

Genomic architecture of eukaryotes

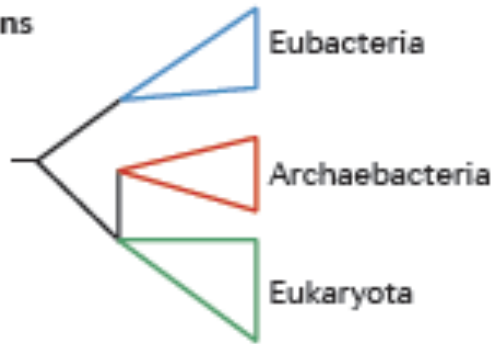
Early days



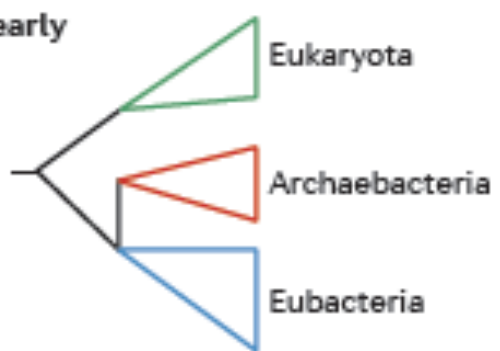
- Eukaryotes are chimeras
- The exact details of the original symbiotic event are still being investigated (mainly using genomics)
 - Hypothesis 1 – relies on biochemistry (Martin et al.)
 - “hydrogen hypothesis”
 - Symbiotic
 - Mito-early
 - Hypothesis 2 – you are what you eat (Calvalier-Smith et al.)
 - Phagocytosis
 - Engulfing
 - Mito-late

Where did eukaryotes come from?

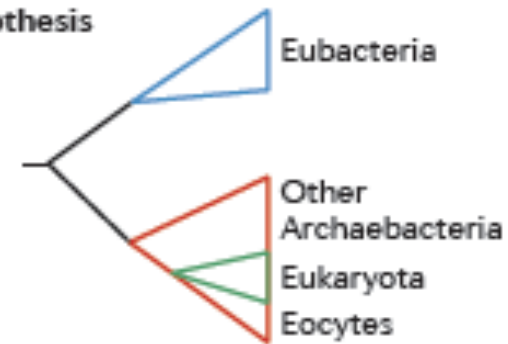
a Three-domains hypothesis



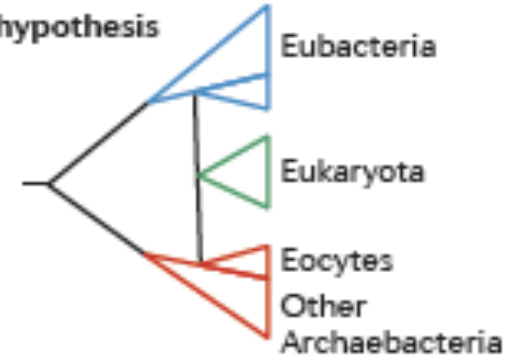
b Eukaryotes-early hypothesis



c Eocyte hypothesis



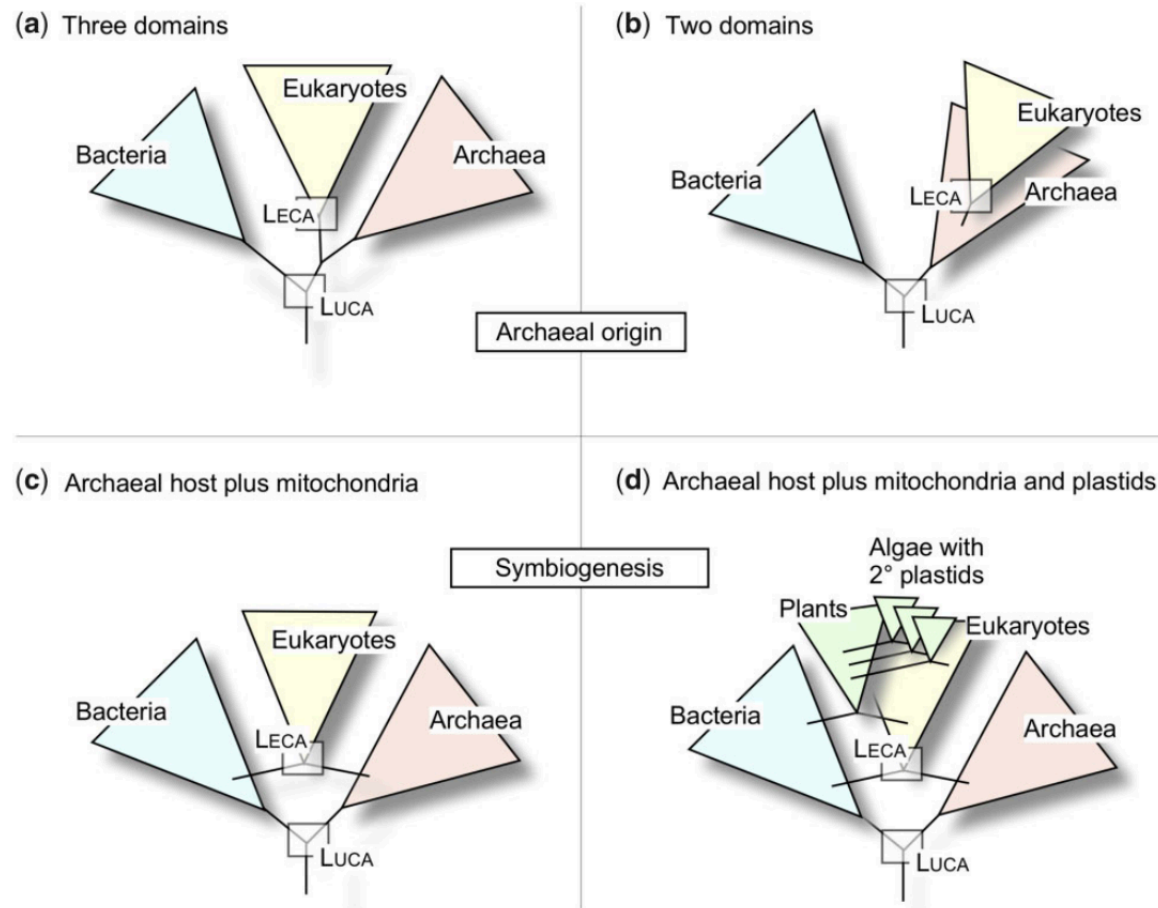
d Ring of life hypothesis



Eukaryotes genomes are chimeric

Table 1
Proportion of Bacterial and Archaeal Derived Genes in Eukaryotic Genomes

Group	Archaeal	Bacterial
All eukaryotes	0.44	0.56
All without plastids ^a	0.47	0.53
All with plastids ^b	0.39	0.61
Land plants	0.33	0.67
Opisthokonts	0.46	0.54
Hacrobia	0.38	0.62
SAR	0.50	0.50
Archaeplastida	0.36	0.64
Mycetozoa	0.50	0.50
Excavata	0.58	0.42
Parasites ^c	0.62	0.38



Shopping bag model

- Most euk bacterial genes are not from alphaproteobacteria

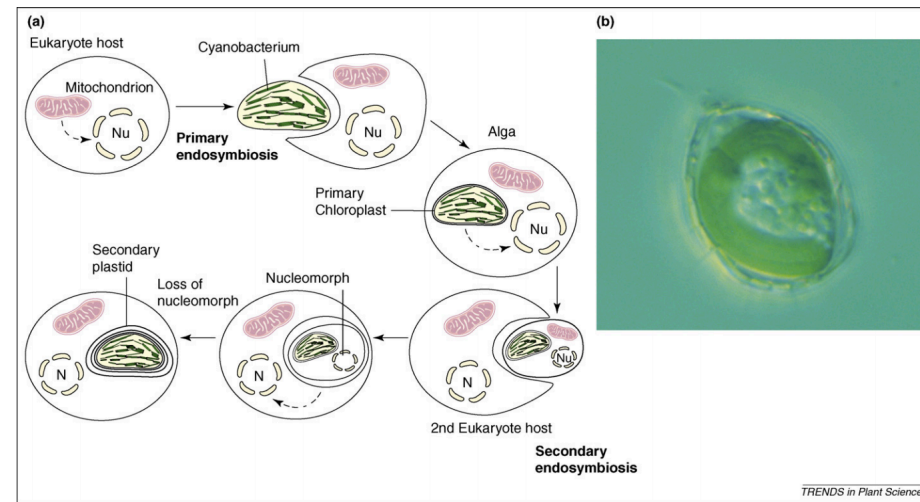
biosis' [57]. It could also be described as the 'shopping bag model'. Your shopping might all be in a bag that came from an identifiable store, and some of the contents of the bag might have come from elsewhere, and you cannot ascribe a single origin to all your shopping.

