

# ENVIRONMENTAL METAGENOMICS

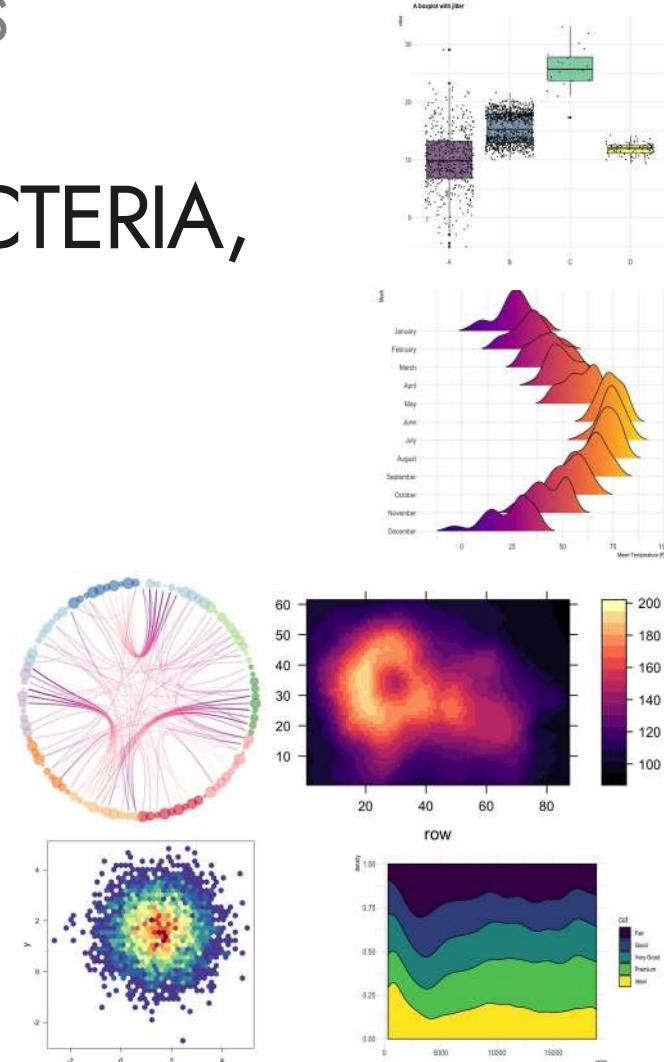
## MICROORGANISMS – BACTERIA, ARCHAEA AND VIRUSES

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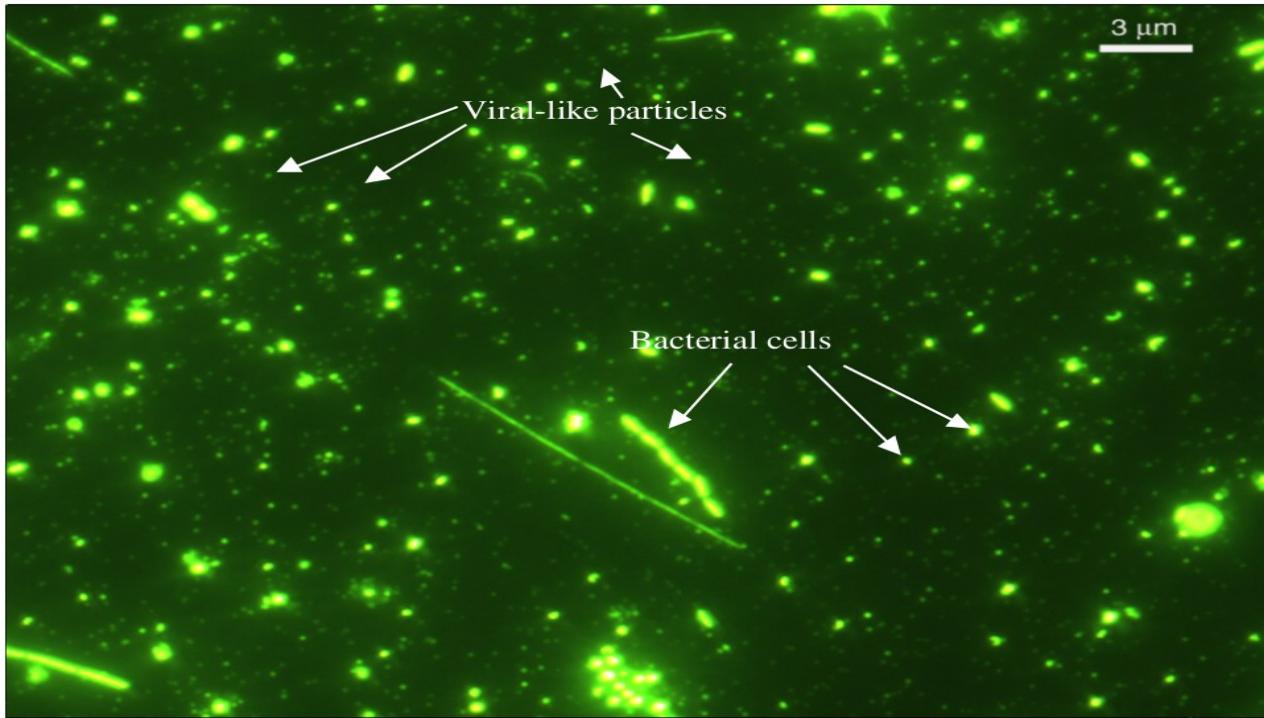
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*Why environmental microbiology?*



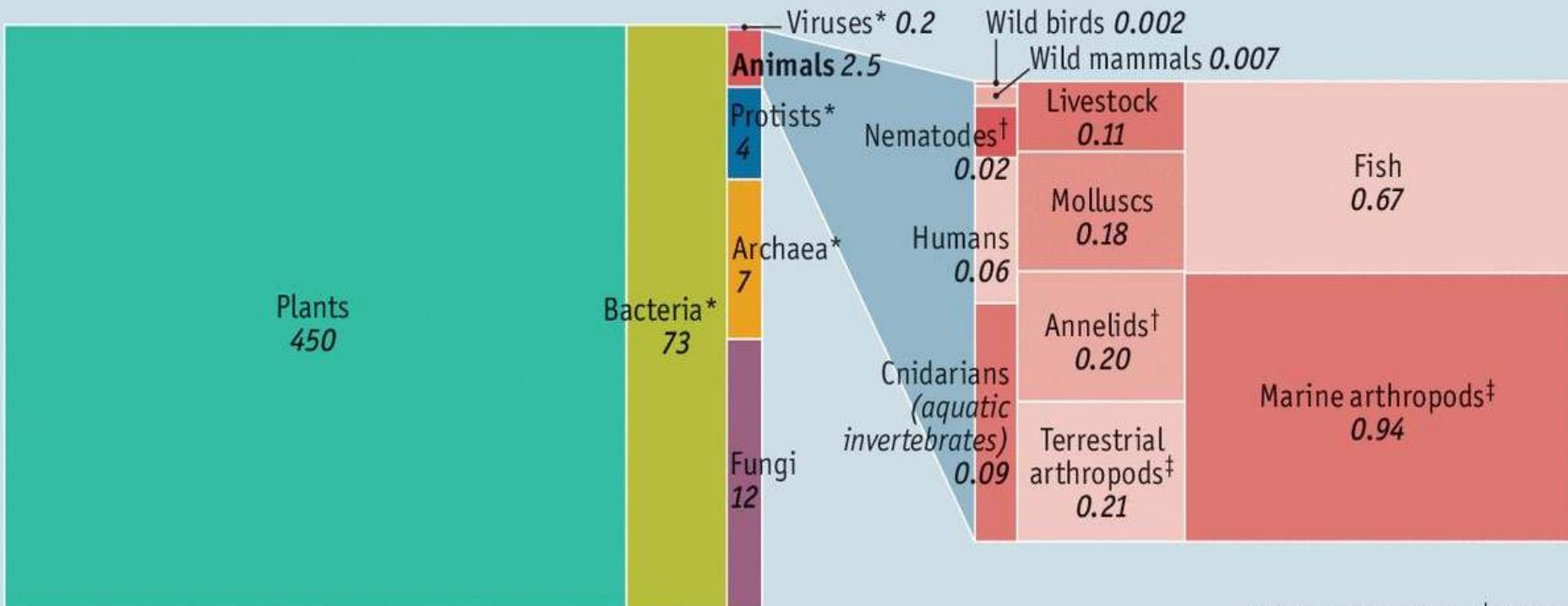
# MICROORGANISMS - WHAT ARE THEY?



Although microorganisms are the smallest forms of life, collectively they constitute the bulk of biomass on Earth and carry out many necessary chemical reactions for higher organisms.

# Life as we know it

Estimated global biomass of selected taxonomic groups, gigatonnes



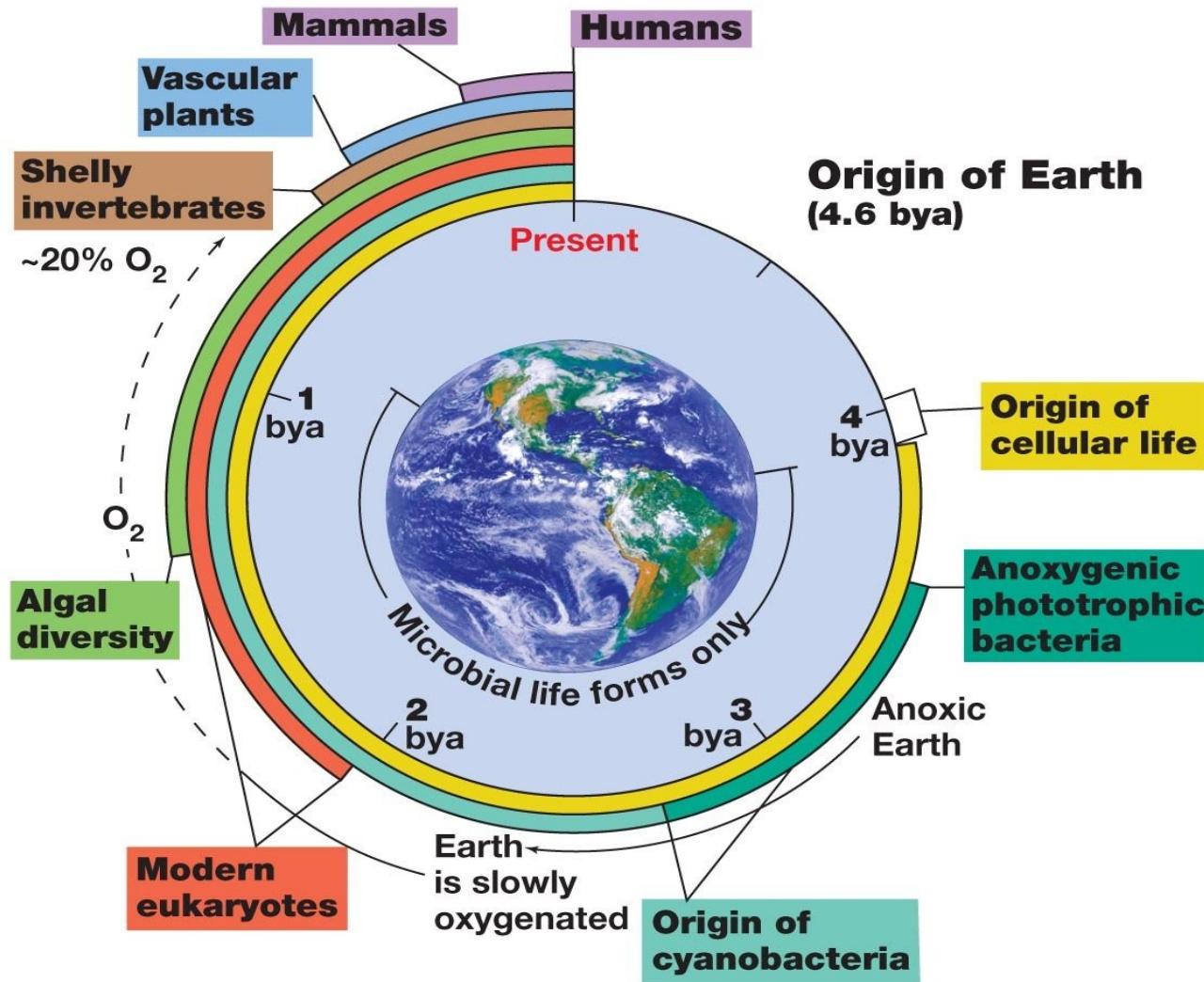
Source: "The biomass distribution on Earth" by Bar-On, Phillips & Milo, PNAS, 2018

## Table 1.2 Distribution of microorganisms in and on Earth<sup>a</sup>

Habitat	Percent of total
Marine subsurface	66
Terrestrial subsurface	26
Surface soil	4.8
Oceans	2.2
All other habitats <sup>b</sup>	1.0

<sup>a</sup>Data compiled by William Whitman, University of Georgia, USA; refer to total numbers (estimated to be about  $2.5 \times 10^{30}$  cells) of *Bacteria* and *Archaea*. This enormous number of cells contains, collectively, about  $5 \times 10^{17}$  grams of carbon.

<sup>b</sup>Includes, in order of decreasing numbers: freshwater and salt lakes, domesticated animals, sea ice, termites, humans, and domesticated birds.



(a)

# MICROBIOLOGY: THE SCIENCE OF MICROORGANISMS

Microbiology is the **study** and **classification** of microorganisms.

Microbiology is also about **diversity** and **evolution** of microbial cells, about **how** different kinds of microorganisms arose and **why**. Microbiology embraces **ecology**, so it is also about where microorganisms live on Earth, how they associate and cooperate with each other, and what they do in the world at large, in soils and waters and in animals and plants.

The science of microbiology revolves around two interconnected themes:

- (1) understanding the nature and functioning of the microbial world;
- (2) applying our understanding of the microbial world for the benefit of humankind and planet Earth.

# The discovery of microorganisms

*The existence of creatures too small to be seen with the naked eye had been suspected and speculated for centuries.*

*The English mathematician and natural historian Robert Hooke (1635–1703) described a series of microscopic observation in his famous book Micrographia (1665).*

*These included, among many other things, the fruiting structures of molds. This was the first known description of microorganisms.*

# Brief History of Microbiology

1665 – Hooke – Discovery of microorganisms

1676 – Van Leeuwenhoek – First bacteria observation

1768 – Spallanzani – Disproved Spontaneous Generation

1866 – Cohn – Beggiatoa sulfur granules

1876 – Kock – Koch's postulates

1880 – Pasteur – The germ theory and first vaccine

1881 – Winogradsky – Chemolithoautotrophy

1884 – Gram – Gram Staining

1916 – Vernadsky – The Biosphere concept

1929 – Fleming – Penicillin

1977 – Woese – Discover the Archaea

1977 – Ballard – Discovery of Hydrothermal Vent

<https://goo.gl/SMoyHc>

# *Prokaryotes: Bacteria and Archaea*

# Bacteria: medical and environmental relevance

Not all bacteria are bad!

About  $>16,000$  bacterial species are known today ( $>150,000$  if we include uncultured).

538 are known pathogens or facultative pathogens ( $\sim 0.36\%$ )

# Taxonomy

Taxonomic nomenclature follows the binomial systems. There are numerous rules and conventions, all established by the International Committee on the Systematics of Prokaryotes.

Domain: Bacteria

Phylum: Proteobacteria

Class: Gammaproteobacteria

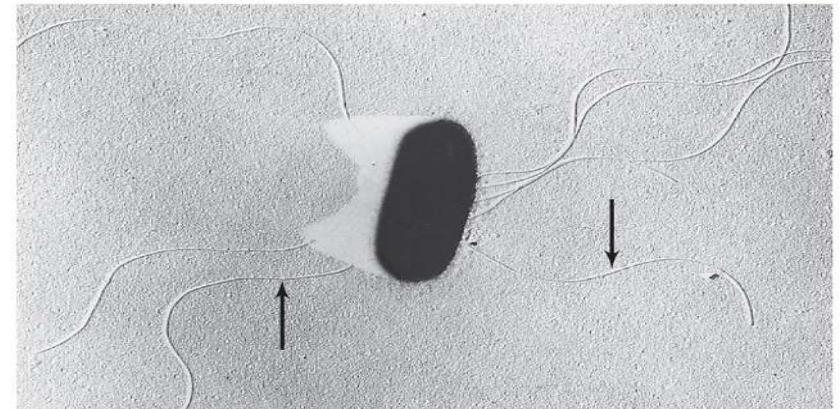
Order: Enterobacterales

Family: Enterobacteraceae

Genus: Escherichia

Species: *Escherichia coli*

Strain: K12

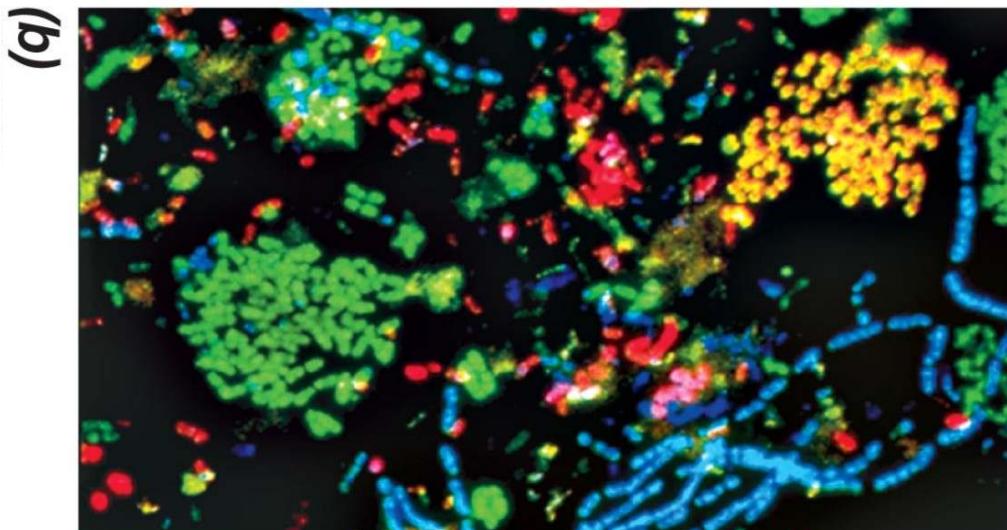


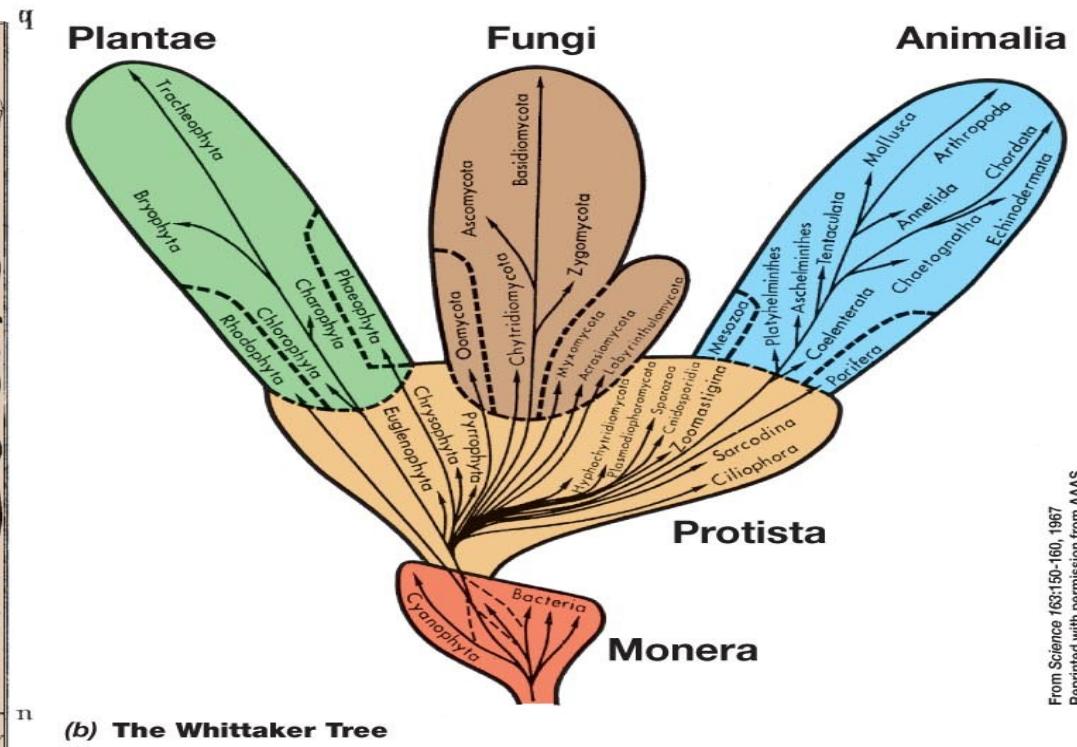
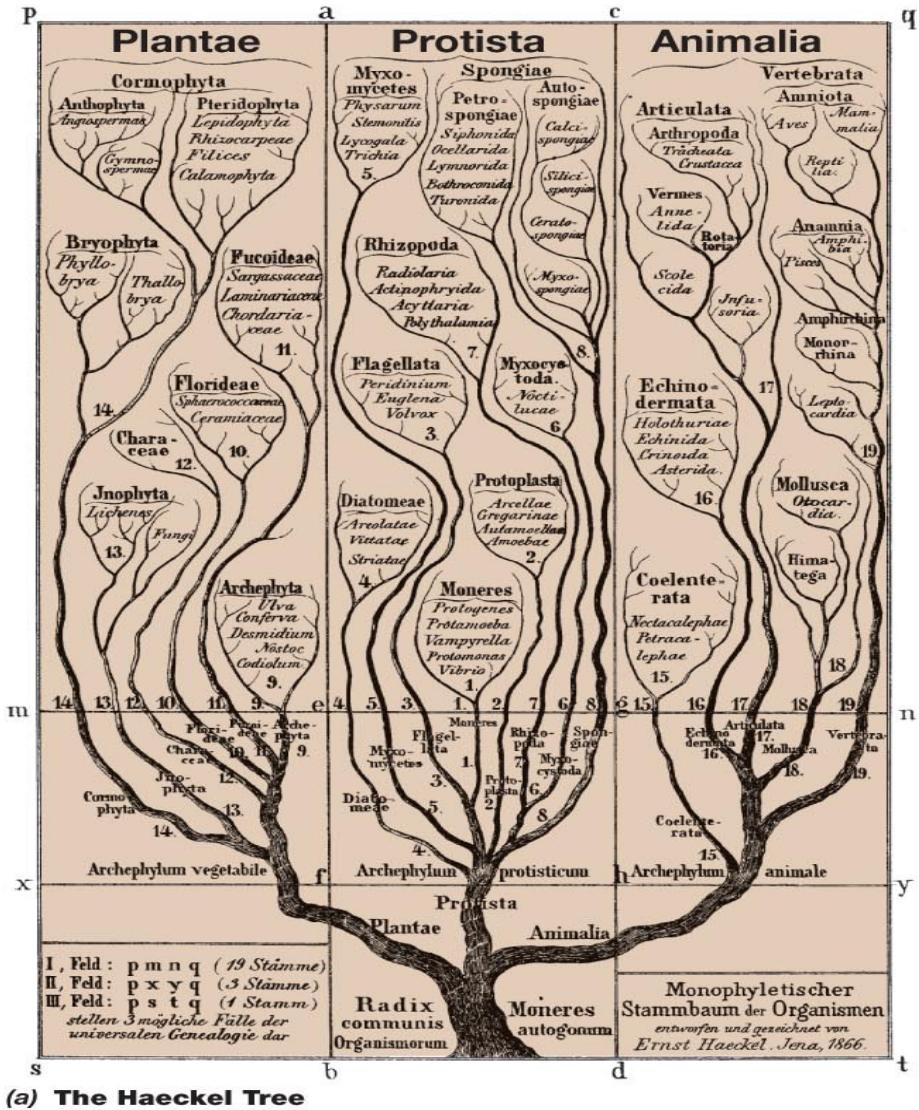
Arthur Kelman

# Prokaryotes: Bacteria and Archaea

Prokaryotes include the Bacteria and the Archaea and consist of small and structurally rather simple cells.

