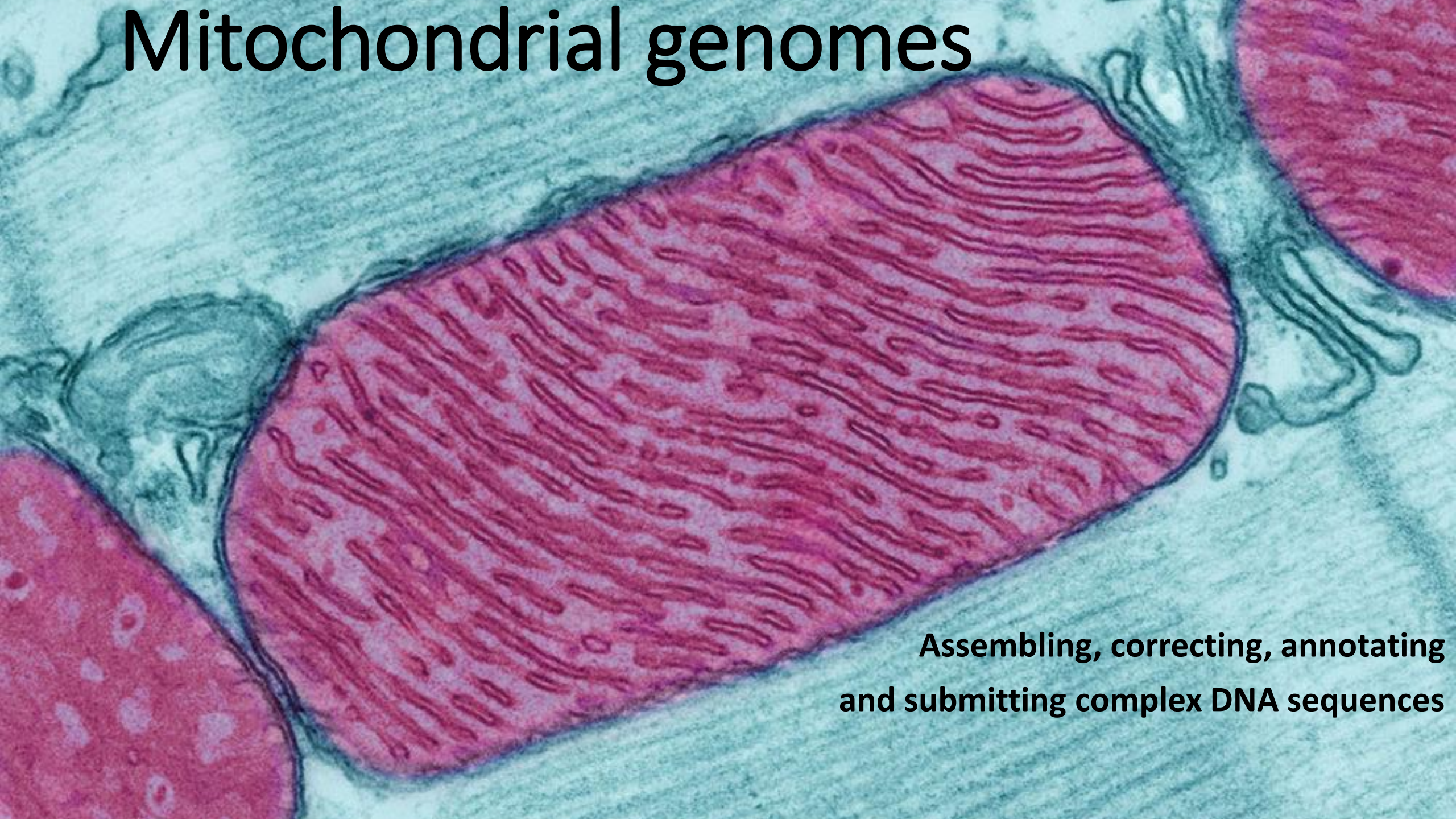
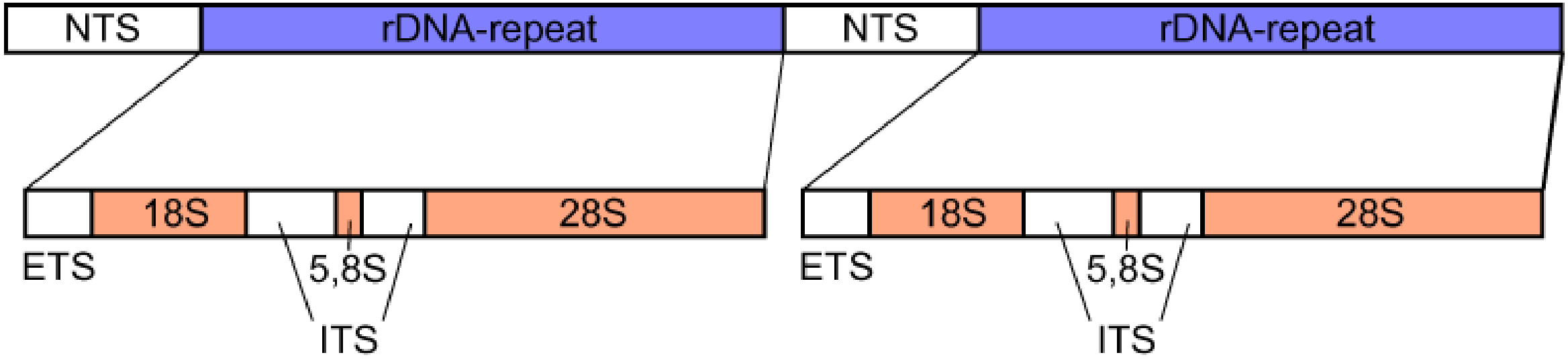
# Mitochondrial genomes



**Assembling, correcting, annotating and submitting complex DNA sequences**

# Finishing up nuclear rDNA

- Finish up correcting errors, annotating, and submitting this week
- In addition to normal office hours, Kyle will  help after 2pm Thursday
- I can help Wednesday morning as well



> Current Issue > vol. 109 no. 16 > Conrad L. Schoch, 6241–6246, doi: 10.1073/pnas.1117018109



# Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for *Fungi*

Conrad L. Schoch[a,1], Keith A. Seifert[b,1], Sabine Huhndorf[c], Vincent Robert[d], John L. Spouge[a], C. André Levesque[b], Wen Chen[b], and Fungal Barcoding Consortium[a,2]

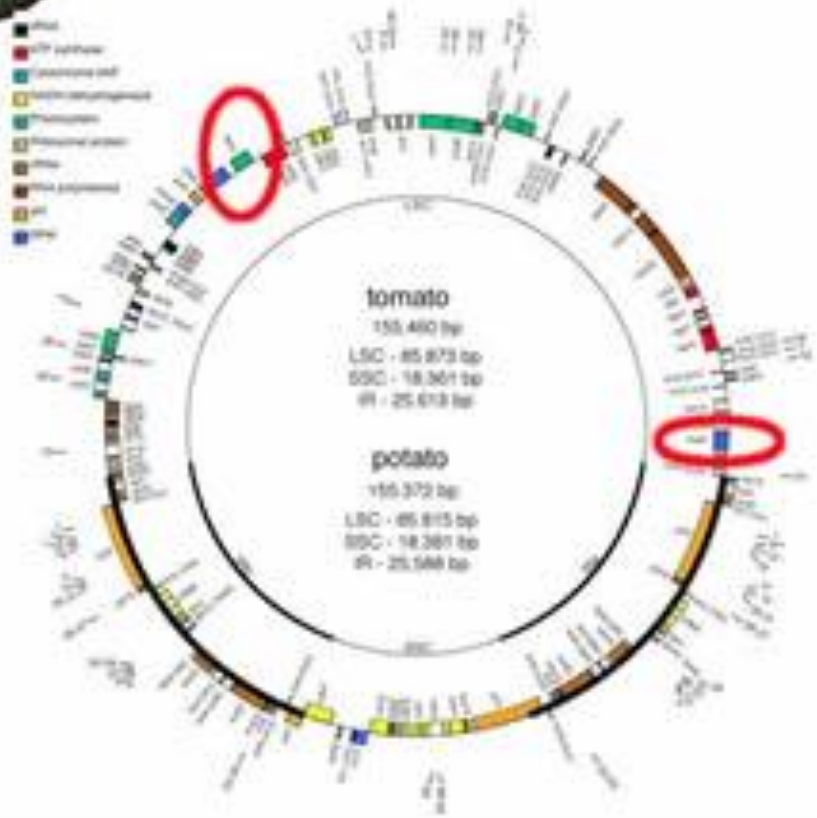
Author Affiliations

Edited* by Daniel H. Janzen, University of Pennsylvania, Philadelphia, PA, and approved February 24, 2012 (received for review October 18, 2011)

