Prokaryote classification and diversity

Different groups of prokaryotes. Evolutionary relationships of bacteria and archaea. Extremophiles.

Key points:

The two prokaryote domains, Bacteria and Archaea, split from each other early in the evolution of life.

Bacteria are very diverse, ranging from disease causing pathogens to beneficial photosynthesizers and symbionts.

Archaea are also diverse, but none are pathogenic and many live in extreme environments.

A DNA sequencing approach called metagenomics lets scientists identify new species of bacteria and archaea, including ones that can't be cultured.

Prokaryotes, which include both bacteria and archaea, are found almost everywhere – in every ecosystem, on every surface of our homes, and inside of our bodies! Some live in environments too extreme for other organisms, such as hot vents on the ocean floor.

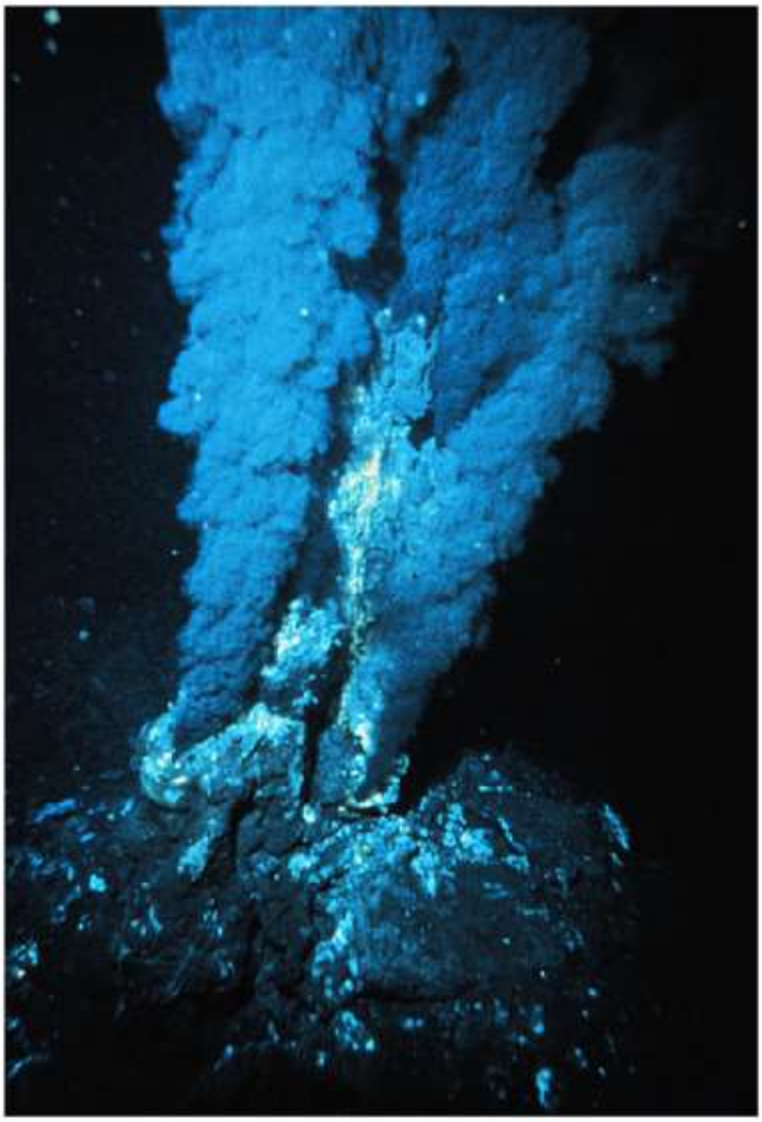


Image credit: "Black smoker in Atlantic ocean," by P. Rona (public domain).

Although they are found all around us, prokaryotes can be hard to detect, count, and classify. The prokaryotic species we know of today are a tiny fraction of all prokaryotic species thought to exist. In fact, the very idea of a “species” becomes complicated in the world of prokaryotes!

In this article, we'll first look at major groups of prokaryotes. Then, we'll explore why it’s often tricky to identify and classify them. Finally, we'll see how DNA sequencing methods are helping us get a better picture of the prokaryotes around us.

A prokaryote "family tree"

For a long time, all prokaryotes were classified into a single domain (the largest taxonomic grouping). However, work by microbiologist Carl Woese in the 1970s showed that prokaryotes are divided into two distinct lineages, or lines of descent: Archaea and Bacteria. Today, these groups are considered to form two out of three domains of life. The third domain (Eukarya) includes all eukaryotes, such as plants, animals, and fungi.

