Taxonomy (Systematics)

Taxon: Group

Taxis+Nomos

Taxis: Arrangement Nomos: Law

Taxonomy

- Taxonomy: Science of Classification
- Classification of living organisms
- Establish a relationship between a group of microorganisms and among the others or seperate them from each other
- Taxonomy offers a common referance for microorganism classification as well.
- Because creates a universal language among scientists, taxonomy is a fundamental and necessary equipment

Taxonomy (Systematic)

1- Identification

2- Classification

3- Nomenclature

1. Identification

Morphological Features

Pathogenic Features

Chemical Features

Cultural Features

Metabolic Features

Ecological Features

Serological Features

Genetic Features(%G+C=G+C/G+C+A+T*100)

Molecular Features

2.Classification

- Natural (phylogenetic)
- Numerical
- Antigenic
- Phage
- Chemotaxonomy

Classification of Bacteria

- Natural (Phylogenetic)

Phylogenetic taxonomy reveals the evolutionary relationship or kinship among the germs and also in all living things. However, in this process the sequence of 16S rRNA/23S rRNA are utilized contrary the others (%G+C=G+C/G+C+A+T*100)

- Numerical

It is the method of the level of relations between the germs with statistical and mathematical methods by coding the various properties of the germs and given certain points.

Numerical taxonomy can be used of microorganisms biochemical,antigenic features , antibiotic susceptibility and nucleic acid sequence

However, genotypic and phenotypic characteristics should be evaluated separately. Namely, numerical taxonomy is made with;

- Phenotypic features
- Genotypic features (with the compared to 16S ribosomal RNA base sequence)

- Antigenic
- Phage
- Chemotaxonomy

Methods of Identification and Classification of Bacteria

- Morphologic Properties
- Staining Properties
- Biochemical Properties
- Antigenic Properties
- Serologic Propertiesfaj
- Phage Typing
- Fatty Acid Profiles
- Flow Cytometry
- DNA Base Composition
- DNA Fingerprinting
- Nucleic Acid Amplification Tests
- Nucleic Acid Hibridization
- DNA Chips
- Ribotyping
- Ribosomal DNA Sequencing

