

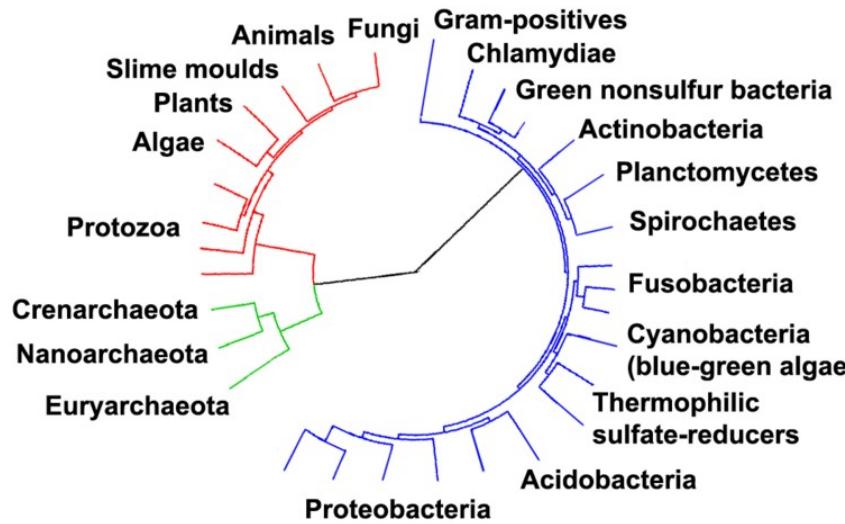
BACTERIA AND ARCHAEA

Phylogeny

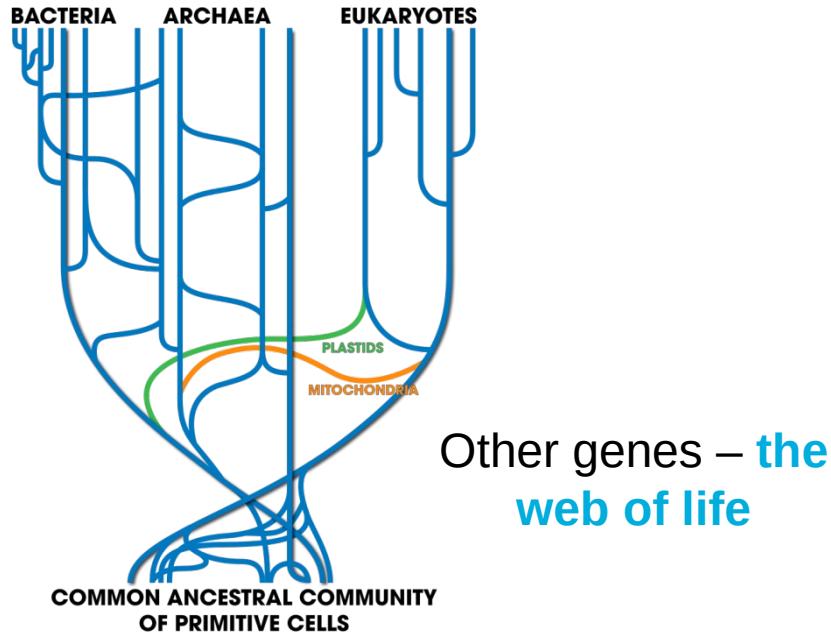
Systematics of Bacteria and Archaea

- Classical approach:
 - based on morphology and biochemistry, which change fast during evolution
 - restricted to cultivated species
- DNA-based approach:
 - no need to cultivate; DNA, isolated from the environment can be used – metagenomics
 - usually rRNA genes are used
 - fewer problems with parallel evolution and trait loss
 - but horizontal gene transfer makes things complicated and challenges the very concept of a tree

Vertical vs horizontal inheritance



Genes involved in replication,
transcription, translation – **the
tree of life**

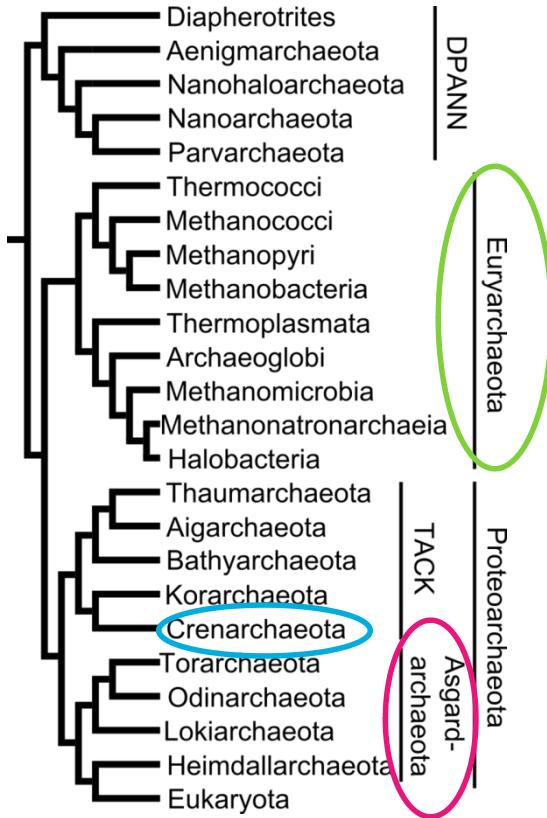


By Andrew Z. Colvin - Barth F. Smets, Ph.D., with permission, CC BY-SA 4.0, <https://commons.wikimedia.org/w/index.php?curid=69411999>

Bacterial phyla (some examples)

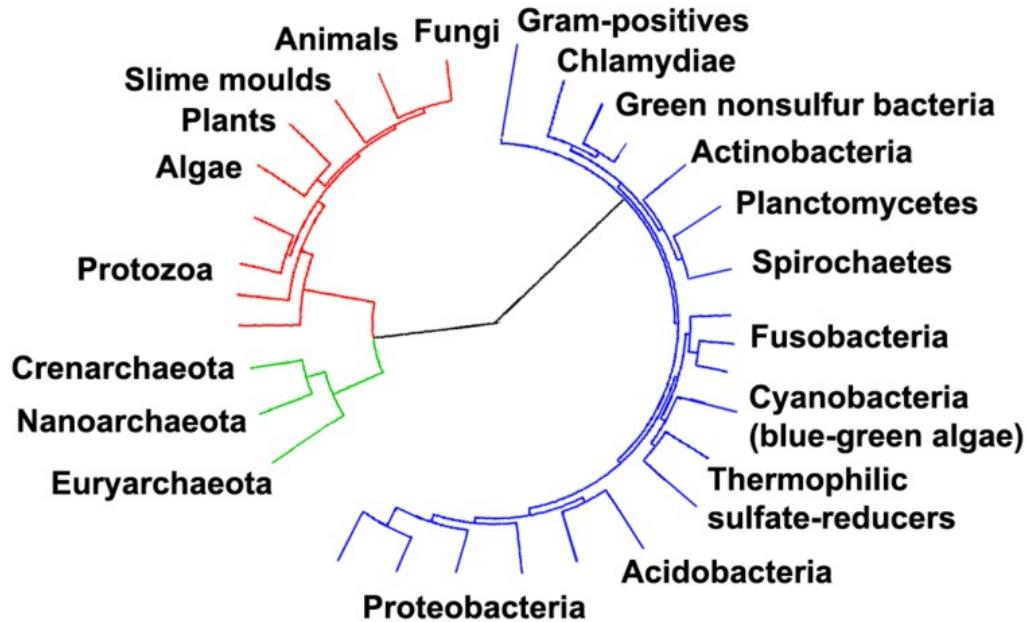
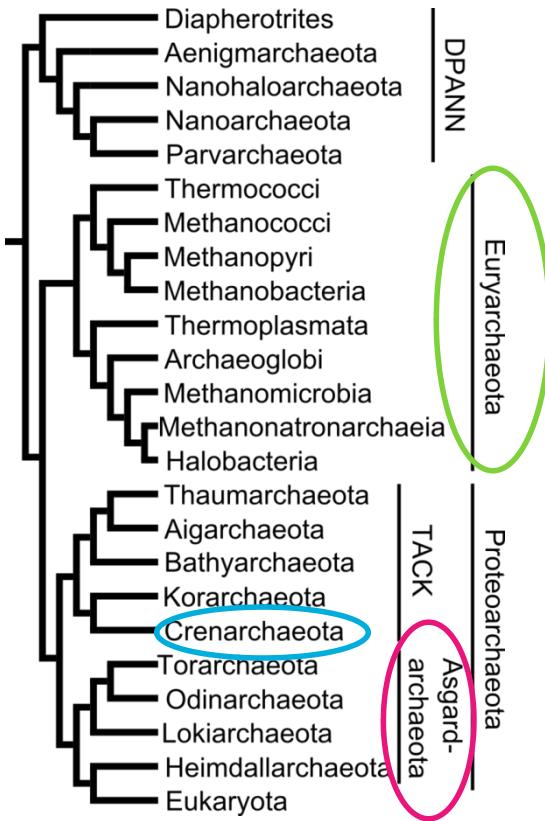
- **Cyanobacteria**
- **Proteobacteria** (incl. *Escherichia coli*, *Vibrio cholerae*, *Yersinia pestis*, *Helicobacter pilori*)
- **Spirochetes** (*Borrelia burgdorferi*, *Treponema pallidum*)
- **Firmicutes** (1 of 2 Gram+, incl. *Staphylococcus*, *Streptococcus*, *Bacillus*, *Clostridium*)
- **Actinobacteria** (2nd Gram+ group, incl. *Mycobacterium tuberculosis*, *M. leprae*, *Streptomyces*)

