

ENVIRONMENTAL METAGENOMICS

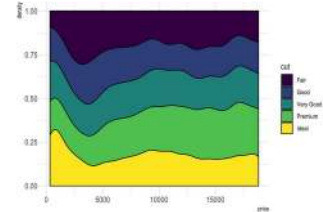
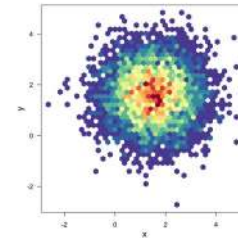
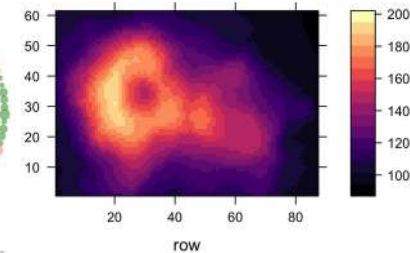
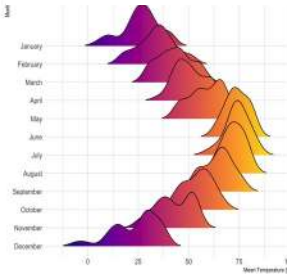
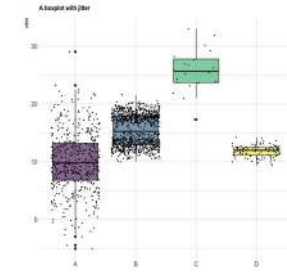
BACTERIA AND ARCHAEA TAXONOMIC DIVERSITY

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Microbial species concept. The species concept is complex when applied to microbiology. In biology species are defined primarily based on their sexual segregation, either by genetic, behavioral or geographical barrier (and even this can be sometimes challenging, as all human-imposed categories).

For microbes the **absence of sexual reproduction, horizontal gene transfer** and a **high genome plasticity** make the classic species concept difficult to apply.

The current golden standard for defining a species is called a **polyphasic approach**, combining **phylogenetics, physiology and chemotaxonomy**.

In more simple terms, microbial species are defined based on their genetic properties, specifically the similarity of the **16S rRNA gene** (since it is a conserved universal marker not subject to HGT) or the **whole genome similarity** (also called ANI, Average Nucleotide Identity).

Current standard are **16S rRNA similarity >97%** for the same species and an **whole genome ANI >70%**.

Proc Natl Acad Sci U S A. 2002 Dec 24;99(26):17020-4. Epub 2002 Dec 5.

Extensive mosaic structure revealed by the complete genome sequence of uropathogenic *Escherichia coli*.

Welch RA¹, Burland V, Plunkett G 3rd, Redford P, Roesch P, Rasko D, Buckles EL, Liou SR, Boutin A, Hackett J, Stroud D, Mayhew GF, Rose DJ, Zhou S, Schwartz DC, Perna NT, Mobley HL, Donnenberg MS, Blattner FR.

⊕ Author information

Abstract

We present the complete genome sequence of uropathogenic *Escherichia coli*, strain CFT073. A three-way genome comparison of the CFT073, enterohemorrhagic *E. coli* EDL933, and laboratory strain MG1655 reveals that, amazingly, only 39.2% of their combined (nonredundant) set of proteins actually are common to all three strains. The pathogen genomes are as different from each other as each pathogen is from the benign strain. The difference in disease potential between O157:H7 and CFT073 is reflected in the absence of genes for type III secretion system or phage- and plasmid-encoded toxins found in some classes of diarrheagenic *E. coli*. The CFT073 genome is particularly rich in genes that encode potential fimbrial adhesins, autotransporters, iron-sequestration systems, and phase-switch recombinases. Striking differences exist between the large pathogenicity islands of CFT073 and two other well-studied uropathogenic *E. coli* strains, J96 and 536. Comparisons indicate that extraintestinal pathogenic *E. coli* arose independently from multiple clonal lineages. The different *E. coli* pathotypes have maintained a remarkable synteny of common, vertically evolved genes, whereas many islands interrupting this common backbone have been acquired by different horizontal transfer events in each strain.

The Tree Of Life: The Bacteria

- *Bacterial diversity is huge!* And there is much uncertainty in the classification and total number of phyla
- As of *January 2016*, there are *30 phyla* in the domain "Bacteria" accepted by LPSN
- The *ARB-Silva database* lists *67 phyla*, of which *37 are candidate phyla*
- The *Ribosomal Database Project 10*, lists *49 phyla*, including *20 candidate phyla*
- *NCBI* lists *120 phyla*, including *90 candidate phyla*
- Despite the unclear branching order for most bacterial phyla, several groups of phyla have clear clustering and are referred to as superphyla: *The FCB Group*, *The PVC Group*, *the Patescibacteria*, *Terrabacteria* and *the Proteobacteria* as superphylum
- *Photosynthesis* only occurs within the Bacteria

International Committee on Systematics of Prokaryotes



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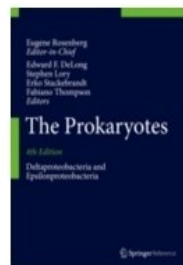
International Journal of Systematic and Evolutionary Microbiology (previously *International Journal of Systematic Bacteriology*) is the journal of record for publication of novel microbial taxa and the official publication of the International Committee on Systematics of Prokaryotes and the Bacteriology and Applied Microbiology Division of the International Union of Microbiological Societies. [More](#)

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Editor-in-Chief: Professor Martha E Trujillo, University of Salamanca, Spain

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IMPORTANT: The ICSP and the Microbiology Society are pleased to announce that our appeal against Clarivate's decision to suppress the journal from the 2019 Journal Citation Reports has been successful. *International Journal of Systematic and Evolutionary Microbiology* will be reinstated in the 2019 Journal Citation Reports (JCR) – the journal's metrics can be found on our Article and journal metrics page. [Read more about our appeal.](#)

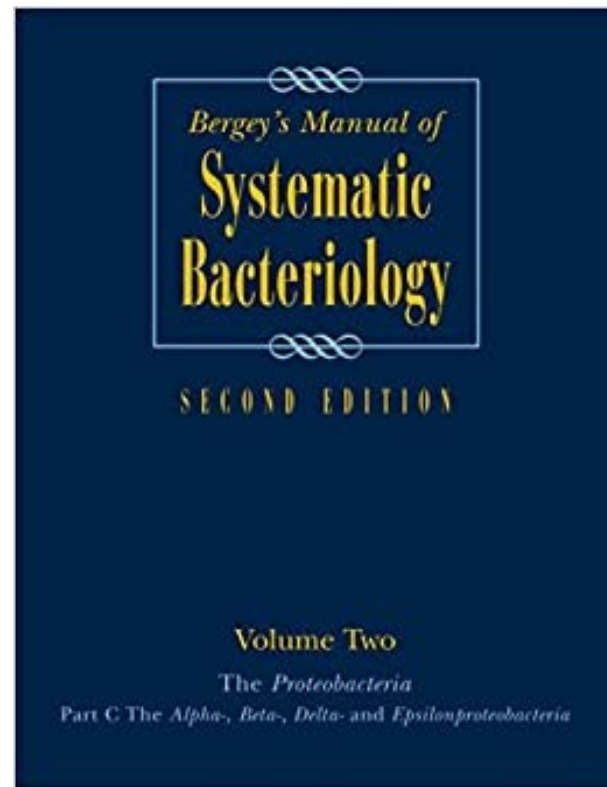


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The Prokaryotes

Deltaproteobacteria and Epsilonproteobacteria

Editors: Editor-in-chief: **Rosenberg, Eugene**
DeLong, E.F., Lory, S., Stackebrandt, E., Thompson, F. (Eds.)



International Committee on Systematics of Prokaryotes

Validly published A name of a prokaryotic species that has appeared on IJSEM validation lists

The new strain need to be **available in a pure culture**

The culture needs to be available in at least **two (2) public culture collections**

The **physiology** and **chemotaxonomy** needs to be known

New species are defined as **Genus species sp. nov.** on their first appearance

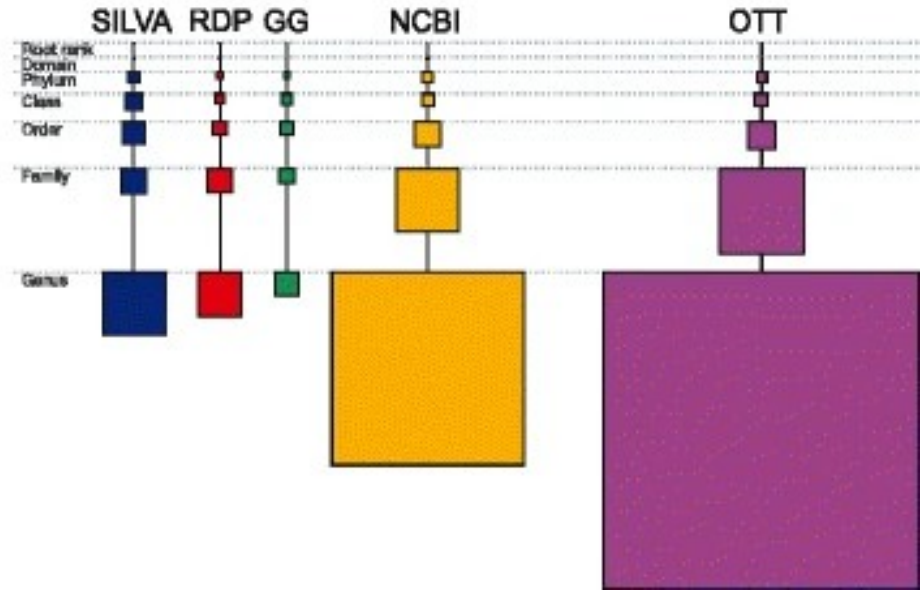
Non validly published prokaryotic species needs to be preceded by the “**Candidatus** Genus species” or “Ca. Genus species”

The **phylum rank is not a validly published** taxonomic rank under ICSP code

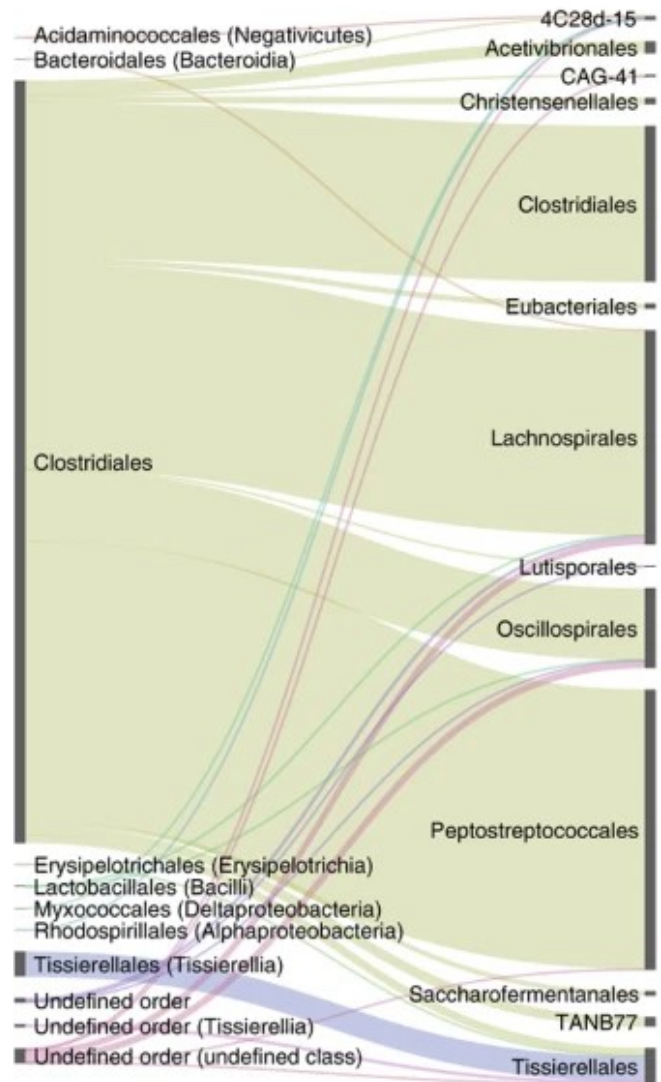
As a reminder, valid prokaryotic taxa needs to be in *Italics* (e.g. *Rhodobacterales*, *Escherichia coli*) while not validly published names cannot appear in italics (Ca. *Pelagibacter ubique*)