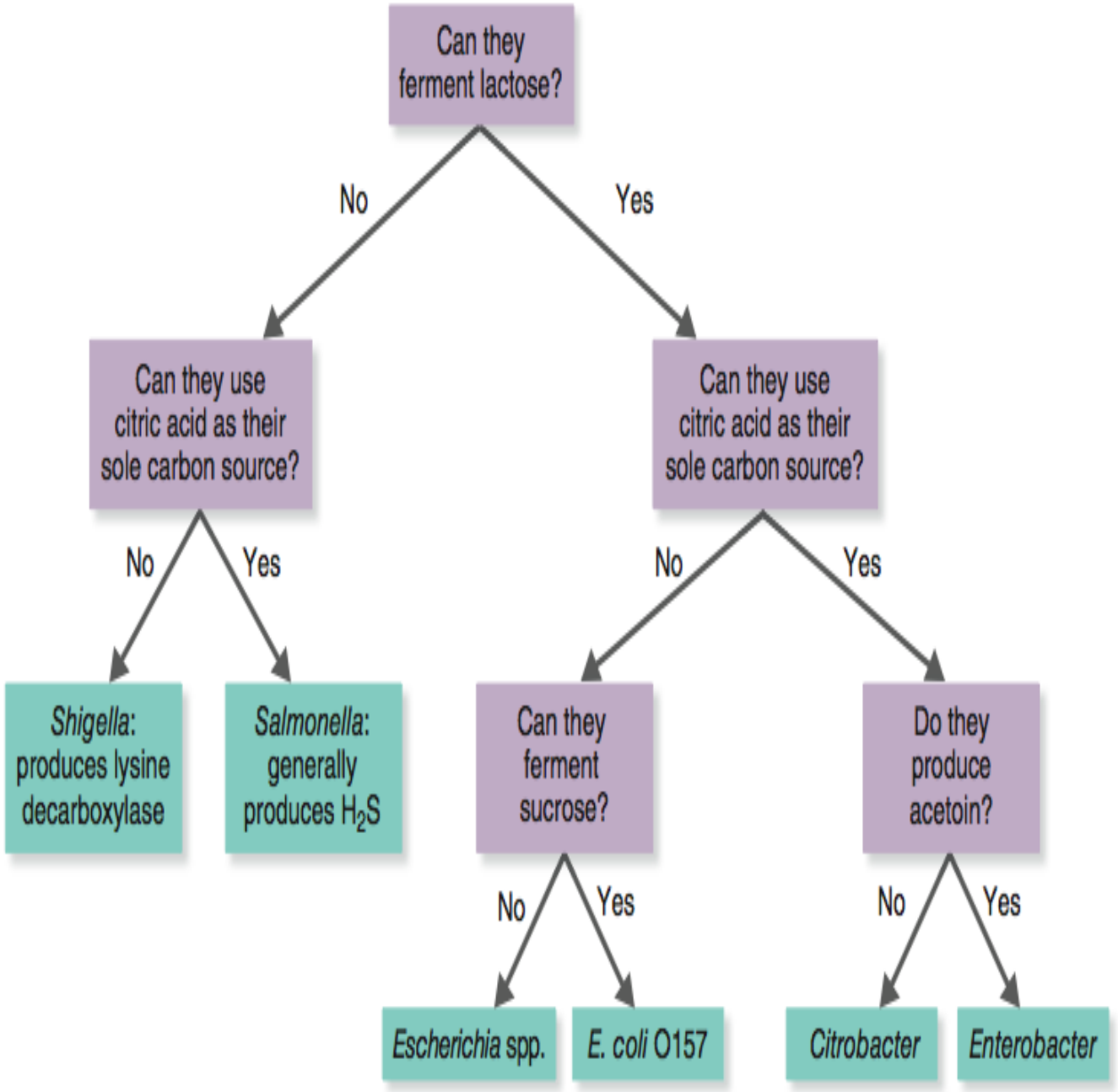
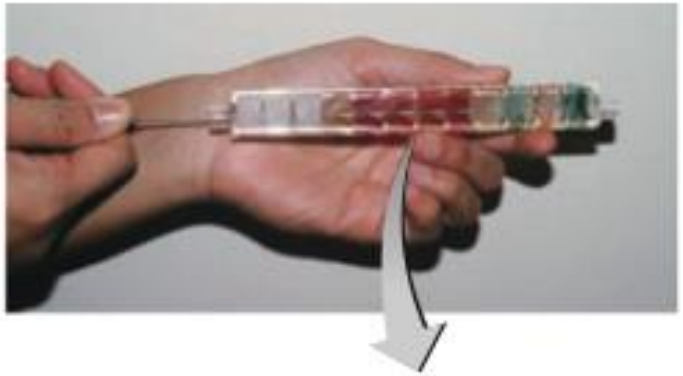


Figure 10.8 **The use of metabolic characteristics to identify selected genera of enteric bacteria.**

