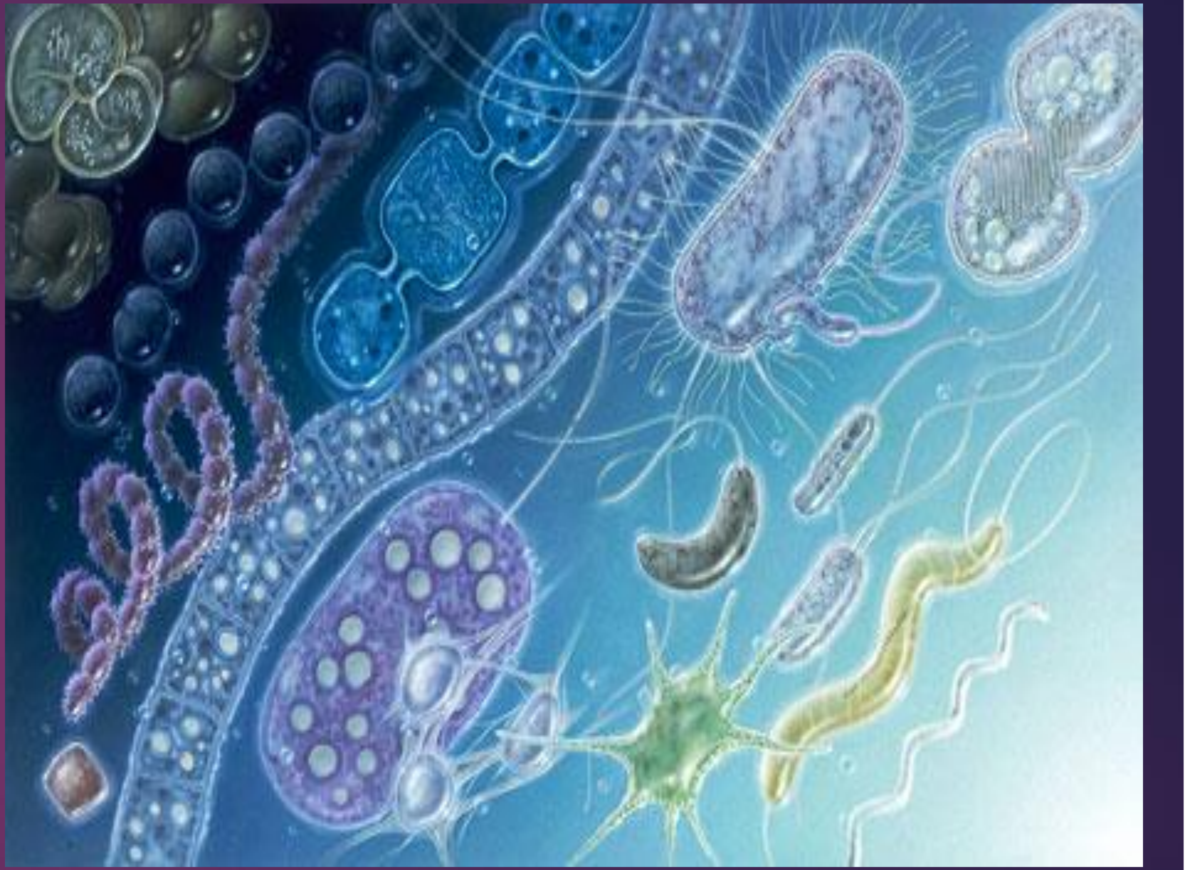
MICROBIAL EVOLUTION, TAXONOMY & BIODIVERITY



08062021

CONTENT

- THEORY OF EVOLUTION
- EVOLUTION OF PROKARYOTES AND EUKARYOTES
- TAXONOMY & CLASSIFICATION SYSTEMS
- LEVELS OF CLASSIFICATION
- DEFINITION OF "SPECIES"
- BINOMIAL NOMENCLATURE
- MAJOR CHARACTERISTICS USED IN TAXONOMY
- MICROBIAL PHYLOGENY
  - ARCHAEA
  - BACTERIA
  - EUKARYA

MICROBIAL EVOLUTION

Microbial evolution refers to the **genetically driven changes** that occur in **microorganisms** and that are retained over time. Some microbial changes can be in response to a **selective pressure**.

The best examples of this are the **various changes** that can occur in bacteria in **response** to the presence of **antibiotics**

EVOLUTION

- Evolution states that living things change gradually through million years and these evolvements result in various types of heritable structural and functional changes through many generations
- Evolution concept:
  1. All new species originate from pre-existing species
  2. Closely related organisms have similar features because they evolved from common ancestral forms

The first discovery of microbial fossils

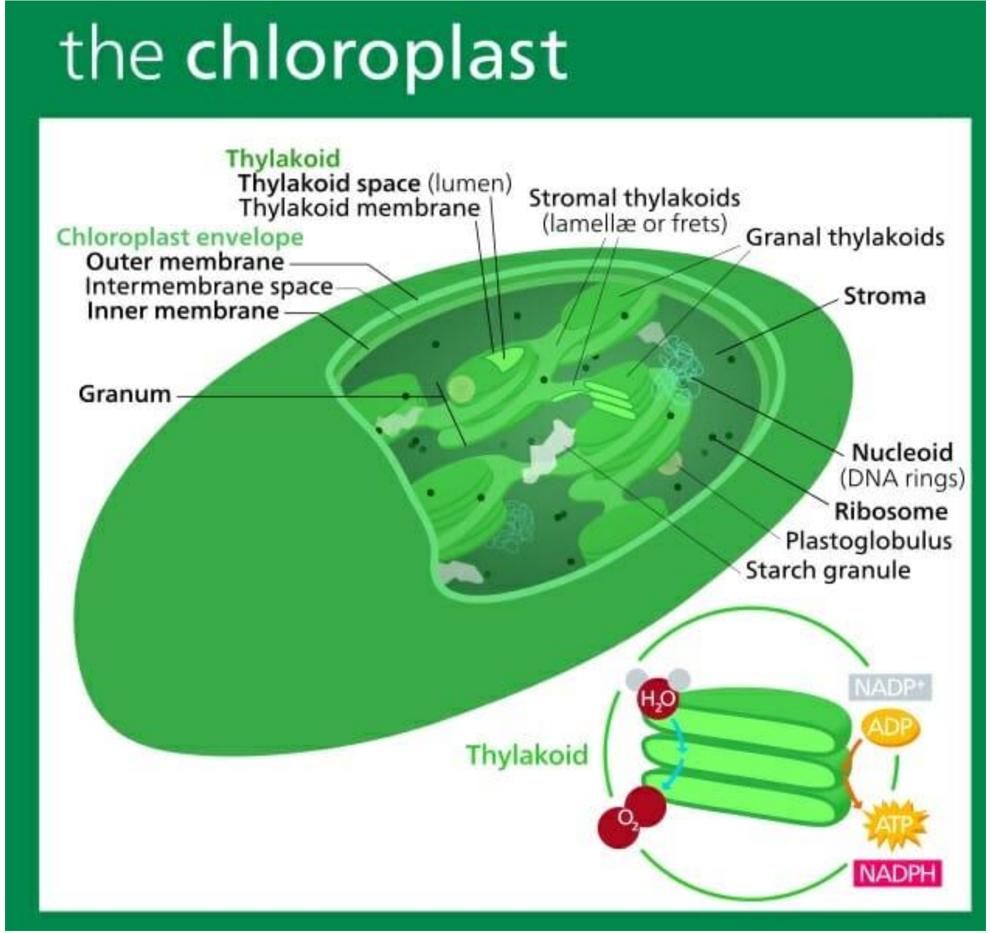
- First prokaryotes probably arose at least 3.5 to 3.8 billion years ago
  - ✓ cyanobacteria
- Fossilized microbial formation called stromatolites is found in sedimentary rock – evidence of life on earth
- **Stromatolites – layered rocks** formed by incorporation of **mineral sediments** into **microbial mats of photosynthetic bacteria**
- Evolutionary scientist believe that the layers of material were formed when mats of cyanobacteria are layered on top of each other, became mineralized

Evolution of prokaryotes

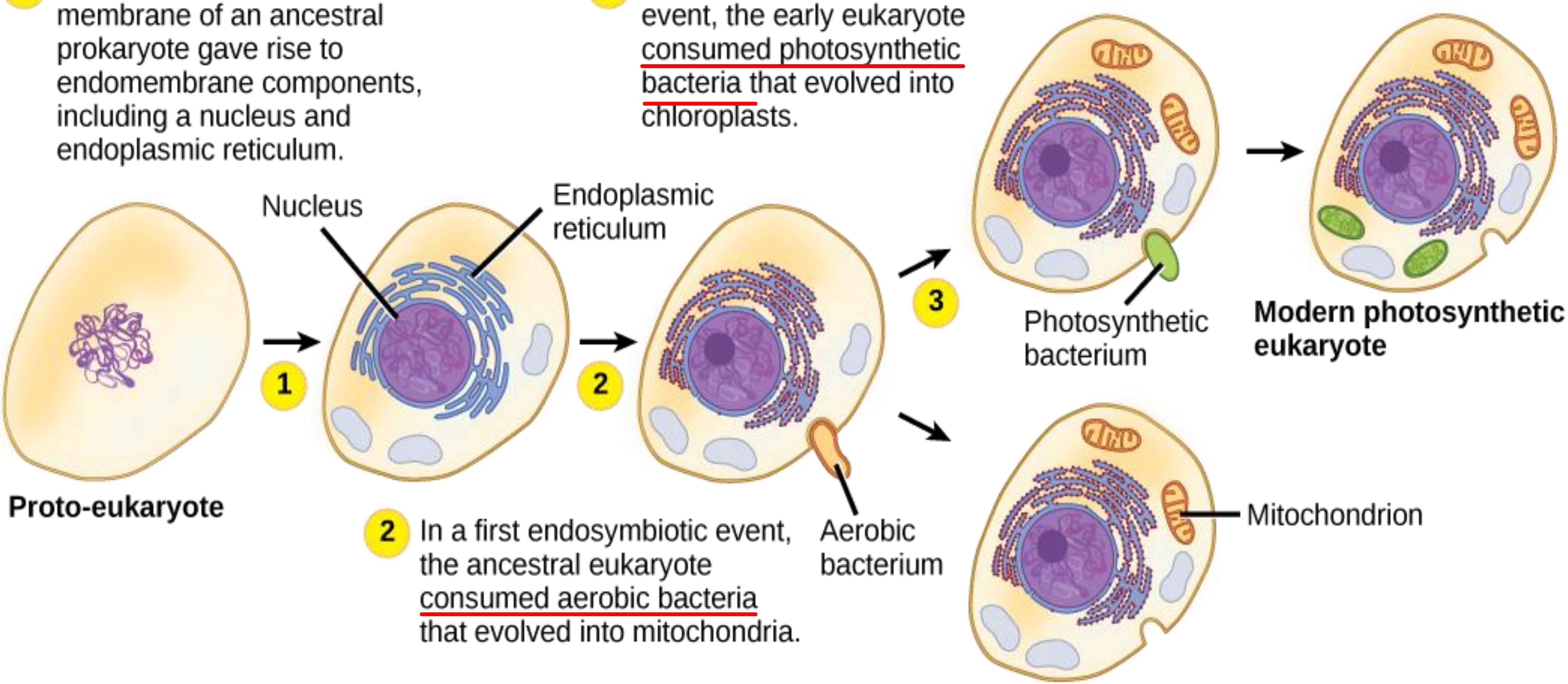
- The evolutionary history was studied primarily through fossil examination
  - Paleontology - the study of the history of life on Earth as based on fossils.
- This approach is useful to understand the evolution of plants and animals
- But, fossil cannot be used to explain microbial evolution
  - Microorganisms do not leaves behind fossils (majority)
  - They do not share any morphological traits with plants & animals
- The evolution of microorganism was explained after the structure of DNA was discovered and the evolutionary history is recorded in DNA sequences
  - Genealogy - the study of families, family history, and the tracing of their lineages.