Archaea phyla



- **Euryarchaeota** – widespread, incl. methanogens
- **Crenarchaeota** – widespread, incl. thermophiles
- **Asgardarchaeota** – deserved a lot of attention

Archaea phyla



B&A: key points

- Morphologically “simple”, but highly adapted to their environment, e.g. by biochemical adaptations > enormous phenotypic diversity
- Phylogenetically highly diverged – old MRCA
- HGT – the concept of the web of life
- Important for understanding the origin of life and the origin of Eukaryotes

EUKARYOTES

Evolution and the Natural World

Lecture 9

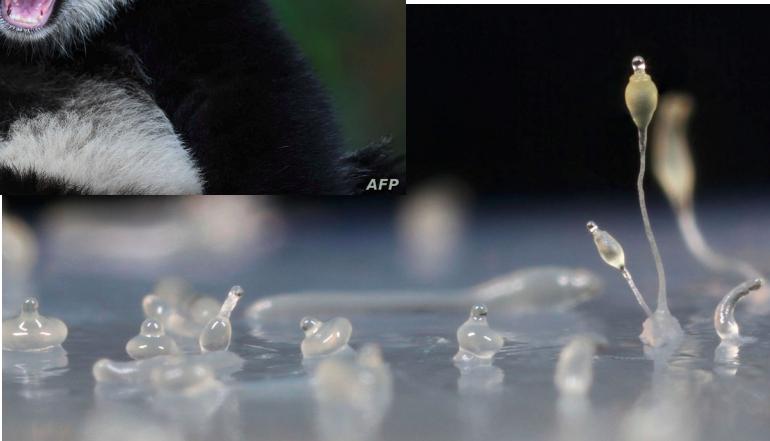
07/10/2021

Vasili Pankratov (vasili.pankratov@ut.ee)

EUKARYOTES

Common features

Diversity of Eukaryotes



- Morphological diversity of eukaryotes is very high
- However the evolutionary diversity (age of the MRCA) is lower than in prokaryotes

<https://en.wikipedia.org/wiki/Dictyostelid>

Eukaryotic cells

C

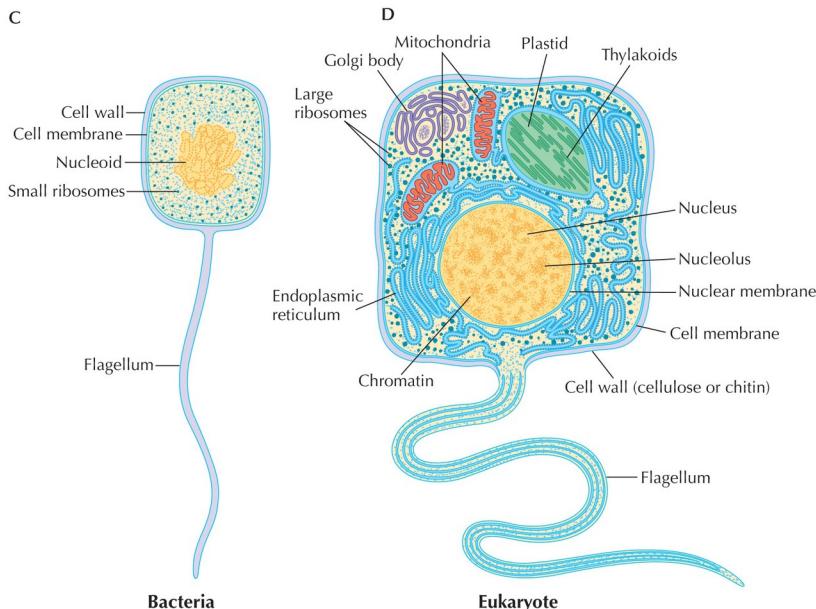


FIGURE 8.1. Bacterial vs. eukaryotic cell (not drawn to scale). (A) Photo of a bacterial cell. (B) Photo of a eukaryotic cell. (C) Diagram of a bacterial cell. (D) Diagram of the main features of eukaryotic cells. Note that both diagrams are composites; not all bacteria or eukaryotes have all such features.

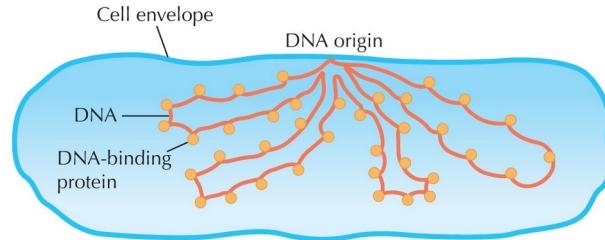
8.1C,D, adapted from Madigan M.T. et al., *Brock Biology of Microorganisms*, 9e, © 2000 Prentice Hall

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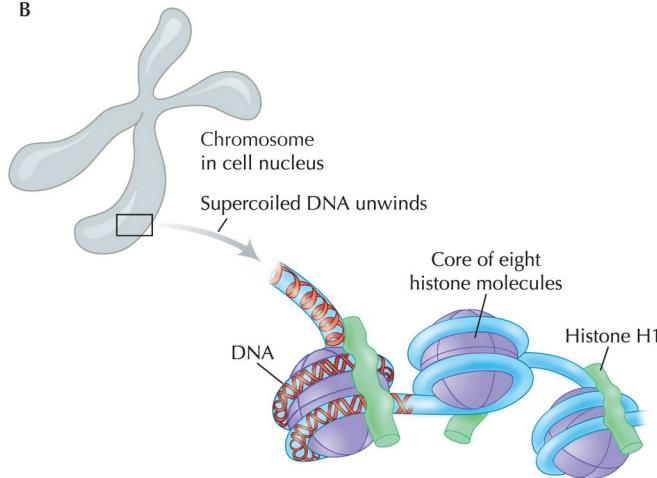
- Membrane-bound nucleus containing most of the DNA
- Mitochondria
- A system of endomembranes: endoplasmic reticulum, Golgi apparatus, lysosomes, peroxisomes
- Complex cytoskeleton (cell shape, movement, flagella, endocytosis)
- Ribosomes are homologous to those of bacteria but are different in size and structure

Eukaryotic DNA

A



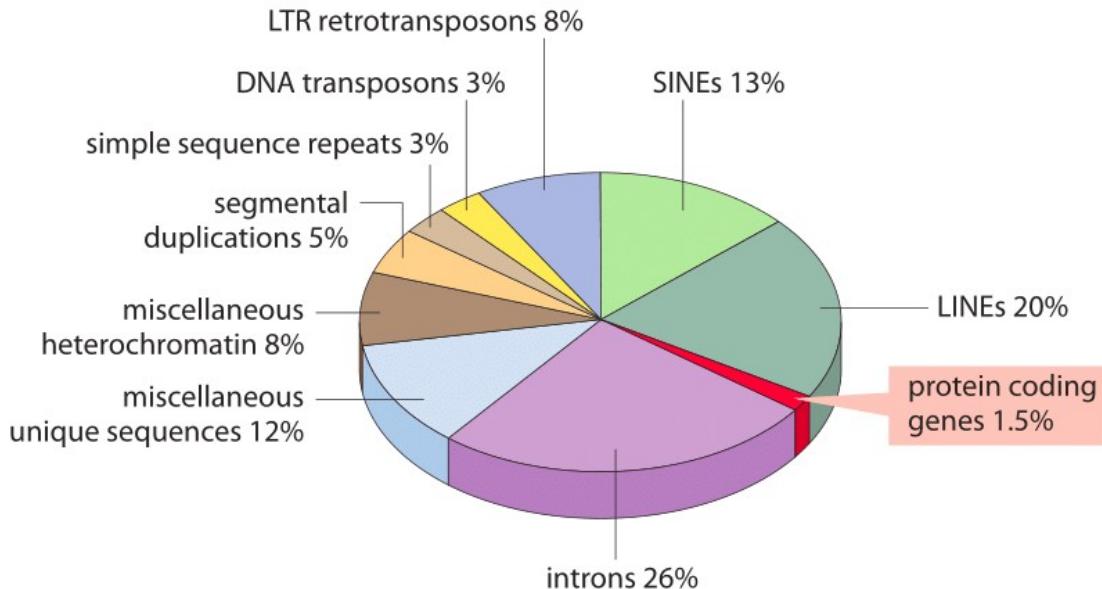
B



- Eukaryotic DNA is associated with proteins (especially histones) = **chromatin**
- Eukaryotic DNA can get very compacted (during cell division) or more relaxed (during gene expression)
- Archaea have histones homologs while bacteria have unrelated DNA-binding proteins