The word “prokaryote” does not imply evolutionary relatedness. Archaea and Bacteria are two distinct domain of life, similarly to Bacteria and Eukarya

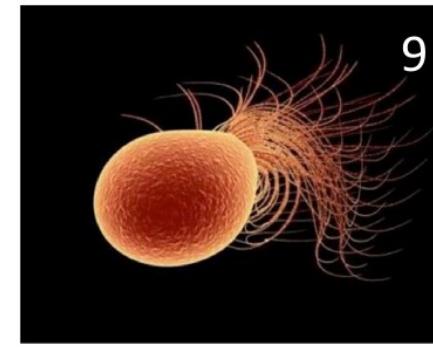
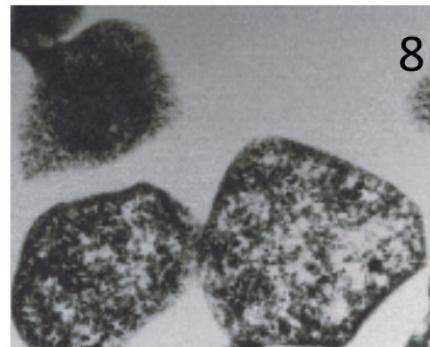
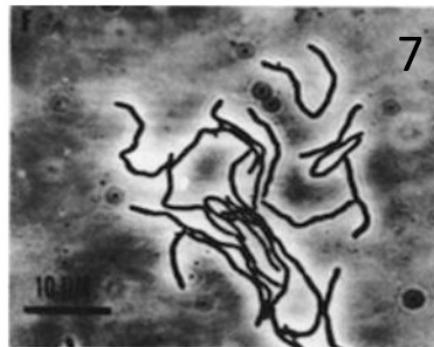
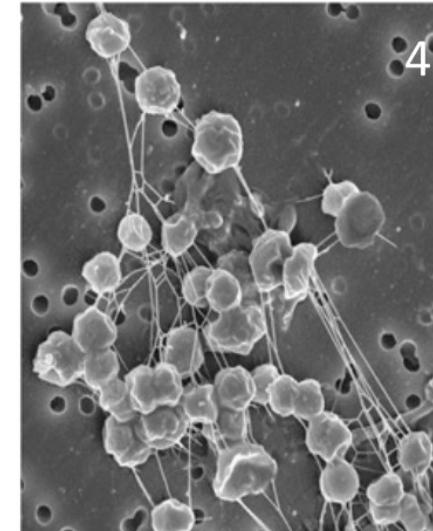
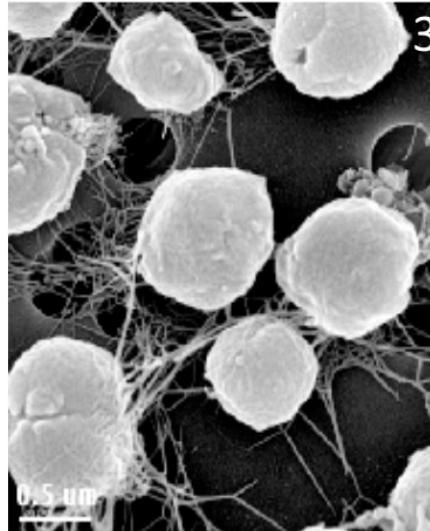
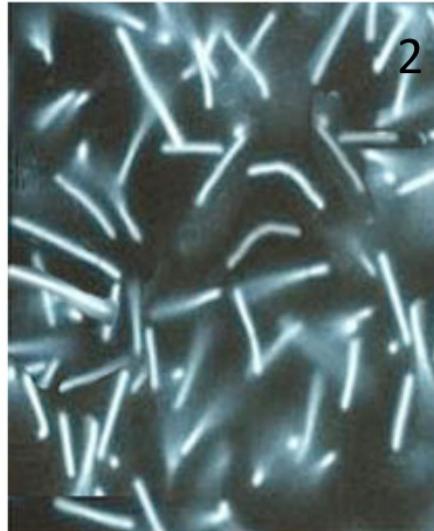




From Science 163:150-160, 1967  
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Early efforts to depict the universal tree of life. (a) Tree of life published in 1866 by Ernst Haeckel in *Generelle Morphologie der Organismen*. (b) Tree of life published by Robert H. Whittaker in 1969. The terms "Monera" and "Moneres" are antiquated terms used to refer to prokaryotic cells.

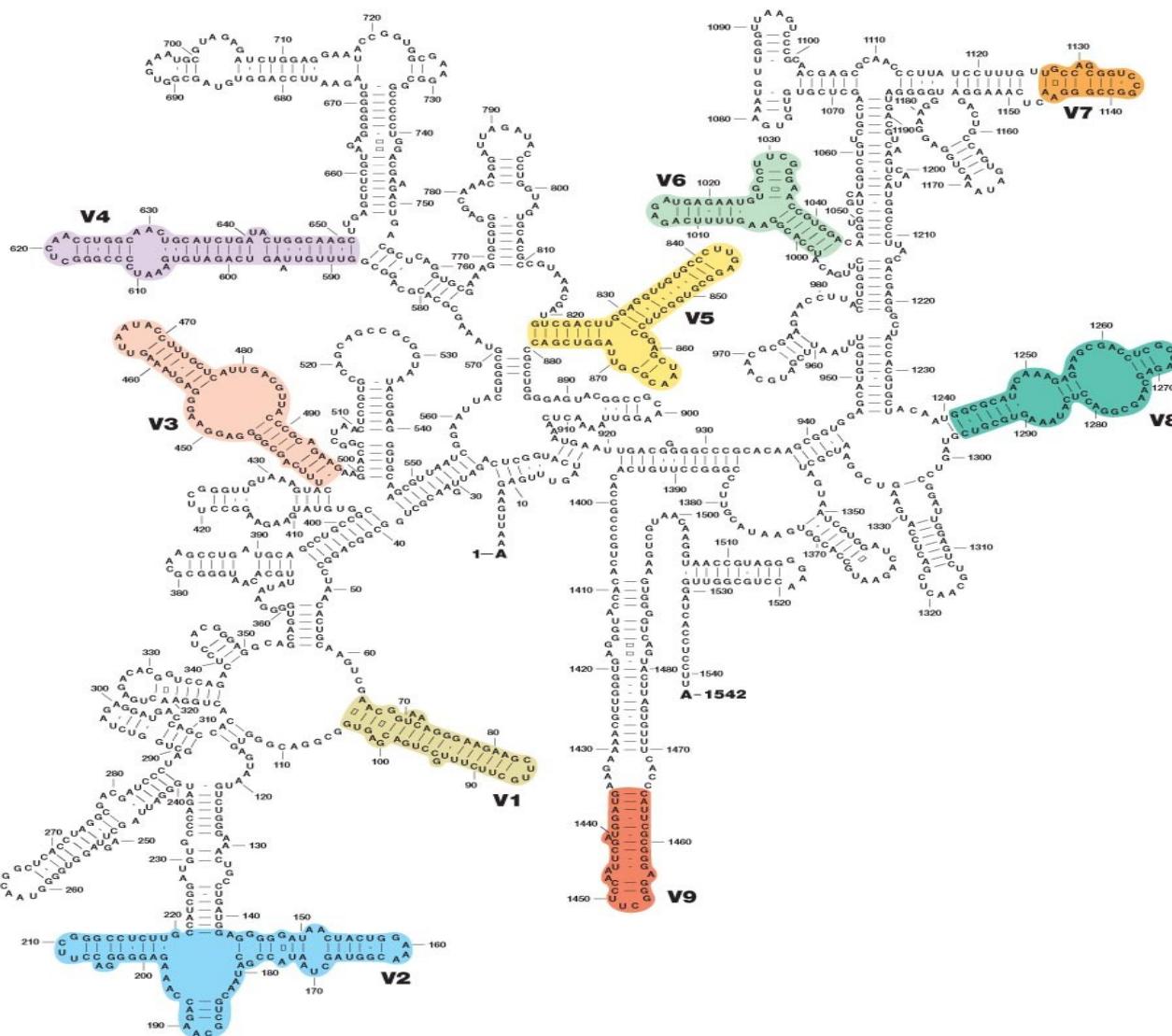
# The discovery of Archaea



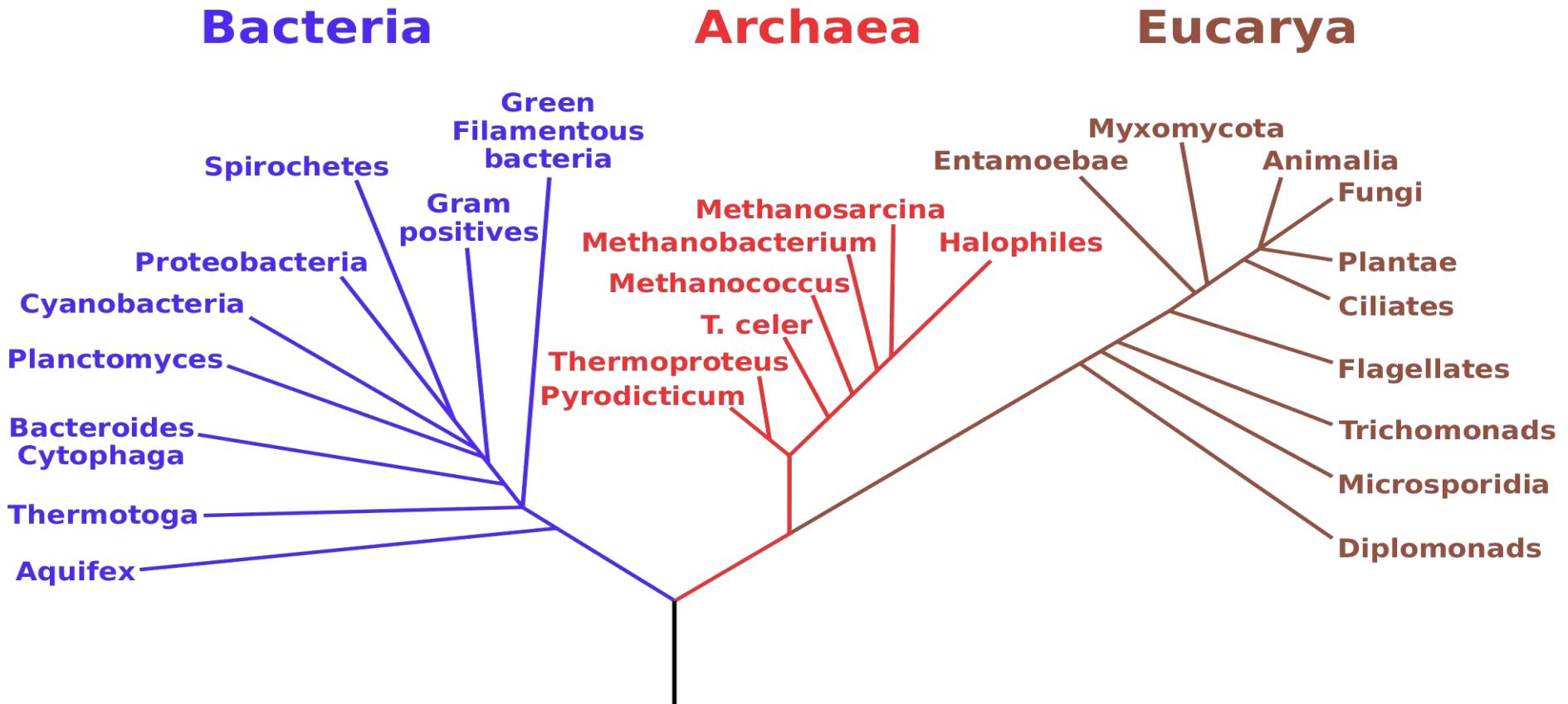
# rRNA as universal marker

In 1977 Carl R. Woese reported the discovery of a new group of organisms, that he called Archeabacteria, previously thought to be Bacteria.

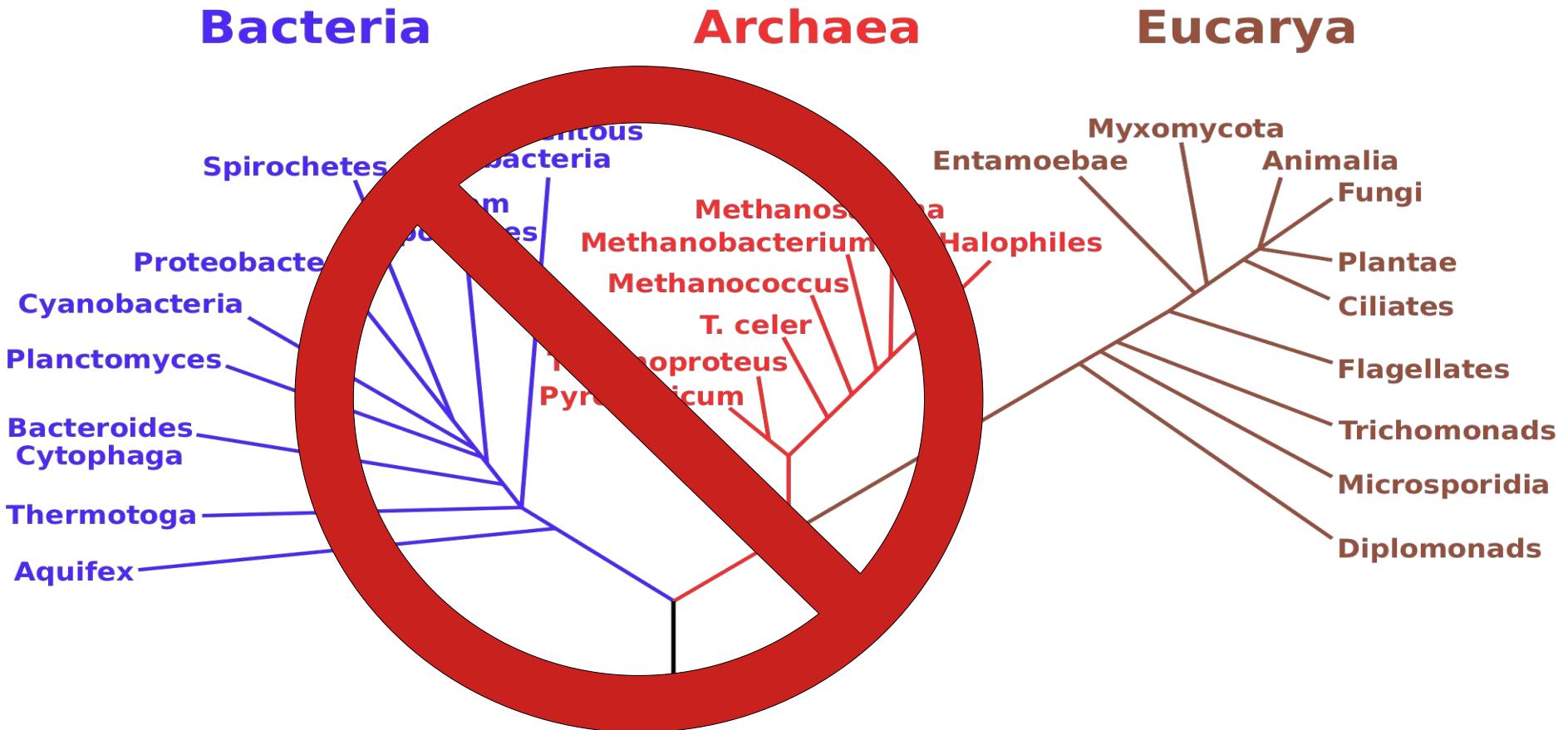
The discovery was possible thanks to sequencing technology and the realization that 16S rRNA could be used as a marker gene for diversity

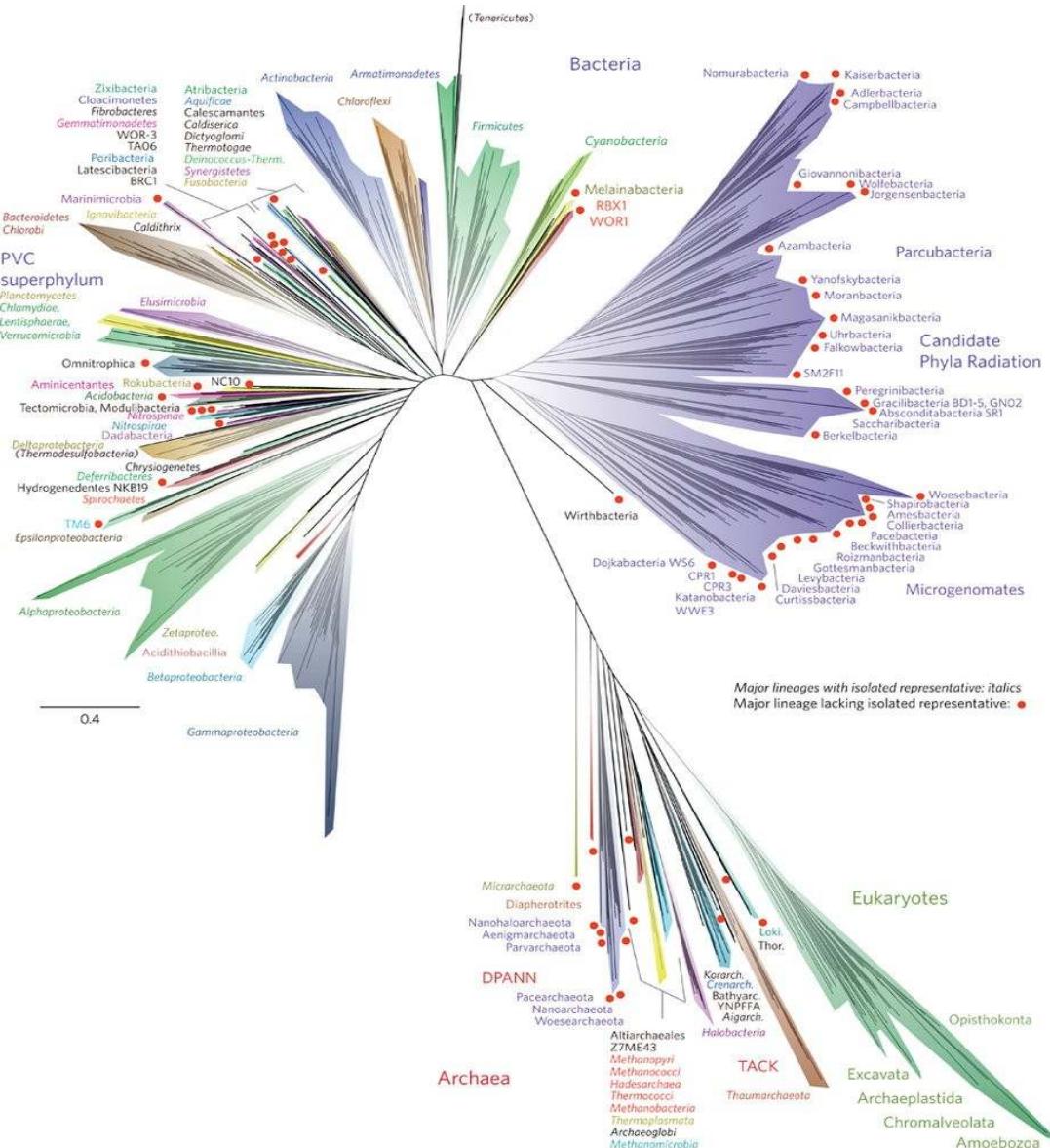


# The textbook tree of life (post Woese)



# The textbook tree of life (post Woese)





# A more accurate view of the tree of life

All the branches with a red dot represent organisms that have no known cultivated representative, and for which their environmental role is often unknown or uncertain.

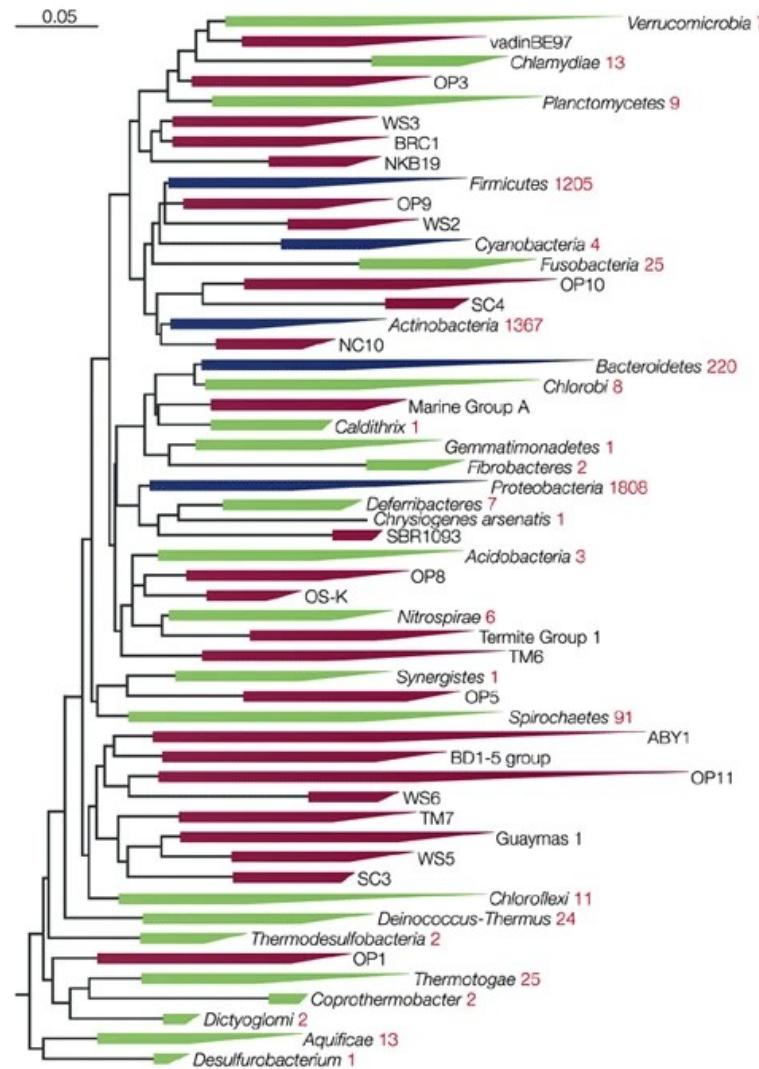
There are more uncultured phyla of Bacteria and Archaea than there are cultured ones.

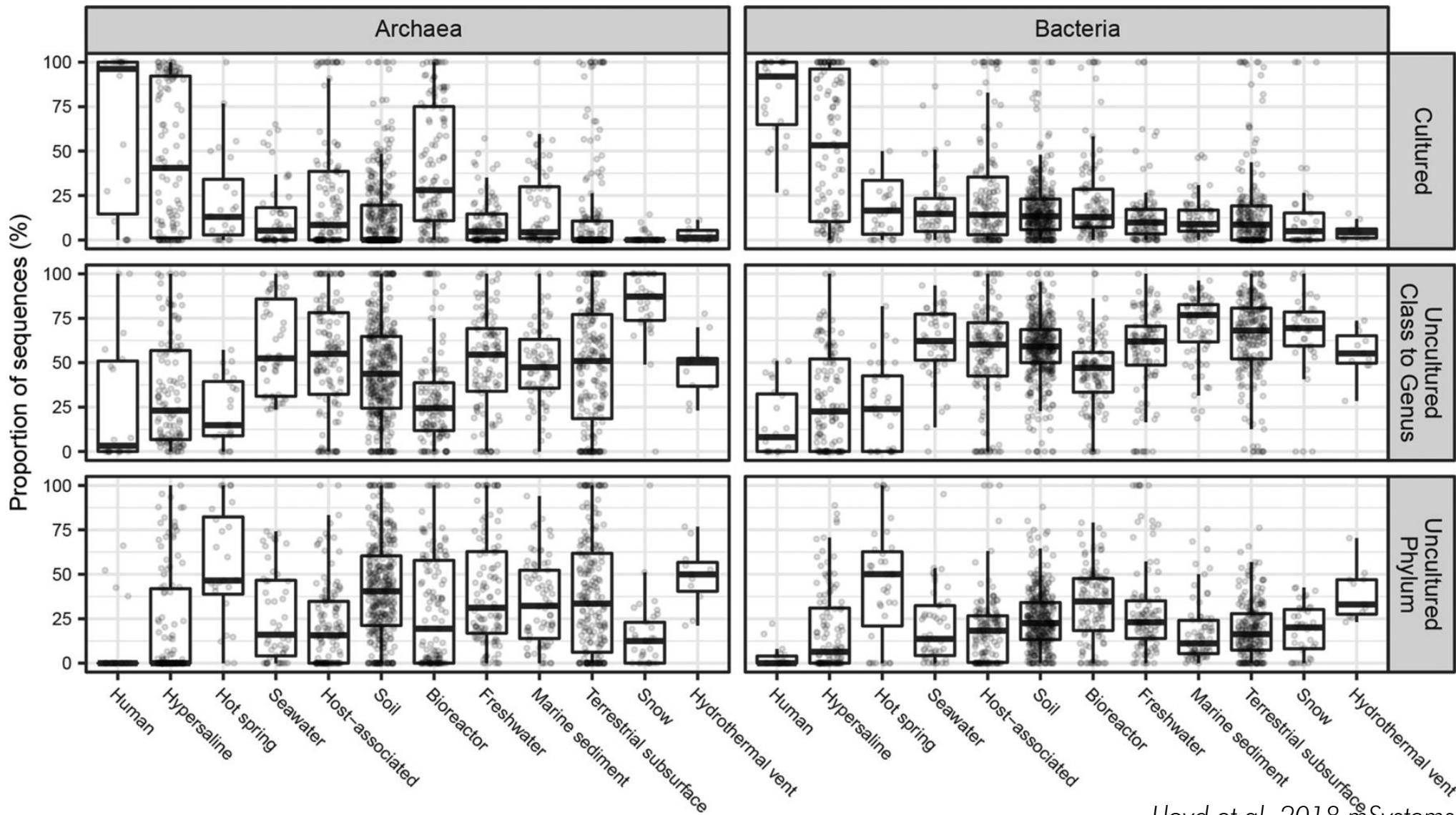
# The Uncultured Majority

The uncultured majority refers to our current inability to cultivate the large majority of microorganisms in many environments. The first description is from Staley and Konopka, 1985, and was later dubbed the “Great Plate Count Anomaly”.

The simple observation that counts of growing microbes on plates differed greatly from counts using microscopy suggested that the known diversity was dwarfed by the actual diversity.

Metagenomic has revolutionized the study of microbial diversity in many ways, allowing us to probe into the unknown.





