COURSE MSc (BIOTECHNOLOGY) 2nd semester

PAPER CODE: MBT-202

MICROBIOLOGY

TOPIC : Microbial Diversity and Systematics
Classification of Bacteria

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MBT -202

Paper Second
Microbiology (Max. marks: 100)

Unit I: Microbial Diversity and Systematics- Classical and modern methods and concepts; Domain and Kingdom concepts in classification of microorganisms; Criteria for classification; Classification of Bacteria; 16S rDNA sequencing and Ribosomal Database Project.

Unit II: Microbial Growth and Physiology: Ultrastructure of Archaea (Methanococcus); Eubacteria (E.coli); Unicellular Eukaryotes (Yeast); Concept of species and strains; Microbial growth: Batch, fed-batch, continuous kinetics, synchronous growth, yield constants, methods of growth estimation, stringent response, death of a bacterial cell. Microbial physiology: Physiological adoption and life style of Prokaryotes; Unicellular Eukaryotes and the Extremophiles (with classical example from each group).

Unit III: Microbial Interactions and Infection; Host–Pathogen interactions; Microbes infecting humans, veterinary animals and plants; Pathogenicity islands and their role in bacterial virulence.

Unit IV: Microbes and Environment: Role of microorganisms in natural system and artificial system; Influence of Microbes on the Earth's Environment and Inhabitants; Ecological impacts of microbes; Symbiosis (Nitrogen fixation and ruminant symbiosis); Microbes and Nutrient cycles; Microbial communication system; Quorum sensing; Microbial fuel cells; Prebiotics and Probiotics. 9

Unit V: General Virology; Morphology and Ultrastructure of viruses (Bacterial, Plant, Animal, Tumor viruses), Satellite viruses; Properties of viruses; Virus like particles-Viroids, prions, Cultivation of viruses in embryonated eggs; General overview of bacteriophages, plant and animal viruses (TMV, CsMV, HIV, Rota, Toga, Rhabdo). Economic loss due to important viruses; Infectivity assays-Sap transmission; insect vector transmission; Agrobacterium mediated; Gene Silencing-Viral suppression.

Texts/References

1. Pelczar MJ Jr., Chan ECS and Kreig NR., Microbiology, 5th Edition, Tata McGraw Hill, 1993.
2. Maloy SR, Cronan JE Jr., and Freifelder D, Microbial Genetics, Jones Bartlett Publishers, Sudbury, Massachusetts, 2006.
3. Crueger and A Crueger, (English Ed., TDW Brock); Biotechnology: A textbook of Industrial Microbiology, Sinaeur Associates, 1990.
4. G Reed, Prescott and Dunn's, Industrial Microbiology, 4th Edition, CBS Publishers, 1987.
5. M.T. Madigan and J.M. Martinko, Biology of Microorganisms, 11th Edition, Pearson Prentice Hall, USA, 2006.

Microbial Diversity and Systematics

Taxonomy (Greek) is defined as the science of biological classification.

It consists of three separate but interrelated parts: classification, nomenclature, and identification.

1. **Classification** is the *arrangement of organisms* into groups or **taxa** (s., **taxon**) based on mutual similarity or evolutionary relatedness.
2. **Nomenclature** is the branch of taxonomy concerned with the assignment of names to taxonomic groups in agreement with published rules.
3. **Identification** is the practical side of taxonomy, the process of determining if a particular isolate belongs to a recognized taxon.
4. **Systematics** "the scientific study of organisms with the ultimate object of characterizing and arranging them in an orderly manner."

Microbial Diversity and Systematics

Classification

- ***Phenetic classification*** **-** Grouping organisms together based on the mutual similarity of their phenotypic characteristics.
- ***Phylogenetic classification-*** These are systems based on evolutionary relationships rather than external appearance

  phylogeny [Greek] refers to the evolutionary development of a species.

  It is based on the direct comparison of genetic materials and/or gene product.

Nomenclature (Binomial system)

- Polynomial system, i.e naming organisms with many names Binomial systems were developed by Swedish biologist Carolus Linnaeus (1707–1778) based on the anatomical characteristics of plants and animals.
- The first word in the binomial is the genus name and is always capitalized
- The second word is species name and never capitalized e.g. honeybee, *Apis mellifera*

Microbial Diversity and Systematics

Taxonomic ranks: (in ascending order)

species ➡ genera ➡ families ➡ orders ➡ classes ➡ phyla ➡ kingdom ➡ domain.

Species is a collection of strains that have a similar G+C composition and *70% or greater similarity* as judged by DNA hybridization.

Strain descended from a single organism or pure culture isolate. Strains within a species *may differ slightly from one another* in many ways.

- **Biovars** are variant prokaryotic strains characterized by *biochemical or physiological differences*,
- **Morphovars** differ *morphologically*,
- **Serovars** have distinctive *antigenic properties* . One strain of a species is designated as the **type strain**

Genus is a well-defined group of one or more species that is clearly separate from other genera.

Divisions of Life

Kingdom systems of classification

- **Five-kingdom system** (Whittaker, 1960s) - based upon cell type, organization, and the means of nutrient acquisition (Monera, Protista, Fungi, Plantae, Animalia)
- **Six-kingdom system** - differs from five-kingdom system by dividing prokaryotes into bacteria and archaea (Bacteria, Archaea, Protista, Fungi, Plantae, Animalia)
- **Eight-kingdom system** (Cavalier-Smith) - further division of the protists using rRNA data and grouping organisms into two empires (Eucaryota and Bacteria) containing a total of eight kingdoms [(Bacteria, Archaea), (Archezoa, Protista, Plantae, Chromista, Fungi, Animalia)]
- Most adapted classification system recognizes three **domains**, a taxonomic level higher than kingdom.
- **Domain** Archaebacteria, **Domain** eubacteria , and **Domain** eukaryotes
- Domain Eukarya is subdivided into four kingdoms plants, animals, fungi, protists.

Microbial Diversity and Systematics

Property	*Bacteria*	*Archaea*	*Eucarya*
Membrane-Enclosed Nucleus with Nucleolus	Absent	Absent	Present
Complex Internal Membranous Organelles	Absent	Absent	Present
Cell Wall	Almost always have peptidoglycan containing muramic acid	Variety of types, no muramic acid	No muramic acid
Membrane Lipid	Have ester-linked, straight-chained fatty acids	Have ether-linked, branched aliphatic chains	Have ester-linked, straight-chained fatty acids
Gas Vesicles	Present	Present	Absent
Transfer RNA	Thymine present in most tRNAs *N*-formylmethionine carried by initiator tRNA	No thymine in T or TψC arm of tRNA Methionine carried by initiator tRNA	Thymine present Methionine carried by initiator tRNA
Polycistronic mRNA	Present	Present	Absent
mRNA Introns	Absent	Absent	Present
mRNA Splicing, Capping, and Poly A Tailing	Absent	Absent	Present
Ribosomes			
Size	70S	70S	80S (cytoplasmic ribosomes)
Elongation factor 2 reaction with diphtheria toxin	Does not react	Reacts	Reacts
Sensitivity to chloramphenicol and kanamycin	Sensitive	Insensitive	Insensitive
Sensitivity to anisomycin	Insensitive	Sensitive	Sensitive
DNA-Dependent RNA Polymerase			
Number of enzymes	One	One	Three
Structure	Simple subunit pattern (6 subunits)	Complex subunit pattern similar to eucaryotic enzymes (8–12 subunits)	Complex subunit pattern (12–14 subunits)
Rifampicin sensitivity	Sensitive	Insensitive	Insensitive
Polymerase II Type Promoters	Absent	Present	Present
Metabolism			
Similar ATPase	No	Yes	Yes
Methanogenesis	Absent	Present	Absent
Nitrogen fixation	Present	Present	Absent
Chlorophyll-based photosynthesis	Present	Absent	Present[a]
Chemolithotrophy	Present	Present	Absent