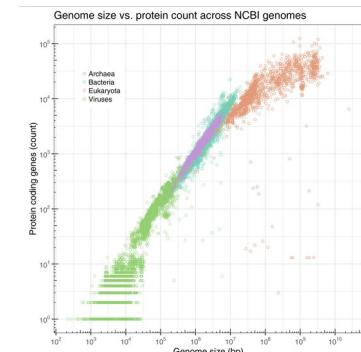
Eukaryotic genomes

main components of the human genome

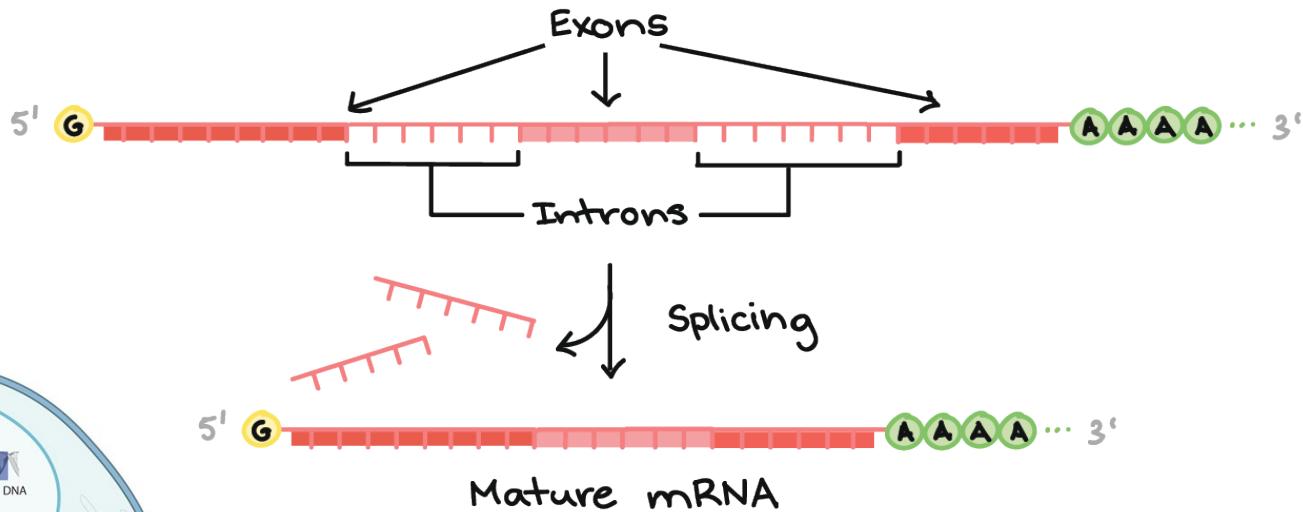
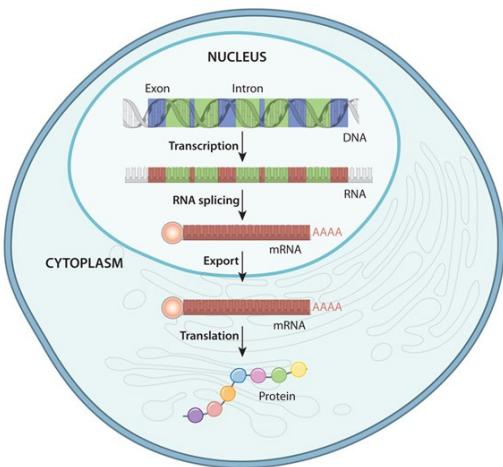


<http://book.bionumbers.org/how-many-genes-are-in-a-genome/>

- Extremely variable in size
- A lot of the DNA doesn't code for proteins



Introns



There are different types of introns which differ in the mechanism of splicing – spliceosomal are the ones found in nuclear genes of Eukaryotes

Eukaryotic genes

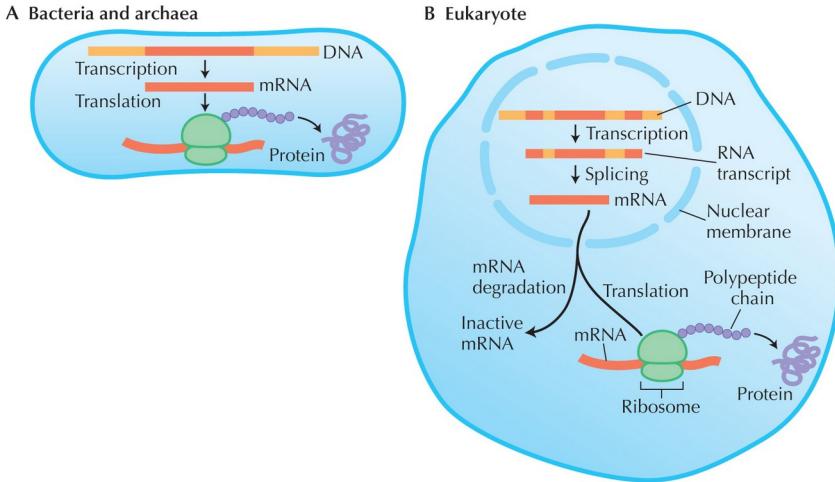
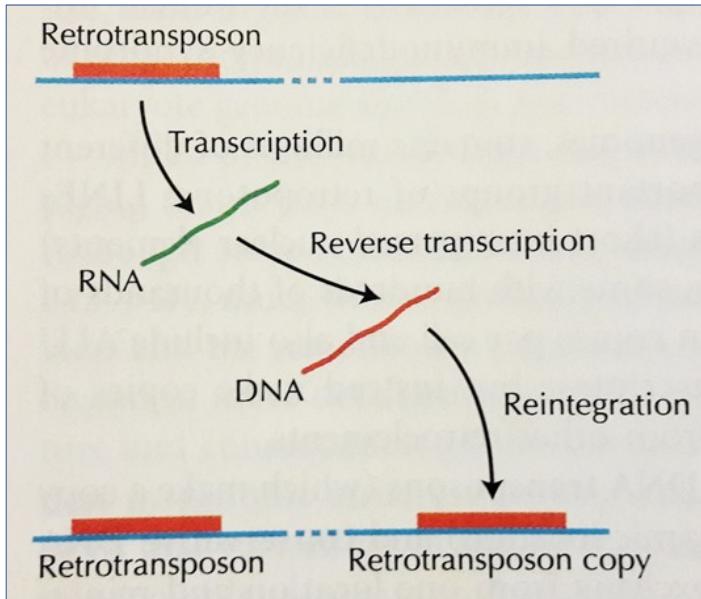


FIGURE 8.3. Eukaryotic vs. bacterial and archaeal transcription and translation. (A) In bacteria and archaea, transcription and translation happen in the same location in the cell and are frequently coupled to each other with translation occurring while an RNA is still being made. (B) In eukaryotes, transcription and splicing occur in the nucleus and then RNA is exported out of the nucleus where translation occurs. Coding regions are in red.

- In eukaryotes transcription happens in the nucleus while translation takes place in the cytoplasm
- Most eukaryotic genes have introns which are spliced out before the mRNA leaves the nucleus

Transposable elements



Element Type	Autonomy	Structure	Length	Copy Number	Fraction of Genome
LINEs	Autonomous	ORF1 ORF2 (pol) AAA	6–8 kb	850,000	21%
SINEs	Nonautonomous	AB AAA	100–300 kb	1,500,000	13%
Retrovirus-like elements	Autonomous	gag pol (env)	6–11 kb	450,000	8%
	Nonautonomous	(gag)	1.5–3 kb		
DNA transposons	Autonomous	Transposase	2–3 kb	300,000	3%
	Nonautonomous	— H —	80–3000 bp		

FIGURE 8.19. Examples of the more abundant repetitive sequences (all of which are some form of transposon) found in the human genome. These can be classified by the type of element and whether they are autonomous (encode the means of transposition) or nonautonomous (depend on exogenous factors for transposition). Shown are four types of elements, their general structure, length, copy number, and fraction of the genome they represent. The first three listed, LINEs, SINEs, and retrovirus-like elements, are forms of retroelements that transpose through an RNA intermediate. LINEs and SINEs are related forms of retroposons; LINEs are autonomous (encoding a pol protein) and SINEs are nonautonomous. Retrovirus-like elements, which include retrotransposons, have long terminal repeats at each end (shown in blue) with autonomous elements encoding a pol protein. DNA transposons are frequently flanked by inverted repeats (small triangles) with autonomous elements encoding a transposase protein.