a

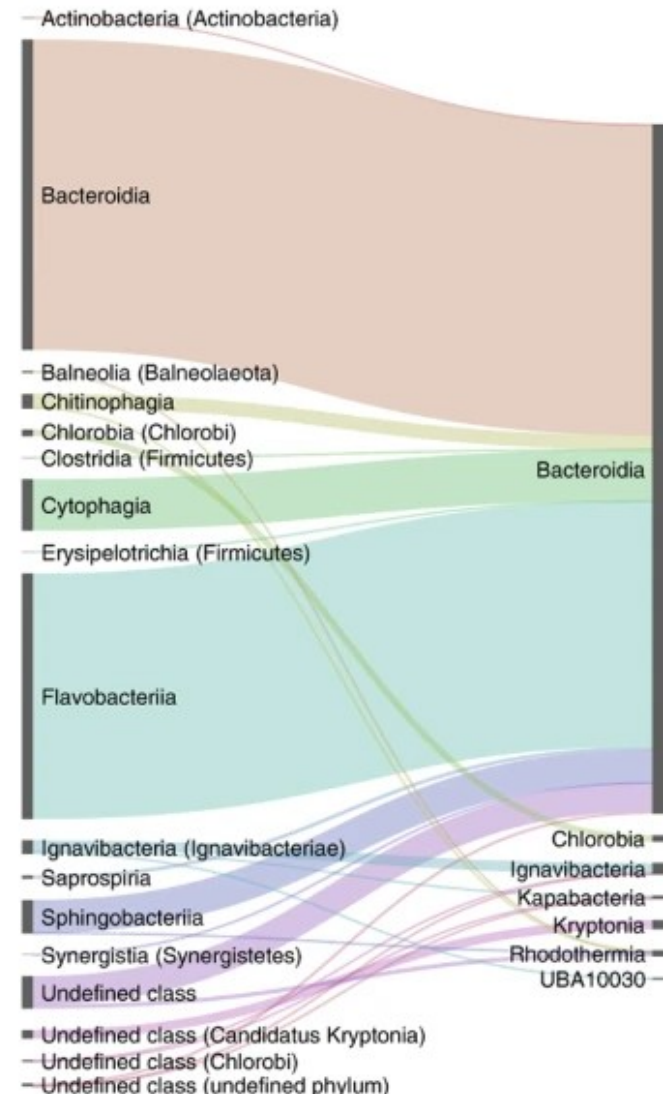
Node percentage

**b**

a NCBI order

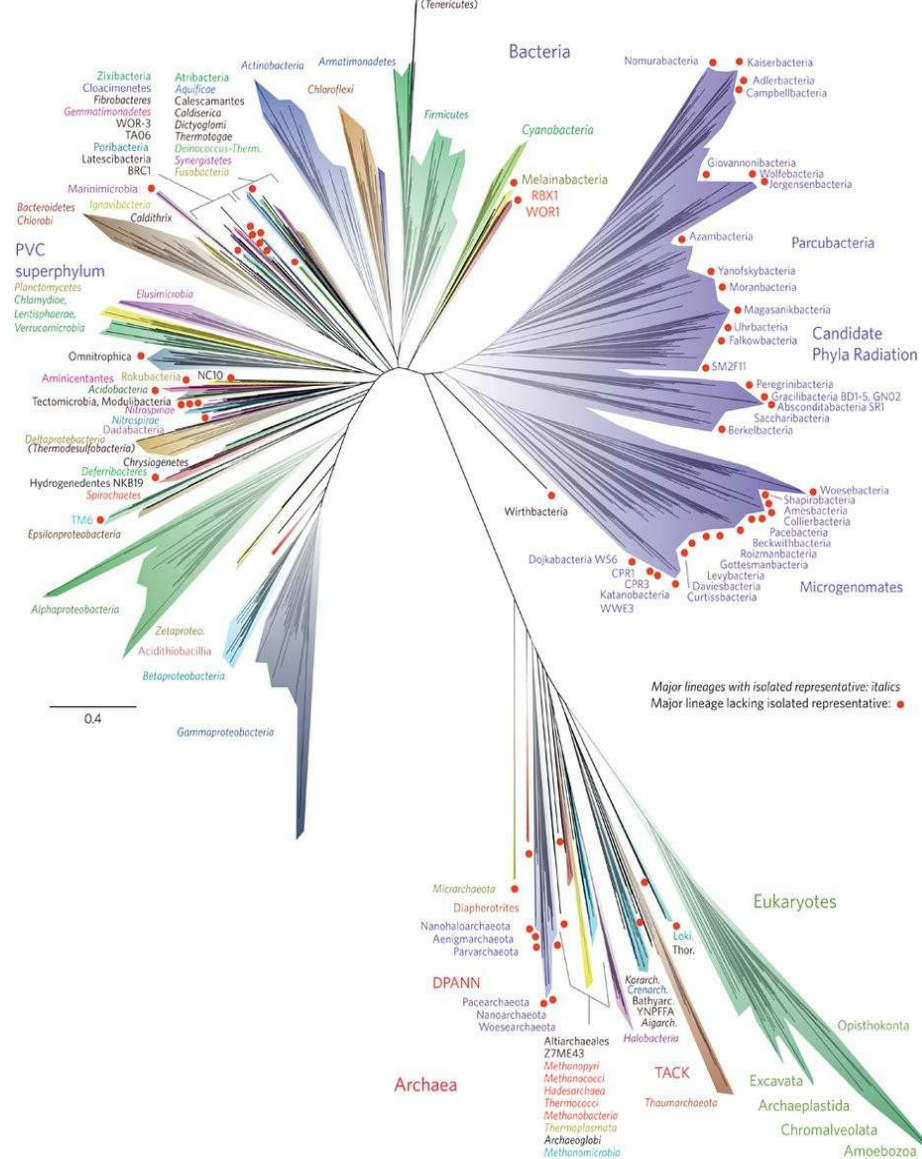


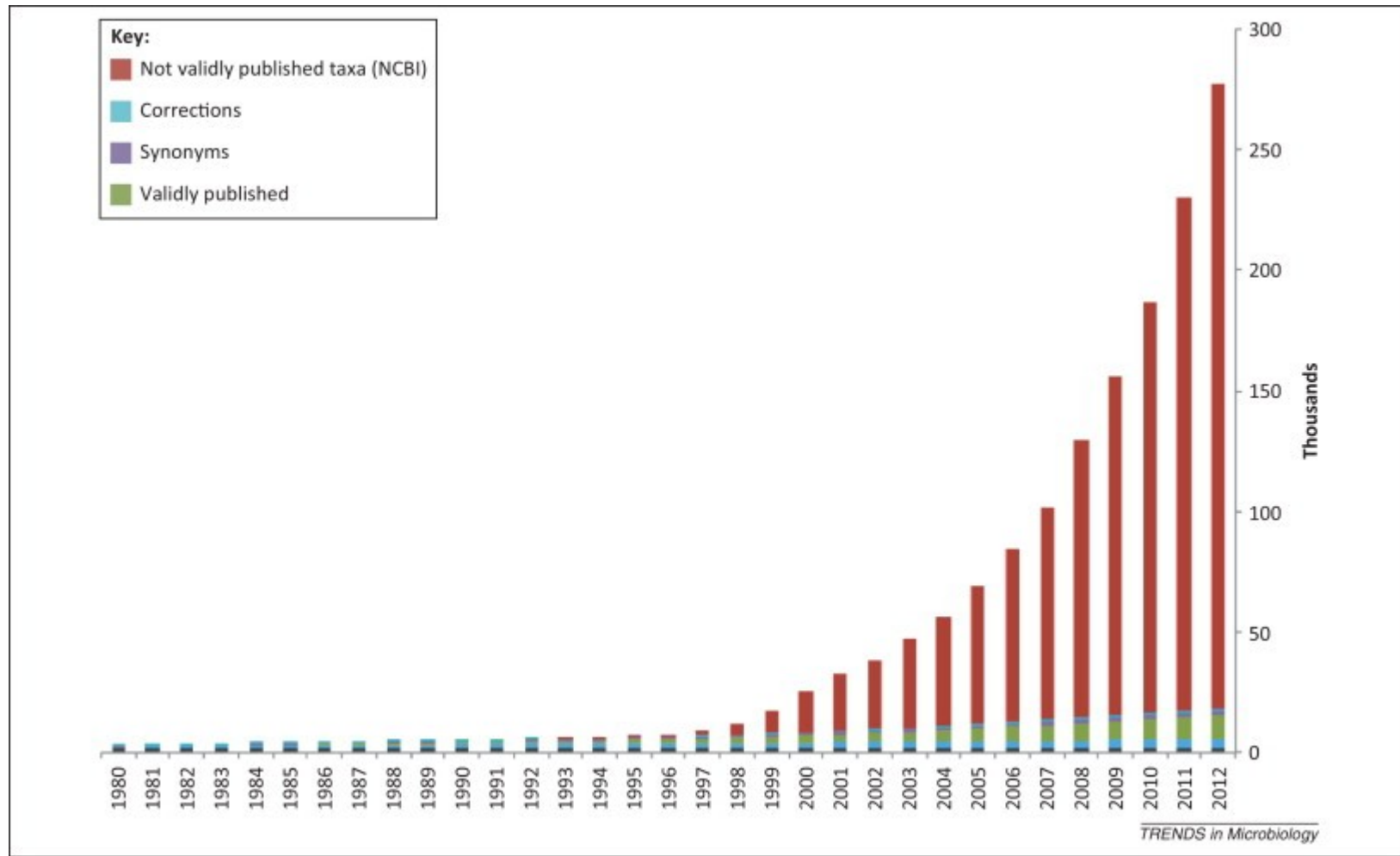
b NCBI class



A new view of the tree of life

Laura A. Hug, Brett J. Baker, Karthik Anantharaman, Christopher T. Brown, Alexander J. Probst, Cindy J. Castelle, Cristina N. Butterfield, Alex W. Hernsdorf, Yuki Amano, Kotaro Ise, Yohey Suzuki, Natasha Dudek, David A. Relman, Kari M. Finstad, Ronald Amundson, Brian C. Thomas & Jillian F. Banfield





Diverse uncultivated ultra-small bacterial cells in groundwater

Birgit Luef, Kyle R. Frischkorn, Kelly C. Wrighton, Hoi-Ying N. Holman, Giovanni Birarda, Brian C. Thomas, Andrea Singh, Kenneth H. Williams, Cristina E. Siegerist, Susannah G. Tringe, Kenneth H. Downing, Luis R. Comolli ✉ & Jillian F. Banfield ✉

Nature Communications **6**, Article number: 6372 (2015) | [Cite this article](#)

2499 Accesses | **127** Citations | **520** Altmetric | [Metrics](#)

REVIEW ARTICLE

Front. Microbiol., 21 August 2018 | <https://doi.org/10.3389/fmicb.2018.01971>

Nano-Sized and Filterable Bacteria and Archaea: Biodiversity and Function

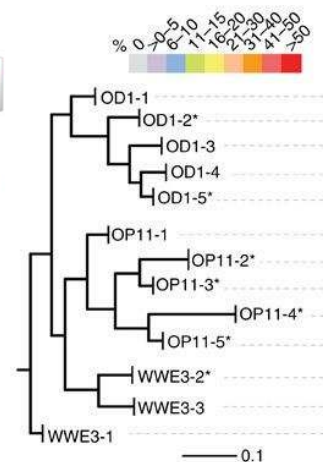
Lydia-Ann J. Ghuneim^{1*}, David L. Jones¹, Peter N. Golyshin² and Olga V. Golyshina²

¹School of Environment, Natural Resources and Geography, Bangor University, Bangor, United Kingdom

