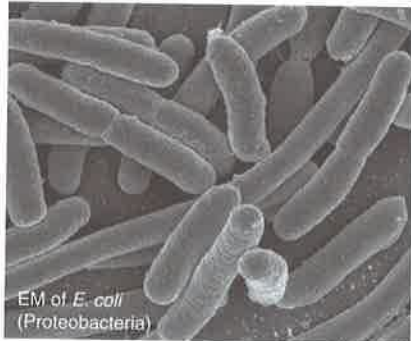


# Descent and Common Ancestry

Name \_\_\_\_\_

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



Xiangyux (PD)



Barfcoz and Josh Grosse (CC 3.0)

## DOMAIN BACTERIA

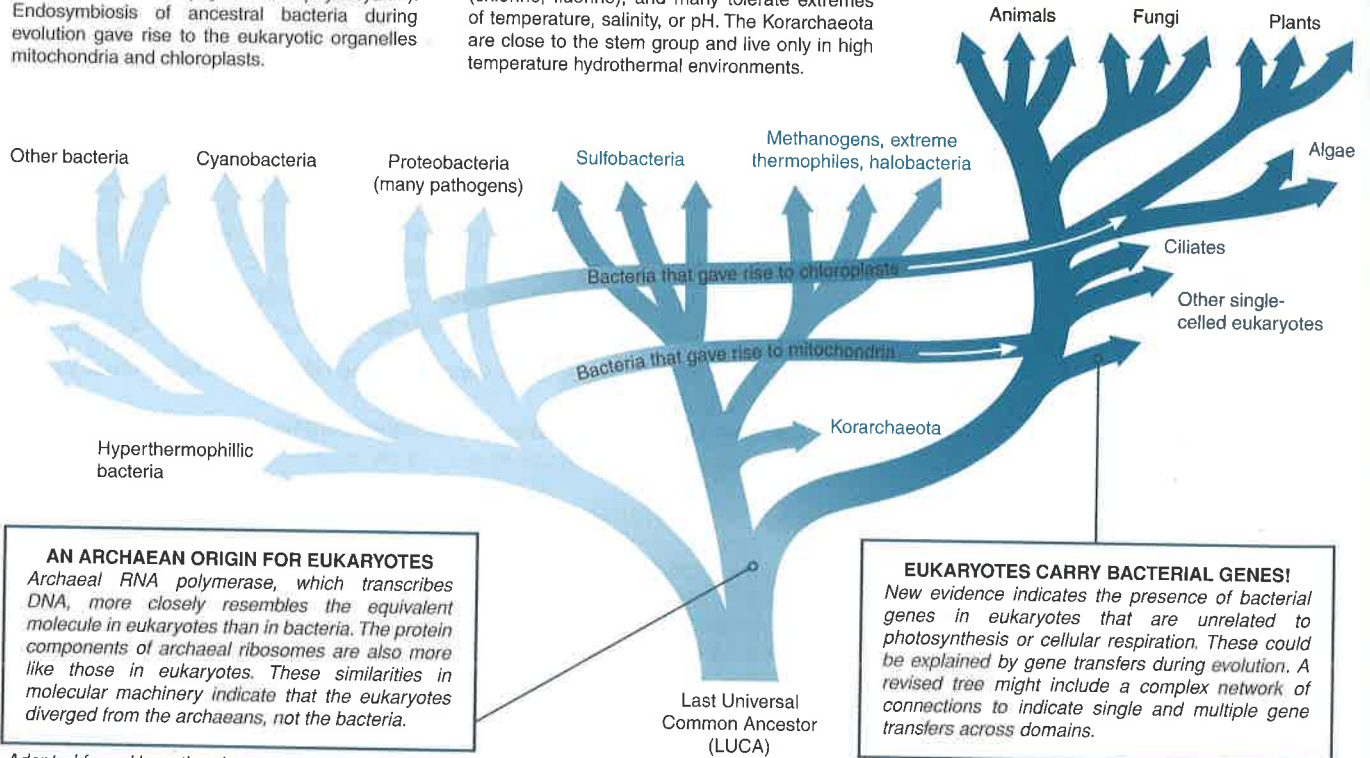
Lack a distinct nucleus and cell organelles. Generally prefer less extreme environments than Archaea. Includes well-known pathogens, many harmless and beneficial species, and the cyanobacteria (photosynthetic bacteria containing the pigments chlorophyll a and phycocyanin). Endosymbiosis of ancestral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

## 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.

## 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):

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

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

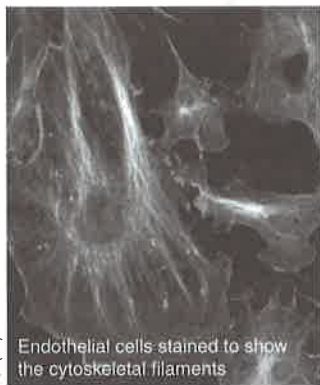
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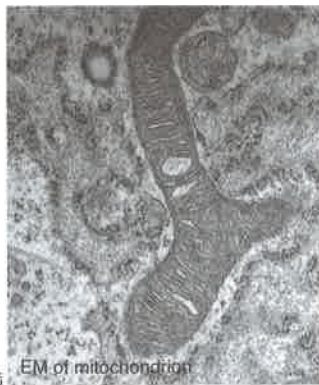