# Size, Morphology and Distribution

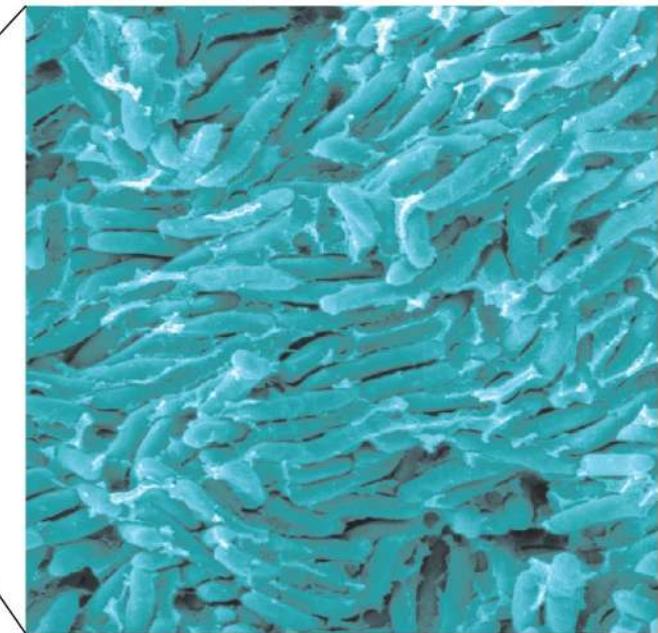
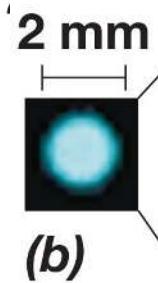
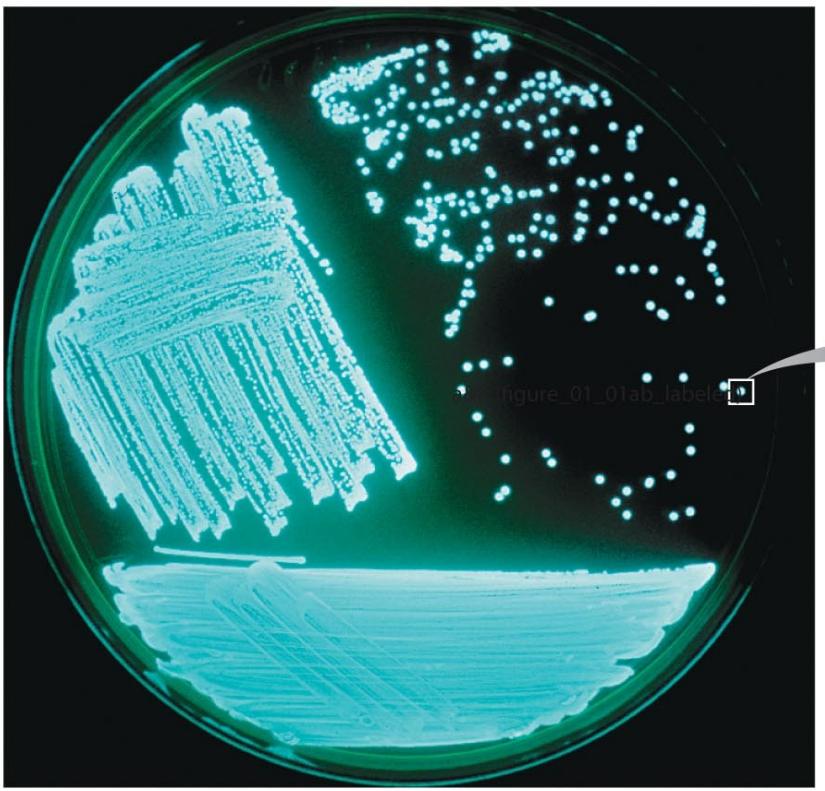
Although cell morphology is easily determined, it is a poor predictor of other properties of a cell. For example, under the microscope many rod-shaped Archaea look identical to rod-shaped Bacteria, yet we know they are of different phylogenetic domains.

Prokaryotes vary in size from cells smaller of about  $0.2\text{ }\mu\text{m}$  in diameter to those more than  $700\text{ }\mu\text{m}$ . The vast majority of rod-shaped prokaryotes that have been cultured are between  $0.5$  and  $4\text{ }\mu\text{m}$  wide and less than  $15\text{ }\mu\text{m}$  long.

**90 mm**

**0.01 mm (10  $\mu$ m)**

Paul V. Dunlap



# Size Variation Among Bacteria

**Table 2.1** Cell size and volume of some cells of *Bacteria*, from the largest to the smallest

Organism	Characteristics	Morphology	Size <sup>a</sup> ( $\mu\text{m}$ )	Cell volume ( $\mu\text{m}^3$ )	E. coli volumes
<i>Thiomargarita namibiensis</i>	Sulfur chemolithotroph	Cocci in chains	750	200,000,000	100,000,000
<i>Epulopiscium fishelsoni</i> <sup>a</sup>	Chemoorganotroph	Rods with tapered ends	80 × 600	3,000,000	1,500,000
<i>Beggiatoa</i> species <sup>a</sup>	Sulfur chemolithotroph	Filaments	50 × 160	1,000,000	500,000
<i>Achromatium oxaliferum</i>	Sulfur chemolithotroph	Cocci	35 × 95	80,000	40,000
<i>Lyngbya majuscula</i>	Cyanobacterium	Filaments	8 × 80	40,000	20,000
<i>Thiovulum majus</i>	Sulfur chemolithotroph	Cocci	18	3,000	1,500
<i>Staphylothermus marinus</i> <sup>a</sup>	Hyperthermophile	Cocci in irregular clusters	15	1,800	900
<i>Magnetobacterium bavaricum</i>	Magnetotactic bacterium	Rods	2 × 10	30	15
<i>Escherichia coli</i>	Chemoorganotroph	Rods	1 × 2	2	1
<i>Pelagibacter ubique</i> <sup>a</sup>	Marine chemoorganotroph	Rods	0.2 × 0.5	0.014	0.007
<i>Mycoplasma pneumoniae</i>	Pathogenic bacterium	Pleomorphic <sup>b</sup>	0.2	0.005	0.0025

<sup>a</sup>Where only one number is given, this is the diameter of spherical cells. The values given are for the largest cell size observed in each species. For example, for *T. namibiensis*, an average cell is only about 200  $\mu\text{m}$  in diameter. But on occasion, giant cells of 750  $\mu\text{m}$  are observed. Likewise, an average cell of *S. marinus* is about 1  $\mu\text{m}$  in diameter. The species of *Beggiatoa* here is unclear and *E. fishelsoni*, *Magnetobacterium bavaricum*, and *P. ubique* are not formally recognized names in taxonomy.

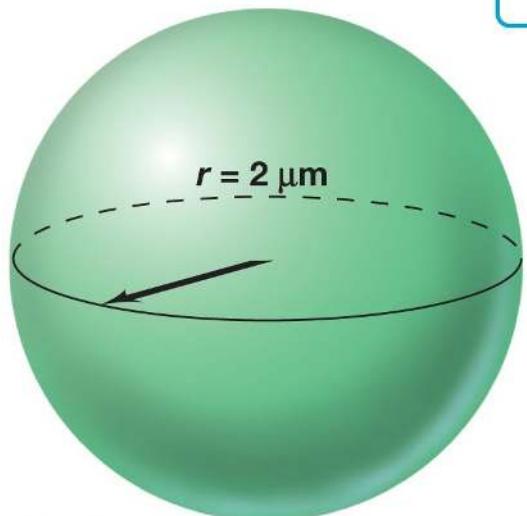
<sup>b</sup>*Mycoplasma* is a bacterium that lacks a cell wall and can thus take on many shapes (*pleomorphic* means “many shapes”).

Source: Data obtained from Schulz, H.N., and B.B. Jørgensen. 2001. *Ann. Rev. Microbiol.* 55: 105–137.

# When Size Matters!



$$\boxed{\begin{aligned}r &= 1 \mu\text{m} \\ \text{Surface area } (4\pi r^2) &= 12.6 \mu\text{m}^2 \\ \text{Volume } (\frac{4}{3}\pi r^3) &= 4.2 \mu\text{m}^3 \\ \frac{\text{Surface}}{\text{Volume}} &= 3\end{aligned}}$$

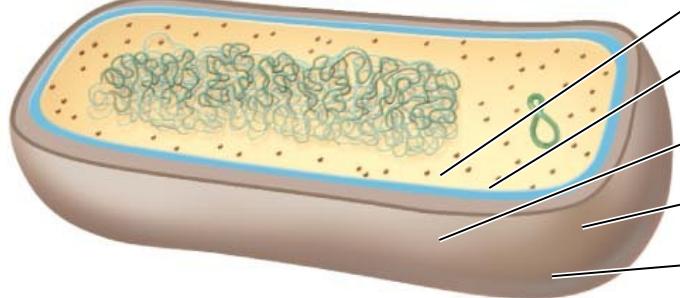


$$\boxed{\begin{aligned}r &= 2 \mu\text{m} \\ \text{Surface area} &= 50.3 \mu\text{m}^2 \\ \text{Volume} &= 33.5 \mu\text{m}^3 \\ \frac{\text{Surface}}{\text{Volume}} &= 1.5\end{aligned}}$$

The lower limit is controlled by volume needed to house the essential components of a free-living cell, calculated around  $0.1 \mu\text{m}$  in diameter.

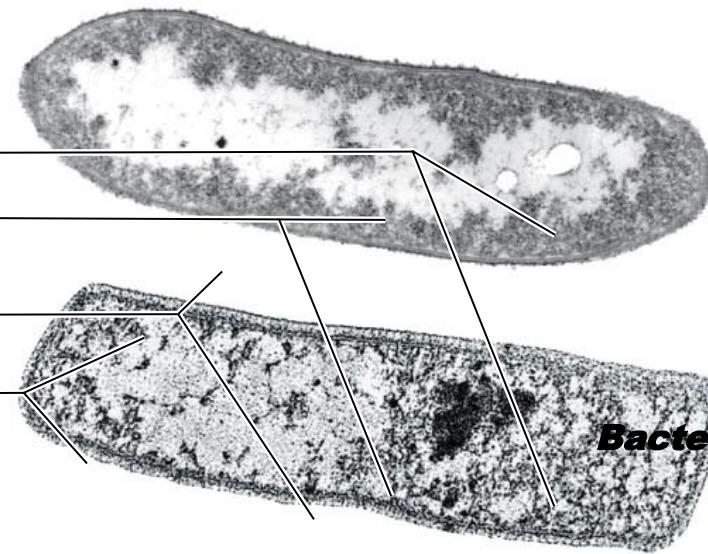
The upper limit is controlled by diffusion limitation of nutrients and waste from and to the surrounding environment.

# Prokaryotic cell structures



**Prokaryote**

- Cell wall
- Cytoplasmic membrane
- Nucleoid
- Cytoplasm
- Plasmid
- Ribosomes

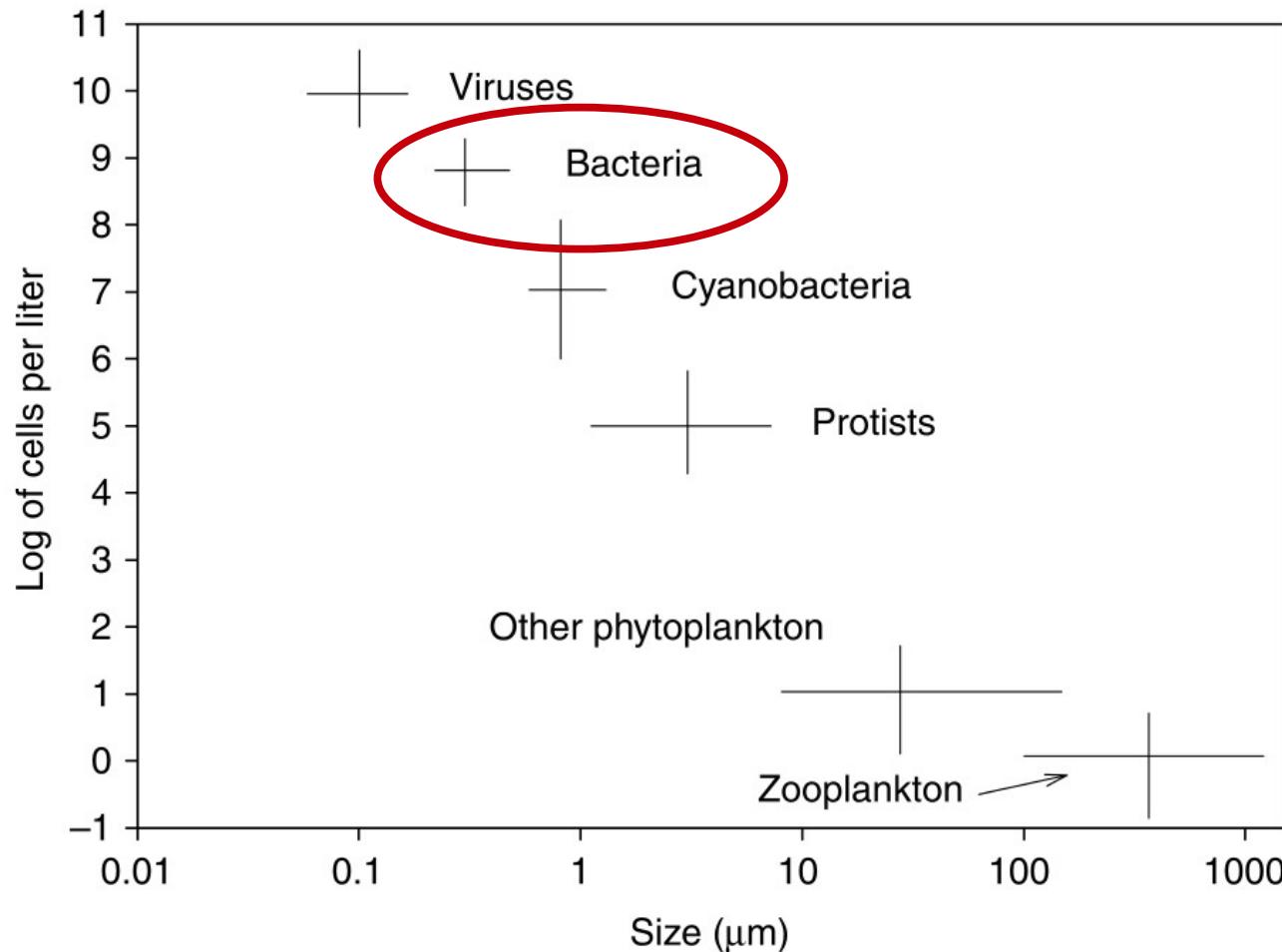


**Archaea**

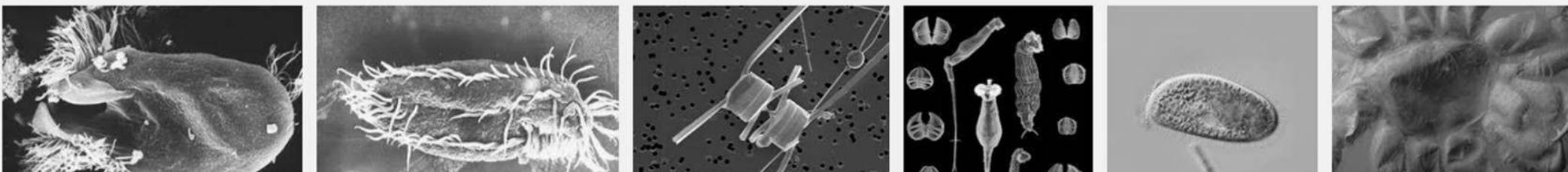
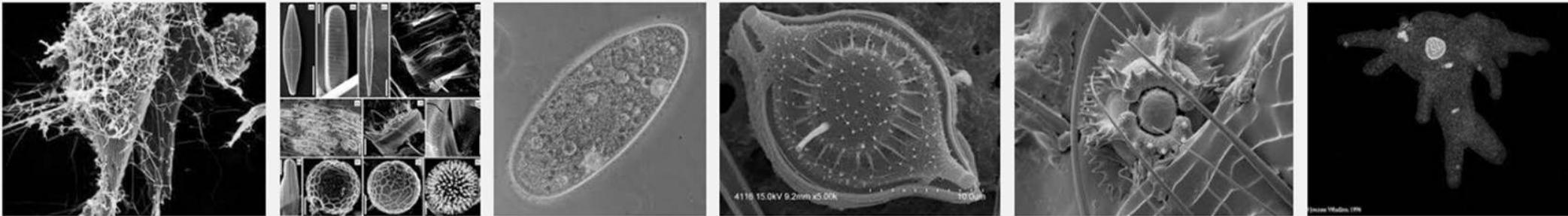
John Bozzola and  
M.T. Madigan

H. König and  
K.O. Stetter

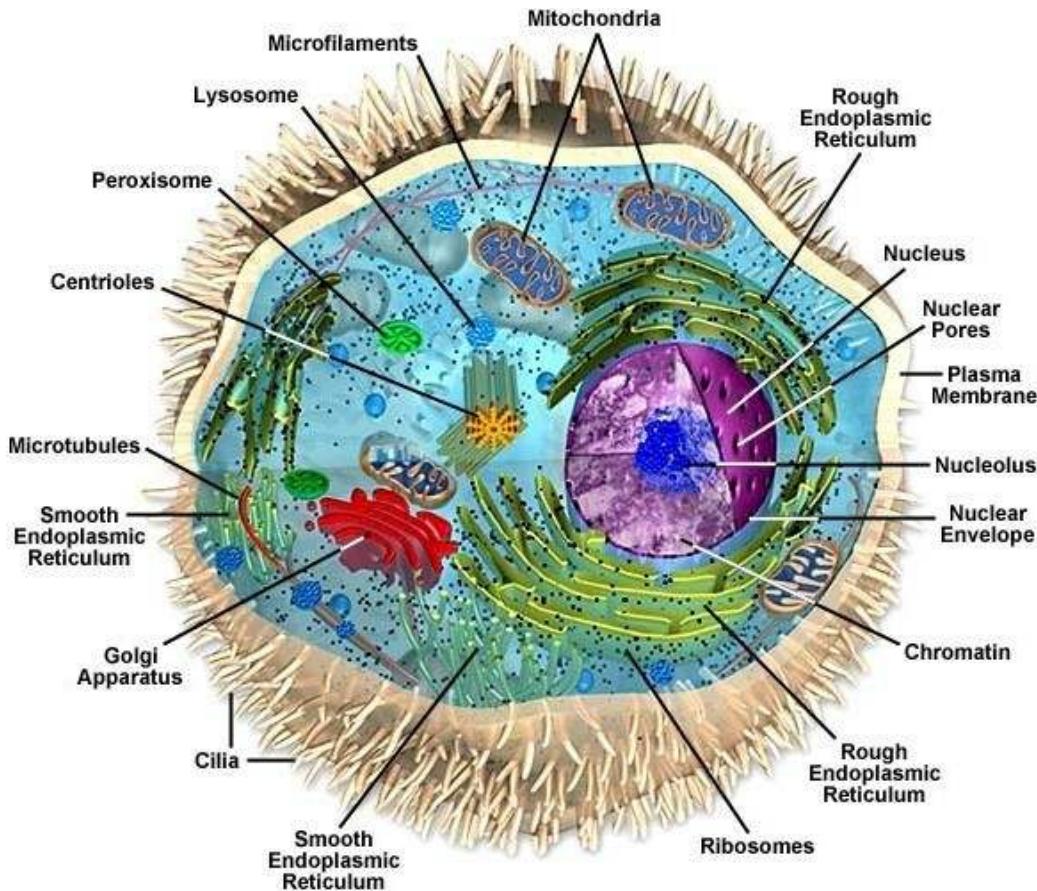
# Abundance and Size



# Microbial Eukaryotes

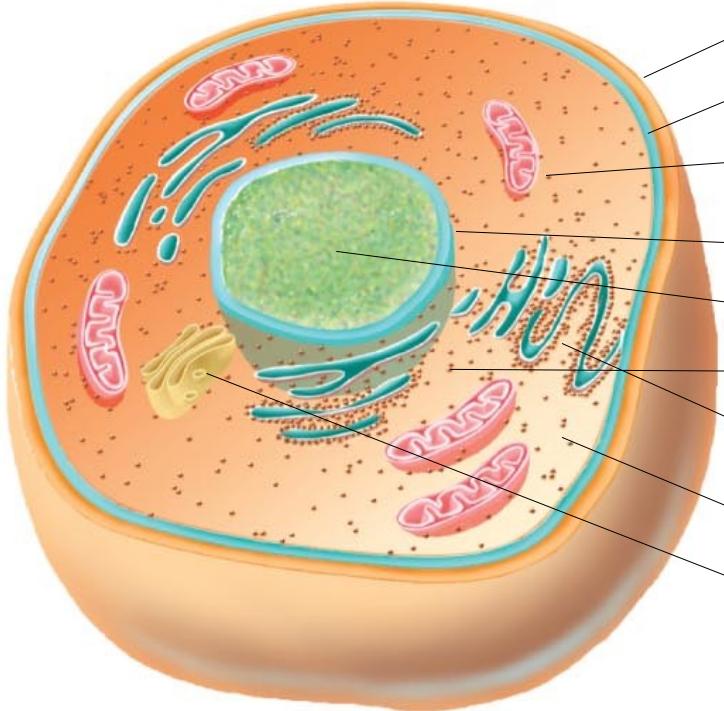


# Eukaryotic cell structures



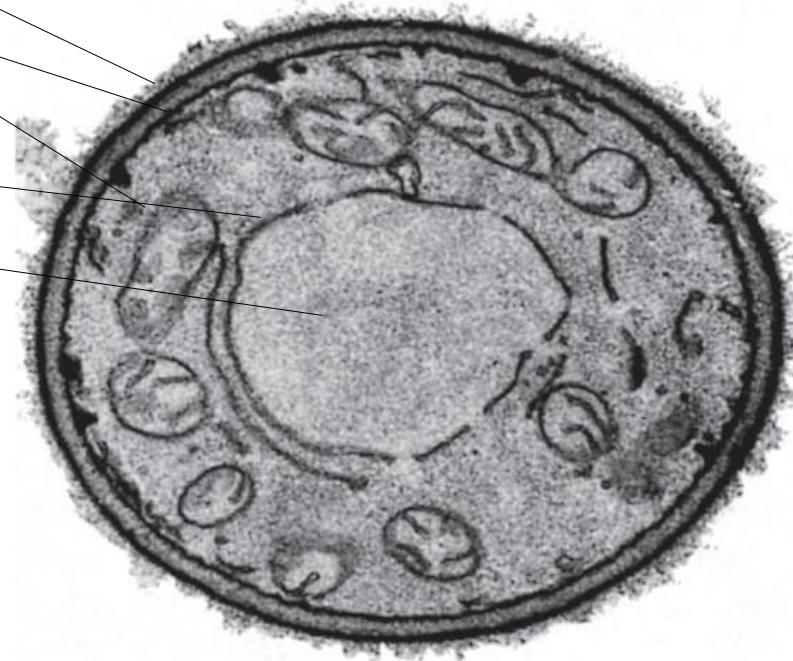
Compared with prokaryotic cells, microbial eukaryotes typically have structurally more complex and much larger cells

# Eukaryotic cell structures



(b)

- Cell wall
- Cytoplasmic membrane
- Mitochondrion
- Nuclear membrane
- Nucleus
- Ribosomes
- Endoplasmic reticulum
- Cytoplasm
- Golgi complex