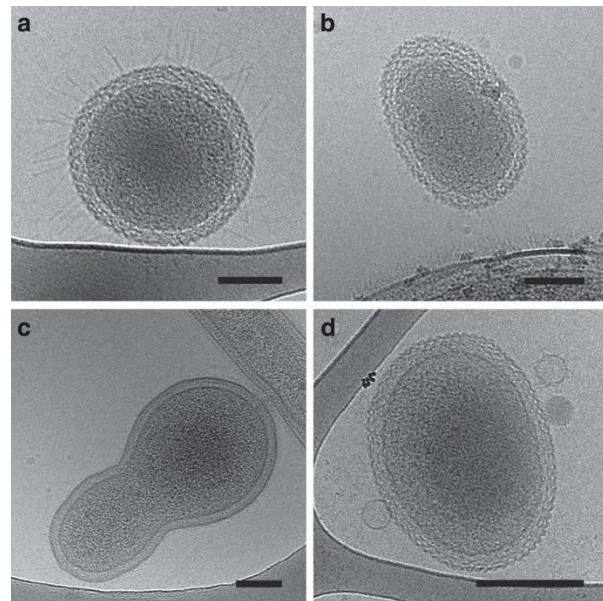
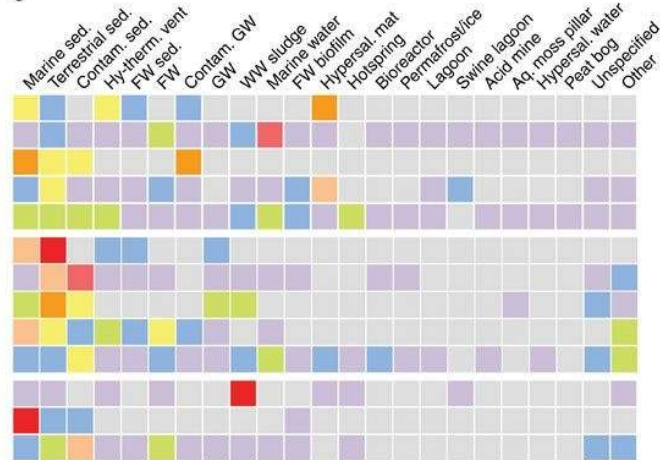
²School of Biological Sciences, Bangor University, Bangor, United Kingdom

CP WWE3
CP CP11
CP OD1
Spirochaetes
Nitrospirae
CP TM7
Proteobacteria
Tenericutes
Euryarchaeota

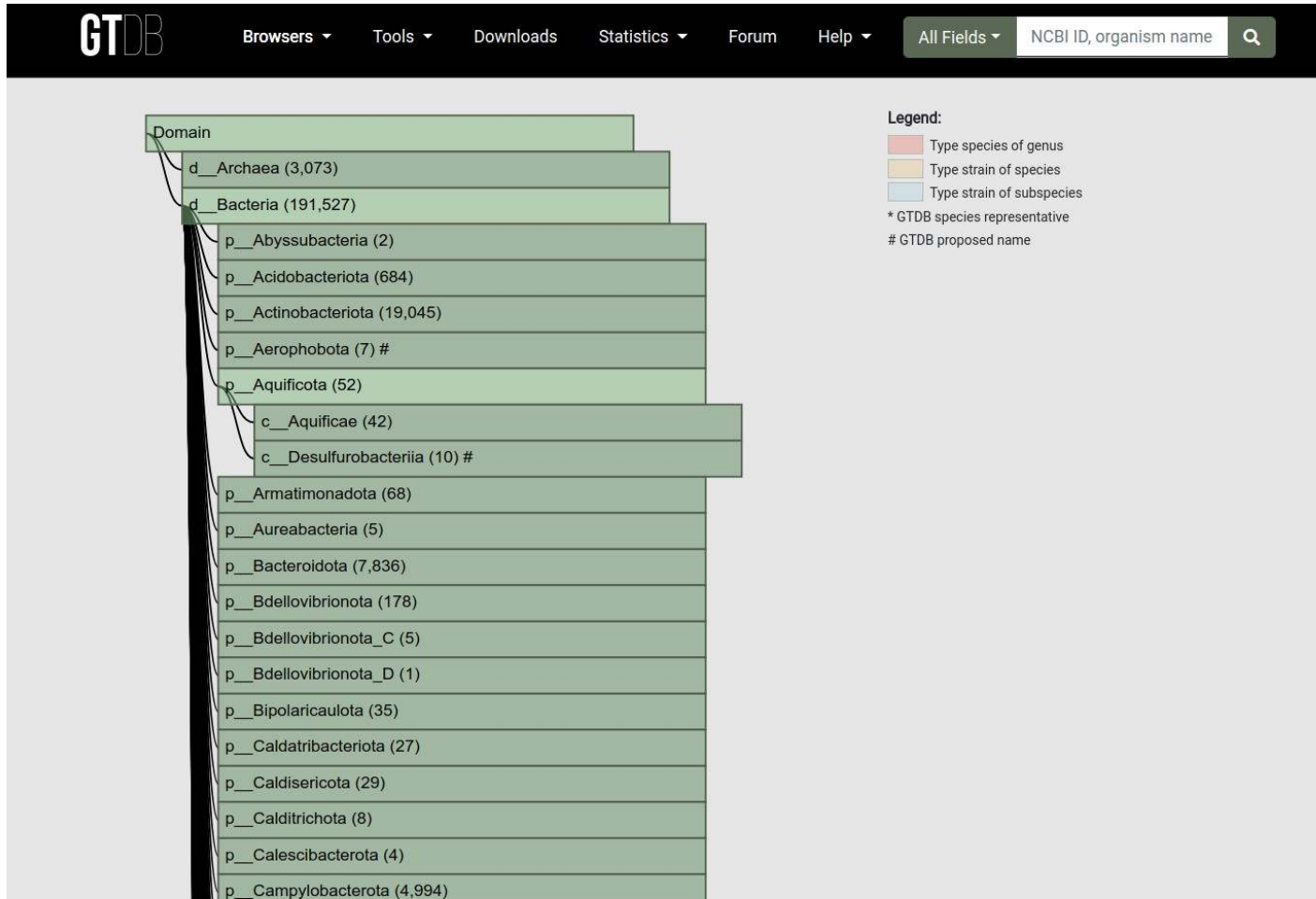
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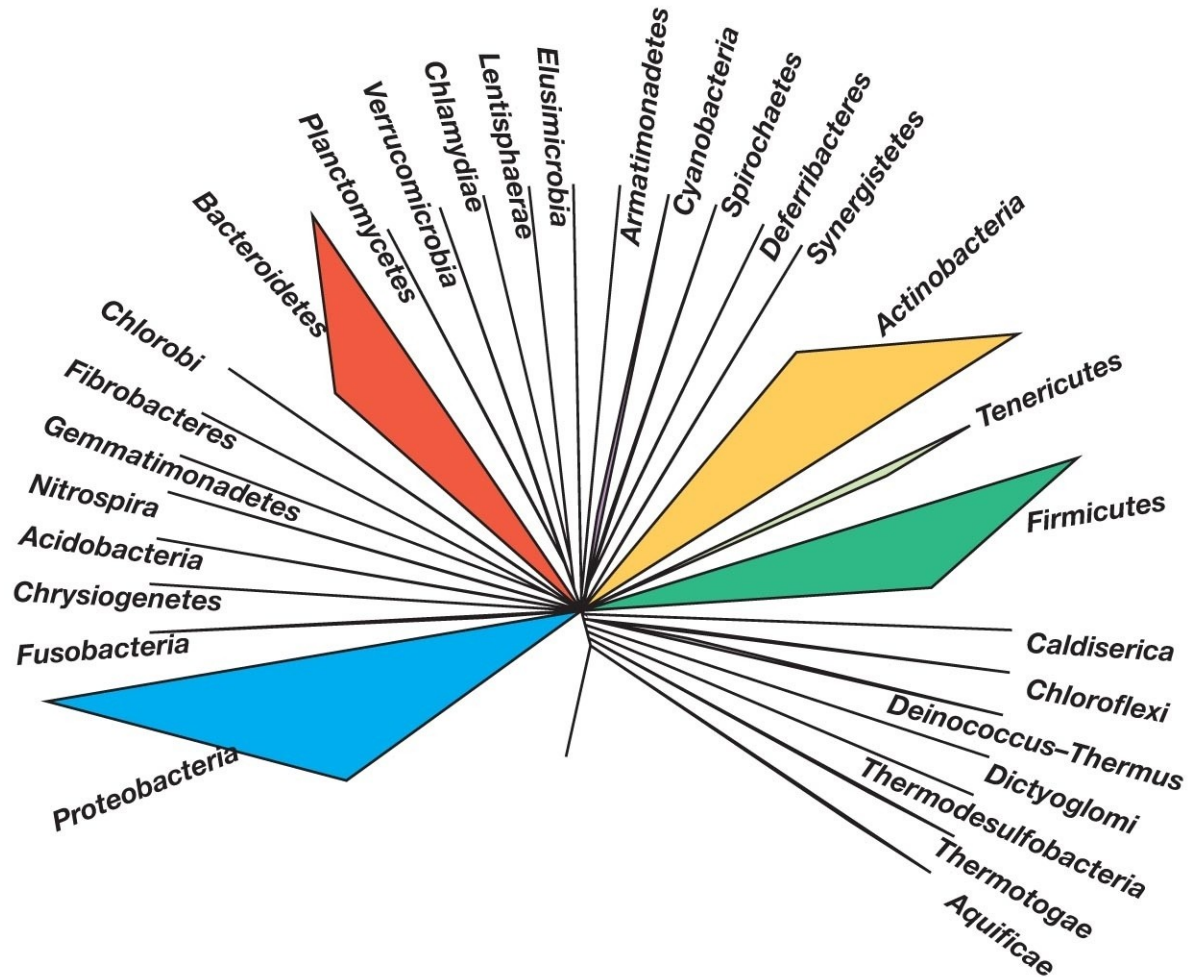
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Gene Taxonomy Database - gtdb.ecogenomic.org