Larkum et al. 2007

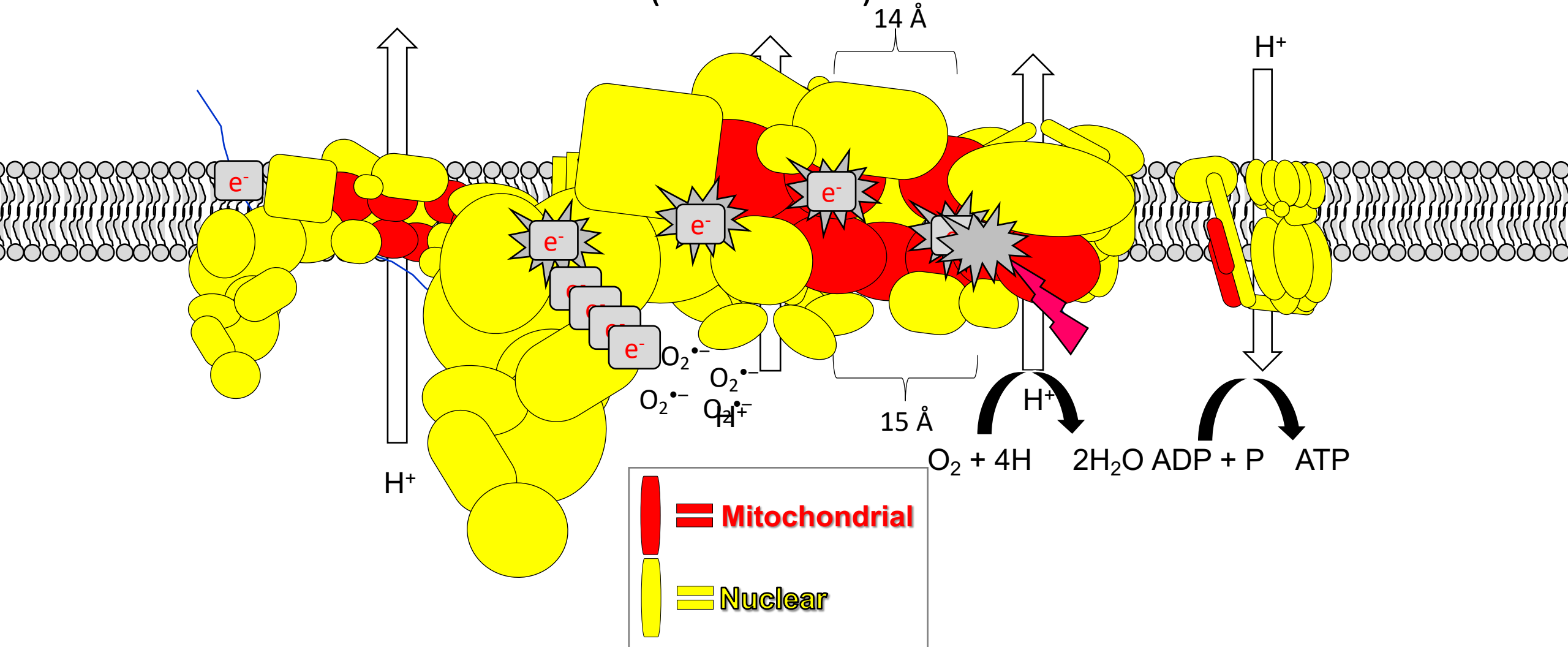
Conclusion

Inherited chimerism is an alternative to the problematic practice of conjuring up additional, gene-donating symbionts at organelle origins to explain gene trees. It merely requires a selective force to associate the symbiont (either plastid or mitochondrion) to its host so that the endosymbiosis (one cell living within another) can be established and gene transfer from the symbiont can commence. It places no constraints on the collections of genes that the plastid and the mitochondrial symbionts possessed, other than that it needs to be a genome-sized collection, not tens of thousands of genes, and it allows freely for LGT among prokaryotes before the endosymbionts become organelles and afterward. LGT among prokaryotes has received much attention in the past decades. Inherited chimerism incorporates LGT among prokaryotes into endosymbiotic theory.

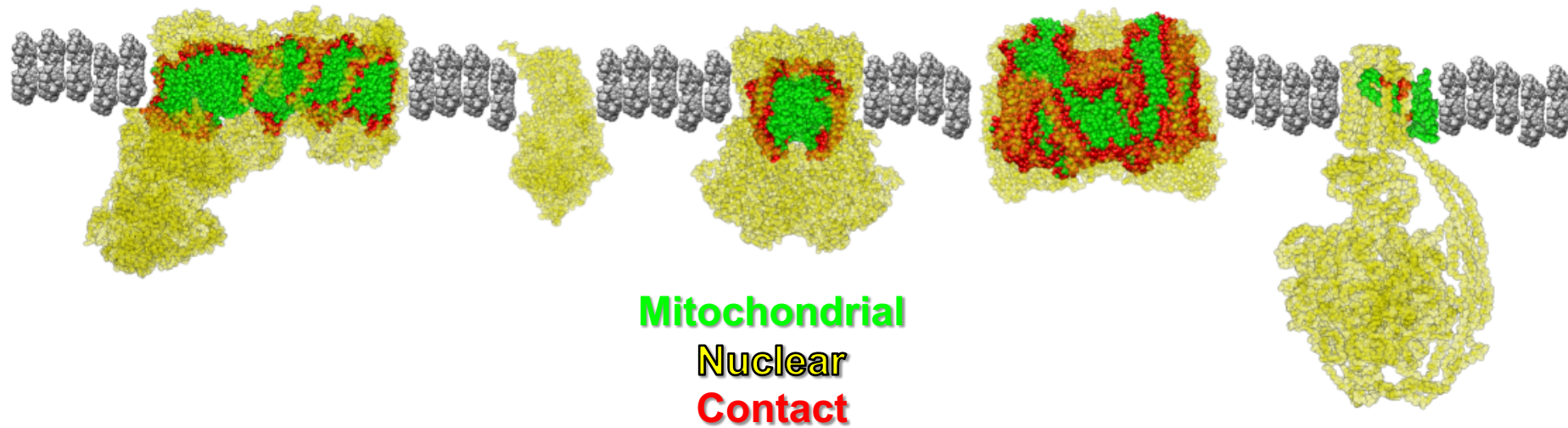
Ku et al. 2015



Oxidative phosphorylation (OXPHOS)