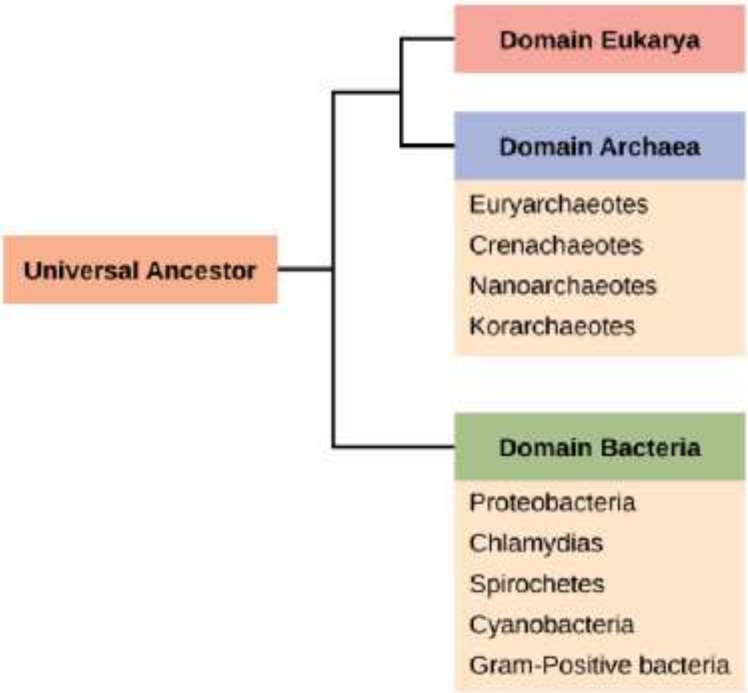


Image credit: "Structure of prokaryotes: Figure 3," by OpenStax College, Biology (CC BY 3.0).

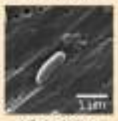
Since splitting off from one another millions of years ago, both Bacteria and Archaea have split off into many groups and species.

Bacteria

Domain Bacteria contains 5 major groups:

proteobacteria, chlamydiae(s), spirochetes, cyanobacteria, and gram-positive bacteria.

The proteobacteria are subdivided into five groups, alpha through epsilon. Species in these groups have a wide range of lifestyles. Some are symbiotic with plants, others live in hot vents deep under the sea, and others yet cause human diseases, such as stomach ulcers (Helicobacter pylori) and food poisoning (Salmonella).

Bacteria of Phylum Proteobacteria		
Class	**Representative organisms**	**Representative micrograph**
Alpha Proteobacteria Some species are photoautotrophic but some are symbionts of plants and animals and others are pathogens. Eukaryotic mitochondria are thought be derived from bacteria in this group.	*Rhizobium* Nitrogen-fixing endosymbiont associated with the roots of legumes *Rickettsia* Obligate intracellular parasite that causes typhus and Rocky Mountain Spotted Fever (but not rickets, which is caused by Vitamin C deficiency)	 *Rickettsia rickettsia*, stained red, grow inside a host cell.
Beta Proteobacteria This group of bacteria is diverse. Some species play an important role in the nitrogen cycle.	*Nitrosomas* Species from this group oxidize ammonia into nitrite. *Spirillum minus* Causes rat-bite fever	 *Spirillum minus*
Gamma Proteobacteria Many are beneficial symbionts that populate the human gut, but others are familiar human pathogens. Some species from this subgroup oxidize sulfur compounds.	*Escherichia coli* Normally beneficial microbe of the human gut, but some strains cause disease *Salmonella* Certain strains cause food poisoning or typhoid fever *Yersinia pestis* Causative agent of Bubonic plague *Psuedomonas aeruginosa* Causes lung infections *Vibrio cholera* Causative agent of cholera *Chromatium* Sulfur-producing bacteria that oxidize sulfur, producing H_2S	 Vibrio cholera
Delta Proteobacteria Some species generate a spore-forming fruiting body in adverse conditions. Others reduce sulfate and sulfur.	*Myxobacteria* Generate spore-forming fruiting bodies in adverse conditions *Desulfovibrio vulgaris* Aneorobic, sulfate-reducing bacterium	 *Desulfovibrio vulgaris*
Epsilon Proteobacteria Many species inhabit the digestive tract of animals as symbionts or pathogens. Bacteria from this group have been found in deep-sea hydrothermal vents and cold seep habitats.	*Campylobacter* Causes blood poisoning and intestinal inflammation *Heliobacter pylori* Causes stomach ulcers	 *Campylobacter*

The other four major groups of bacteria are similarly diverse. Chlamydia’s are pathogens that live inside host cells, while cyanobacteria are photosynthesizers that make much of Earth's oxygen. Spirochetes include both harmless bacteria and harmful ones, like the

Borrelia burgdorferi that cause Lyme disease. The same is true of Gram-positive bacteria, which range from probiotic bacteria in yogurt to the Bacillus anthraces that cause anthrax.