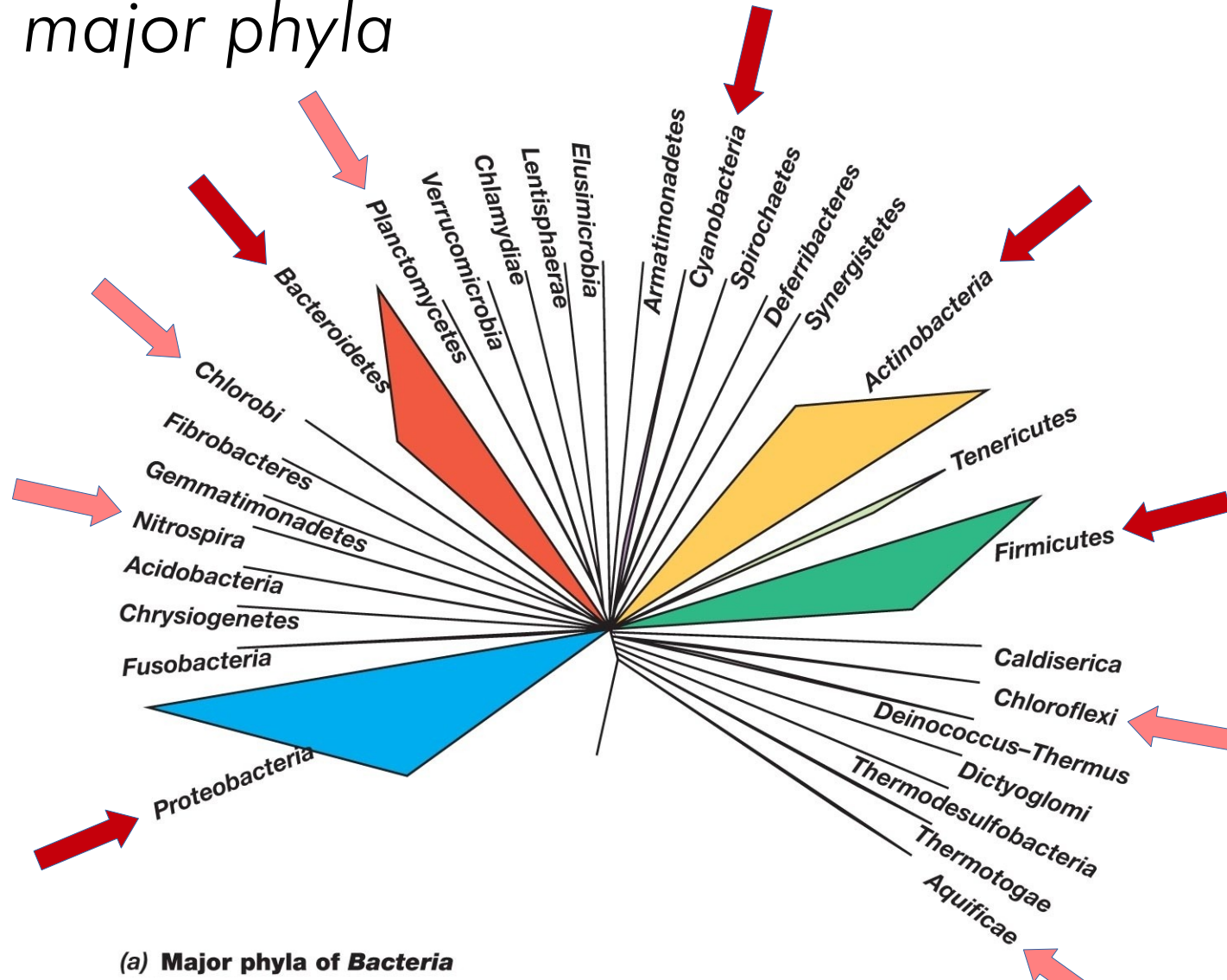


Bacteria: major phyla



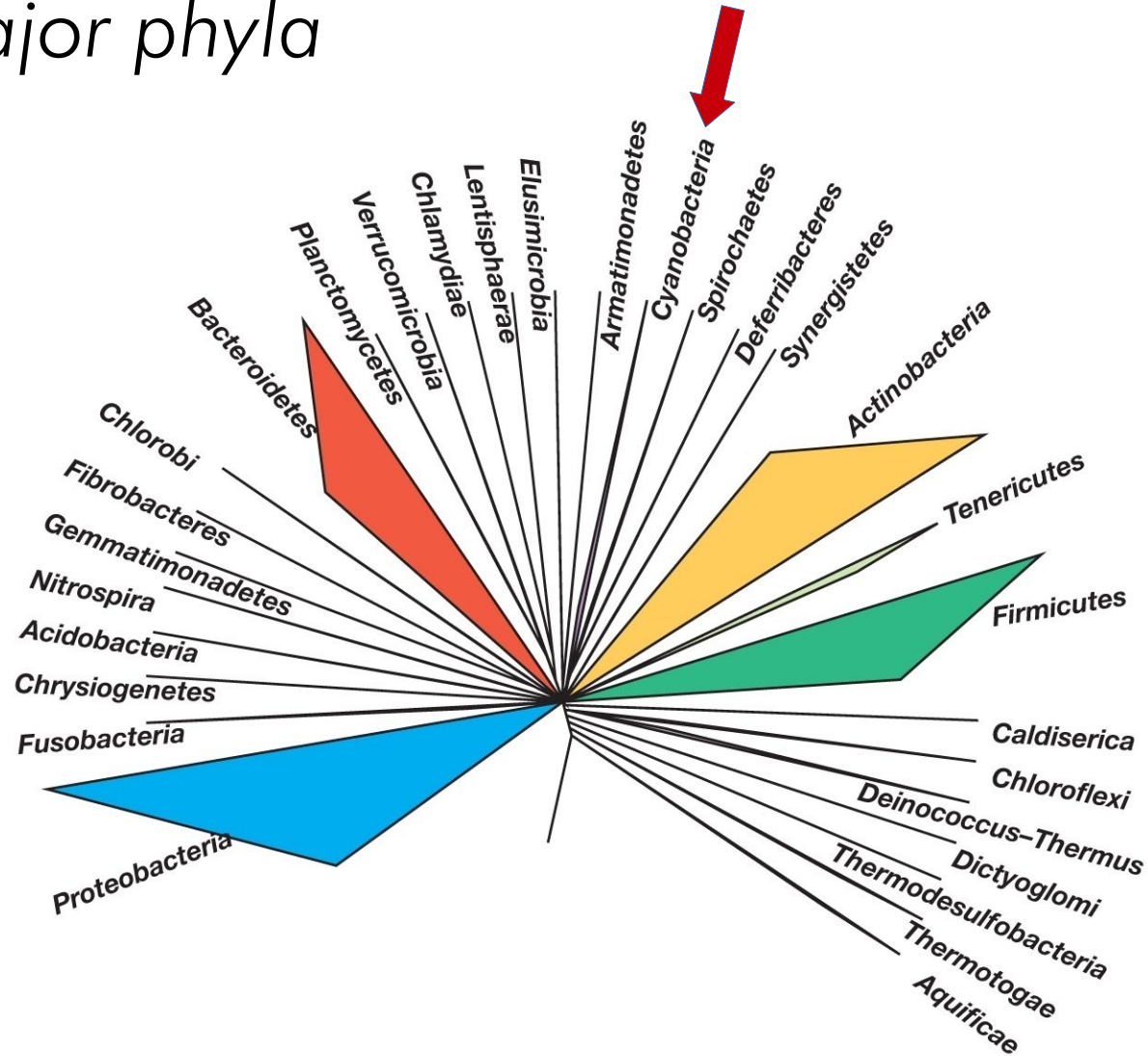
(a) Major phyla of *Bacteria*

Bacteria: major phyla



(a) Major phyla of *Bacteria*

Bacteria: major phyla



(a) Major phyla of *Bacteria*

Cyanobacteria

- Cyanobacteria (once known as Cyanophyta), are a phylum of *photosynthetic, nitrogen fixing* bacteria
- Cyanobacteria can be found in almost *every terrestrial and aquatic habitat*—oceans, fresh water, damp soil, temporarily moistened rocks in deserts, bare rock and soil, and even Antarctic rocks. They can occur as *planktonic cells* or form *phototrophic biofilms*. They are found in almost every *endolithic ecosystem* and can form *symbiosis*.
- The morphological diversity of the Cyanobacteria is huge. Cyanobacterial cells range in size from 0.5 μm in diameter to cells as large as 100 μm in diameter. They range from *unicellular to filamentous* and include colonial species, forming filaments, sheets, or even hollow balls. In filamentous species cells can differentiate into several different cell types: *vegetative cells, akinetes and heterocysts*
- Photosynthesis is performed in distinctive folds in the outer membrane of the cell. *Chloroplasts found in eukaryotes*, have their ancestry in Cyanobacteria, via a process called endosymbiosis.

Cyanobacteria

- Cyanobacteria are **oxygenic phototrophs**, having both type I and type II photosystems. All species fix CO₂ by the **Calvin cycle**, and many can fix N₂. Some Cyanobacteria can assimilate simple organic compounds if light is present (**photoheterotrophy**). A few cyanobacteria, mainly filamentous species, can also grow in the dark on glucose or sucrose, using the sugar as both carbon and energy source. When sulfide concentrations are high, some cyanobacteria are able to **switch from oxygenic photosynthesis to anoxygenic photosynthesis** using hydrogen sulfide rather than water as electron donor
- Cyanobacteria are thought to have been the main contributor to the **Great Oxygenation Event**, ca. 2.5 Ga
- Cyanobacteria are of central importance to the **productivity of the oceans**. Small unicellular cyanobacteria of the genera *Synechococcus* and *Prochlorococcus* are the most abundant phototrophs in the oceans. Together these organisms contribute ~80% of marine photosynthesis and ~35% of all photosynthetic activity on Earth

Bacteria: major phyla



(a) Major phyla of *Bacteria*

Firmicutes

- The Firmicutes are phylum of bacteria, most of which have **Gram-positive** cell wall structure. The Firmicutes, has been recently defined to contain related forms called the **low-G+C group**, while Actinobacteria now contains the high-G+C group
- They generally have round cells, called cocci (singular coccus), or rod-like forms (bacillus). They are found in **various environments**, and the group includes some **notable pathogens**. They play an important role in beer, wine, and food fermentations
- Many Firmicutes produce **endospores**, which are resistant to desiccation and can survive extreme conditions. They are **generally heterotrophs and/or fermenters**. Those in one family, the Heliobacteria, produce energy through photosynthesis
- The group is typically divided into the **Clostridia**, which are obligate anaerobes, the **Bacilli**, which are obligate or facultative aerobes
- The Clostridia are a **highly polyphyletic** class of Firmicutes, including Clostridium and other similar genera. They are **obligate anaerobes**.
- Bacillus species are almost **ubiquitous in nature**, e.g. in soil, but also occur in extreme environments such as high pH (*B. alcalophilus*), high temperature (*B. thermophilus*), or high salt (*B. halodurans*)

Actinobacteria

- Actinobacteria is a phylum of **gram-positive** bacteria. They are found in both terrestrial and aquatic environments.
- They have been **extensively studied in soils**, where they behave much like fungi, helping to **decompose the organic matter** of dead organisms so that the molecules can be taken up anew by plants. In this role the colonies often grow extensive mycelia, and the name of an important order of the phylum, Actinomycetales, reflects that they were long believed to be fungi
- Currently understood primarily as soil bacteria, their role in the **aquatic environment is not yet clear**
- They are of **great economic importance** to humans because agriculture and forests depend on their contributions to soil systems. Streptomyces, one of the largest bacterial genera, and other Actinobacteria are source of **many antibiotics**

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Microbial dormancy in the marine subsurface: Global endospore abundance and response to burial

Lars Wörmer^{1,*}, Tatsuhiko Hoshino², Marshall W. Bowles³, Bernhard Viehweger¹, Rishi R. Adhikari¹, Nan Xiao², Go-ichiro Ur...

+ See all authors and affiliations

Science Advances 20 Feb 2019;
Vol. 5, no. 2, eaav1024
DOI: 10.1126/sciadv.aav1024