8.19, redrawn from International Human Genome Sequencing Consortium, *Nature* **409**: 860–921, © 2001 Macmillan, www.nature.com

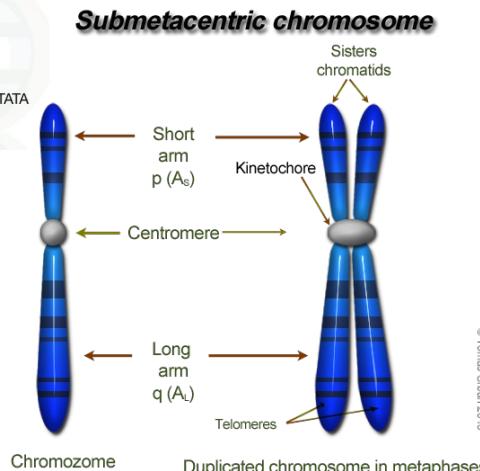
Tandem repeats

Short Tandem Repeats

AGACAGACAGACAGACAGACAGACAGACATT CGCGTAC GCGCTTTATA
Short sequence of "AGAC"
© Genetic Education Inc.

AGACAGACAGACAGACAGACAGACAGACAGACATT CGCGTAC GCGCTTTATA
Located one after another, tandem repeats

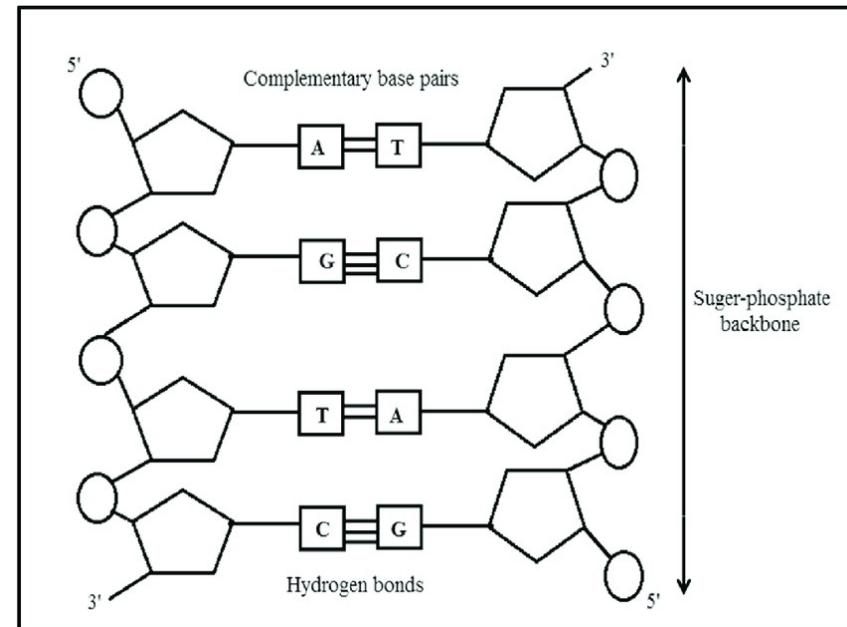
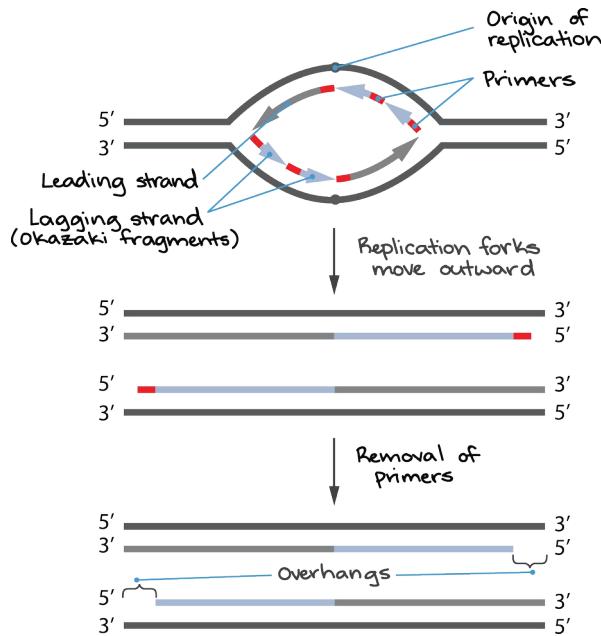
AGAOAGAOAGACAGACAGACAGACAGACATT CGCGTAC GCGCTTTATA
Repeatedly present in the sequence



- **SATELLITE DNA:** repeats of 100-1000 bp in lengths. It is very abundant especially in centromeric regions and in heterochromatin
- **MINISATELLITES:** repeats of 10-100 bp
- **MICROSATELLITES:** repeats of 2-10 bp. Also called STR (Short Tandem Repeats)

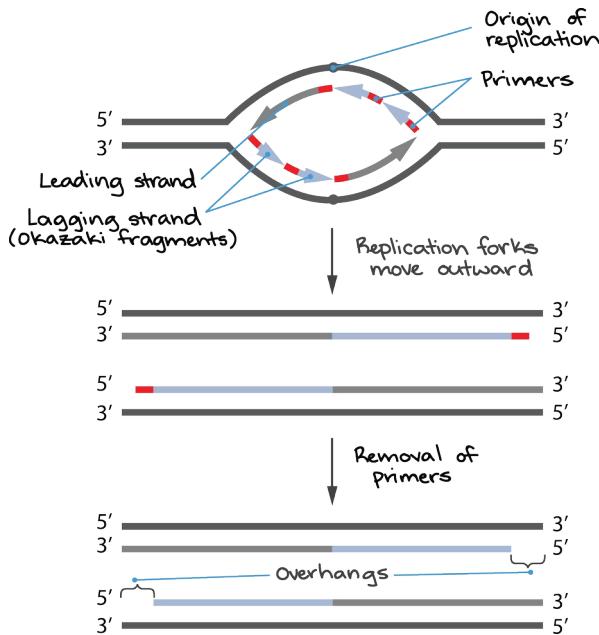
Telomeres

The lagging strand cannot be replicated to the end of the chromosome.

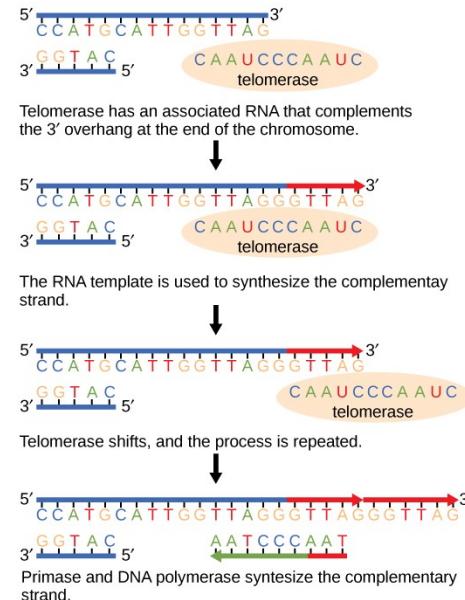


Telomeres

The lagging strand cannot be replicated to the end of the chromosome.