The Approaches Commonly Used To Determine Taxonomic Classification

CLASSICAL APPROACHES

- Morphological Characteristics
- Physiological and Metabolic Characteristics
- Biochemical Characteristics
- Ecological Characteristics

MOLECULAR APPROACHES

- Nucleic Acid Base Composition
- Nucleic Acid Hybridization
- Nucleic Acid Sequencing
- Genomic Fingerprinting

The Approaches Commonly Used To Determine Taxonomic Classification

Morphological Characteristics

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

*Reference- Prescott's Microbiology Tenth edition

The Approaches Commonly Used To Determine Taxonomic Classification

Physiological and Metabolic Characteristics

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

*Reference- Prescott's Microbiology Tenth edition

The Approaches Commonly Used To Determine Taxonomic Classification

Biochemical Characteristics

- **FAME** *f*atty *a*cid *m*ethyl *e*ster (FAME) analysis
- **MS** mass spectrometry (MS) for fast and accurate identification of bacteria based on the presence of specific, highly abundant proteins.

Ecological Characteristics

- The ability of a microorganism to colonize a specific environment

MOLECULAR CHARACTERISTICS

- Phylogenetic inferences based on molecular approaches provide the most robust analysis of microbial evolution
- **Nucleic Acid Base Composition**

$$\text{mol\% G + C} = \frac{\text{G + C}}{\text{G + C + A + T}} \times 100$$

*Reference- Prescott's Microbiology Tenth edition

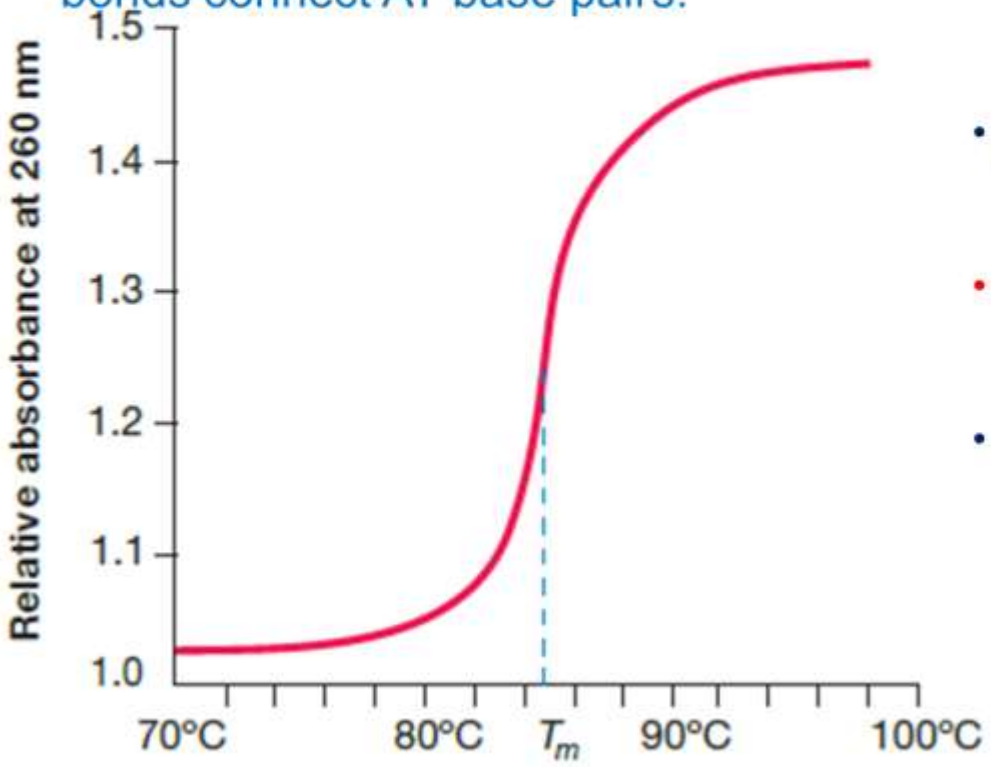
Molecular Approaches for Taxonomic Classification

Nucleic Acid Base Composition

$$\text{mol\% G + C} = \frac{\text{G + C}}{\text{G + C + A + T}} \times 100$$

DNA melting temperature (*Tm*)

- In double-stranded DNA, three hydrogen bonds join GC base pairs and two bonds connect AT base pairs.



A DNA Melting Curve. The T_m is indicated.

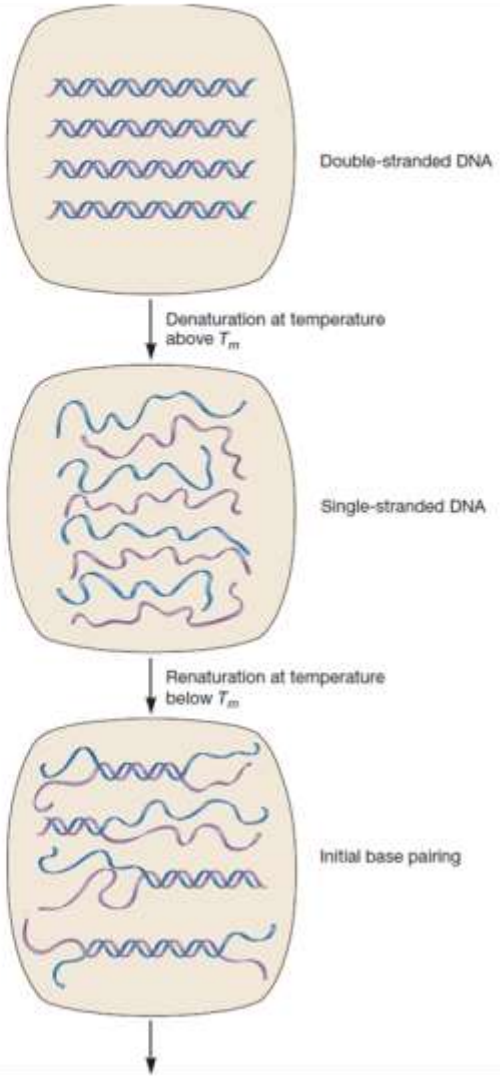
- Strands of DNA with a greater G + C has a higher melting temperature
- DNA melting can be easily followed spectrophotometrically
- The absorbance of DNA at 260 nm increases during strand separation
- The absorbance increases as hydrogen bonds are broken and reaches a plateau when all the DNA has become single-stranded

*Reference- Prescott's Microbiology Tenth edition

Molecular Approaches for Taxonomic Classification

Nucleic Acid Hybridization

- The similarity between genomes can be compared more directly by use of nucleic acid hybridization studies, also called **DNA-DNA hybridization** (**DDH**)
- The genomes of two microbial isolates are heated to become single-stranded (ss) DNA and then cooled and held at a temperature about 258C below the *Tm*, strands with complementary base sequences will reassociate to form stable double-stranded (ds) DNA.



