

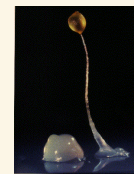
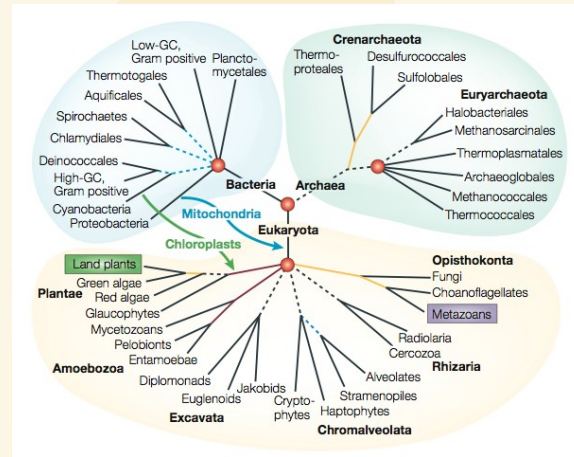
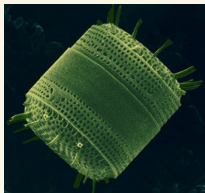
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# Evolution of the ribosome: testing eukaryotic origins

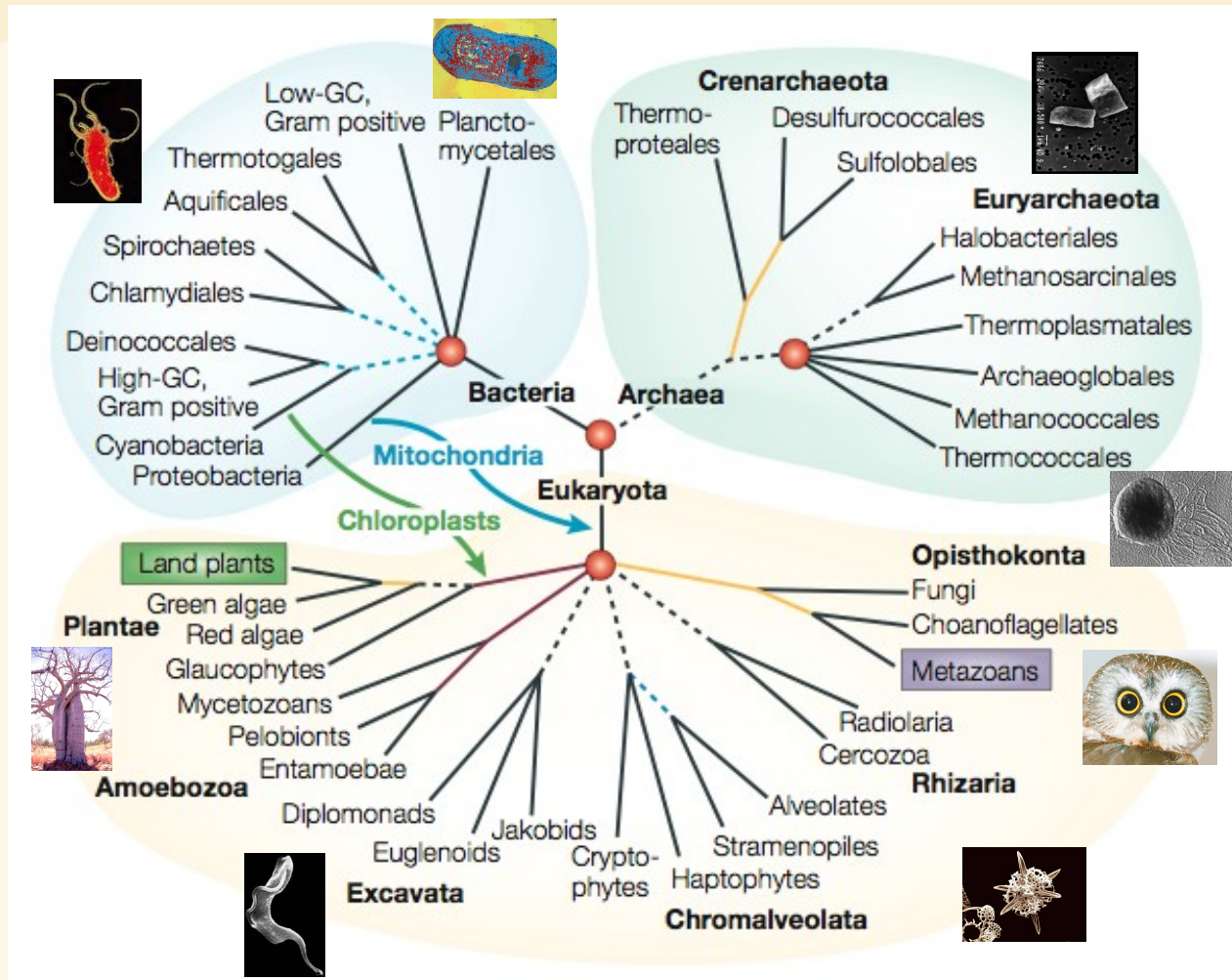
**Elie Desmond**

Unité de Biologie Moléculaire du Gène chez les Extrêmophiles





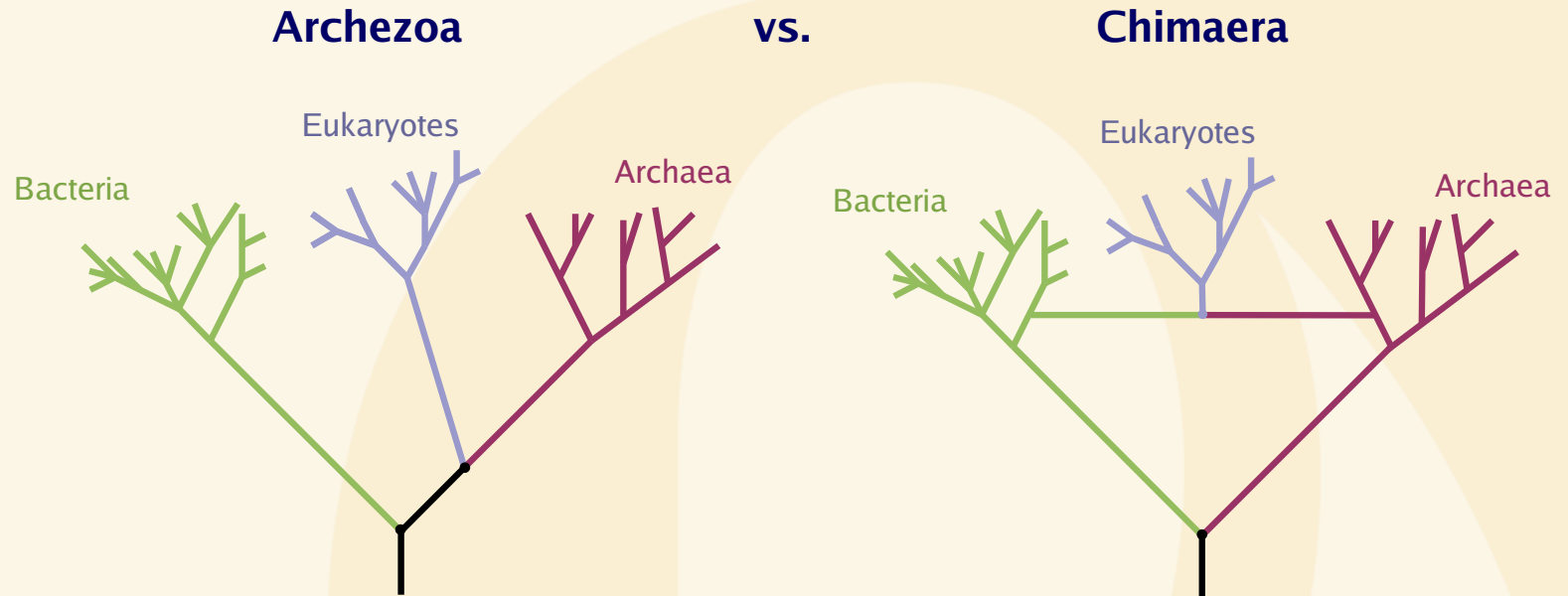
# Molecular phylogeny and the tree of life



From Delsuc F (2005) Nat Rev Genet. 6(5):361-75



# The origin of eukaryotes : hypotheses



- **Hydrogen hypothesis Martin & Muller (1998)**
- **Syntrophic hypothesis Moreira & Lopez-Garcia (1998)**
- ...



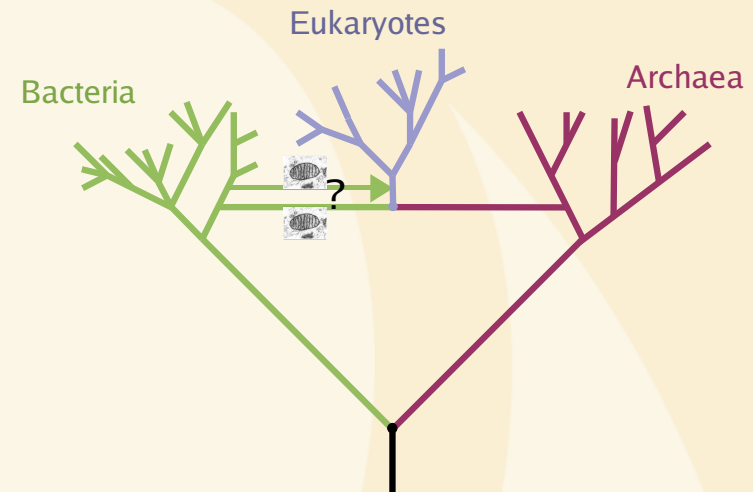
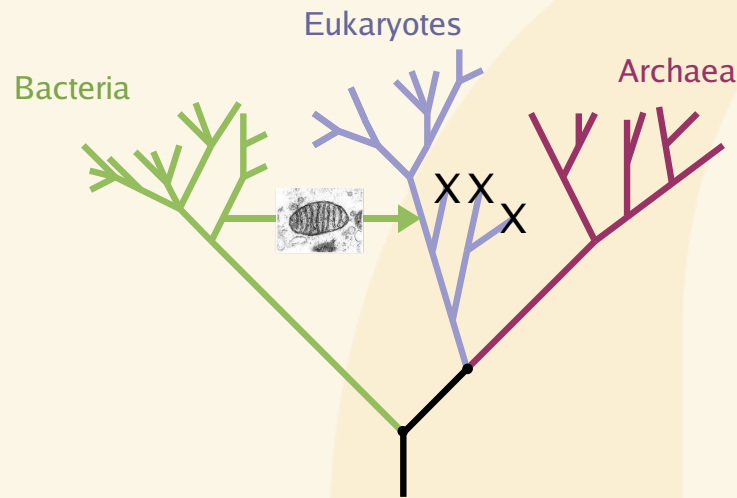
# The origin of eukaryotes : the Last Eukaryotic Common Ancestor had already a mitochondrion



## Archezoa

vs.

## Chimaera



- **Hydrogen hypothesis** Martin & Muller (1998)
- **Syntrophic hypothesis** Moreira & Lopez-Garcia (1998)
- ...