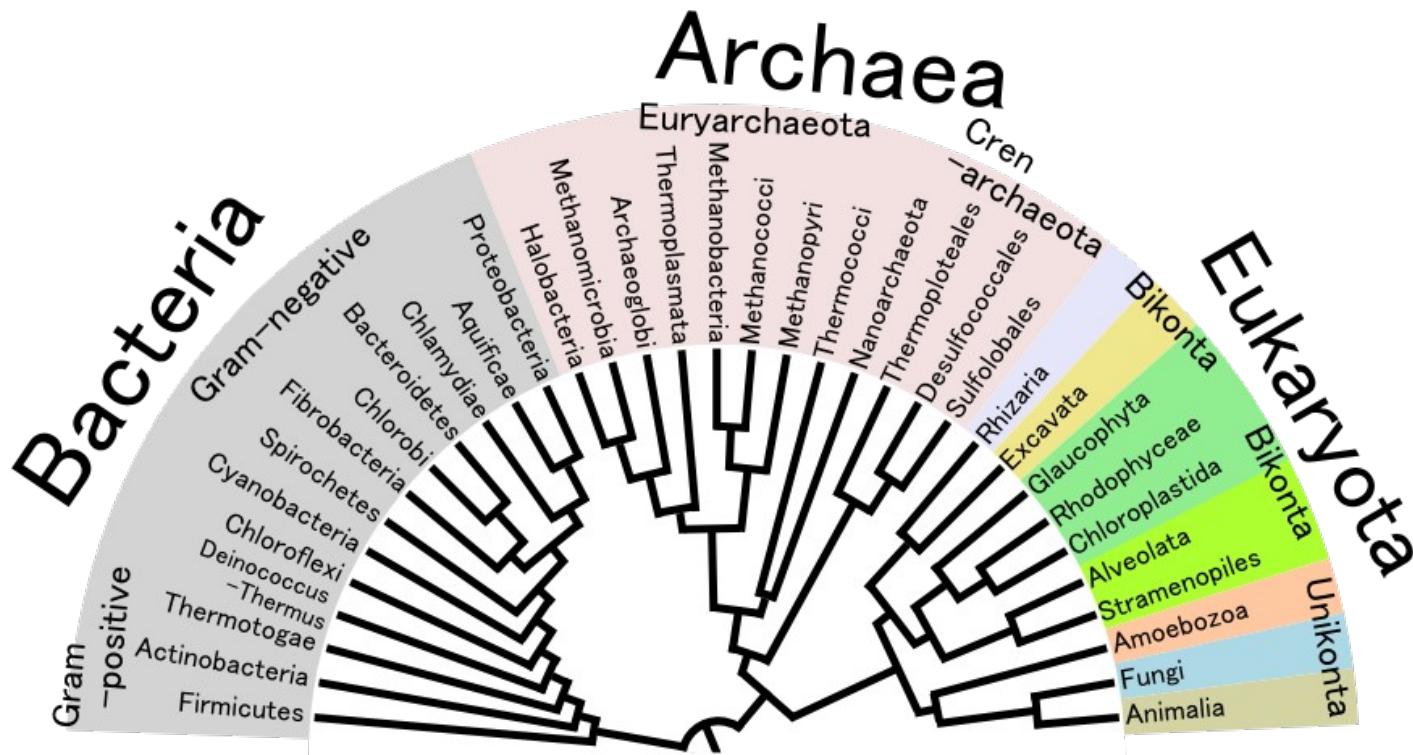
Telomeres are shortened with every cell division + they can be re-synthesized in some cells



EUKARYOTES

Origin

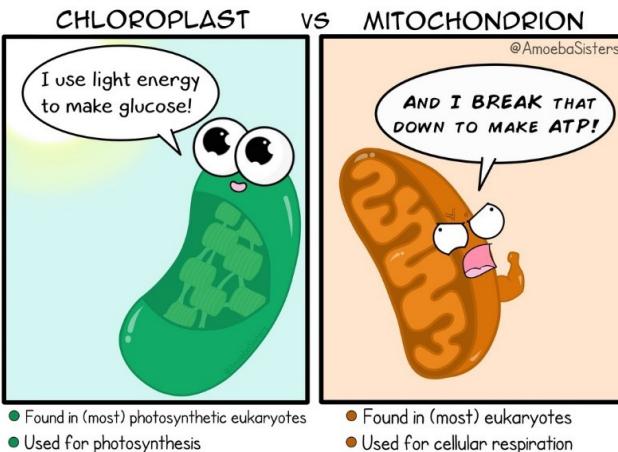
Relationship to Bacteria and Archaea



Relationship to Bacteria and Archaea

Similarities to Archaea	Similarities to Bacteria	Unique features
Enzymes involved in replication, transcription and translation	Enzymes involved in metabolism	Nucleus
Cytoskeleton	Cellular membranes	Various organelles
Histones		Complex cytoskeleton

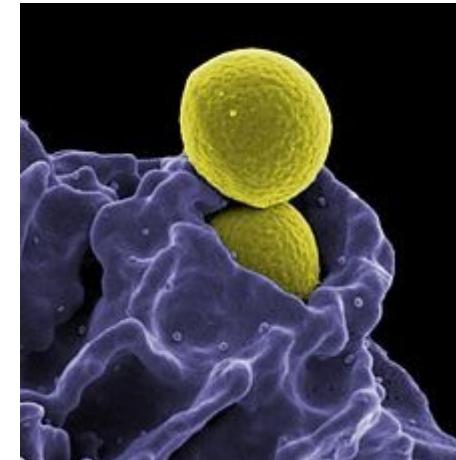
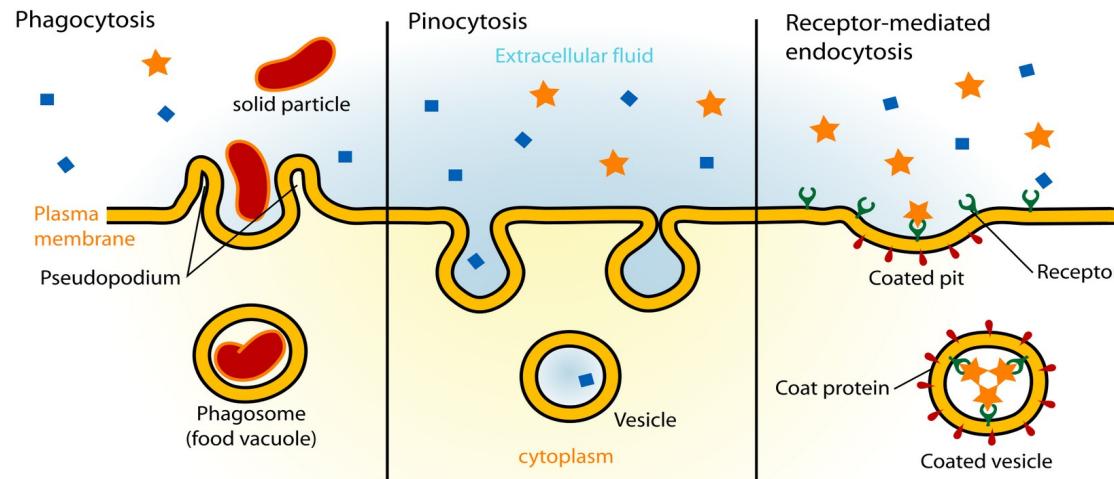
Mitochondria (mt) and plastids (pl) are derived from bacteria as a result of an endosymbiosis event



- At least 2 membranes like in Gram-negative bacteria
- Circular DNA
- Transcription and translation similar to that in bacteria
- Reproduce by simple division
- Enzymes and other components involved in respiration/photosynthesis in mt/pl are similar to that of α -proteobacteria / cyanobacteria
- α -proteobacteria include intracellular parasites

Endocytosis

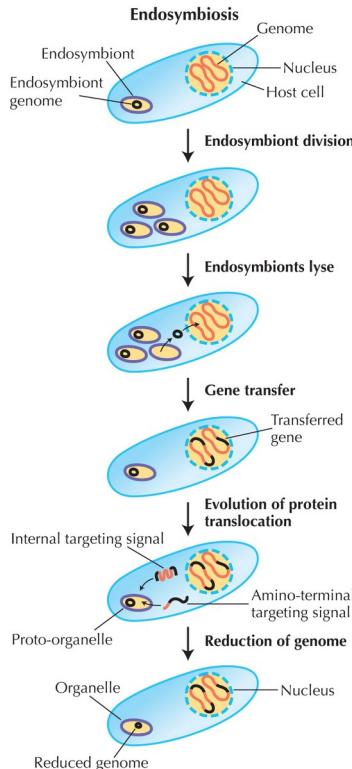
Endocytosis



<https://www.biomadam.com/difference-between-phagocytosis-and-pinocytosis>

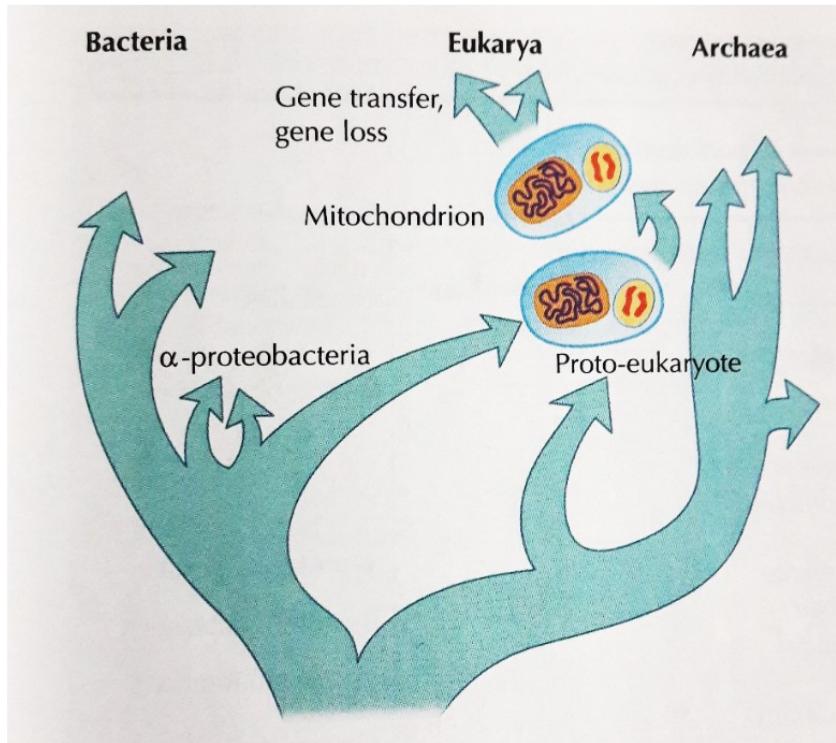
File: Methicillin-resistant *Staphylococcus aureus* (MRSA) Ingestion by a Neutrophil (6830921049).jpg