Evolution of eukaryotes

- Eukaryotes arose from prokaryotes through fusion of ancient bacteria and archaea ~ 1.4 billion years ago
  - endosymbiotic hypothesis
- Organelles
  - chloroplasts arose from free-living phototrophic bacterium that entered symbiotic relationships with primitive eukaryotes
  - mitochondria arose by similar mechanism



The ENDOSYMBIOTIC THEORY



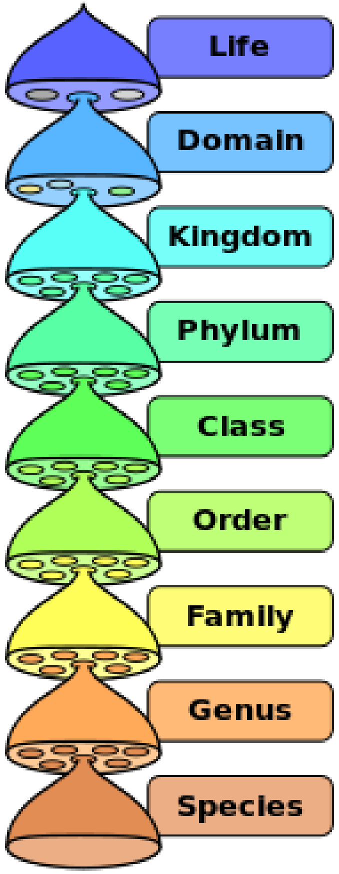
1 Infoldings in the plasma membrane of an ancestral prokaryote gave rise to endomembrane components, including a nucleus and endoplasmic reticulum.

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.

Taxonomy

- science of biological classification
- consists of three separate but interrelated parts
  - **classification** – arrangement of organisms into groups (taxa; s.,taxon)
  - **nomenclature** – the process of assigning names to the various taxonomic rankings of each microbial species
  - **identification** – determination of taxon to which an isolate belongs



Importance of Taxonomy

- allows scientists to organize huge amounts of knowledge
- allows scientists to make predictions and frame hypotheses about organisms
- places organisms into meaningful, useful groups, with precise names, thus facilitating scientific communication
- essential for accurate identification of organisms

Classification system

Old classification system

- Natural classification based on anatomical characteristics
- Arranges organisms into groups whose members share many characteristics

  e.g. human is classified as mammals because they have hair, self-regulating body temperature, and milk-producing mammary gland

- Most desirable system because it reflects biological nature of organisms
- However, it is only suitable for higher organisms (animals, plants)

Current practice

- Polyphasic taxonomy is used to determine the genus and species of newly isolated microbes.
- This approach includes these features
  - Phenetic
  - Phylogenetic
  - Genotypic

Classification system

Phenetic classification

- phenotypes is the observable characteristics of organism
- organisms are classified based on mutual similarity of phenotypes. E.g. flagella involve in motility of certain microorganism
- can reveal possible evolutionary relationships, but it is not enough

Phylogenetic / phyletic classification

- To compare the organisms based on the basis of evolutionary relationship
- phylogeny refers to the evolutionary development of a species
- usually based on direct comparison of genetic material and gene products
- Current theories based largely on characterization of rRNA sequences

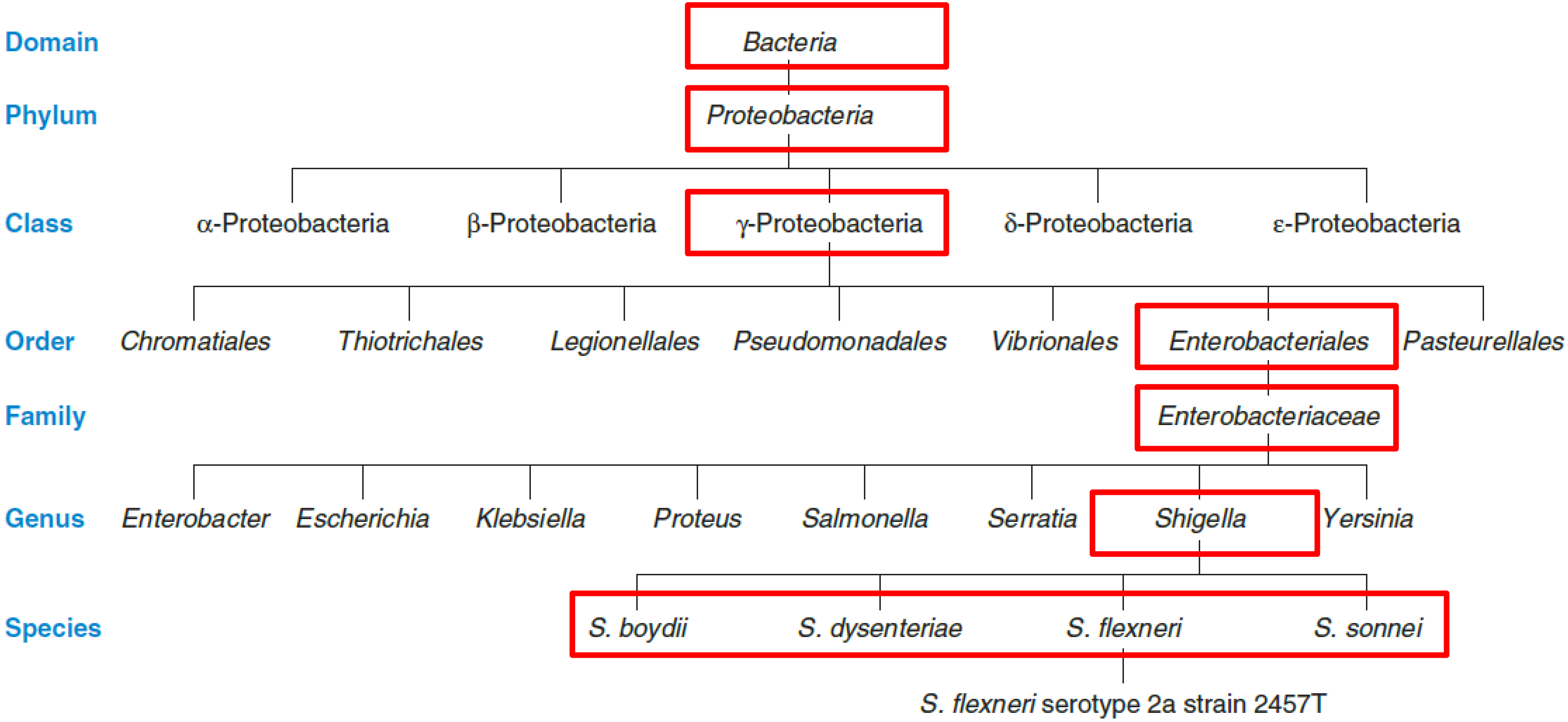
Genotypic classification

- Compare genetic similarity between organisms
- Individual or whole genome can be compared
- Bacteria that have 70% homologous genome belong to the same species

Levels of Classification

- Taxon is a group or “level” of classification
- Hierarchical; broad divisions are divided up into smaller divisions:
    - Domain
    - Kingdom
    - Phylum (Called “Division” by botanists)
    - Class
    - Order
    - Family
    - Genus (plural: Genera)
    - Species (Both singular & plural)

Domain	Bacteria
Phylum	Proteobacteria
Class	Gammaproteobacteria
Order	Enterobacteriales
Family	Enterobacteriaceae
Genus	*Escherichia*
Species	*Escherichia coli*



Domain *Bacteria*

Phylum *Proteobacteria*

Class α-Proteobacteria β-Proteobacteria γ-Proteobacteria δ-Proteobacteria ε-Proteobacteria

Order *Chromatiales* *Thiotrichales* *Legionellales* *Pseudomonadales* *Vibrionales* *Enterobacteriales* *Pasteurellales*

Family *Enterobacteriaceae*

Genus *Enterobacter* *Escherichia* *Klebsiella* *Proteus* *Salmonella* *Serratia* *Shigella* *Yersinia*

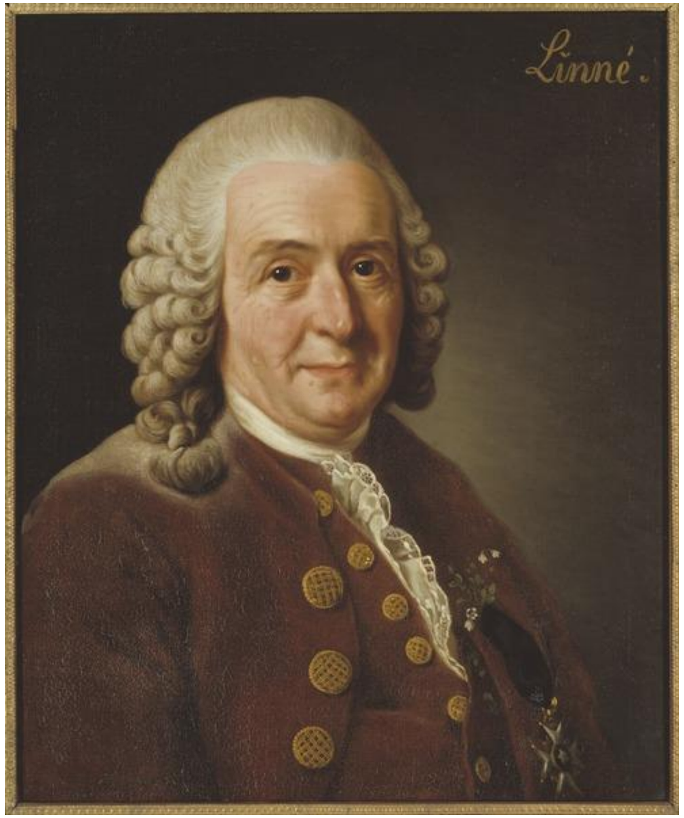
Species *S. boydii* *S. dysenteriae* *S. flexneri* *S. sonnei*

S. flexneri serotype 2a strain 2457T

Figure 19.1 Hierarchical Arrangement in Taxonomy. In this example, members of the genus *Shigella* are placed within higher taxonomic ranks. Not all classification possibilities are given for each rank to simplify the diagram. Note that -*ales* denotes order and -*ceae* indicates family.

Binomial system of nomenclature

- Carolus Linnaeus is the father of taxonomy
- The method of assigning the scientific name of different organisms.
- The scientific name is always a combination of the generic (genus) name followed by the species name
- each organism has two names
    1. genus name - italicized and capitalized (e.g. *Escherichia*)
    2. species epithet – italicized but not capitalized (e.g. *coli*)
- Can be abbreviated after first use (e.g., *E. coli*)



Definition of “Species”

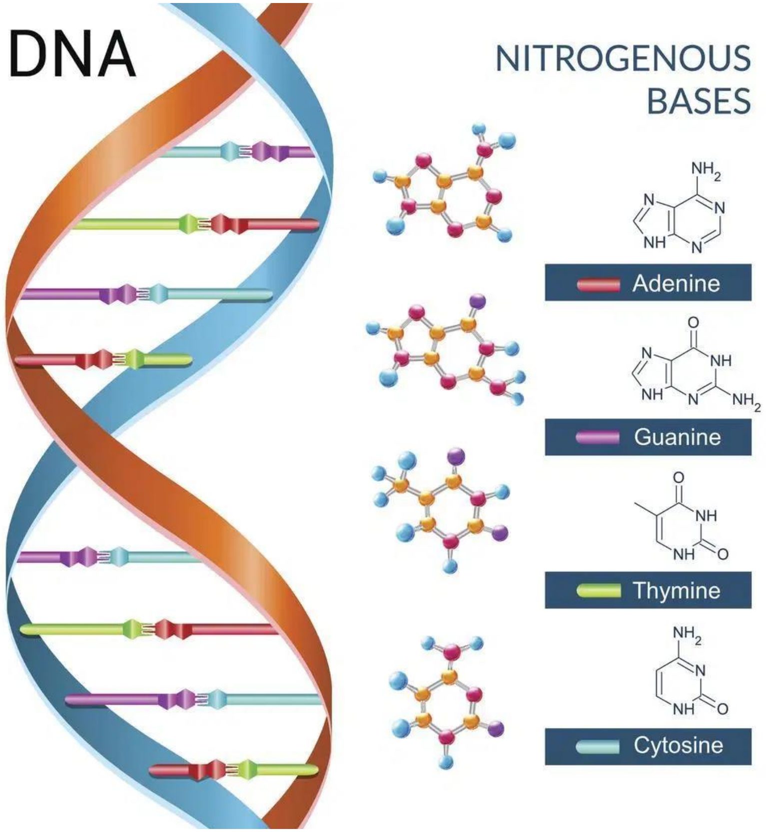
- The “basic unit” of taxonomy, representing a specific, recognized type of organism
- For sexually reproducing organisms (e.g.plants/animals), a “species” is defined as a group of organisms, in which any two individuals of the appropriate sexes/ mating types can produce fertile offspring
- However, this definition fails for many microbial species (including bacteria), because they do not reproduce sexually

Domain	Bacteria
Phylum	Proteobacteria
Class	Gammaproteobacteria
Order	Enterobacteriales
Family	Enterobacteriaceae
Genus	*Escherichia*
Species	*Escherichia coli*

How to define prokaryotic species?