# Why DNA barcoding works: genes with the right number of differences

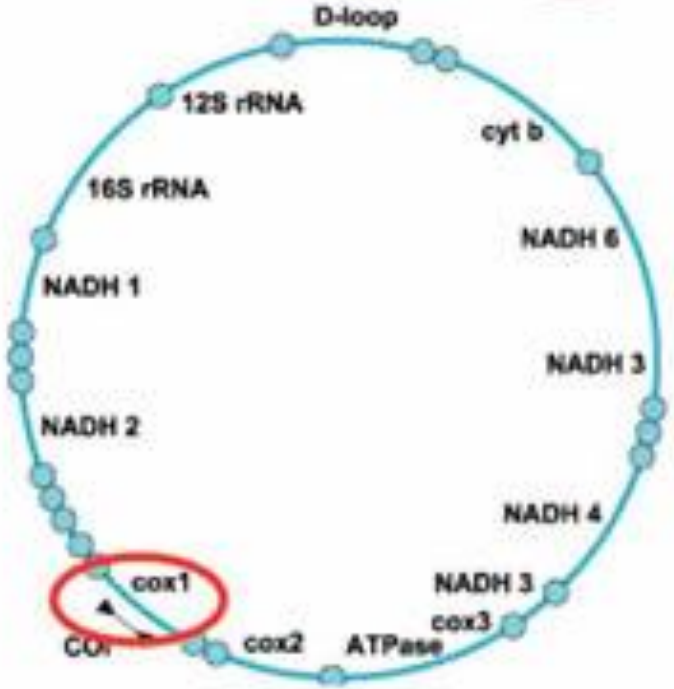
## CHLOROPLAST

rbcL




## MITOCHONDRION

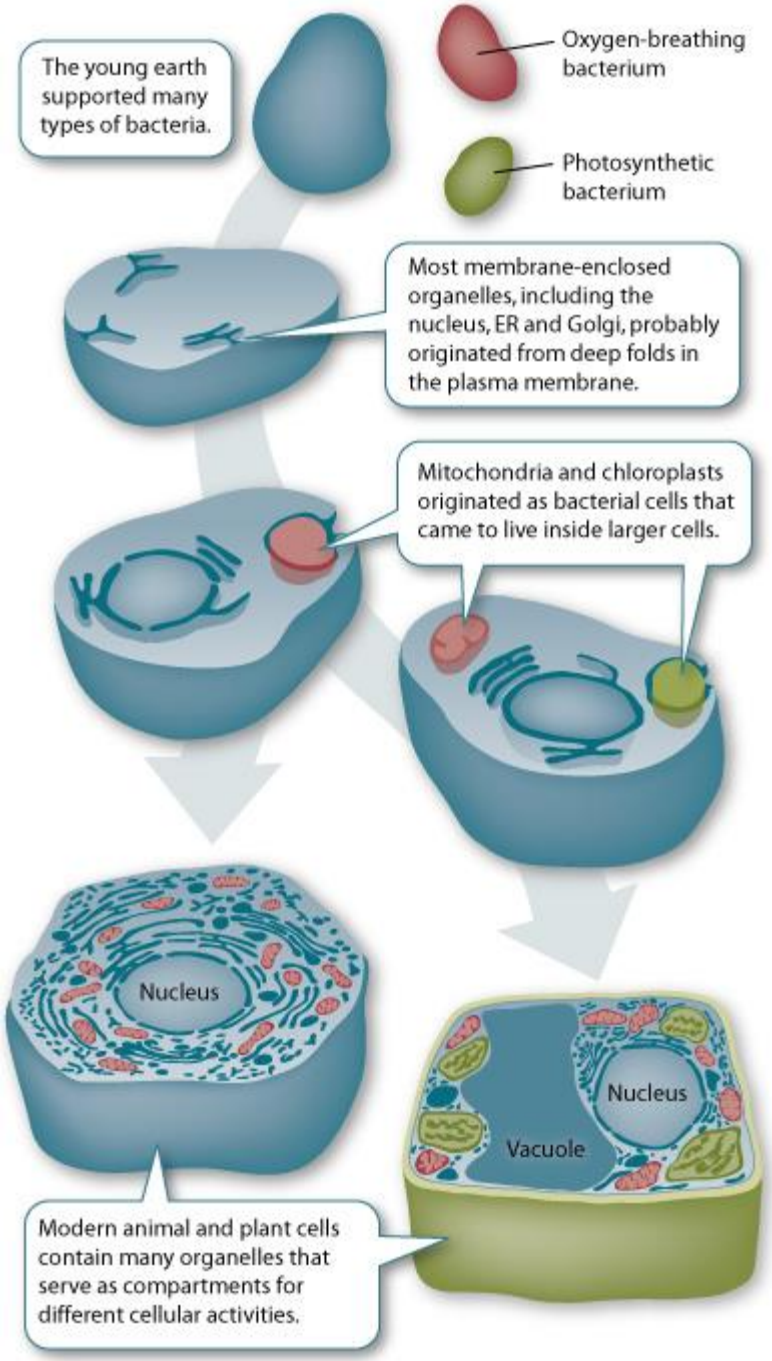
COX1



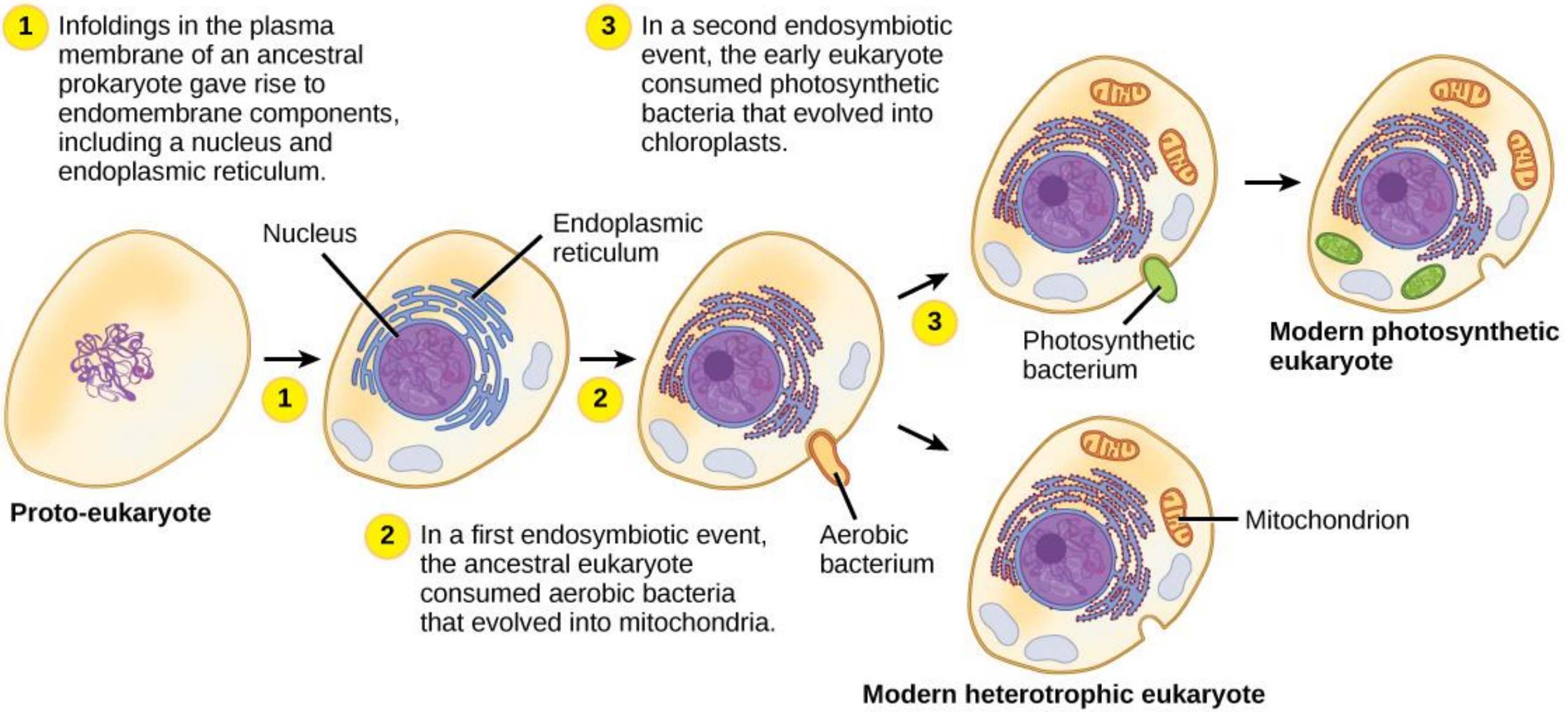