Gene transfer from mt and pl to the nucleus



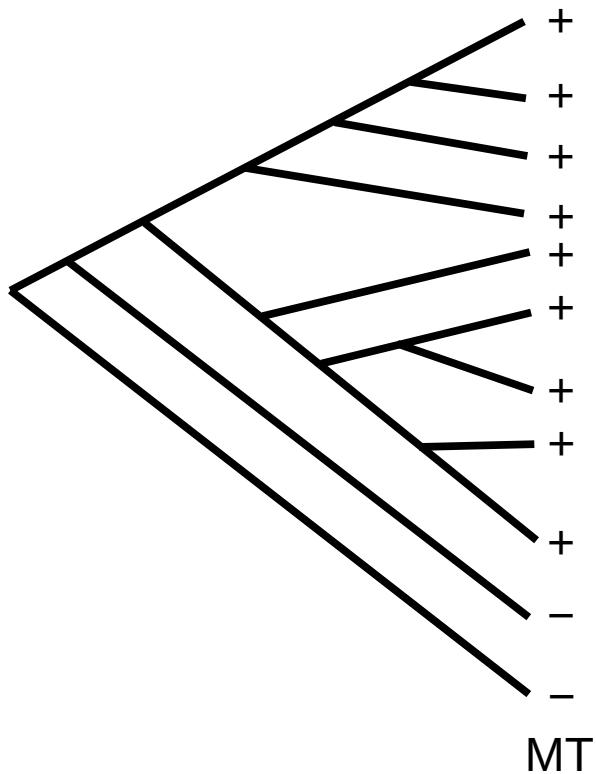
- Mt and pl genomes are small (only 38 genes in human mtDNA)
- Many proteins needed by mt and pl are encoded by the nucleus and transferred to mt and cp
- Some parts of the nuclear genome have homologs in the mt genome
- We believe that many of the genes of the endosymbiont got incorporated into the host's nuclear genome

Mitochondria



- All mt come from one endosymbiosis event between an archaeon and an alpha-proteobacterium
- This happened during early evolution of eukaryotes
- What was the role of this event in the evolution of eukaryotes?

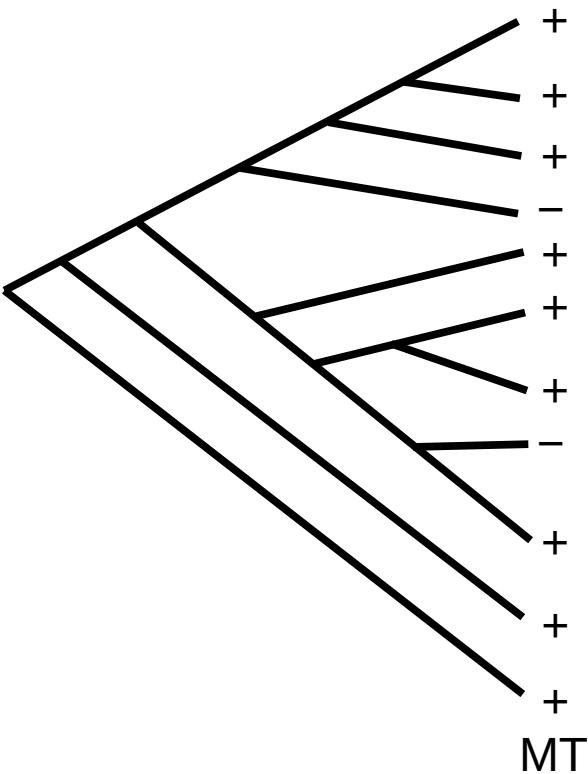
Not all eukaryotes have mitochondria



Old view:

- Eukaryotes without mitochondria are the most diverged from the rest
- This supports the idea that mt were acquired after other traits of eukaryotes (like the nucleus)

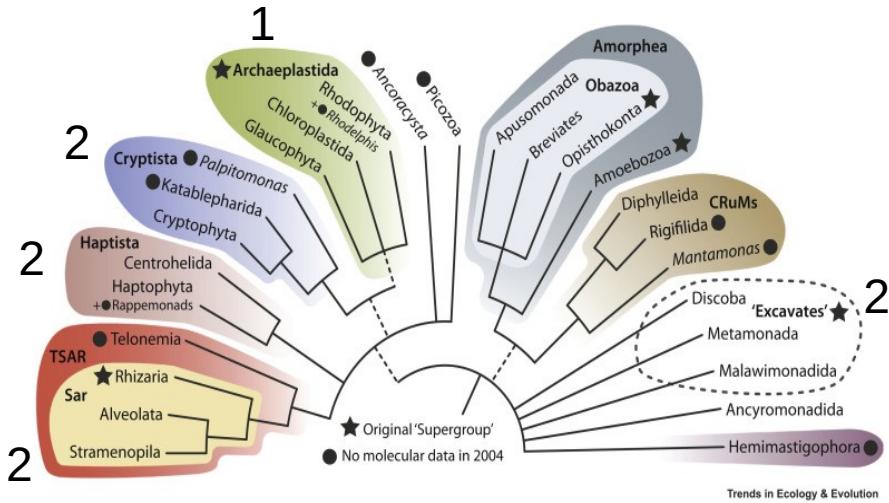
Not all eukaryotes have mitochondria



Current view:

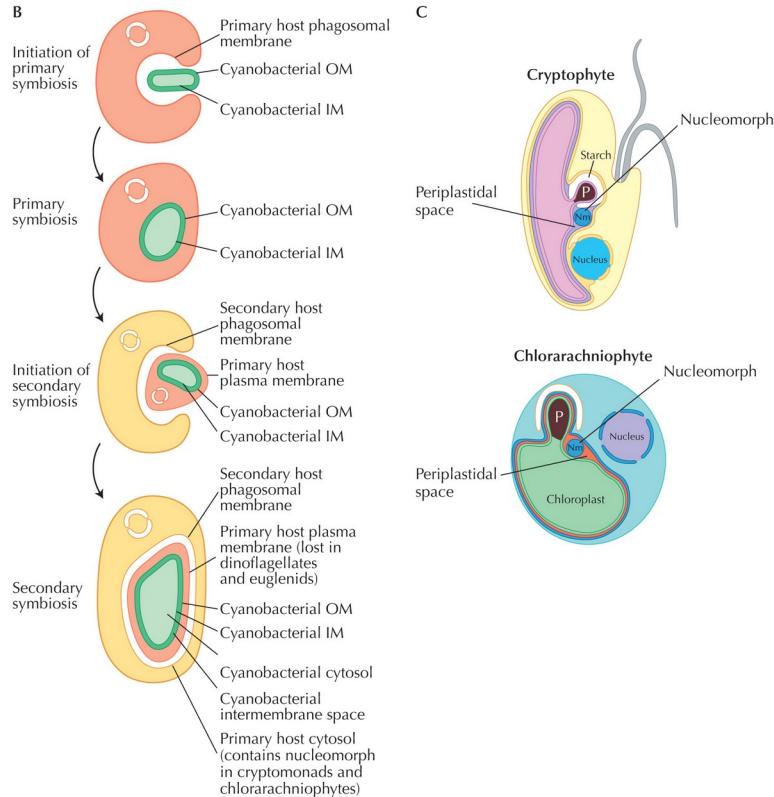
- Those species are not close to the root
- They are mostly parasites and/or anaerobes
- All of such species have mitochondrial genes in their nuclear genomes
- Some have organelles similar to mt in structure (hydrogenosomes in *Trichomonas*; mitosomes in *Microsporidia*, *Giardia* and *Entamoeba*)
- *Monocercomonoides* → only known eukaryote with no mitochondria or derived organelles still has mt genes in the nuclear genome