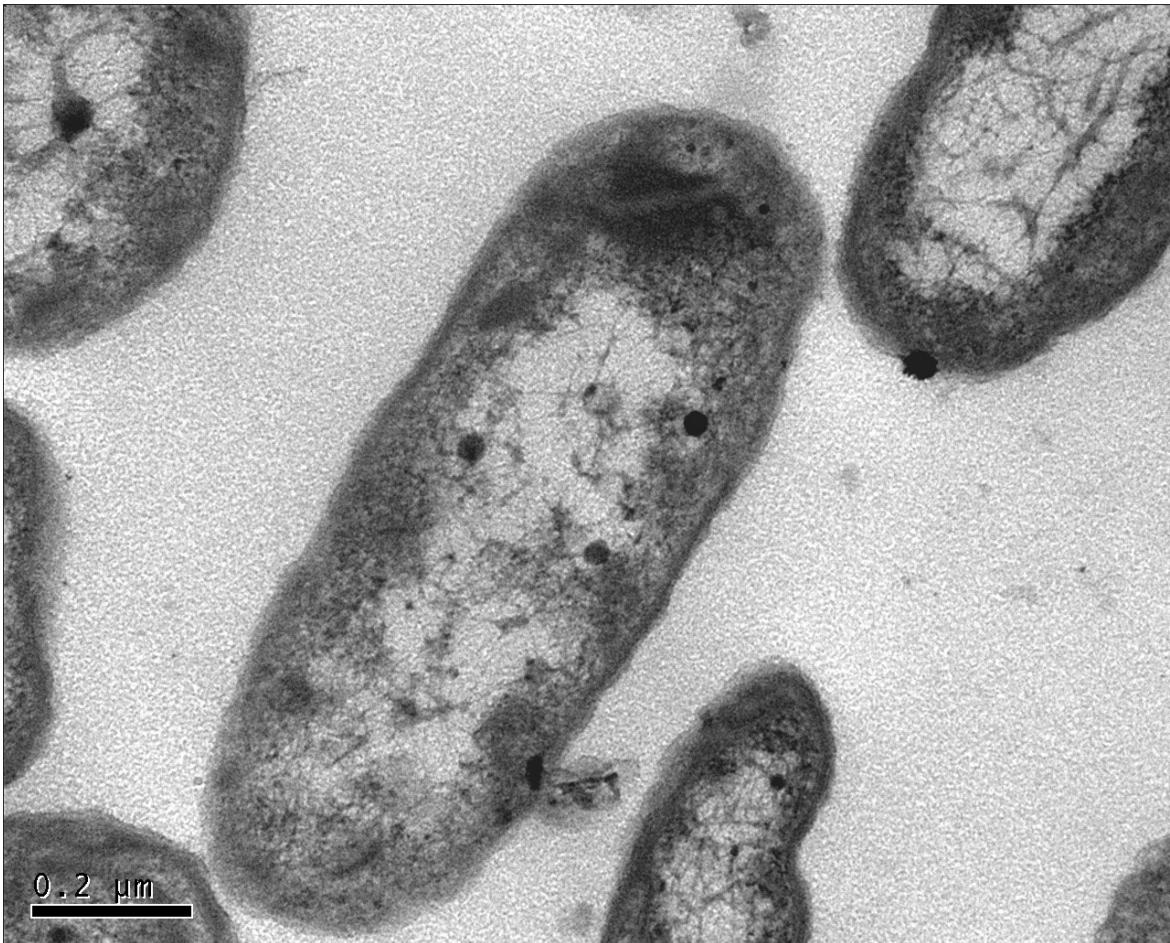


# *Prokaryote or Eukaryote?*

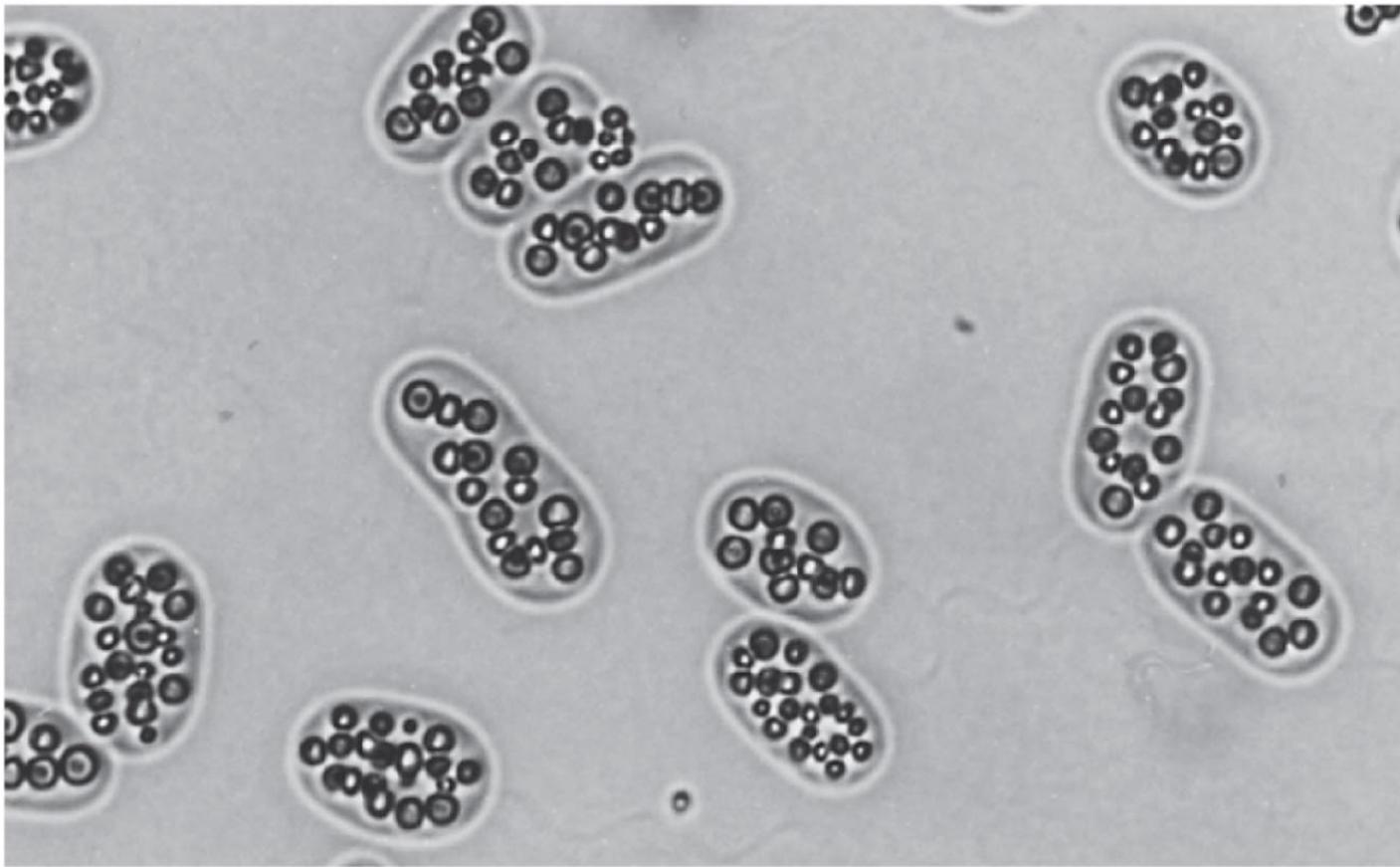


M.T. Madigan

# *Prokaryote or Eukaryote?*



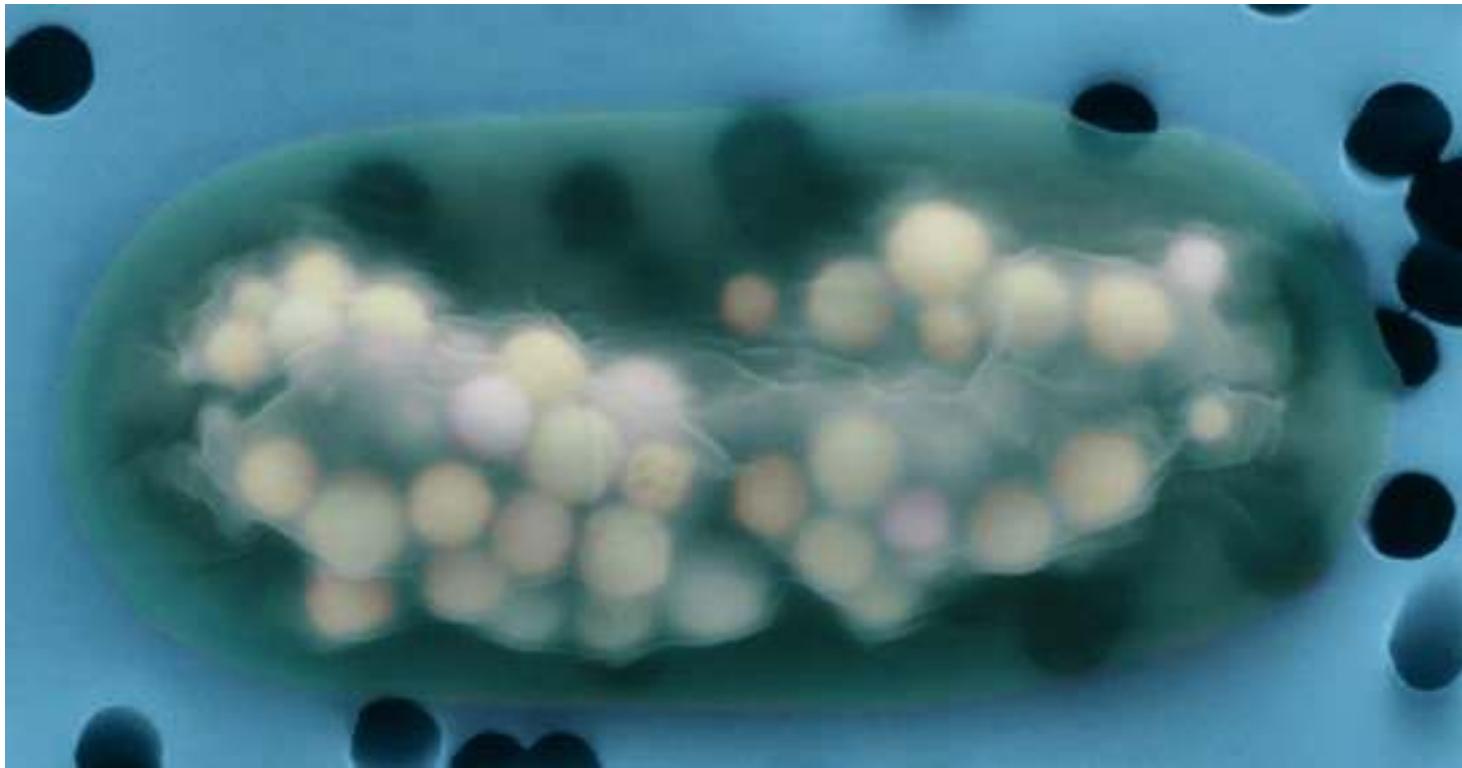
# *Prokaryote or Eukaryote?*



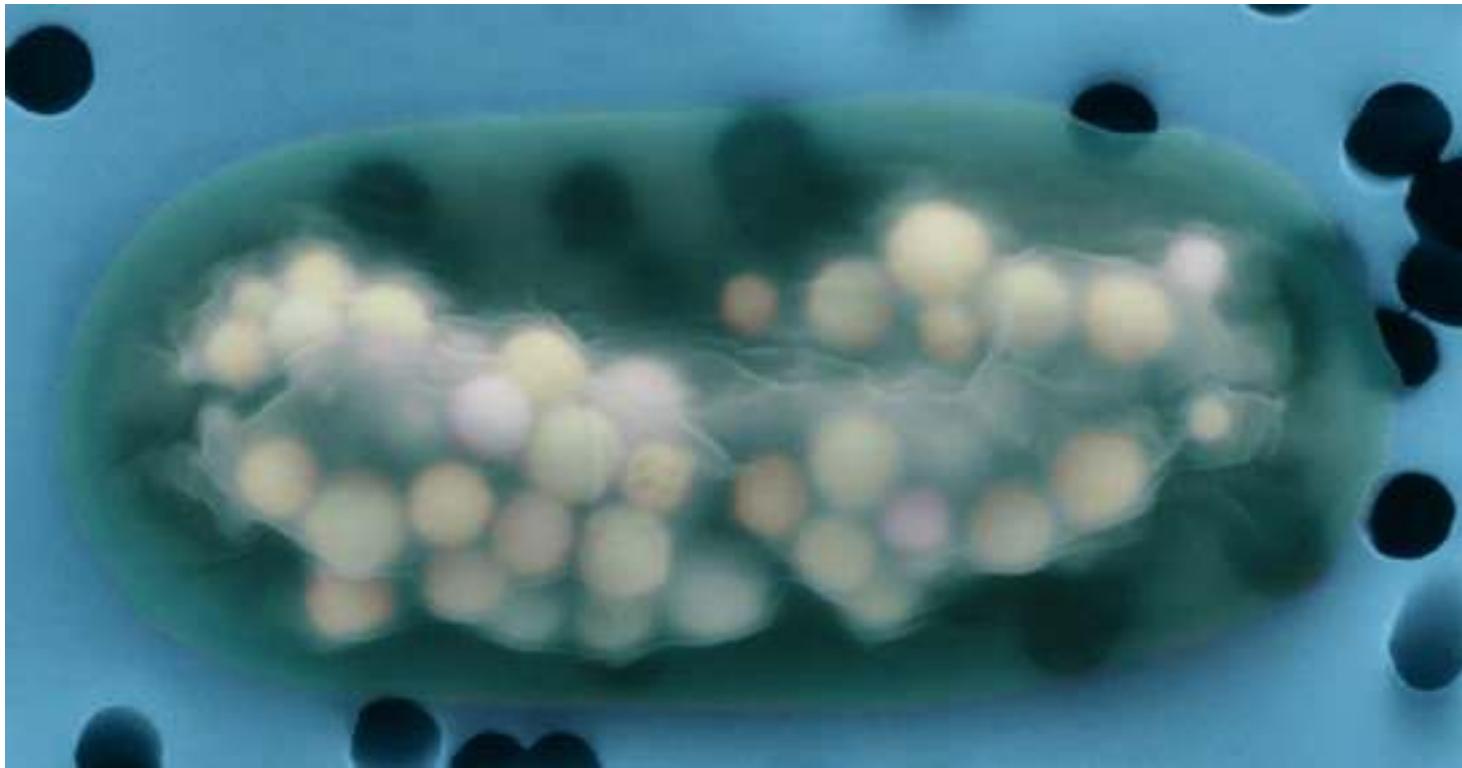
**(b)**

Norbert Pfennig

# Prokaryote or Eukaryote?

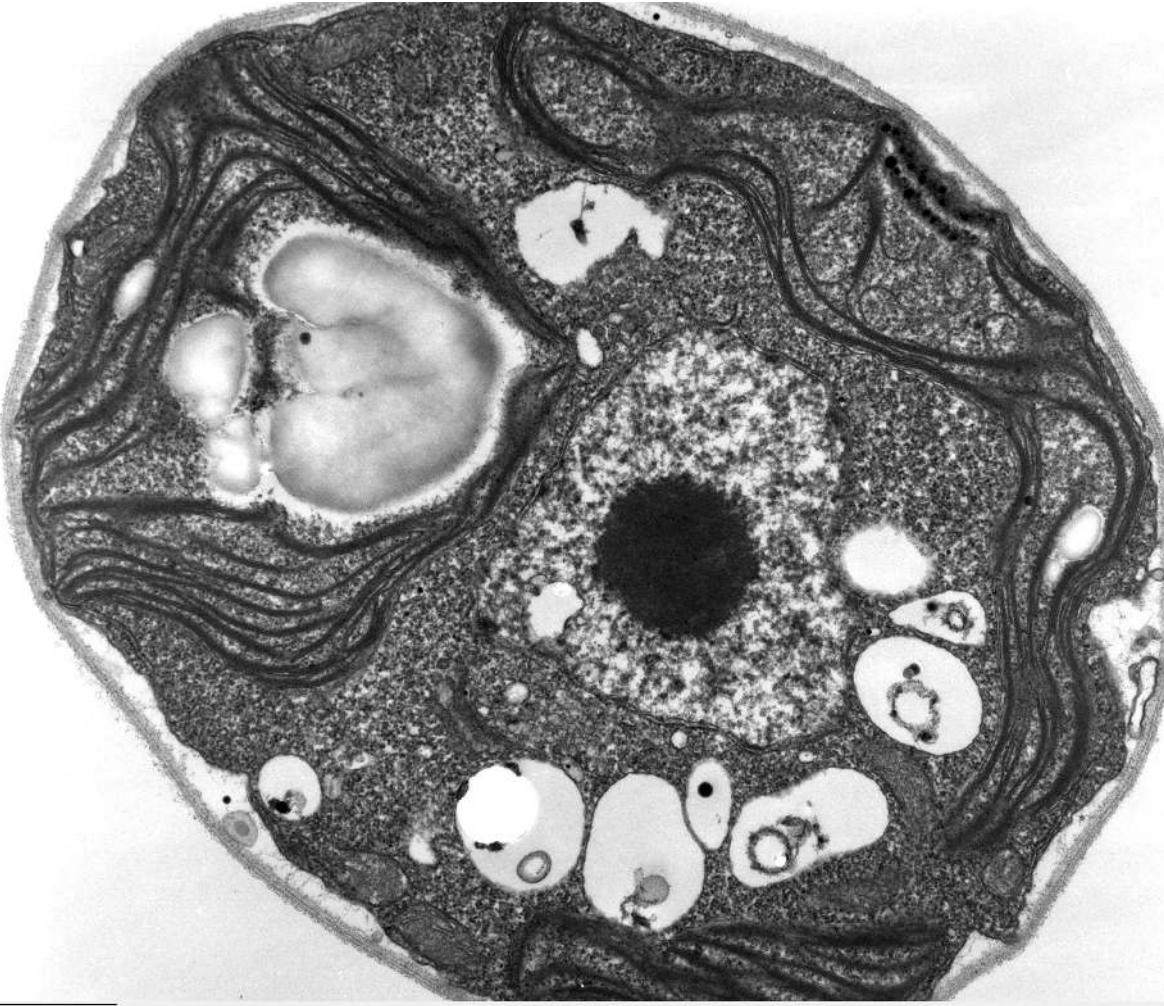


# Prokaryote or Eukaryote?

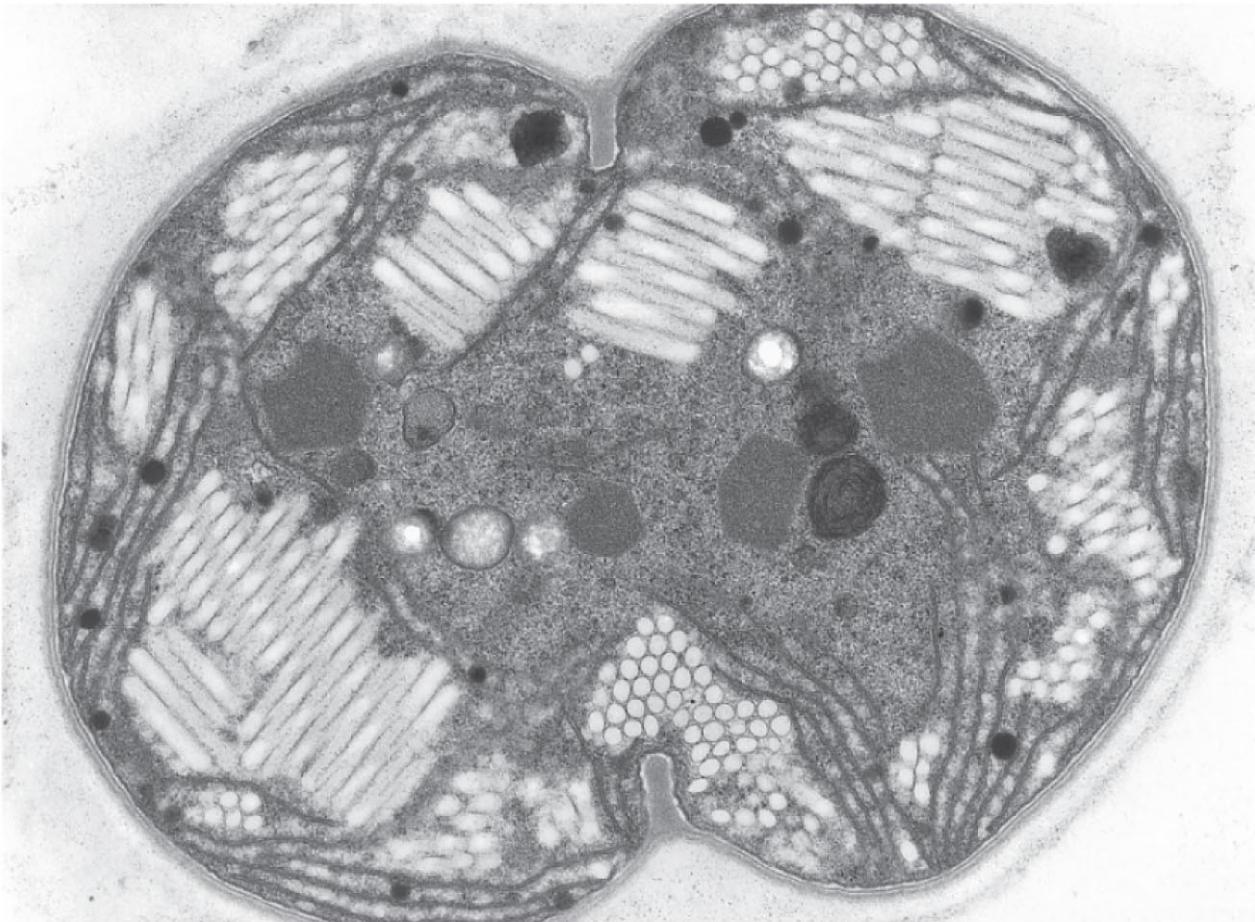


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# Prokaryote or Eukaryote?



# Prokaryote or Eukaryote?



S. Pellegrini and M. Grilli Caiola



# How did Eukaryotes form?

Symbiogenesis, or endosymbiotic theory (Mereschowsky 1910 and Lynn Margulis in 1967) is a theory on the evolution of eukaryotes.

Primary endosymbiosis is the process in which a eukaryote engulfs another living prokaryote.

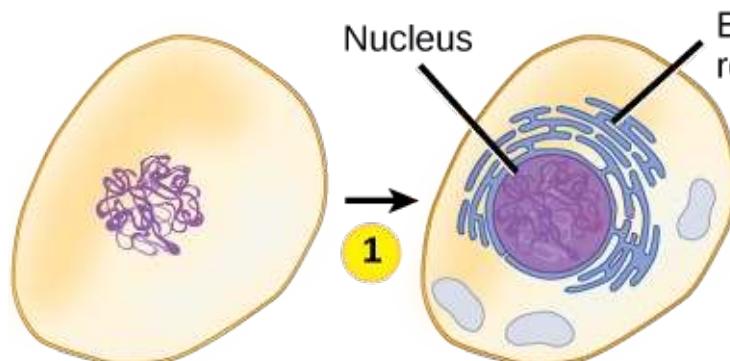
The mitochondria and plastids (for example chloroplasts), and possibly other organelles of eukaryote cells are thought to represent formerly free-living prokaryotes taken one inside the other in endosymbiosis around 1.5 billion years ago.

Molecular and biochemical evidence suggest that mitochondria developed from Proteobacteria (Alphaproteobacteria, like SAR11) and chloroplasts from Cyanobacteria (in particular, nitrogen-fixing filamentous cyanobacteria).

# Primary endosymbiosis

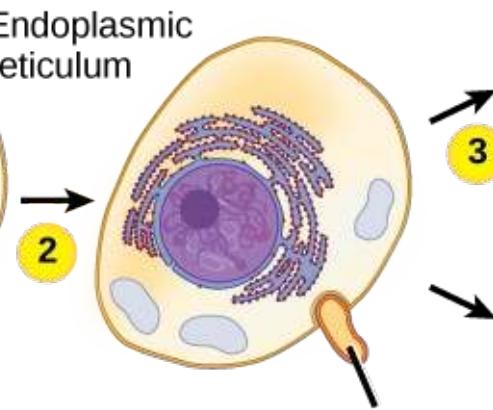
## The ENDOSYMBIOTIC THEORY

1 Infoldings in the plasma membrane of an ancestral prokaryote gave rise to endomembrane components, including a nucleus and endoplasmic reticulum.

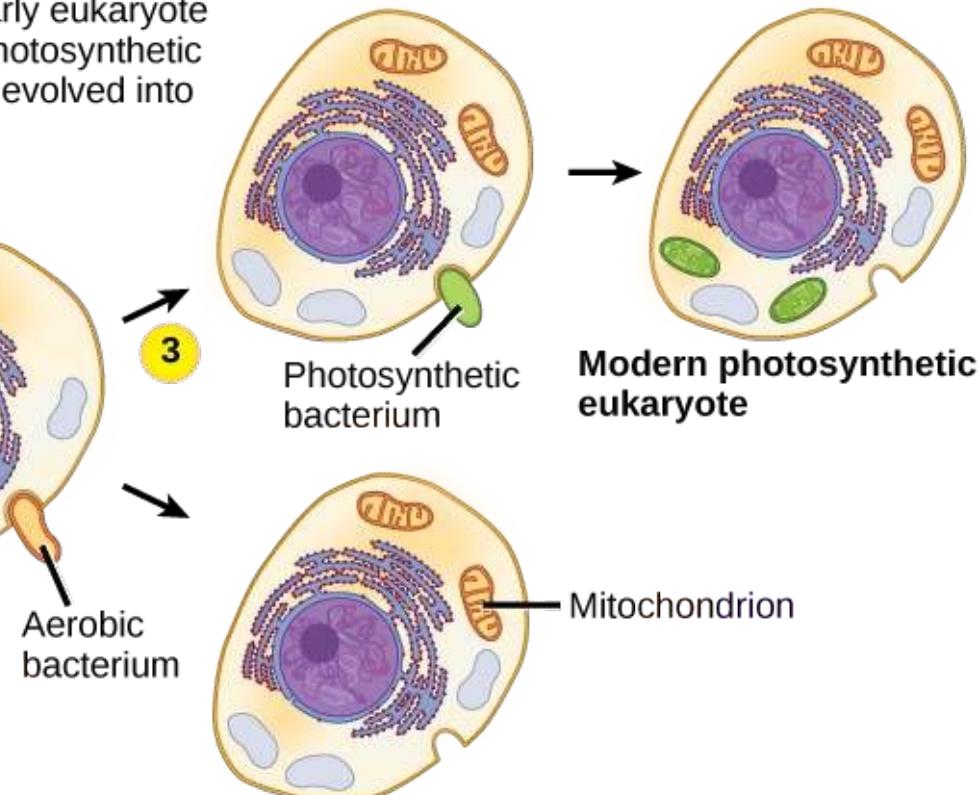


Proto-eukaryote

3 In a second endosymbiotic event, the early eukaryote consumed photosynthetic bacteria that evolved into chloroplasts.



2 In a first endosymbiotic event, the ancestral eukaryote consumed aerobic bacteria that evolved into mitochondria.



Modern heterotrophic eukaryote

# Primary endosymbiosis: evidence

- Both mitochondria and chloroplasts can arise only from preexisting mitochondria and chloroplasts. They cannot be formed in a cell that lacks them because nuclear genes encode only some of the proteins of which they are made.
- Both mitochondria and chloroplasts have their own genome, and it resembles that of bacteria not that of the nuclear genome.
- Both genomes consist of a single circular molecule of DNA.
- There are no histones associated with the DNA.
- Both mitochondria and chloroplasts have their own protein-synthesizing machinery, and it more closely resembles that of bacteria than that found in the cytoplasm of eukaryotes, and are sensitive to a number of antibiotics (e.g. streptomycin, rifampicin).
- Genes for the functioning of both mitochondria and chloroplast are shared between their own genomes and the nuclear genomes.

