

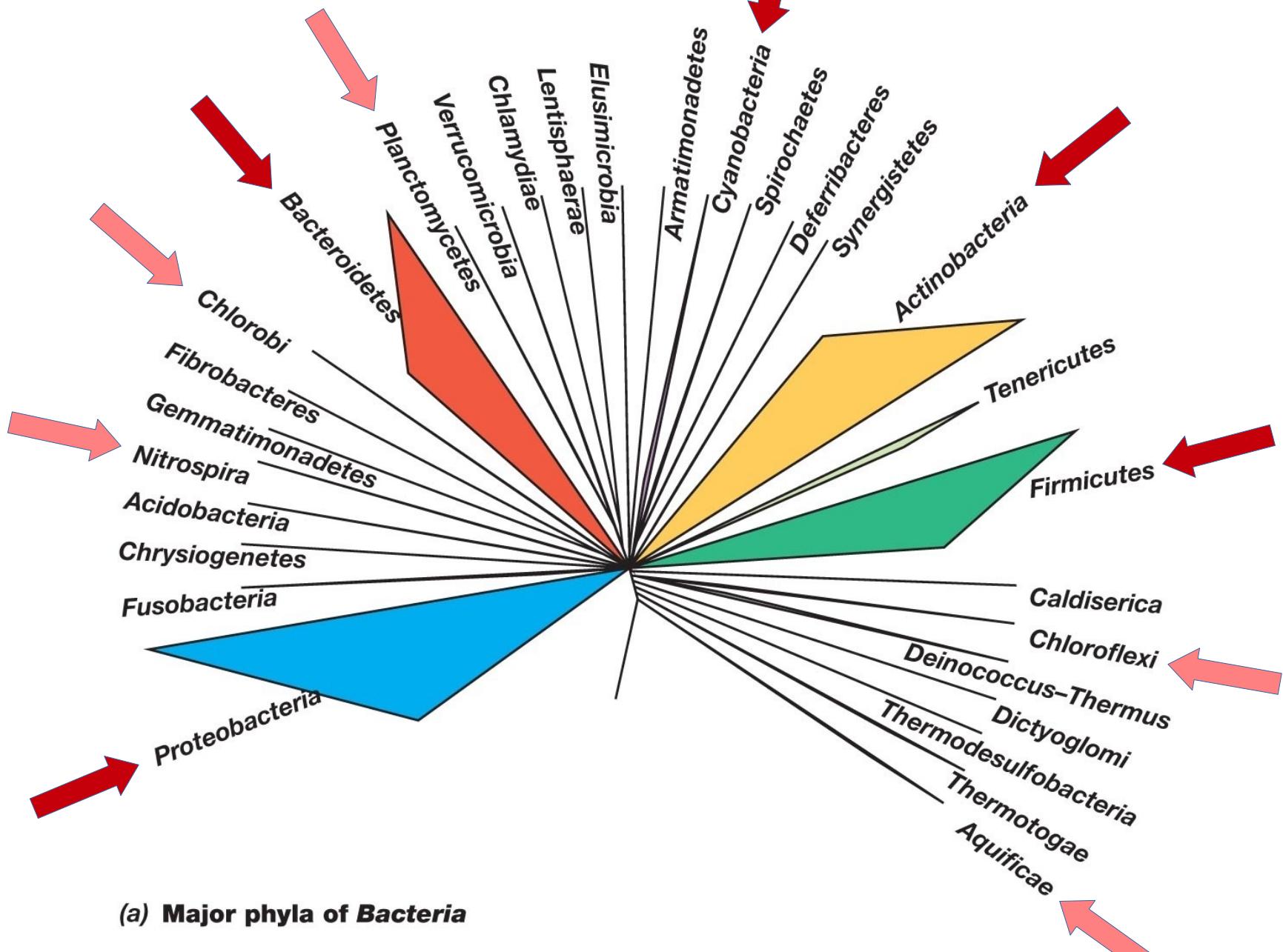


University of Naples "Federico II"

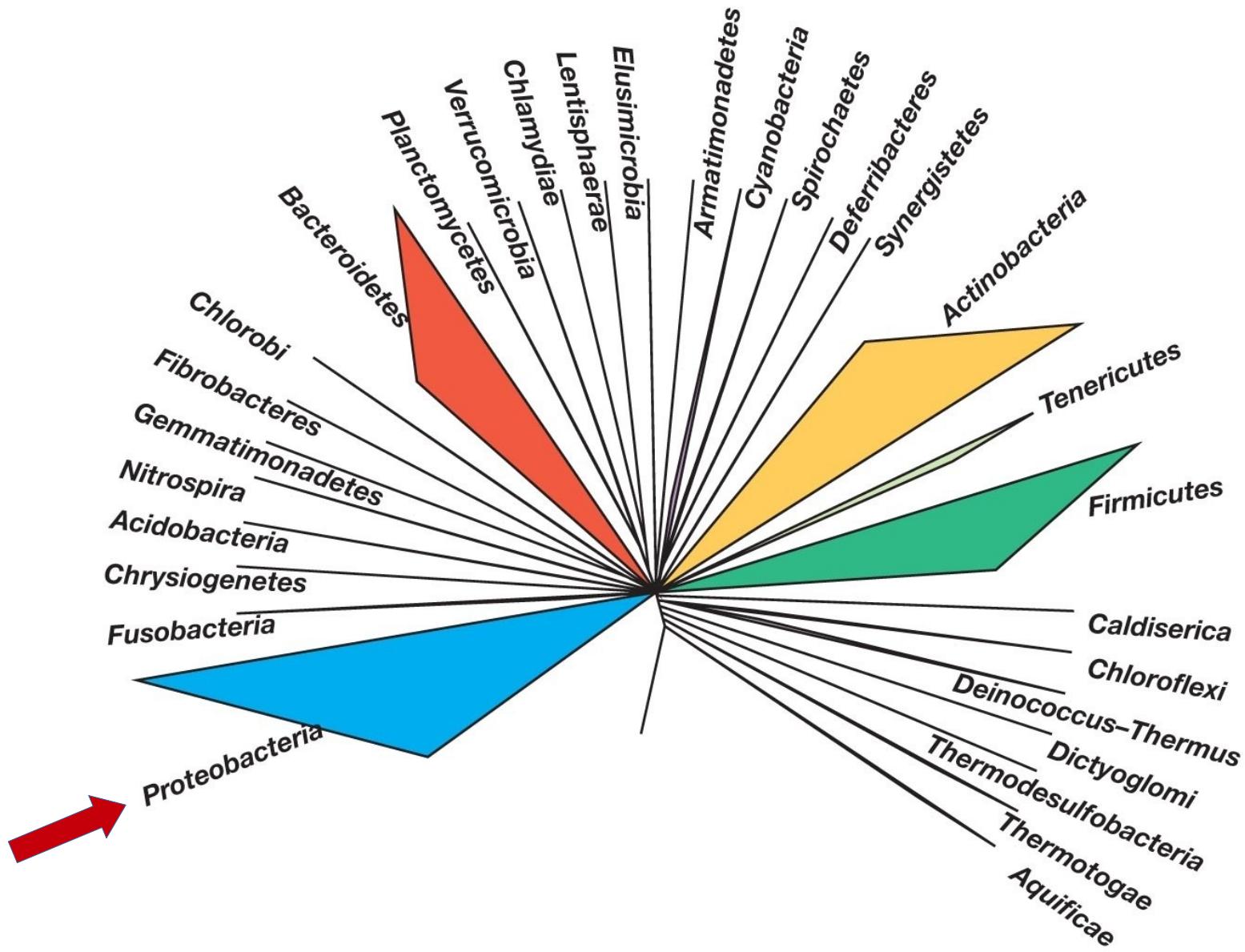
Marine Microbial Diversity

Know your Beasts 2: Bacterial and Archaeal Diversity in Marine Environments

Bacteria: major phyla



Bacteria: major phyla



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

Table 15.3 Characteristics of key genera of *Epsilonproteobacteria*

Genus	Habitat	Descriptive characters	Physiology and metabolism
<i>Campylobacter</i>	Reproductive organs, oral cavity, and intestinal tract of humans and other animals; pathogenic	Slender, spirally curved rods; corkscrew-like motility by single polar flagellum	Microaerophilic; chemoorganotrophic
<i>Arcobacter</i>	Diverse habitats (freshwater, sewage, saline environments, animal reproductive tract, plants); some species pathogenic for humans and other animals	Slender, curved rods; motile by single polar flagellum	Microaerophilic; aerotolerant or aerobic; chemoorganotrophic; oxidation of sulfide to elemental sulfur (S^0) by some species; nitrogen fixation in one species
<i>Helicobacter</i>	Intestinal tract and oral cavity of humans and other animals; pathogenic	Rods to tight spiral; some species with tightly coiled periplasmic fibers	Microaerophilic, chemoorganotrophic; produce high levels of urease (nitrogen assimilation)
<i>Sulfurospirillum</i>	Freshwater and marine habitats containing sulfur	Vibrioid to spiral-shaped cells; motile by polar flagella	Microaerophilic; reduces elemental sulfur (S^0)
<i>Thiovulum</i>	Freshwater and marine habitats containing sulfur; not yet in pure culture (Figure 14.29)	Cells contain orthorhombic S^0 granules; rapid motility by peritrichous flagella	Microaerophilic; chemolithotrophic oxidizing H_2S
<i>Wolinella</i>	Bovine rumen	Rapidly motile by polar flagellum; single species known: <i>W. succinogenes</i>	Anaerobe; anaerobic respiration using fumarate, nitrate, or other compounds as terminal electron acceptor, and with H_2 or formate as electron donor