Article Figures & Data Info & Metrics eLetters PDF

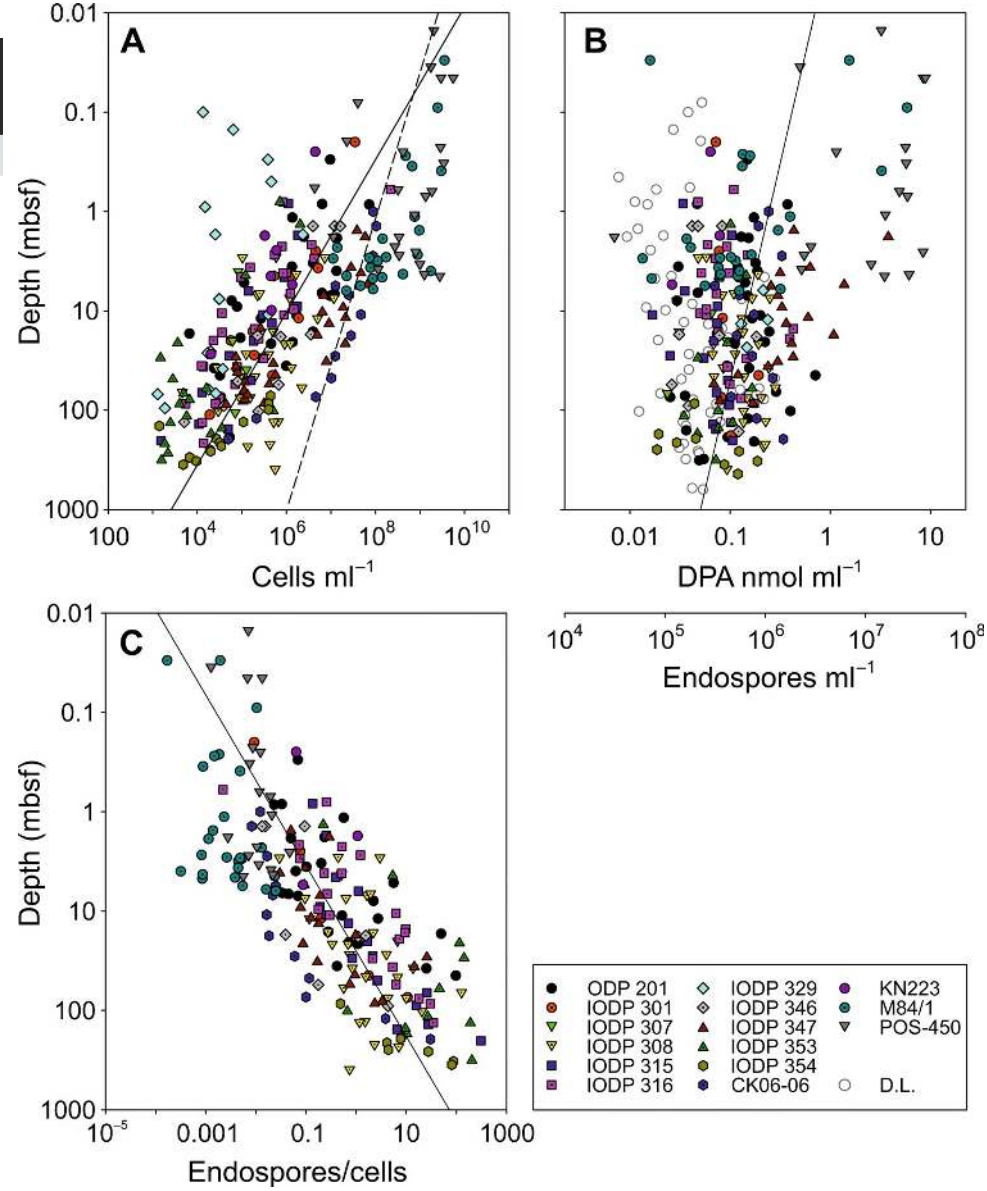
HYPOTHESIS AND THEORY ARTICLE

Front. Microbiol., 13 January 2012 | <https://doi.org/10.3389/fmicb.2011.00284>

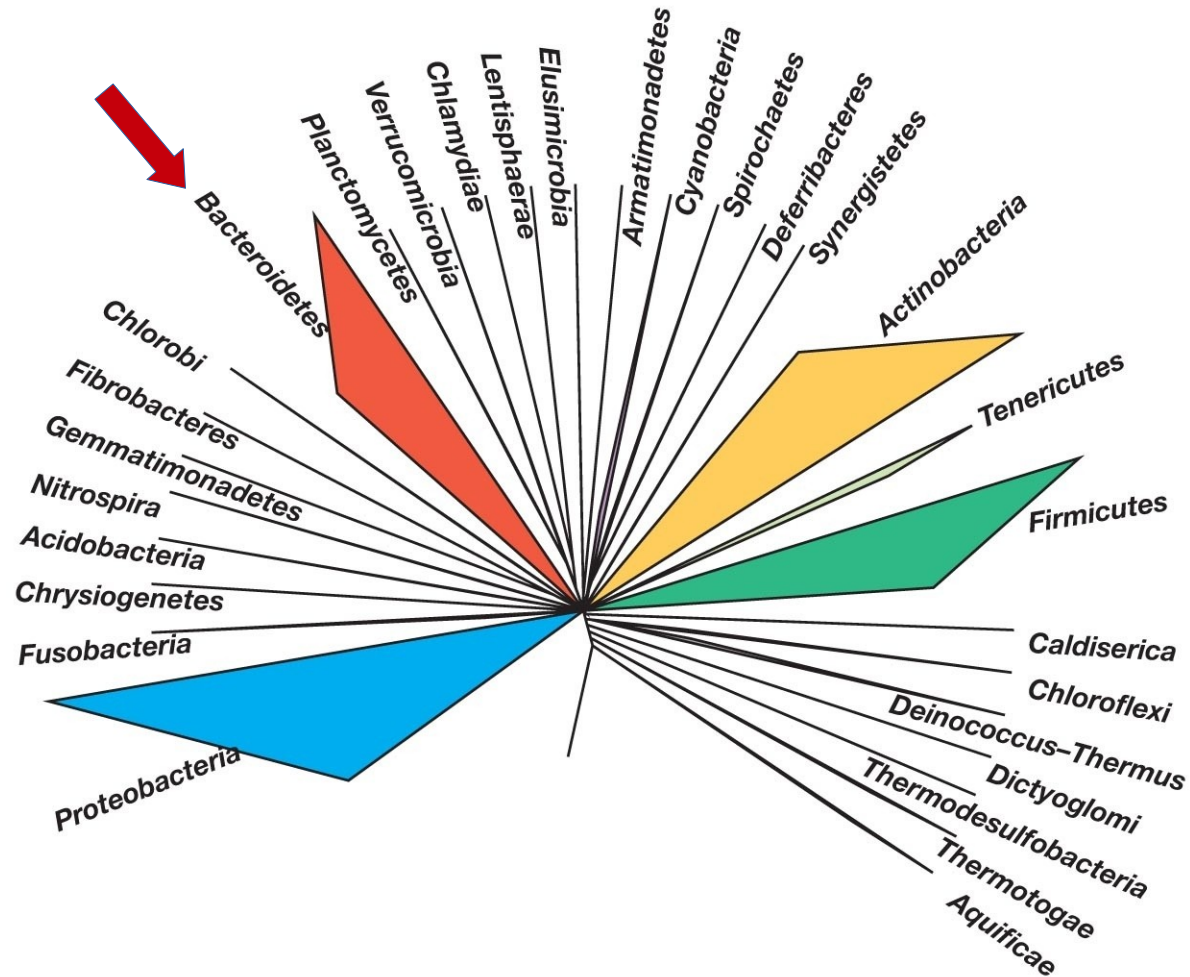
Acetogenesis in the energy-starved deep biosphere – a paradox?

Mark Alexander Lever*

Department of Bioscience, Center for Geomicrobiology, Aarhus University, Aarhus, Denmark



Bacteria: major phyla

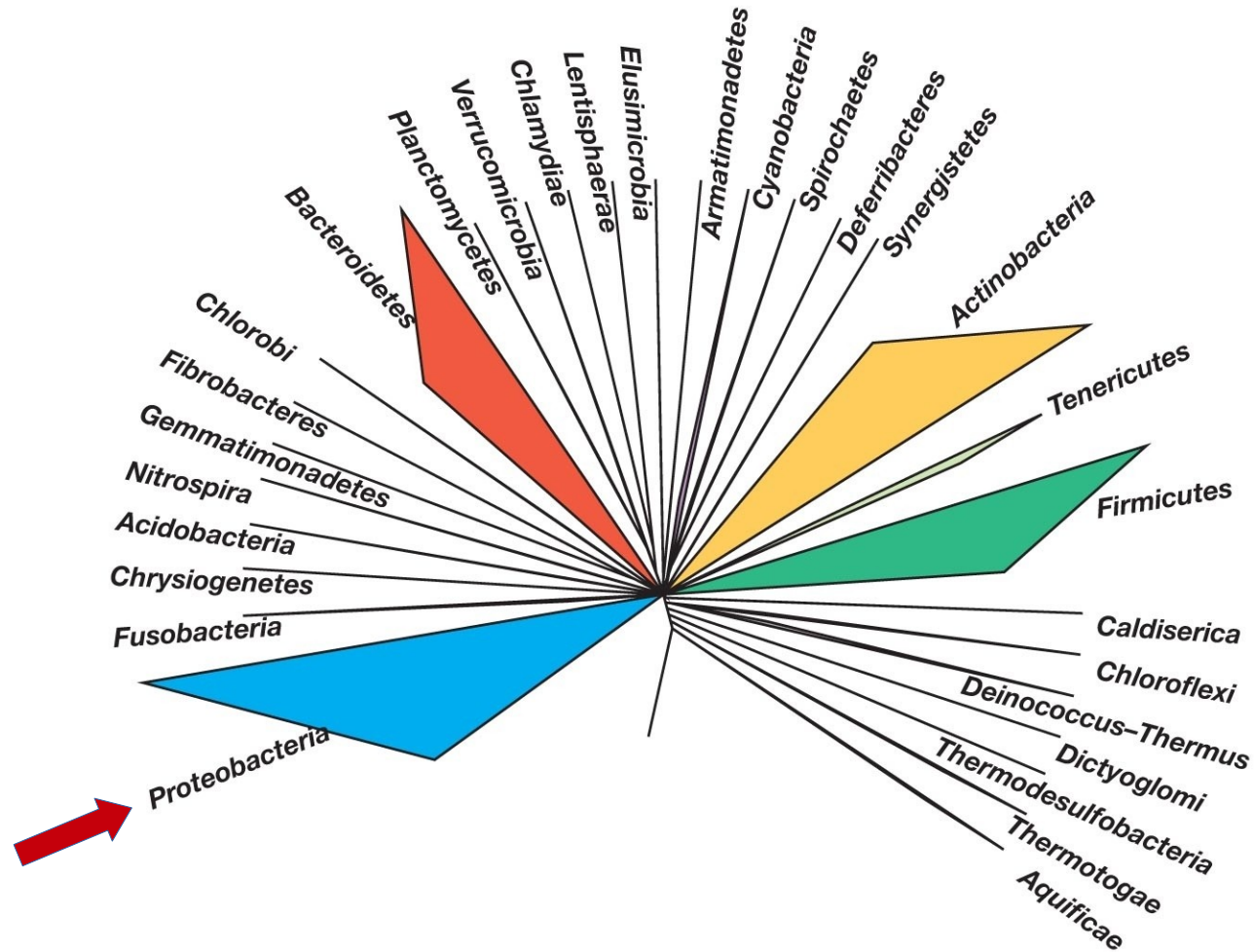


(a) Major phyla of *Bacteria*

Bacteroidetes

- The phylum Bacteroidetes (known as the CFB group) is composed of three large classes of *nonsporeforming, anaerobic or aerobic*, and rod-shaped bacteria that are *widely distributed in the environment*, including in soil, sediments, and sea water, as well as in the guts and on the skin of animals comprising 7,000 different species
- In the marine environment they are ubiquitous, and believed to play a major role in *degrading organic matter*, and decomposing complex recalcitrant compounds in the form of polysaccharides and proteins
- By far, the ones in the Bacteroidia class are the most well-studied, including the genus Bacteroides (an abundant organism in the feces of warm-blooded animals including humans), and Porphyromonas, a group of organisms inhabiting the human oral cavity. Yet, the *marine diversity has been poorly investigated*
- Bacteroidetes can represent the dominant phylum in *marine snow aggregates*

Bacteria: major phyla



(a) Major phyla of *Bacteria*

Proteobacteria

- The Proteobacteria are a major phylum of Gram-negative bacteria. Carl Woese established this grouping in 1987, calling it informally the “purple bacteria and their relatives”. Because of the great diversity of forms found in this group, the Proteobacteria are named after Proteus, a Greek god of the sea capable of assuming many different shapes
- They are **ubiquitous in the environments** and possess a **huge metabolic diversity**, encompassing facultatively or obligately anaerobes, chemolithoautotrophy, heterotrophy and anoxygenic phototrophy. They include free living, commensal, symbiotic and pathogenic species
- They are currently divided into six classes: **Alphaproteobacteria**, **Betaproteobacteria**, **Gammaproteobacteria**, **Deltaproteobacteria**, **Epsilonproteobacteria** and **Zetaproteobacteria**
- Given their diversity they have been proposed as **superphylum**, with the classes promoted to distinct phyla

Proteobacteria: Alphaproteobacteria

- With nearly one thousand described species, the Alphaproteobacteria are the second largest class of Proteobacteria
- The Alphaproteobacteria is a diverse taxon and comprises several phototrophic genera, several genera metabolising C1-compounds (e.g., Methylobacterium spp.), symbionts of plants (e.g., Rhizobium spp.), endosymbionts of arthropods (Wolbachia) and intracellular pathogens (e.g. Rickettsia). A total of 10 orders have been described within the Alphaproteobacteria
- Most species are obligate aerobes or facultative aerobes and many are oligotrophic, preferring to grow in environments that have low nutrient concentration. Several species play a key role in nitrogen fixation in various types of plants
- The class includes the protomitochondrion, the bacterium that was engulfed by the eukaryotic ancestor and gave rise to the mitochondria through endosymbiosis