# Alternative Eukaryogenesis theories

In 1996, Woese and colleagues (University of Illinois professor Gary Olsen and researchers from the Institute for Genomic Research) published in the journal Science the first complete genome structure of an archaeon, *Methanococcus jannaschii*. Based on this work, they concluded that the Archaea are more closely related to humans than to bacteria. "The Archaea are related to us, to the eukaryotes; they are descendants of the microorganisms that gave rise to the eukaryotic cell billions of years ago" Woese said at the time.

This led to the current idea that the protoeukaryotes and the Archaea had a common ancestor, but new evidence has emerged thanks to advanced metagenomic approaches



nature

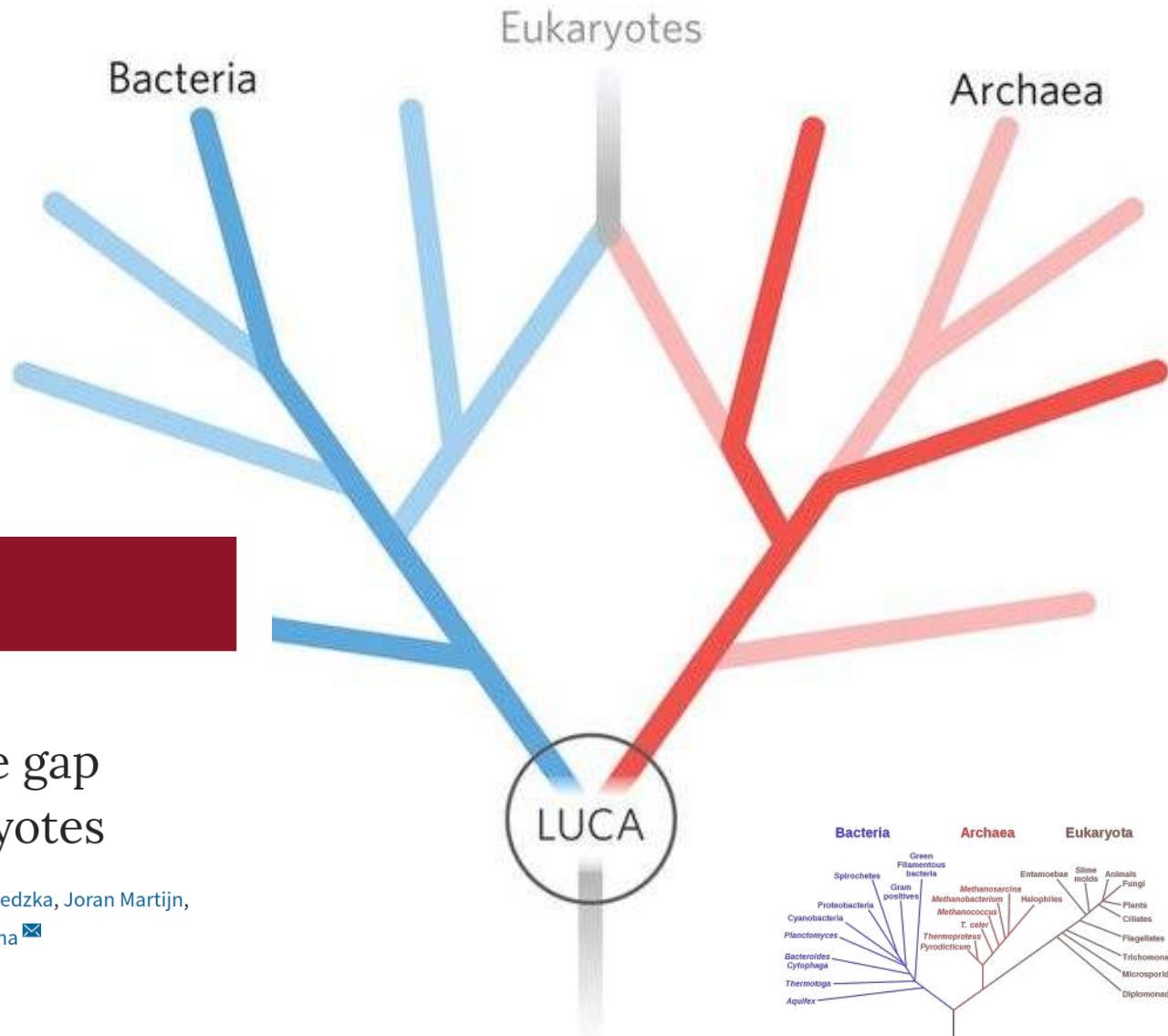
International journal of science

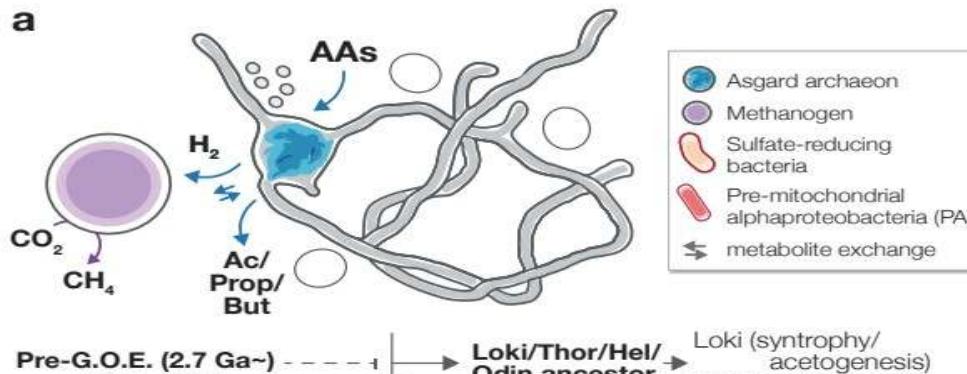
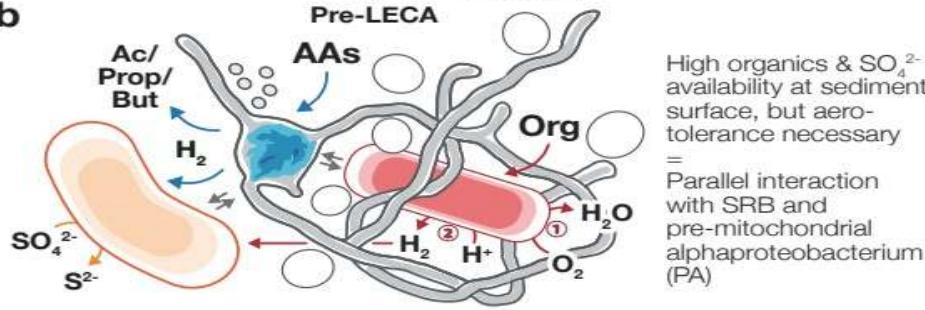
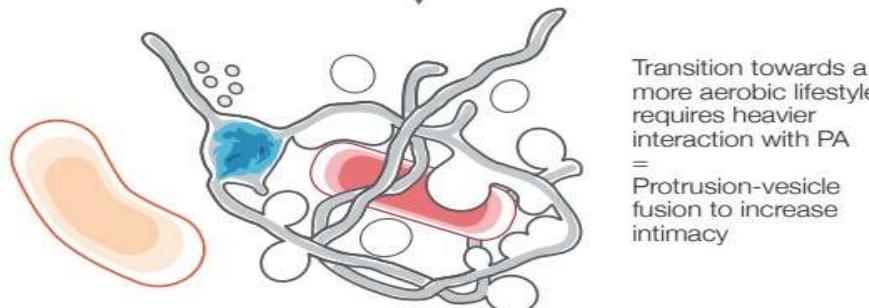
Article | Published: 06 May 2015

# Complex archaea that bridge the gap between prokaryotes and eukaryotes

Anja Spang, Jimmy H. Saw, Steffen L. Jørgensen, Katarzyna Zaremba-Niedzwiedzka, Joran Martijn,  
Anders E. Lind, Roel van Eijk, Christa Schleper, Lionel Guy & Thijs J. G. Ettema

Nature 521, 173–179 (14 May 2015) | Download Citation ↓



**a****b****c**

## Isolation of an archaeon at the prokaryote-eukaryote interface

Hiroyuki Imachi, Masaru K. Nobu, Nozomi Nakahara, Yuki Morono, Miyuki Ogawara, Yoshihiro Takaki, Yoshinori Takano, Katsuyuki Uematsu, Tetsuro Ikuta, Motoo Ito, Yohei Matsui, Masayuki Miyazaki, Kazuyoshi Murata, Yumi Saito, Sanae Sakai, Chihong Song, Eiji Tasumi, Yuko Yamanaka, Takashi Yamaguchi, Yoichi Kamagata, Hideyuki Tamaki, Ken Takai  
 doi: <https://doi.org/10.1101/726976>

This article is a preprint and has not been certified by peer review [what does this mean?].

**Abstract**

**Full Text**

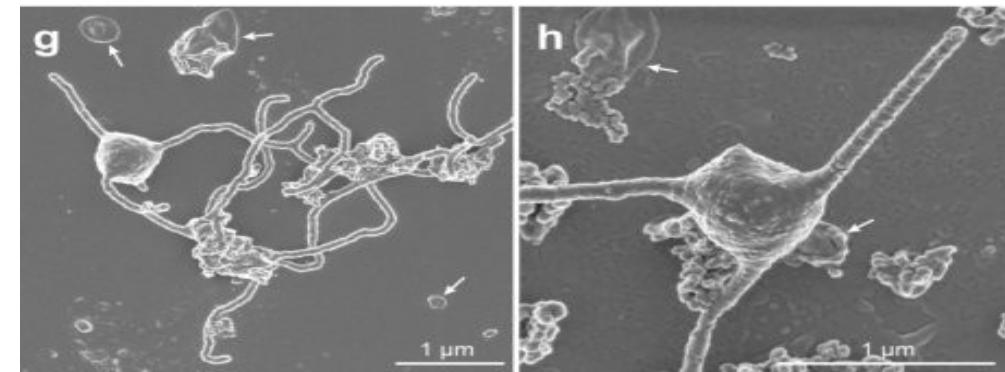
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**Metrics**

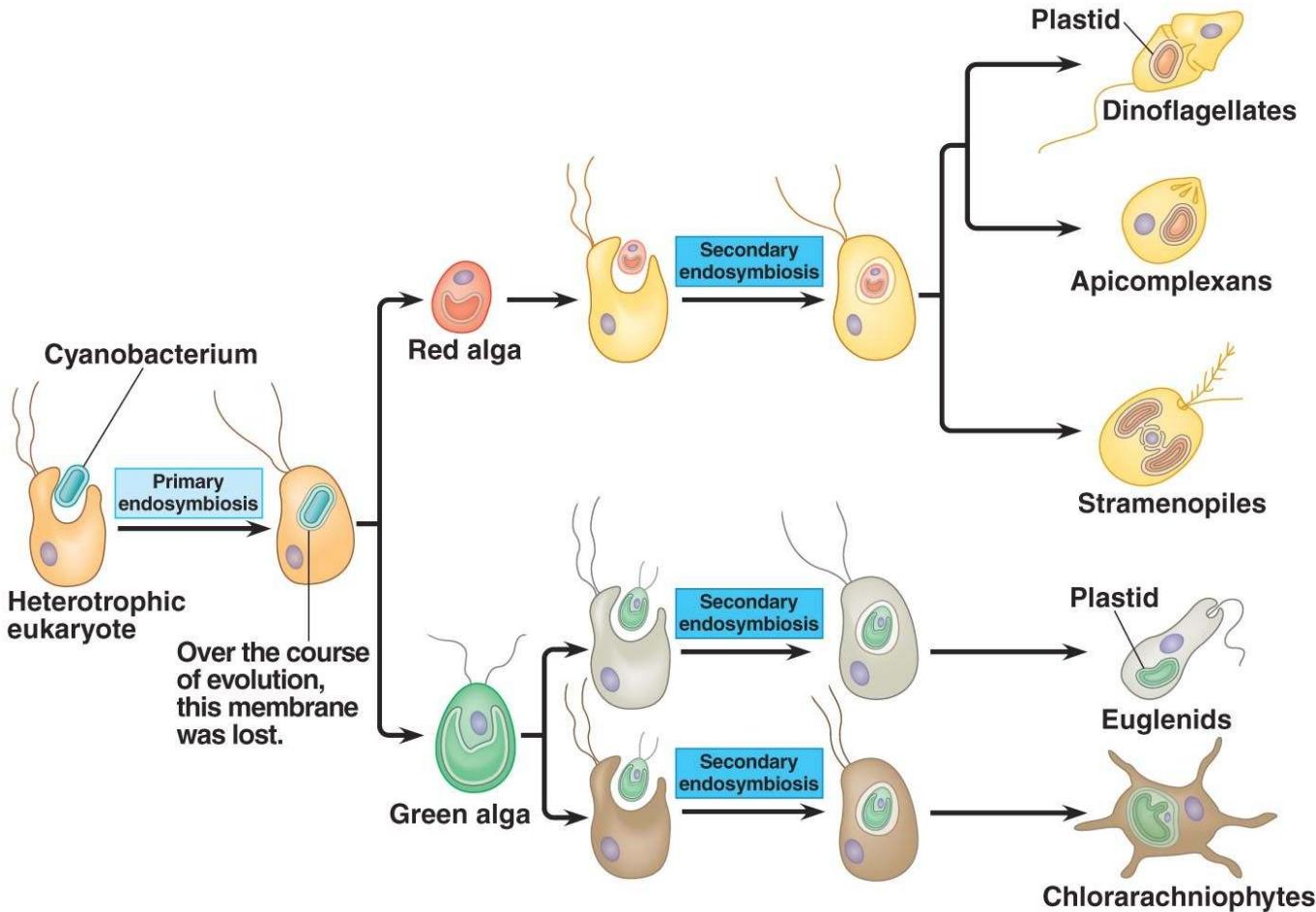
**Preview PDF**

### Abstract

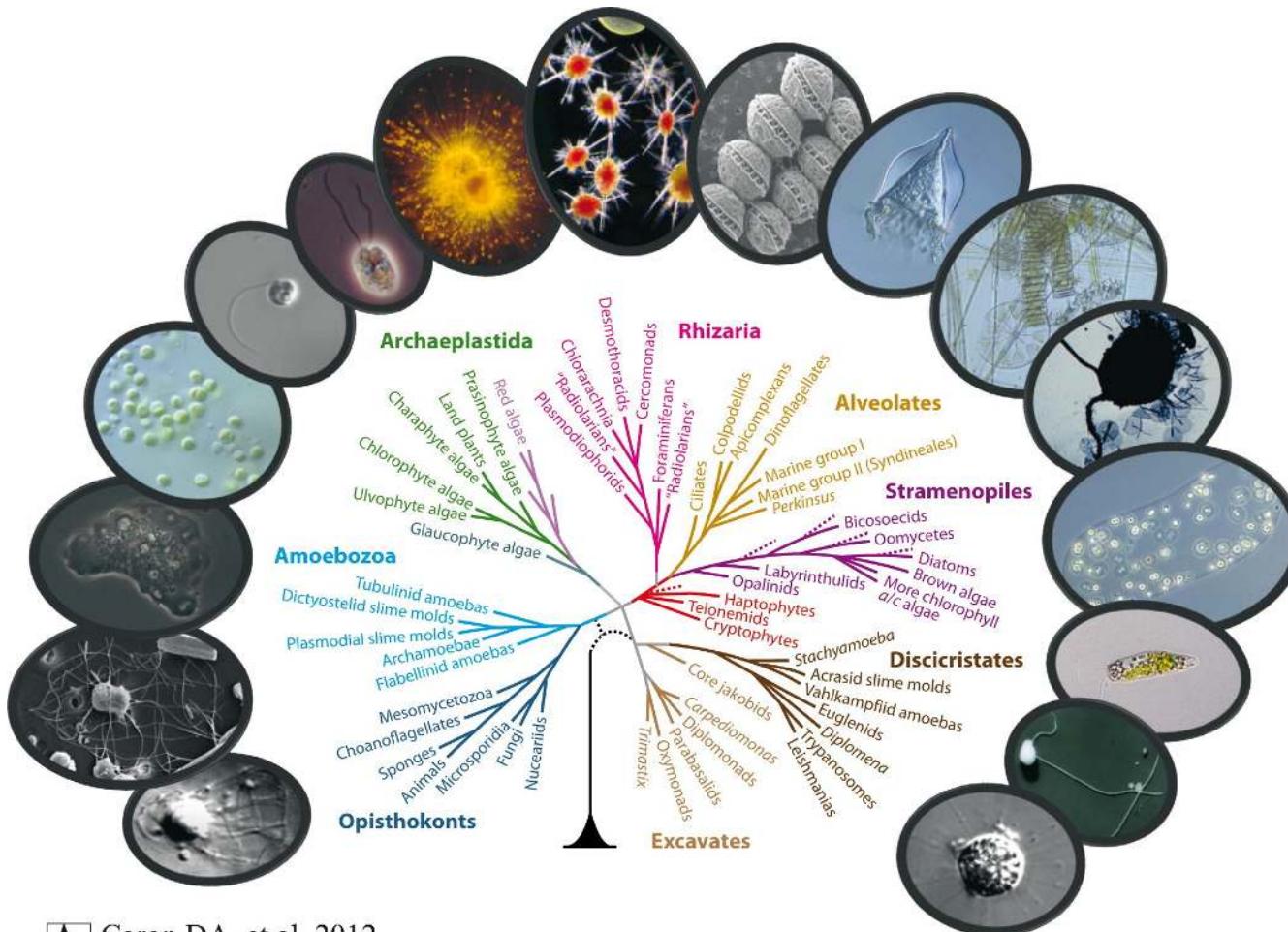
The origin of eukaryotes remains enigmatic. Current data suggests that eukaryotes may have risen from an archaeal lineage known as "Asgard archaea". Despite the eukaryote-like genomic features found in these archaea, the evolutionary transition from archaea to eukaryotes remains unclear due to the lack of cultured representatives and corresponding physiological insight. Here we report the decade-long isolation of a Lokiarchaeota-related Asgard archaeon from deep marine sediment. The archaeon, "*Candidatus Prometheoarchaeum syntrophicum* strain MK-D1", is an anaerobic, extremely slow-growing, small cocci (~550 nm), that degrades amino acids through syntrophy. Although eukaryote-like intracellular complexities have been proposed for Asgard archaea, the isolate has no visible organella-like structure. *Ca. P. syntrophicum* instead displays morphological complexity – unique long, and often, branching protrusions. Based on cultivation and genomics, we propose an "Entangle-Engulf-Enslave (E<sup>3</sup>) model" for eukaryogenesis through archaea-alphaproteobacteria symbiosis mediated by the physical complexities and metabolic dependency of the hosting archaeon.



# Secondary endosymbiosis



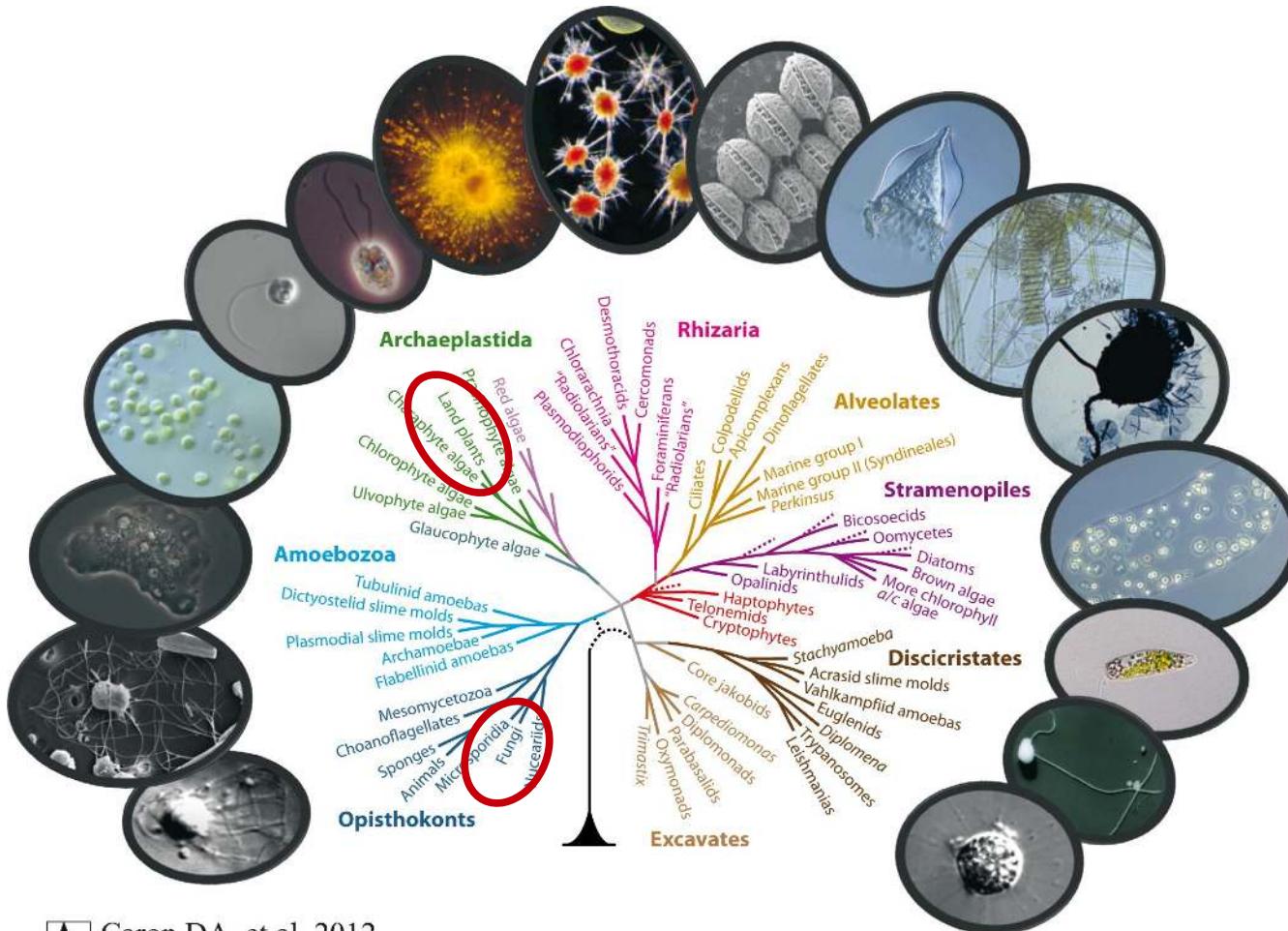
## Protist



Caron DA, et al. 2012.