Nucleic Acid Melting and Hybridization.
Complementary strands are shown in purple and blue.

*Reference- Prescott's Microbiology Tenth edition

Molecular Approaches for Taxonomic Classification

AVERAGE NUCLEOTIDE IDENTITY (ANI)

- which uses pairwise alignment between sequenced DNA from two organisms, is a promising replacement for DDH

NUCLEIC ACID SEQUENCING

- **Small subunit rRNAs** (**SSU rRNAs**) are almost ideal for studies of microbial evolution, relatedness, and genus identification
- The rRNAs from small ribosomal subunits (16S from bacterial and archaeal cells and 18S from eukaryotes) have become the molecules of choice for inferring microbial phylogenies and making taxonomic assignments at the genus level
- **Oligonucleotide signature sequences** These are short, conserved nucleotide sequences that are specific for phylogenetically defined groups of organisms.
- **Indels** A particular nucleotide sequence that is inserted or deleted at fixed positions of many genes may be found exclusively among all members of a phylum. These taxon specific insertions and deletions are called conserved **indels** which can be used as signature sequences

Molecular Approaches for Taxonomic Classification

Genomic Fingerprinting

SSU rRNA can also be analyzed by methods that do not require nucleotide sequencing. Instead, the differences in rRNA gene sequences can be discerned by digestion with restriction enzymes.

Restriction fragment length polymorphism (RFLP), requires PCR amplification of the gene encoding the rRNA to provide enough DNA for analysis. The DNA is then digested with restriction enzymes and run on a gel

Ribotyping, omits the need for PCR because the rRNA genes are detected by a labeled nucleotide probe.

The microbe's entire genome is cut with one or more restriction enzymes.

The digested DNA is run on a gel and transferred to a nylon filter, and the rRNA encoding DNA fragments are visualized after hybridization with a labeled rRNA gene probe

Genomic fingerprinting RFLP and ribotyping generate specific patterns that are used to reveal microbial identity, they are often referred to as **genomic fingerprinting**

Molecular Approaches for Taxonomic Classification

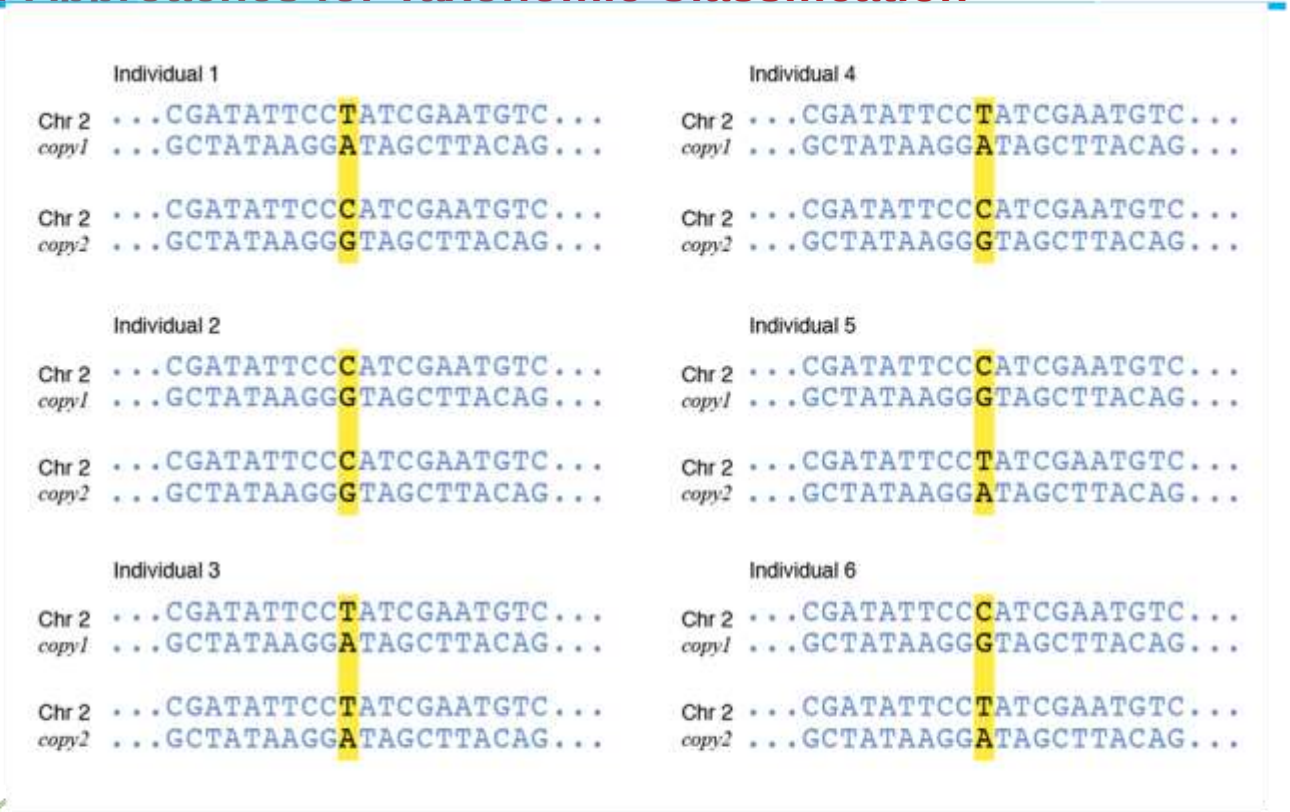
- **Phylotype** Any uncultivated microorganism that is identified solely on its nucleic acid sequence is called a **phylotype**
- **Multilocus sequence analysis** (**MLSA**) a technique, in which five to seven conserved housekeeping genes can be sequenced and compared rather than using a single gene ,
- **Multilocus sequence typing** (**MLST**), which is used to discriminate among strains belonging to the same pathogenic species.
- Three families of **repetitive sequences** are typically used for microbial identification: These sequences are intergenic and are conserved among genera.
- The 154 bp BOX elements, **BOX-PCR**
- The 124–127 bp enterobacterial repetitive intergenic consensus (ERIC) sequence, **ERIC-PCR**
- 35–40 bp repetitive extragenic palindromic (REP) sequences. **REP-PCR**

Molecular Approaches for Taxonomic Classification

Single nucleotide polymorphisms

SNP analysis looks at single nucleotide changes, or polymorphisms, in specific genes, intergenic regions, or other noncoding regions.