# organelles

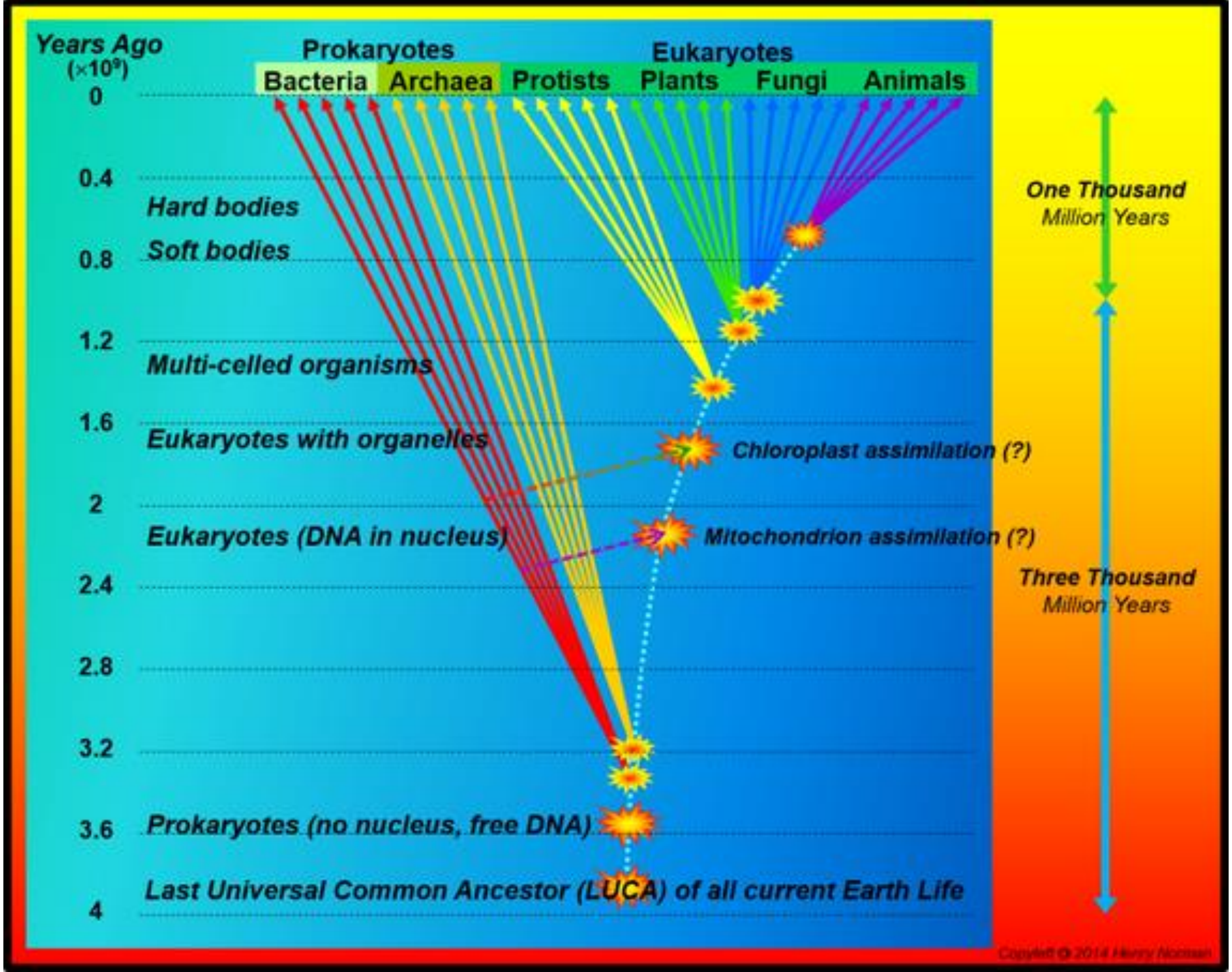
# Origins

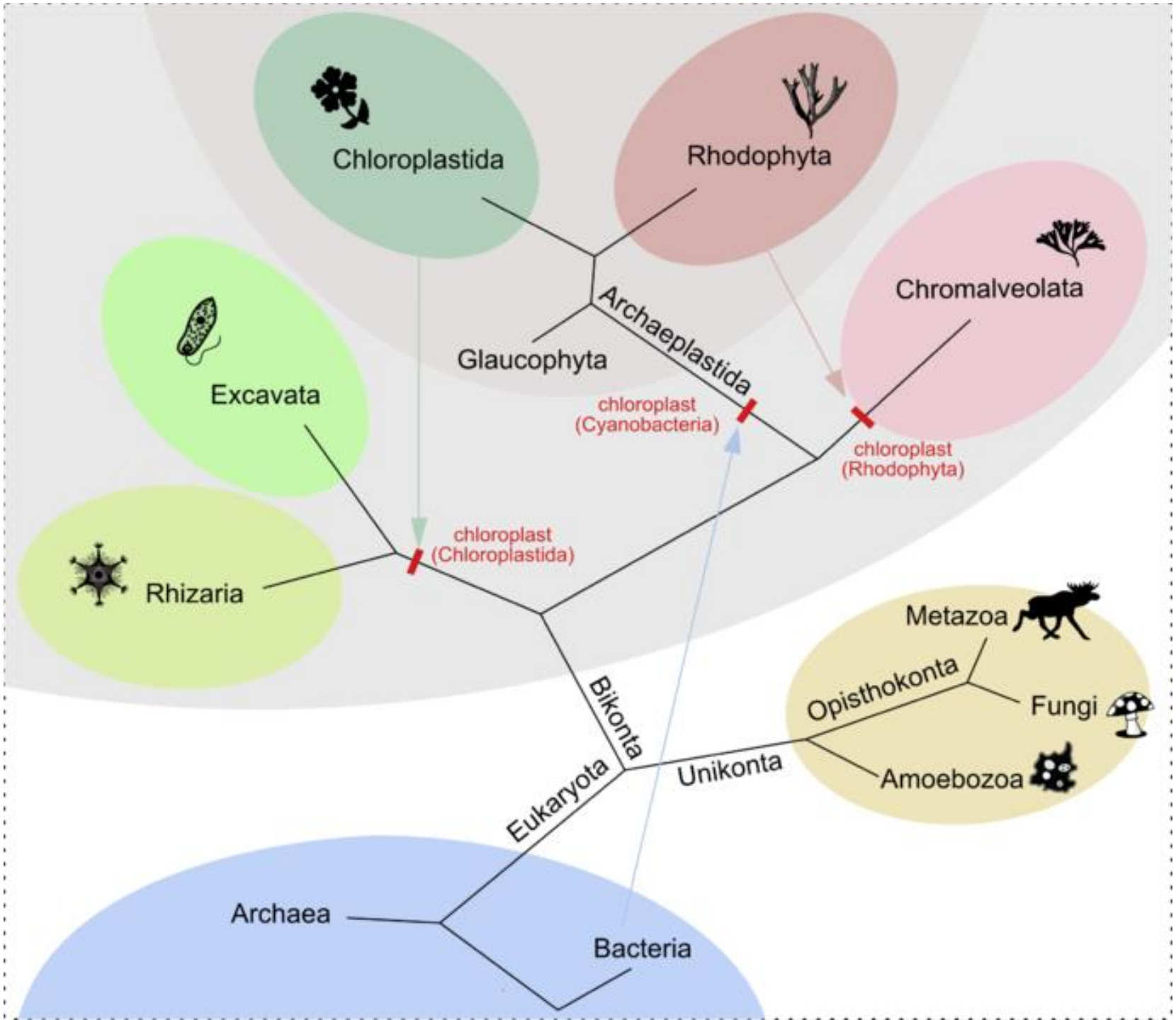
- Endosymbiosis 1.5-2.5 Billion years ago
- Lost most of their genes
  - Genes / gene functions transferred to nucleus
- Genome size heavily reduced