Possible definitions:

- collection of strains that share many stable properties and differ significantly from other groups of strains
- collection of strains with **similar G + C composition** and **≥ 70% sequence similarity**
- collection of organisms that **share** the **same sequences** in their core **housekeeping genes** (genes that are required for the maintenance of basic cellular function, e.g ribosomes)



Definition of “Species”

- Definition of “**species**” in microbiology:
  - Classic definition: A **collection of microbial strains** that **share many properties** and **differ significantly from other groups** of strains
  - Species are identified by **comparison** with known “**type strains**”: well-characterized pure cultures; references for the identification of unknowns
  - There are several collections of type strains, including the American Type Culture Collection (**ATCC**)

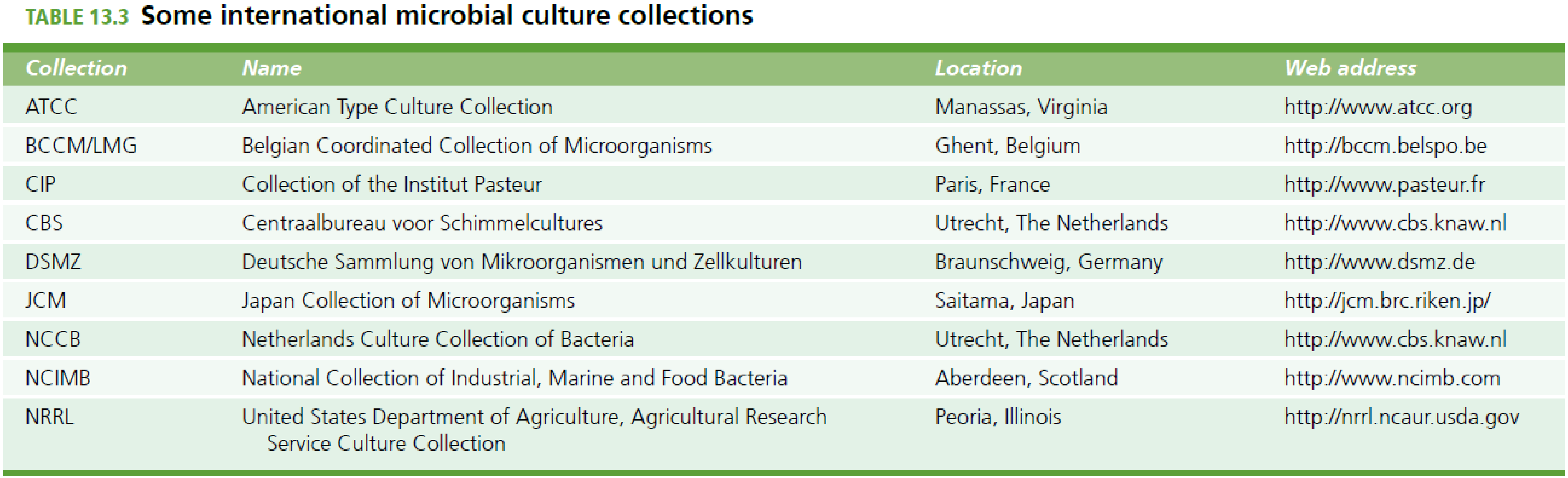
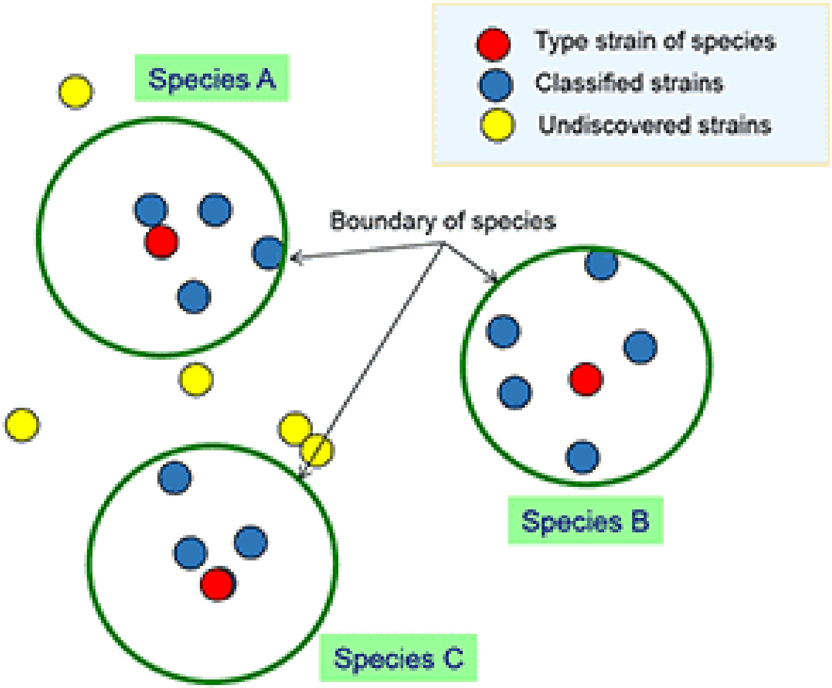


TABLE 13.3 Some international microbial culture collections

Collection	*Name*	*Location*	*Web address*
ATCC	American Type Culture Collection	Manassas, Virginia	http://www.atcc.org
BCCM/LMG	Belgian Coordinated Collection of Microorganisms	Ghent, Belgium	http://bccm.belspo.be
CIP	Collection of the Institut Pasteur	Paris, France	http://www.pasteur.fr
CBS	Centraalbureau voor Schimmelcultures	Utrecht, The Netherlands	http://www.cbs.knaw.nl
DSMZ	Deutsche Sammlung von Mikroorganismen und Zellkulturen	Braunschweig, Germany	http://www.dsmz.de
JCM	Japan Collection of Microorganisms	Saitama, Japan	http://jcm.brc.riken.jp/
NCCB	Netherlands Culture Collection of Bacteria	Utrecht, The Netherlands	http://www.cbs.knaw.nl
NCIMB	National Collection of Industrial, Marine and Food Bacteria	Aberdeen, Scotland	http://www.ncimb.com
NRRL	United States Department of Agriculture, Agricultural Research Service Culture Collection	Peoria, Illinois	http://nrrl.ncaur.usda.gov

What is a “strain”?

- A population of microbes **descended from a single individual** or pure culture
- It is a subgroup of a species with one or more characteristics that distinguish it other subgroups of the same species
- Different strains represent **genetic variability within a species**
- **Biovars:** Strains that differ in biochemical or physiological differences
- **Morphovars:** Strains that vary in morphology
- **Serovars:** Strains that vary in their antigenic properties
- Each strain is identified by a name, number, letter, etc. (E.g. *Lactobacillus acidophilus* LA-5)



Major characteristics used in taxonomy

- Different approaches are used in classifying and identifying new microorganism that have isolated and grown in pure culture

- 2 major characteristics used in taxonomy:
  1. **Classical characteristics** – The basis of phenetic classification, useful in identification & may provide phylogenetic information.
  2. **Molecular characteristics** – important for microbial identification & evolution

Classical Characteristics

Morphological characteristics

- Structural features depend on the gene expression (e.g. protein)
- Thus, morphological similarity indicates phylogenetic relatedness

Physiological & metabolic characteristics

- Directly related to the nature & activity of microbial enzymes & transport protein
- provide indirect comparison of microbial genome

Biochemical characteristics

- Bacterial fatty acids is a useful biochemical characteristics
- Same fatty acid profile in the same species

Ecological characteristics

- Life-cycle pattern
- symbiotic relationship
- ability to cause disease
- habitat preferences
- growth requirement

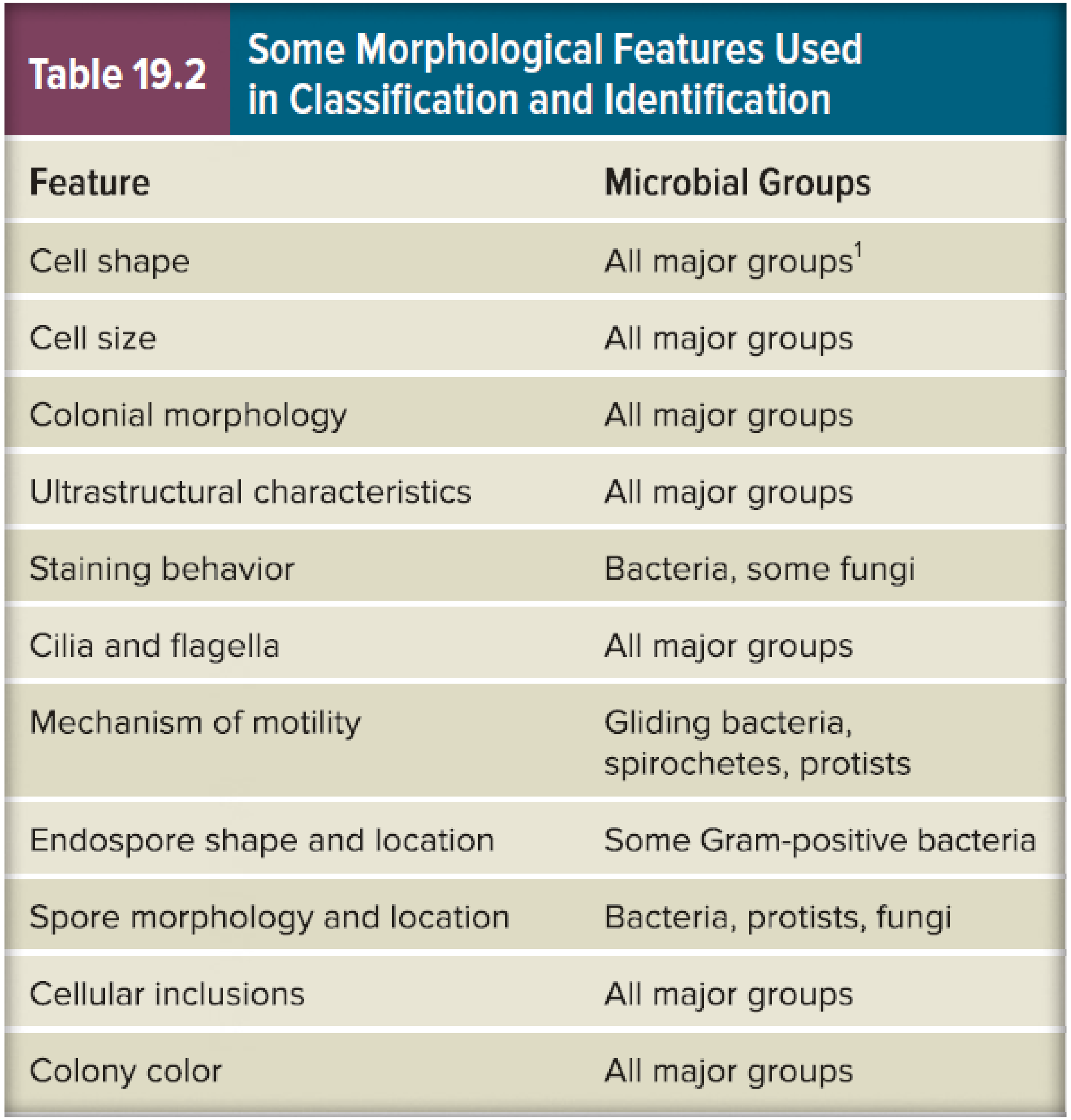


Table 19.2 Some Morphological Features Used in Classification and Identification

Feature	Microbial Groups
Cell shape	All major groups[1]
Cell size	All major groups
Colonial morphology	All major groups
Ultrastructural characteristics	All major groups
Staining behavior	Bacteria, some fungi
Cilia and flagella	All major groups
Mechanism of motility	Gliding bacteria, spirochetes, protists
Endospore shape and location	Some Gram-positive bacteria
Spore morphology and location	Bacteria, protists, fungi
Cellular inclusions	All major groups
Colony color	All major groups

[1] Used in classifying and identifying at least some bacteria, archaea, fungi, and protists.