Almost all common SNPs have only two alleles.



- A SNP in which both forms lead to the same polypeptide sequence is termed *synonymous* (sometimes called a silent mutation) — if a different polypeptide sequence is produced they are *nonsynonymous*.
- These particular region are targeted because they are normally conserved, so single base-pair differences reveal evolutionary change.

Molecular Approaches for Taxonomic Classification

The Ribosomal Database Project website is a repository of hundreds of thousands of rRNA sequences and facilitates accurate comparative analysis.

Ribosomal Database Project (RDP; http://rdp.cme.msu.edu/) provides the research community with aligned and annotated rRNA gene sequence data, along with tools to allow researchers to analyze their own rRNA gene sequences in the RDP framework.

RDP data and tools are utilized in fields as diverse as human health, microbial ecology, environmental microbiology, nucleic acid chemistry, taxonomy and phylogenetics.

In addition to aligned and annotated collections of bacterial and archaeal small subunit rRNA genes, RDP now includes a collection of fungal large subunit rRNA genes.

RDP tools, including Classifier and Aligner, have been updated to work with this new fungal collection.

With release 11, RDP is providing an expanded set of tools to facilitate analysis of high-throughput data, including both single-stranded and paired-end reads.

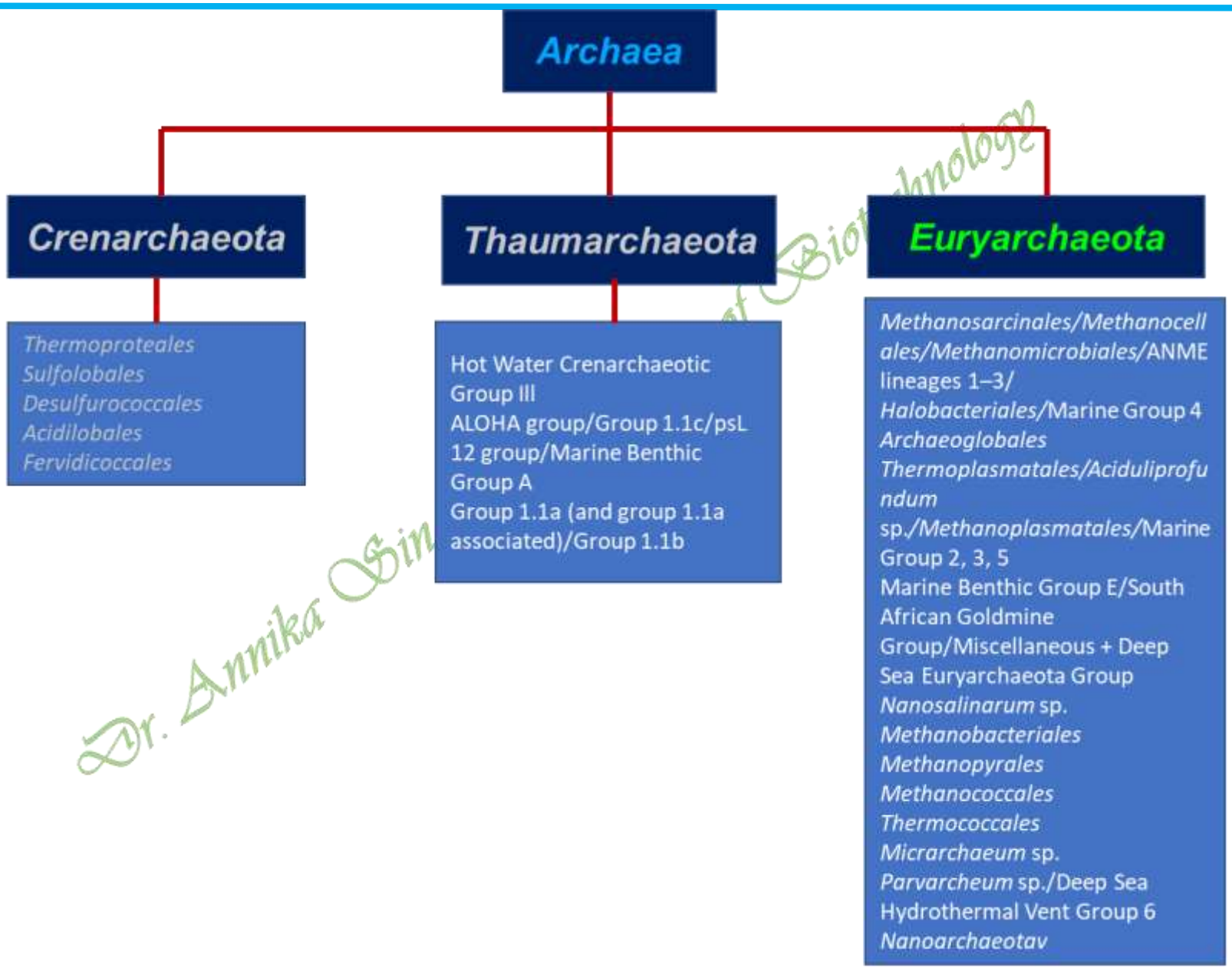
Classification of Bacteria

- In 1923 David Bergey (1860–1937), professor of bacteriology at the University of Pennsylvania, and four colleagues published *Bergey's Manual of Determinative Bacteriology,* a classification of bacteria
- In 1984 the first edition of *Bergey's Manual of Systematic Bacteriology* was published. It contained descriptions of all bacterial and archaeal species then identified.
- A more recent second edition consists of five volumes published over a number of years, starting in 2001.
- Microbial classification in the first edition was phenetic (based on phenotypic characterization)
- Classification in the second edition of *Bergey's Manual* is largely phylogenetic
- In addition to the reorganization based on phylogeny, the second edition has more ecological information about individual taxa.