Caminibacter mediatlanticus

- *Caminibacter mediatlanticus* is a member of the *Nautiliales* order of the *Epsilonproteobacteria*
- *C. mediatlanticus* is a thermophilic chemolithoautotroph able to fix CO₂ using the rTCA cycle
- It oxidizes hydrogen while reducing either nitrate or elemental sulfur to ammonia or hydrogen sulfide respectively
- It is an abundant member of the deep-sea hydrothermal vent community where can be found near vents in the temperature range of 50-65°C



Isolated from a deep-sea hydrothermal vent,
Middle Atlantic Ridge

Opt. T: 55°C

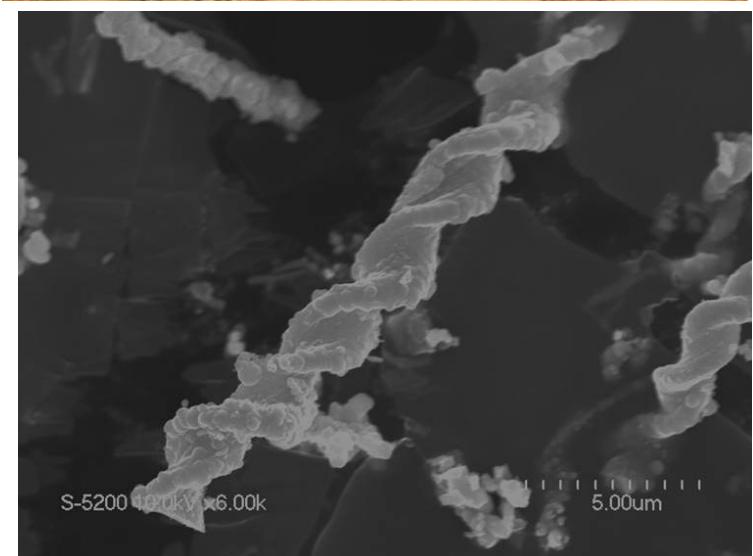


Proteobacteria: Zetaproteobacteria

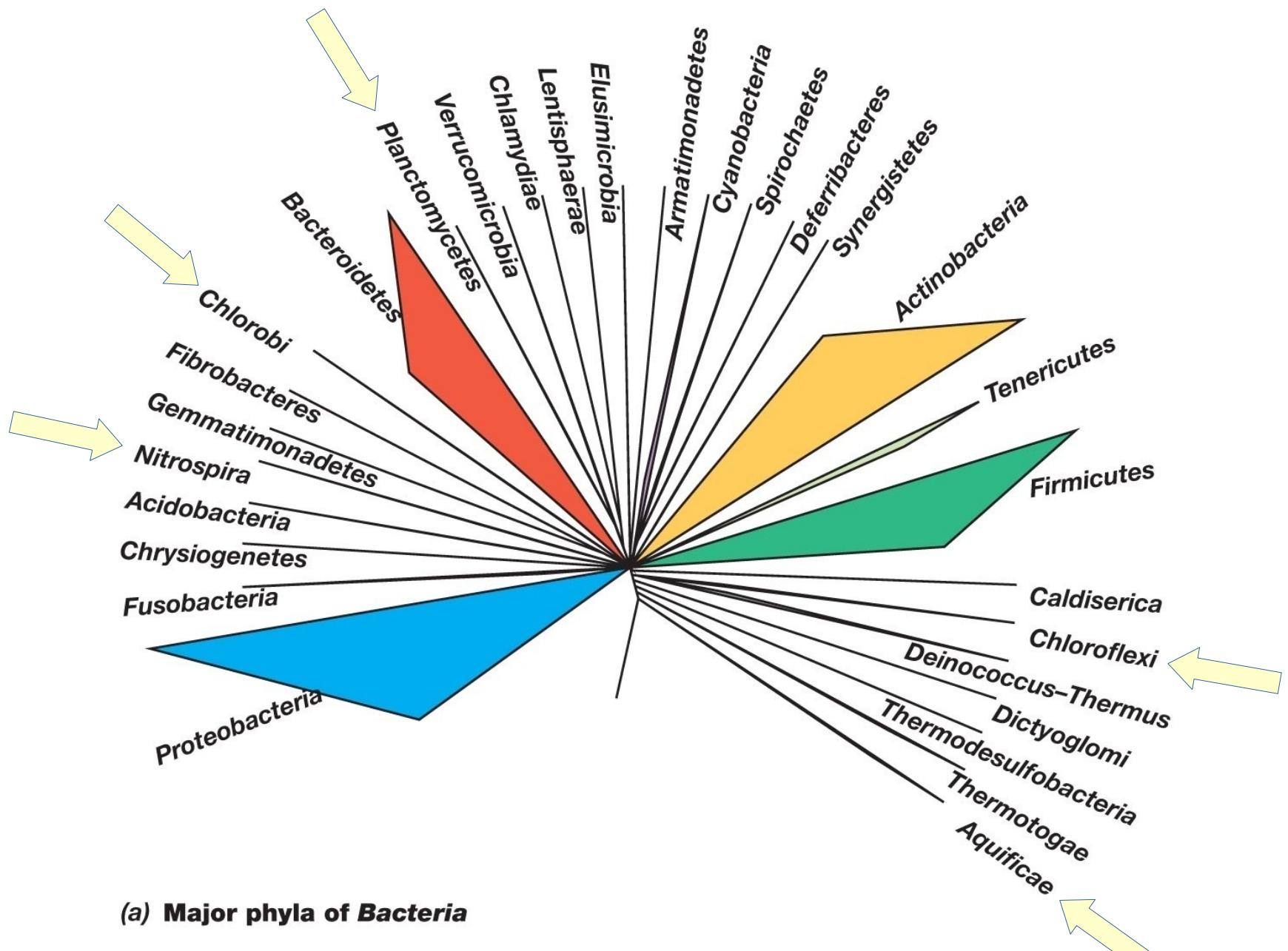
- Zetaproteobacteria are a *new class* within the Proteobacteria consisting of a *single cultivated genus and species Mariprofundus hydrothermalis*
- Zetaproteobacteria are now believed to be *key player in the marine iron biogeochemical cycle*
- *M. ferrooxydans* was first isolated from Lō'ihi Seamount, a submarine volcano found near Hawaii
- *M. ferrooxydans* is a *neutrophilic aerobic iron-oxidizers*, forming a twisted stalklike structure containing Fe(OH)3 from the oxidation of ferrous iron. The iron-encrusted stalk contains an organic matrix on which Fe(OH)3 accumulates as it is excreted from the cell surface. Stalk formation is presumably an adaptation that prevents cells from becoming entombed in an iron oxide crust
- *M. ferrooxydans* is a *autotrophic chemolithotrophs* fixing CO₂ using the *Calvin cycle*

Mariprofundus ferrooxydans

- *Mariprofundus ferrooxydans* is an iron-oxidizing neutrophilic chemolithoautotroph
- Only cultured member of the genus
- Zetaproteobacteria have been most commonly found at deep-sea hydrothermal vents, though recent discovery of members of this class in near-shore environments has led to the reevaluation of Zetaproteobacteria distribution and significance
- Thought to be a major player in iron cycle in the marine ecosystem



Bacteria: major phyla



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. *Methylomirabilis 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

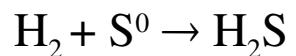
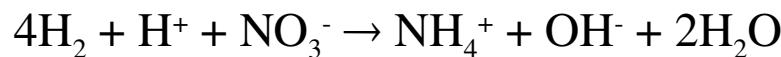
Other bacterial groups

- **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
- **Aquifcae** 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