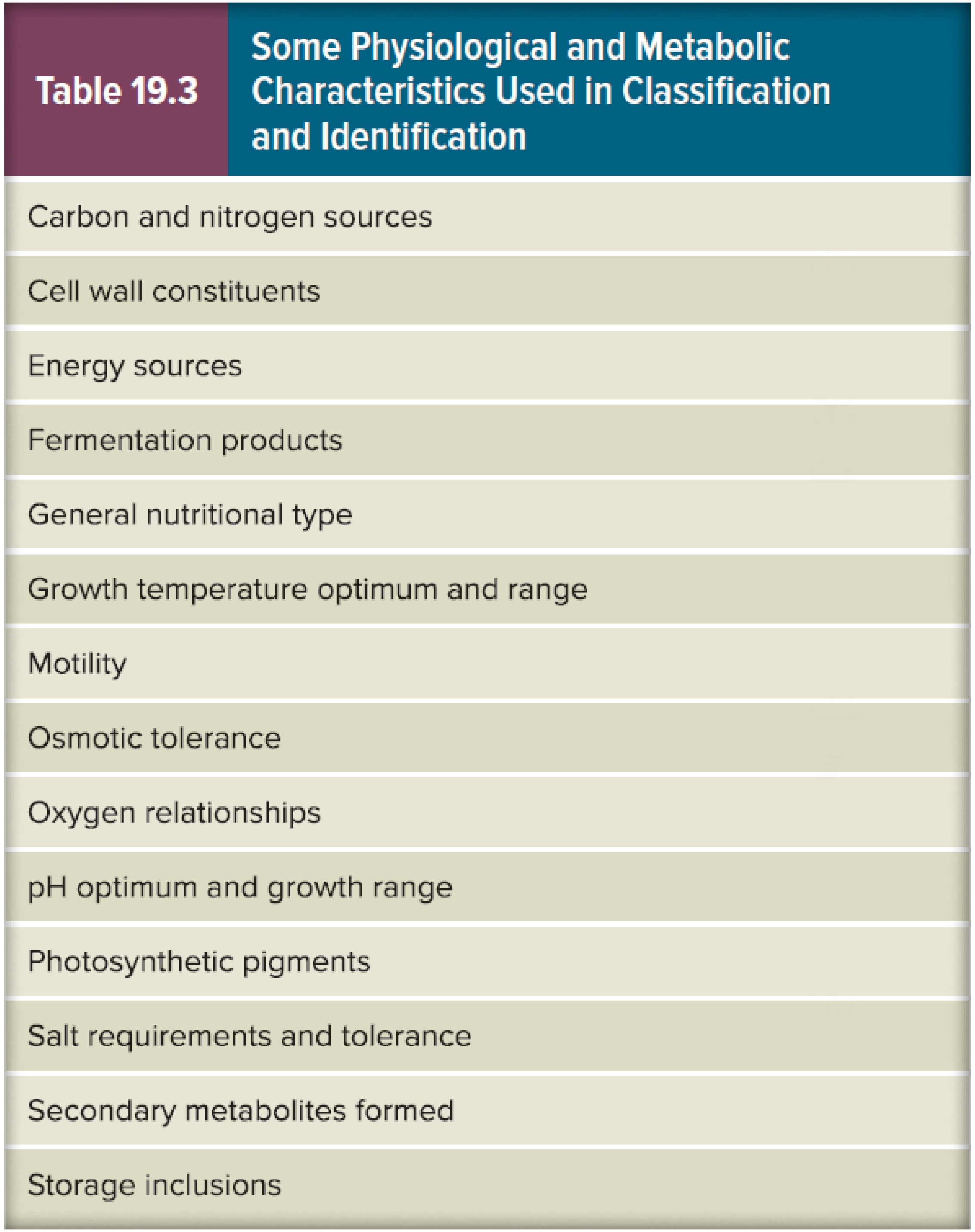


Table 19.3 Some Physiological and Metabolic Characteristics Used in Classification and Identification

Carbon and nitrogen sources
Cell wall constituents
Energy sources
Fermentation products
General nutritional type
Growth temperature optimum and range
Motility
Osmotic tolerance
Oxygen relationships
pH optimum and growth range
Photosynthetic pigments
Salt requirements and tolerance
Secondary metabolites formed
Storage inclusions

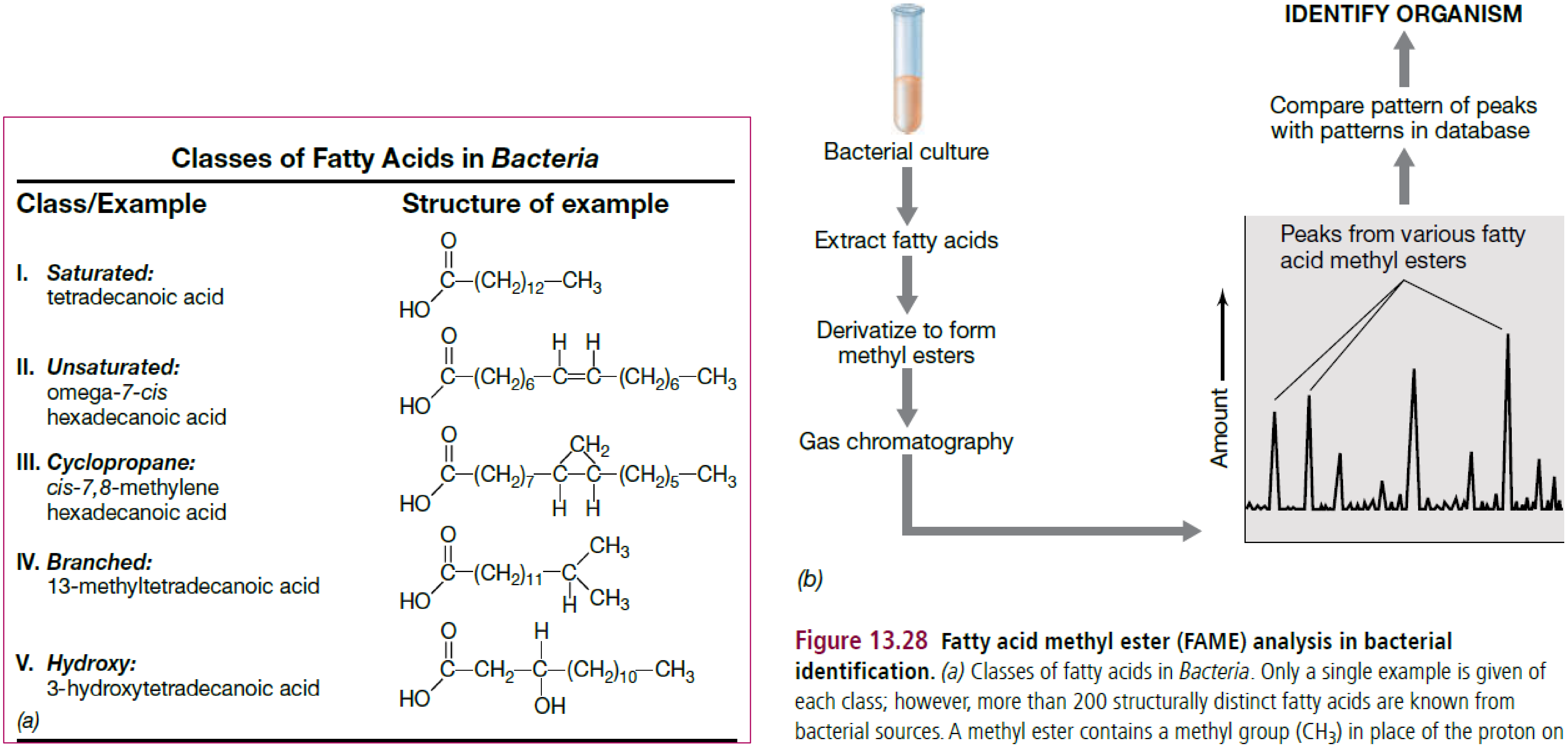


Figure 13.28 Fatty acid methyl ester (FAME) analysis in bacterial identification. *(a)* Classes of fatty acids in *Bacteria*. Only a single example is given of each class; however, more than 200 structurally distinct fatty acids are known from bacterial sources. A methyl ester contains a methyl group (CH_3) in place of the proton on the carboxylic acid group (COOH) of the fatty acid. *(b)* Procedure. Each peak from the gas chromatograph is due to one particular fatty acid methyl ester, and the peak height is proportional to the amount.

Molecular characteristics

- Nucleic acid base composition
  - Determination of the DNA base composition based on the G + C content
- Nucleic acid hybridization
  - Also known as DNA-DNA hybridization
- Nucleic acid sequencing
  - 16S ribosomal RNA
- Genomic fingerprinting
  - Digestion of rRNA gene sequences by the restriction enzymes
- Comparison of proteins
  - Serological test
  - Reaction between antibody and antigen (unknown m/o)

Nucleic acid base composition

- G + C content

$$\text{Mol\%}(G+C)=\frac{G+C}{G+C+A+T}\times 100\%$$

- Estimated by determining the melting temperature (T_m) of the DNA
- Higher G + C gives a higher melting temperature

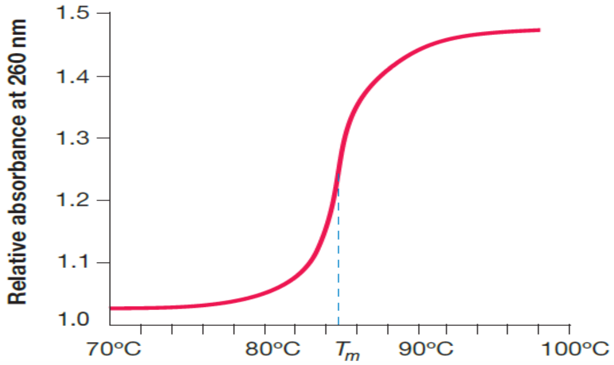


Figure 19.2 **A DNA Melting Curve.** The T_m is indicated.

- G + C content of strains within a particular species is constant & varies very little within a genus.