Classification of Bacteria

- **Volume 1,** *The Archaea and the Deeply Branching and Phototrophic Bacteria*
- **Volume 2,** *The Proteobacteria*
- **Volume 3,** *The Firmicutes*
- **Volume 4,** *The Bacteroidetes, Spirochaetes, Tenericutes (Mollicutes), Acidobacteria, Fibrobacteres, Fusobacteria, Dictyoglomi, Gemmatimonadetes, Lentisphaerae, Verrucomicrobia, Chlamydiae, and Planctomycetes*
- **Volume 5,** *The Actinobacteria*

Domain Archaea



Domain Archaea

- *Archaea* contains a highly diverse group of microbes with respect to morphology, reproduction, physiology, and ecology.
- best known for their growth in anoxic, hypersaline, and high-temperature habitats, they also inhabit marine Arctic, temperate, and tropical waters.
- Archaea may be divided into six physiological groups: methanogenic archaea, sulfate reducers, extreme halophiles, cell wall-less archaea, extremely thermophilic S0-metabolizers, and mesophilic ammonia oxidizers
- The second edition of *Bergey's Manual* divides *Archaea* into two phyla, *Crenarchaeota* and *Euryarchaeota*; however, the phylum *Thaumarchaeota* was recently recognized.
- Autotrophic archaea generally use one of three pathways for CO2 assimilation: the reductive acetyl-CoA pathway, the 3-hydroxypropionate/4-hydroxybutyrate (HP/HB) cycle, or the dicarboxylate/4-hydroxybutyrate (DC/HB) cycle. Acetate is incorporated either by the glyoxylate or methylaspartate cycle. Most other anabolic pathways appear to be similar to those found in bacteria
- Although much of archaeal catabolism appears similar to that of bacteria, archaea differ with respect to glucose catabolism, using modified versions of the Embden-Meyerhof and Entner-Doudoroff pathways

Domain Archaea

Volume 1. ***The Archaea and the Deeply Branching and Phototrophic Bacteria***	
Domain *Archaea*	
Phylum *Crenarchaeota*	
Class I. *Thermoprotei*	*Thermoproteus, Pyrodictium, Sulfolobus*
Phylum *Euryarchaeota*	
Class I. *Methanobacteria*	*Methanobacterium*
Class II. *Methanococci*	*Methanococcus*
Class III. *Methanomicrobia*	*Methanomicrobium*
Class IV. *Halobacteria*	*Halobacterium, Halococcus*
Class V. *Thermoplasmata*	*Thermoplasma, Picrophilus, Ferroplasma*
Class VI. *Thermococci*	*Thermococcus, Pyrococcus*
Class VII. *Archaeoglobi*	*Archaeoglobus*
Class VIII. *Methanopyri*	*Methanopyrus*

Domain Archaea

Table 20.1 Characteristics of the Major Archaeal Physiological Groups

Group	General Characteristics	Representative Genera
Methanogenic archaea	Strict anaerobes. Methane is the major metabolic end product. S^0 may be reduced to H_2S without yielding energy. Cells possess coenzyme M, factors 420 and 430, and methanopterin.	*Methanobacterium (E)*[1] *Methanococcus (E)* *Methanomicrobium (E)* *Methanosarcina (E)*
Archaeal sulfate reducers	Regular and irregular cocci. H_2S formed from thiosulfate and sulfate. Autotrophic growth with thiosulfate and H_2. Can grow heterotrophically. Traces of methane also formed. Extremely thermophilic and strictly anaerobic. Possess factor 420 and methanopterin but not coenzyme M or factor 430.	*Archaeoglobus (E)*
Extremely halophilic archaea	Rods, cocci, or irregular shaped cells that may include pyramids or cubes. Primarily chemoorganoheterotrophs. Most species require sodium chloride ≥1.5 M, but some survive in as little as 0.5 M. Most produce characteristic bright-red colonies; some are unpigmented. Neutrophilic to alkalophilic. Generally mesophilic; however, at least one species is known to grow at 55°C. Possess either archaerhodopsin or halorhodopsin and can use light energy to produce ATP.	*Halobacterium (E)* *Halococcus (E)* *Natronobacterium (E)*
Cell wall-less archaea	Pleomorphic cells. Thermoacidophilic and chemoorganotrophic. Facultatively anaerobic. Plasma membrane contains mannose-rich glycoproteins and lipoglycans.	*Thermoplasma (E)*
Extremely thermophilic S^0-metabolizers	Rods, filaments or cocci. Obligately thermophilic (optimum growth temperature between 70–100°C). Usually strict anaerobes but may be aerobic or facultative. Acidophilic or neutrophilic. Autotrophic or heterotrophic. Most are sulfur metabolizers. S^0 reduced to H_2S anaerobically; H_2S or S^0 oxidized to H_2SO_4 aerobically.	*Desulfurococcus (C)* *Pyrodictium (C)* *Pyrococcus (E)* *Sulfolobus (C)* *Thermococcus (E)* *Thermoproteus (C)*
Mesophilic aerobic ammonia-oxidizers	Globally distributed in marine and soil environments, chemolithoautotrophic, using ammonia as electron donor and oxygen as terminal electron acceptor. Use HP/HB[2] pathway for carbon fixation. Evidence that some deep-ocean thaumarchaea may use urea as carbon and nitrogen source.	*Cenarchaeum symbiosum (T)* *Nitrosopumilus maritimus (T)*

Classification of Bacteria

Volume 1. *The Archaea and the Deeply Branching and Phototrophic Bacteria*

Domain *Bacteria*	
Phylum *Aquificae*	*Aquifex, Hydrogenobacter*
Phylum *Thermotogae*	*Thermotoga, Geotoga*
Phylum *Thermodesulfobacteria*	*Thermodesulfobacterium*
Phylum *Deinococcus-Thermus*	*Deinococcus, Thermus*
Phylum *Chrysiogenetes*	*Chrysogenes*
Phylum *Chloroflexi*	*Chloroflexus, Herpetosiphon*
Phylum *Thermomicrobia*	*Thermomicrobium*
Phylum *Nitrospira*	*Nitrospira*
Phylum *Deferribacteres*	*Geovibrio*
Phylum *Cyanobacteria*	*Prochloron, Synechococcus, Pleurocapsa, Oscillatoria, Anabaena, Nostoc, Stigonema*
Phylum *Chlorobi*	*Chlorobium, Pelodictyon*

Classification of Bacteria

Volume 2. *The Proteobacteria*	
Phylum *Proteobacteria*	
Class I. *Alphaproteobacteria*	*Rhodospirillum, Rickettsia, Caulobacter, Rhizobium, Brucella, Nitrobacter, Methylobacterium, Beijerinckia, Hyphomicrobium*
Class II. *Betaproteobacteria*	*Neisseria, Burkholderia, Alcaligenes, Comamonas, Nitrosomonas, Methylophilus, Thiobacillus*
Class III. *Gammaproteobacteria*	*Chromatium, Leucothrix, Legionella, Pseudomonas, Azotobacter, Vibrio, Escherichia, Klebsiella, Proteus, Salmonella, Shigella, Yersinia, Haemophilus*
Class IV. *Deltaproteobacteria*	*Desulfovibrio, Bdellovibrio, Myxococcus, Polyangium*
Class V. *Epsilonproteobacteria*	*Campylobacter, Helicobacter*
Volume 3. *The Low G + C Gram-Positive Bacteria*	
Phylum *Firmicutes*	
Class I. *Clostridia*	*Clostridium, Peptostreptococcus, Eubacterium, Desulfotomaculum, Heliobacterium, Veillonella*
Class II. *Mollicutes*	*Mycoplasma, Ureaplasma, Spiroplasma, Acholeplasma*
Class III. *Bacilli*	*Bacillus, Caryophanon, Paenibacillus, Thermoactinomyces, Lactobacillus, Streptococcus, Enterococcus, Listeria, Leuconostoc, Staphylococcus*