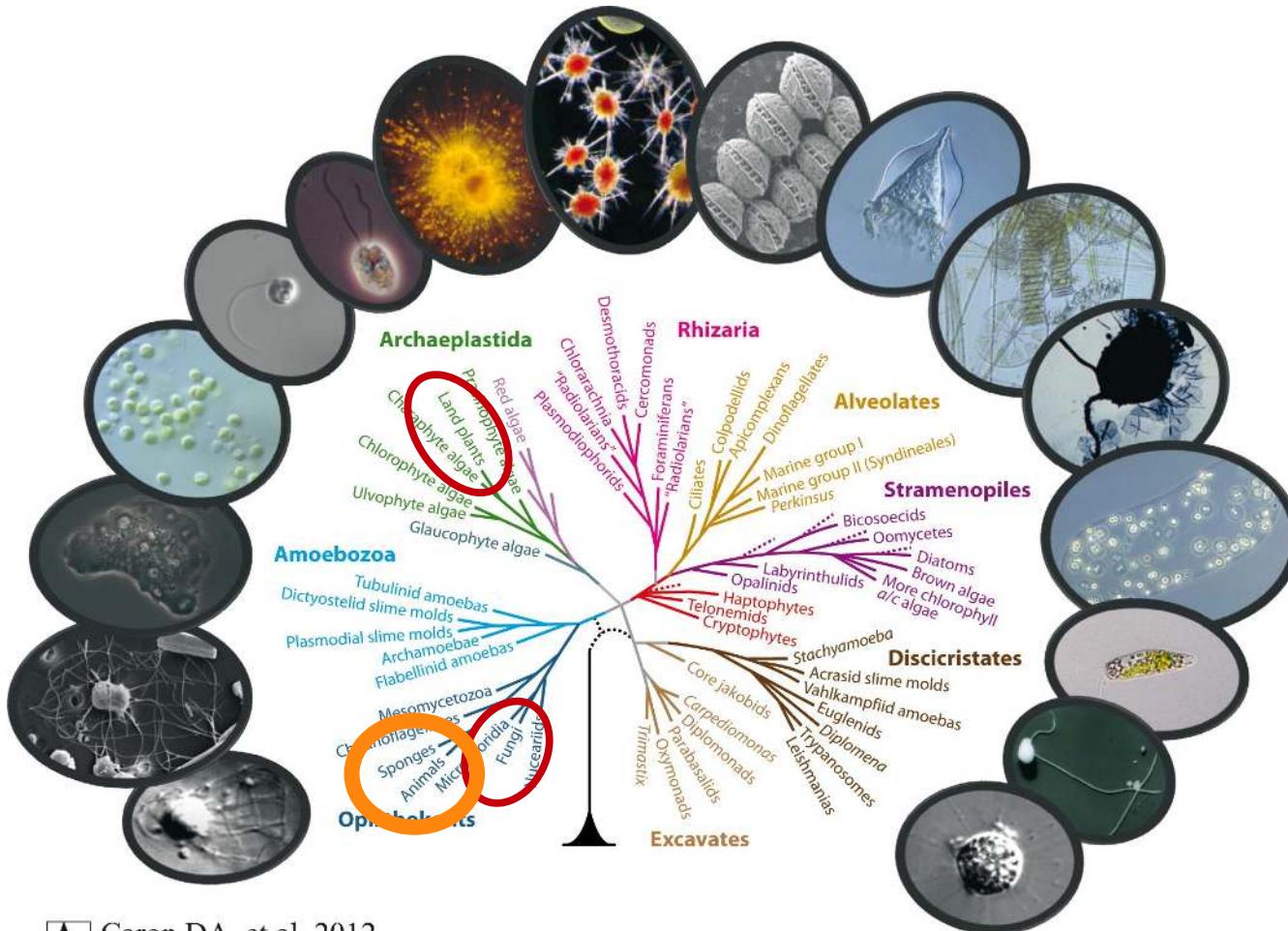
Annu. Rev. Mar. Sci. 4:467–93

# Protist



Caron DA, et al. 2012.  
Annu. Rev. Mar. Sci. 4:467–93

# Protist

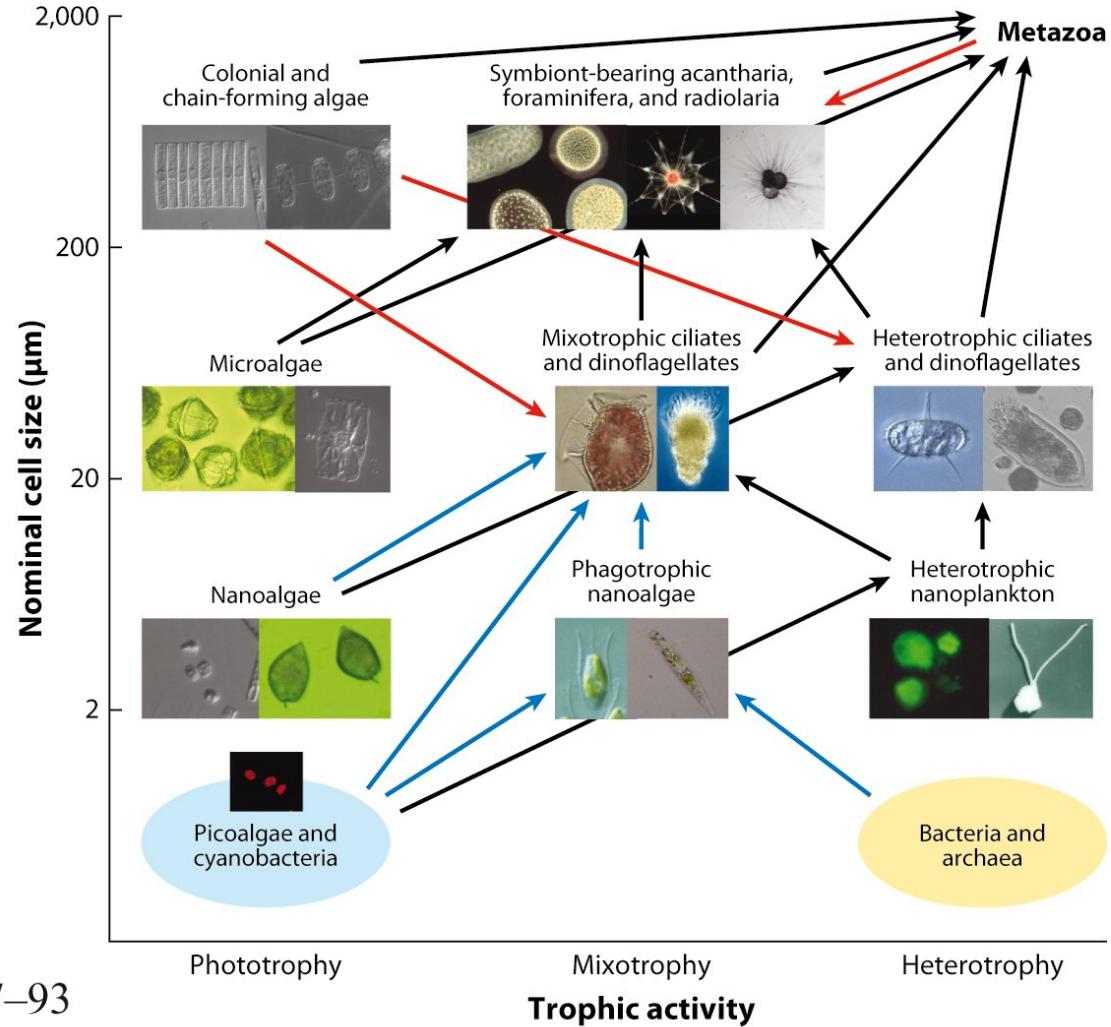


Caron DA, et al. 2012.  
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# Protist

- Protists have fascinated microbiologists since their discovery nearly 350 years ago
- Single-celled, eukaryotic species span an incredible range of sizes, forms, and functions and, despite their generally diminutive size, constitute much of the genetic diversity within the domain Eukarya
- Complex taxonomy with numerous paraphyletic groups
- Protists in marine ecosystems play fundamental ecological roles as primary producers, consumers, decomposers, and trophic links in aquatic food webs

# Protist: why important?

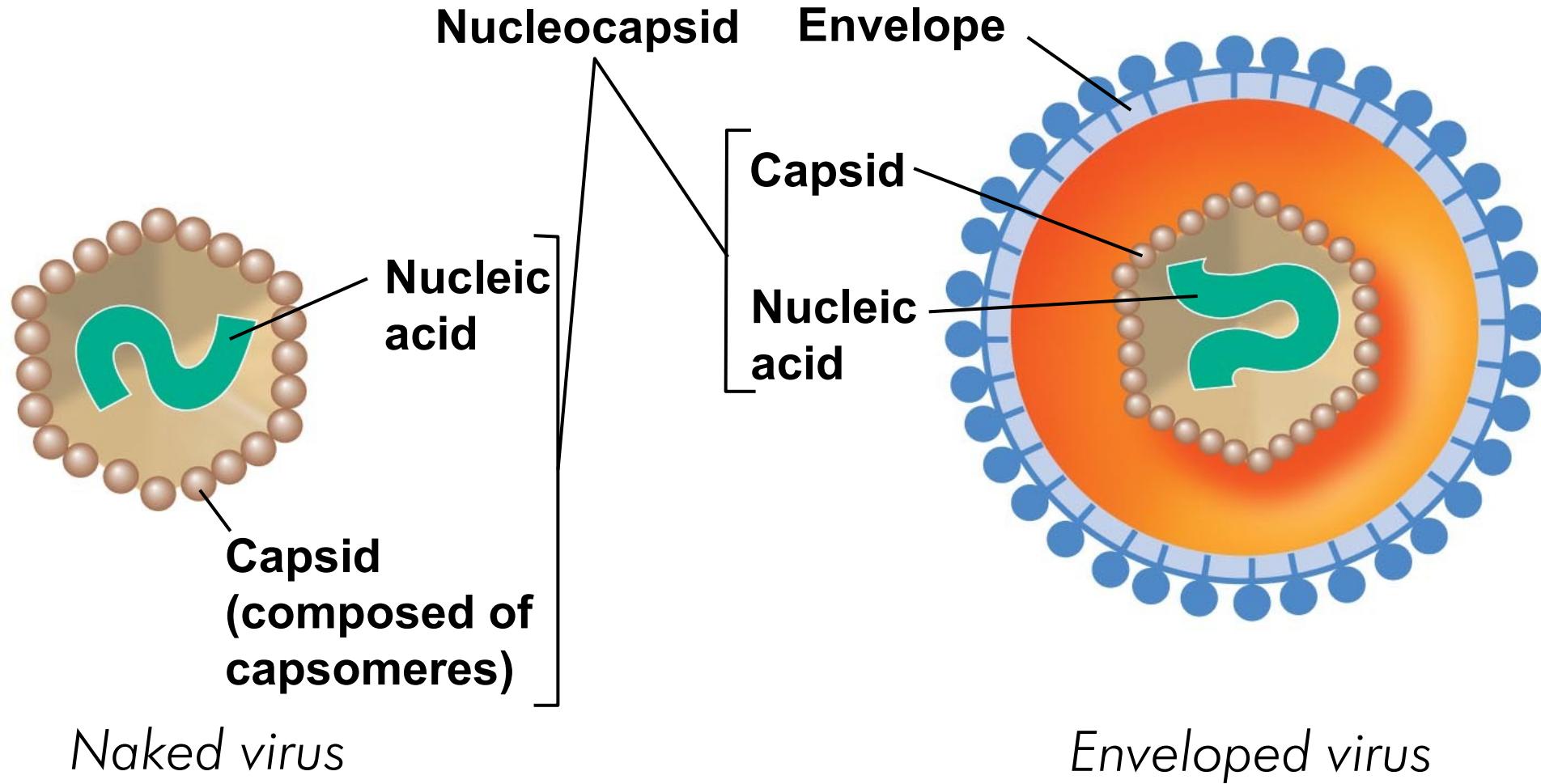


# *The Viruses*

# What is a virus

- A **virus** is a genetic element that can replicate only inside a living cell, called the host cell
- The word virus comes from the Latin, poison (syn. Venum)
- Viruses can only replicate themselves by infecting a host cell and therefore cannot reproduce on their own
- At the most basic level, viruses consist of genetic material contained within a **protective protein coat** called a **capsid**. They infect a wide variety of organisms: both eukaryotes and prokaryotes
- A virus that infects bacteria is known as a **bacteriophage**, often shortened to phage
- The study of viruses is known as virology, and those who study viruses are known as virologists
- Simply stated a virus is a “piece of bad news wrapped in a protein case”

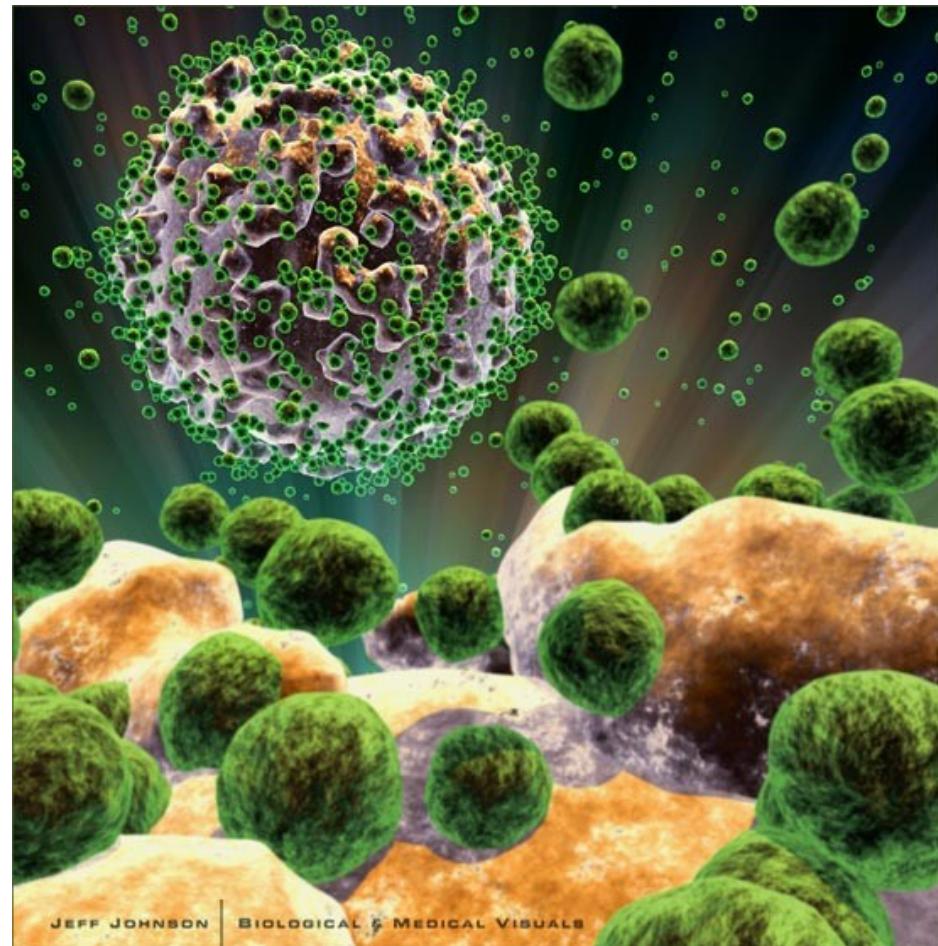
## *Viral structure*

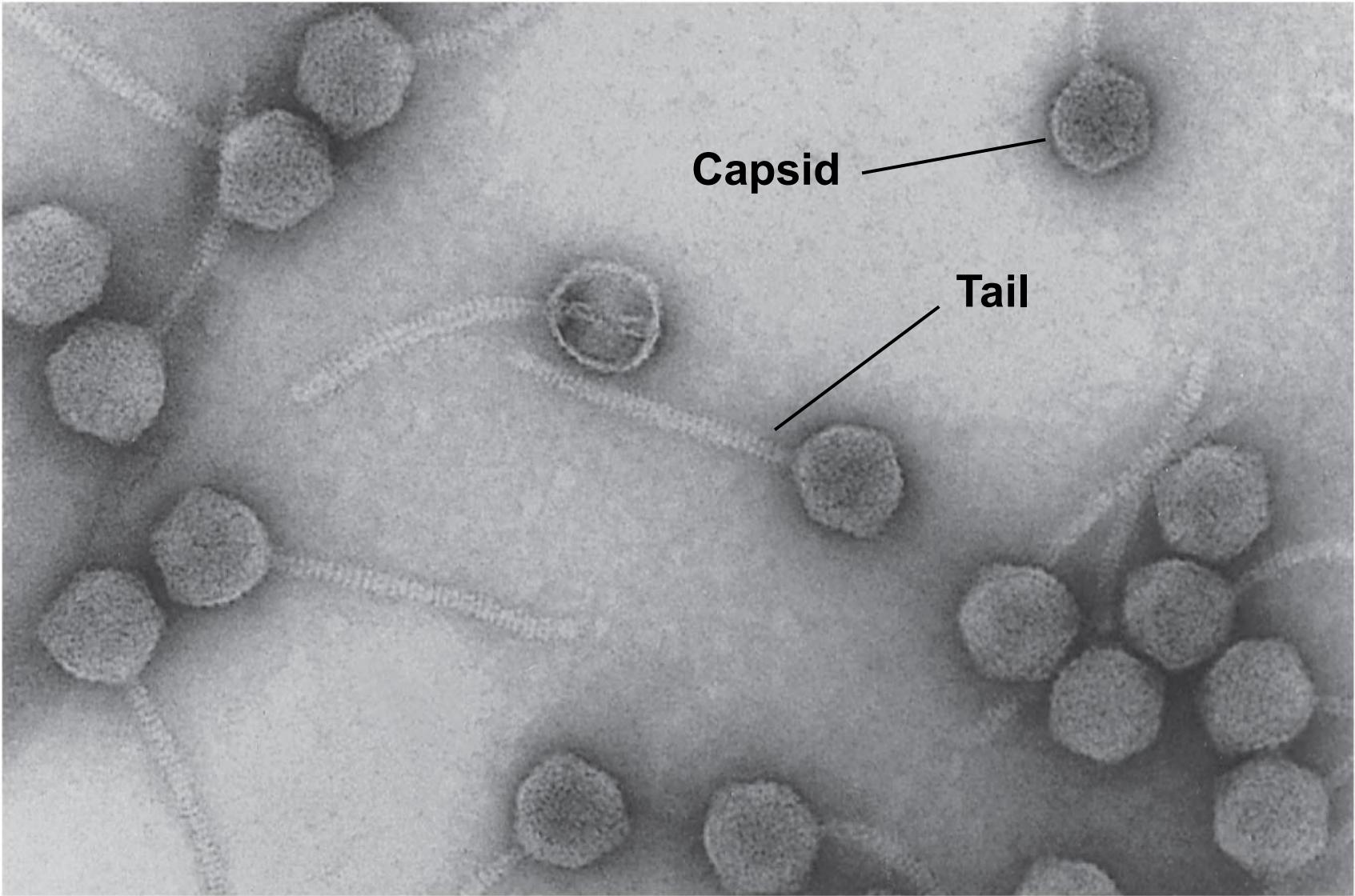


# An Sea of Viruses

There are an estimated  $10^{31}$  viruses on Earth.

The sheer number of viruses and their intimate relationship with microbial life suggest that viruses play a critical role in the planet's biosphere.





D. Kaiser



VISUAL SCIENCE  
Scientific illustration, animation, design

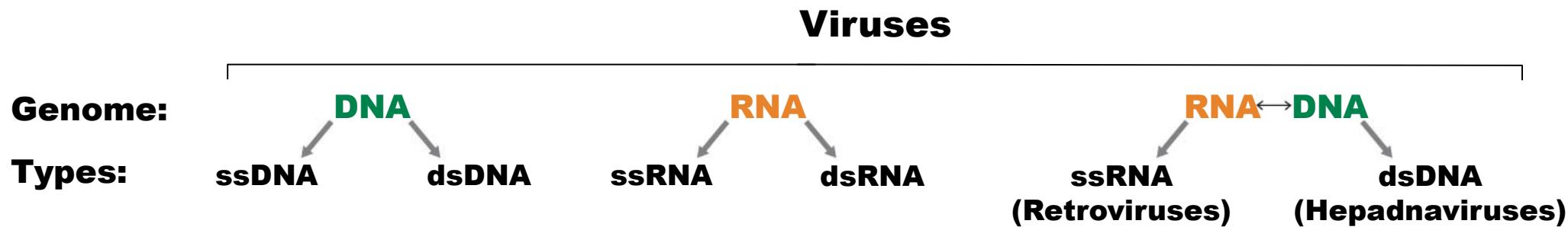


VISUAL SCIENCE  
Scientific illustration, animation, design



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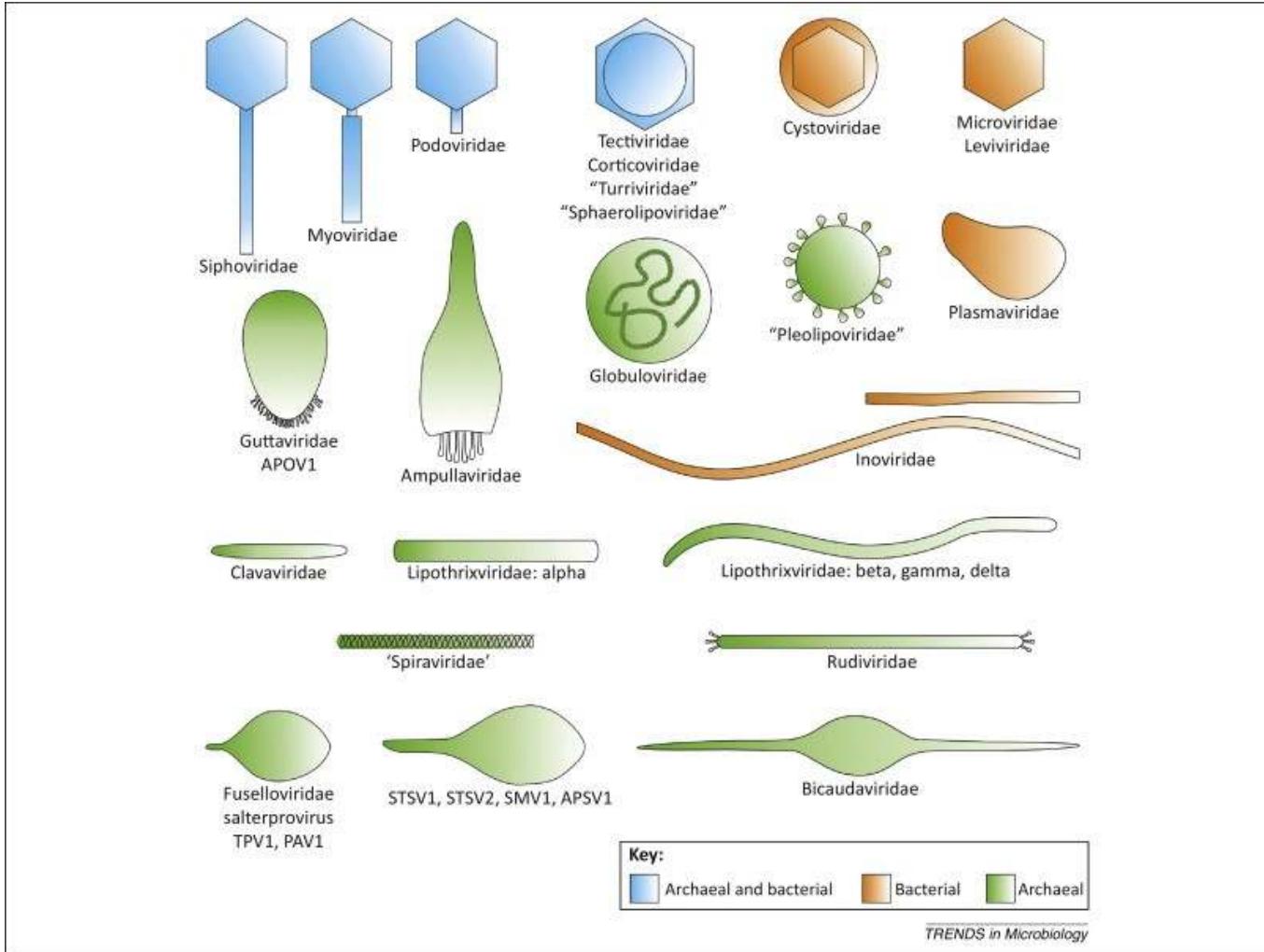
# Virus: Structure and Morphology



All cells contain double-stranded DNA genomes

By contrast, viral genomes consist of either DNA or RNA and are further subdivided based on whether the genome is single-stranded or double-stranded

# Virus: Structure and Morphology



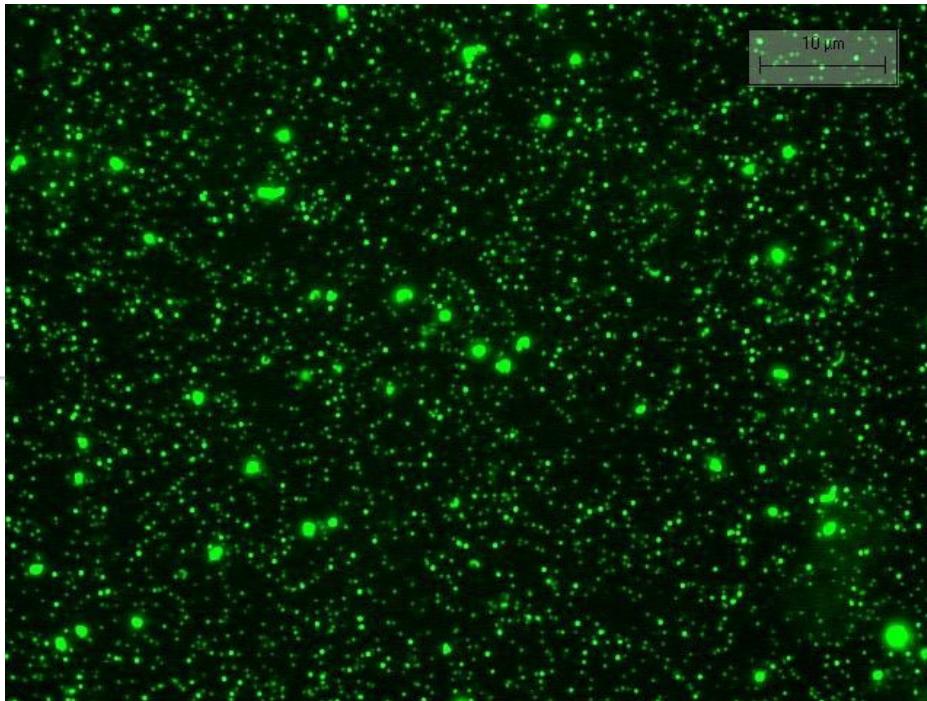
## Use of SYBR Green I for rapid epifluorescence counts of marine viruses and bacteria

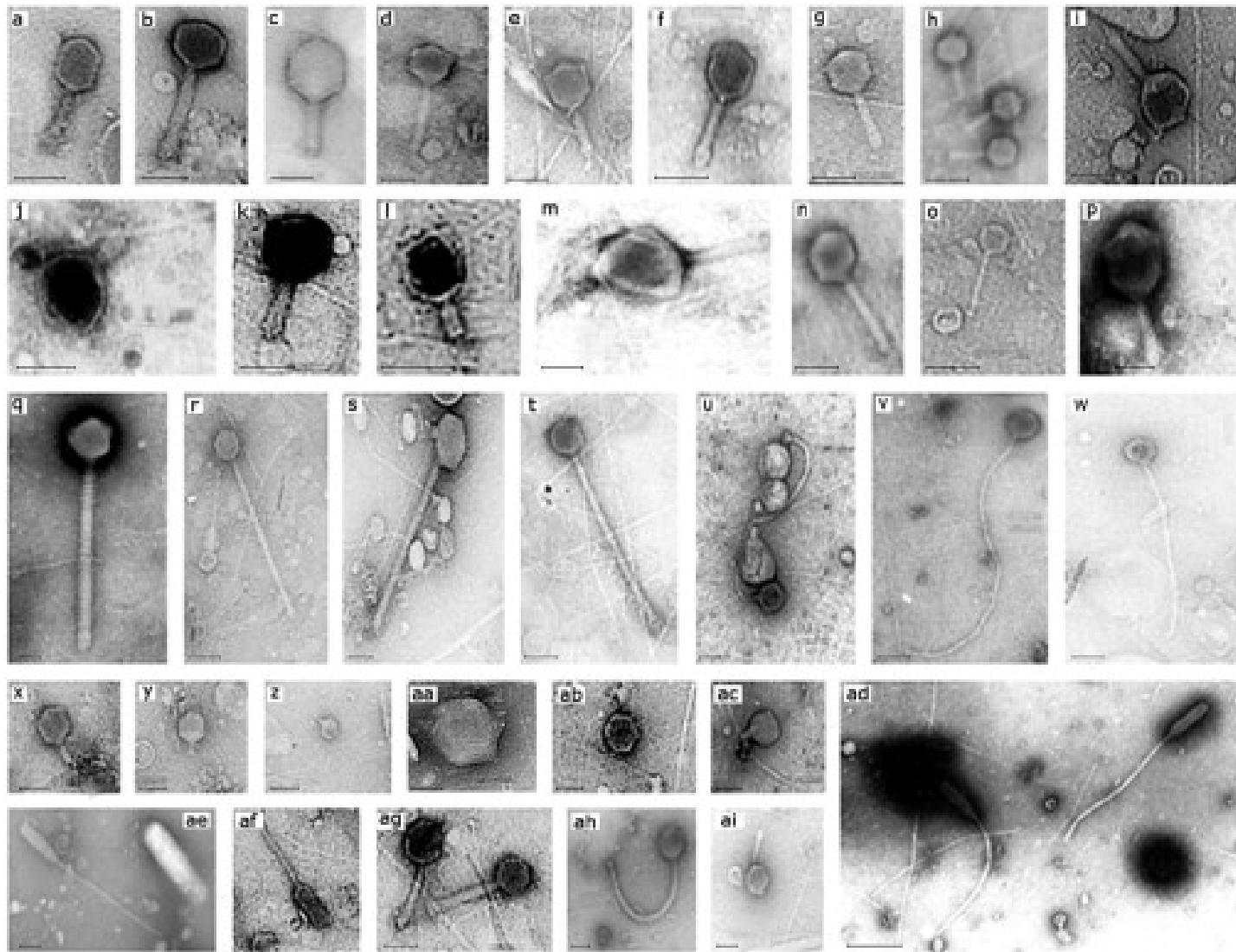
Rachel T. Noble\*, Jed A. Fuhrman

University of Southern California, Department of Biological Sciences, AHF 107, University Park, Los Angeles, California 90089-0371, USA

**ABSTRACT:** A new nucleic acid stain, SYBR Green I, can be used for the rapid and accurate determination of viral and bacterial abundances in diverse marine samples. We tested this stain with formalin-preserved samples of coastal water and also from depth profiles (to 800 m) from sites 19 and 190 km offshore, by filtering a few ml onto 0.02  $\mu\text{m}$  pore-size filters and staining for 15 min. Comparison of bacterial counts to those made with acridine orange (AO) and virus counts with those made by transmission electron microscopy (TEM) showed very strong correlations. Bacterial counts with AO and SYBR Green I were indistinguishable and almost perfectly correlated ( $r^2 = 0.99$ ). Virus counts ranged widely, from 0.03 to  $15 \times 10^3$  virus  $\text{ml}^{-1}$ . Virus counts by SYBR Green I were on the average higher than those made by TEM, and a SYBR Green I versus TEM plot yielded a regression slope of 1.28. The correlation between the two was very high with an  $r^2$  value of 0.98. The precision of the SYBR Green I method was the same as that for TEM, with coefficients of variation of 2.9%. SYBR Green I stained viruses and bacteria are intensely stained and easy to distinguish from other particles with both older and newer generation epifluorescence microscopes. Detritus is generally not stained, unlike when the alternative dye YoPro I is used, so this approach may be suitable for sediments. SYBR Green I stained samples need no desalting or heating, can be fixed with formalin prior to filtration, the optimal staining time is 15 min (resulting in a total preparation time of less than 25 min), and counts can be easily performed at sea immediately after sampling. This method may facilitate incorporation of viral research into most aquatic microbiology laboratories.