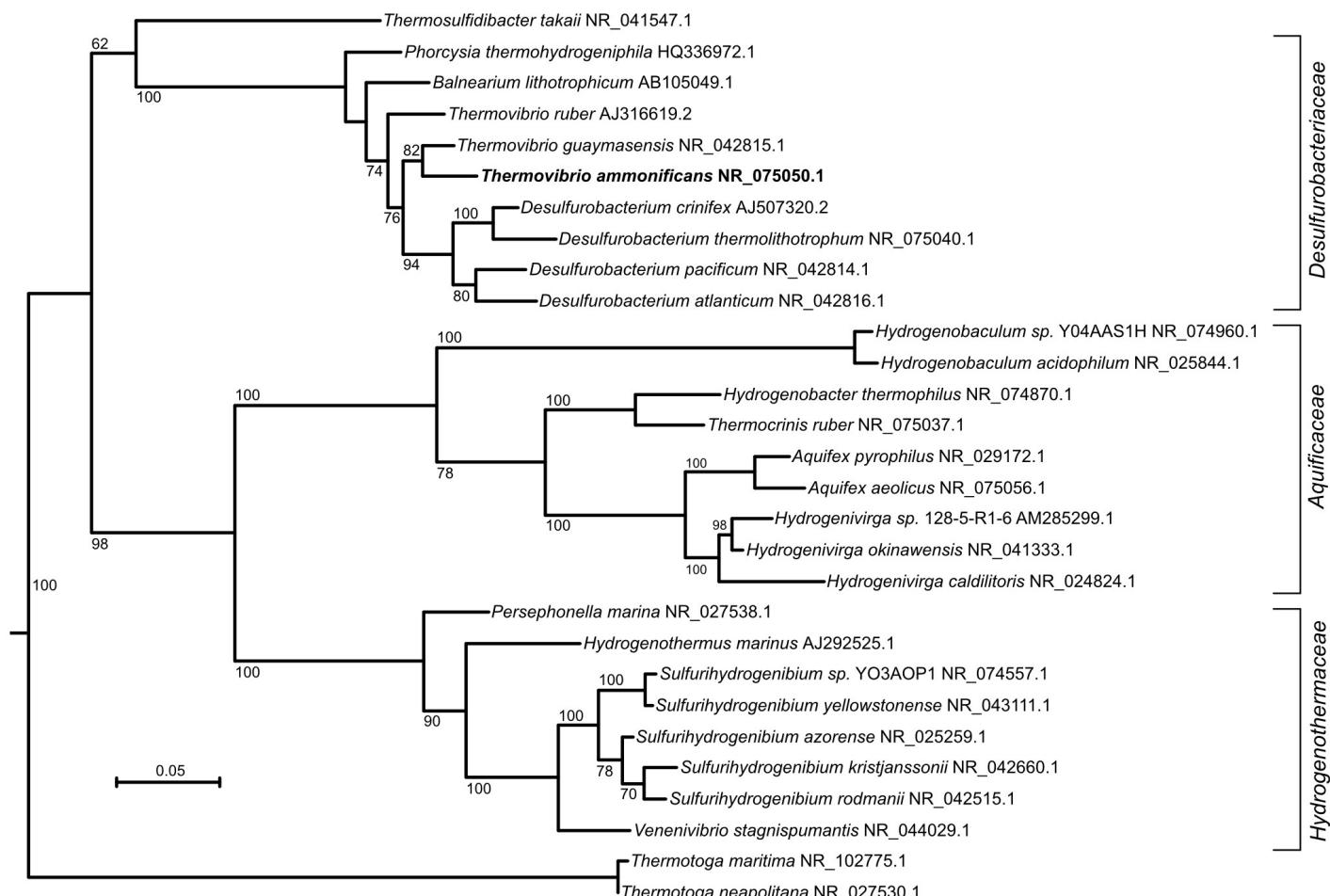
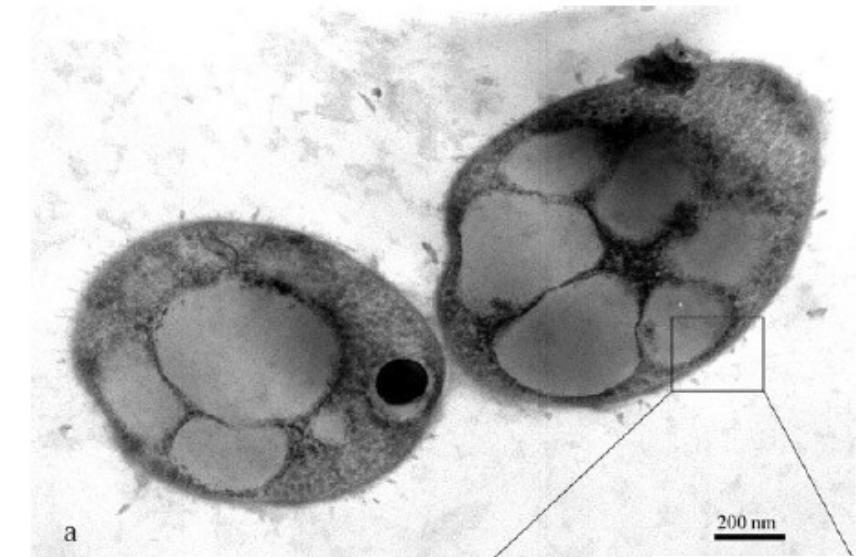
Thermovibrio ammonificans

Phylum Aquificae - Isolated from a deep-sea hydrothermal vent, EPR

Opt. T: 75°C

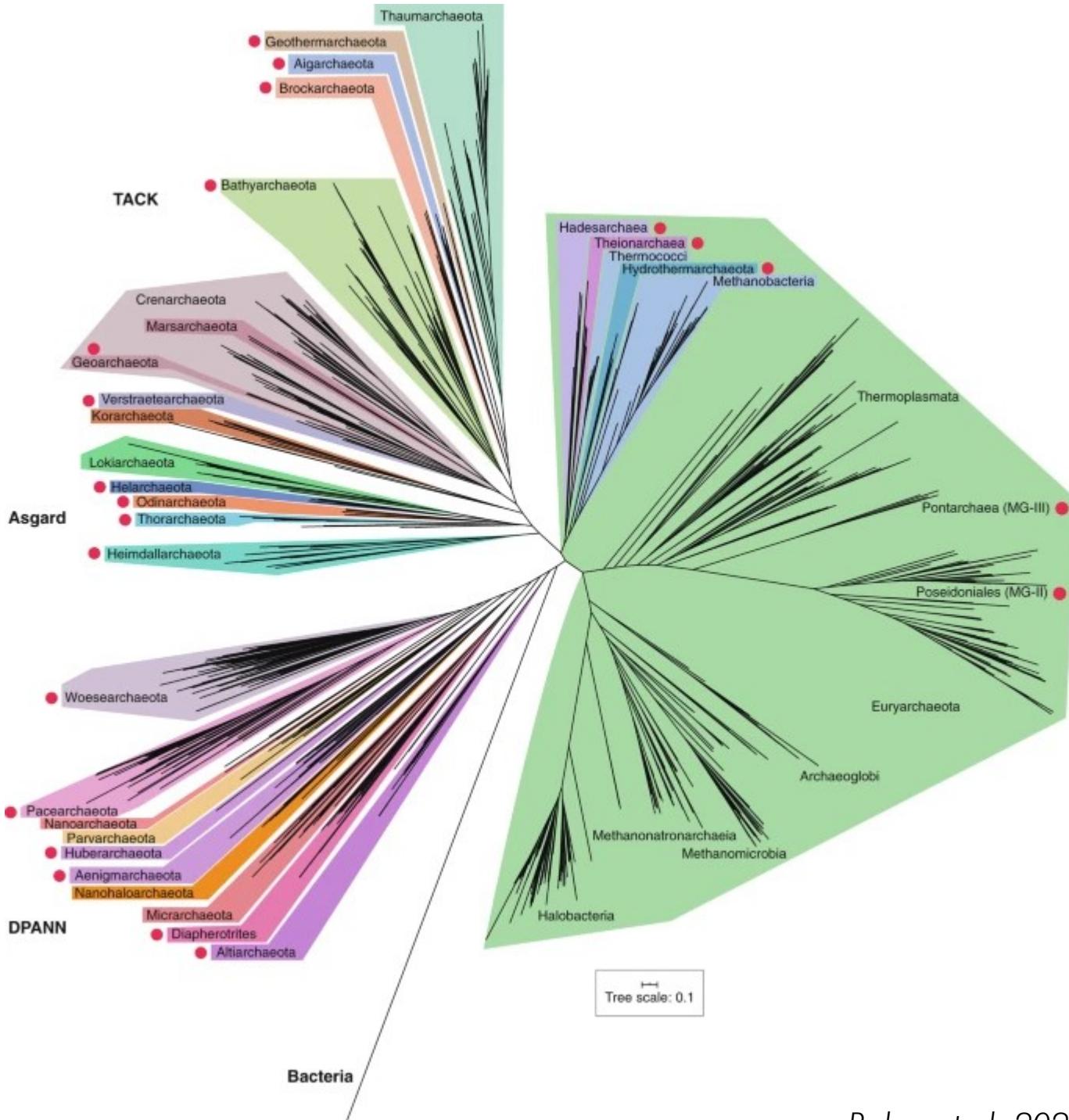


Chemolithoautotrophic H₂ oxidation (anaerobic)



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 reflect a primitive metabolism. Archaea were *initially classified as bacteria*, receiving the name Archaebacteria
- 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 phyla 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



Archaea Diversity

Euryarchaeota Woese et al. 1990

"Aenigmarchaeota" Rinke et al. 2013

"Diapherotrites" Rinke et al. 2013

Nanoarchaeota Huber et al. 2002

"Nanohaloarchaeota" Rinke et al. 2013

"Micrarchaeota" Baker et al. 2010

"Pacearchaeota" Castelle et al. 2015

"Parvarchaeota" Rinke et al. 2013

"Woesearchaeota" Castelle et al. 2015

"Proteoarchaeota" Petitjean et al. 2014

"Aigarchaeota" Nunoura et al. 2011

"Bathyarchaeota" Meng et al. 2014

Crenarchaeota Garrity & Holt 2002

"Geoarchaeota" Kozubal et al. 2013

"Korarchaeota" Barns et al. 1996

"Lokiarchaeota" Spang et al. 2015

"Thorarchaeota" Seitz et al. 2016

Thaumarchaeota Brochier-Armanet et al. 2008

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	Diapherotrites	pMC2A384	29
DPANN	Woesearchaeota	Previously undescribed	88
DPANN	Altarchaeota	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	Verstraetarchaeota	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.