- Two microorganism are not closely-related if their G + C content differ by more than 10%

Nucleic acid hybridization

- Nucleic acid hybridization
  - By mixing ssDNA from two different species and determining the percentage of the DNA that can form dsDNA hybrids
  - The greater the percent hybridization, the closer the species
  - Two strains are considered as the same species if their DNA show at least 70% relatedness under optimal hybridization condition,

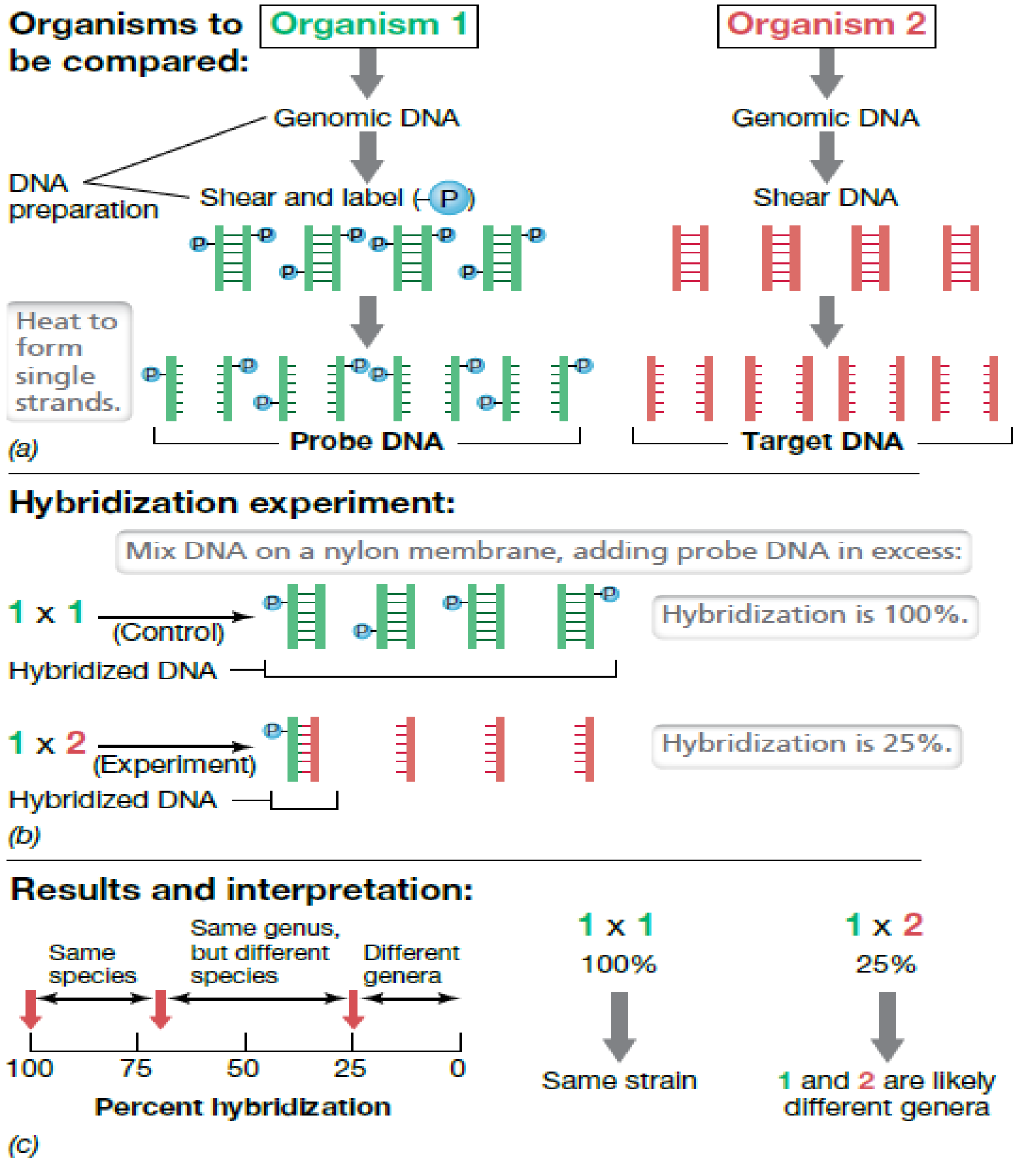
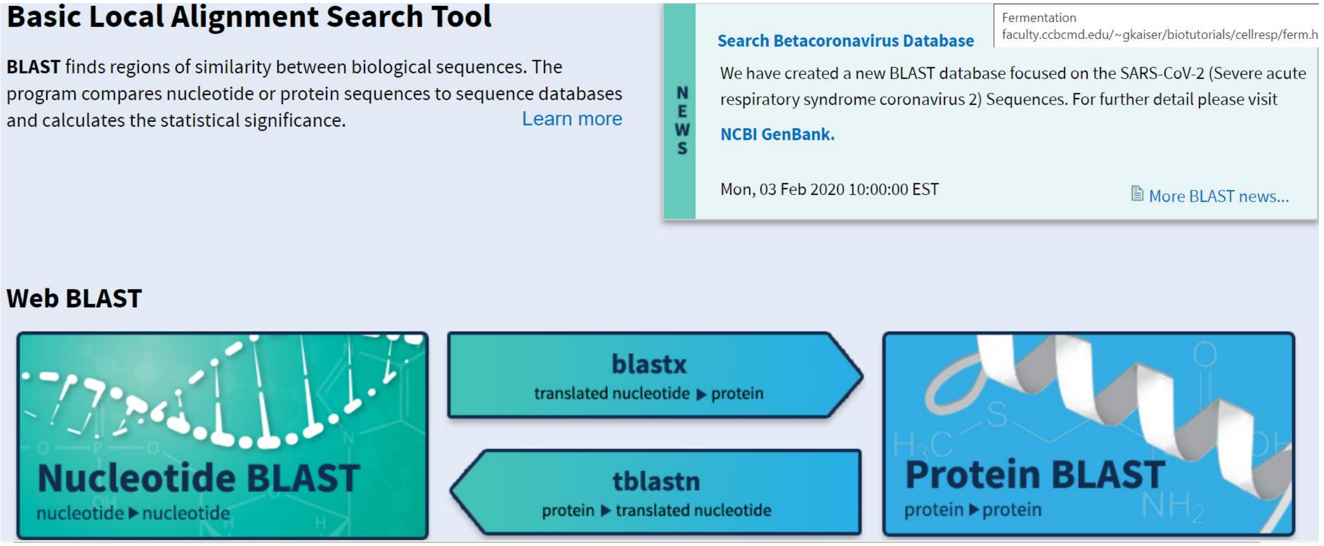


Figure 13.22 Genomic hybridization as a taxonomic tool. *(a)* Genomic DNA is isolated from the organisms to be compared and then sheared and denatured. Probe DNA is prepared from organism 1 by shearing, denaturing, and labeling the DNA (shown here as radioactive phosphate). *(b)* Sheared single-stranded target DNA from each genome is immobilized on a membrane and then hybridized with the labeled probe DNA from organism 1. Radioactivity in the hybridized DNA is measured. *(c)* Radioactivity in the control (organism 1 DNA hybridizing to itself) is taken as the 100% hybridization value.

Nucleic acid sequencing

- The nucleic acid sequence for the complete genome of several species is now available
- 16S rRNA (ribosomal RNA) sequences; comparison of these sequences has been extensively used to determine the phylogenetic relationships of microbial groups
- Polymerase chain reaction (PCR) is used to amplify regions of rRNA genes from the genome of organisms and sequence the DNA using automated sequencing technology.



Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

Learn more

NEWS

Search Betacoronavirus Database

Fermentation
faculty.ccbcmd.edu/~gkaiser/biotutorials/cellresp/ferm.h

We have created a new BLAST database focused on the SARS-CoV-2 (Severe acute respiratory syndrome coronavirus 2) Sequences. For further detail please visit **NCBI GenBank.**

Mon, 03 Feb 2020 10:00:00 EST

More BLAST news...

Web BLAST

Comparison of proteins

- Serological Tests
- Use group specific antiserum isolated from the plasma of animals that have been sensitized to the organism
  - The antiserum contains antibody proteins that react with antigens on the unknown organism.
  - The reaction can be detected by examining agglutination or by using sera labeled with colorimetric or fluorescent labels

- Advantages:
  - Highly specific
  - Does not usually require the organism to be isolated into pure culture
  - Can be used to identify organisms that can't be grown on medium

Bergey’s Manual of Systematic Bacteriology

- Bergey’s Manual of Determinative Bacteriology
  - published by David Bergey and 4 collegues in 1923.
  - Grouped bacteria into phenetic groups
  - Used as a reference guide for bacterial identification based on physiological and morphological traits
- Bergey’s Manual of Systematic Bacteriology (1st ed)
  - Published in 1984
  - Contained description of all bacterial and archaeal species
- Bergey’s Manual of Systematic Bacteriology (2nd ed)
  - Consist of 5 volumes, Published over a number of years starting in 2005,
  - Provides the morphology, physiology, growth condition, ecology
  - gives the most up-to-date phylogenic classification of prokaryotic organisms
- The classification in Bergey’s Manual is accepted by most microbiologists as the best consensus for prokaryotic taxonomy.

10 min break

THE MAJOR DIVISIONS OF LIFE

ARCHAEA

BACTERIA

EUKARYA

The tree of Life based on rRNA genes

(phylogenetic tree)

LUCA
- The Last universal common ancestor
- The root of phylogenetic tree

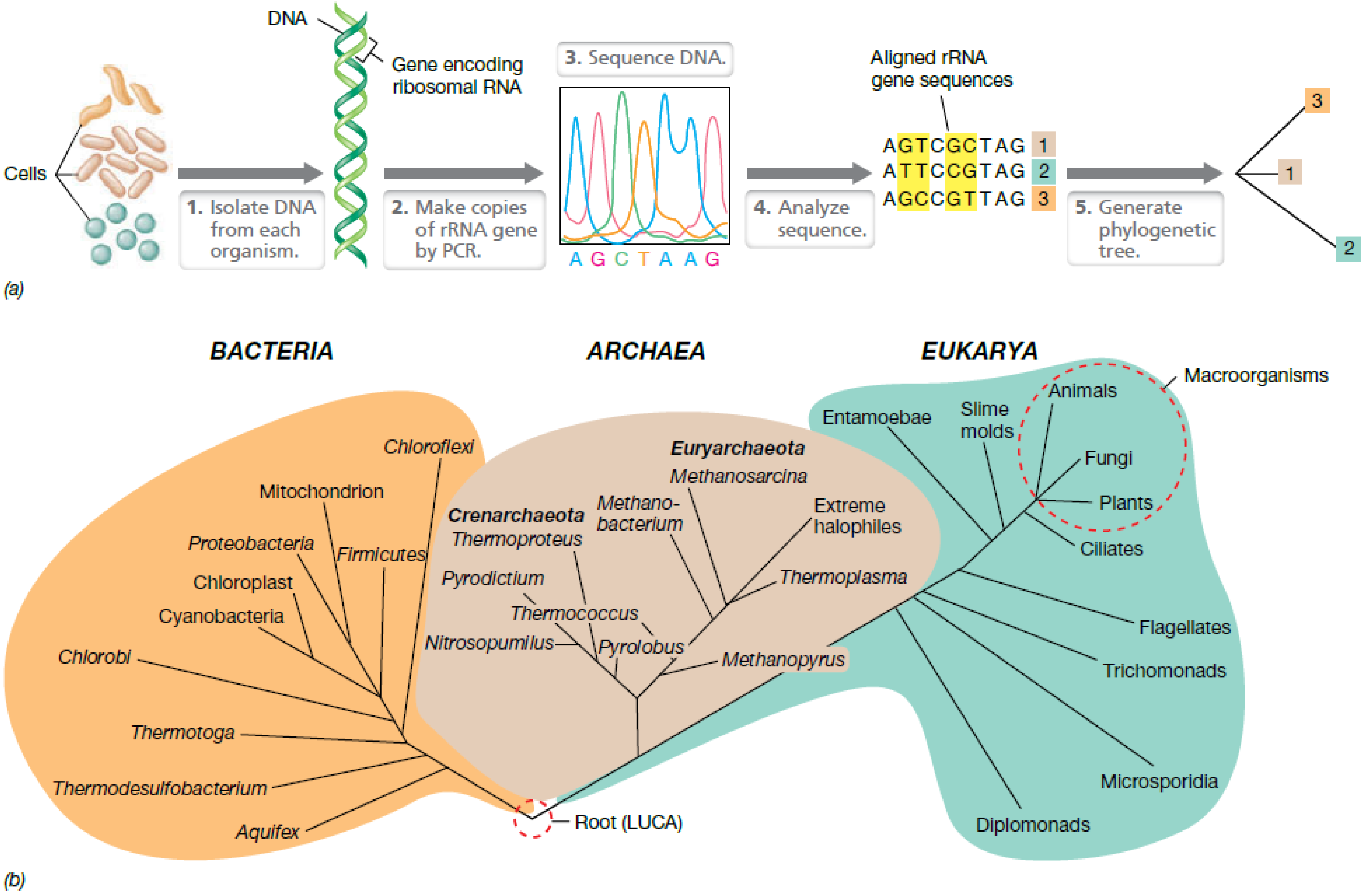
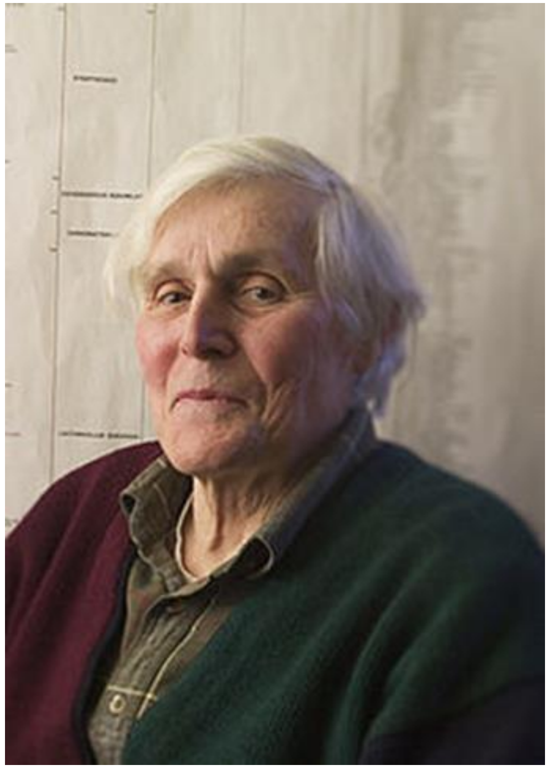