# Testing hypotheses on the origin of Eukaryotes with molecular phylogeny

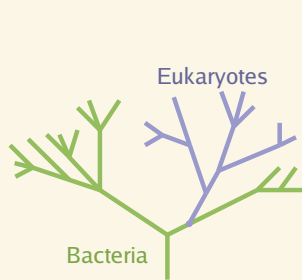


Archezoa

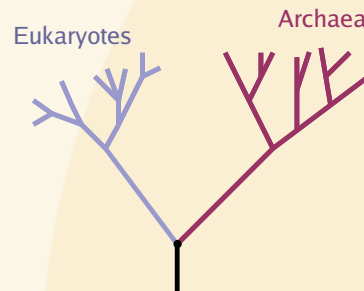
vs.

Chimaera

Expected Phylogenies :

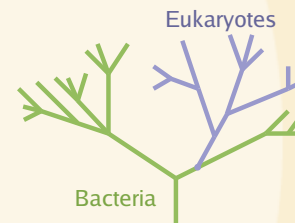


genes shared with Bacteria

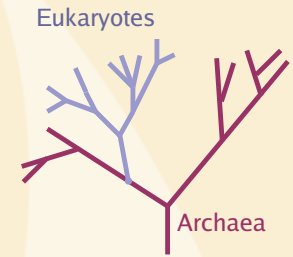


genes shared with Archaea

vs.



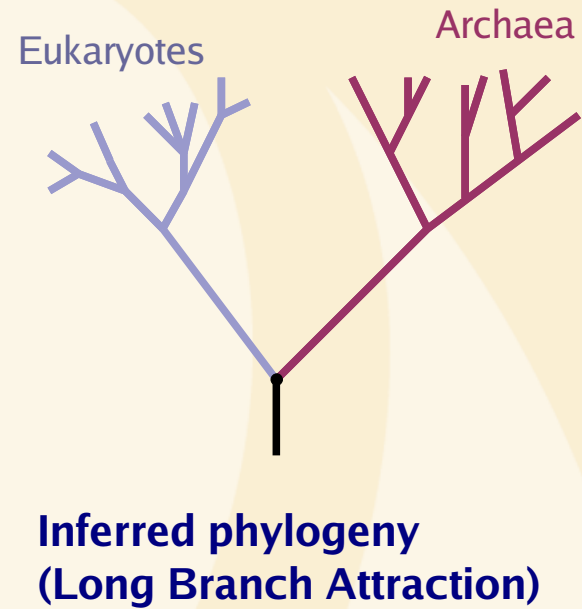
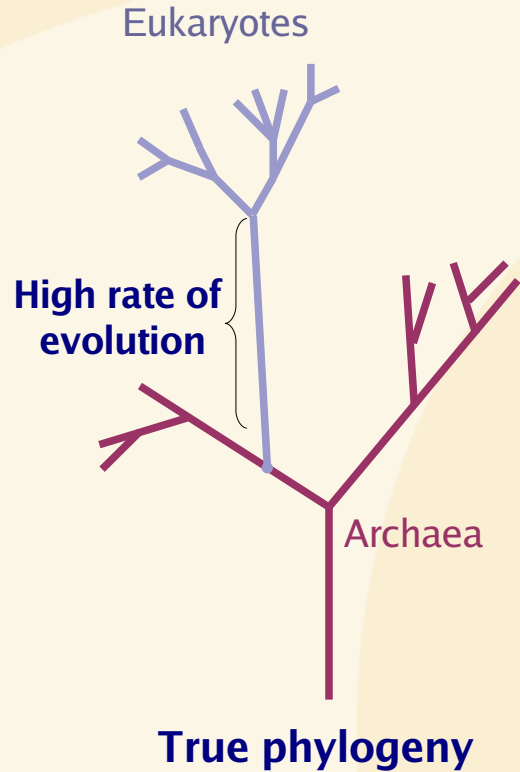
genes shared with Bacteria



genes shared with Archaea

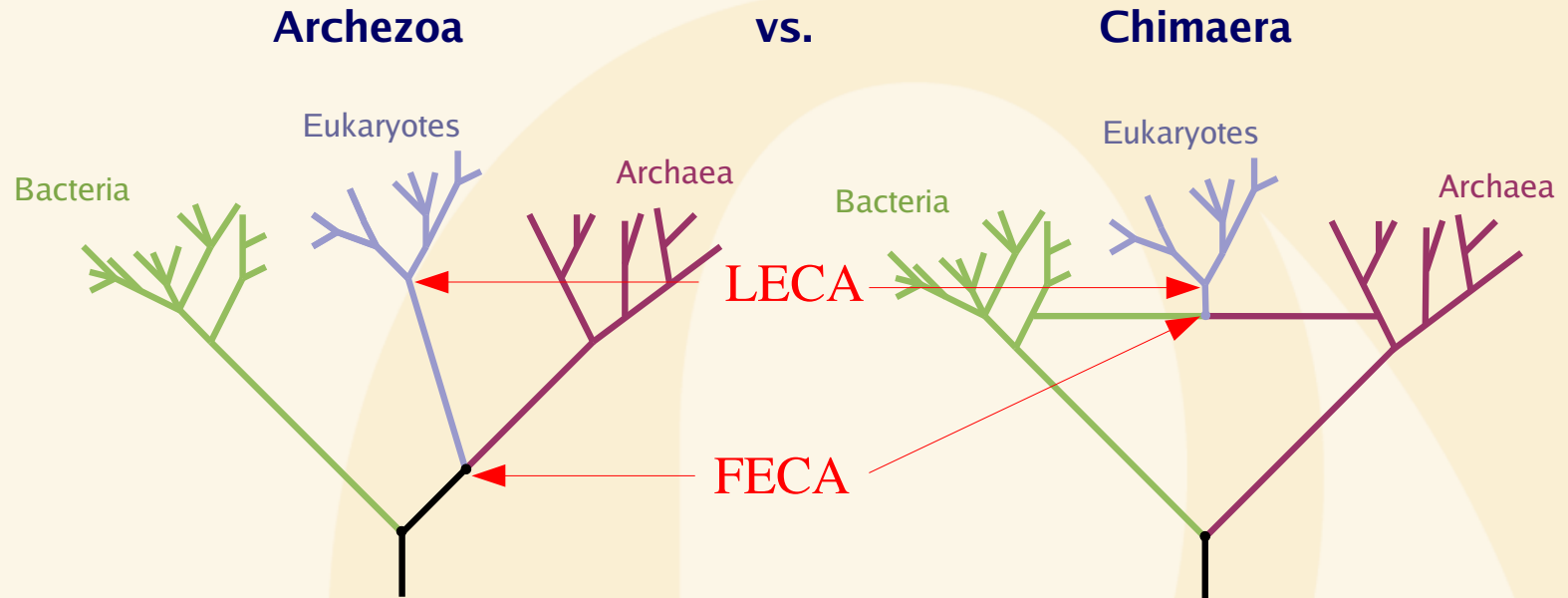


# Reconstruction artefacts in molecular phylogeny





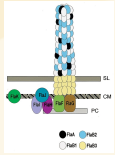
# First Eukaryotic Common Ancestor & Last Eukaryotic Common Ancestor



- Shared characters within eukaryotes => reconstruction of the LECA
- Shared characters in Eukaryotes/Archaea, Eukaryotes/Bacteria or Eukaryotes/Archaea/Bacteria => reconstruction of the FECA



# Phylogenomics : evolution of biological systems

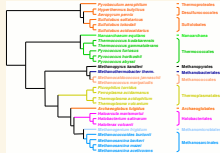


**Components of a biological system**

**Complete genomes**



**Taxonomic distribution & Gene phylogeny**



**Reference species tree**

**Gene origins**

**Evolutionary events:**

- Gene duplications
- Gene losses
- Horizontal Gene Transfers



**Ancestral composition of the biological system and its evolution**





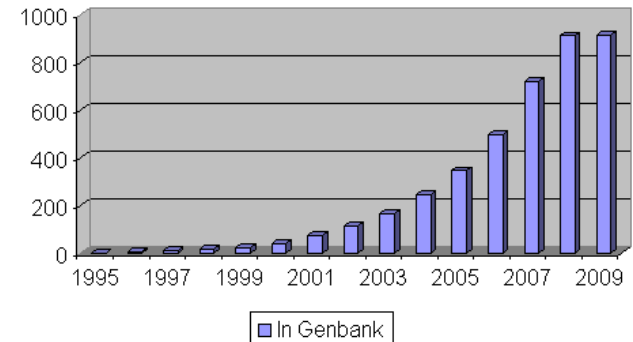
# Phylogenomics and the reconstruction of the FECA and the LECA



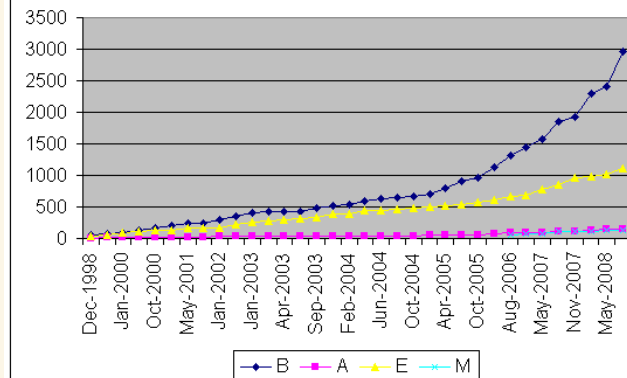
May 2009 → 987 complete genomes published :