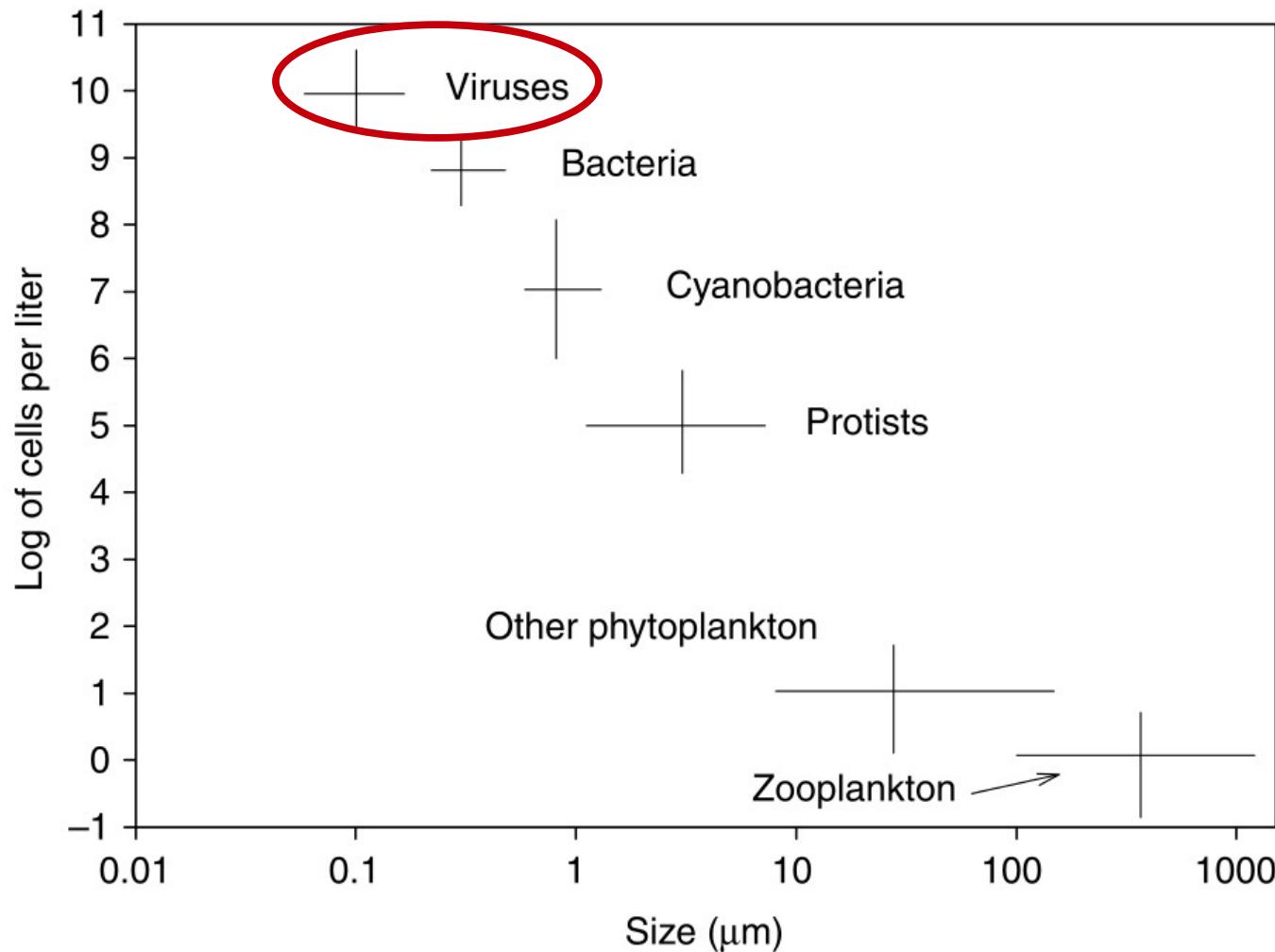
**KEY WORDS:** Virus · Epifluorescence · SYBR Green I · Marine ecology

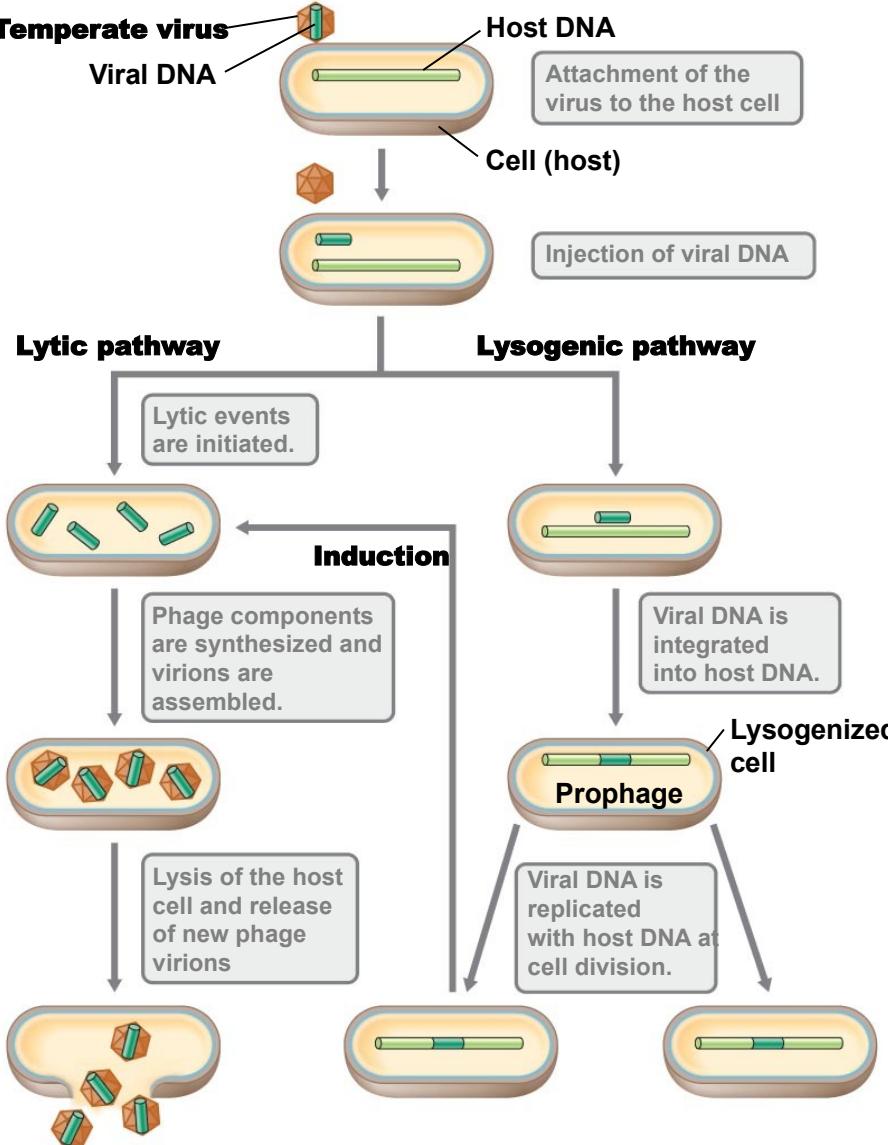




Given the lack of conserved genes across the viral groups, for a while viral diversity was only studied based on their morphology or general genome properties (pulse field gel electrophoresis)

# Abundance and Size





# Virus Life Cycle

**Lytic pathway.** The phage infects and lyse the host cell immediately after reaching burst size

**Lysogenic pathway.** The phage becomes dormant (i.e. integrated) into the host genome until induced. Integration can become permanent

**Chronic pathway.** The virus remains inside the host cell releasing viral particle without lysing the cell

# Virus Life Cycle

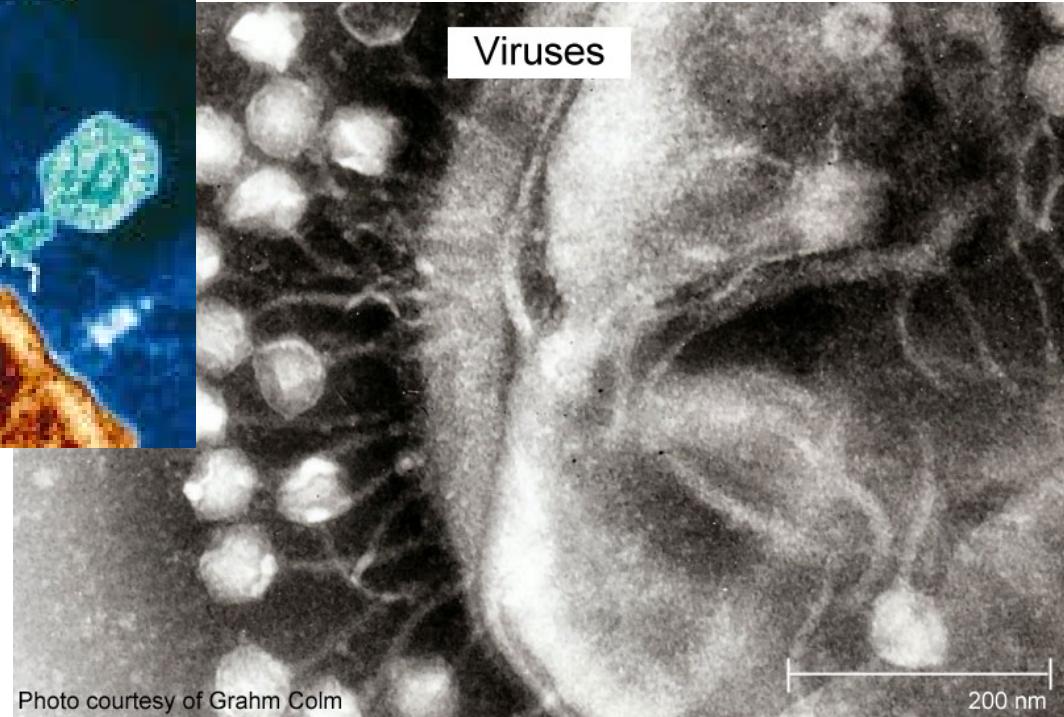
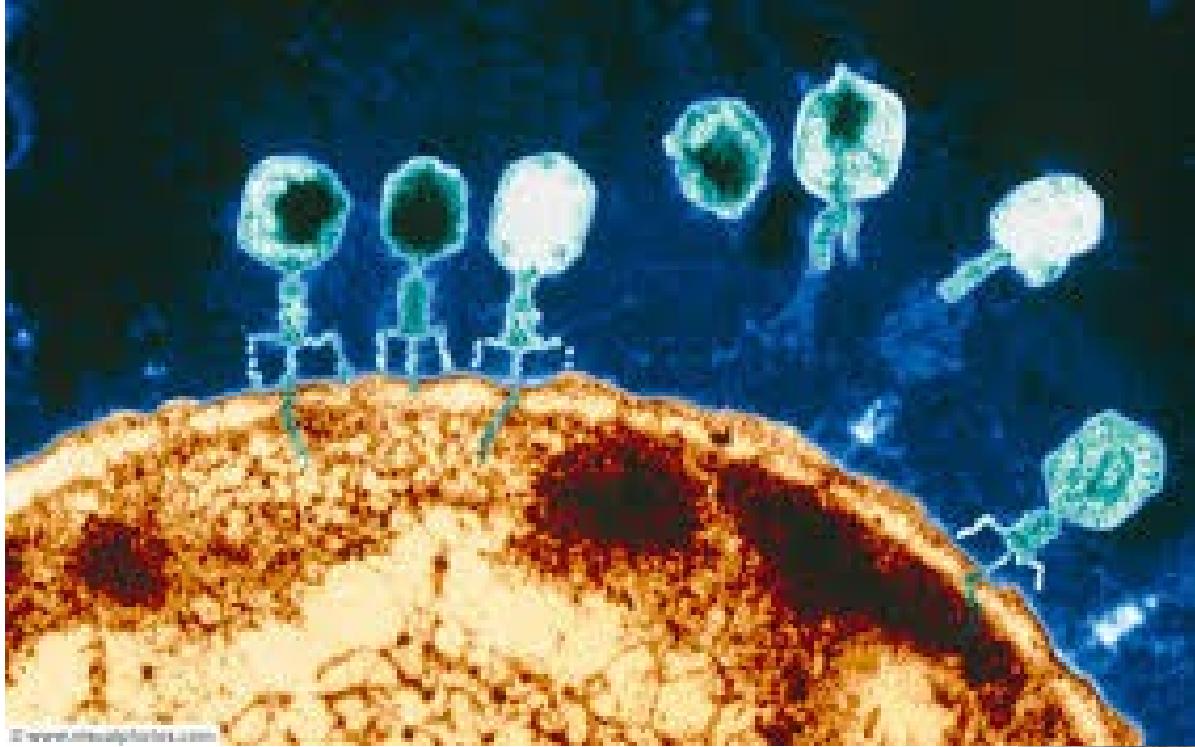
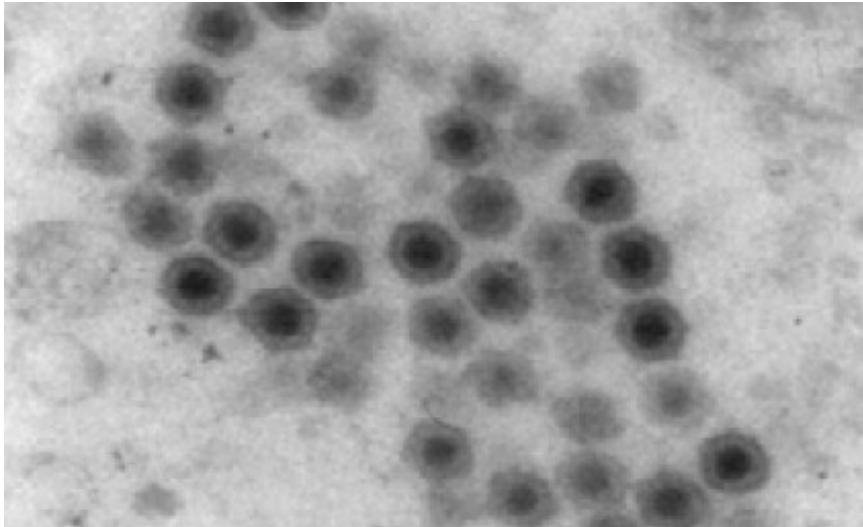


Photo courtesy of Graham Colm

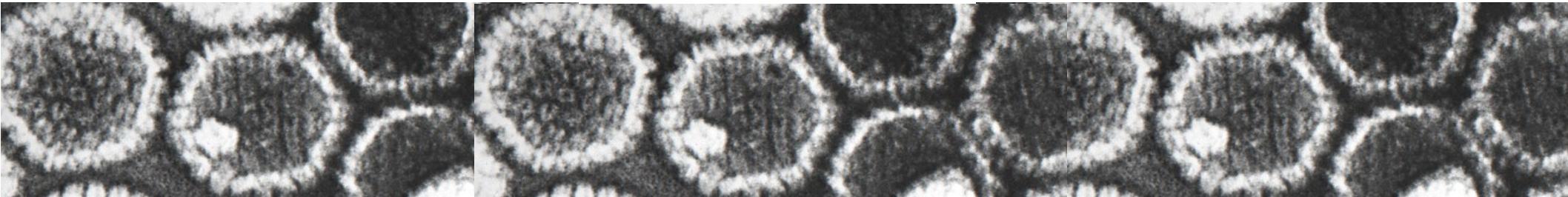
# Virus Life Cycle



An important modeling parameter: **Burst Size**  
i.e. the average number of virus released by a cell

# *Viral diversity in the environment*

- Highest diversity of unknown genes with no matches in databases
- Highest number of unknown viral families
- Lowest number of “cultured” types available, mostly from model organisms
- Huge potential to influence diversity, evolution and biogeochemistry



# *Effects on biogeochemistry*

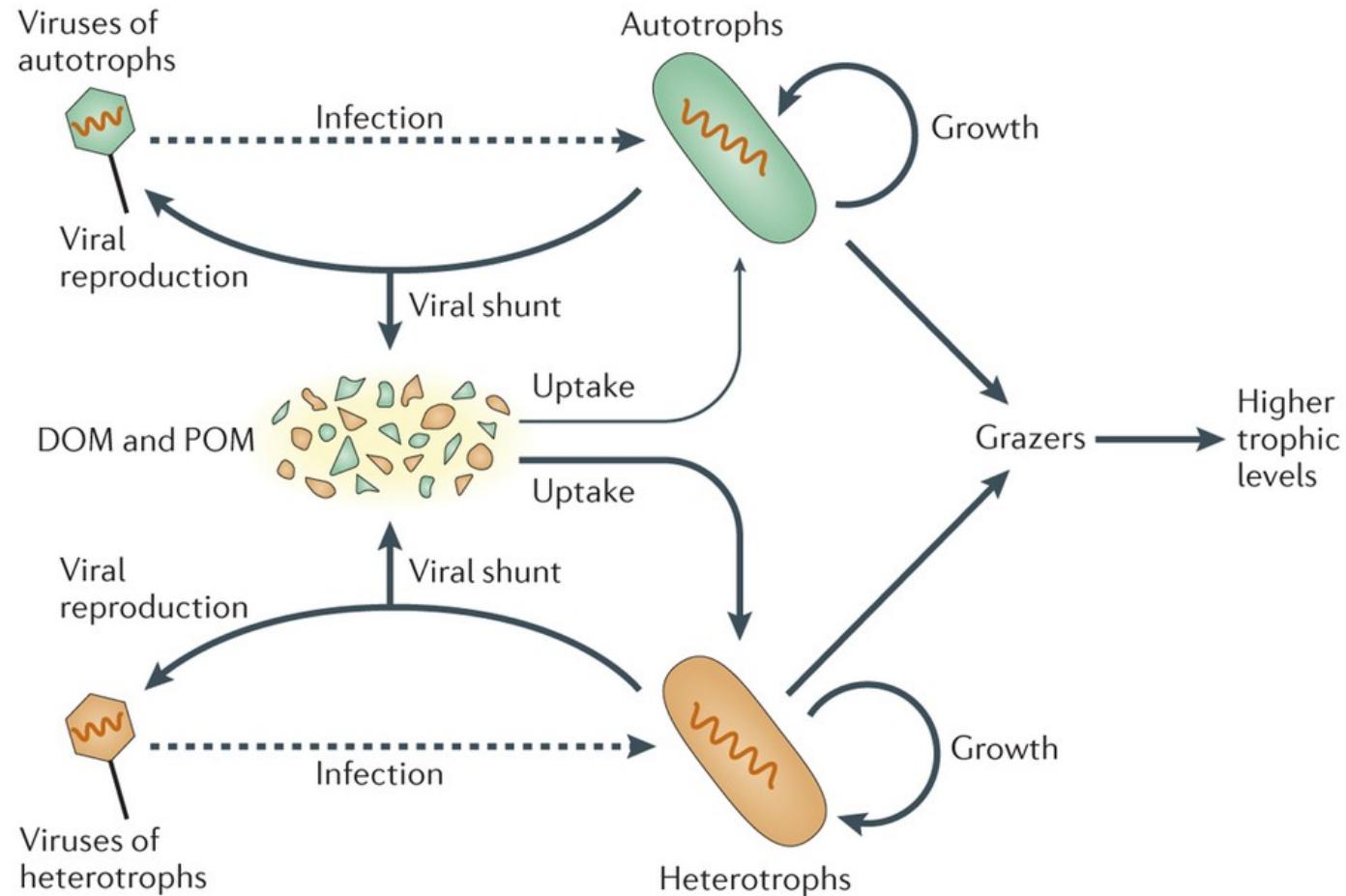
*By infecting and lysing prokaryotic cells, virus are potentially responsible for cycling huge amounts of organic carbon and other nutrients in many ecosystems*

*For example in the Ocean, viruses may turn over as much as 150 gigatons of carbon per year—more than 30 times the standing abundance of carbon in marine plankton (though **Viral shunt**)*

*Top-Down control of prokaryotic and phytoplankton populations, and effect on community structure (**Killing the winner hypothesis**)*

*They are evolutionary drivers through transduction and horizontal gene transfer (**Red queen hypothesis**)*