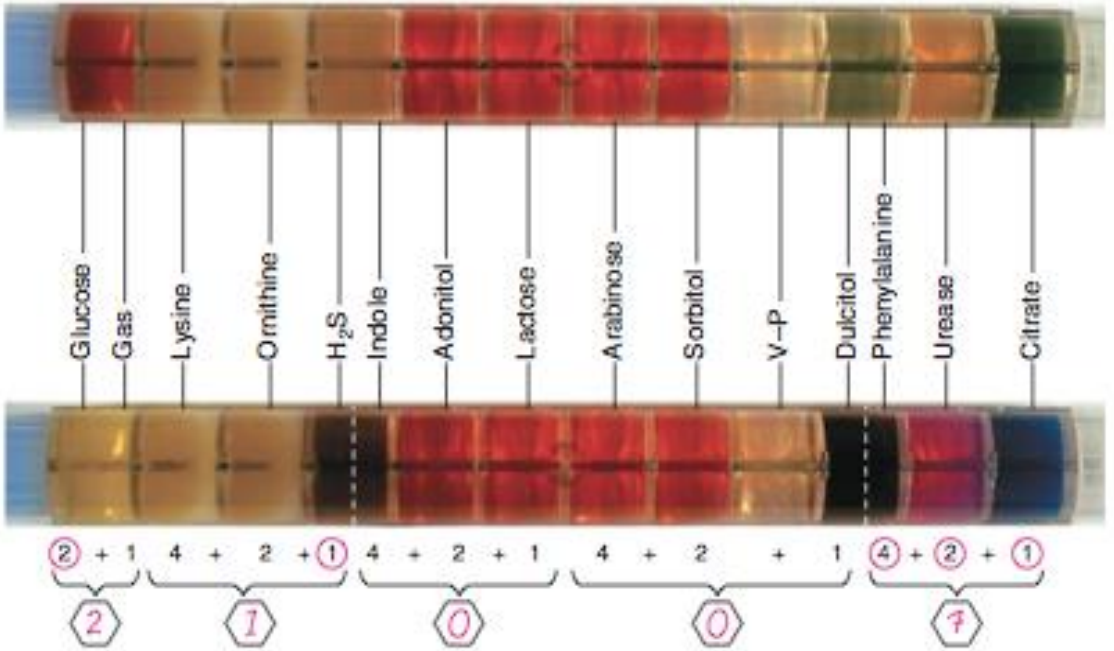
Q Assume you have a gram-negative bacterium that produces acid from lactose and cannot use citric acid as its sole carbon source. What is the bacterium?

1. One tube containing media for 15 biochemical tests is inoculated with an unknown enteric bacterium.



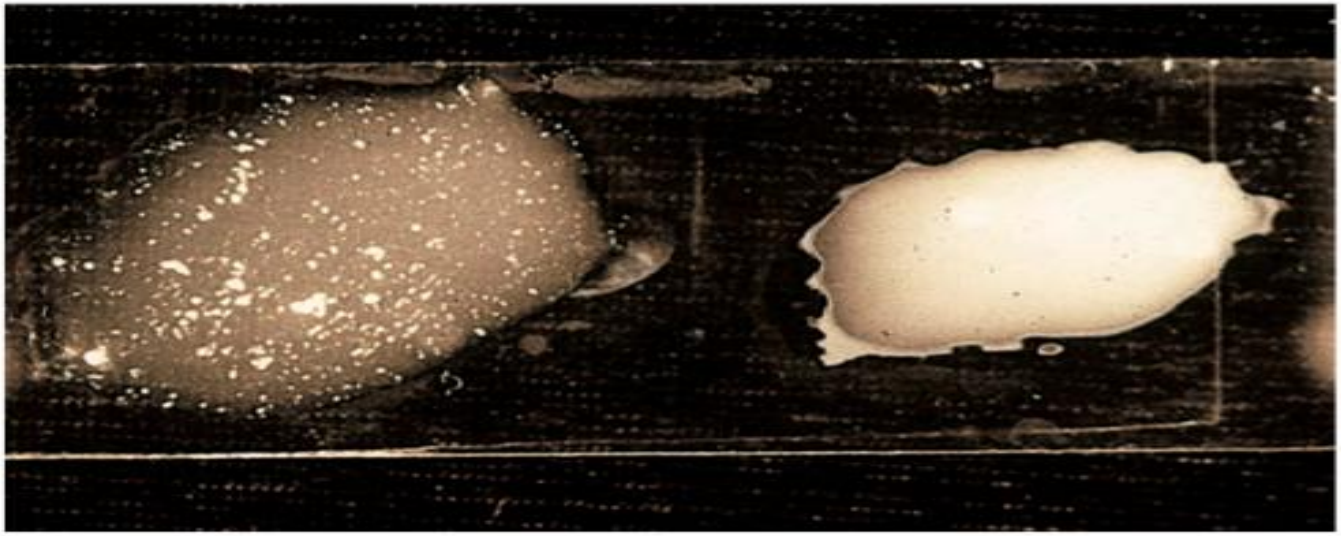
2. After incubation, the tube is observed for results.