- 825 bacteria
- 104 eukaryotes
- 58 archaea

Completely Sequenced Genomes ©  
January 2009

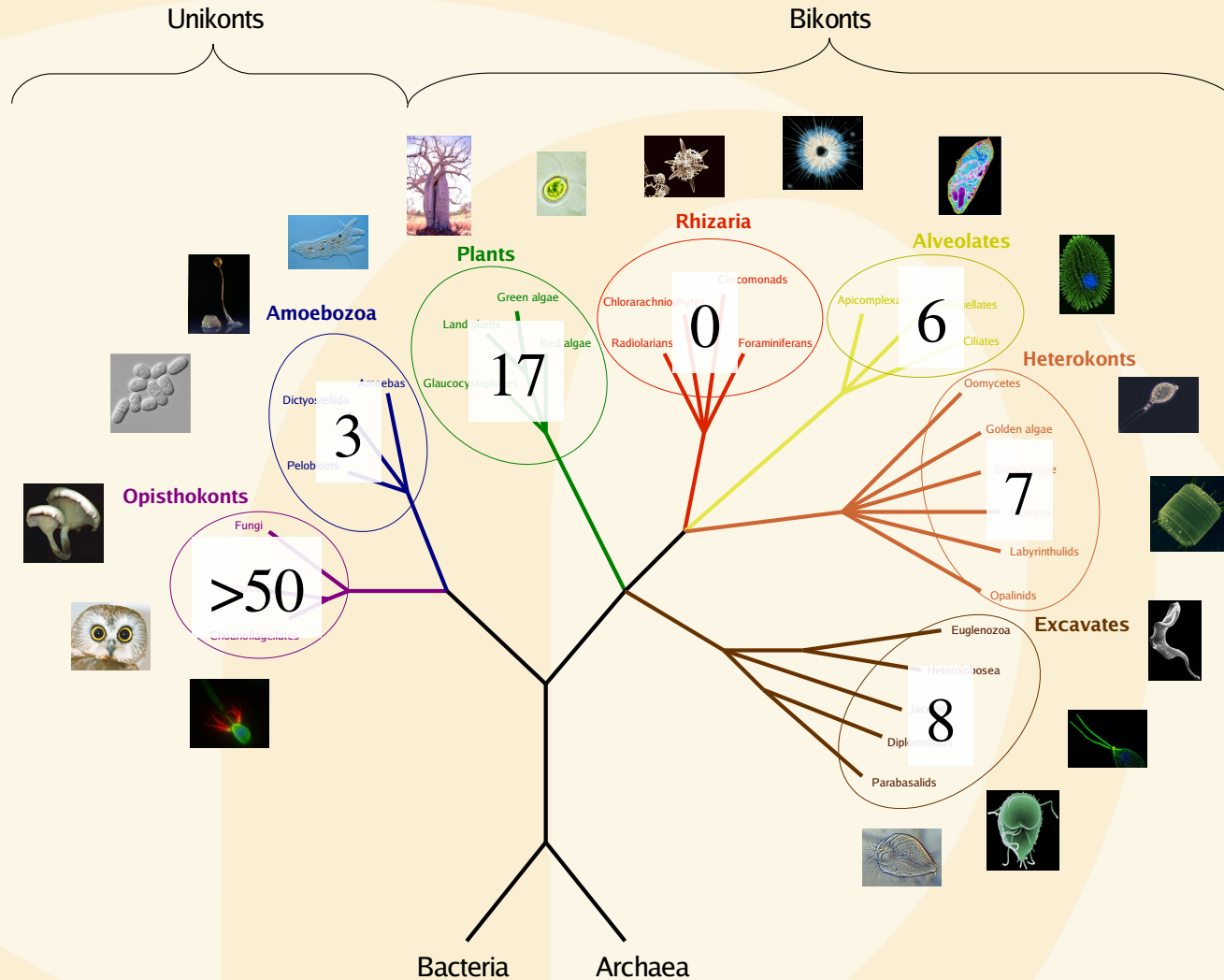


Genome Projects on GOLD according to Phylogenetic Groups ©  
Jan 2009 - 4370 Projects