# The ENDOSYMBIOTIC THEORY

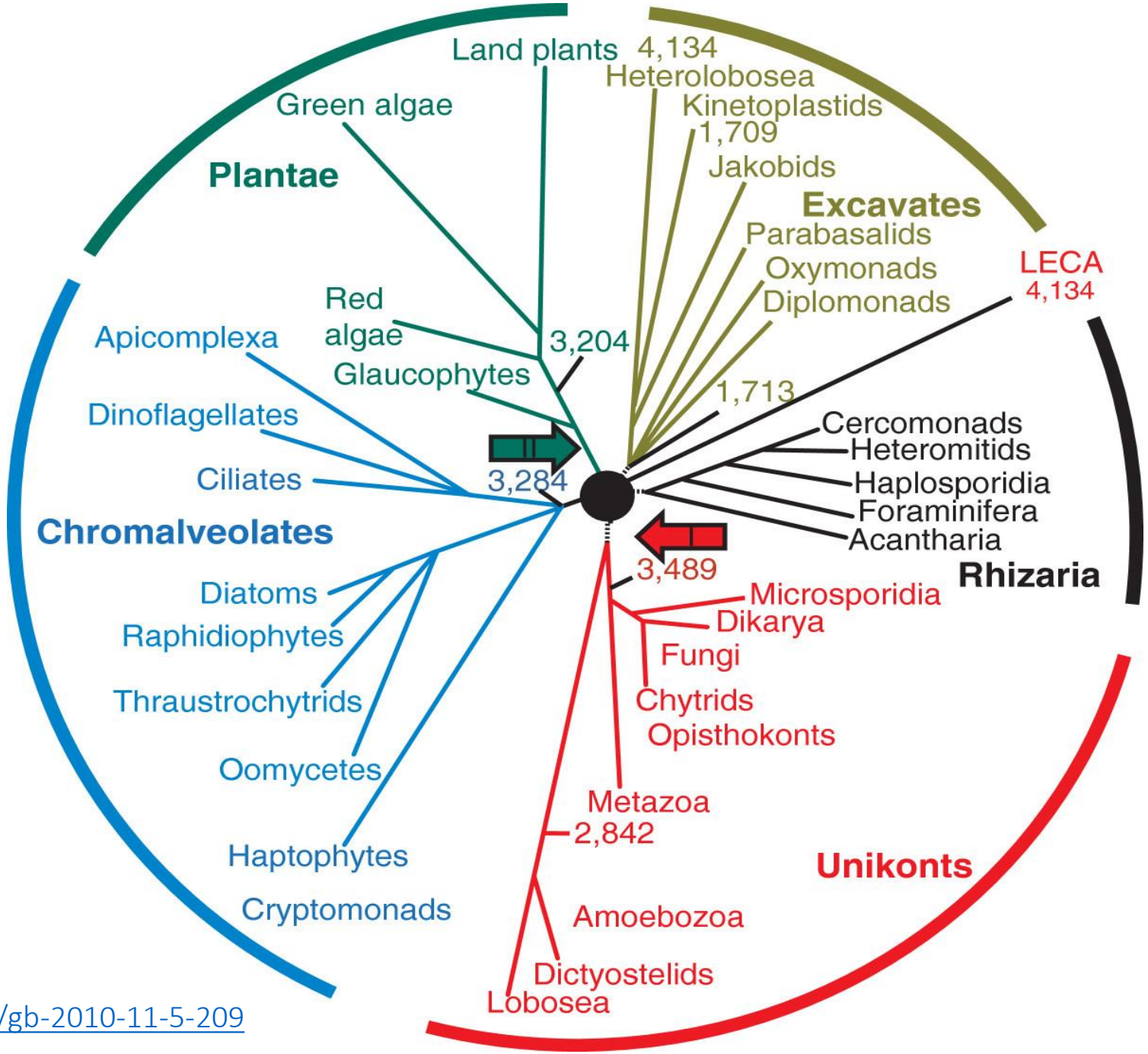



Years Ago
(×10⁹)
Prokaryotes
Eukaryotes
Bacteria
Archaea
Protists
Plants
Fungi
Animals
0
0.4
0.8
1.2
1.6
2
2.4
2.8
3.2
3.6
4
Hard bodies
Soft bodies
Multi-celled organisms
Eukaryotes with organelles
Eukaryotes (DNA in nucleus)
Prokaryotes (no nucleus, free DNA)
Last Universal Common Ancestor (LUCA) of all current Earth Life
Chloroplast assimilation (?)
Mitochondrion assimilation (?)
One Thousand
Million Years
Three Thousand
Million Years


Chloroplastida
Rhodophyta
Chromalveolata
Archaeplastida
Glaucophyta
Excavata
chloroplast
(Cyanobacteria)
chloroplast
(Rhodophyta)
chloroplast
(Chloroplastida)
Rhizaria
Metazoa
Opisthokonta
Fungi
Bikonta
Unikonta
Amoebozoa
Eukaryota
Archaea
Bacteria

- The origin and early evolution of eukaryotes in the light of phylogenomics
- Eugene V Koonin
- *Genome Biology*2010**11**:209

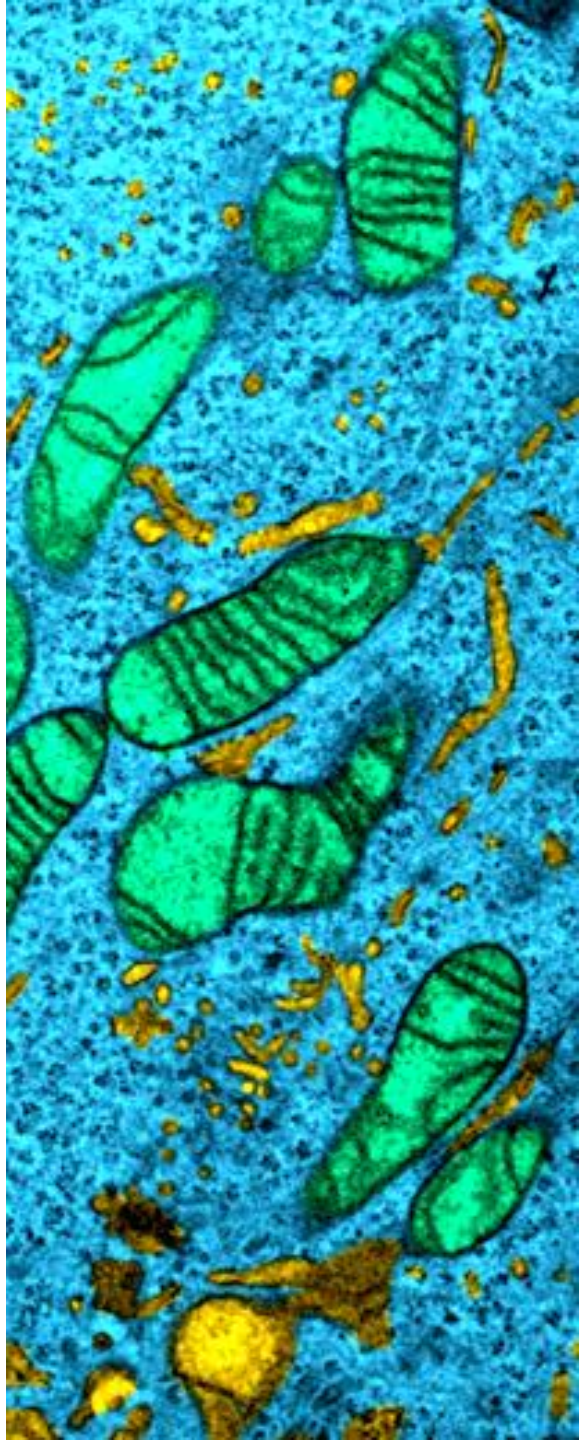
- Phylogenomics of eukaryote supergroups suggest a highly complex last common ancestor of eukaryotes and a key role of mitochondrial endosymbiosis in the origin of eukaryotes.