3. The value for each positive test is circled, and the numbers from each group of tests are added to give the ID value.



4. Comparing the resultant ID value with a computerized listing shows that the organism in the tube is *Proteus mirabilis*.

ID Value	Organism	Atypical Test Results	Confirmatory Test
21006	*Proteus mirabilis*	Ornithine⁻	Sucrose
21007	*Proteus mirabilis*	Ornithine⁻	
21020	*Salmonella choleraesuis*	Lysine⁻	

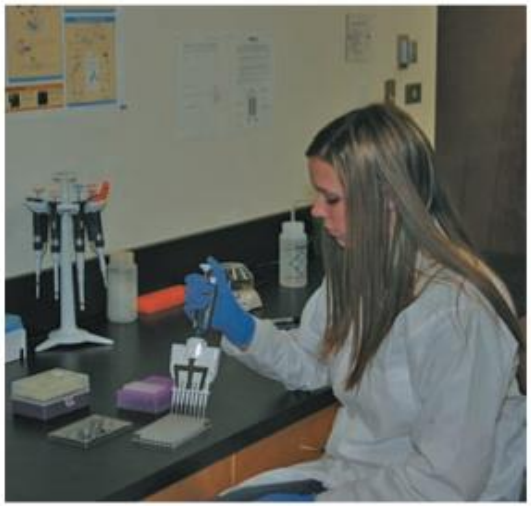


(a) Positive test **(b)** Negative test

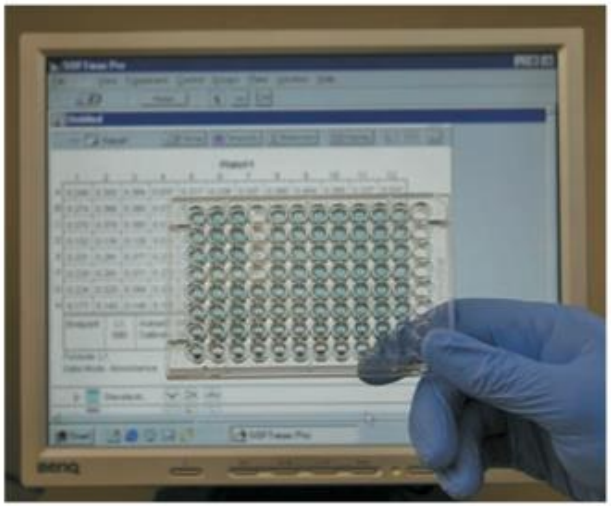
Figure 10.10 A slide agglutination test. (**a**) In a positive test, the grainy appearance is due to the clumping (agglutination) of the bacteria. (**b**) In a negative test, the bacteria are still evenly distributed in the saline and antiserum.

Figure 10.11 An ELISA test.

Q What are the similarities between the slide agglutination test and the ELISA test?



(a) A technician uses a micropipette to add samples to a microplate for an ELISA.



(b) ELISA results are then read by the computer scanner.

1. If Lyme disease is suspected in a patient: Electrophoresis is used to separate *Borrelia burgdorferi* proteins in the serum. Proteins move at different rates based on their charge and size when the gel is exposed to an electric current.

2. The bands are transferred to a nitrocellulose filter by blotting. Each band consists of many molecules of a particular protein (antigen). The bands are not visible at this point.

3. The proteins (antigens) are positioned on the filter exactly as they were on the gel. The filter is then washed with patient's serum followed by anti-human antibodies tagged with an enzyme. The patient antibodies that combine with their specific antigen are visible (shown here in red) when the enzyme's substrate is added.

4. The test is read. If the tagged antibodies stick to the filter, evidence of the presence of the microorganism in question—in this case, *B. burgdorferi*—has been found in the patient's serum.