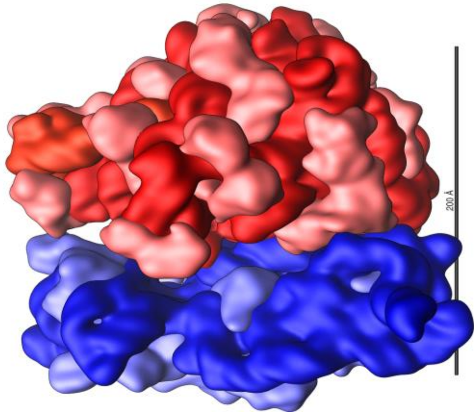
Figure 1.36 Evolutionary relationships and the phylogenetic tree of life. *(a)* The technology behind ribosomal RNA gene phylogenies. 1. DNA is extracted from cells. 2. Copies of the gene encoding rRNA are made by the polymerase chain reaction (PCR; Section 12.1). 3, 4. The gene is sequenced and the sequence aligned with sequences from other organisms. A computer algorithm makes pairwise comparisons at each base and generates a phylogenetic tree, 5, that depicts evolutionary relationships. In the example shown, the sequence differences are highlighted in yellow and are as follows: organism 1 versus organism 2, three differences; 1 versus 3, two differences; 2 versus 3, four differences. Thus organisms 1 and 3 are closer relatives than are 2 and 3 or 1 and 2. *(b)* The phylogenetic tree of life. The tree shows the three domains of organisms and a few representative groups in each domain.

Tree of Life

- Carl Woese (1928–2012) realized that the sequence of ribosomal RNA (rRNA) molecules and the genes that encode them could be used to infer evolutionary relationship between organisms.
- Woese is famous for defining the Archaea in 1977
- Current theories based largely on characterization of rRNA sequences
- 16S rRNA gene provides a species specific signature sequence which is useful for bacterial identification process



Professor in the University of Illinois (USA)



Ribosomes: Large (red) and small (blue) subunit fit together

- Genes encoding rRNAs are excellent for phylogenetic analysis because
  1. Universally distributed
  2. Functionally constant
  3. Highly conserved (slowly changing)
  4. Adequate length to provide a deep view of evolutionary relationship

- **16S rRNA**
  - A component of 30S small subunit of ribosomes
  - The genes coding for it are referred to as 16S rRNA gene
  - The region is conserved – slow rates of evolution
  - Used in constructing phylogenies

Domain Archaea

Overview of the Archaea

- Composed of 5 phyla
  - *Euryarchaeota, Crenarchaeota, Thaumarchaeota, Korarchaeota,* and *Nanoarchaeota*.
- Multiplication by binary fission, budding, fragmentation
- Inhabit extreme environments (extremophiles)
  - very high/low temp./pH, concentrated salts, completely anoxic
- Diverse physiology
  - Aerobic, facultative anaerobic, strictly anaerobic
- Diverse morphology
  - Spherical, rod-shape, spiral, cuboidal, irregular, etc.
- None of them are pathogenic

Microbial phylogeny in Domain Archaea

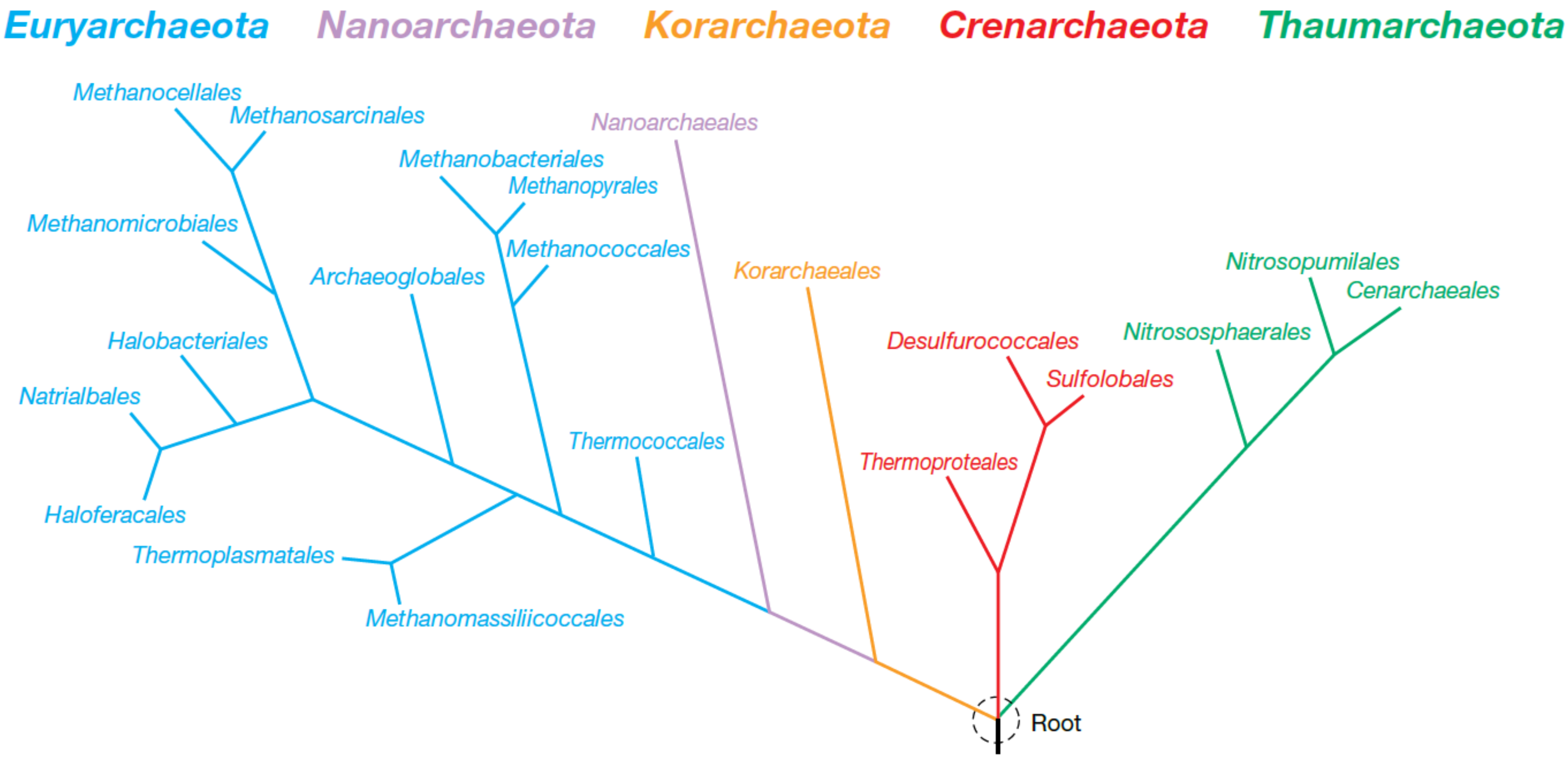


Figure 17.1 Schematic representation of the phylogeny of the major taxonomic orders within the domain *Archaea*. Each of the five archaeal phyla and their major orders are indicated in a different color.

Phylum *Crenarchaeota*

- Metabolically diverse thermophiles
- Contain thermophylic and hyperthermophilic sulfur-metabolizing archaea
- Most of the thermophiles are sulfur dependant
  - Sulfur as electron acceptor in anaerobic respiration or electron donor by litothrophs.
  - Grow in geothermal heated water that contain sulfur
  - Optimum growth temp. 105°C

Figure 20.8 Habitat for Thermophilic Archaea. The Sulfur Cauldron in Yellowstone National Park. The water is at its boiling point and very rich in sulfur. *Sulfolobus* spp. grow well in such habitats.