https://genomebiology.biomedcentral.com/articles/10.1186/gb-2010-11-5-209

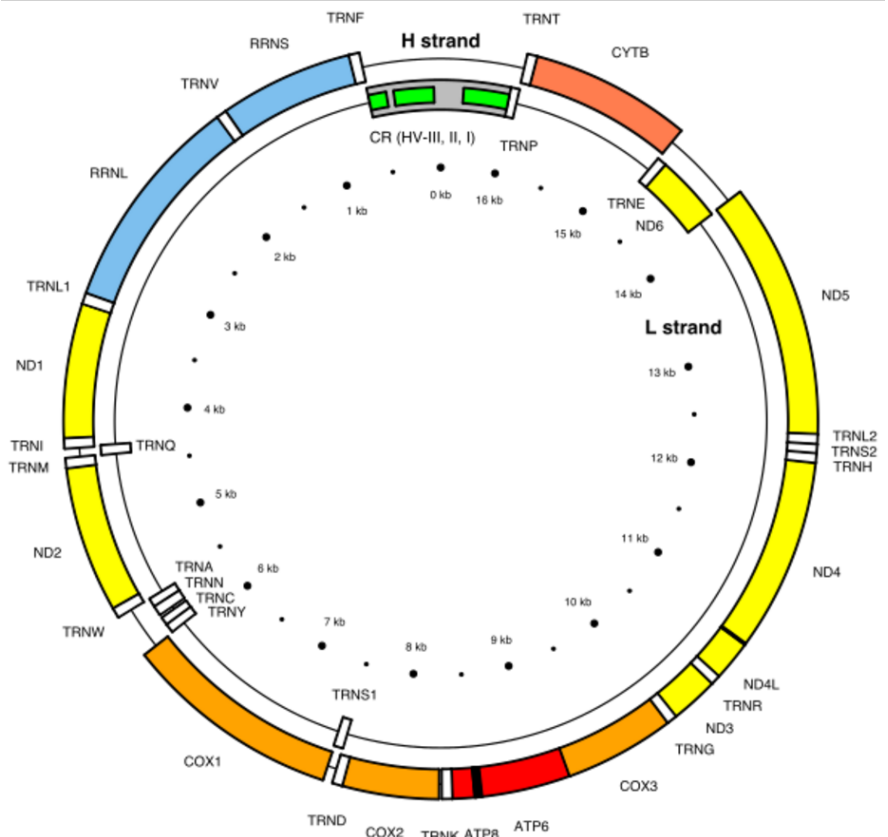
# Evolution of mitochondrial genome

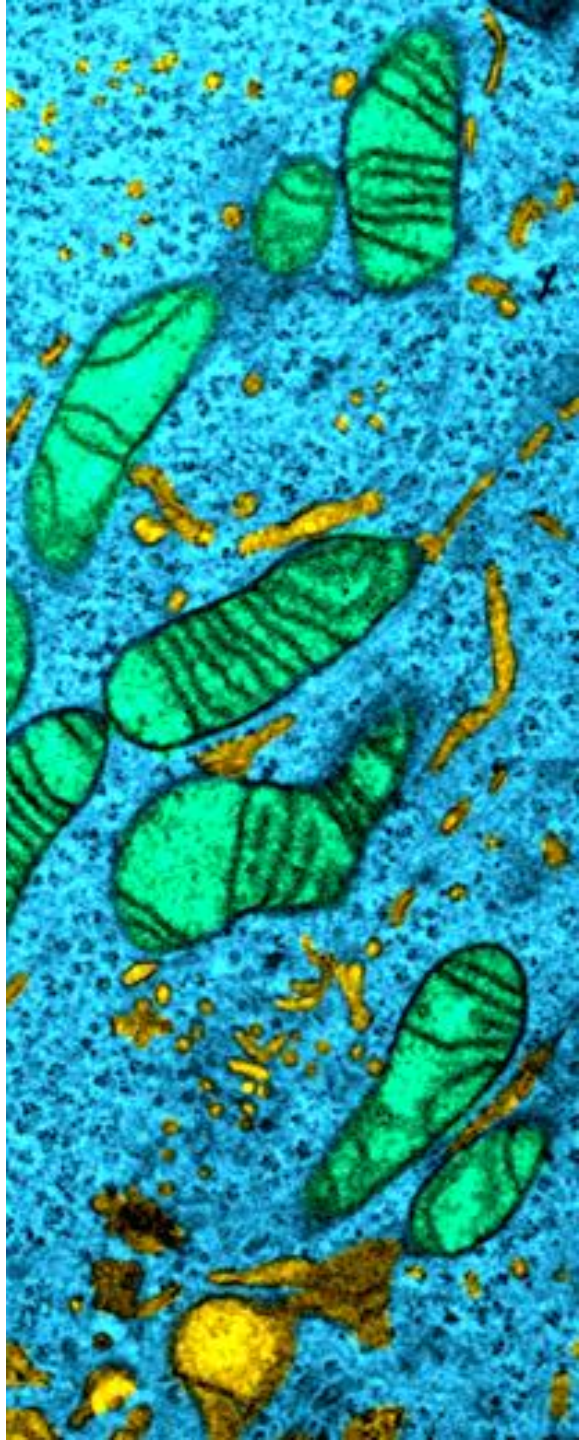
- free-living α-proteobacterial ancestor probably had ~1600+ protein-coding genes
- Today, far fewer – many have been lost or transferred to the nuclear genome