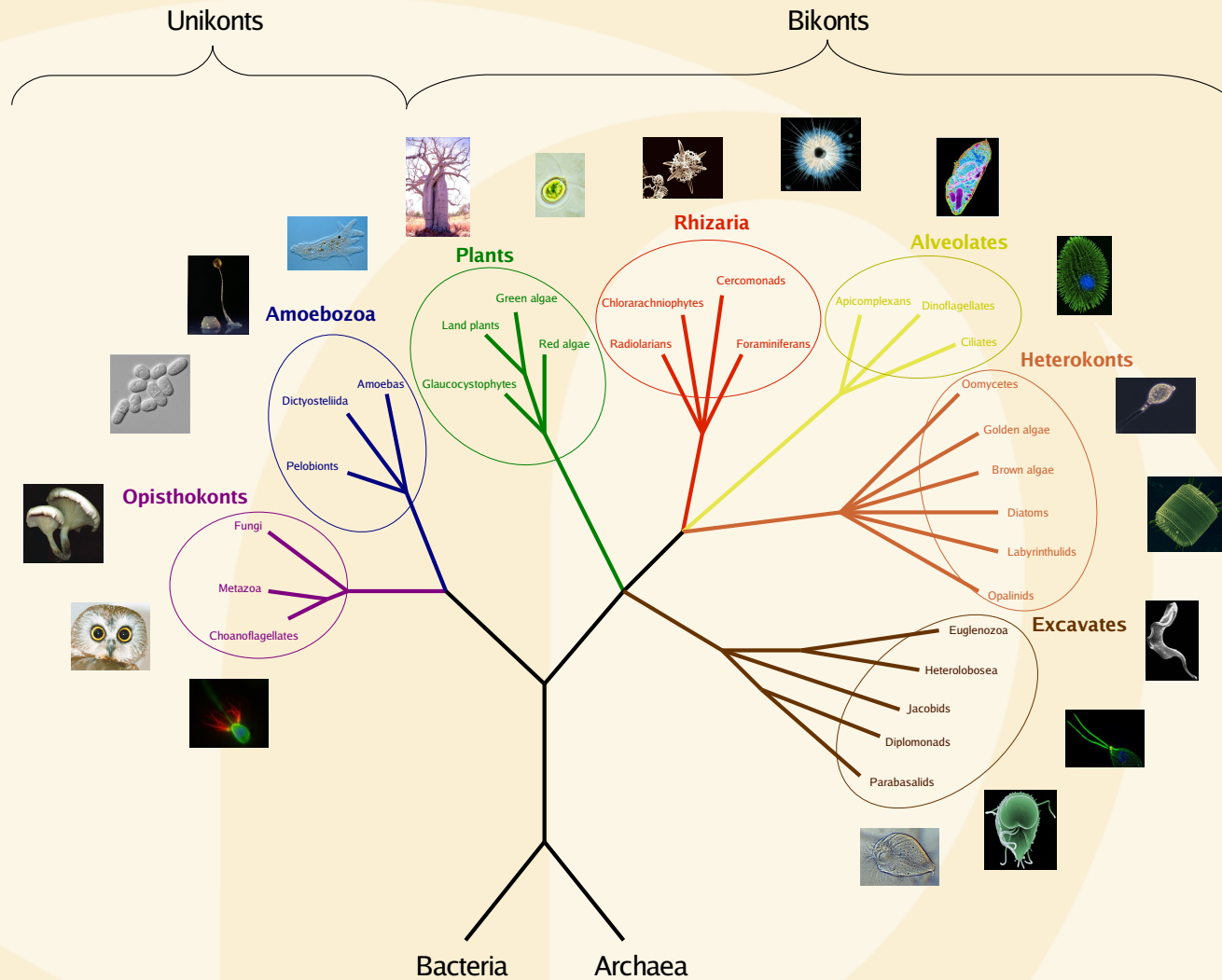


# Phylogenomics of eukaryotic systems : the phylogeny of eukaryotes



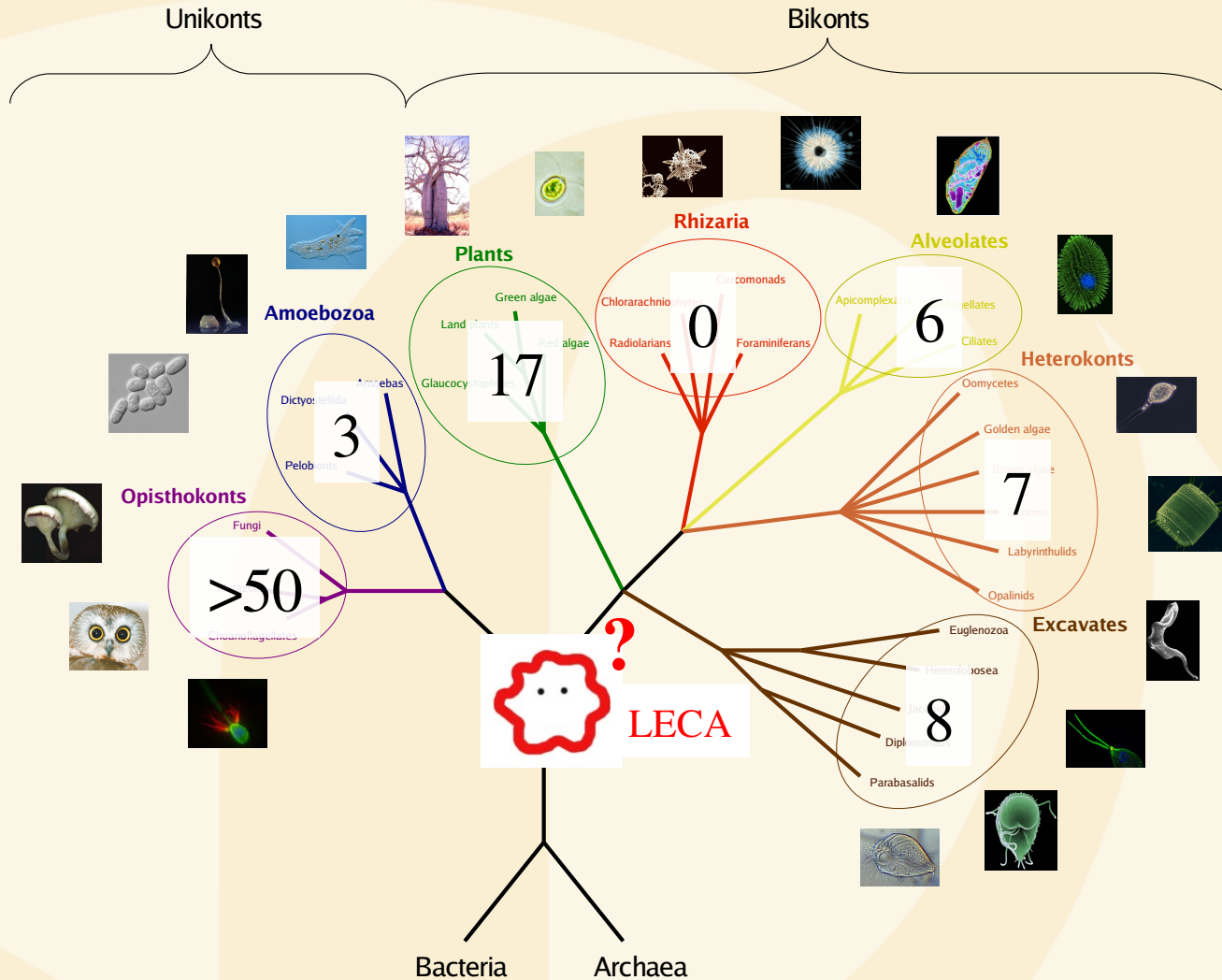


# Phylogenomics of eukaryotic systems : inferring the nature of the LECA



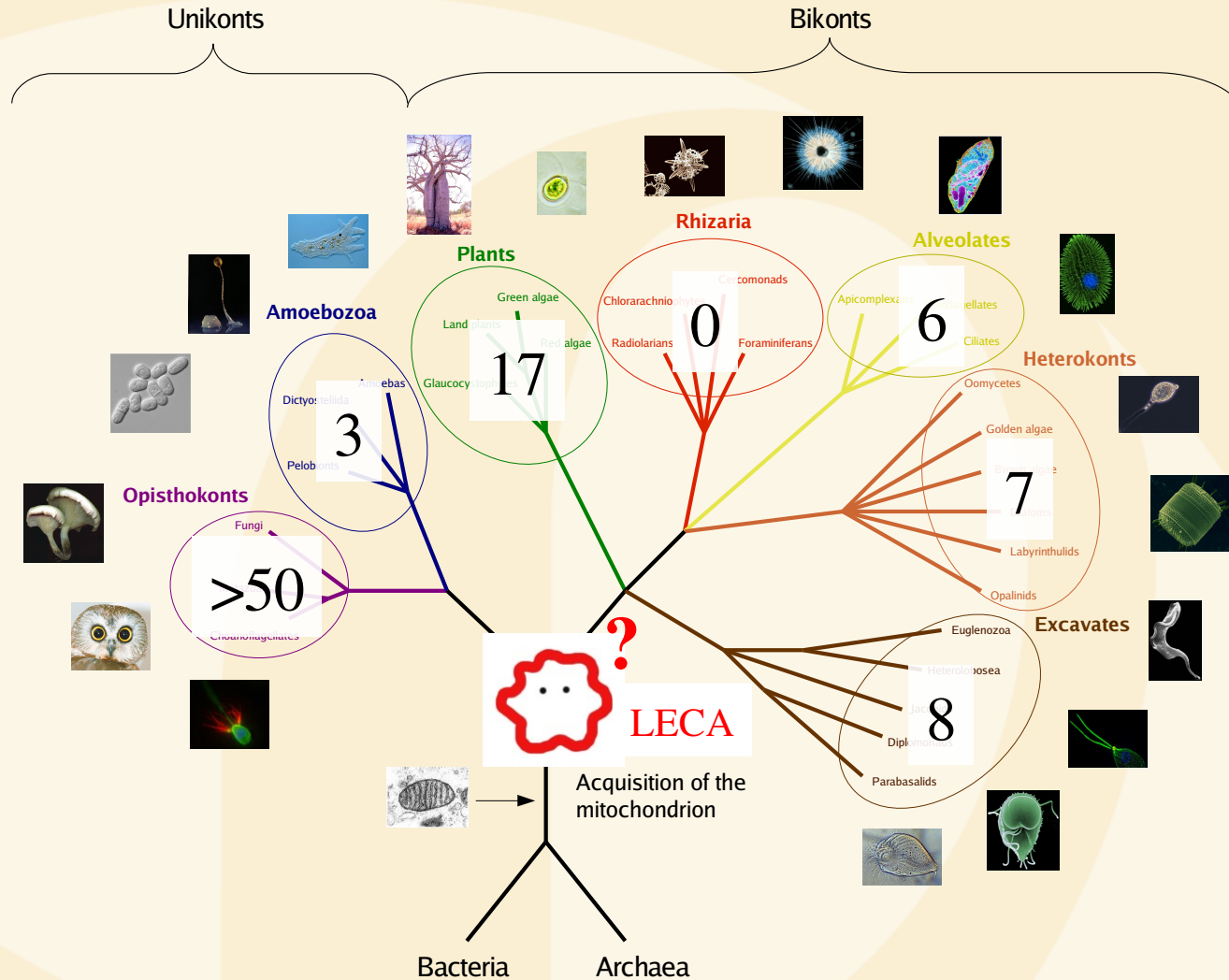


# Phylogenomics of eukaryotic systems : inferring the nature of the LECA



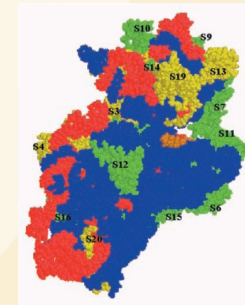
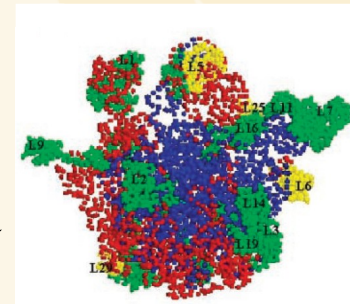
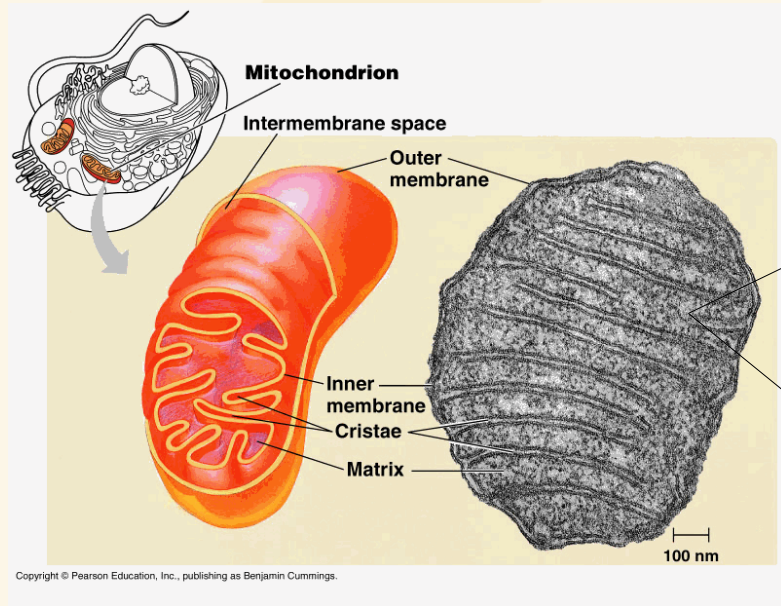


# Phylogenomics of eukaryotic systems : inferring the nature of the LECA





## Phylogenomics of mitochondrial ribosomes



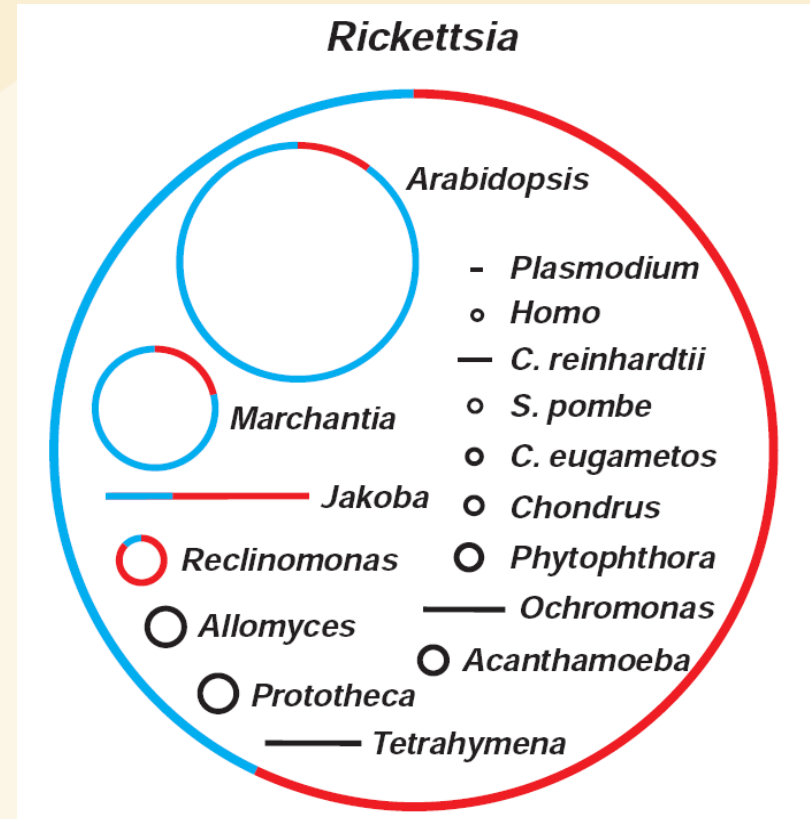


# The mitochondrial genome



Size, topology and gene content of mitochondrial genomes compared to a Rickettsia ( $\alpha$ -proteobacteria) :

- For genomes > 60 kbp  
Red line : coding DNA  
Blue line : non-identified ORFs and non-coding DNA
- Mitochondrial genome tends to reduce with many genes transferred to the host nuclear genome

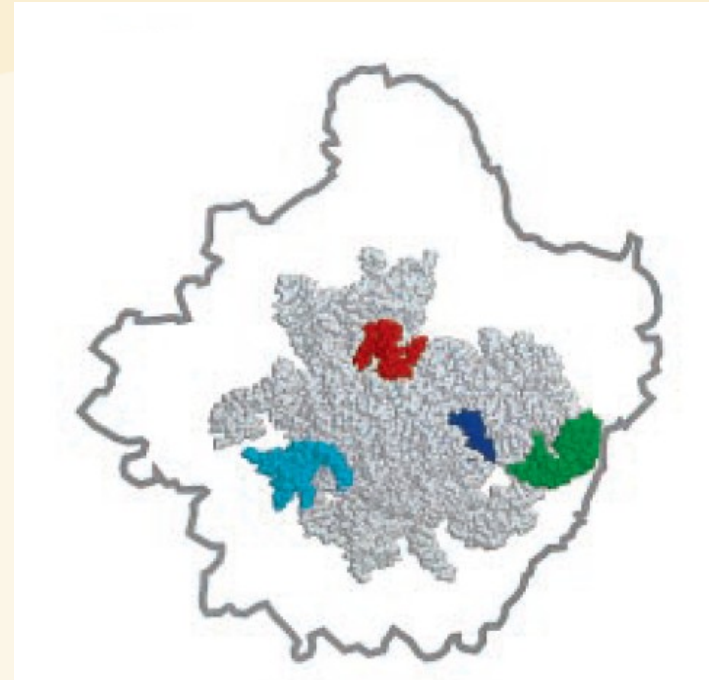


Gray MW & al., Science vol. 283, March 1999

# ➔ The mitochondrial ribosome



- Ratio of protein:RNA in the mitochondrial ribosome (~69:~31) is inverse of the ratio in the bacterial ribosome (~33:~67)
- Proteins are more abundant in mitochondrial ribosomes than in bacterial ribosomes (~70-80 against ~60) and are larger



The 3D structure of the RNA of the mitochondrial ribosomal LSU of *C. elegans* (in plain dots) is compared to the 3D structure of a bacterial rRNA (suggested in gray line)

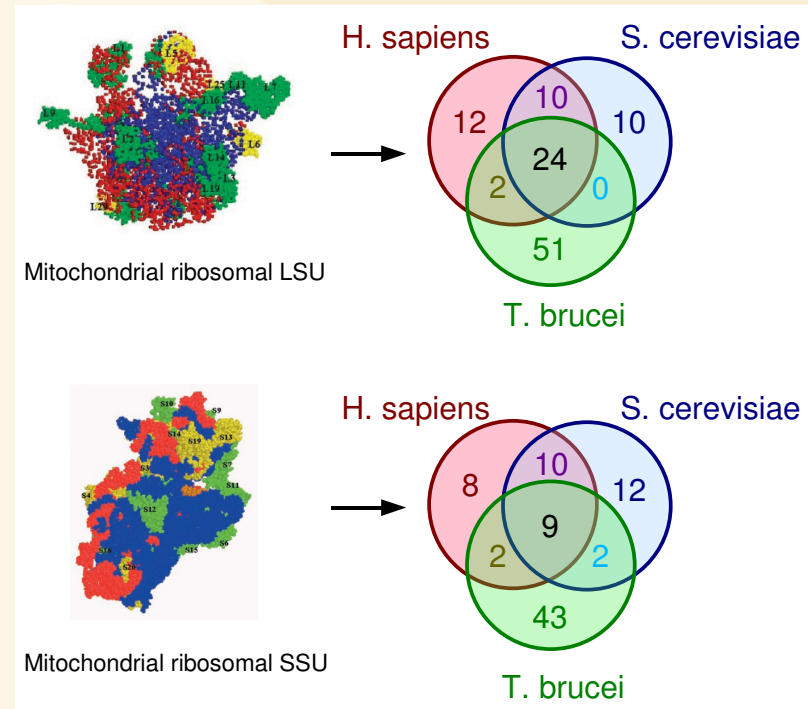
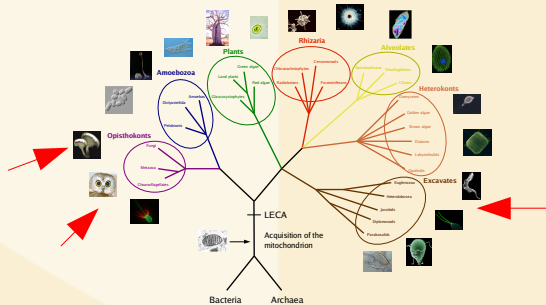