# Ecological Role: Viral Shunt



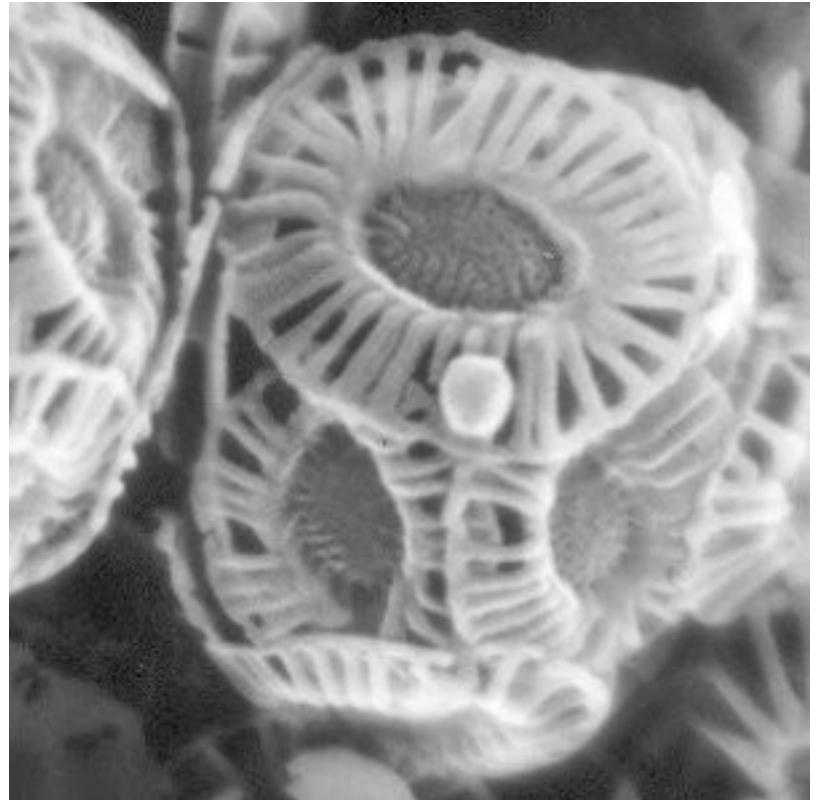
# *How virus influence climate*



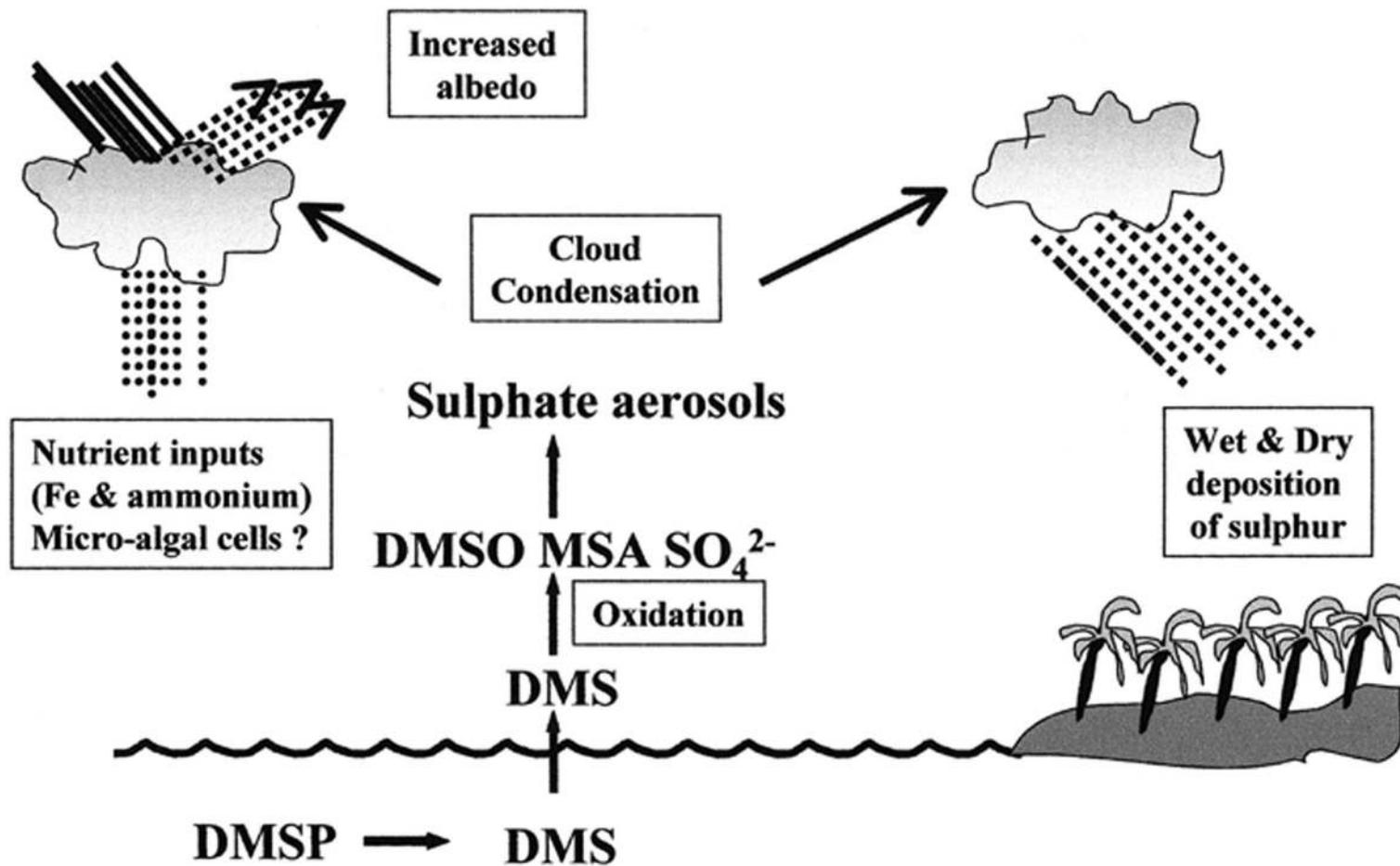
# How virus influence climate

- Virus infect phytoplankton
- Since their infection is controlled by random contact (they are not motile), most abundant organisms are more likely to be infected
- This can trigger bloom termination due to viral infection

On the side: EhV1 infecting the coccolithophore *Emiliania heuxleyi*



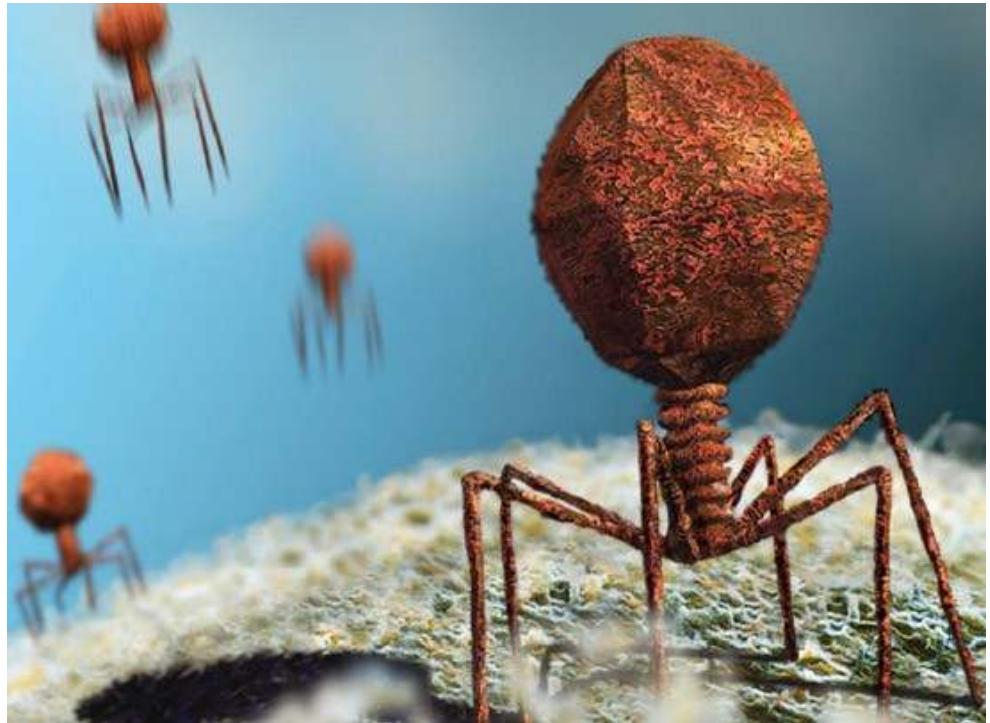
# How virus influence climate



Virus affect the amount of released DMSP in the Oceans, thus affecting climate

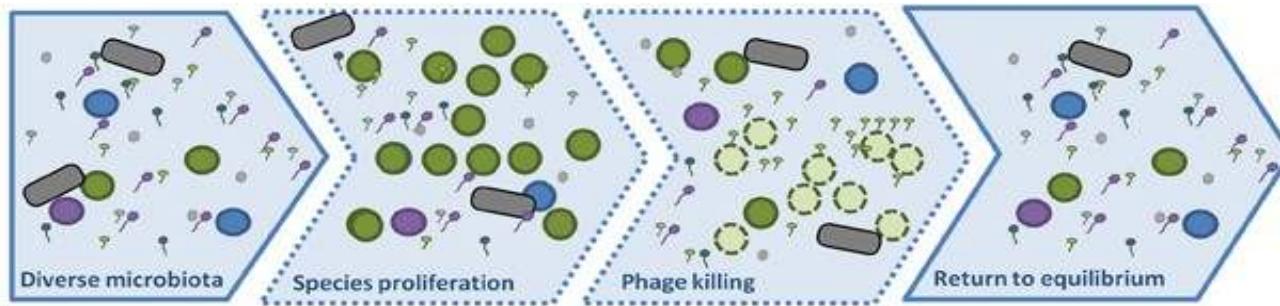
# Killing the Winner Hypothesis

- The theory states that virus kill the most abundant organisms in a population (frequency dependent selection)
- Supported by both experimental and modeling data
- Alternative models are possible



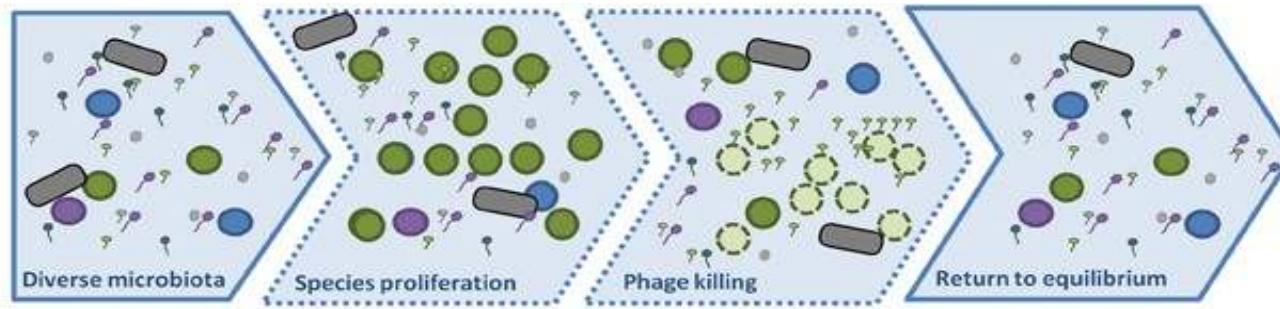
**A**

Kill the  
winner



**A**

Kill the  
winner

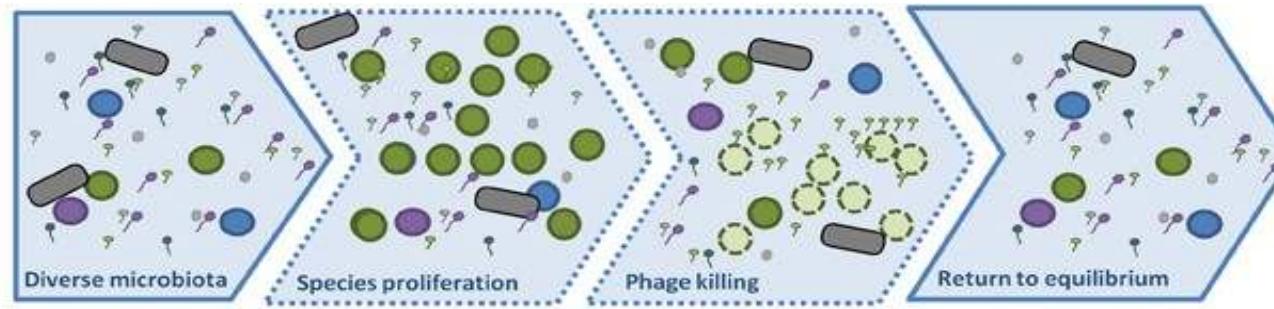
**B**

Kill the  
relative

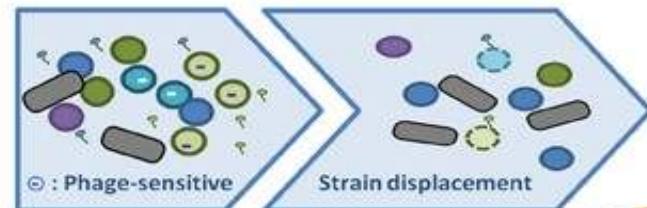


**A**

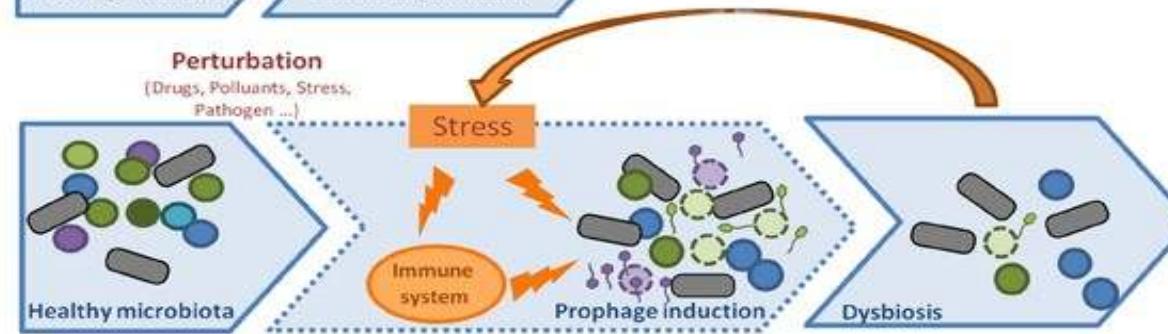
Kill the  
winner

**B**

Kill the  
relative

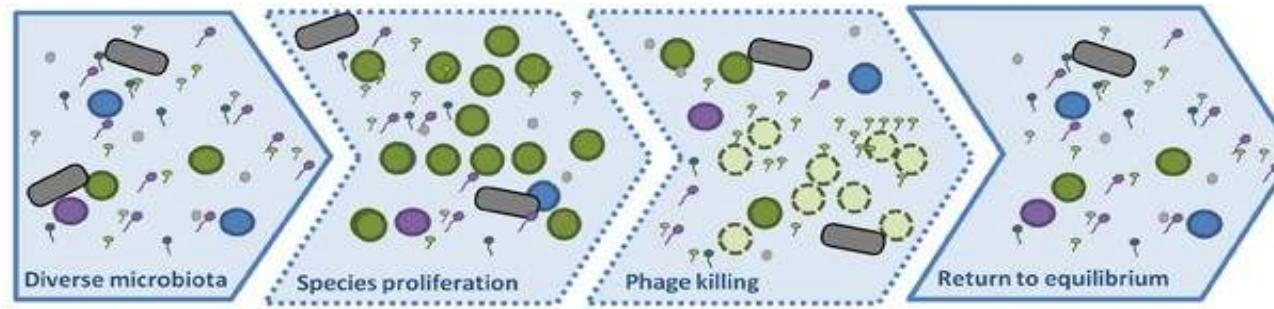
**C**

Community  
shuffling

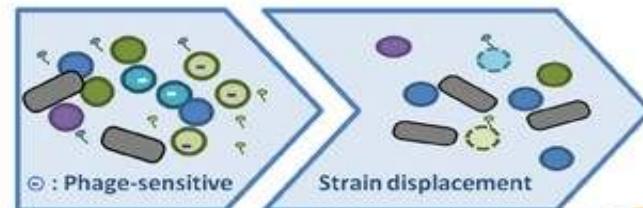


**A**

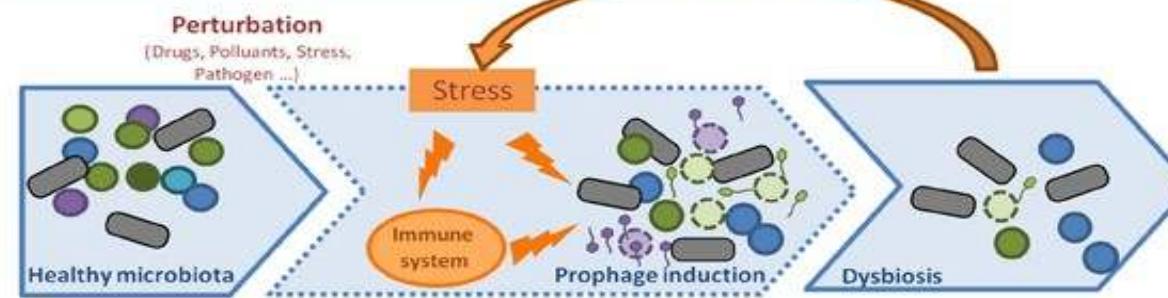
Kill the  
winner

**B**

Kill the  
relative

**C**

Community  
shuffling

**D**

Invoke the  
relative



# The Red Queen Hypothesis

The Red Queen hypothesis is an evolutionary hypothesis which proposes that organisms must constantly adapt, evolve, and proliferate not merely to gain reproductive advantage, but also simply to survive while pitted against ever-evolving opposing organisms in an ever-changing environment, and intends to explain two different phenomena

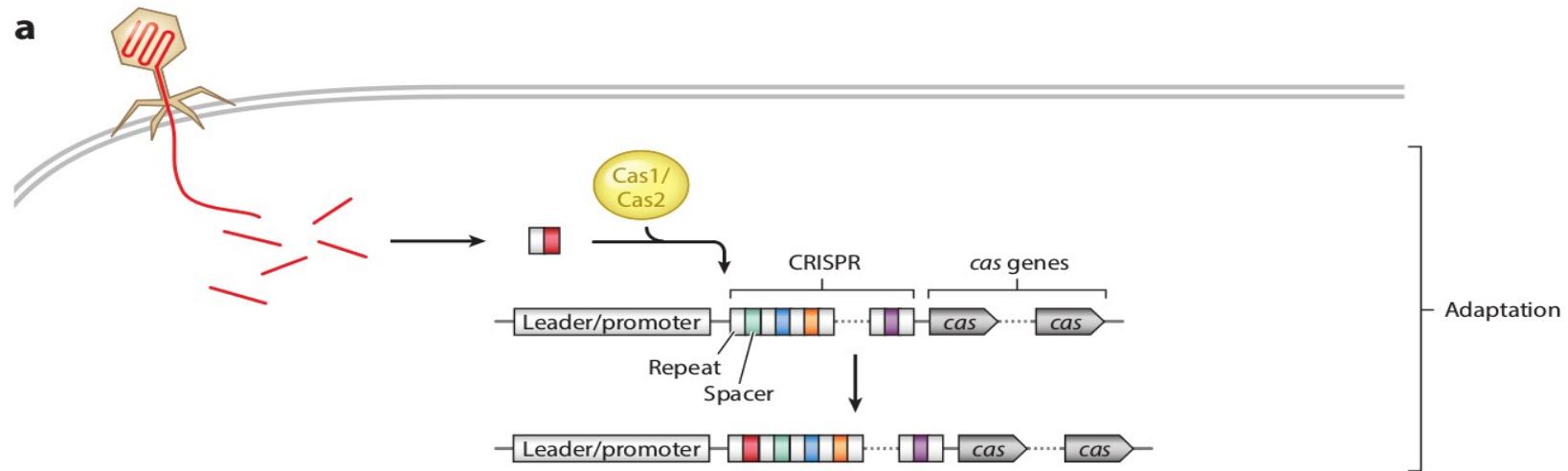


"The Red Queen has to run faster and faster in order to keep still where she is. That is exactly what you all are doing!"

# CRISPR-Cas System

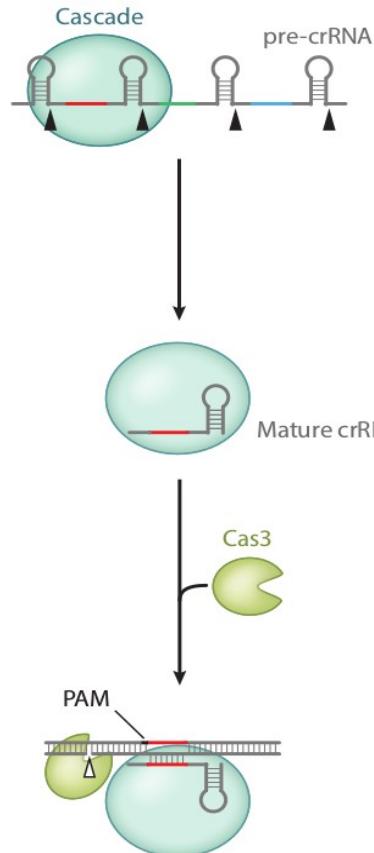
Clustered regularly interspaced short palindromic repeats (CRISPR) and their associated Cas proteins function as an adaptive, small-RNA-based immune system that protects prokaryotes from infectious viruses and plasmids.

CRISPR-Cas immunity develops in three phases:

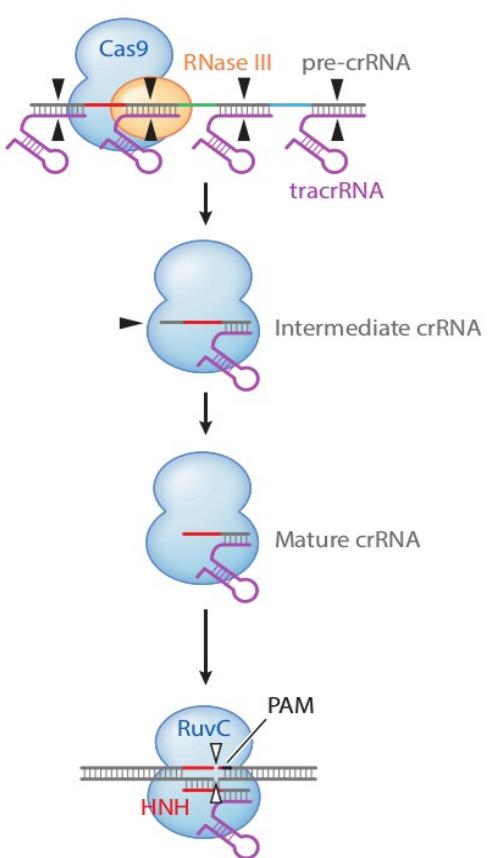


# CRISPR-Cas System

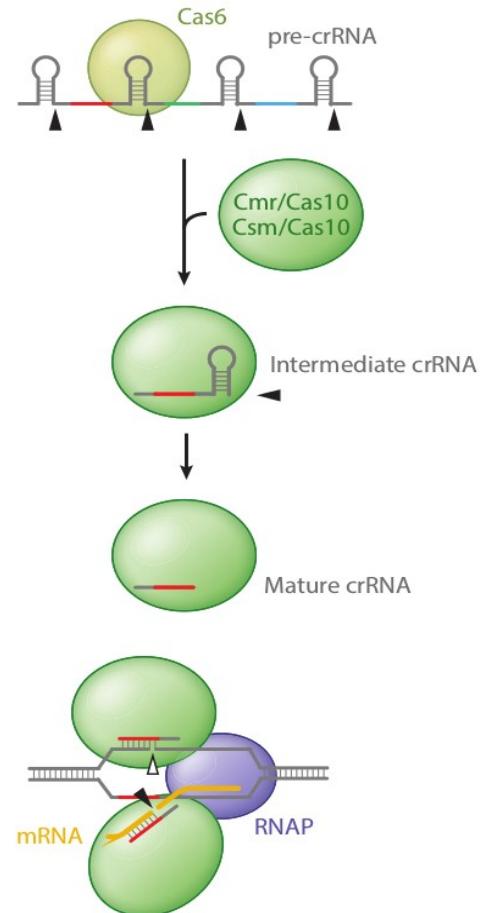
**b** Type I



**c** Type II



**d** Type III



crRNA biogenesis      Targeting

# *Virus role in controlling metabolism*

*Infection of microbes can alter host metabolism. Virus-induced changes in host metabolism make it biochemically and metabolically a very different cell.*

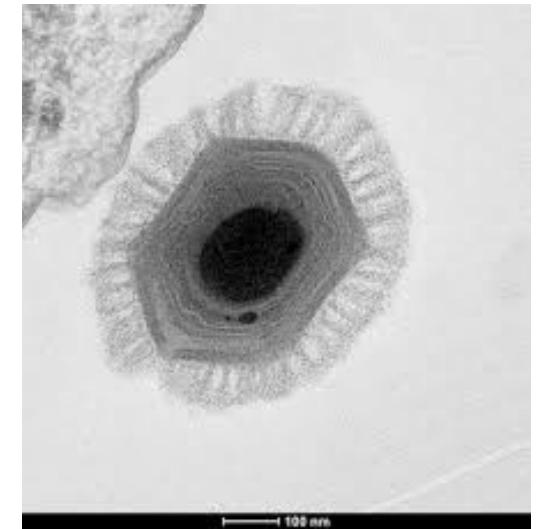
## ***Examples:***

*Phage-infected cyanobacteria exhibit a higher rate of photosynthesis than their noninfected counterparts.*

*Bacterial cells undergoing active phage infections can also have altered distributions of other major elements, such as nitrogen and phosphorus, making them biochemically unique.*

# Megavirus, and emerging group

- Capsid cross-sections that can exceed 500 nm, an order of magnitude larger than prototypical viruses
- Giant viruses infect eukaryotic hosts, including the protists and unicellular green algae
- Carry genomes larger than nearly all previously identified viral types, in some cases upwards of 1 million base pairs
- In both marine and non-marine contexts, researchers have even identified viruses that can infect giant viruses, the so-called virophages



## Two “specials”: Viroids and Prions

**Viroids** are particle exclusively constituted by RNA (240-400 bp). Those are copied by the host RNA polymerase and proliferate inside the nucleus where they interfere with gene regulations

**Prions:** Infective particles made exclusively by a single protein (208 aa). They accumulate inside cells preventing correct folding of host protein and accumulate cell damage.

# This Week Reads

Woese, C. R., and Fox, G. E. (1977). Phylogenetic structure of the prokaryotic domain: The primary kingdoms. PNAS 74, 5088–5090. doi:10.1073/pnas.74.11.5088.

Pace, N. R., Sapp, J., and Goldenfeld, N. (2012). Phylogeny and beyond: Scientific, historical, and conceptual significance of the first tree of life. PNAS 109, 1011–1018. doi:10.1073/pnas.1109716109.