# Mammalian mitochondria

- 37 protein-coding genes
- 22 tRNA
- 11-28kb genome size (most ~16kb), 1 circle



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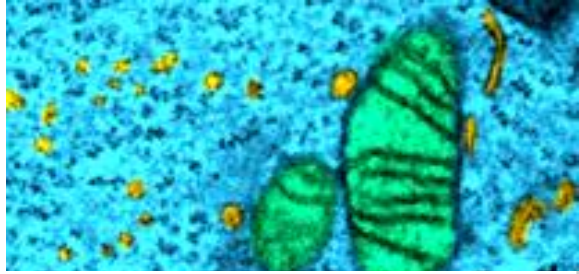
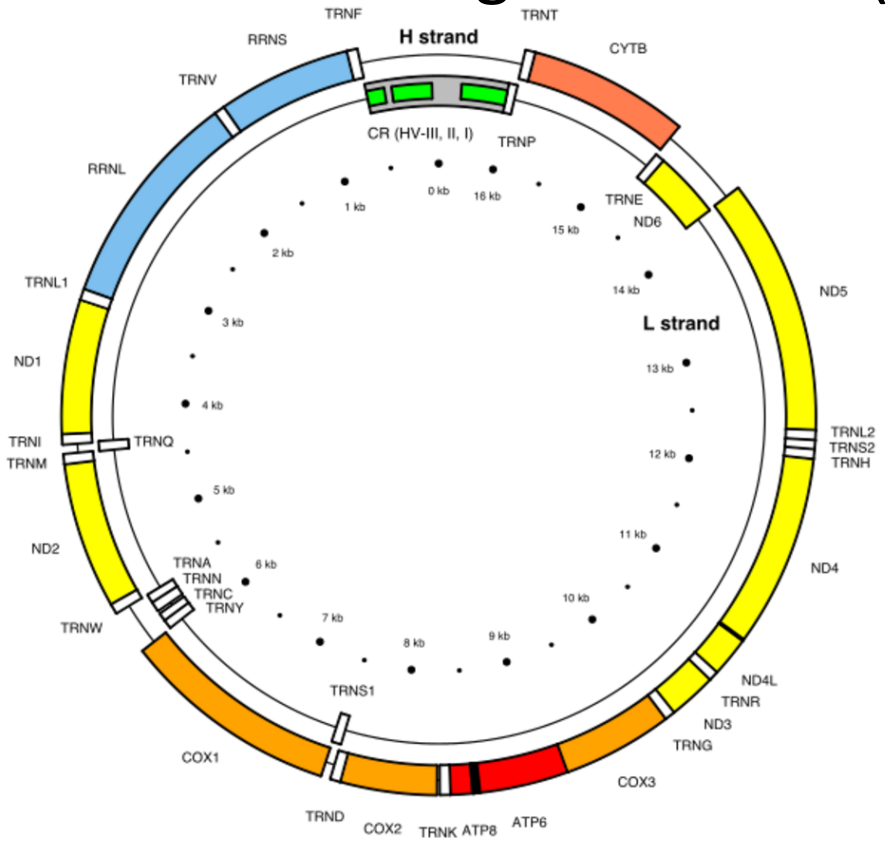
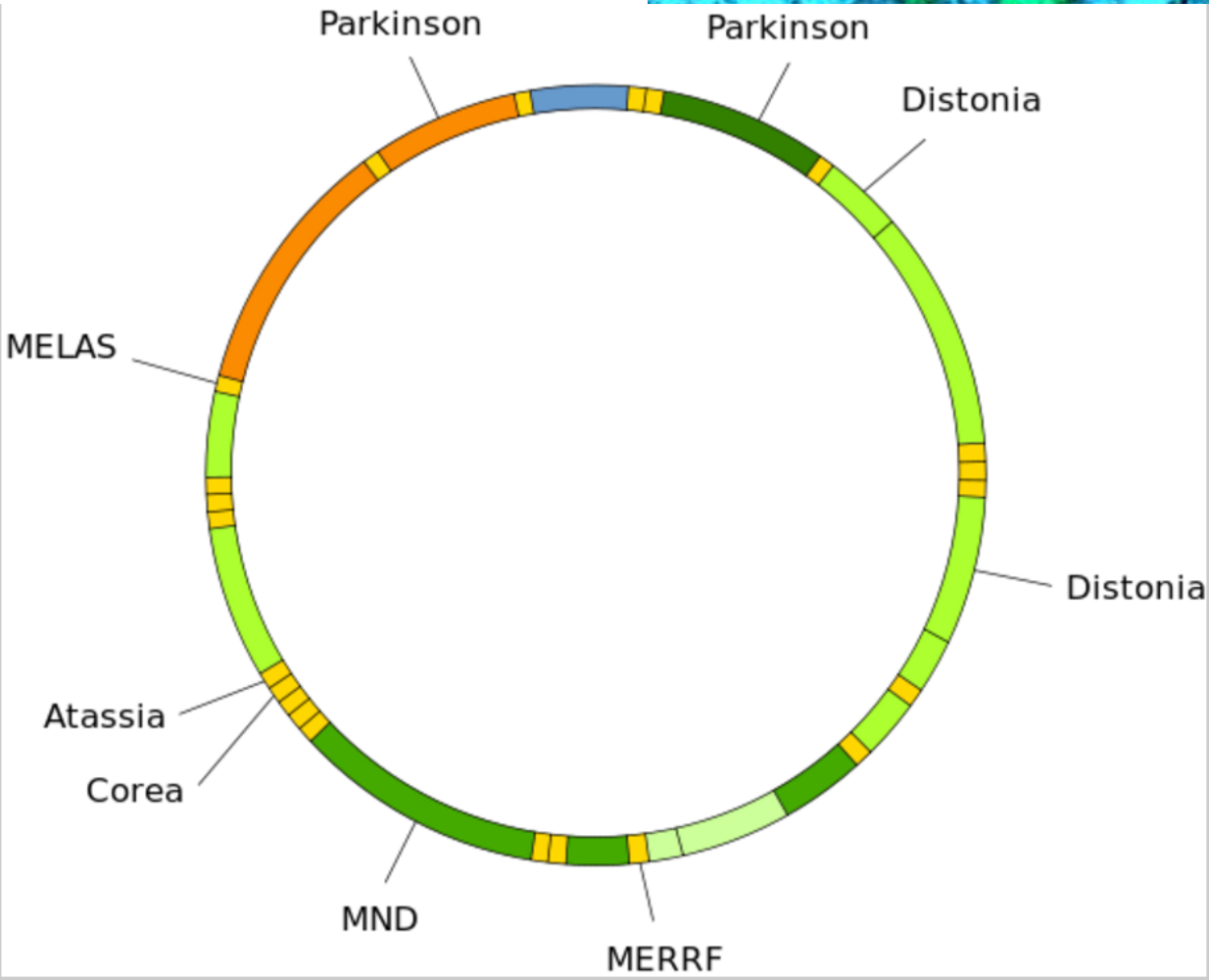
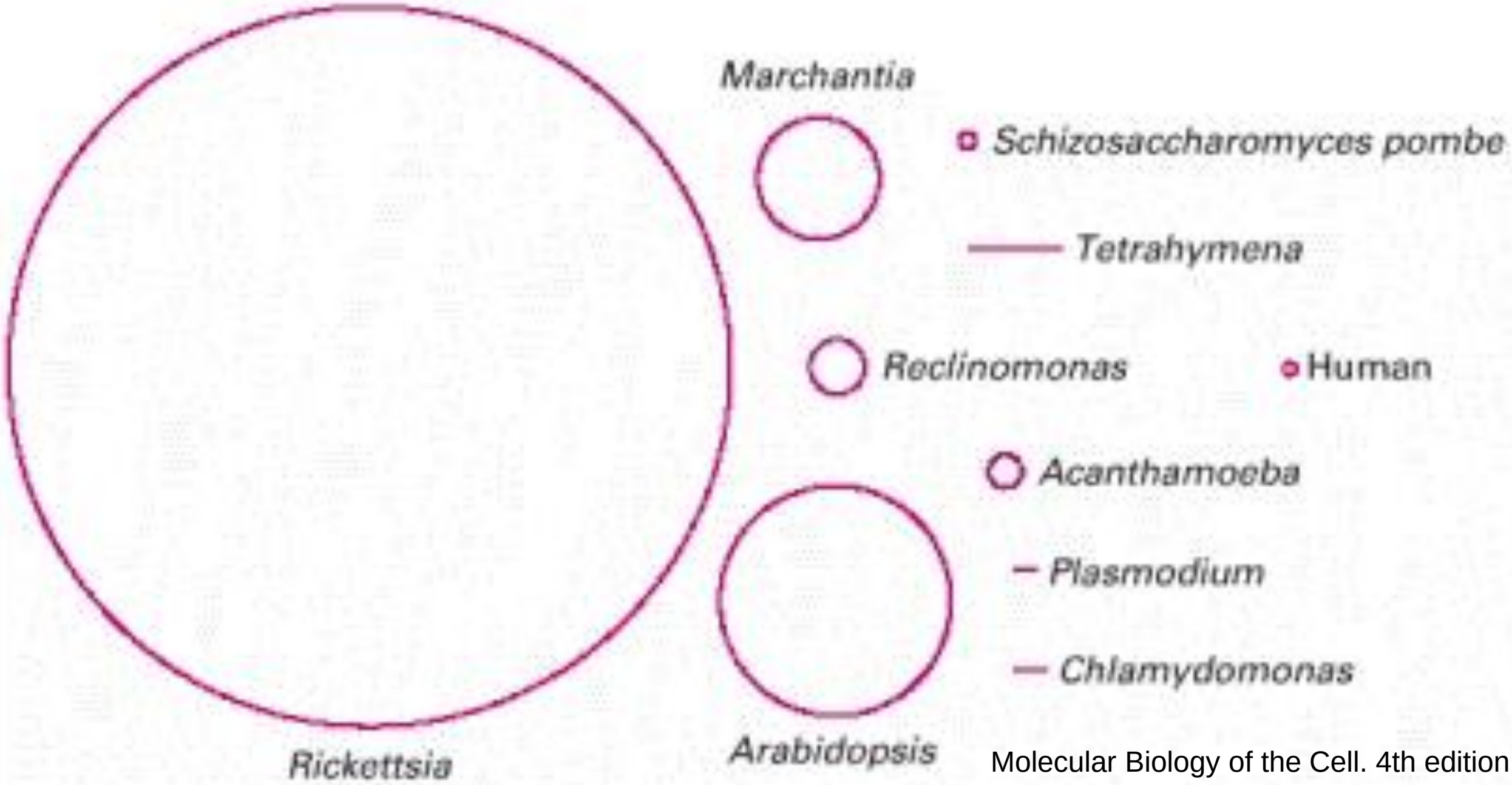