Baker at al. 2020 *Nature Microbiol*

Bacteria

Eukaryotes

Archaea

LUCA



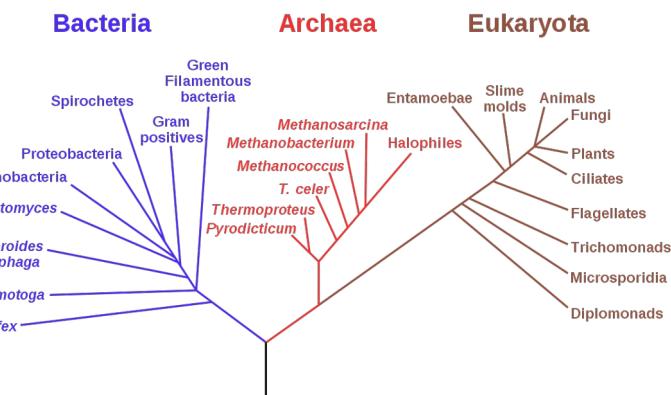
nature
International journal of science

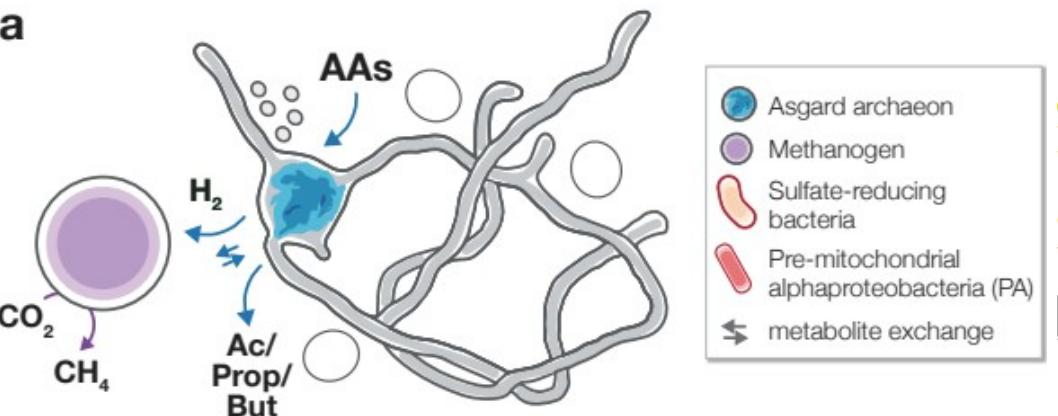
Article | Published: 06 May 2015

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

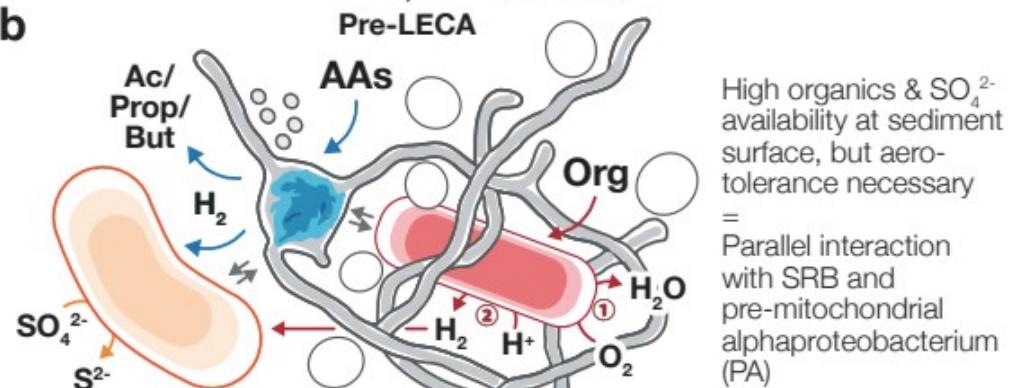
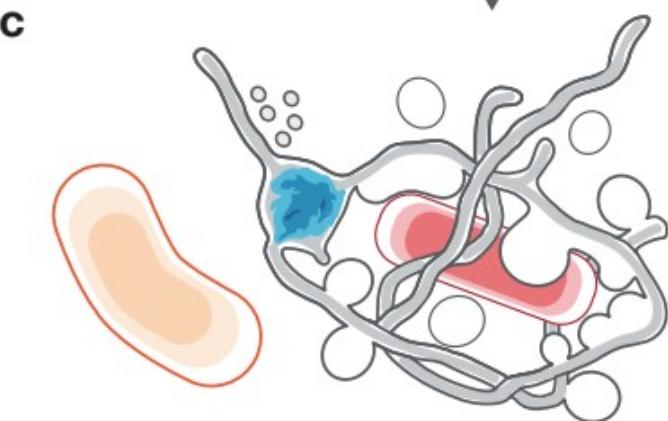
Pre-G.O.E. (2.7 Ga~)
ox. of S^{2-} to SO_4^{2-}

Loki/Thor/Hel/
Odin ancestor

Heimdall-Eukarya
ancestor

Loki (syntrophy/
acetogenesis)
Thor (acetogenesis)
Odin (fermentation?)
Hel (alkane metabolism)

→ Heim (O_2 respiration)

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

Info/History

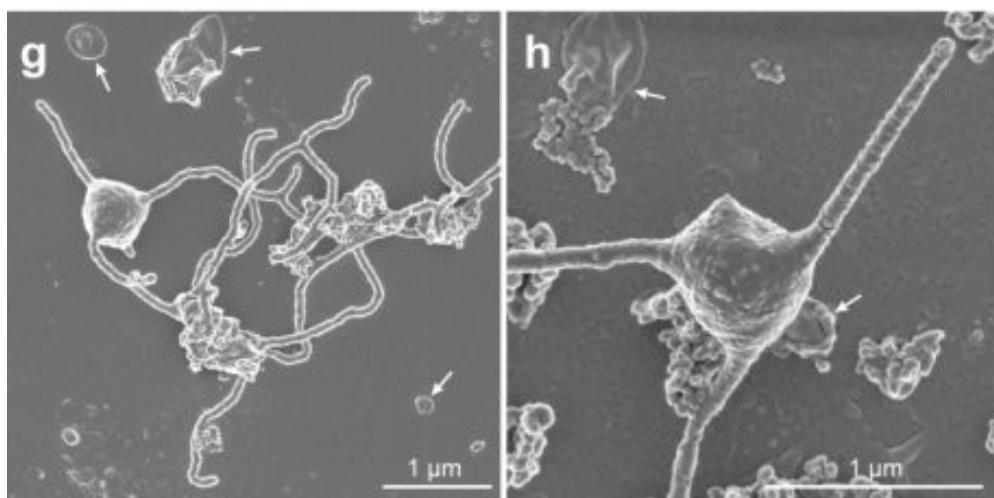
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Preview PDF

