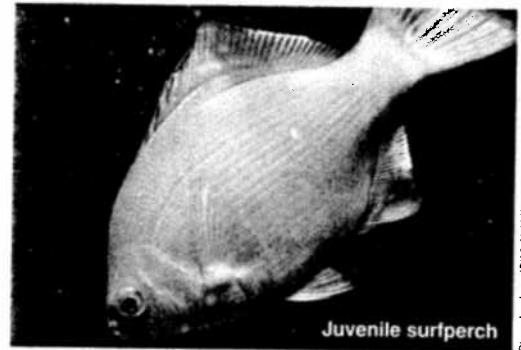
Using DNA Data

DNA analysis has allowed scientists to confirm many phylogenies and refute or redraw others. In a similar way to morphological differences, DNA sequences can be tabulated and analyzed. The ancestry of whales has been in debate since Darwin. The radically different morphologies of whales and other mammals makes it difficult work out the correct phylogenetic tree. However recently discovered fossil ankle bones, as well as DNA studies, show whales are more closely related to hippopotami than to any other mammal. Coupled with molecular clocks, DNA data can also give the time between each split in the lineage.

The DNA sequences on the right show part of the nucleotide subset 141-200 and some of the matching nucleotides used to draw the cladogram. Although whales were once thought most closely related to pigs, based on the DNA analysis the most parsimonious tree disputes this.



CHARACTER													
Taxon	1	2	3	4	5	6	7	8	9	10	11	12	13
Zebra-perch sea chub	0	0	0	0	0	0	0	0	0	0	0	0	0
Barred surfperch	1	0	0	0	0	0	0	0	0	1	1	0	0
Walleye surfperch	1	0	0	0	0	1	0	1	0	1	1	0	0
Black perch	1	1	1	0	0	0	0	0	0	0	0	1	0
Rainbow seaperch	1	1	1	0	0	0	0	0	0	0	0	1	0
Rubberlip surfperch	1	1	1	1	1	0	0	0	0	0	0	0	1
Pile surfperch	1	1	1	1	1	0	0	0	0	0	0	0	1
White seaperch	1	1	1	1	1	0	0	0	0	0	0	0	0
Shiner perch	1	1	1	1	1	1	0	0	0	0	0	0	0
Pink seaperch	1	1	1	1	1	1	1	1	0	0	0	0	0
Kelp perch	1	1	1	1	1	1	1	1	1	0	0	0	0
Reef perch	1	1	1	1	1	1	1	1	1	0	0	0	0



Steve Lonhart (SIMON / MBRMS) / PD NOAA

Surfperches are viviparous (live bearing) and the females give birth to relatively well developed young. Some of the characters (below, left) relate to adaptations of the male for internal fertilization. Others relate to deterring or detecting predators. In the matrix, characters are assigned a 0 or 1 depending on whether they represent the ancestral (0) or derived (1) state. This coding is common in cladistics because it allows the data to be analyzed by computer.

Data after Cailliet et al. 1986

Selected characters for cladogram assembly

- | | | |
|----------------------------------|------------|----------|
| 1. Viviparity (live bearing) | 0 No | 1 Yes |
| 2. Males with flask organ | 0 No | 1 Yes |
| 3. Orbit without bony front wall | 0 Yes | 1 No |
| 4. Tail length | 0 Short | 1 Long |
| 5. Body depth | 0 Deep | 1 Narrow |
| 6. Body size | 0 Large | 1 Small |
| 7. Length of dorsal fin base | 0 Long | 1 Short |
| 8. Eye diameter | 0 Moderate | 1 Large |
| 9. Males with anal crescent | 0 No | 1 Yes |
| 10. Pectoral bone with process | 0 No | 1 Yes |
| 11. Length of dorsal sheath | 0 Long | 1 Short |
| 12. Body mostly darkish | 0 No | 1 Yes |
| 13. Flanks with large black bars | 0 No | 1 Yes |

1. This activity provides the taxa and character matrix for 11 genera of marine fishes in the family of surfperches. The outgroup given is a representative of a sister family of rudderfishes (zebra-perch sea chub), which are not live-bearing. Your task is to create the most parsimonious cladogram from the matrix of character states provided. To help you, we have organized the matrix with genera having the smallest blocks of derived character states (1) at the top following the outgroup representative. Use a separate sheet of graph paper, working from left to right to assemble your cladogram. Identify the origin of derived character states with horizontal bars, as shown in the examples earlier in this activity. CLUE: You should end up with 15 steps. Two derived character states arise twice independently. Staple your cladogram to this page.

2. In the cladogram you have constructed for the surfperches, two characters have evolved twice independently:

(a) Identify these two characters: _____

(b) What selection pressures do you think might have been important in the evolution of these two derived states?

3. What assumption is made when applying the rule of parsimony in constructing a cladogram? _____

4. (a) Describe the contribution of biochemical evidence to clarifying some evolutionary relationships: _____

(b) When might it not be advisable to rely on biochemical evidence alone? _____

5. In the DNA data for the whale cladogram (previous page) identify the DNA match that shows a mutation event must have happened twice in evolutionary history.

6. A phylogenetic tree is a hypothesis for an evolutionary history. How could you test it? _____