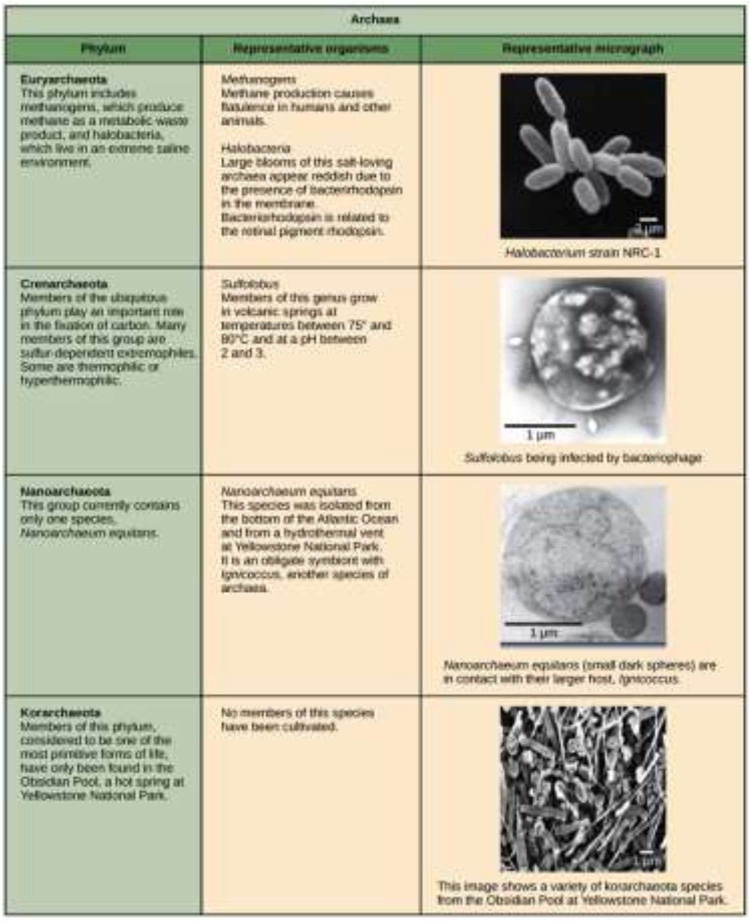
Bacteria: Chlamydia, Spirochaetae, Cyanobacteria, and Gram-positive		
Phylum	**Representative organisms**	**Representative micrograph**
Chlamydias All members of this group are obligate intracellular parasites of animal cells. Cells walls lack peptidoglycan.	*Chlamydia trachomatis* Common sexually transmitted disease that can lead to blindness	 In this pap smear, *Chlamydia trachomatis* appear as pink inclusions inside cells.
Spirochetes Most members of this species, which has spiral-shaped cells, are free-living aneaerobes, but some are pathogenic. Flagella run lengthwise in the periplasmic space between the inner and outer membrane.	*Treponema pallidum* Causative agent of syphilis *Borrelia burgdorferi* Causative agent of Lyme disease	 *Treponema pallidum*
Cyanobacteria Also known as blue-green algae, these bacteria obtain their energy through photosynthesis. They are ubiquitous, found in terrestrial, marine, and freshwater environments. Eukaryotic chloroplasts are thought be derived from bacteria in this group.	*Prochlorococcus* Believed to be the most abundant photosynthetic organism on earth; responsible for generating half the world's oxygen	 *Phormidium*
Gram-positive Bacteria Soil-dwelling members of this subgroup decompose organic matter. Some species cause disease. They have a thick cell wall and lack an outer membrane.	*Bacillus anthracis* Causes anthrax *Clostridium botulinum* Causes Botulism *Clostridium difficile* Causes diarrhea during antibiotic therapy *Streptomyces* Many antibiotics, including streptomycin, are derived from these bacteria. *Mycoplasmas* These tiny bacteria, the smallest known, lack a cell wall. Some are free-living, and some are pathogenic.	 *Clostridium difficile*

Archaea

Domain Archaea contains 4 major groups. Intriguingly, so far, no archaea that are human pathogens have yet been discovered.