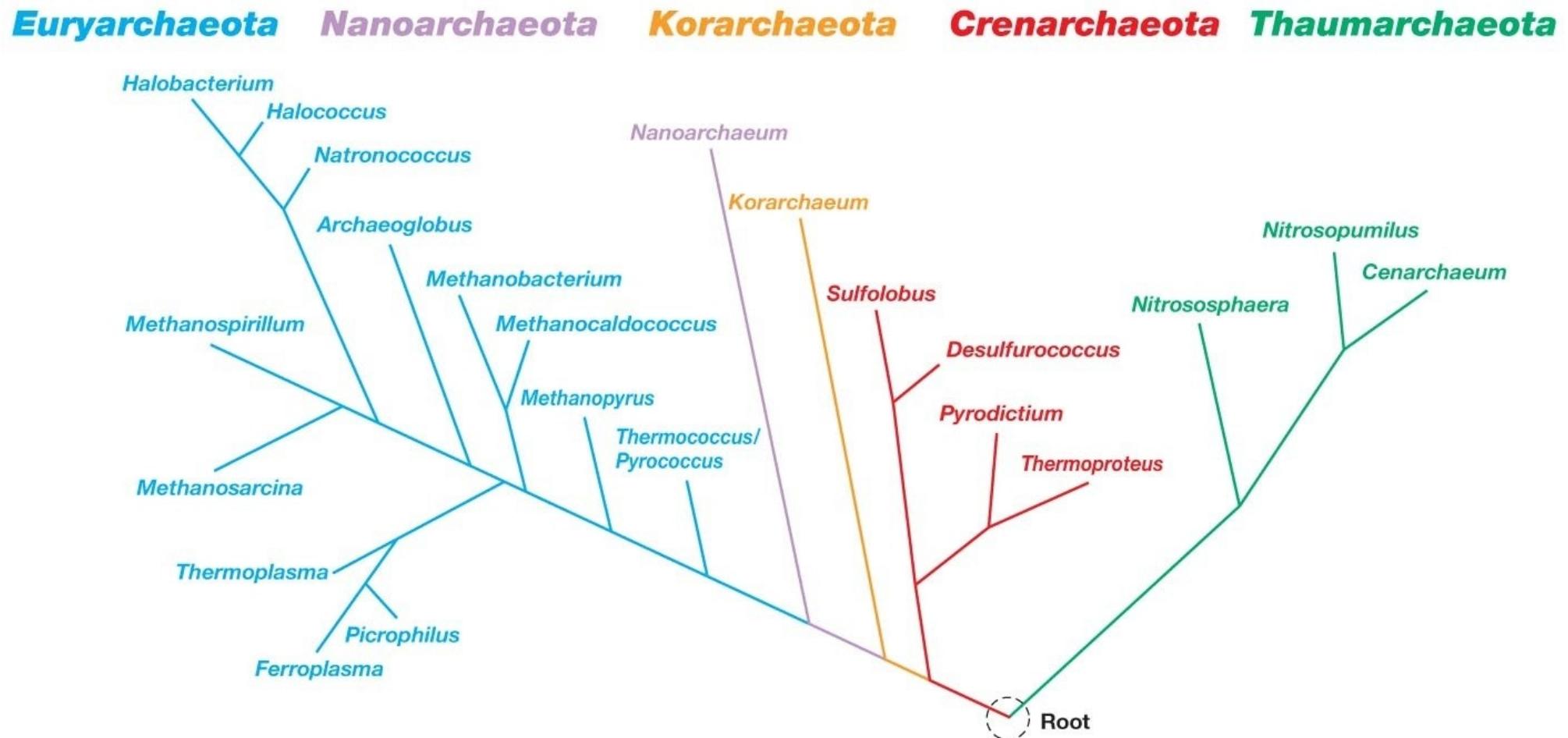
Abstract

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.

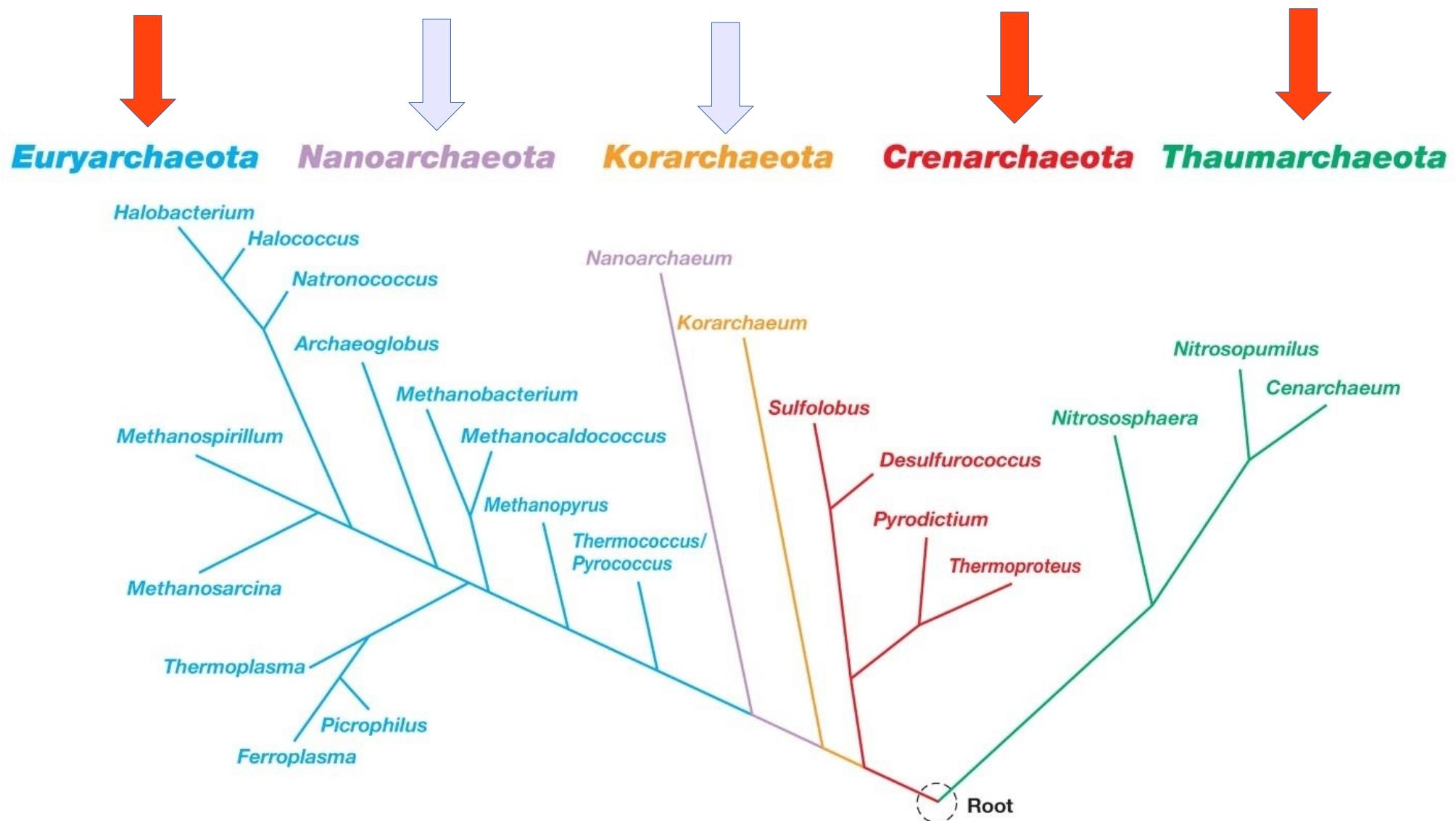
Here we report the decade-long isolation of a Lokiarchaeota-related Asgard archaeon from deep marine sediment. The archaeon, *Candidatus Prometheoarchaeum syntrophicum* strain MK-D1, is an anaerobic, extremely slow-growing, small cocci (~550 nm), that degrades amino acids through syntrophy. Although 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 (E³) model” for eukaryogenensis through archaea-alphaproteobacteria symbiosis mediated by the physical complexities and metabolic dependency of the hosting archaeon.



Archaea: major phyla



Archaea: major phyla

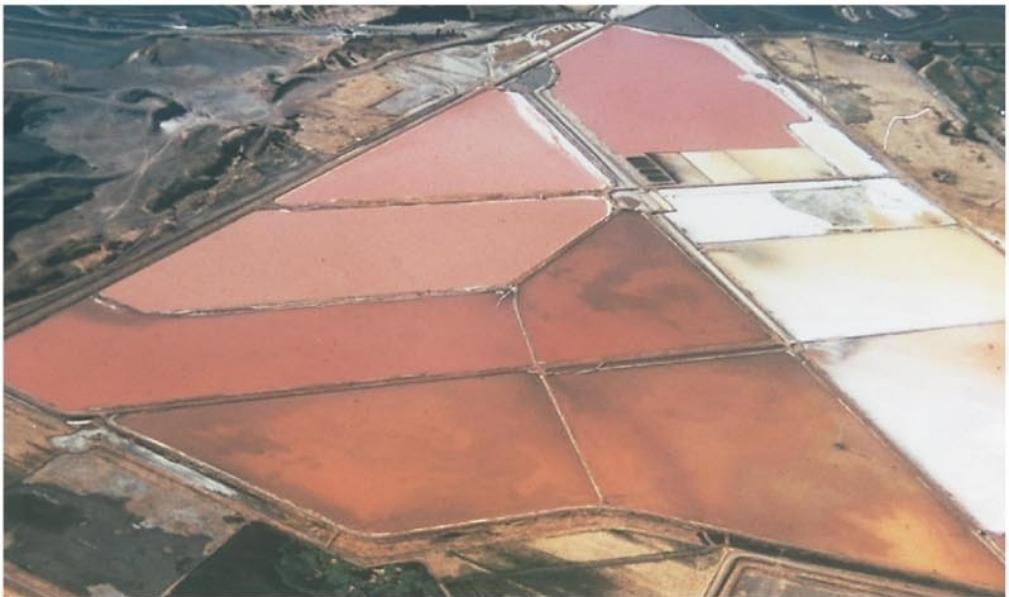


Euryarchaeota

- 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



(a)