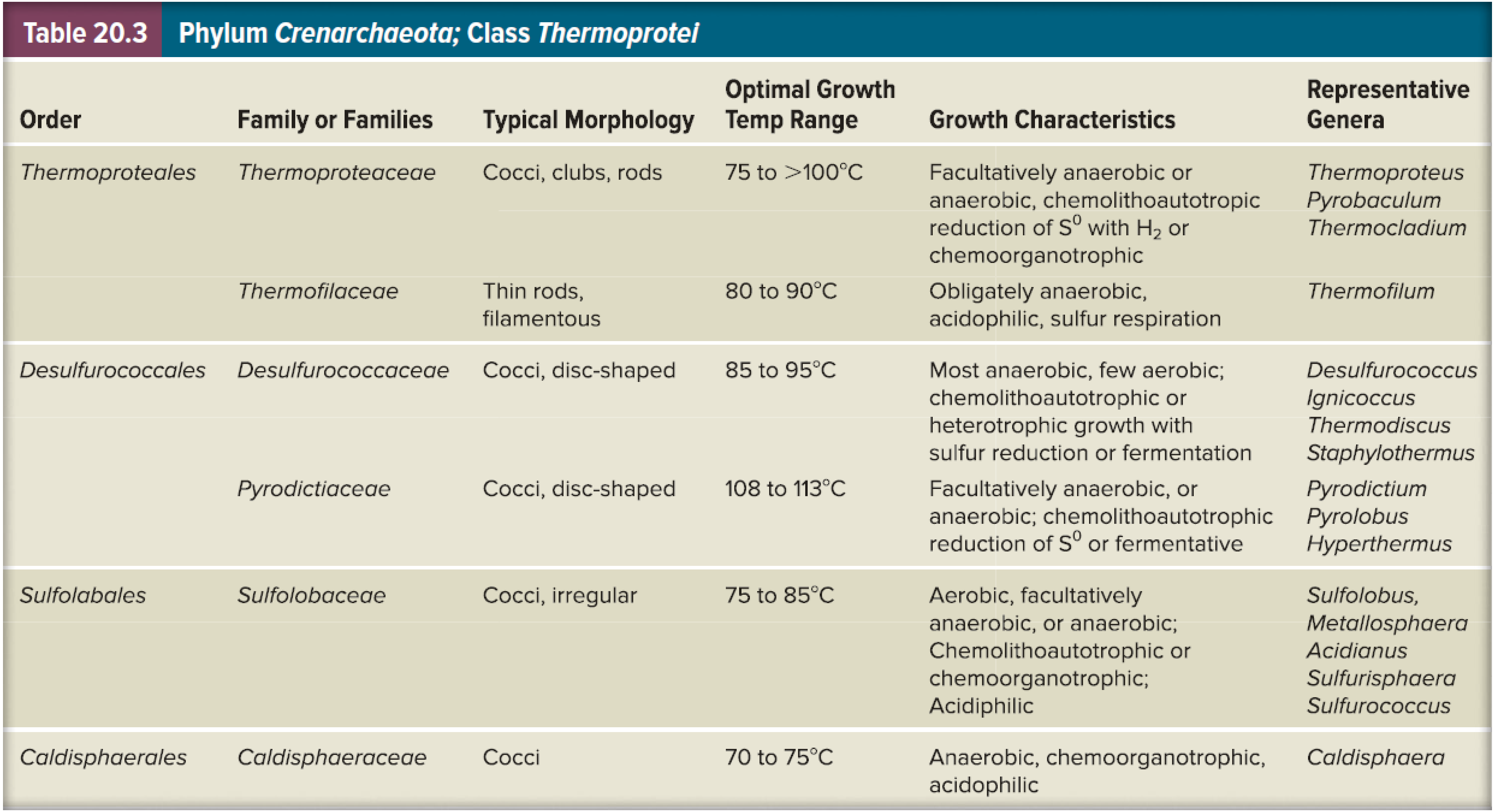


Table 20.3 Phylum *Crenarchaeota; Class Thermoprotei*

Order	Family or Families	Typical Morphology	Optimal Growth Temp Range	Growth Characteristics	Representative Genera
Thermoproteales	*Thermoproteaceae*	Cocci, clubs, rods	75 to >100°C	Facultatively anaerobic or anaerobic, chemolithoautotropic reduction of S^0 with H_2 or chemoorganotrophic	*Thermoproteus* *Pyrobaculum* *Thermocladium*
	Thermofilaceae	Thin rods, filamentous	80 to 90°C	Obligately anaerobic, acidophilic, sulfur respiration	*Thermofilum*
Desulfurococcales	*Desulfurococcaceae*	Cocci, disc-shaped	85 to 95°C	Most anaerobic, few aerobic; chemolithoautotrophic or heterotrophic growth with sulfur reduction or fermentation	*Desulfurococcus* *Ignicoccus* *Thermodiscus* *Staphylothermus*
	Pyrodictiaceae	Cocci, disc-shaped	108 to 113°C	Facultatively anaerobic, or anaerobic; chemolithoautotrophic reduction of S^0 or fermentative	*Pyrodictium* *Pyrolobus* *Hyperthermus*
Sulfolabales	*Sulfolobaceae*	Cocci, irregular	75 to 85°C	Aerobic, facultatively anaerobic, or anaerobic; Chemolithoautotrophic or chemoorganotrophic; Acidiphilic	*Sulfolobus,* *Metallosphaera* *Acidianus* *Sulfurisphaera* *Sulfurococcus*
Caldisphaerales	*Caldisphaeraceae*	Cocci	70 to 75°C	Anaerobic, chemoorganotrophic, acidophilic	*Caldisphaera*

Phylum *Euryarchaeota*

- Contains primarily methanogenic archaea, halophilic archaea, and thermophilic, sulfur-reducing archaea
- Methanogens are the largest group of Archea, strictly anaerobes (5 orders)
  - Generate methane from H_2 and CO_2 or organic molecule such as formate, acetate, and methanol
- Haloarcheae are extreme halophiles
  - Grow only in high-salinity habitats such as Dead sea in Jordan and Great Salt Lake in Utah.

The pond is extremely high in salt and mineral content. Haloarchea dominate the area and produce brilliant red pigments

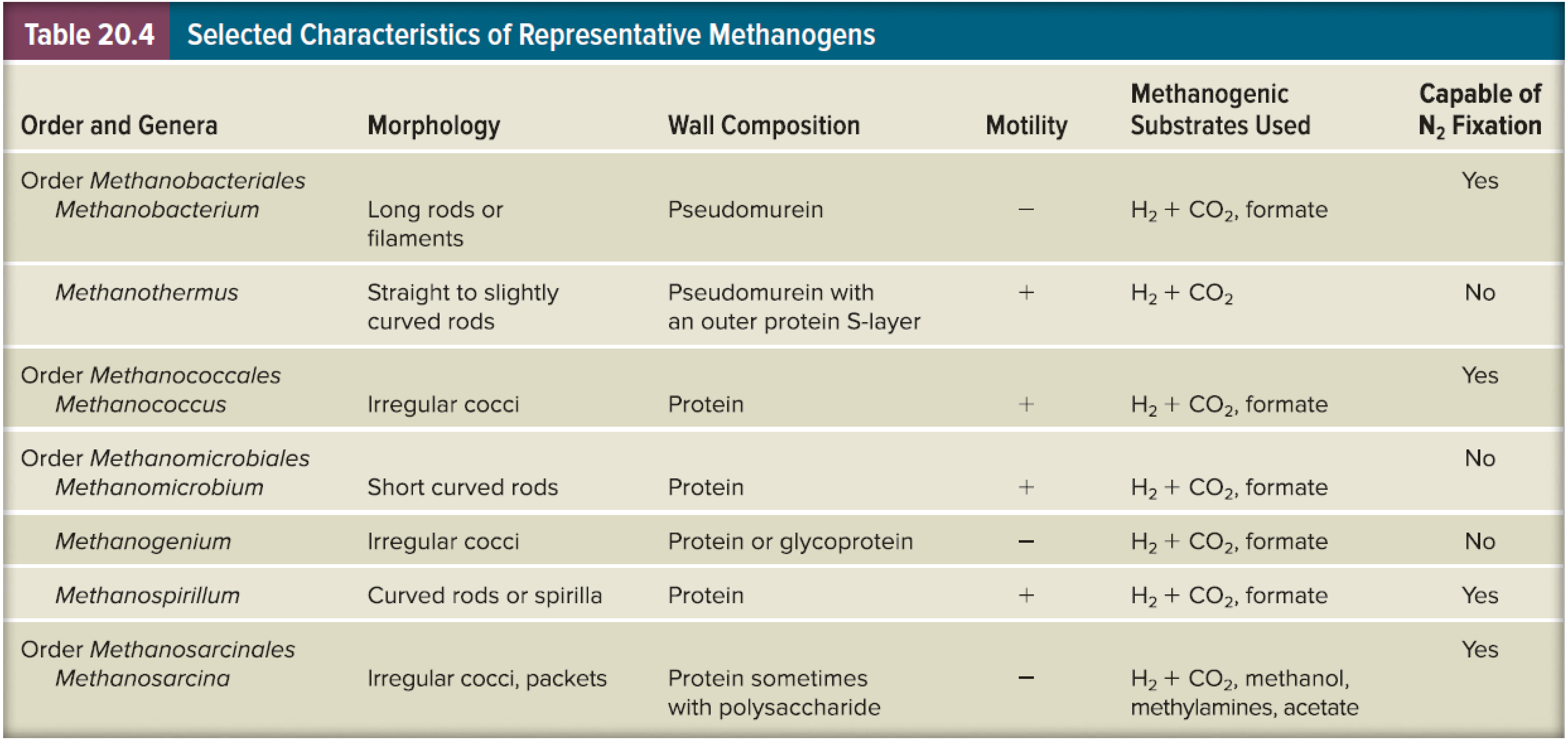


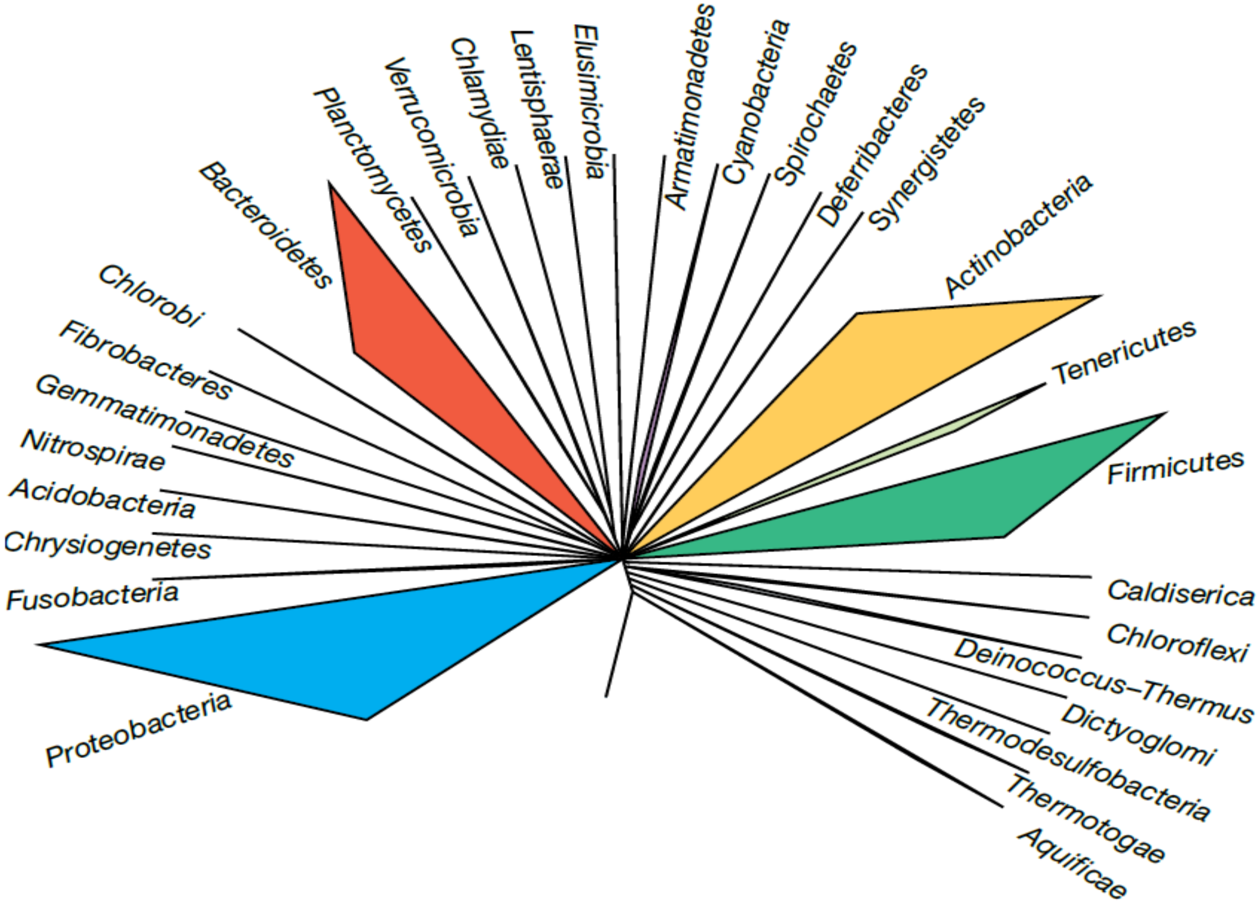
Table 20.4 Selected Characteristics of Representative Methanogens

Order and Genera	Morphology	Wall Composition	Motility	Methanogenic Substrates Used	Capable of N_2 Fixation
Order *Methanobacteriales*					Yes
Methanobacterium	Long rods or filaments	Pseudomurein	–	$H_2 + CO_2$, formate	
Methanothermus	Straight to slightly curved rods	Pseudomurein with an outer protein S-layer	+	$H_2 + CO_2$	No
Order *Methanococcales*					Yes
Methanococcus	Irregular cocci	Protein	+	$H_2 + CO_2$, formate	
Order *Methanomicrobiales*					No
Methanomicrobium	Short curved rods	Protein	+	$H_2 + CO_2$, formate	
Methanogenium	Irregular cocci	Protein or glycoprotein	–	$H_2 + CO_2$, formate	No
Methanospirillum	Curved rods or spirilla	Protein	+	$H_2 + CO_2$, formate	Yes
Order *Methanosarcinales*					Yes
Methanosarcina	Irregular cocci, packets	Protein sometimes with polysaccharide	–	$H_2 + CO_2$, methanol, methylamines, acetate	