Classification of Bacteria

Volume 4. ***The Planctomycetes, Spirochaetes, Fibrobacteres, Bacteriodetes, and Fusobacteria***

Phylum *Planctomycetes*	*Planctomyces, Gemmata*
Phylum *Chlamydiae*	*Chlamydia*
Phylum *Spirochaetes*	*Spirochaeta, Borrelia, Treponema, Leptospira*
Phylum *Fibrobacteres*	*Fibrobacter*
Phylum *Acidobacteria*	*Acidobacterium*
Phylum *Bacteroidetes*	*Bacteroides, Porphyromonas, Prevotella, Flavobacterium, Sphingobacterium, Flexibacter, Cytophaga*
Phylum *Fusobacteria*	*Fusobacterium, Streptobacillus*
Phylum *Verrucomicrobia*	*Verrucomicrobium*
Phylum *Dictyoglomi*	*Dictyoglomus*
Phylum *Gemmatimonadetes*	*Gemmatimonas*

Classification of Bacteria

Volume 5 *The High G + C Gram-Positive Bacteria*

Phylum *Actinobacteria*

Class *Actinobacteria*	*Actinomyces, Micrococcus, Arthrobacter, Corynebacterium, Mycobacterium, Nocardia, Actinoplanes, Propionibacterium, Streptomyces, Thermomonospora, Frankia, Actinomadura, Bifidobacterium*

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- Most Bacteria and Archaea Reproduce by Binary Fission
- Binary fission is a relatively simple type of cell division: the cell elongates as new material is synthesized, replicates its chromosome, and separates the newly formed DNA molecules so there is one chromosome in each half of the cell.
- Finally, a septum (cross wall) is formed at midcell, dividing the parent cell into two progeny cells, each having its own chromosome and a complement of other cellular constituents.

Some bacteria reproduce by forming a bud. Certain cyanobacteria undergo multiple fission.
The progeny cells, called baeocytes, are held within the cell wall of the parent cell until they are released.

Binary Fission

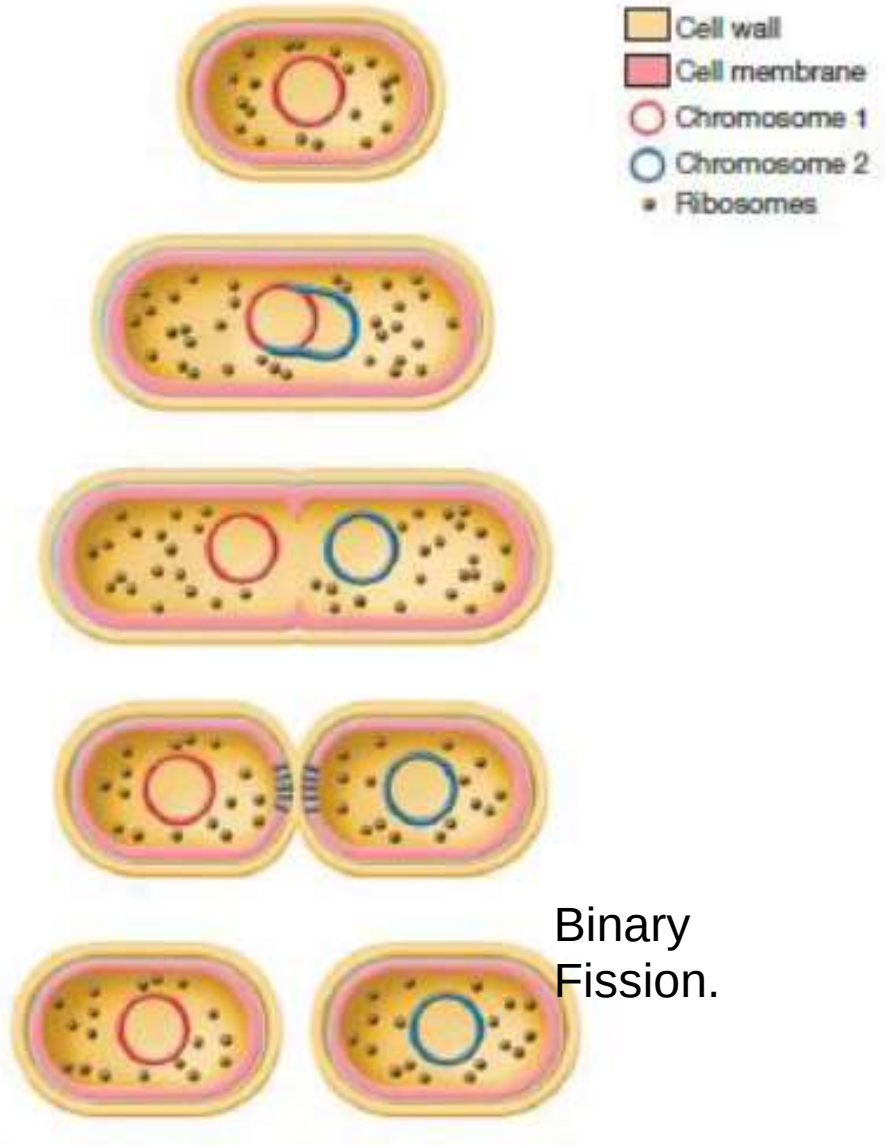
(a) A young cell at early phase of cycle

(b) A parent cell prepares for division by enlarging its cell wall, plasma membrane, and overall volume. DNA replication then starts.

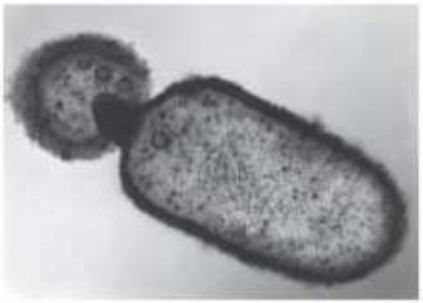
(c) The septum begins to grow inward as the chromosomes move toward opposite ends of the cell. Other cytoplasmic components are distributed to the two developing cells.

(d) The septum is synthesized completely through the cell center, creating two separate cell chambers.

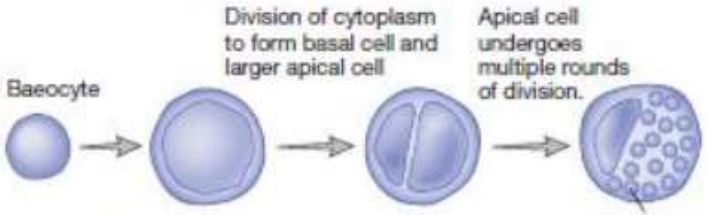
(e) At this point, the daughter cells are divided. Some species separate completely as shown here, while others remain attached, forming chains, doublets, or other cellular arrangements.