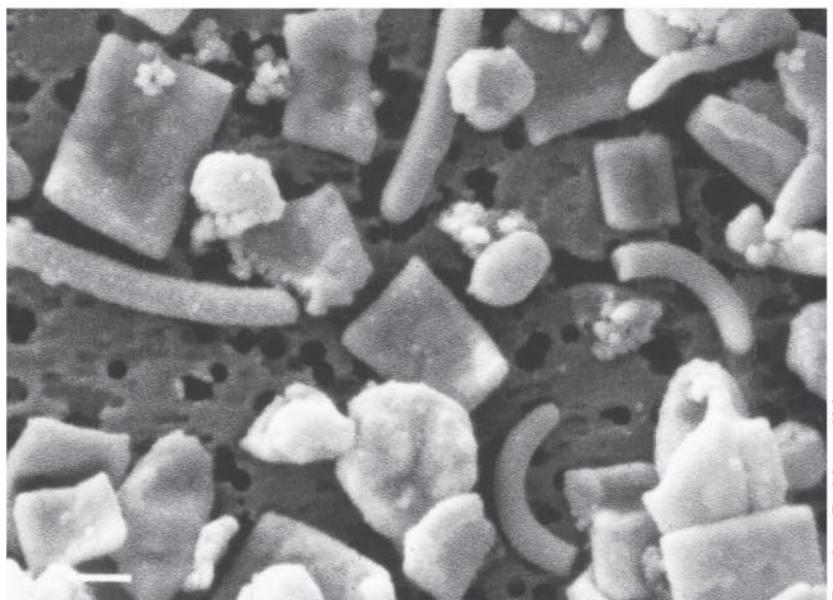


(b)



Michael T. Madigan

(c)



Francisco Rodriguez-Valera

(d)

Table 16.1 Some genera of extremely halophilic *Archaea*

Genus	Morphology	Habitat
<i>Extreme halophiles</i>		
<i>Halobacterium</i>	Rods	Salted fish; hides; hypersaline lakes; saltrens
<i>Halorubrum</i>	Rods	Dead Sea; saltrens
<i>Halobaculum</i>	Rods	Dead Sea
<i>Haloferax</i>	Flattened discs	Dead Sea; saltrens
<i>Haloarcula</i>	Irregular discs	Salt pools, Death Valley, CA; marine saltrens
<i>Halococcus</i>	Cocci	Salted fish; saltrens
<i>Halogeometricum</i>	Pleomorphic flat cells	Solar saltrens
<i>Haloterrigena</i>	Rods, ovals	Saline soil
<i>Haloquadratum</i>	Flat squares	Saltrens
<i>Haloalkaliphiles</i>		
<i>Natronobacterium</i>	Rods	Highly saline soda lakes
<i>Natrinema</i>	Rods	Salted fish; hides
<i>Natrialba</i>	Rods	Soda lakes; beach sand
<i>Natronomonas</i>	Rods	Soda lakes
<i>Natronococcus</i>	Cocci	Soda lakes
<i>Natronorubrum</i>	Flattened cells	Soda lakes

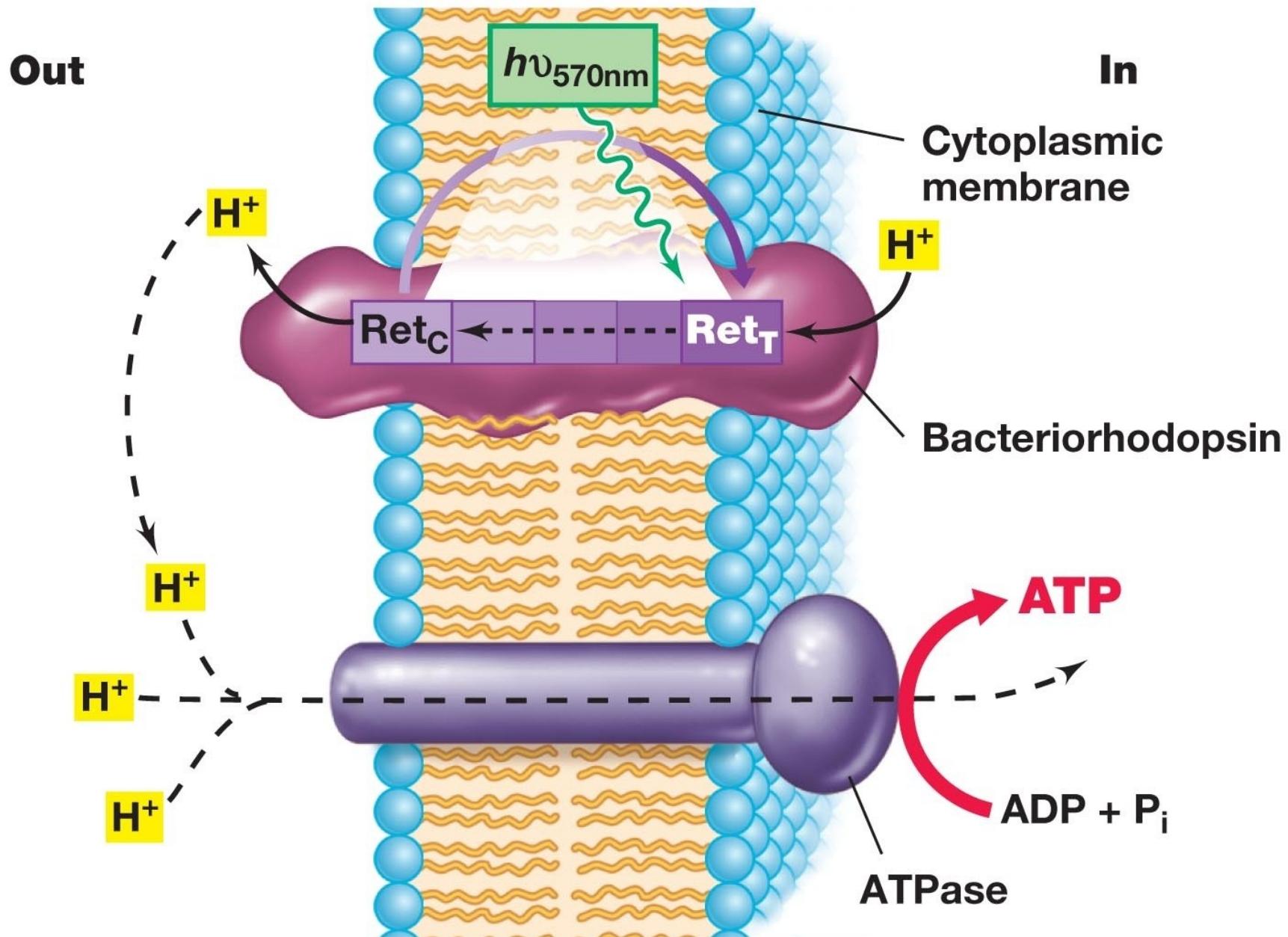


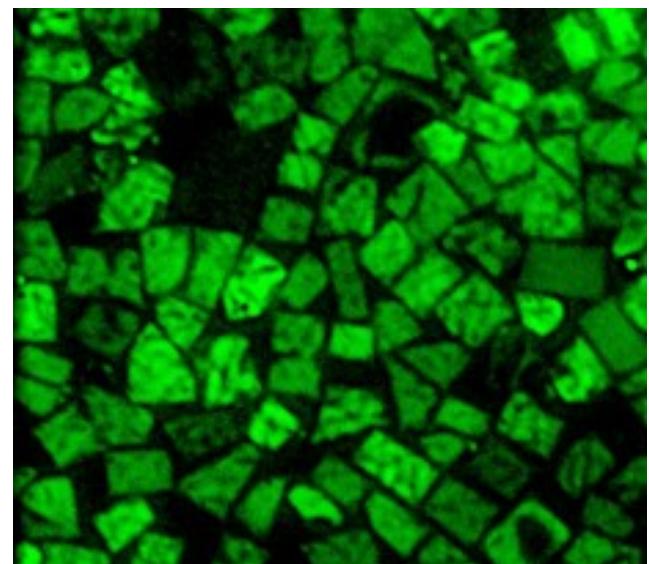
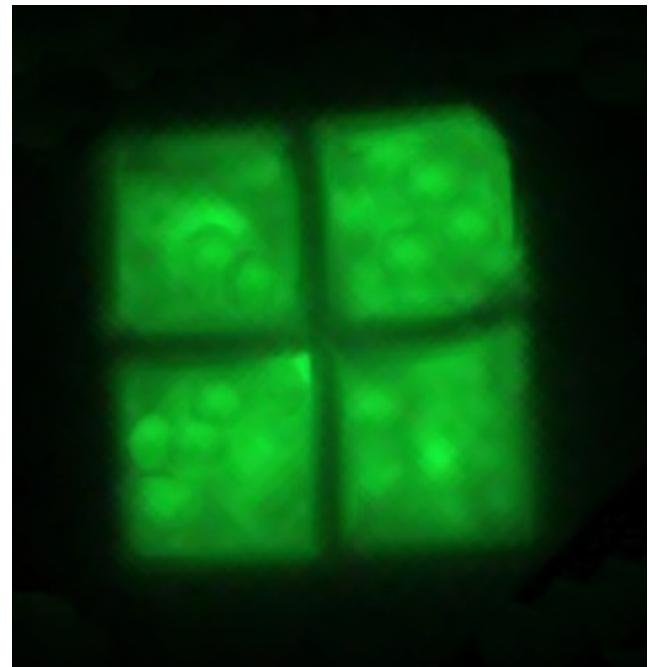
Table 16.2 Concentration of ions in cells of *Halobacterium salinarum*^a

<i>Ion</i>	<i>Concentration in medium (M)</i>	<i>Concentration in cells (M)</i>
Na ⁺	4.0	1.4
K ⁺	0.032	4.6
Mg ²⁺	0.13	0.12
Cl ⁻	4.0	3.6

^aData from *Biochim. Biophys. Acta* 65: 506–508 (1962).