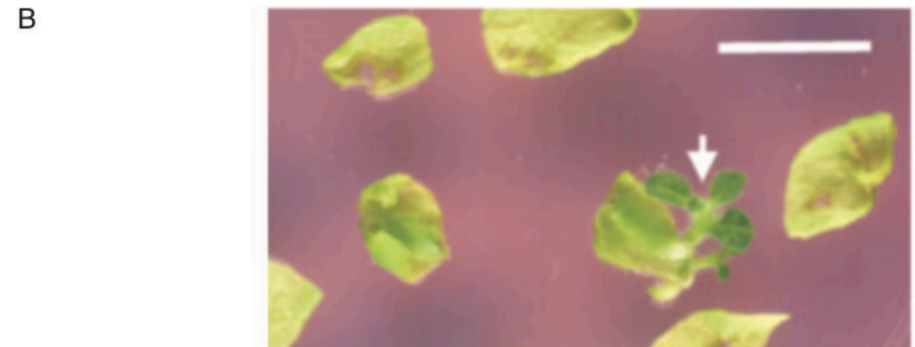
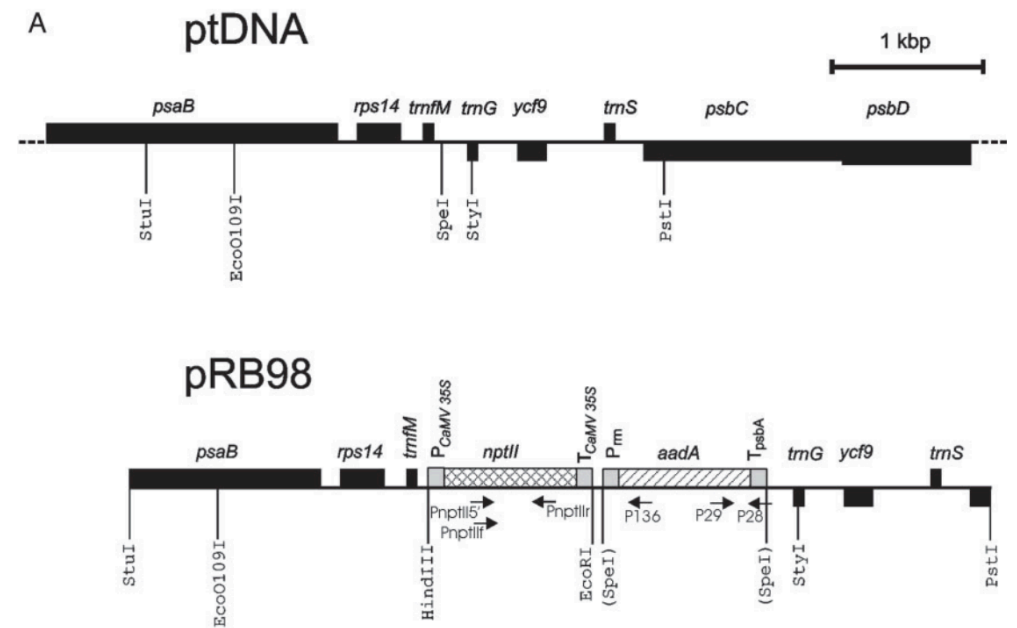
Close up of mammalian ETS



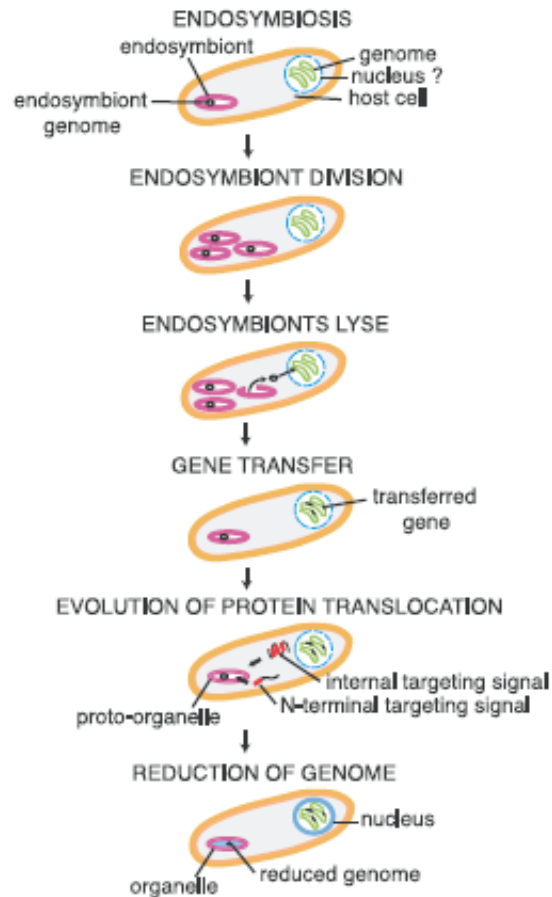
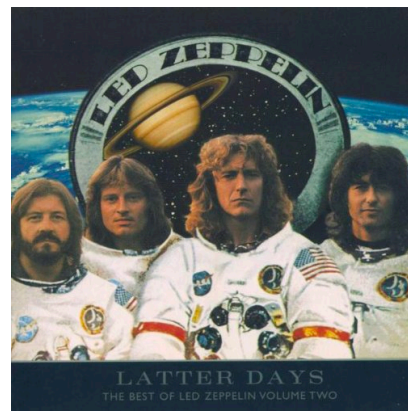
- Coenzyme Q
- Cyt c
- Other complexes in other taxa

Genomic changes after endosymbiosis

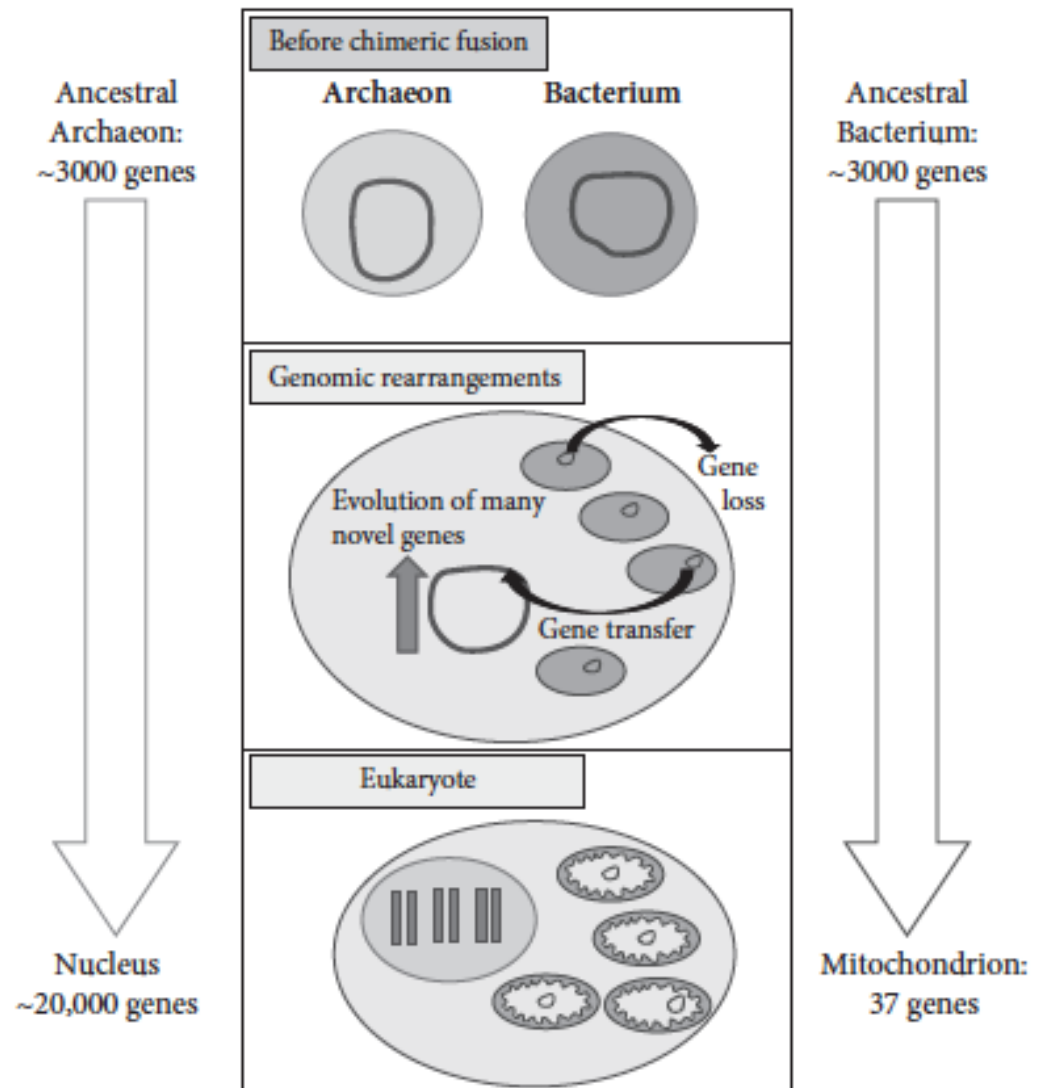
- Loss
- Gain
- Transfer
 - Adaptive reasons
 - Non-adaptive reasons (transfer ratchet)
- Ongoing transfer in plants as a model