Plastids



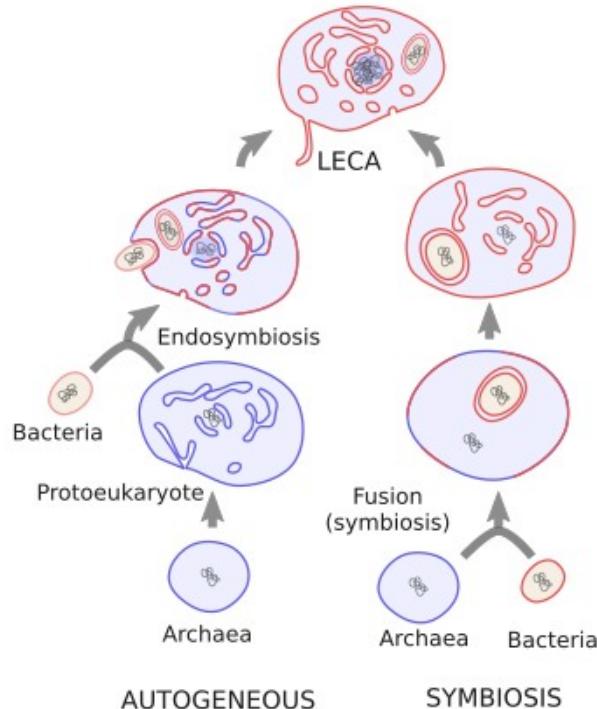
- Primary plastids (1) have 2 membranes; are found in land plants, green and red algae; originate from cyanobacteria and were acquired once
- Secondary plastids (2) often have more than 2 membranes and a nucleomorph – remnant of a nucleus; some come from the green algae, others from red algae; are found in different groups of eukaryotes – several symbiosis events;

Plastids



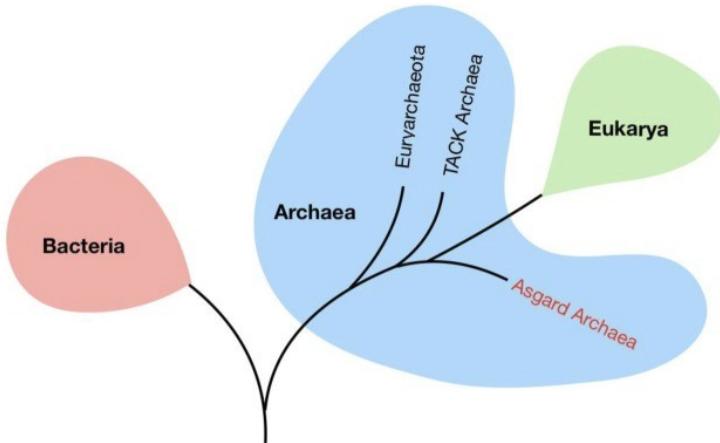
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Origin of eukaryotes



- Modern eukaryotes are a result of symbiosis between an archaeon and an alpha-proteobacterium and eukaryotic genomes have genes from both sources
- How complex was the archaeon and if it had some eukaryotic traits before the symbiosis is unknown
- Symbiosis with cyanobacteria happened later and only in one lineage

Origin of eukaryotes



- It seems that some groups of Archaea are closer to Eukaryotes than others
- But those groups are described using the metagenomics approach and we know very little about their morphology and life style
- If you find this interesting here is a read for you:
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7015854/>

<https://mmegias.webs.uvigo.es/02-english/5-celulas/1-origen-eucariotas.php>

Origin of the nucleus

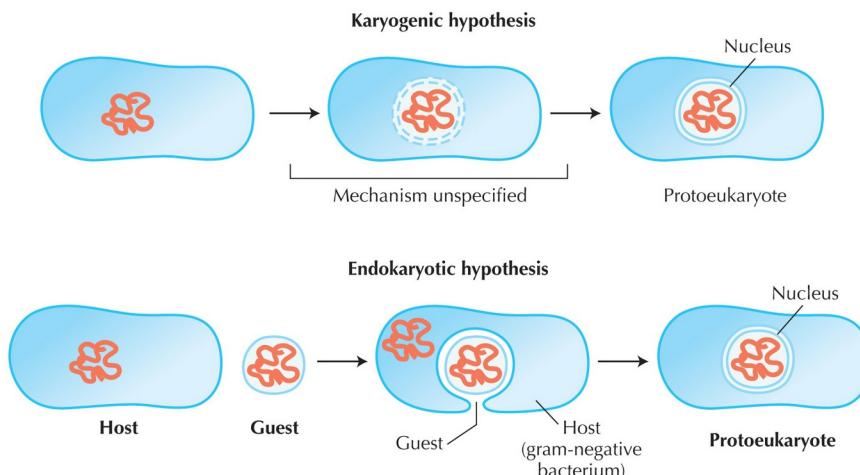


FIGURE 8.16. Origin of nucleus.

8.16, modified from Lake J.A. et al., *Proc. Natl. Acad. Sci.* **91**: 2880–2881, © 1994 National Academy of Sciences, U.S.A.

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- Nuclear membrane is closely related to the endoplasmic reticulum
- Chemically eukaryotic membranes are similar to the bacterial ones
- The nuclear genome has both archaeal and bacterial genes