Haloquadratum walsbyi

- *Haloquadratum* ("salt square") is a genus of the family Halobacteriaceae containing a single genus and a single species, *Haloquadratum walsbyi*
- Discovered in 1980 in the Gavish Sabkha, a coastal brine pool on the Sinai Peninsula in Egypt, the archaeon was not cultured until 2004
- *H. walsbyi* can be found anywhere in hypersaline waters. During the final stage of halite formation, *H. walsbyi* flourishes and can make up 80% of the brine's biomass
- The cells typically contain polyhydroxyalkanoate granules, and a large numbers of gas-filled vacuoles which provide buoyancy and may help to position the cells to maximise light-harvesting



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 CO₂ have been depleted
- They have been found in *several extreme environments* on Earth. They are known to be the *most common archaebacteria 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 CH₃COO⁻ are classed as *chemotroph* instead
- Closely related to the methanogens are the *anaerobic methane oxidizers* (ANME)

Table 16.3 Habitats of methanogens

- I. Anoxic sediments: marsh, swamp, and lake sediments, paddy fields, moist landfills
- II. Animal digestive tracts:^a
 - A. Rumen of ruminant animals such as cattle, sheep, elk, deer, and camels
 - B. Cecum of cecal animals such as horses and rabbits
 - C. Large intestine of monogastric animals such as humans, swine, and dogs
 - D. Hindgut of cellulolytic insects (for example, termites)
- III. Geothermal sources of H₂ + CO₂: hydrothermal vents
- IV. Artificial biodegradation facilities: sewage sludge digesters
- V. Endosymbionts of various anaerobic protozoa

^aSee Sections 22.6 and 22.7 and Figures 22.27 and 22.28.

Table 16.5 Substrates converted to methane by various methanogenic *Archaea*

I. CO₂-type substrates

Carbon dioxide, CO₂ (with electrons derived from H₂, certain alcohols, or pyruvate)

Formate, HCOO⁻

Carbon monoxide, CO

II. Methylated substrates

Methanol, CH₃OH

Methylamine, CH₃NH₃⁺

Dimethylamine, (CH₃)₂NH₂⁺

Trimethylamine, (CH₃)₃NH⁺

Methylmercaptan, CH₃SH

Dimethylsulfide, (CH₃)₂S

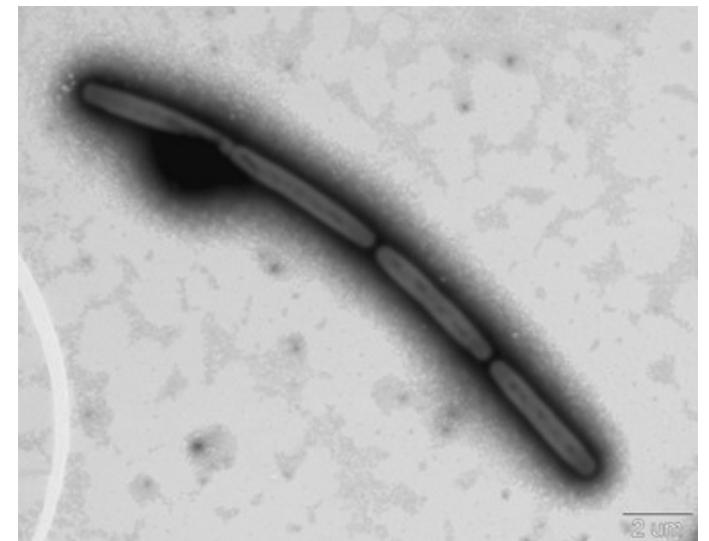
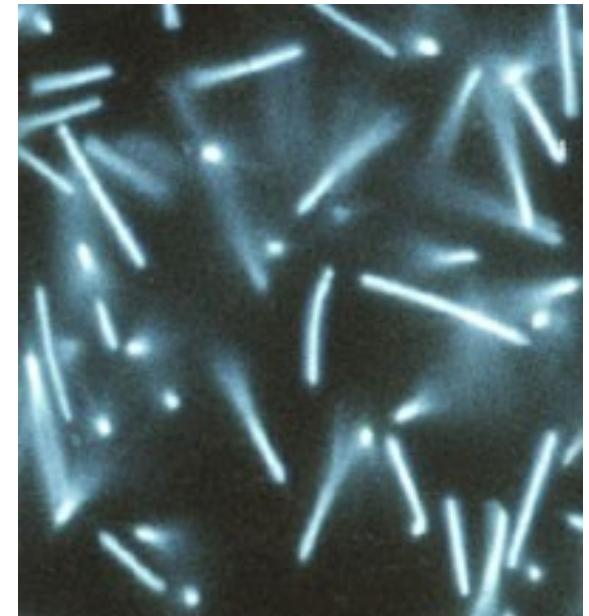
III. Acetotrophic substrates

Acetate, CH₃COO⁻

Pyruvate, CH₃COCOO⁻

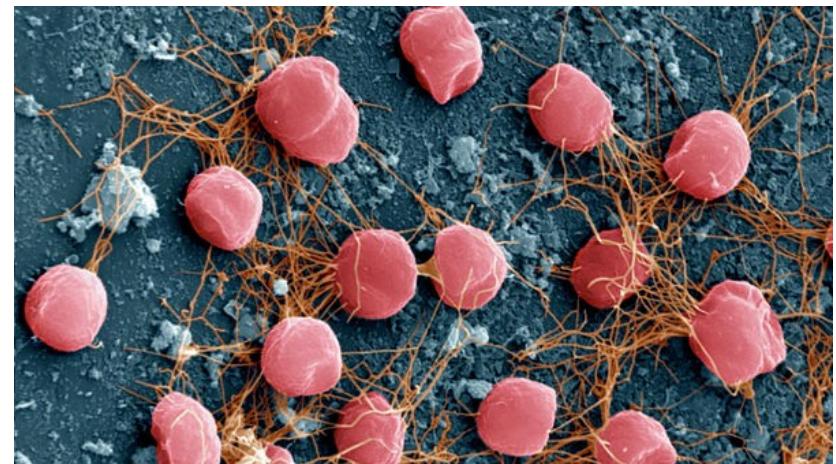
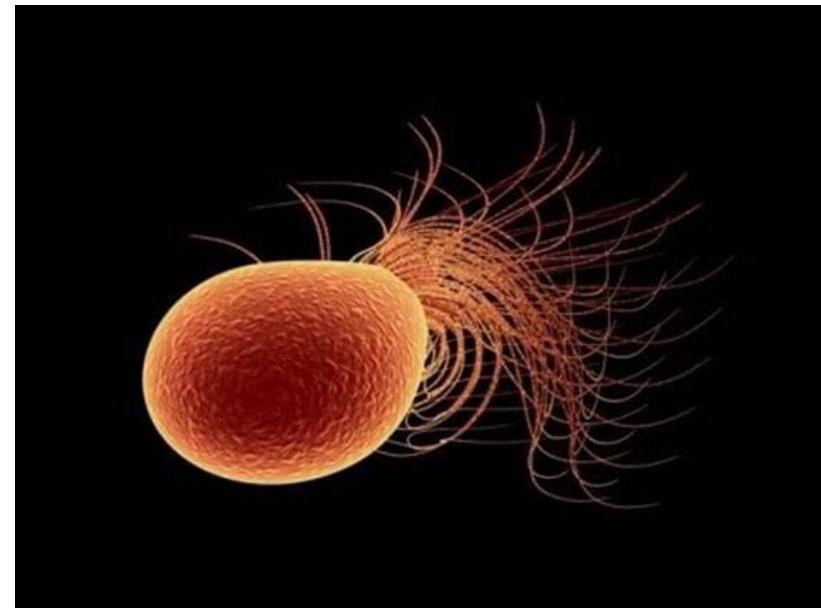
Methanopyrus kandleri

- *Methanopyrus kandleri* is a Gram-positive hyperthermophilic halophilic archaeon, discovered on the wall of a black smoker from the Gulf of California at a depth of 2000 m, at temperatures of 84–110 °C
- Strain 116 was discovered in black smoker fluid of the Kairei hydrothermal field; it can survive and reproduce at 122 °C
- lives in a hydrogen-carbon dioxide rich environment, and like other methanogens reduces the latter to methane
$$4\text{H}_2 + \text{CO}_2 \rightarrow \text{CH}_4 + 2\text{H}_2\text{O}$$
- the genome was determined to be a single chromosome that was 1,694,969 base pairs (bp) long. it is considered the most divergent methanogen based on its 16S rRNA sequence



