

Microbial Taxonomy and the Evolution of Diversity

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Introduction to Microbial Taxonomy

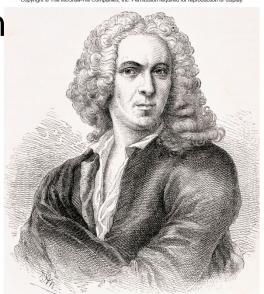
- Taxonomy
 - science of biological classification
 - consists of three separate but interrelated parts
 - classification arrangement of organisms into groups (taxa; s., taxon)
 - nomenclature assignment of names to taxa
 - identification determination of taxon to which an isolate belongs

Natural Classification

- Arranges organisms into groups whose members share many characteristics
 - first such classification in 18th century developed by Linnaeus

-based on anatomical characteristics

 This approach to classification does not necessarily provide information on evolutionary relatedness



Polyphasic Taxonomy

- Used to determine the genus and species of a newly discovered prokaryote
- Incorporates information from genetic, phenotypic, and phylogenetic analysis

Phenetic Classification

- Groups organisms together based on mutual similarity of phenotypes
- Can reveal evolutionary relationships, but not dependent on phylogenetic analysis

- i.e., doesn't weigh characters

 Best systems compare as many attributes as possible

Phylogenetic Classification

- Also called phyletic classification systems
- Phylogeny
 - evolutionary development of a species
- Usually based on direct comparison of genetic material and gene products
 - Woese and Fox proposed using small subunit (SSU) rRNA nucleotide sequences to assess evolutionary relatedness of organisms

Genotypic Classification

- Comparison of genetic similarity between organisms
 - individual genes or whole genomes can be compared
 - 70% homologous belong to the same species

Taxonomic Ranks - 1

- Microbes are placed in hierarchical taxonomic levels with each level or rank sharing a common set of specific features
- Highest rank is domain
 - Bacteria and Archaea microbes only
 - Eukarya microbes and macroorganisms
- Within domain
 - phylum, class, order, family, genus, species
 epithet, some microbes have subspecies

Species

- Definition
 - collection of strains that share many stable properties and differ significantly from other groups of strains
- Also suggested as a definition of species
 - collection of organisms that share the same sequences in their core housekeeping genes

Strains

- Descended from a single, pure microbial culture
- Vary from each other in many ways
 - biovars differ biochemically and physiologically
 - morphovars differ morphologically
 - serovars differ in antigenic properties

Type Strain

- Usually one of first strains of a species studied
- Often most fully characterized
- Not necessarily most representative member of species
- Cataloged by the ATCC American Type
 Culture Collection

Genus

- Well-defined group of one or more strains
- Clearly separate from other genera
- Often disagreement among taxonomists about the assignment of a specific species to a genus

Binomial System of Nomenclature

- Devised by Carl von Linné (Carolus Linnaeus)
- Each organism has two names
 - genus name italicized and capitalized (e.g., *Escherichia*) or underlined
 - species epithet italicized but not capitalized (e.g., *coli*) or underlined
- Can be abbreviated after first use (e.g., *E. coli*)
- A new species cannot be recognized until it has been published in the International Journal of Systematic and Evolutionary Microbiology

Techniques for Determining Microbial Taxonomy and Phylogeny

- Classical characteristics
 - morphological
 - physiological
 - biochemical
 - ecological
 - genetic

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Table 19.1Some 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.

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| Table 19.2 | 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 | | | |
| Luminescence | | | |
| Mechanisms of energy conversion | | | |
| Motility | | | |
| Osmotic tolerance | | | |
| Oxygen relationships | | | |
| pH optimum and growth range | | | |
| Photosynthetic pigments | | | |
| Salt requirements and tolerance | | | |
| Secondary metabolites formed | | | |
| Sensitivity to metabolic inhibitors and antibiotics | | | |
| Storage inclusions | | | |

Ecological Characteristics

- Life-cycle patterns
- Symbiotic relationships
- Ability to cause disease
- Habitat preferences
- Growth requirements

Molecular Approaches

- Extremely important because almost no fossil record was left by microbes
- Allows for the collection of a large and accurate data set from many organisms
- Phylogenetic inferences based on these provide the best analysis of microbial evolution currently available

Molecular Characteristics

- Nucleic acid base composition
 - G + C content Mol% G + C = (G + C/G + C + A + T)100
 - variation within a genus usually <10%
- Nucleic acid hybridization
- Nucleic acid sequencing
 - Small subunit rRNAs (SSU rRNAs)
 - sequences of 16S and 18S rRNA most powerful and direct method for inferring microbial phylogenies and making taxonomic assignments at genus level
 - When comparing rRNA sequences between 2 organisms, their relatedness is represented by percent sequence homology
 - 70% is cutoff value for species definition
- Genomic fingerprinting
- Amino acid sequencing