Latter days

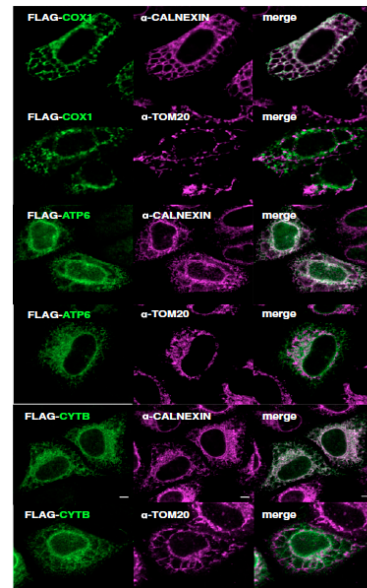


Dyall et al., 2004

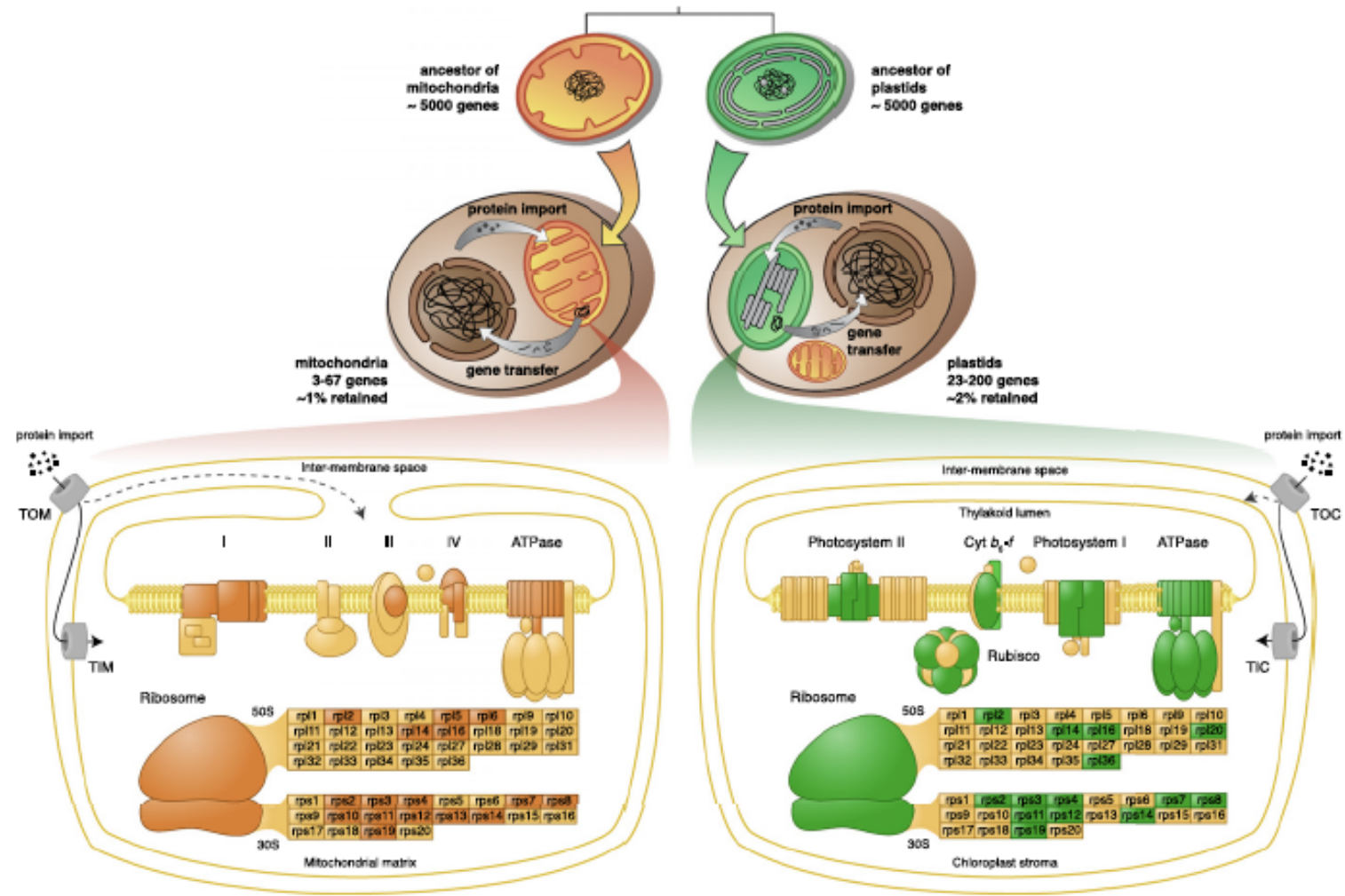


Retention of an mt genome

- CORR hypothesis
- Hydrophobicity hypothesis



Bjorkholm 2015



Allen 2015

Mt genomes: anything goes