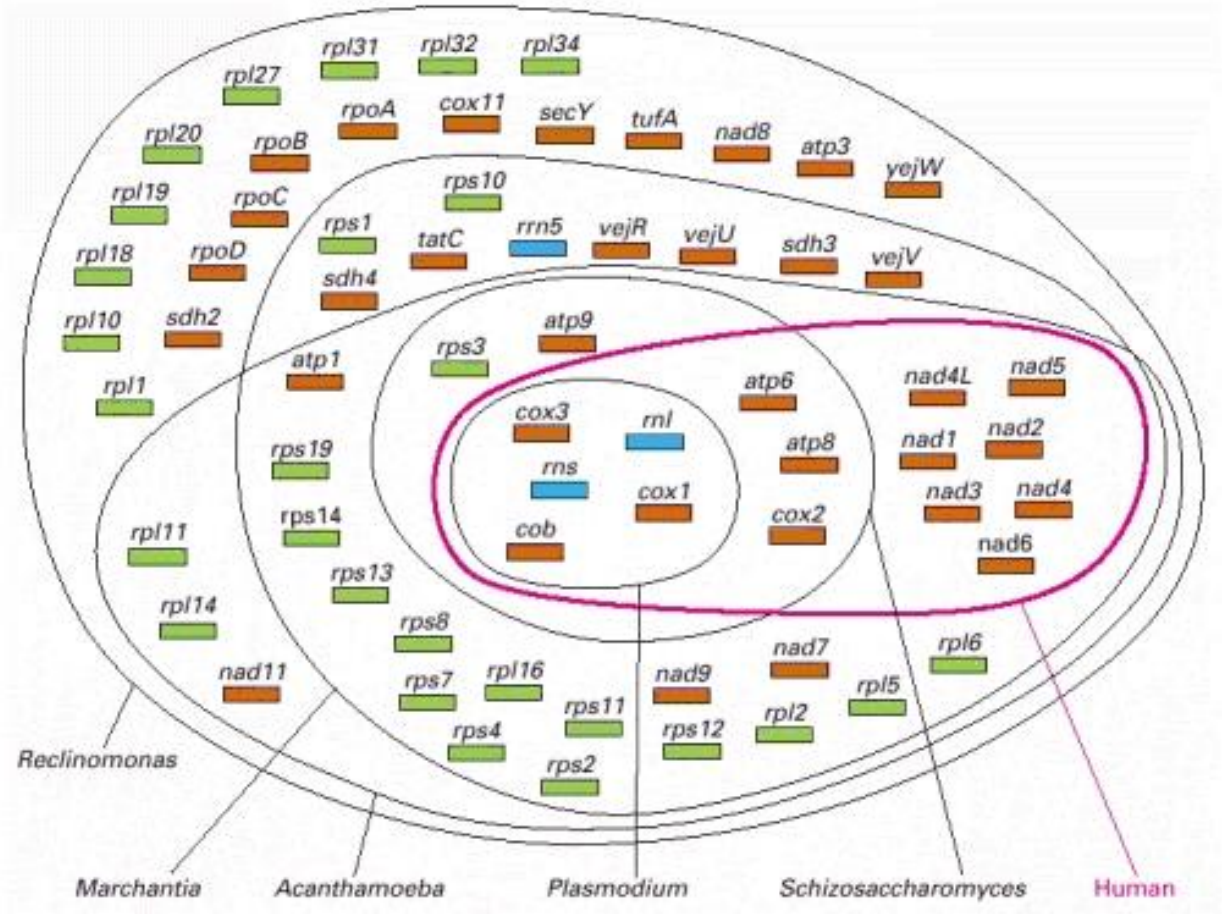



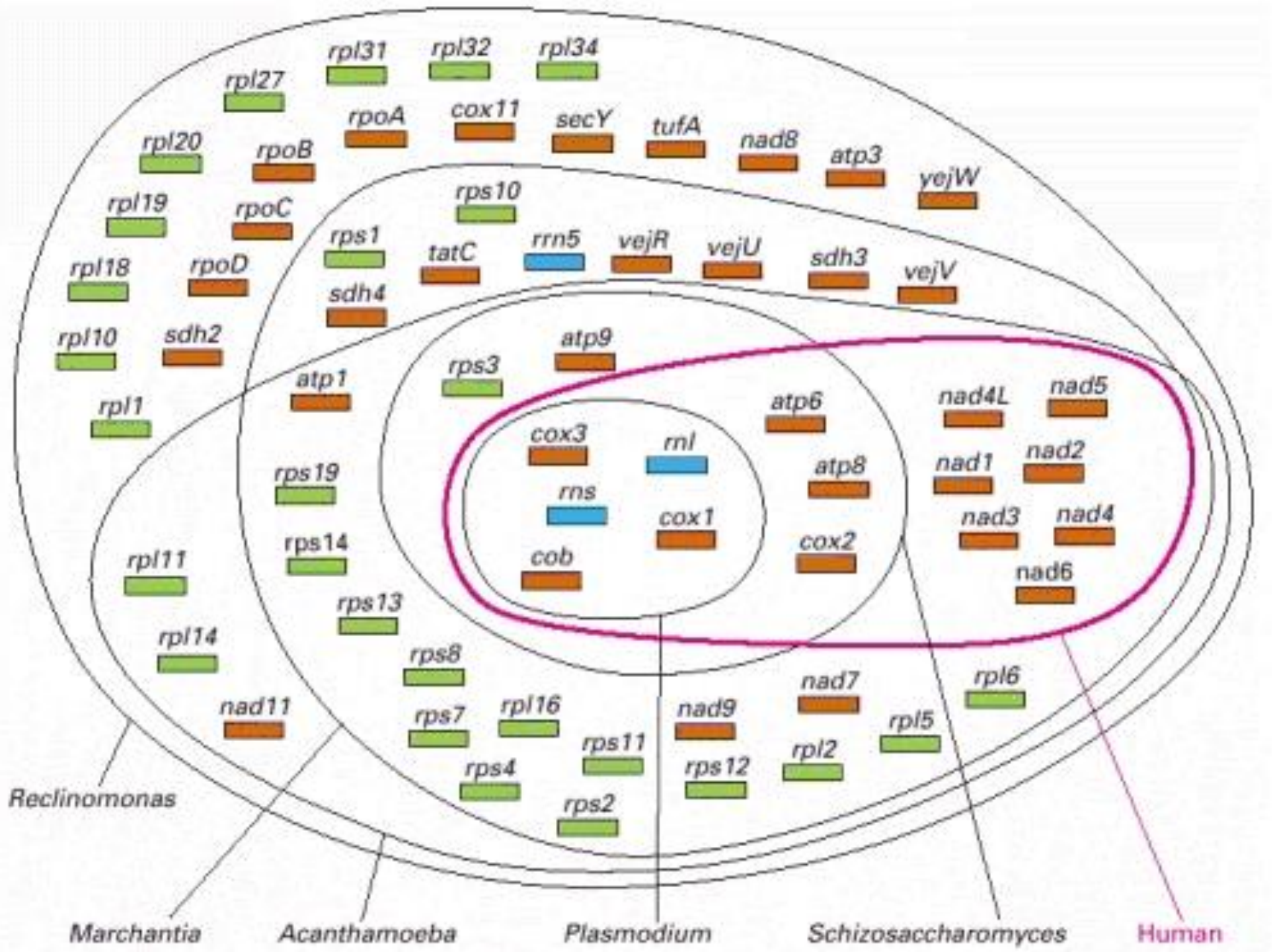

The involvement of mitochondrial DNA in several human diseases.




Molecular Biology of the Cell. 4th edition.
Alberts B, Johnson A, Lewis J, et al.
New York: Garland Science; 2002.

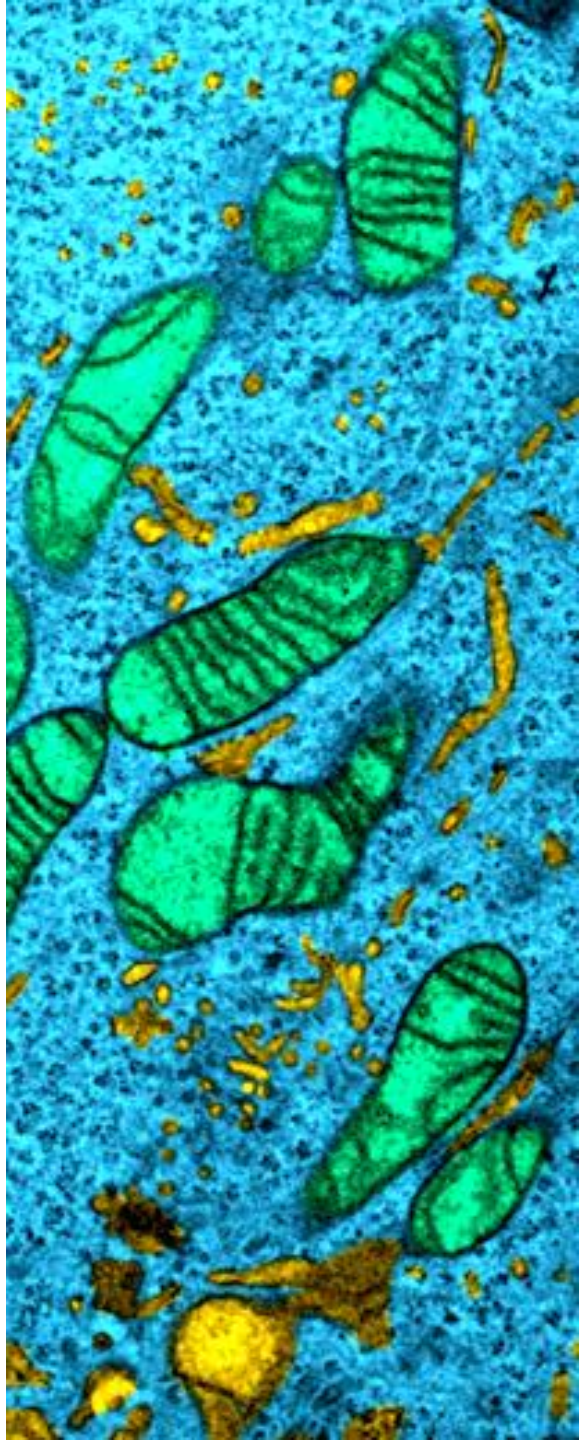
Less complex mitochondrial genomes encode subsets of the proteins and ribosomal RNAs that are encoded by large mitochondrial genomes. The five genes present in all known mitochondrial genomes encode ribosomal RNAs *(rns* and *rnl),* cytochrome *b (cob),* and two cytochrome oxidase subunits *(cox1* and *cox3).* (Adapted from M.W. Gray et al., *Science* 283:1476–1481, 1999.)