Proteobacteria: *Betaproteobacteria*

- With nearly 500 described species, the Betaproteobacteria are the third largest class of Proteobacteria.
- The *Burkholderiales* contain species with a wide range of metabolic and ecological characteristics. Species include *strictly aerobic, facultatively aerobic, and obligately anaerobic chemoorganotrophs, anoxygenic phototrophs, obligate and facultative chemolithotroph*
- The Betaproteobacteria contain an immense amount of functional diversity, and consist of several groups of *aerobic or facultative anaerobic bacteria* that are often *highly versatile in their degradation capacities*, but also contain *chemolithotrophic* genera (e.g., the ammonia-oxidising genus *Nitrosomonas*) and some *phototrophs* (members of the genera *Rhodocyclus* and *Rubrivivax*). *Pathogenic* species within this class are the Neisseriaceae (gonorrhea and meningitis) and species of the genus *Burkholderia*
- The *Methylophilales* and *Nitrosomonadales* contain metabolically specialized organisms. *Methylophilus* species are *obligate and facultative methylotrophs* that grow on methanol and other C1 compounds, but not on CH₄. The order Nitrosomonadales contains obligately *chemolithotrophic ammonia-oxidizing bacteria*, the key genera being *Nitrosomonas* and *Nitrospira*

Proteobacteria: Gammaproteobacteria

- The Gammaproteobacteria comprise several medically, ecologically and scientifically important groups of bacteria
- Gammaproteobacteria are major players in diverse marine ecosystems, including extreme environments
- The class contains a huge variety of taxonomic and metabolic diversity, including aerobic and anaerobic species, chemolithoautotrophic, chemoorganotrophic and phototrophic species and include free living, biofilms formers, commensal and symbionts
- Chemolithoautotrophic species use the Calvin cycle to fix CO₂, with the exception of the symbionts of the vent tubeworm *Riftia* which possess also the rTCA cycle
- Families of interest include the Thiotrichales and Chromatiales, Pseudomonadales, Vibrionales, Methylococcales and Enterobacterales

Proteobacteria: *Deltaproteobacteria*

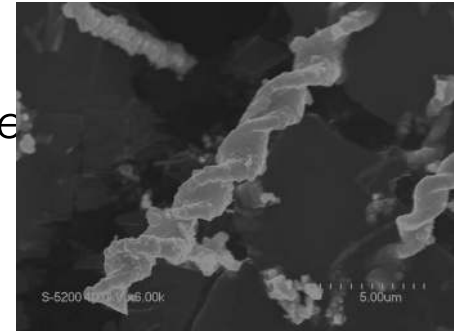
- The Deltaproteobacteria are *ubiquitous in marine sediments*, and contains *most of the known sulfate-* (Desulfovibrio, Desulfobacter, Desulfococcus, Desulfonema, etc.) and *sulfur-reducing bacteria* (e.g. Desulfuromonas spp.) alongside several other anaerobic bacteria with different physiology (e.g. ferric iron-reducing Geobacter spp. and syntrophic Pelobacter and Syntrophus spp.)
- The largest and most common order containing sulfate reducers is the *Desulfovibrionales*, followed by the *Desulfobacterales* and *Desulfarcuiales*. These organisms are readily cultivated from marine sediments and nutrient-rich anoxic environments that contain sulfate
- Some but not all *Syntrophobacterales* are able to reduce sulfate. In nature, however, species of Syntrophobacterales primarily interact with *H₂-consuming bacteria* in a metabolic partnership called *syntrophy*

Proteobacteria: *Epsilonproteobacteria*

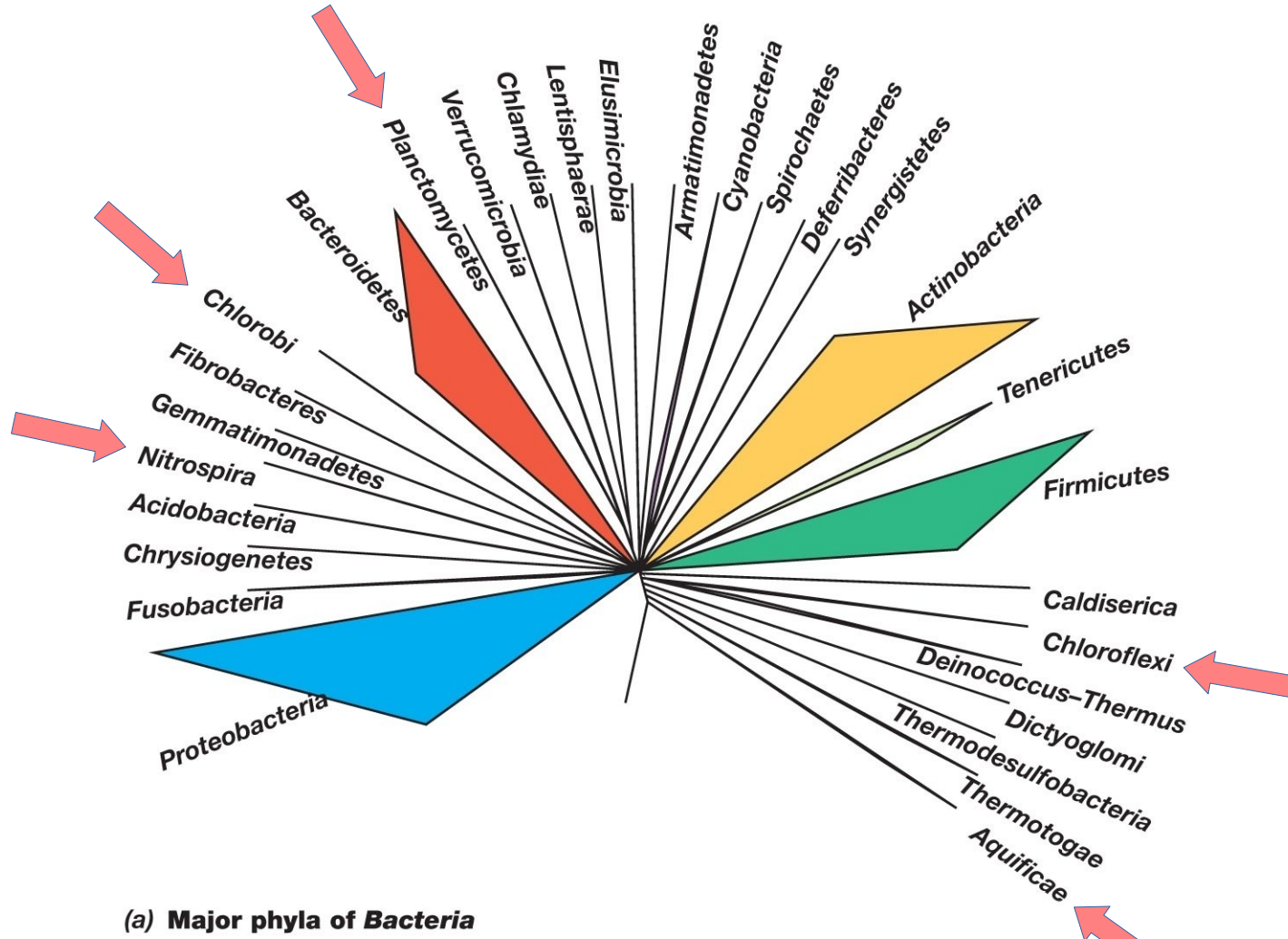
- The *Epsilonproteobacteria* consist of few known genera, encompassing either free-living and symbionts species found in *sulfidic environments*, or *mammalian commensal and pathogens*
- *Epsilonproteobacteria* are *major player in sulfidic marine environments*. Numerous environmental sequences and isolates of *Epsilonproteobacteria* have been recovered from *hydrothermal vents and cold seep habitats*. Examples of isolates include *Sulfurimonas autotrophica*, *Sulfurovum lithotrophicum* and *Caminibacter mediatlanticus*
- The *Epsilonproteobacteria* found at deep-sea hydrothermal vents are typically *anaerobic or microaerophilic chemolithotrophs*, and *oxidize reduced sulfur, formate, or hydrogen* coupled to the *reduction of nitrate or oxygen*. They use the *rTCA cycle to fix carbon dioxide* into biomass, a pathway originally thought to be of little environmental significance

Proteobacteria: *Zetaproteobacteria*

- Zetaproteobacteria are a *new class* within the Proteobacteria consisting of a *single cultivated genus and species Mariprofundus hydrothermalis*
- Zetaproteobacteria are now believed to be *key player in the marine iron biogeochemical cycle*
- *M. ferrooxydans* was first isolated from Lō'ihī Seamount, a submarine volcano found near Hawaii
- *M. ferrooxydans* is a *neutrophilic aerobic iron-oxidizers*, forming a twisted stalklike structure containing $\text{Fe}(\text{OH})_3$ from the oxidation of ferrous iron. The iron-encrusted stalk contains an organic matrix on which $\text{Fe}(\text{OH})_3$ accumulates as it is excreted from the cell surface.
- *M. ferrooxydans* is a *autotrophic chemolithotrophs* fixing CO_2 using the *Calvin cycle*



Bacteria: major phyla



(a) Major phyla of *Bacteria*

Other bacterial groups

- Other bacterial phyla of interest in the marine environments are *Nitrospirae*, *Plancomycetes*, *Chlorobi*, *Chroloflexi* and *Aquificae*.
- Other groups are likely to play major roles in marine ecosystems, however our knowledge of their ecology and diversity is very limited. An example of the breadth of future discoveries is the recent description of the metabolic potential of ca. *Methyloirabilis oxyfera*, within the candidate division NC10
- Our current understanding of bacterial (and archaeal) diversity and ecosystem role is currently hampered by our ability to cultivate and constrain the metabolic diversity of the numerous candidate phyla found in the environment