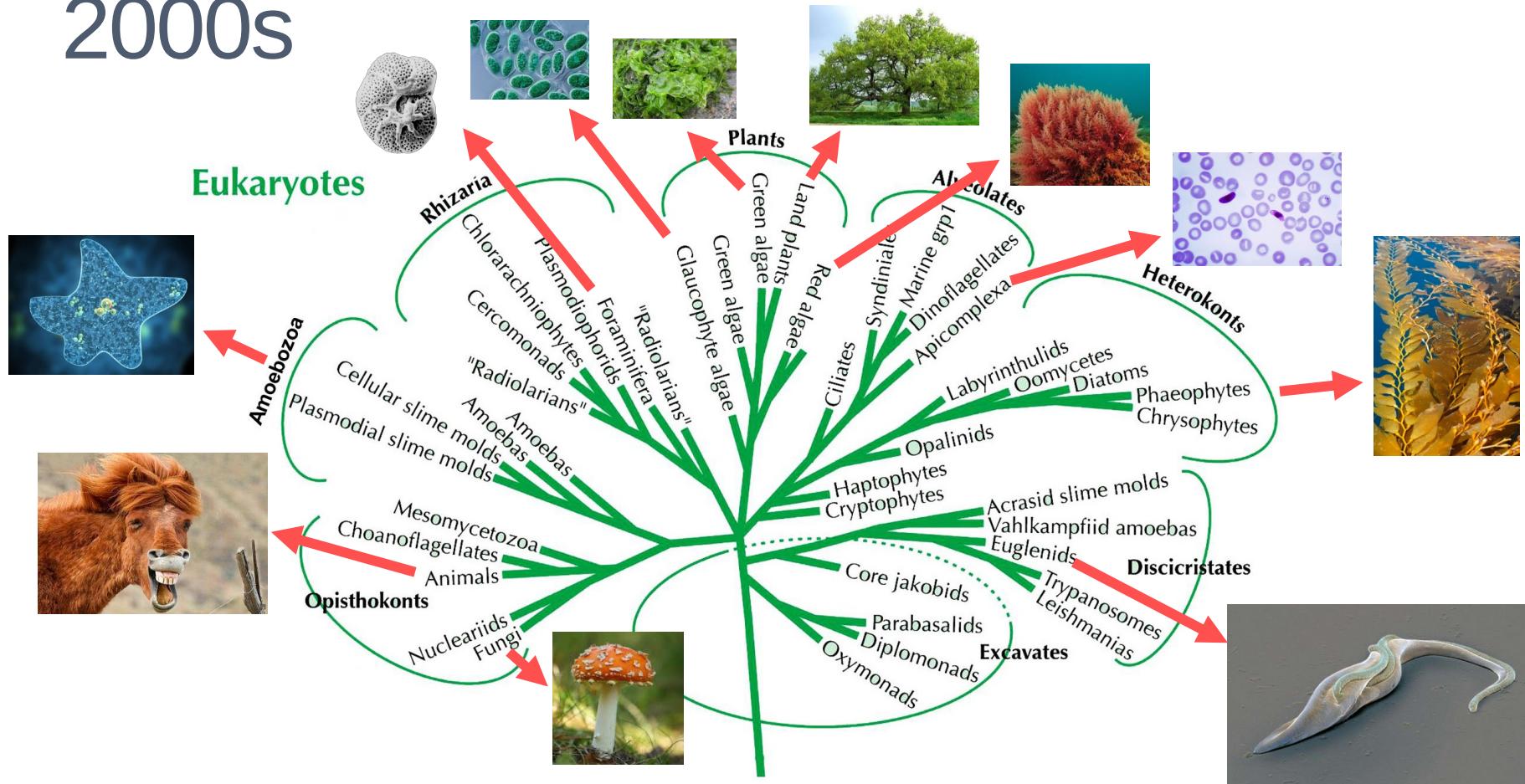
EUKARYOTES

Diversity

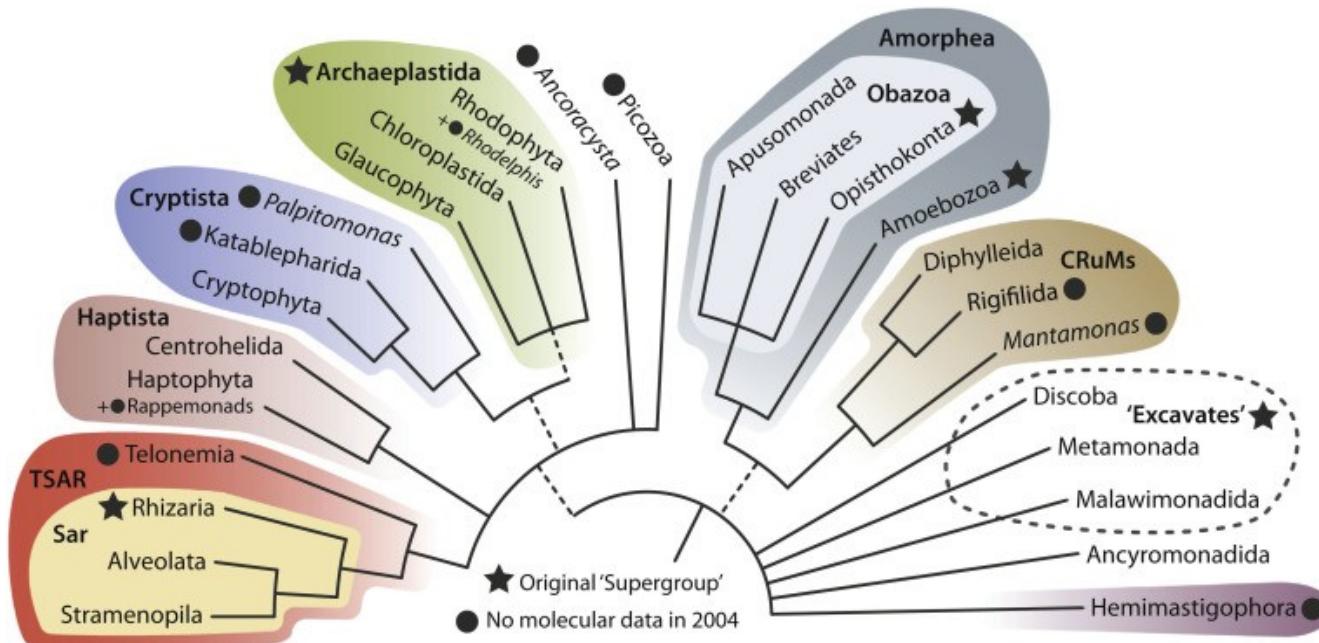
Early views

- Plants, Animals and Fungi (with all 3 groups having unicellular species)
- Plants, Animals, Fungi and Protists

2000s



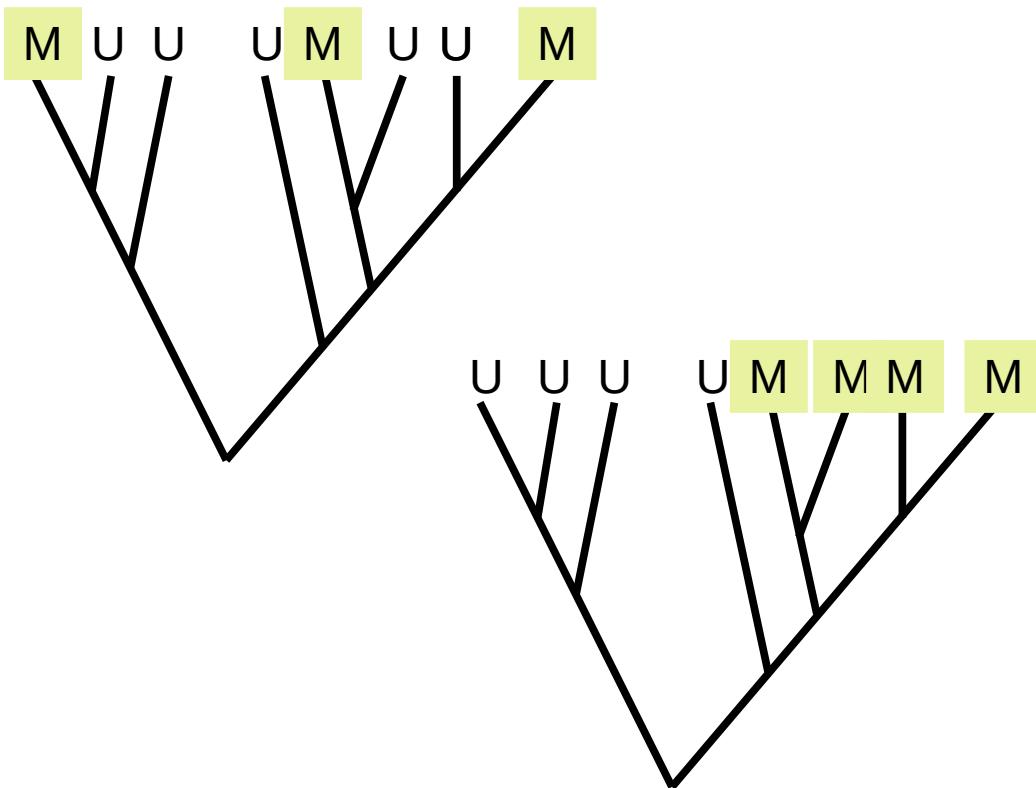
Modern view



Trends in Ecology & Evolution

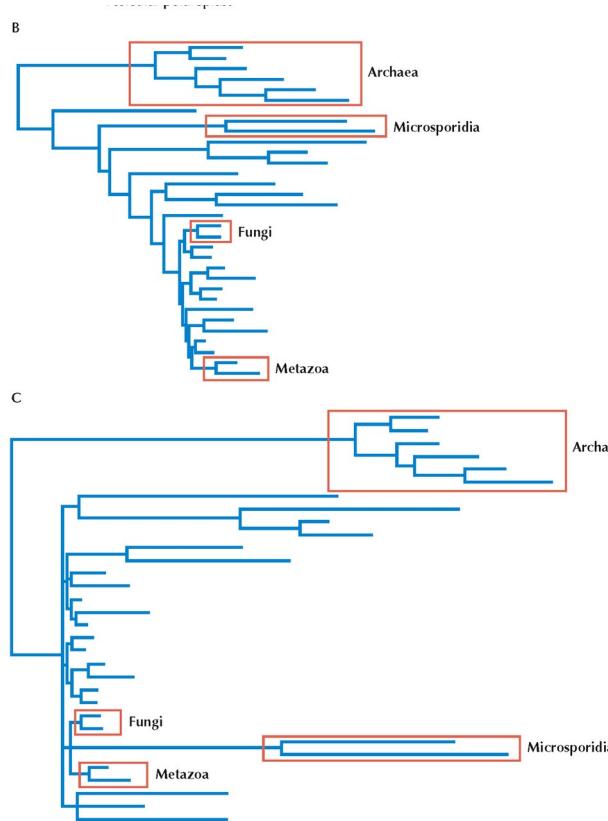
[https://www.cell.com/trends/ecology-evolution/fulltext/S0169-5347\(19\)30257-5](https://www.cell.com/trends/ecology-evolution/fulltext/S0169-5347(19)30257-5)

Why is reconstructing phylogenies important?

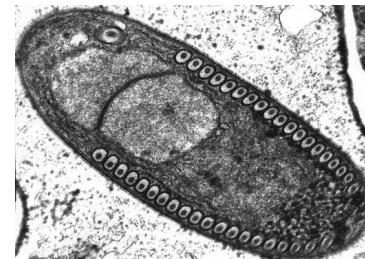


Knowing the phylogeny
one can understand
evolution of traits =
phylogenetic
reconstructions

Why is reconstructing phylogenies important?



Microsporidia shown to be related to fungi and hence can be treated with anti-fungal drugs



Summary

- Modern Eukaryotes have both unique traits and traits shared with Bacteria and Archaea
- Endosymbiosis between an Archaeal host and an alpha-proteobacterium happened early during Eukaryotic evolution and could have been the trigger for «eukaryotization»
- Eukaryotes have genomes with a lot of different types of sequences that don't code for proteins
- The early evolution and diversification of eukaryotes is complex making it hard to reconstruct the deep topology
- Unicellular eukaryotes make for the major part of their evolutionary diversity