rpl31
rpl32
rpl34
rpl27
rpoA
cox11
secY
tufA
nad8
atp3
yejW
rpl20
rpoB
rpl19
rpoC
rps10
rps1
tatC
rrn5
vejR
vejU
sdh3
vejV
rpl18
rpoD
sdh4
rpl10
sdh2
atp9
rps3
atp1
rpl1
atp6
nad4L
nad5
cox3
rnl
atp8
nad1
nad2
rps19
rns
cox1
nad3
nad4
rpl11
rps14
cob
cox2
nad6
rps13
rpl14
rps8
nad7
rpl6
nad11
rps7
rpl16
nad9
rpl5
rps11
rpl2
rps4
rps12
rps2
Reclinomonas
Marchantia
Acanthamoeba
Plasmodium
Schizosaccharomyces
Human

# Plant and fungal mitochondria

- ?8-127+ protein-coding genes (NCBI)
- 22 tRNA
- 19,000-1,000,000+bp genome size
- Can be 1 circle, 2+ circles, or 1 linear molecule



# Your final project : a compete organellar genome

1. Identify the correct sequence(s)
2. Construct a complete, assembled genome – may be done
3. Error correct (you know how!)
4. Annotate
   - Much more complicated if you have more genes
   - More challenging due to differences in gene order, gene content

5. Submit
   - Much more complicated if you have more genes

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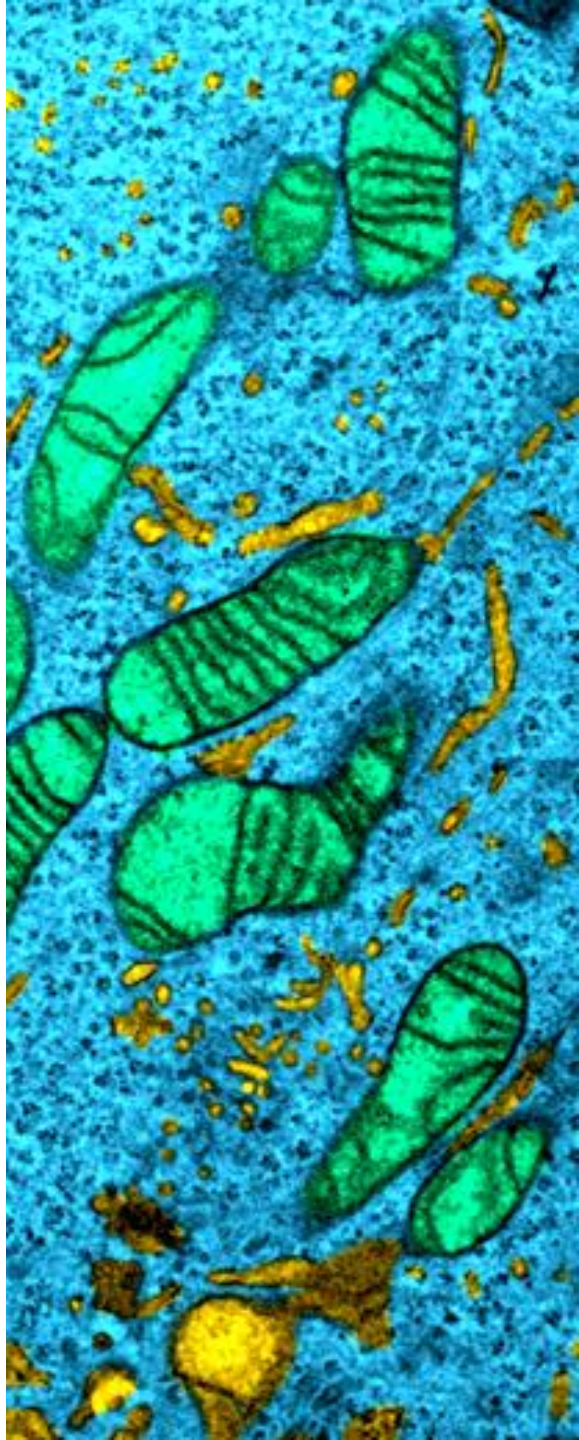
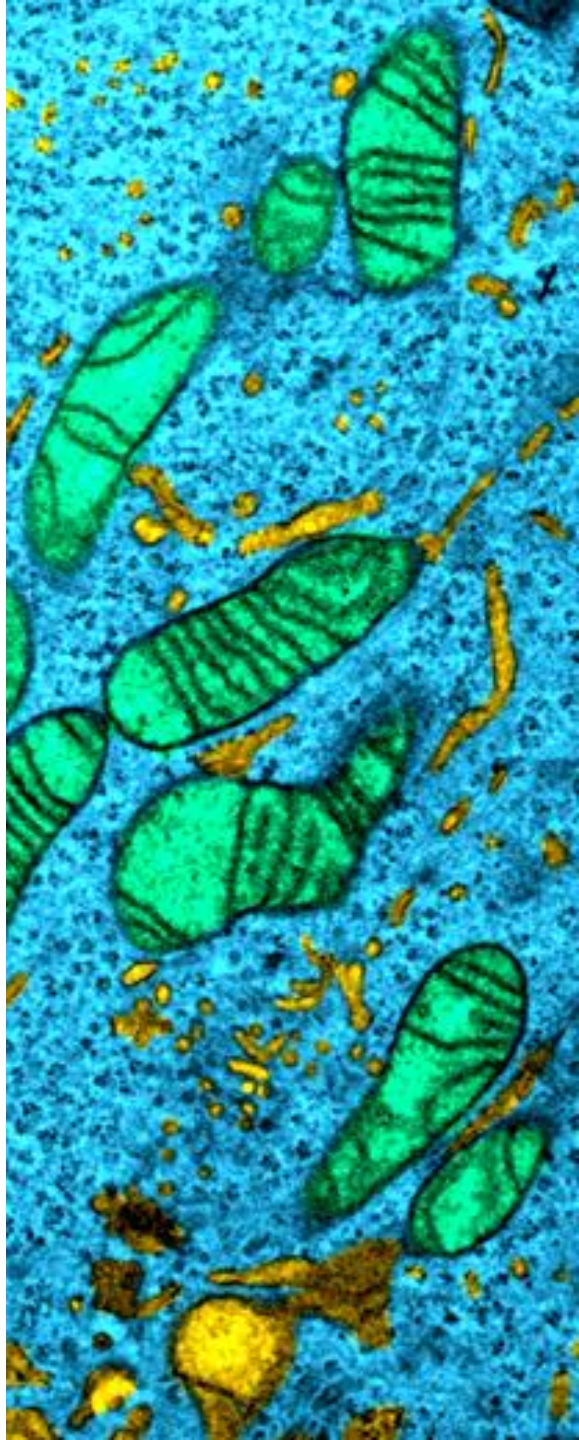


# Your fungal mitochondria

- All ascomycete lichenized fungi
- 20kb-90kb
- Lots of variation in gene order
- Less variation in gene content



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# First steps- by next Tuesday

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