Other bacterial groups

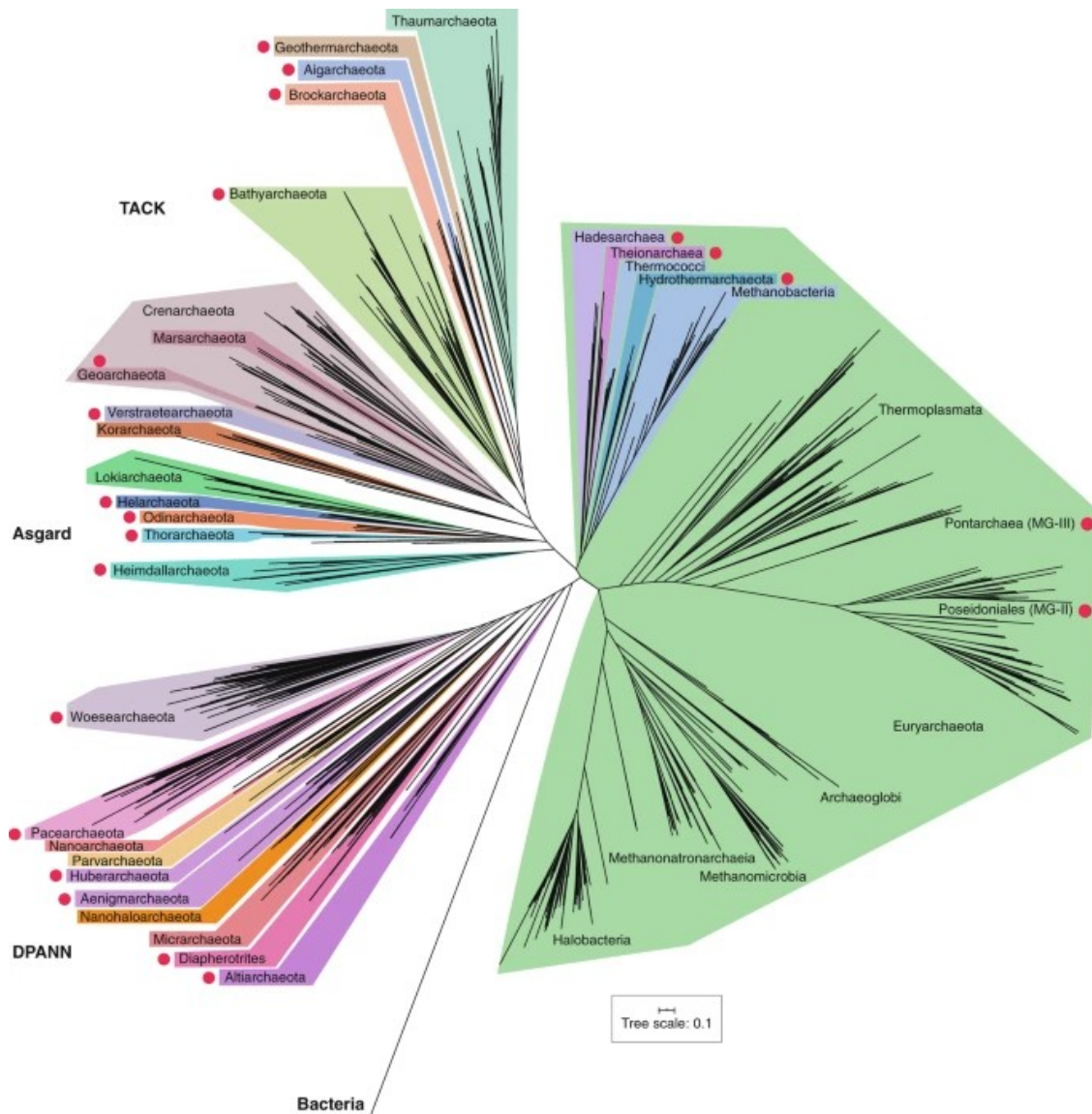
- **Nitrospirae** is a phylum of bacteria containing only one class, Nitrospira, which itself contains one order (Nitrospirales) and one family (Nitrospiraceae). They are **chemolithoautotrophs** using the **rTCA cycle** to fix CO₂ and **oxidizing nitrite to nitrate**. They likely represent major nitrifiers in marine ecosystems
- **Planctomycetes** are a phylum of **aquatic bacteria** and are found in brackish, marine and fresh water. They are likely to play a major role in **complex organic matter degradation** in sediments and include species known to carry out **ANAMMOX metabolism**, thus playing a major role in the global nitrogen cycle

Other bacterial groups

- **Chrolobi** include the *non-photosynthetic Ignavibacteriaceae* and the green sulfur bacteria (*Chlorobiales*), a family of *obligately anaerobic photoautotrophic* bacteria. Photosynthesis is achieved using a *Type I reaction centre* using bacteriochlorophyll (BChl) a and in chlorosomes which employ BChl c, d, or e. They use *sulfide ions, hydrogen or ferrous iron* as an electron donor. Elemental sulfur deposited outside the cell may be further oxidized
- **Chloroflexi** are a phylum of bacteria containing isolates with a diversity of phenotypes including members that are *aerobic thermophiles*, *anoxygenic phototrophs* (green non-sulfur bacteria), and *anaerobic halorespirers*, which uses halogenated organics (such as the toxic chlorinated ethenes and polychlorinated biphenyls) as energy sources. Member of this phylum are believed to be important player in the subsurface
- **Aquificae** are an *early branching* phylum of *thermophilic* and *hyperthermophilic* bacteria that live in extreme environmental settings. They have been found in both terrestrial and marine geothermal environments. They generally use *hydrogen* as electron donor, fix CO₂ using the *rTCA cycle* and may use either *nitrate, sulfur* or low partial pressure of *oxygen* as electron acceptor

The Tree Of Life: The Archaea

- The Archaea (archaea; singular archaeon) constitute a domain of single-celled microorganisms. The word archaea comes from Greek, meaning "ancient things", as the first representatives of the domain Archaea were methanogens, assumed to reflected a primitive metabolism. Archaea were *initially classified as bacteria*, receiving the name Archaeobacteria
- Archaeal cells have *unique properties* separating them from the other two domains of life, Bacteria and Eukaryota. The Archaea are further divided into multiple recognized phyla, however only few pbhyla have cultured representatives
- Archaea were initially viewed as *extremophiles* living in harsh environments, such as hot springs and salt lakes, but they have since been *found in a broad range of habitats*, including soils, oceans, marshlands and the human colon, oral cavity, and skin
- Archaea include species that carry out *chemoorganotrophic* or *chemolithotrophic* metabolisms, and both *aerobic* and *anaerobic* species are common. *Methanogenesis* only occurs within the Archaea
- Archaea are particularly numerous in the oceans, and may *play key roles in both the carbon cycle and the nitrogen cycle*
- *No clear examples of archaeal pathogens* or parasites are known, but they are often mutualists or commensals

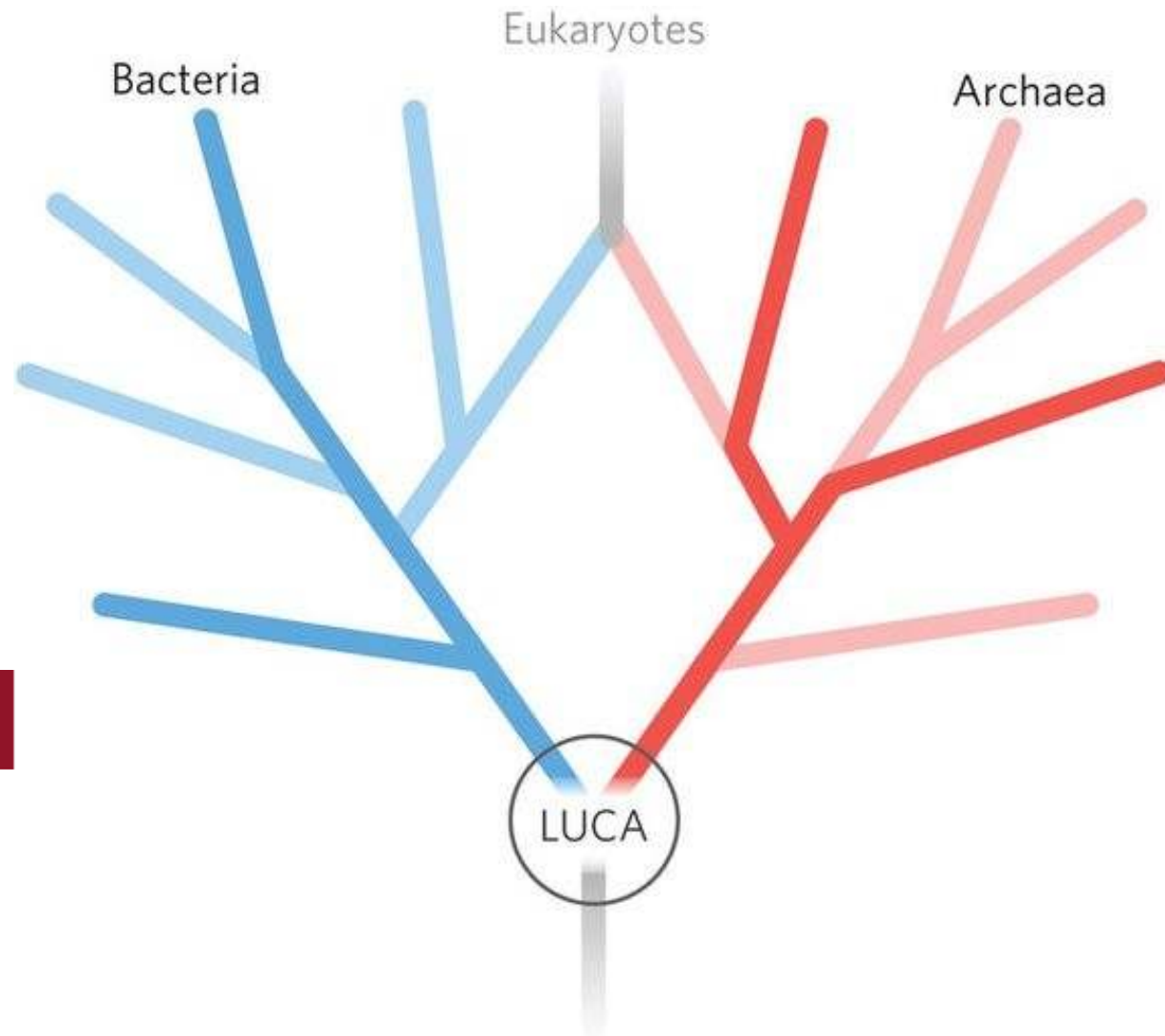
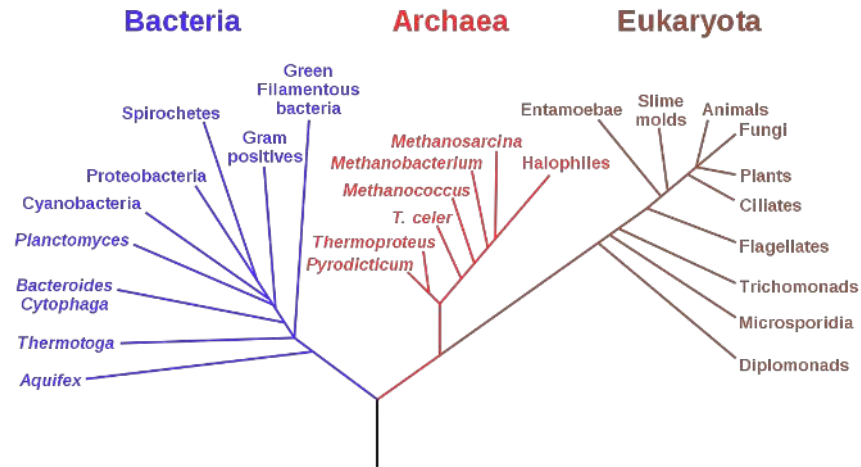


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| Superphylum | Phylum | Previous designation | References |
|-------------|---------------------|------------------------|------------|
| | Euryarcheota | Numerous | 7 |
| | Hydrothermarchaeota | MBG-E | 45 |
| Asgard | Lokiarchaeota | MBG-B and DSAG | 148 |
| Asgard | Thorarchaeota | Previously undescribed | 48 |
| Asgard | Odinarchaeota | Previously undescribed | 151 |
| Asgard | Heimdallarchaeota | AAG and MHVG | 151 |
| Asgard | Helarcheota | Previously undescribed | 152 |
| DPANN | Micrarchaeota | ARMAN-1 and -2 | 88,86 |
| DPANN | Parvarchaeota | ARMAN-4 and -5 | 88,86 |
| DPANN | Pacearcheota | DHVEG-6 | 88 |
| DPANN | Aenigmarchaeota | DSEG | 29 |
| DPANN | Diapherotites | pMC2A384 | 29 |
| DPANN | Woesearchaeota | Previously undescribed | 88 |
| DPANN | Altiarchaeota | SM1 | 49 |
| DPANN | Nanoarchaeota | Previously undescribed | 49,83 |
| DPANN | Nanohaloarchaeota | Previously undescribed | 29,87 |
| DPANN | Huberarchaeota | Previously undescribed | 49 |
| TACK | Korarchaeota | Previously undescribed | 19 |
| TACK | Verstraetearchaeota | TMCG | 45,100 |
| TACK | Nezhaarchaeota | Previously undescribed | 39 |
| TACK | Crenarchaeota | Many | 7 |
| TACK | Aigarchaeota | HWCG-I | 169 |
| TACK | Thaumarchaeota | MG-I, MBG-A | 97 |
| TACK | Bathyarchaeota | MCG | 135 |
| TACK | Geothermarchaeota | THSCG | 45 |
| TACK | Geoarcheota | NAG1 | 107 |
| TACK | Marsarchaeota | NAG2 | 170 |

AAG, ancient archaeal group; DHVEG, deep-sea hydrothermal vent group; DSEG, deep-sea euryarchaeotal group; SBAR, Santa Barbara Archaea; SM1, Sippenauer Moor; HWCG, hot water crenarchaeotic group.