# ➔ The mitochondrial ribosome



## Experimental characterizations :

- 48 proteins in the LSU and 29 in the SSU in mammals
- 44 proteins in the LSU and 33 in the SSU in yeast
- 77 proteins in the LSU and 56 in the SSU in kinetoplastids

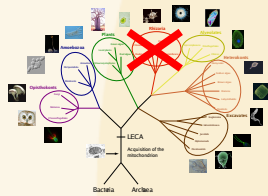




## Construction of HMM models for the 195 known mitochondrial ribosomal protein families

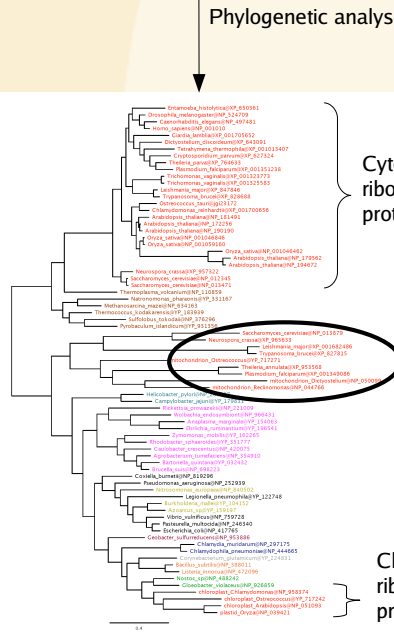
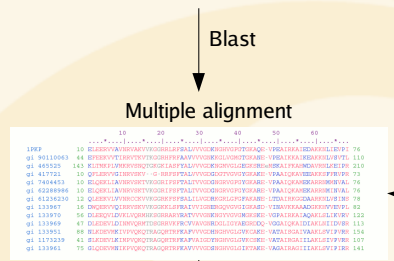
### Database :

• 38 complete eukaryotic genomes from 6 supergroups



• 50 complete bacterial and archaeal genomes from all phyla

For each MRP characterized experimentally ( $\alpha$ -proteobacteria, mammals, yeast, kinetoplastids)



HMM homology searches

N iterations

Presence/absence table

MRPs	Species				
	A	B	C	D	E
1	X	X	X	X	X
2	X	X	X	X	X
3	X	X	X	X	X
4	X	X	X	X	X
5	X	X	X	X	X
6	X	X	X	X	X
7	X	X	X	X	X
8	X	X	X	X	X

Identification of proteins of mitochondrial origin with respect to cytoplasmic or chloroplastic counterparts.

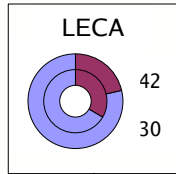
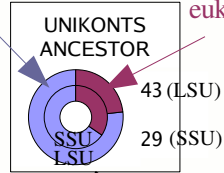


# 19 new proteins between the FECA and the LECA

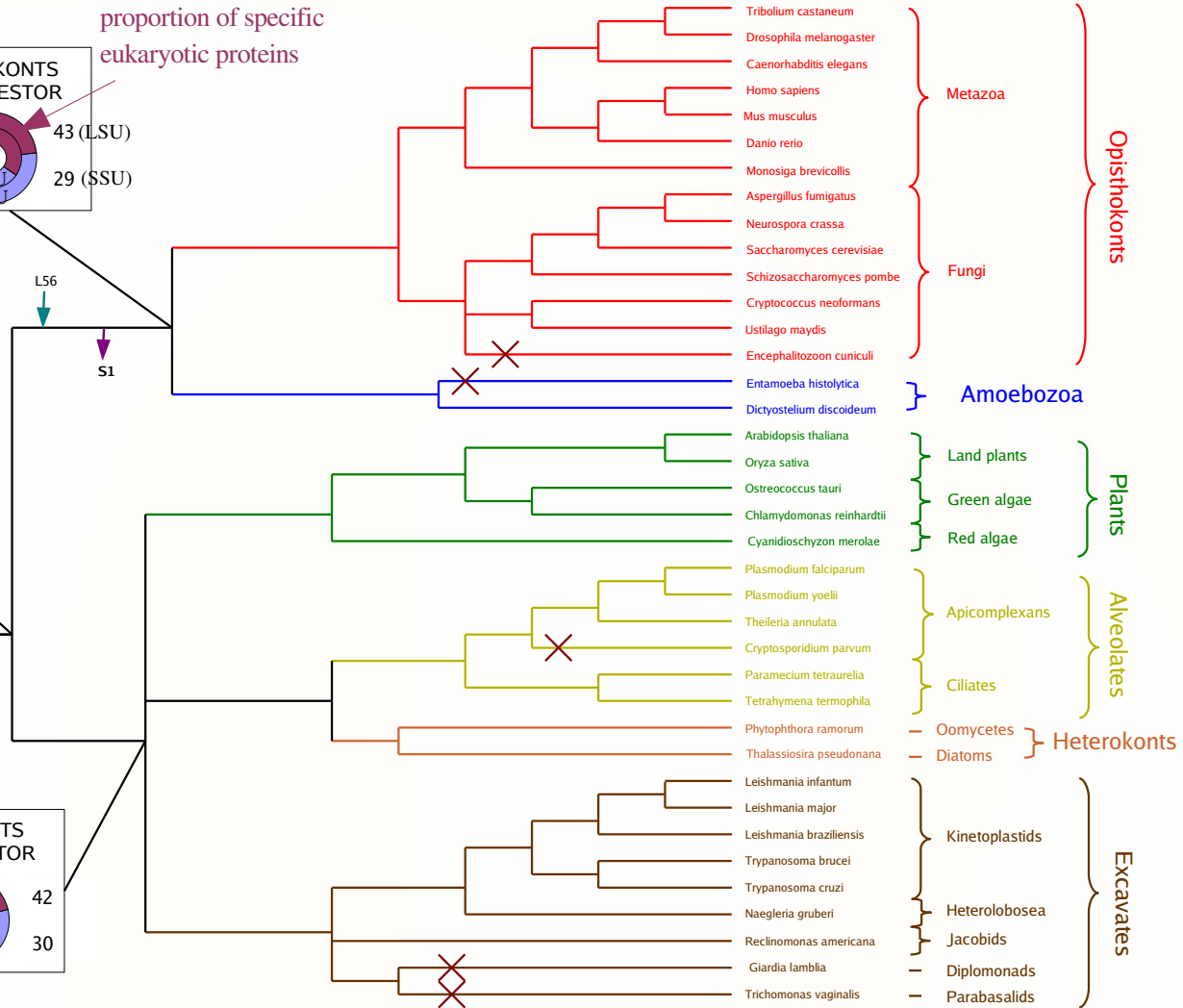
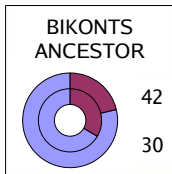