DOMAIN BACTERIA

Overview of domain Bacteria

- There are over 80 phyla in Bacteria based on the analyses of 16S rRNA gene sequences from natural environments.
- Major phyla of bacteria that have cultivated species
  - *Proteobacteria*
  - *Firmicutes*
  - *Actinobacteria*
  - *Bacteroidetes*



(a) **Major phyla of *Bacteria***

Phylum *Proteobacteria*

- The largest group of gram-negative bacteria
- Extremely complex group, with over 400 genera and 1300 named species
- Proteobacteria constitute the majority of known bacteria of medical, industrial, and agricultural significance.
- All major nutritional types are represented: phototrophy, heterotrophy, and several types of chemolithotrophy
- Sometimes called the "**purple bacteria**," although very few are purple; the term refers to a hypothetical purple **photosynthetic bacterium** from which the group is believed to have evolved

Phylum *Proteobacteria*

Divided into 5 classes:

- Alphaproteobacteria (α)
  - Purple nonsulfur bacteria, *Rickettsia, Rhizobium,*
- Betaproteobacteria (β)
- Gammaproteobacteria (γ)
  - Purple sulfur bacteria
- Deltaproteobacteria (δ)
  - Sulfate or sulfur-reducing bacteria
- Epsilonproteobacteria (ε)
  - Include genera: *Camplylobacter* and *Helicobacter*

Phylum *Proteobacteria*

- Significant groups and genera include:
  - Photosynthetic genera such as *Rhodospirillum* (a purple non-sulfur bacterium) and *Chromatium* (a purple sulfur bacterium)
  - Sulfur chemolithotrophs, genera *Thiobacillus* and *Beggiatoa*
  - Nitrogen chemolithotrophs (nitrifying bacteria), genera Nitrobacter and *Nitrosomonas*
  - Other chemolithotrophs, genera *Alcaligenes, Methylobacilllus, Burkholderia*
  - *The family Enterobacteriaceae, the "Gram-negative enteric bacteria," which includes genera Escherichia, Proteus, Enterobacter, Klebsiella, Salmonella, Shigella, Serratia, and others*
  - *The family Pseudomonadaceae, which includes genus Pseudomonas and related genera*
  - *Other medically important Proteobacteria include genera Haemophilus, Vibrio, Campylobacter, Helicobacter, Rickessia, Brucella*

Phylum *Firmicutes*

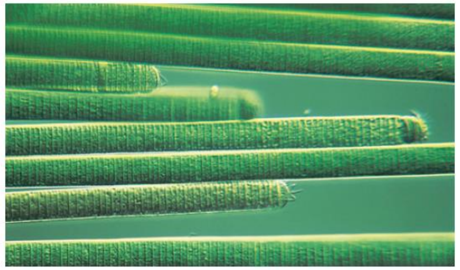
- Latin: firmus, strong + cutis, skin (as in reference to cell wall)
- Gram +ve cell wall structure
- "Low G + C gram-positive" bacteria
- Divided into 3 classes
  - Class I – Clostridia; includes genera *Clostridium* and *Desulfotomaculatum*, and others
  - Class II – *Mollicutes*; bacteria in this class cannot make peptidoglycan and lack cell walls; includes genera *Mycoplasma*, *Ureaplasma*, and others
  - Class III – Bacilli; includes genera *Bacillus, Lactobacillus, Streptococcus, Lactococcus, Geobacillus, Enterococcus, Listeria, Staphylococcus*, and others

Phylum *Aquificae*

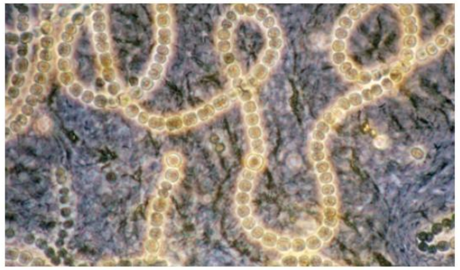
- Hyperthermophiles bacteria
- Represent the earliest "deepest" branch of the Bacteria
- Contains genera *Aquifex* and *Hydrogenobacter* that can obtain energy from hydrogen via chemolithotrophic pathways
- *Aquifex pyrophilus*
  - Extreme thermophiles
  - 85°C-95°C
  - Gram-negative rod
- Grow in active geothermal area

Phylum *Cyanobacteria*

- Cyanobacteria / blue-green algae are the largest and most diverse group of photosynthetic bacteria
- Cyano "Colour of the bacteria" Greek "Blue"
- Obtain energy through photosynthesis
- Photosynthetic prokaryotes produce O_2
- The photosynthetic apparatus closely resemble that of eukaryotes
- Diverse morphology
- Reproduce by binary fission, budding, fragmentation

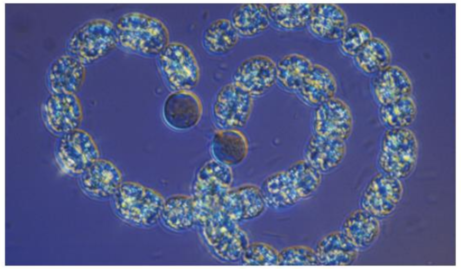


(a) *Oscillatoria*



(c) *Nostoc*

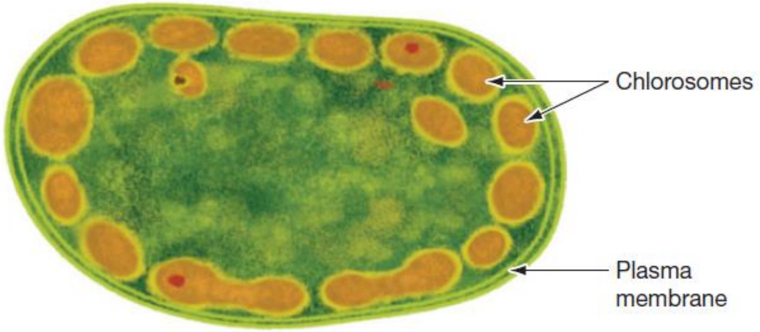
(b) *Chroococcus turgidus*



(d) *Anabaena spiroides*

Phylum *Chlorobi*

- Anaerobic photosynthetic bacteria
- The "green sulfur bacteria"
- Obligate anaerobic photolithotrophs that use hydrogen sulfide, sulfur, and hydrogen as electron source
- Found in sulfide-rich muds at the bottom of lakes and ponds
- Green-grass or chocolate brown in colour
- Includes genera *Chlorobium*



Phylum *Spirochaetes*

- Greek: *spira* - a coil; *chaete* - hair
- Morphologically unique – long bacteria with a flexible & helical shape.
- Cell moves in corkscrew like movement
- Gram negative, chemoorganotrophic bacteria
- Important pathogenic genera include *Treponema, Borrelia,* and *Leptospira*
- Often grow in anoxic and sulfide-rich freshwater and marine environment

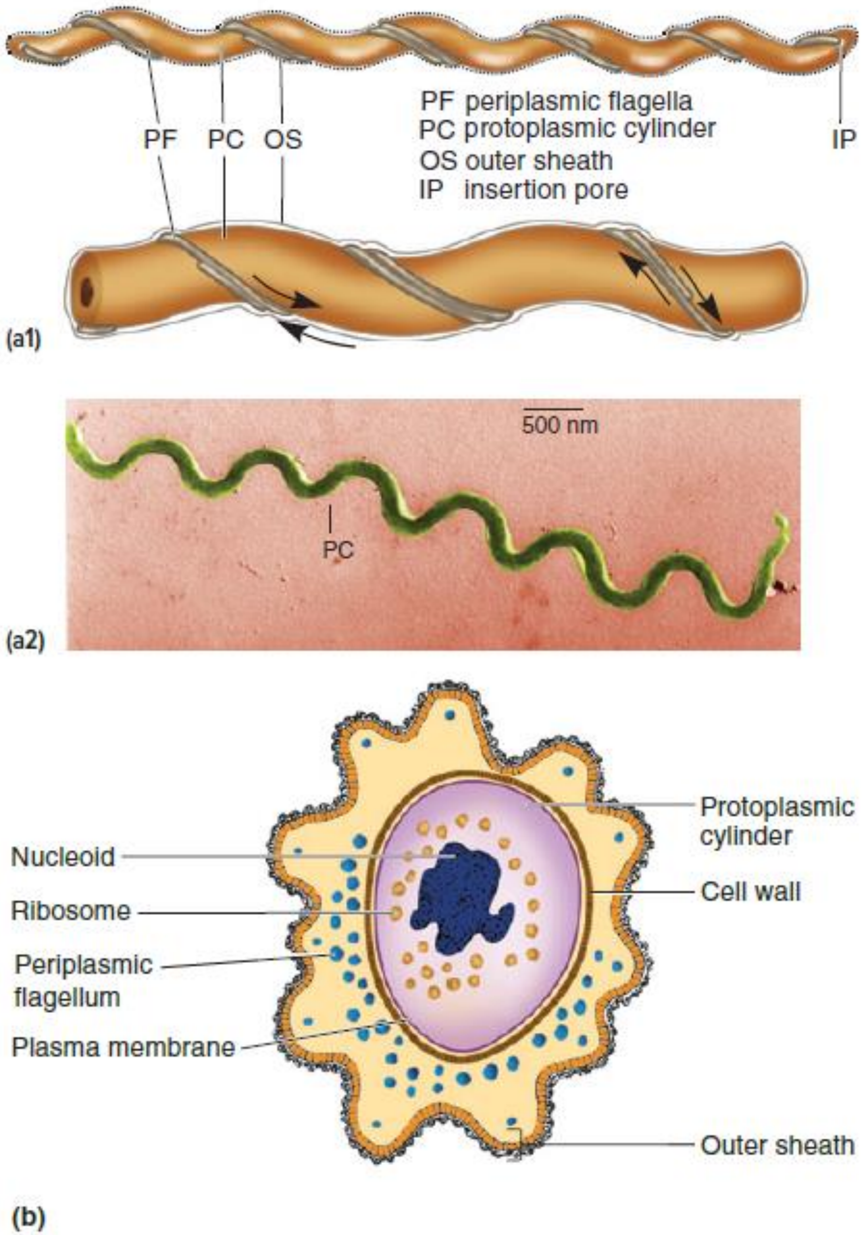


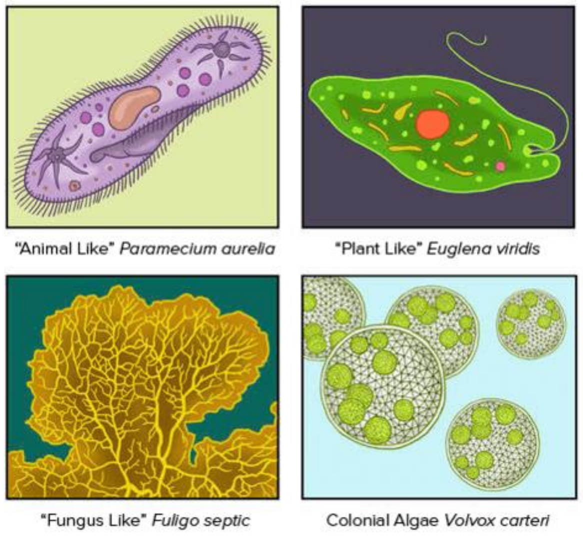
Figure 21.19 Spirochete Morphology. (a1) A surface view of spirochete structure as interpreted from electron micrographs. (a2) A longitudinal view of *Treponema pallidum*. (b) A cross section of a typical spirochete showing morphological details.

Phylum *Actinobacteria*

- "High G + C gram-positive" bacteria
- Includes genera *Actinomyces, Streptomyces, Corynebacterium, Micrococcus, Mycobacterium, Propionibacterium*

DOMAIN EUKARYA

- The domain Eucarya is divided into four kingdoms by most biologists:
  - Kingdom Protista, including the protozoa and algae
  - Kingdom Fungi, the fungi (molds, yeast, and fleshy fungi)
  - Kingdom Animalia, the multicellular animals
  - Kingdom Plantae, the multicellular plants


"Animal Like" *Paramecium aurelia*
"Plant Like" *Euglena viridis*
"Fungus Like" *Fuligo septic*
Colonial Algae *Volvox carteri*

THANK YOU