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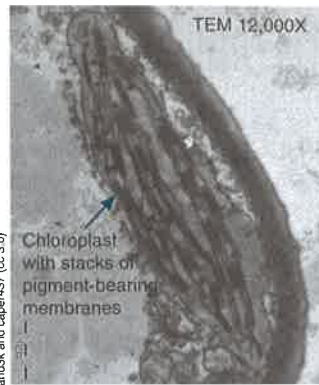


NH (PD)

Endothelial cells stained to show the cytoskeletal filaments



EM of mitochondrion



TEM 12,000X

andisk and caper437 (cc 3.0)

Chloroplast with stacks of pigment-bearing membranes

Eukaryotic cells are characterized by large linear chromosomes within the cell's nucleus (above). These nuclear chromosomes are packaged by proteins into a condensed structure called chromatin. The evolution of linear chromosomes was related to the appearance of microtubule-dependent cell division (mitosis and meiosis).

The cytoskeleton (CSK) is an intracellular scaffold of protein filaments, important in intracellular movement of materials and cell division in eukaryotic cells. The CSK was once thought to be unique to eukaryotic cells, but homologs to all the major proteins of the eukaryotic cytoskeleton have also been found in prokaryotes.

The endosymbiotic origin of eukaryotic mitochondria is supported by the evidence from mitochondrial gene sequences, ribosomes, and protein synthesis that indicate a prokaryotic origin. Mitochondria are characteristic of eukaryotic cells and arose in a common ancestor to eukaryotic cells.

Chloroplasts are assumed to have been acquired, via endosymbiosis, after mitochondria and there is much evidence to suggest that they were acquired independently by more than one type of cyanobacterial cell (i.e. their origin is polyphyletic). The prokaryotic origin of chloroplasts is supported by ribosomal evidence.



Most organisms share the same genetic code, i.e. the same combination of three DNA bases code for the same amino acid, although there are some minor variations (e.g. in mitochondria). Evidence suggests the code was subject to selection pressure which acted to minimize the effect of point mutations or errors in translation.



Ribosomes in translation

In all living systems, the genetic machinery consists of self-replicating DNA molecules. Some DNA is transcribed into RNA, some of which is translated into proteins. The machinery for translation (above) involves proteins and RNA. Ribosomal RNA analyses support a universal common ancestor.

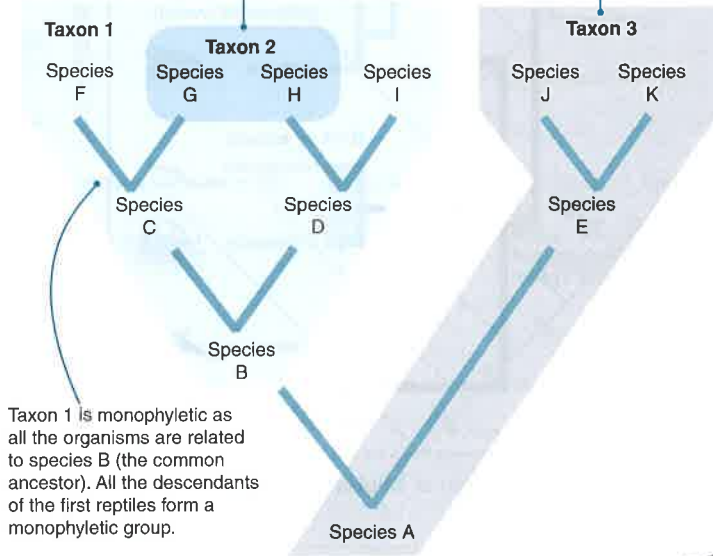
**Determining Phylogenetic Relationships**

Increasingly, analyses to determine evolutionary relationships rely on cladistic analyses of character states. Cladism groups species according to their most recent common ancestor on the basis of shared derived characteristics or **synapomorphies**. All other characters are ignored. A phylogeny constructed using cladistics thus includes only **monophyletic groups**, i.e. the common ancestor and all of its descendants. It excludes both paraphyletic and polyphyletic groups (right). It is important to understand these terms when constructing cladograms. The cladist restriction to using only synapomorphies creates an unambiguous branching tree. One problem with this approach is that a strictly cladistic classification could theoretically have an impractically large number of taxonomic levels and may be incompatible with a Linnaean system.

Cladistic schemes have traditionally used morphological characteristics, with gain (or loss) of a character indicating a derived state. Increasingly, molecular comparisons are being used, particularly for highly conserved genes such as those coding for ribosomal RNA. For prokaryotes, molecular phylogeny studies have been the most important tool in revealing evolutionary relationships and revolutionizing traditional classification schemes.

Taxon 2 is polyphyletic as it includes organisms with different ancestors. The group "warm-blooded (endothermic) animals" is polyphyletic as it includes birds and mammals.

Taxon 3 is paraphyletic. It includes species A without including all of A's descendants. The traditional grouping of reptiles is paraphyletic because it does not include birds.



Taxon 1 is monophyletic as all the organisms are related to species B (the common ancestor). All the descendants of the first reptiles form a monophyletic group.

Intro. to Cladistics

Relatedness of Organisms

4. (a) Briefly describe how eukaryotic organelles, such as mitochondria and chloroplasts, are thought to have evolved:

(b) What evidence is there to support this?

5. Discuss the benefits of cladistics for establishing evolutionary relationships. What useful groupings might it exclude?

See video linked to website

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