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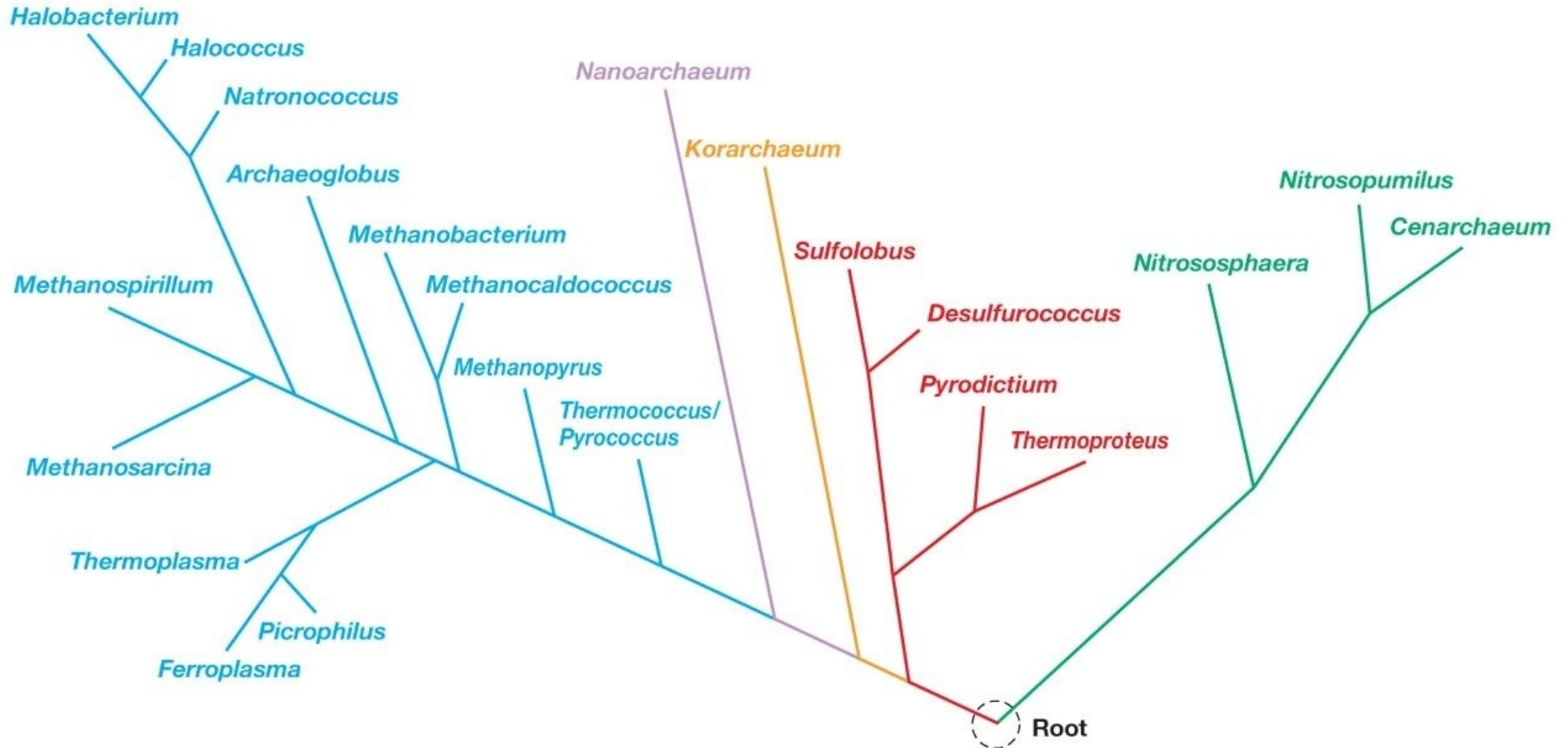


Complex archaea that bridge the gap between prokaryotes and eukaryotes

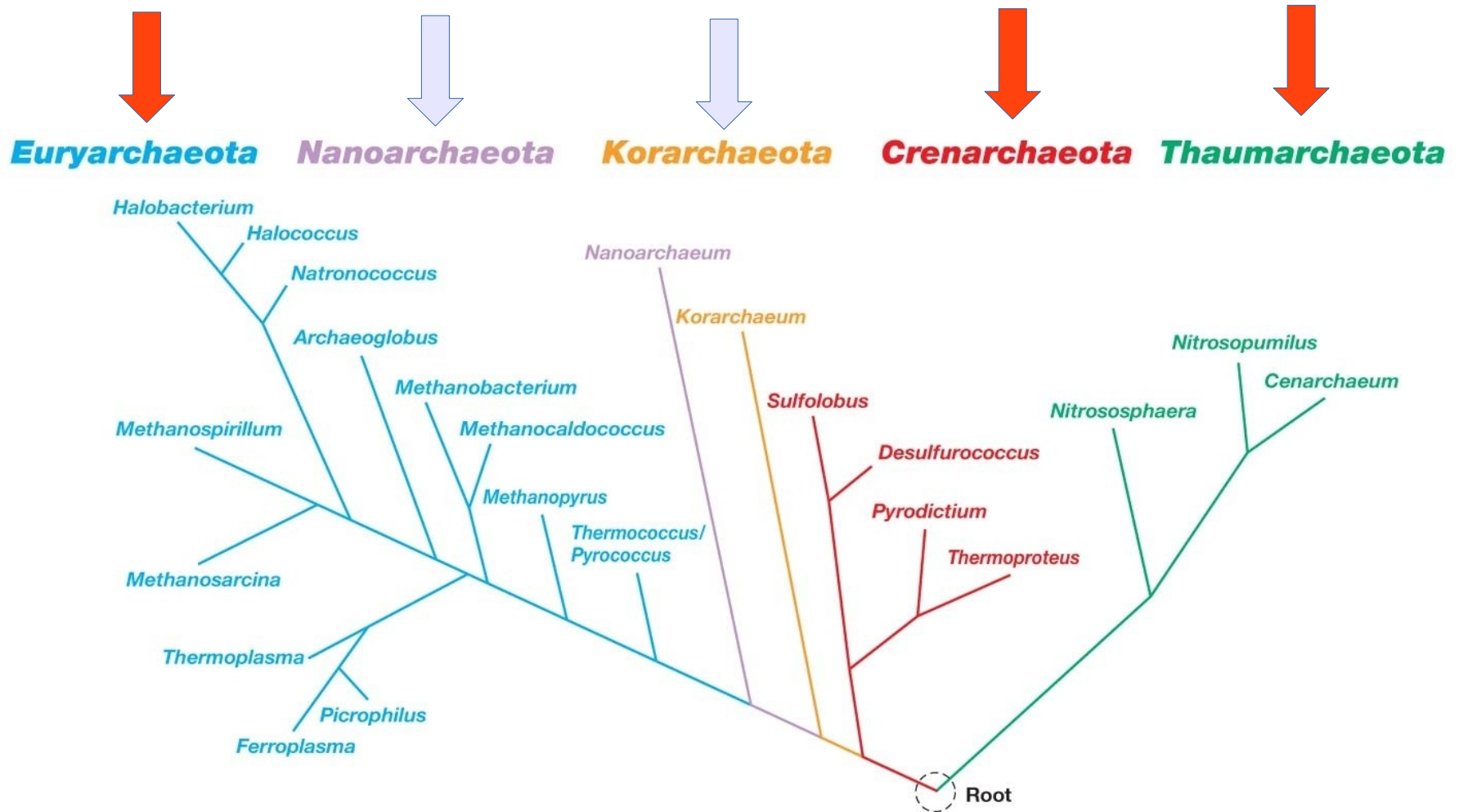
Anja Spang, Jimmy H. Saw, Steffen L. Jørgensen, Katarzyna Zaremba-Niedzwiedzka, Joran Martijn, Anders E. Lind, Roel van Eijk, Christa Schleper, Lionel Guy & Thijs J. G. Ettema

Archaea: major phyla

Euryarchaeota **Nanoarchaeota** **Korarchaeota** **Crenarchaeota** **Thaumarchaeota**



Archaea: major phyla



Euryarchaeota

- The Euryarchaeota (Greek for "broad old quality") are a phylum of the Archaea comprising a *large variety of metabolic strategies*
- The Euryarchaeota include the *methanogens, ANME, halophilic species* which survive extreme concentrations of salt, and some extremely *thermophilic aerobes and anaerobes*
- Within the halophilic Halobacteria, there are species able to catalyze the *light-driven synthesis of ATP using bacteriorhodopsin*
- Methanogenesis has been shown only within this phylum, although new evidence suggest that (at least) another candidate phylum of Archaea could be capable of methanogenesis

Methanogens

- Methanogens are coccoid or bacilli shaped archaea belonging to the Euryarchaeota phylum. There are over 50 described species of methanogens, which do not form a monophyletic group, although all methanogens belong to Archaea
- They are strict anaerobic organisms and cannot function under aerobic conditions. Methanogens typically thrive in environments in which all electron acceptors other than CO_2 have been depleted
- They have been found in several extreme environments on Earth. They are known to be the most common archaeobacteria in deep subterranean habitats
- They play a key ecological role in anaerobic environments removing excess hydrogen and fermentation products and contributing to organic matter decay
- The thermal breakdown of water, serpentinisation and water radiolysis are other possible sources of hydrogen
- Most methanogens are autotrophic producers, but those that oxidize CH_3COO^- are classed as chemotroph instead
- Closely related to the methanogens are the anaerobic methane oxidizers (ANME)

Crenarchaeota

- The Crenarchaeota were initially thought to be composed only by *acidophilic sulfur-dependent extremophiles*.
- Approximately *15 genera* are known, and most of the hyperthermophilic species have been isolated from marine or terrestrial volcanic environments, such as hot springs and shallow or deep-sea hydrothermal vents
- Recent analyses of genetic sequences obtained directly from environmental samples, however, indicate the existence of *low temperature Crenarchaeota*, which have not yet been cultivated
- Cells range in size from cocci *<1μm in diameter to filaments over 100μm in length*. Species display a *wide range of cell shapes*, including regular cocci clustered in grape-like aggregates (*Staphylothermus*), irregular, lobed cells (*Sulfolobus*), discs (*Thermodiscus*), very thin filaments (*<0.5μm* diameter; *Thermofilum*), and almost rectangular rods (*Thermoproteus*, *Pyrobaculum*). Most species possess flagella and *are motile*
- Metabolically, Crenarchaeota are quite diverse, ranging from *chemoorganotrophs* to *chemolithoautotrophs*. They are *anaerobes, facultative anaerobes or aerobes*, and many utilize *sulfur* in some way for energy metabolism

Thaumarchaeota

- The Thaumarchaeota (from the Greek 'thaumas', meaning wonder) are a phylum of the Archaea proposed in 2008 after the genome of *Cenarchaeum symbiosum* (the first isolate of this group) was sequenced and found to differ significantly from other members of the hyperthermophilic phylum Crenarchaeota
- Sequences belonging to this phylum have been identified in numerous marine and soil environments and are now believed to be ubiquitous
- All organisms of this lineage thus far identified are chemolithoautotrophic ammonia-oxidizers and may play important roles in biogeochemical cycles, such as the nitrogen cycle and the carbon cycle
- Only few species have been isolated in addition to *C. symbiosum*: *Nitrosopumilus maritimus*, *Nitrososphaera viennensis*, and *Nitrososphaera gargensis*

Other archaeal groups

- **Nanoarchaeota** (Greek, "dwarf or tiny ancient one") are a phylum of the small Archaea. This phylum currently has **only one representative**, *Nanoarchaeum equitans*. They are found living attached to other archaea cells and are believed to **be parasites**.
- **Korarchaeota** (Greek, "young ancient man") are a newly proposed phylum of the Archaea. Analysis of their 16S rRNA gene sequences suggests that they are a deeply branching lineage. They have only been found in hydrothermal environments.

This week reads

*Baker, Brett J., Valerie De Anda, Kiley W. Seitz, Nina Dombrowski, Alyson E. Santoro, e Karen G. Lloyd. 2020. «Diversity, Ecology and Evolution of Archaea». Nature Microbiology 5 (7): 887–900.
<https://doi.org/10.1038/s41564-020-0715-z>*