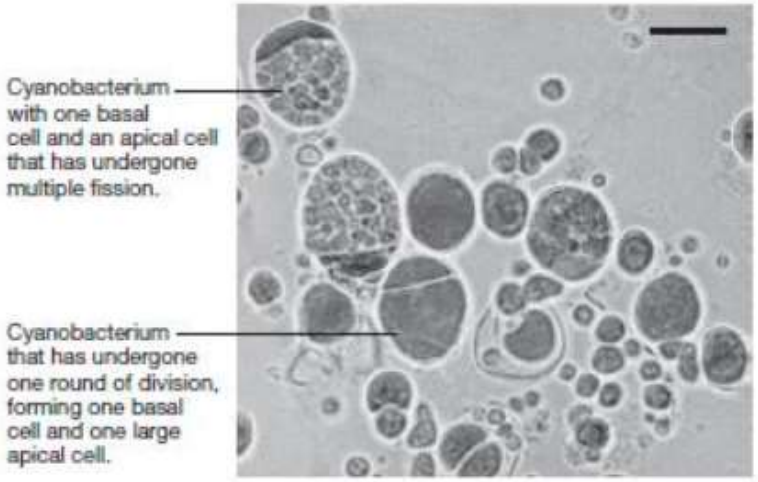
Binary Fission.

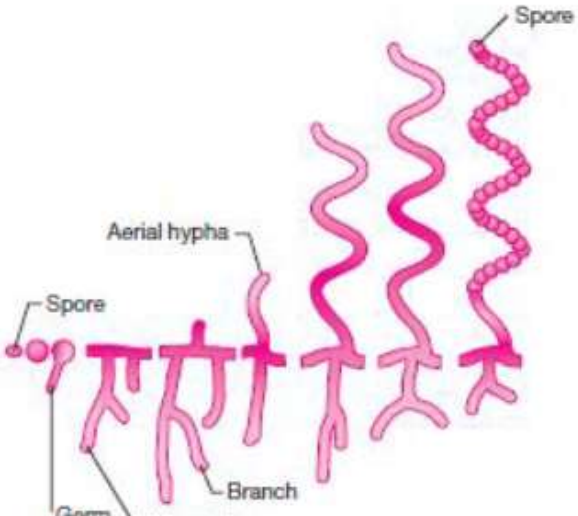


(a) *Listeria monocytogenes* mother cell and bud



(b) Baeocyte formation





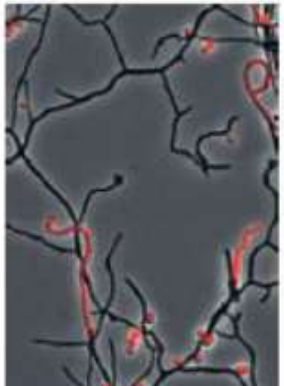
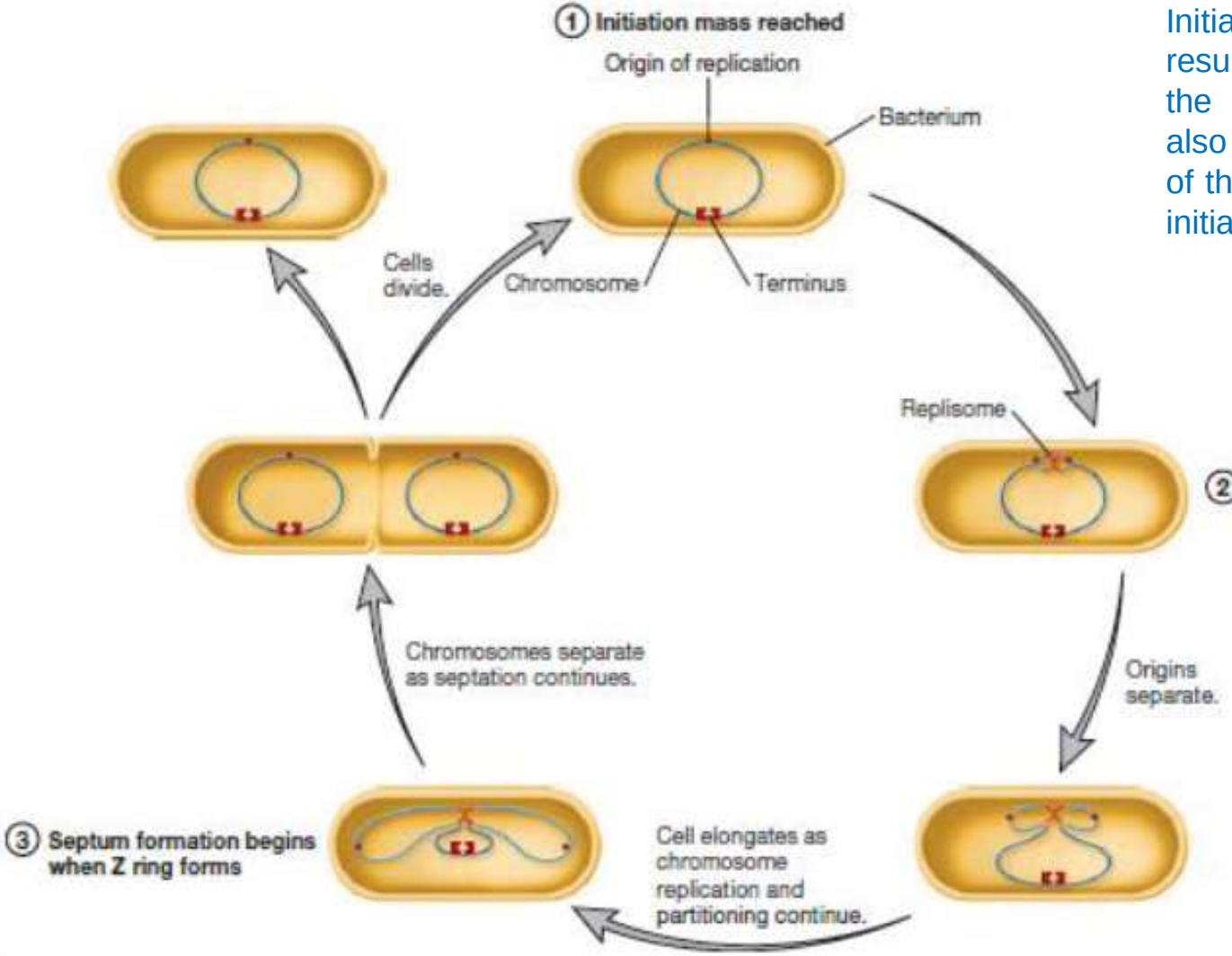


Figure 7.2 **Some Bacteria Reproduce by Methods Other than Binary Fission.**
(a) Transmission electron micrograph (TEM) of a budding *Listeria monocytogenes* cell. (b) On the left is a drawing illustrating baeocyte formation. On the right is a photo of baeocytes produced by the cyanobacterium *Dermocarpella*. Bar = 10 μm. (c) Spore formation by *Streptomyces coelicolor*.