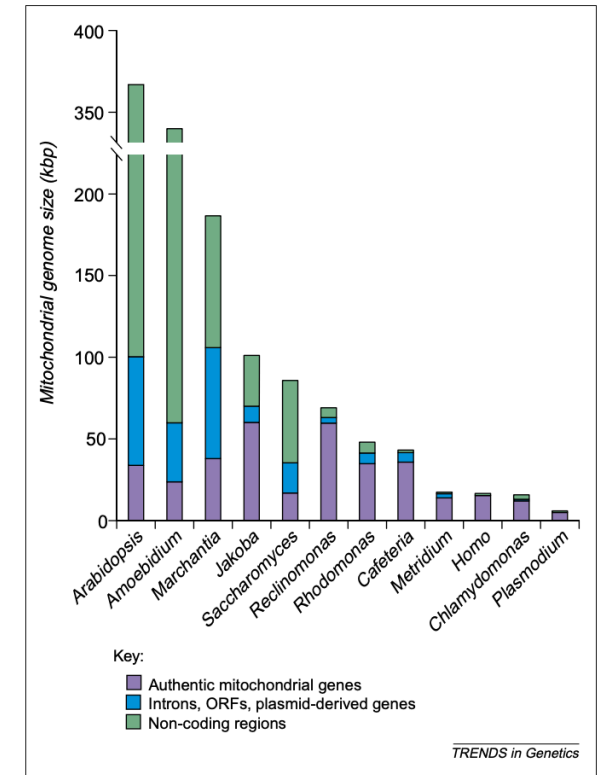
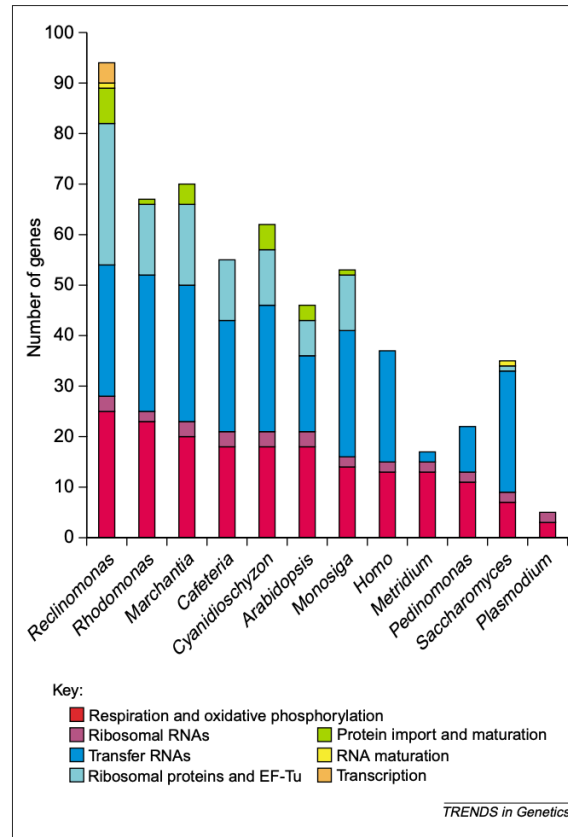
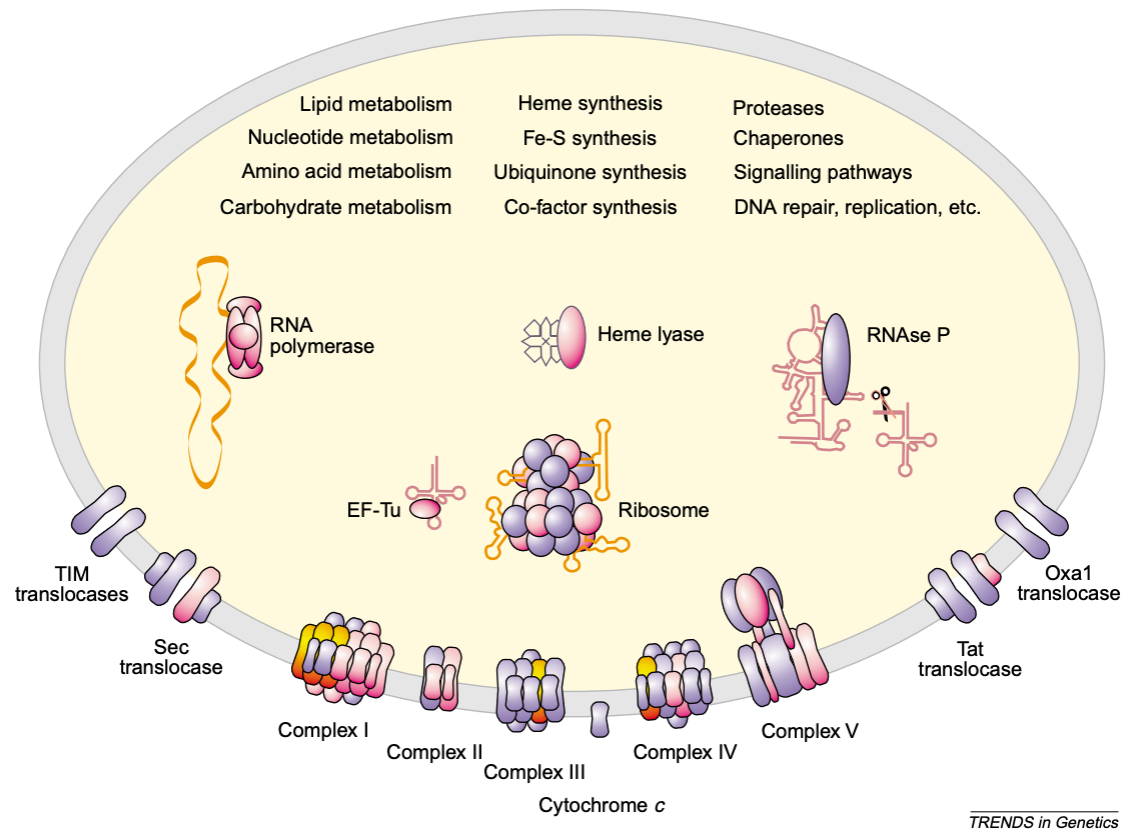
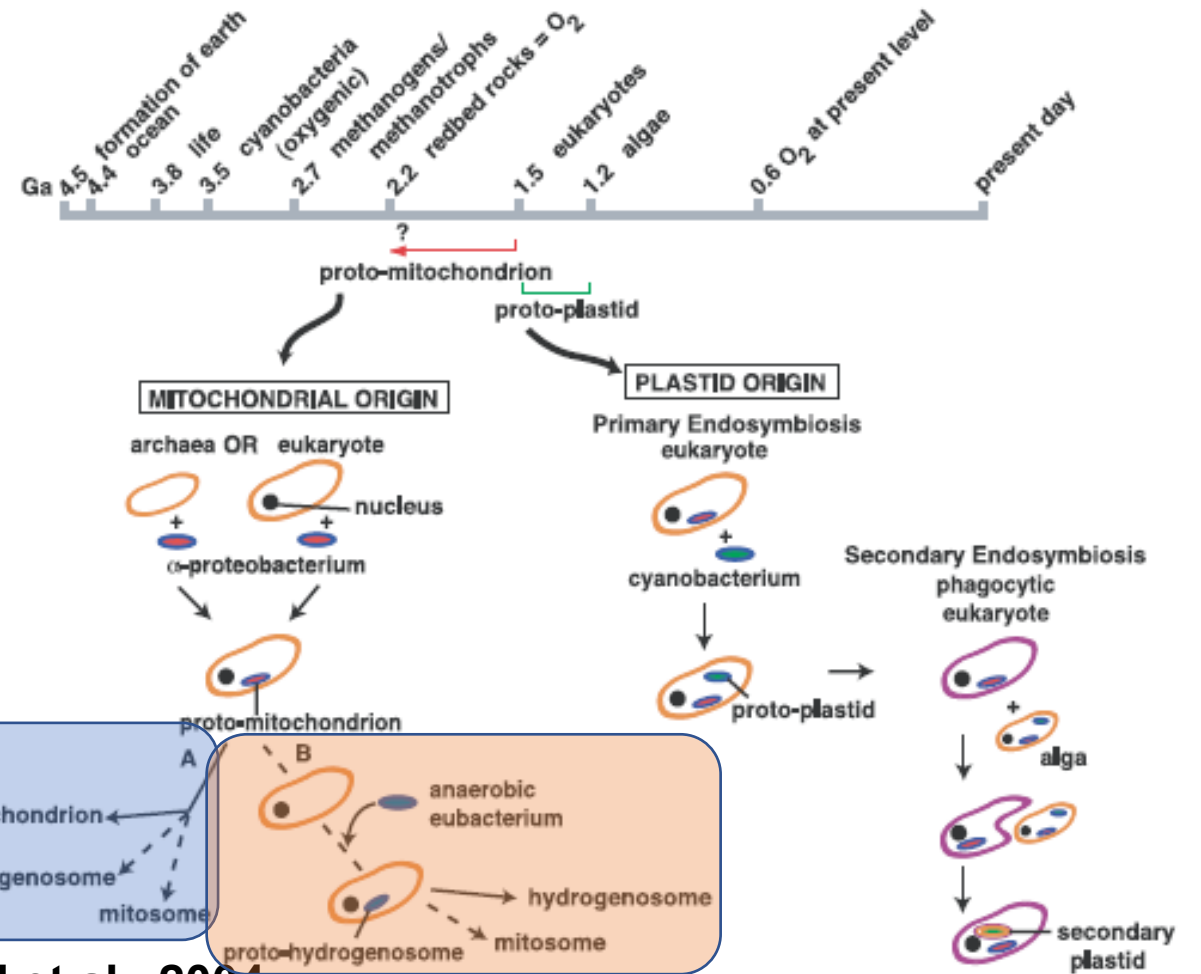
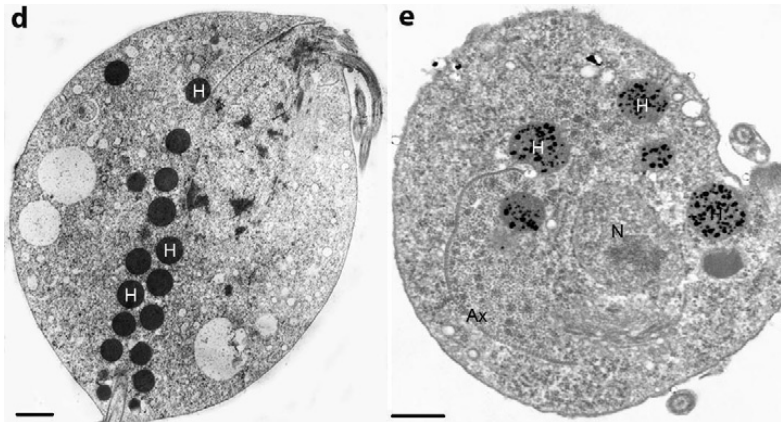
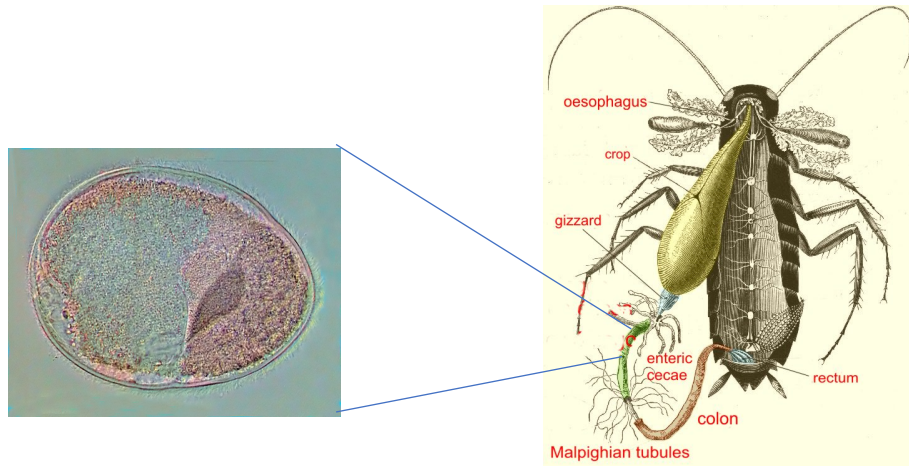