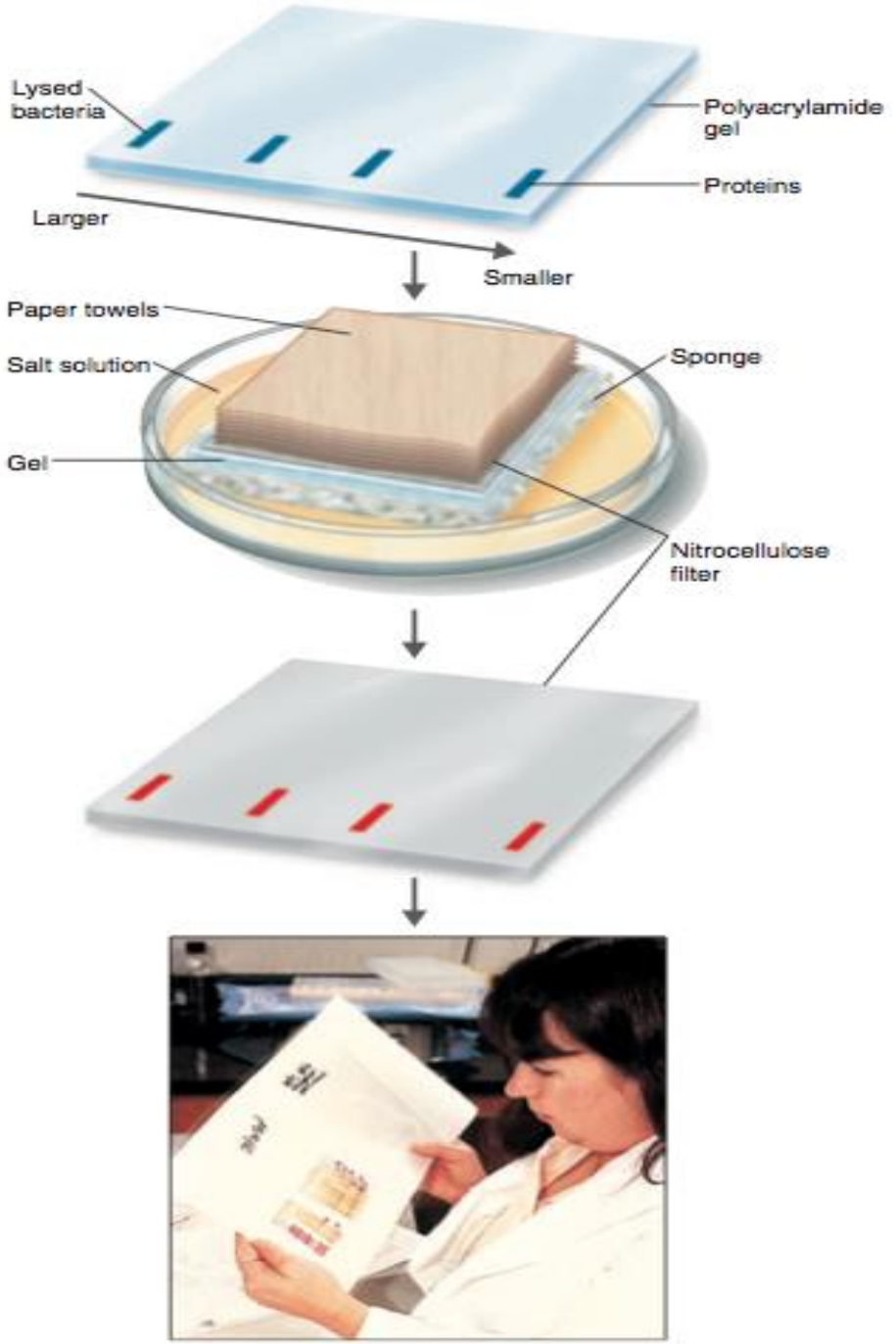


Figure 10.12 The Western blot. Proteins separated by electrophoresis can be detected by their reactions with antibodies.