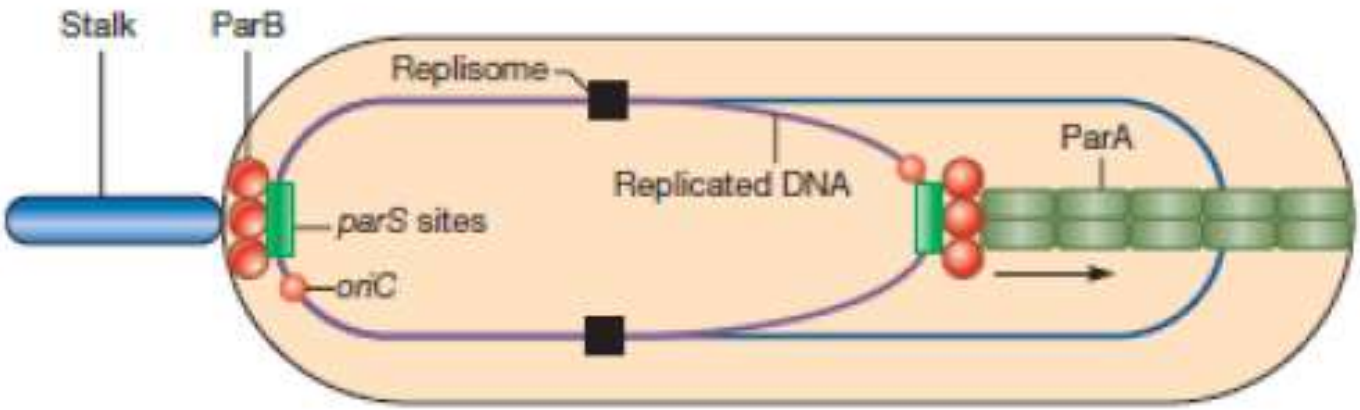
Cell Cycle of E. coli

Initiation of the cell cycle results from an increase in the mass of a cell, which also results in accumulation of the Dna A protein, which initiates DNA replication.



As the cell readies for DNA replication, the origin of replication migrates to the center of the cell and proteins that make up the replisome assemble.

Cell Cycle of E. coli



- The ParAB/parS Partitioning System of Caulobacter crescentus.
- ParB binds each parS site on the two daughter chromosomes.
- ParA is a cytoskeletal protein that pulls one
- daughter chromosome to the pole opposite the stalk pole of the cell.
- Other proteins are involved in localizing ParA and ParB to their respective poles

Cytokinesis

Cytokinesis, a term that has been used to describe the formation of two eukaryotic daughter cells, is now used to describe this process in all cells.

Septation is the process of forming a cross wall between two daughter cells.

Septation is divided into several steps:

(1) selection of the site where the septum will be formed;

(2) assembly of the Z ring, which is composed of the cytoskeletal protein FtsZ;

(3) assembly of the cell wall–synthesizing machinery

(4) constriction of the cell and septum formation

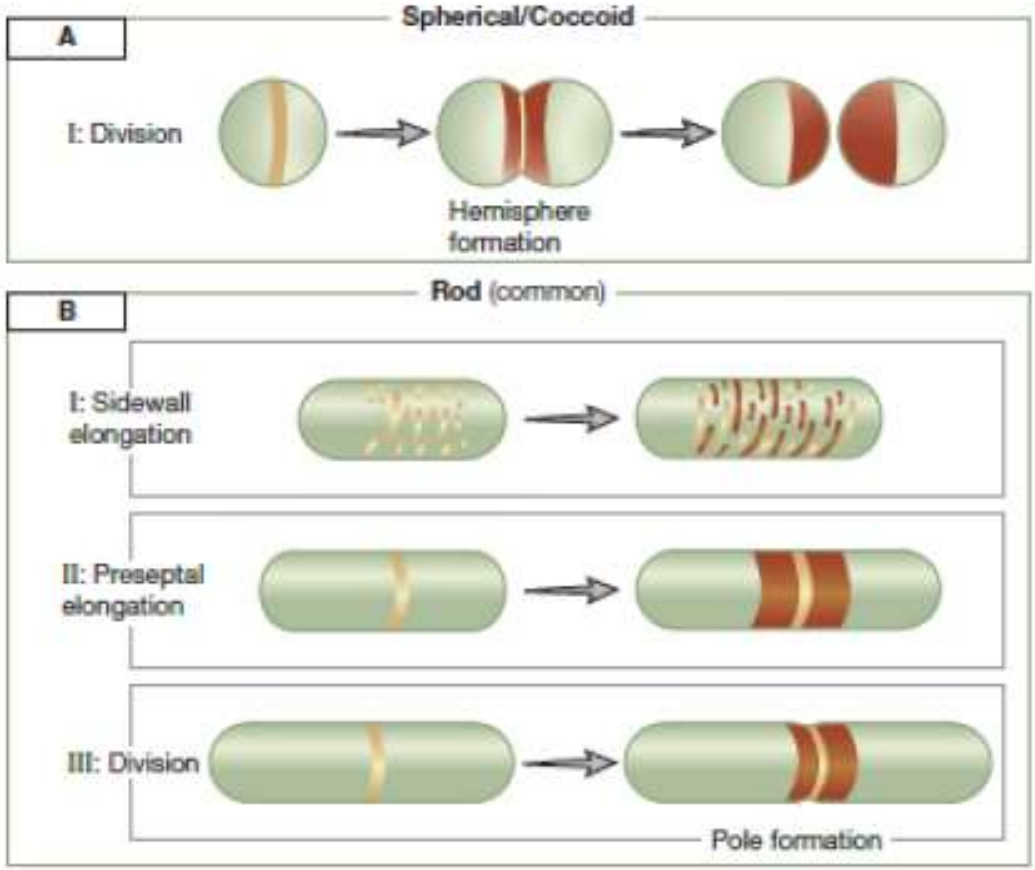
Nucleoid occlusion is a mechanism ensure that the Z ring forms only after most of the daughter chromosomes have segregated from each other.

AI. Spherical cells build new peptidoglycan only at midcell, where the septum will form during division. This leads to daughter cells that have one old and one new cell wall hemisphere.

BI. During growth, prior to division, new cell wall is made along the side of the cell but not at the poles. This placement is thought to be determined by the position of MreB homologues.

BII. As division begins, FtsZ polymerization forms a Z ring and new cell wall growth is confined to the midcell.

BIII. Rod-shaped daughter cells are formed with one new pole and one old pole.



Microbial Growth Curve

- Growth is also used to refer to growth in the size of a population.
- Population growth is often studied by analyzing the growth of microbes in liquid (broth) culture.
- **Batch culture** that is, microbes are incubated in a closed culture vessel with a single batch of medium.
- **Growth Curves Consist of Five Phases**
- Lag phase
- Log phase
- Stationary phase
- Death phase
- Long-term stationary phase