Evolution of the Three Domains of Life

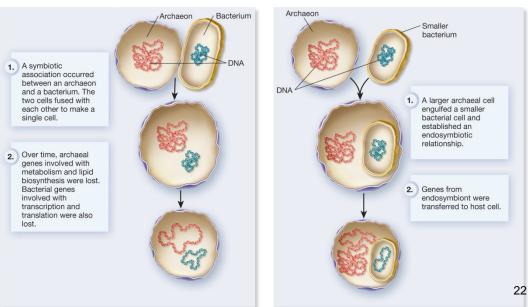
- Hypothesized that when RNA became enclosed in a lipid sphere, the first primitive life forms were generated
- Last universal common ancestor (LUCA)
 - the root of the tree of life, based on SSU rRNA, shows the earliest region is on the bacterial branch
 - thought that Archaea and Eukarya evolved independently of Bacteria

| Property | Bacteria | Archaea | Eukarya |
|---|--|---|--|
| | | | |
| 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; some have pseudomurein | No muramic acid |
| Membrane Lipid | Have ester-linked, straight- chained fatty acids | Have ether-linked, branched isoprene-derived chains | Have ester-linked, straight-chained fatty acids |
| Gas Vesicles | Present | Present | Absent |
| Transfer RNA | Thymine present in most tRNAs | No thymine in T or T Ψ C arm of tRNA | Thymine present |
| | <i>N</i> -formylmethionine carried by initiator tRNA | Methionine carried by initiator tRNA | Methionine carried by initiator tRNA |
| Polycistronic mRNA | Present | Present | Present in some protists |
| mRNA Introns | Rare | Rare | Present |
| mRNA Splicing, Capping, and Poly-A Tailing | Absent | Absent | Present |
| Ribosomes | | | |
| Size | 70S | 70S | 80S (cytoplasmic ribosome |
| 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 eukaryotic enzymes (8–12 subunits) | Complex subunit pattern (12–14 subunits) |
| Rifampicin sensitivity | Sensitive | Insensitive | Insensitive |
| RNA Polymerase II Type Promoters | Absent | Present | Present |
| Metabolism | | | |
| Similar ATP synthase | No | Yes | Yes |
| Methanogenesis | Absent | Present | Absent |
| Nitrogen fixation | Present | Present | Absent |
| Chlorophyll-based photosynthesis | Present | Absent | Present ¹ |
| Chemolithotrophy | Present | Present | Absent |

1 Present in chloroplasts (of bacterial origin).

Steps in Endosymbiotic Hypothesis

- Ancestral eukaryotic cell had lost cell wall
- Engulfment of an endosymbiote occurred
 - produced needed product such as ATP
- Genome reduction occurred
- Evolution of organelles
 - mitochondria
 - hydrogenosome
 - chloroplasts



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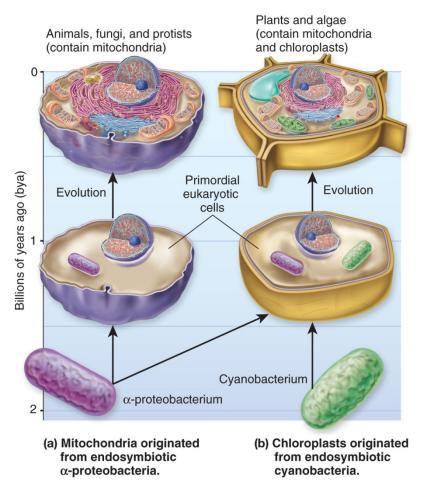
(a) Origin from cellular fusion

(b) Origin from endosymbiotic relationship

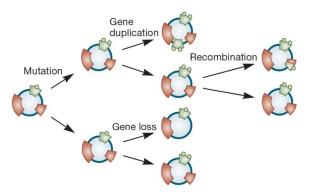
Mitochondria and Chloroplasts

- Believed to be descended from *Rickettsiae* and *Prochlorococcus*, engulfed in a precursor cell
 - provided essential function for host
 - engulfed organism thought to be aerobic, thereby eliminating oxygen toxicity to the host cell
 - host provided nutrients/safety for engulfed organism

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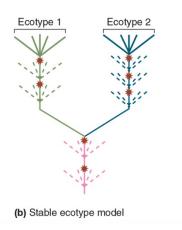


Microbial Evolutionary Processes



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(a) Mechanisms of genetic variation within a homogeneous population



- Bacteria and Archaea are asexual
- Heritable changes occur
 - mutation and natural selection
 - gene loss or gain
 - intragenomic recombination
 - horizontal gene transfer (HGT)

Anagenesis Model of Microbial Diversity

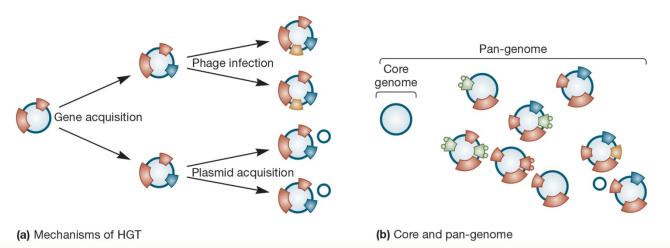
- Microevolution
 - also known as genetic drift
- Small, random genetic changes over generations which slowly drive either speciation or extinction, both of which are forms of macroevolution
 - only adaptive mutants are selected

Ecotype Model for Microbial Diversity

- Genetically similar population of microbes is ecologically distinct
- Members of specific ecosystem diversify and gain adaptive mutation to compete for resources
- Extinction occurs in other ecosystems and reduced genetic variation
- Punctuated equilibria

Horizontal Gene Transfer (HGT) Model for Microbial Diversity

- Pan-genome is complete gene repertoire of a taxon
 - includes the core genome plus "housekeeping" and dispensable genes
 - pan-genome genes acquired through HGT
 - requires genetically heterogeneous group of microbes



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Bergey's Manual of Systematic Bacteriology

- Accepted system of bacterial taxonomy
- Detailed work containing descriptions of all bacterial species currently identified
- First edition published in 1984, with significantly updated editions since