proportion of proteins of bacterial origin

proportion of specific eukaryotic proteins

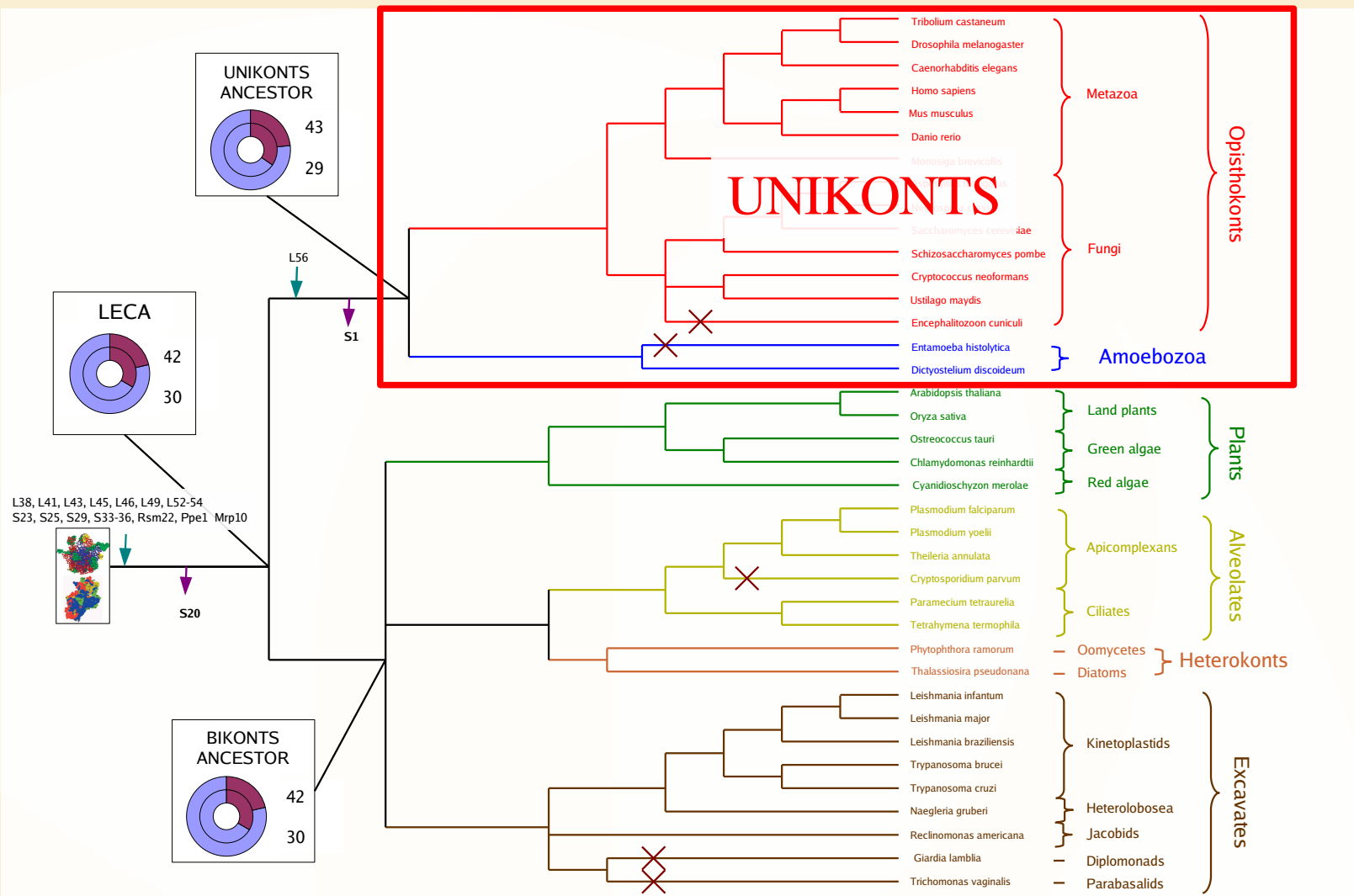


L38, L41, L43, L45, L46, L49, L52-54  
S23, S25, S29, S33-36, Rsm22, Ppe1, Mrp10



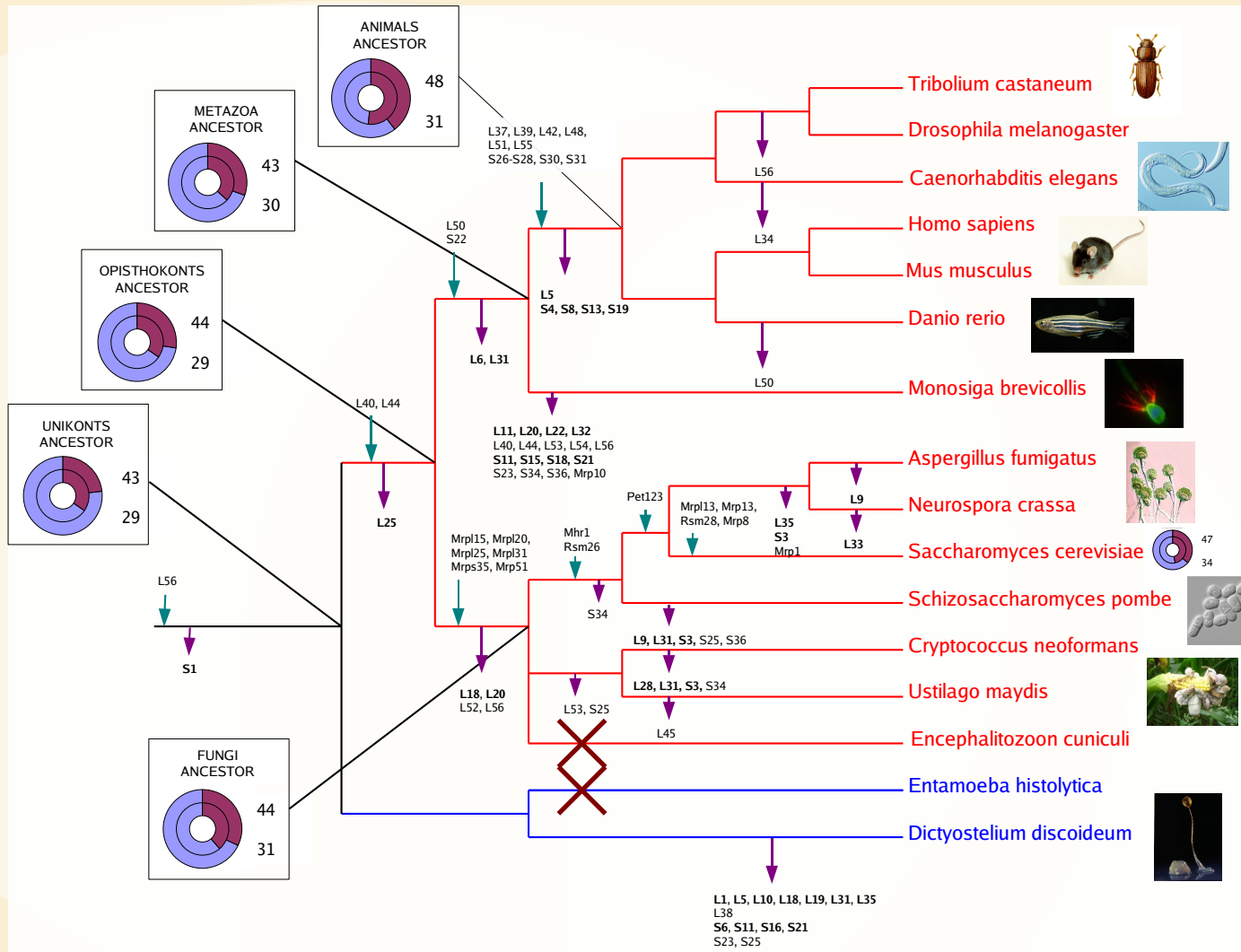


# A very dynamic evolution



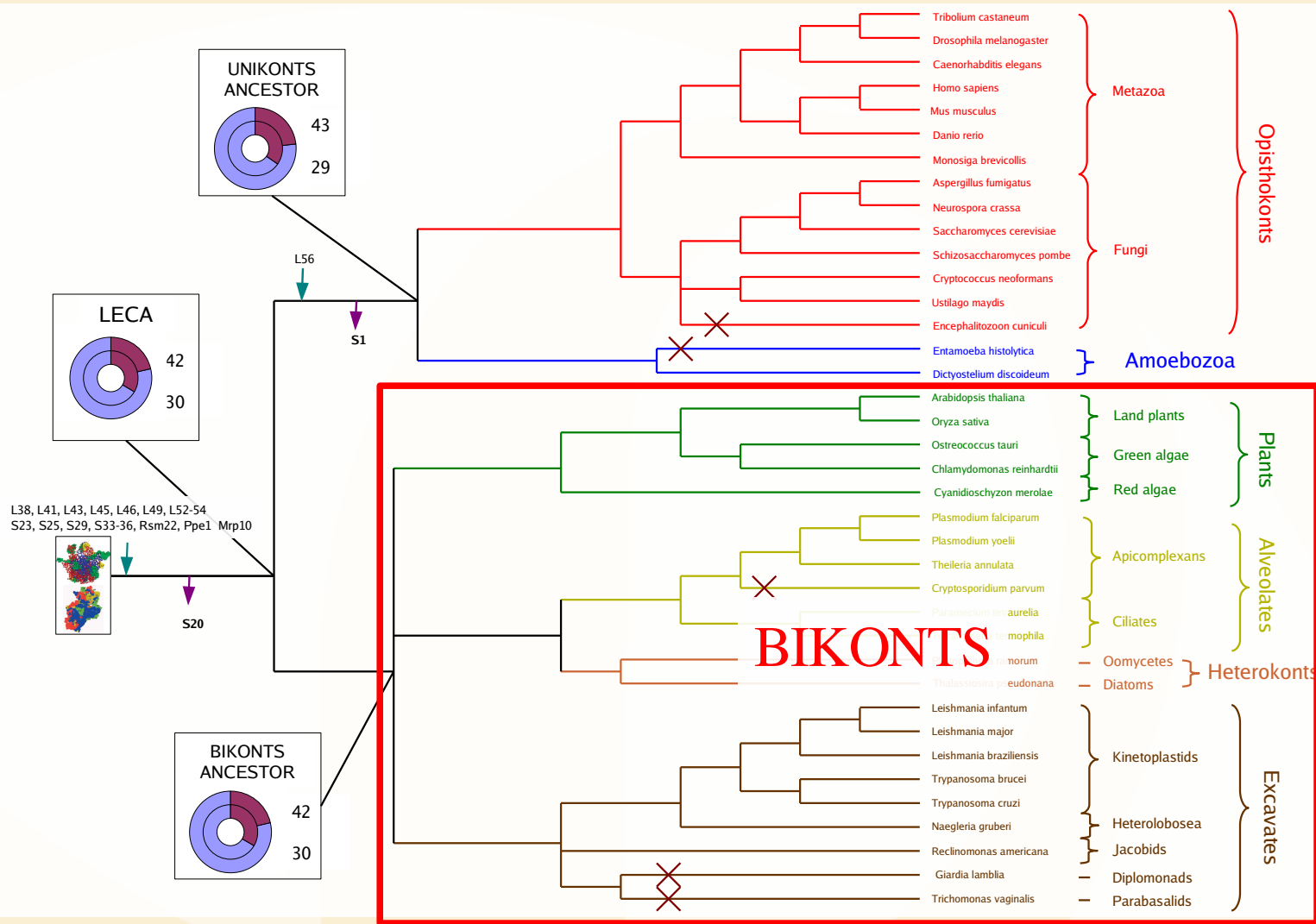


# A very dynamic evolution



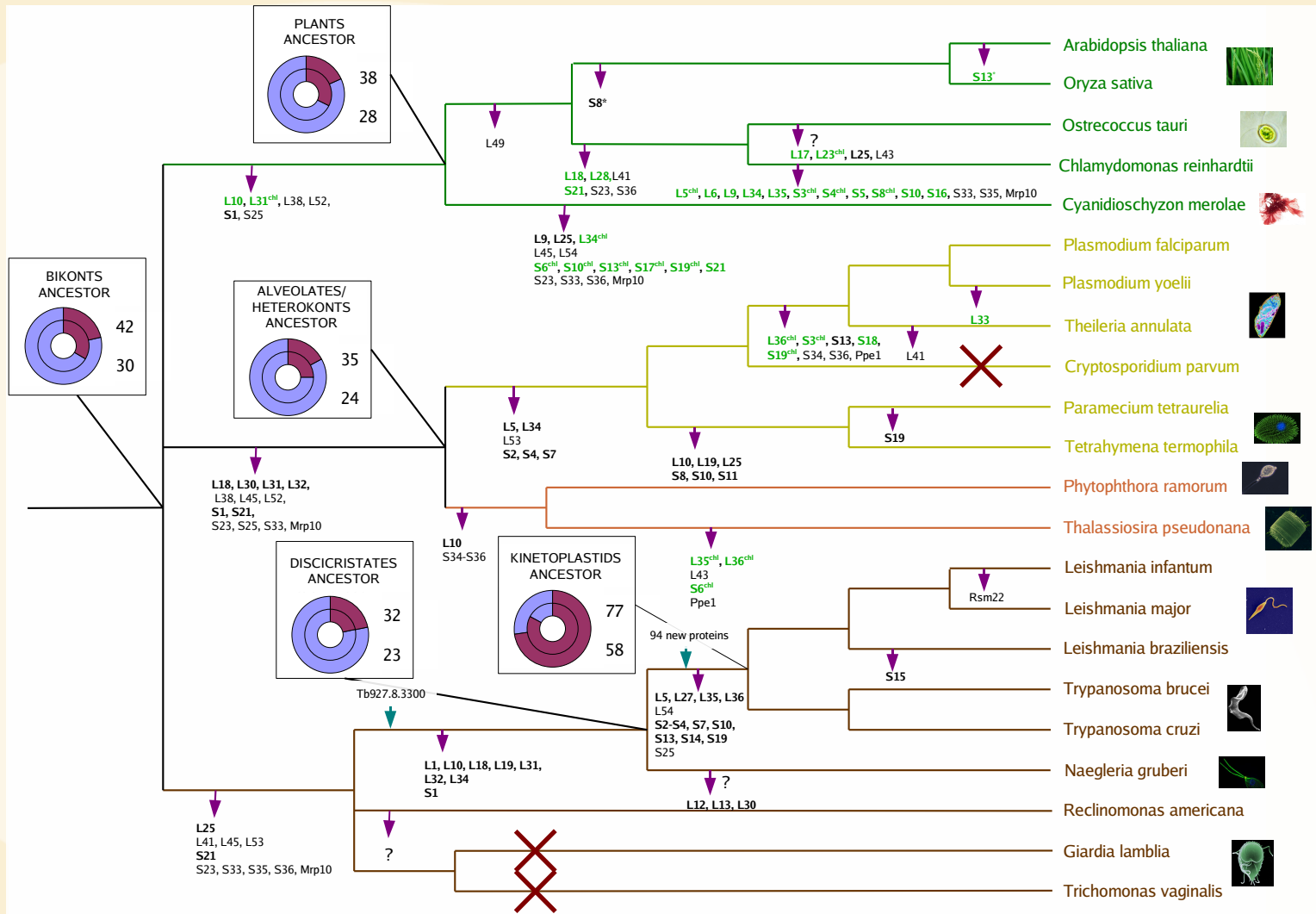


# The importance of experimental characterizations





# The importance of experimental characterizations



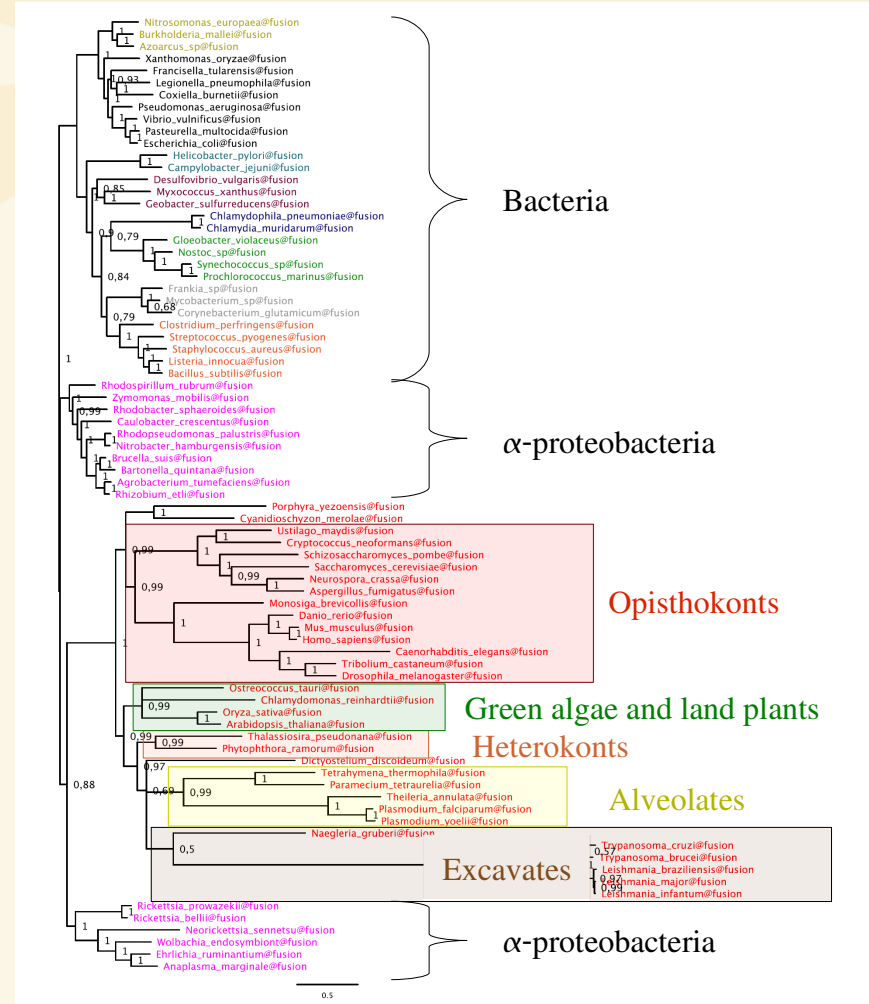


# Strong support for the $\alpha$ -proteobacterial origin of the mitochondrial ribosomal proteins despite their rapid evolution



56 proteins concatenated (4133 positions)

= > Despite the rapid evolution of mitochondrial ribosomal proteins, the  $\alpha$ -proteobacterial origin is well recovered