Figure 5. Mitochondrial genome size and coding content across eukaryotes. Length of coding regions of authentic mitochondrial genes (purple), introns, intronic ORFs, phage-like reverse transcriptases and DNA polymerases (blue), and

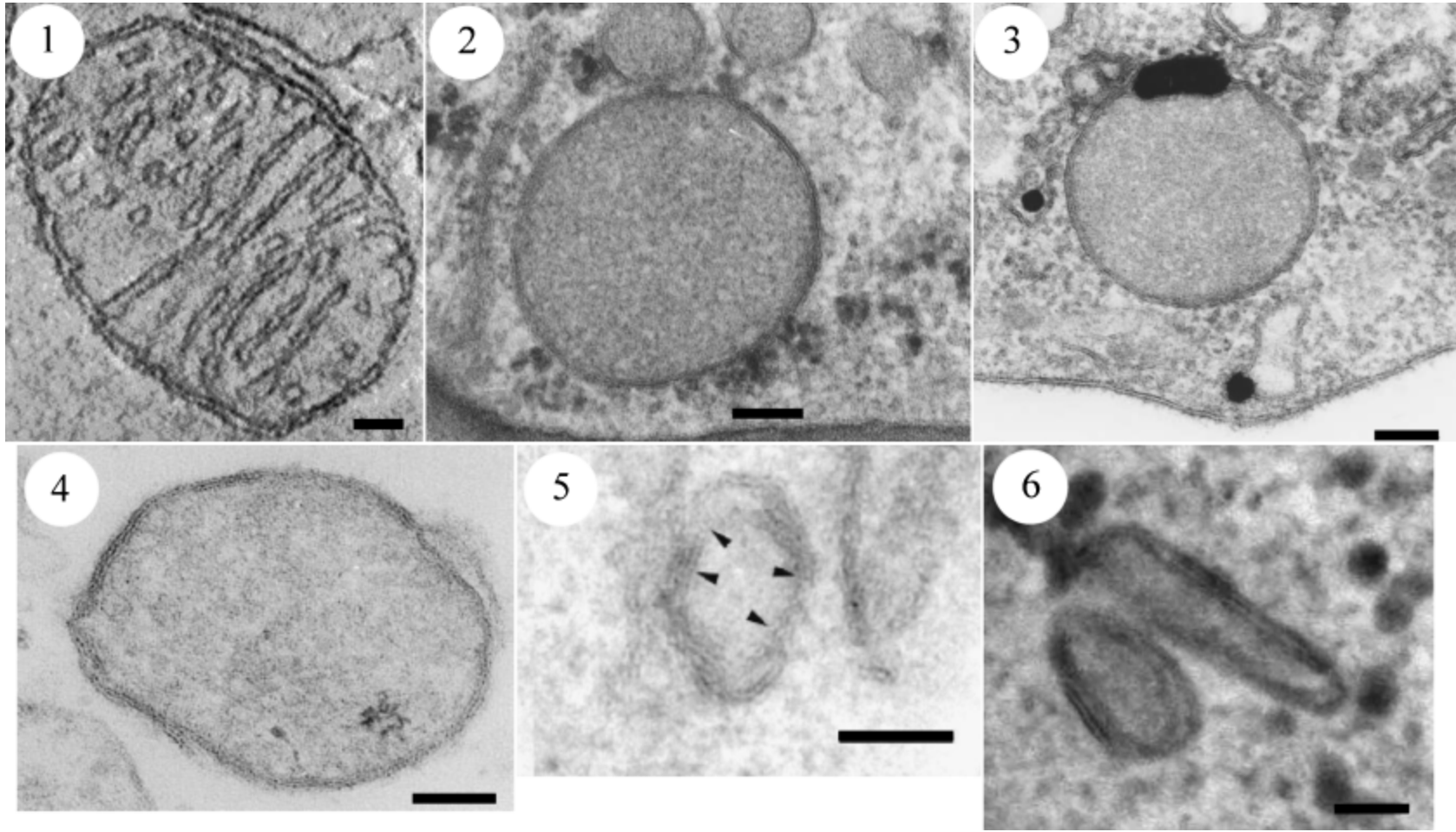
Burger et al. 2012

Hydrogenosomes



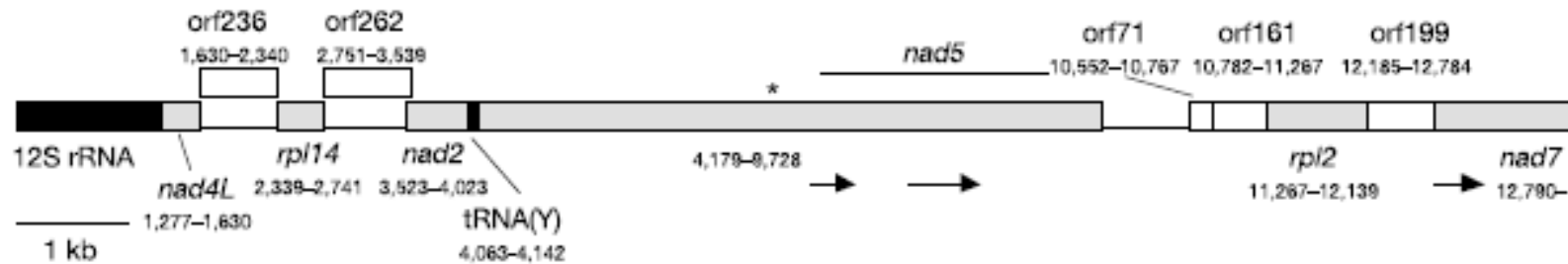
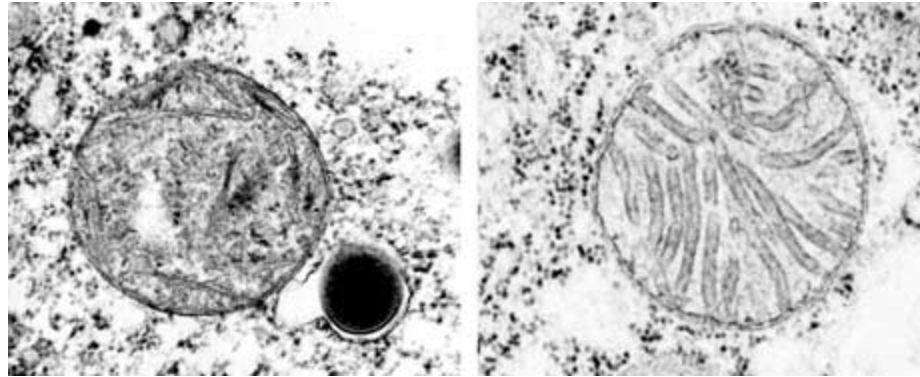
Dyall et al., 2004

Mitosomes



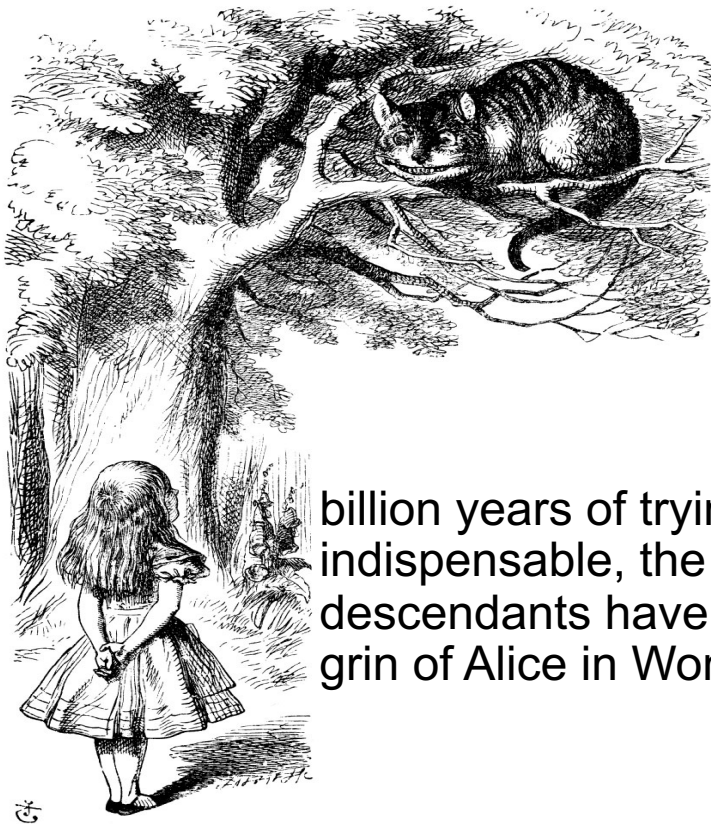