Pyrococcus furiosus

- *Pyrococcus furiosus* is an extremophilic species of Euryarchaeota phylum, in the *Thermococcales* order
- The optimum growth temperature is 100 °C with a rapid doubling time of 37 minutes under optimal conditions
- It grows well on yeast extract, maltose, cellobiose, β -glucans, starch, and protein sources (tryptone, peptone, casein, and meat extracts)
- The presence of hydrogen severely inhibits its growth and metabolism; this effect can be circumvented, however, by introducing sulfur into the organism's environment
- It possesses an aldehyde ferredoxin oxidoreductase enzymes containing tungsten, an element rarely found in biological molecules



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



T. D. Brock

(a)



T. D. Brock

(b)



T. D. Brock

(c)

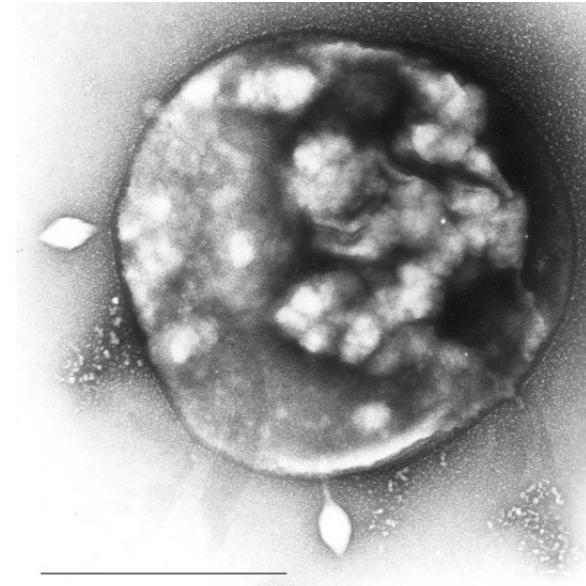
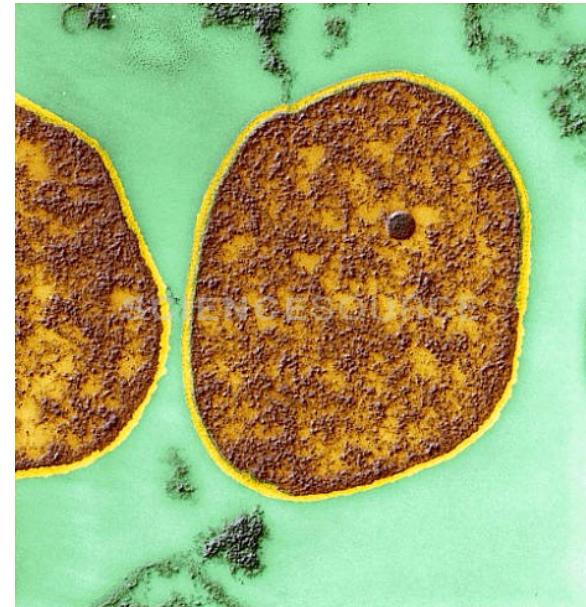


T. D. Brock

(d)

Sulfolobus solfataricus

- *Sulfolobus solfataricus* is a species of thermoacidophilic Crenarchaeota isolated and discovered in the Solfatara volcano near Naples
- The species grows best in temperatures around 80° C, a pH between 2 and 4, and sulfur
- *Sulfolobus* can grow either lithoautotrophically by oxidizing sulfur, or chemoheterotrophically using sulfur to oxidize simple reduced carbon compounds.
- Heterotrophic growth has only been observed, however, in the presence of oxygen
- The genome consist of a single chromosome, there are 2,992,245 base pairs which encode for 2,977 proteins

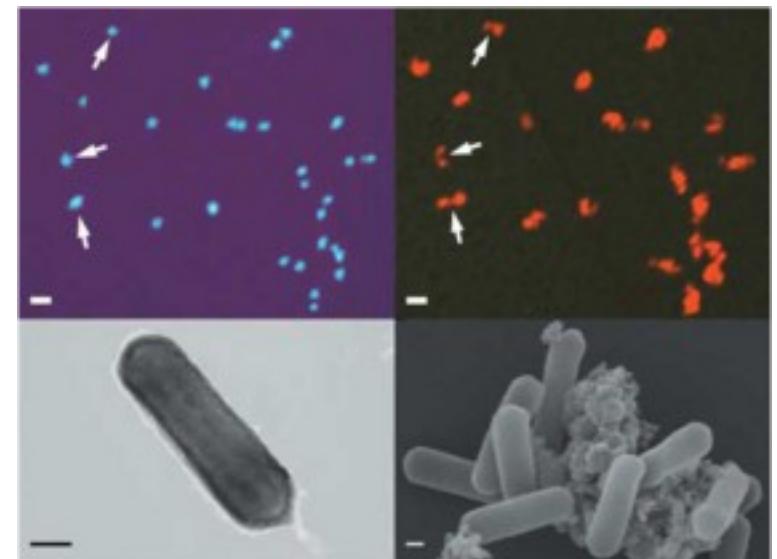


Thaumarchaeota

- 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. symbosum*: *Nitrosopumilus maritimus*, *Nitrososphaera viennensis*, and *Nitrososphaera gargensis*

Nitrosopumilus maritimus

- *Nitrosopumilus maritimus* is a member of the newly proposed archaea phylum Thaumarchaeota
- *N. maritimus* was the first non-thermophilic archaeon to be maintained in axenic culture. The original isolate was obtained from a tropical salt-water aquarium
- Gene sequences closely related to *N. maritimus* have been amplified from numerous aquatic environments and soils
- It was the first reported chemolithoautotroph ammonia oxidizer (nitrifier) in the domain archaea
- It is believed to be a key player in marine nitrification. This hypothesis is supported by the parallels between the depth of the marine nitrite maximum and the vertical distribution of Thaumarchaeota in the ocean

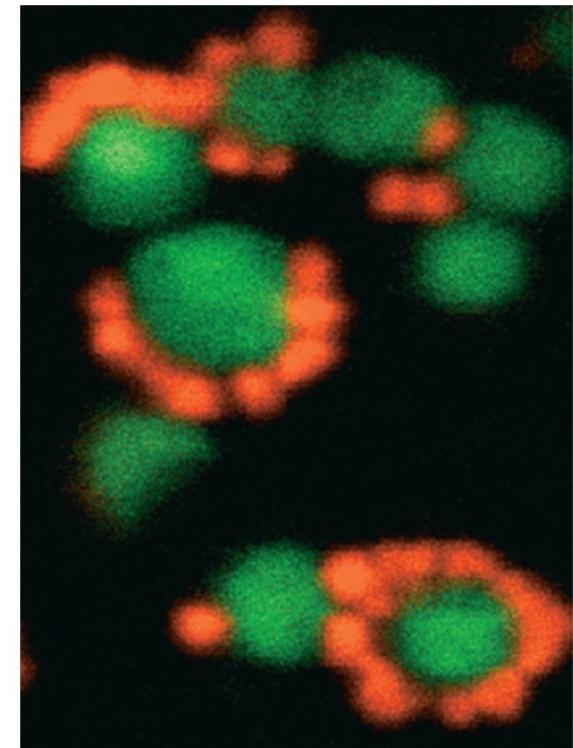
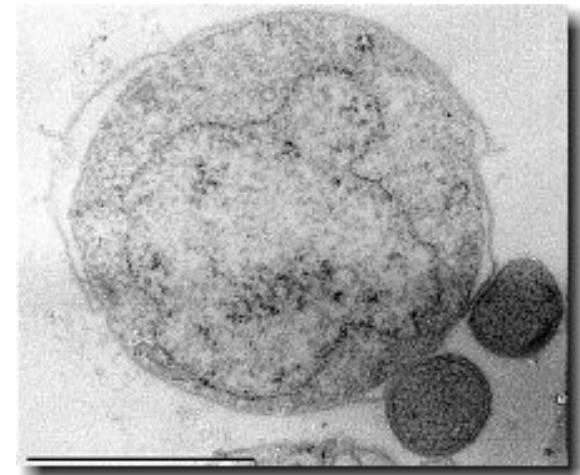


Other archaeal groups

- **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

Nanoarchaeum equitans

- *Nanoarchaeum equitans* is a species of marine Archaea “parasite” that was discovered in 2002 in a hydrothermal vent off the coast of Iceland
- *Nanoarchaeum* appears to be an obligate symbiont on the archaeon *Ignicoccus*; it must be in contact with the host organism to survive. It cannot synthesize lipids but obtains them from its host. Whether it obtains energy from biological molecules imported from *Ignicoccus*, or whether it receives ATP directly is currently unknown
- Its cells are only 400 nm in diameter, making it one of the smallest known cellular organisms, and the smallest known archaeon
- *N. equitans*' genome consists of a single circular chromosome of 0.49 Mbp, coding for 540 genes



Reinhard Rachel and Harald Huber

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>