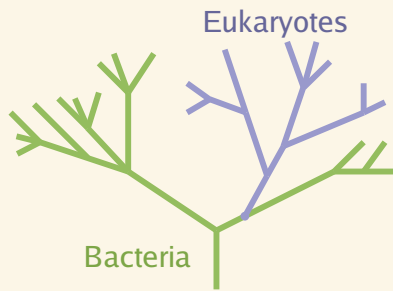




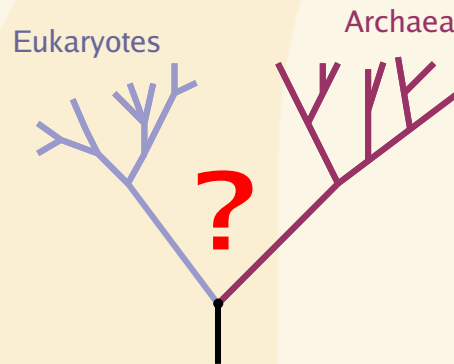
# What about cytosolic ribosomes ?



**$\alpha$ -proteobacterial origin  
of the mitochondrial  
ribosome**



**evolution of the cytosolic  
ribosome ?**

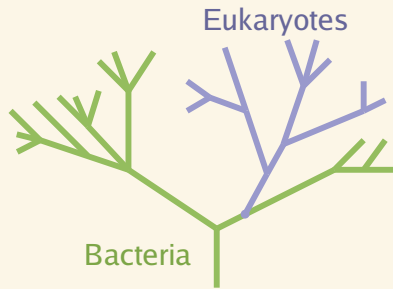




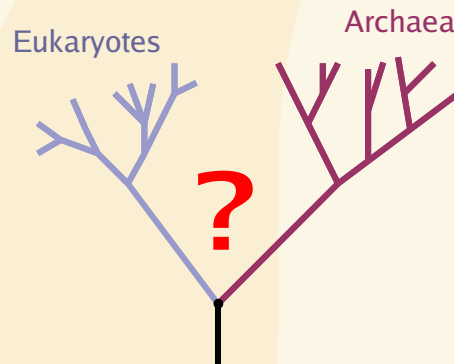
# What about cytosolic ribosomes ?



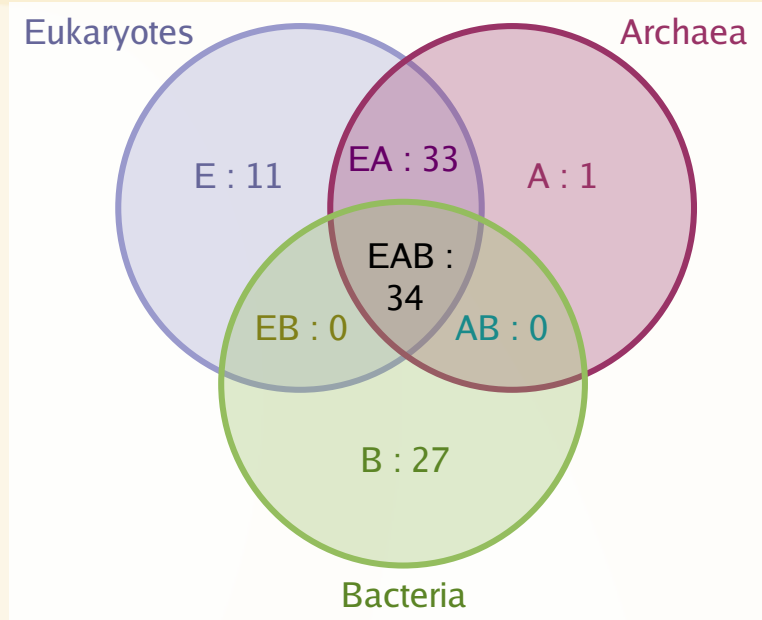
**$\alpha$ -proteobacterial origin of the mitochondrial ribosome**



**evolution of the cytosolic ribosome ?**



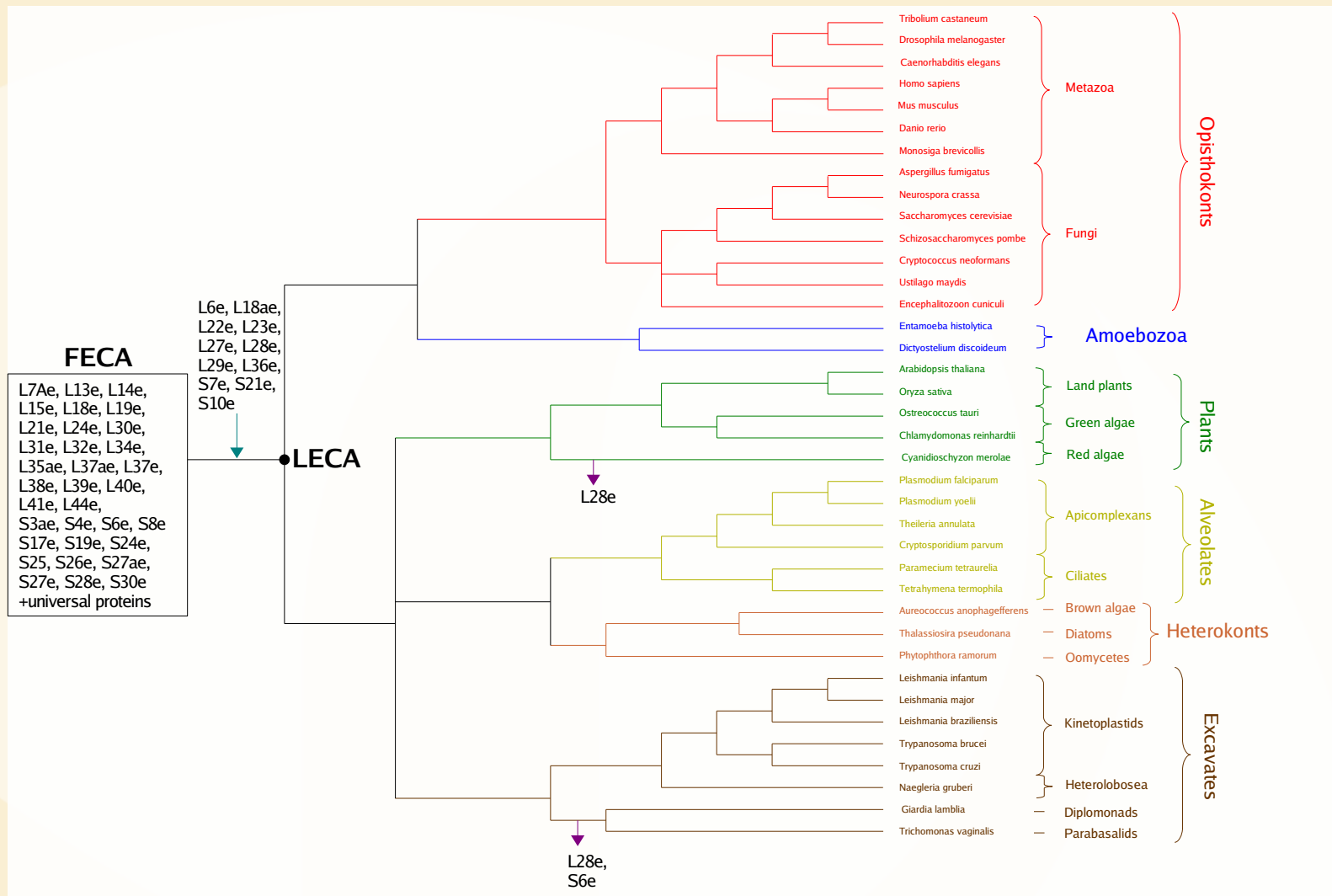
**Families of ribosomal proteins :**



ref. Lecompte O., NAR, 2002



# The slow evolution of the cytosolic ribosome

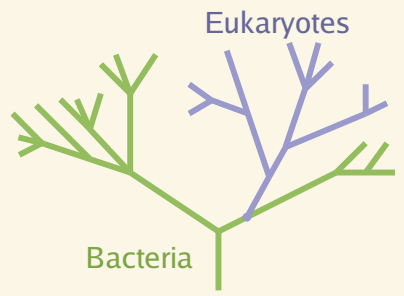




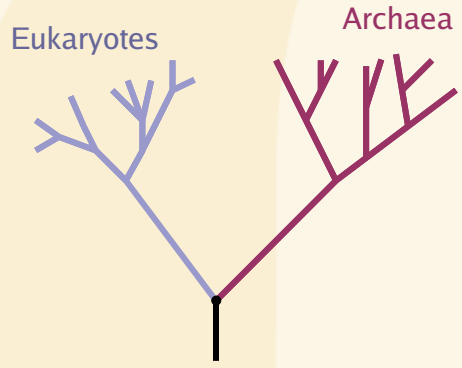
# Comparative analysis of mitochondrial and cytosolic ribosomes evolution plead for the Archezoa hypothesis