Van Der Giezen, 2009

Archeozoa hypothesis debunked



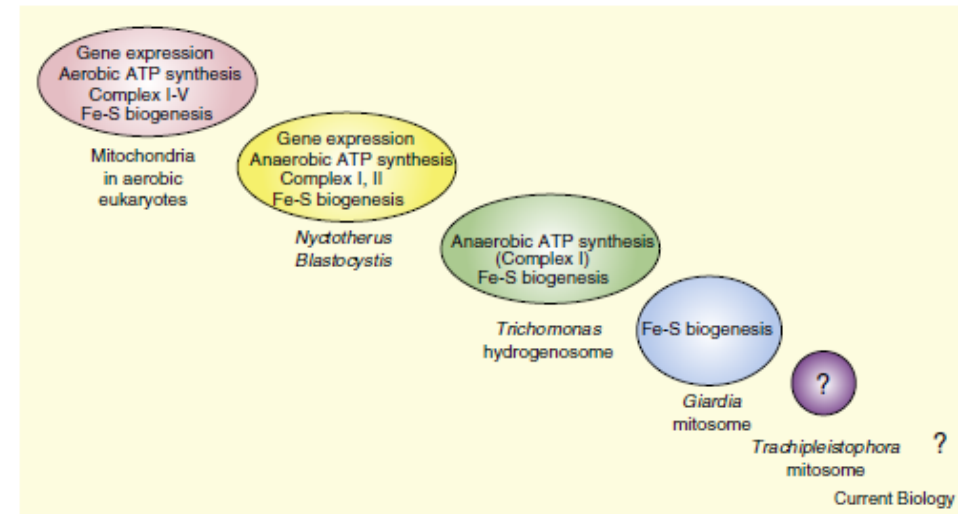
Boxma et al. 2005

MLOs

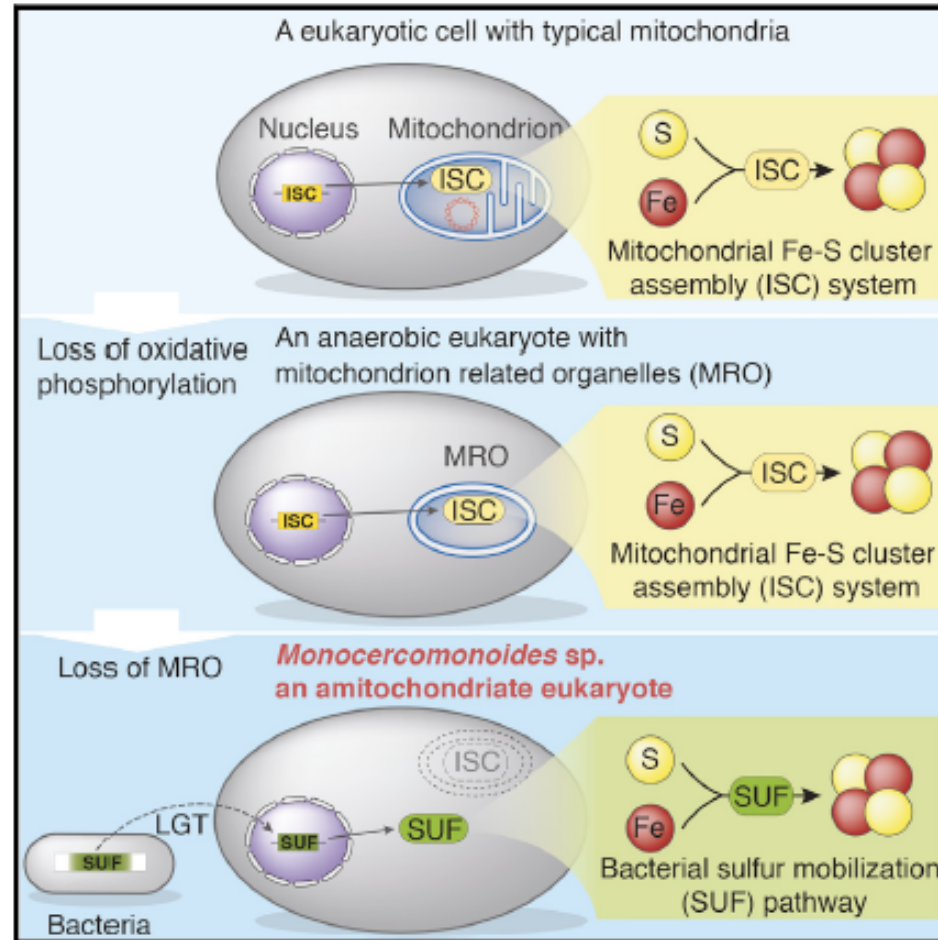


“So there may well be organisms where the whole of this role has been delegated by the mitochondrion, and where after over a billion years of trying to make themselves indispensable, the mitochondrion and its descendants have finally disappeared, like the grin of Alice in Wonderland’s Cheshire Cat.”