Archaea do live in our bodies and those of animals—for instance, in the gut—but all of them seem to be harmless or beneficial. Although there are hypotheses, no one yet knows exactly why archaea are all "friendly," i.e., why no disease-causing species have evolved.

Alongside the archaea that enjoy the comfy environment of the human gut, there are many extremophile species that live in much more inhospitable places. These include volcanic hot springs, undersea hot vents, and very salty places like the Dead Sea.



Archaea		
Phylum	Representative organisms	Representative micrograph
Euryarchaeota This phylum includes methanogens, which produce methane as a metabolic waste product, and halobacteria, which live in an extreme saline environment.	Methanogens Methane production causes flatulence in humans and other animals. Halobacteria Large blooms of this salt-loving archaea appear reddish due to the presence of bacterirhodopsin in the membrane. Bacteriorhodopsin is related to the retinal pigment rhodopsin.	1 µm *Halobacterium* strain NRC-1
Crenarchaeota Members of the ubiquitous phylum play an important role in the fixation of carbon. Many members of this group are sulfur-dependent extremophiles. Some are thermophilic or hyperthermophilic.	Sulfolobus Members of this genus grow in volcanic springs at temperatures between 75° and 80°C and at a pH between 2 and 3.	1 µm Sulfolobus being infected by bacteriophage
Nanoarchaeota This group currently contains only one species, *Nanoarchaeum equitans*.	*Nanoarchaeum equitans* This species was isolated from the bottom of the Atlantic Ocean and from a hydrothermal vent at Yellowstone National Park. It is an obligate symbiont with Ignicoccus, another species of archaea.	1 µm *Nanoarchaeum equitans* (small dark spheres) are in contact with their larger host, *Ignicoccus*.
Korarchaeota Members of this phylum, considered to be one of the most primitive forms of life, have only been found in the Obsidian Pool, a hot spring at Yellowstone National Park.	No members of this species have been cultivated.	1 µm This image shows a variety of korarchaeota species from the Obsidian Pool at Yellowstone National Park.

The many "mystery prokaryotes"

For many years, the main approach to studying prokaryotes was to grow them in the lab. If an organism could be grown on an agar plate or in a liquid culture, then it could be studied, analysed, and added to our growing catalogue of prokaryotic species and strains.

Some prokaryotes, however, can't grow in a laboratory setting (at least, not under the conditions scientists have tried). In fact, an estimated 99% of bacteria and archaea are un-cultivable!

This represents a pretty huge gap in our understanding of what prokaryotes are out there. For context, there are 8.7 million known eukaryotic species. If the cultivability problem applied to eukaryotes in the same degree as prokaryotes, we would only know of 87,000 of these species. This would make for a very empty tree of life, and a very incomplete understanding of what eukaryotes (as a group) are like. For instance, we might know that there were animals, but be in the dark about plants or fungi!

What is a prokaryotic species?

In order to talk about finding prokaryotic species, we probably need to define what they are. This may seem like a basic question, but it's a complex and even controversial one if you're a microbiologist.

For eukaryotes, most scientists define a species as a group of organisms that can interbreed and have fertile offspring. This definition makes sense for species that reproduce sexually, but it doesn't work so well for organisms like bacteria. Bacteria reproduce asexually to make clones of themselves—they don't interbreed.

Scientists instead classify bacteria and archaea into taxonomic groups based on similarities in appearance, physiology, and genes. Many are given names using traditional Linnaean taxonomy, with a genus and species. Still, the question of how and whether prokaryotes should be grouped into species remains a topic of debate among scientists. The right “species concept” for these organisms is still a work in progress.

Metagenomics: A new window on microbes

Scientists estimate there may be millions of prokaryotic species (or species-like groups), but we know very little about most of them. This is starting to change thanks to large-scale DNA sequencing.
DNA sequencing makes it possible for scientists to study entire prokaryotic communities in their natural habitats – including the many prokaryotes that are uncultivable, and would previously have been "invisible" to researchers.

The collective genome of such a community is called its metagenome, and the analysis of metagenome sequences is known as metagenomics. Prokaryotic metagenomics is one of the areas of biology that I find coolest and most mysterious.

For example, a DNA sample can be taken from a hot spring microbial mat, such as the beautiful, multi-coloured mats found in Yellowstone National Park. Even a tiny sample from this rich community includes many, many individuals of different species.

By sequencing and analysing metagenome DNA samples, scientists can sometimes piece together entire genomes of previously unknown species. In other cases, they use sequence information from specific genes to figure out what types of prokaryotes are present (and how they are related to each other or to known species).