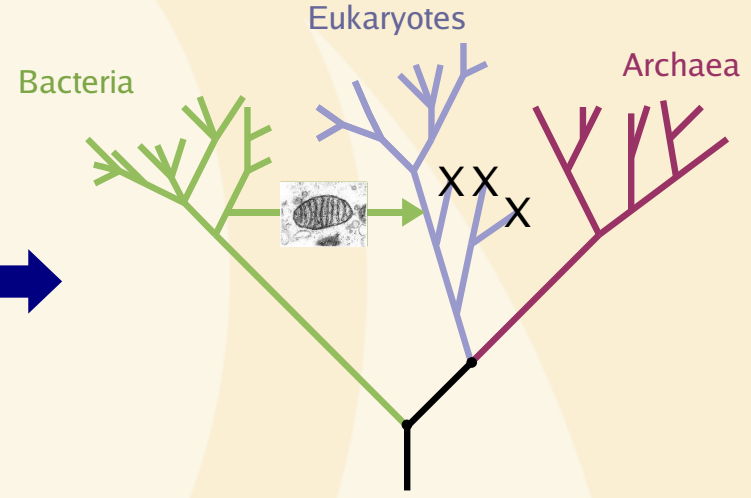
**$\alpha$ -proteobacterial origin of the mitochondrial ribosome**



**Archaea and Eukaryotes share a common ancestor**



**Archezoa tree**



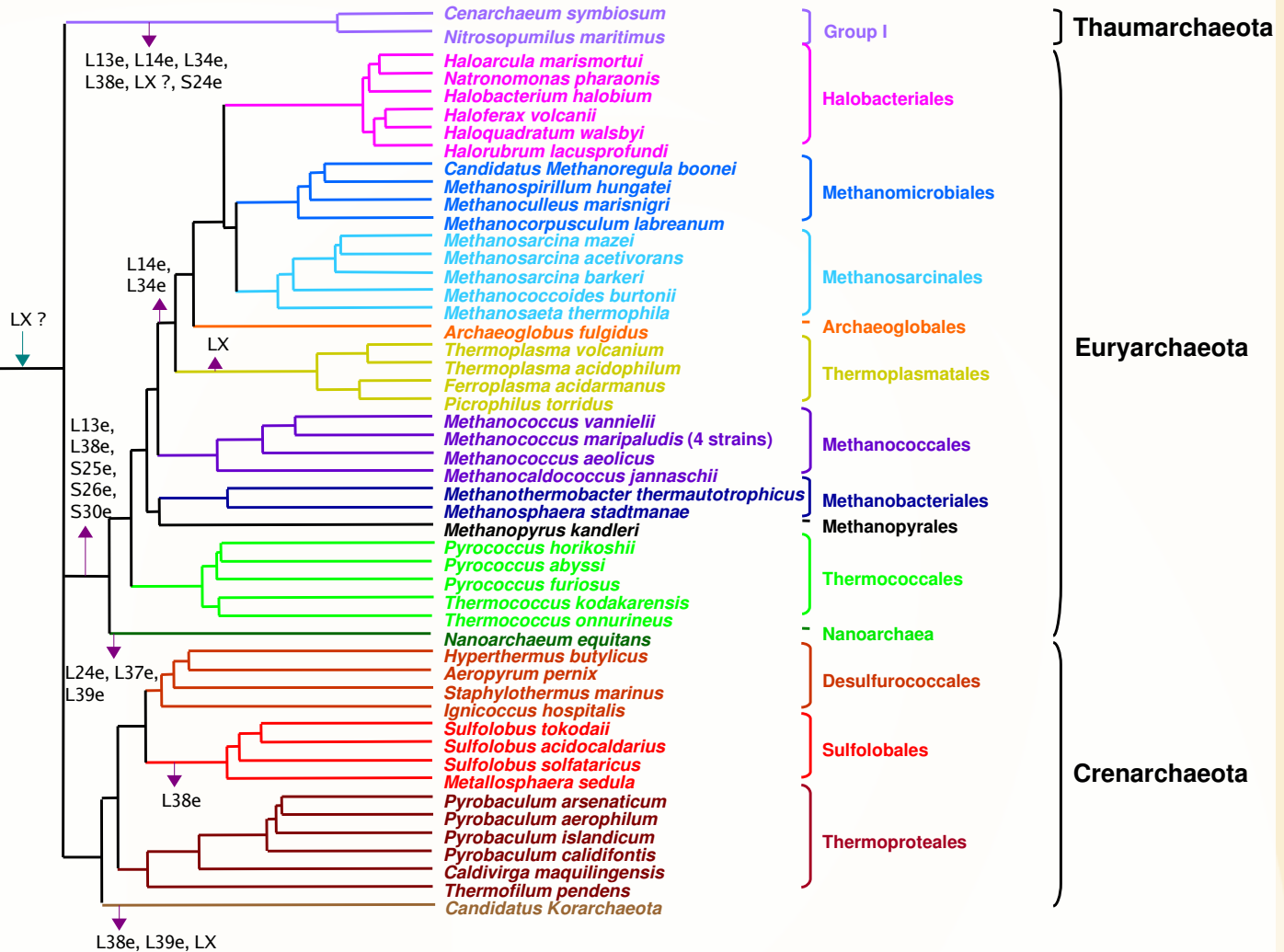


# The archaeal ribosome : a reductive evolution



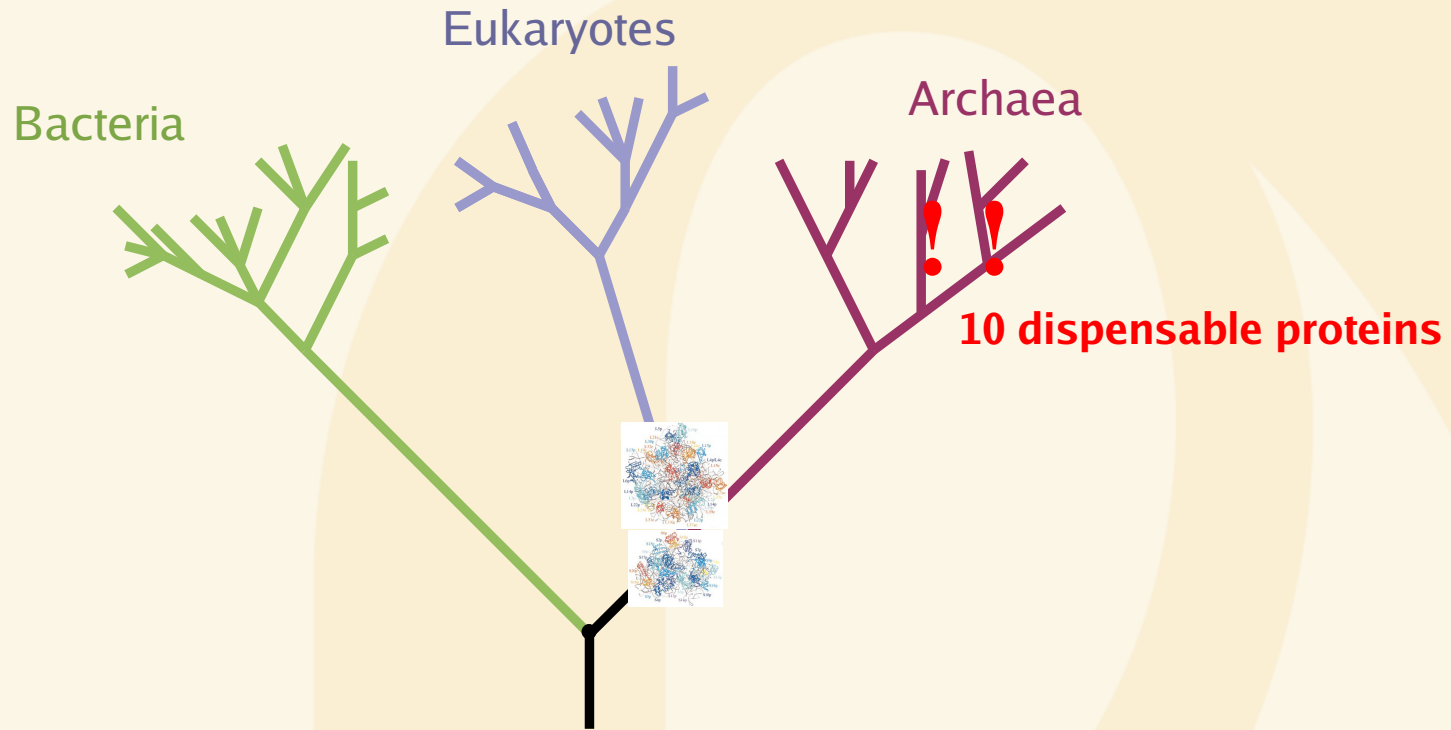
## First archaeal ancestor

L7Ae, L13e, L14e, L15e, L18e, L19e, L21e, L24e, L30e, L31e, L32e, L34e, L35ae, L37ae, L37e, L38e, L39e, L40e, L41e, L44e, S3ae, S4e, S6e, S8e, S17e, S19e, S24e, S25, S26e, S27ae, S27e, S28e, S30e + universal proteins



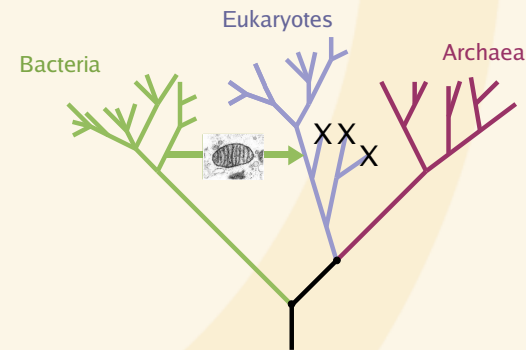


# Different tendencies in the evolution of archaeal and eukaryotic ribosomes





- **Phylogenomic is a powerful tool to reconstruct the origin and evolution of cellular systems**
- **Importance of the combination with proteomics**
- **Eukaryotic mitochondrial ribosomes evolve very fast but their origin from within bacteria is well recovered by molecular phylogeny**
- **Eukaryotic cytosolic ribosomes evolve much more slowly and indicate a sister relationship between archaea and eukaryotes**





INSTITUT PASTEUR

**Merci !**

**Special thanks :**

**to Simonetta Gribaldo, Patrick Forterre, Celine Petitjean,  
Alexis Criscuolo and all other BMGE members (Institut  
Pasteur)**

**to Celine Brochier (Université de Provence - Aix-Marseille I)**