—Howe, 2009



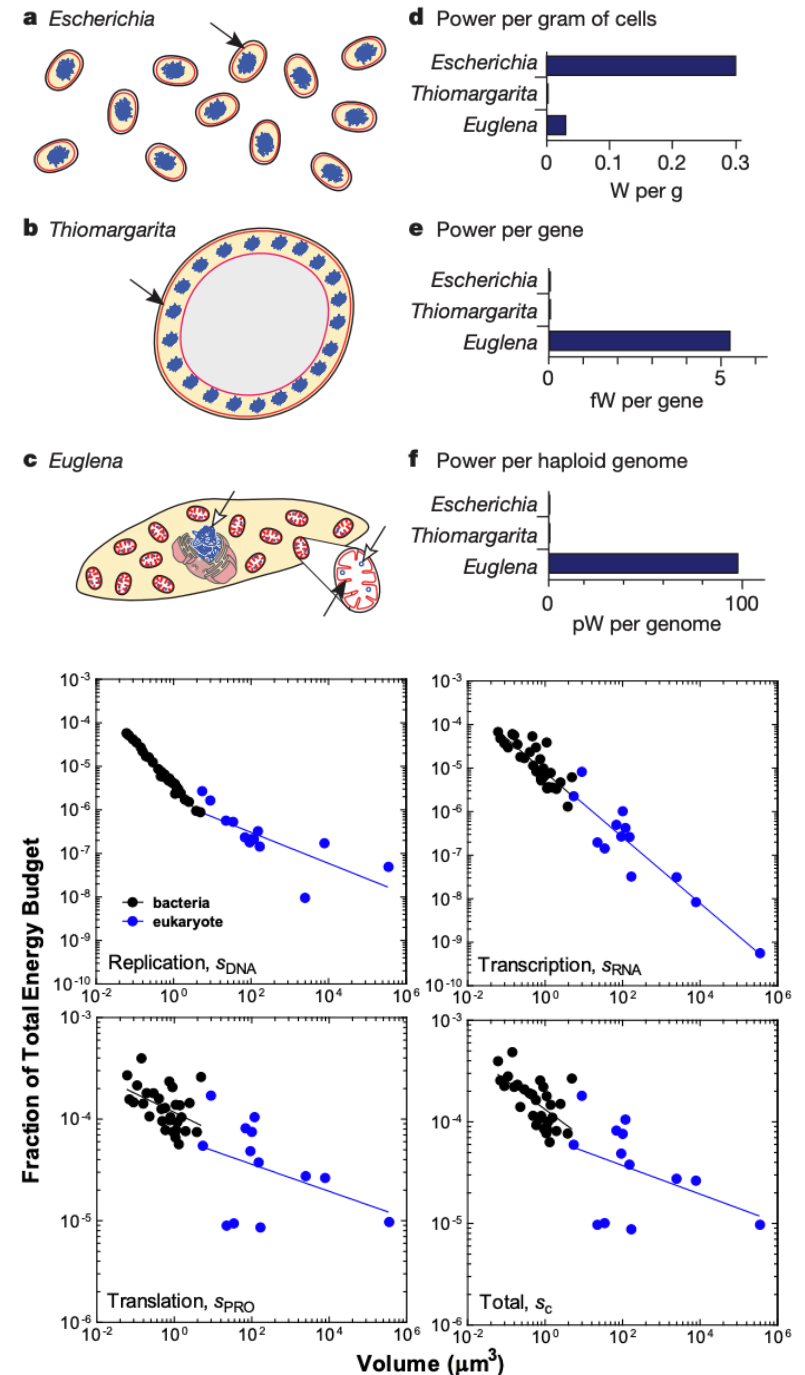
An amitochondrial eukaryote?



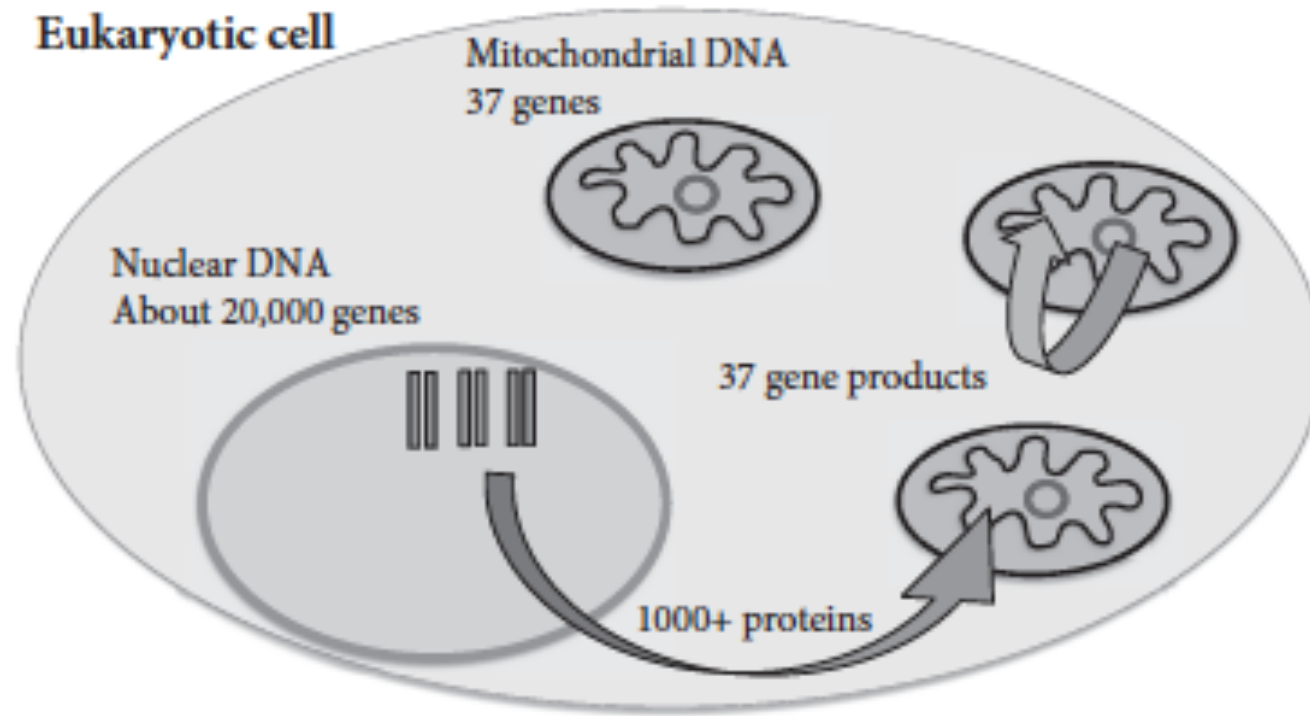
Karnkowska et al. 2016

Hill's deductions

- The train of deductions proceeds as follows:
- complexity requires a large genome;
- a large genome requires a lot of energy (Martin and Lane 2015; Lynch and Marinov 2015);
- massive energy production is only possible via the combined output of many mitochondria;
- and control of such a power system necessitates independent genomes in each mitochondrion.



N-mt genes



Mt mutation rates are variable