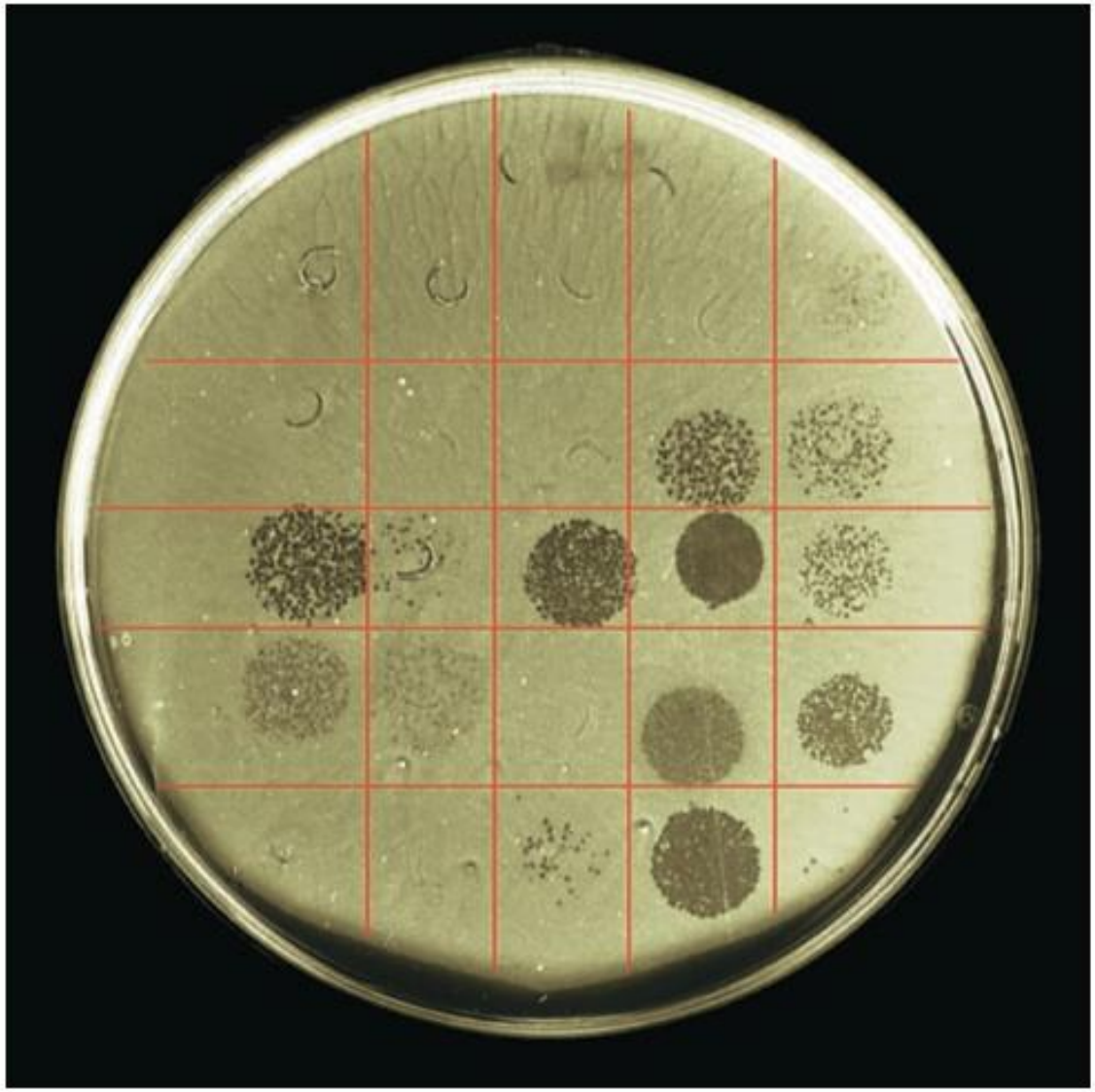


Figure 10.13 Phage typing of a strain of *Salmonella enterica*. The tested strain was grown over the entire plate. Plaques, or areas of lysis, were produced by bacteriophages, indicating that the strain was sensitive to infection by these phages. Phage typing is used to distinguish *S. enterica* serotypes and *Staphylococcus aureus* types.

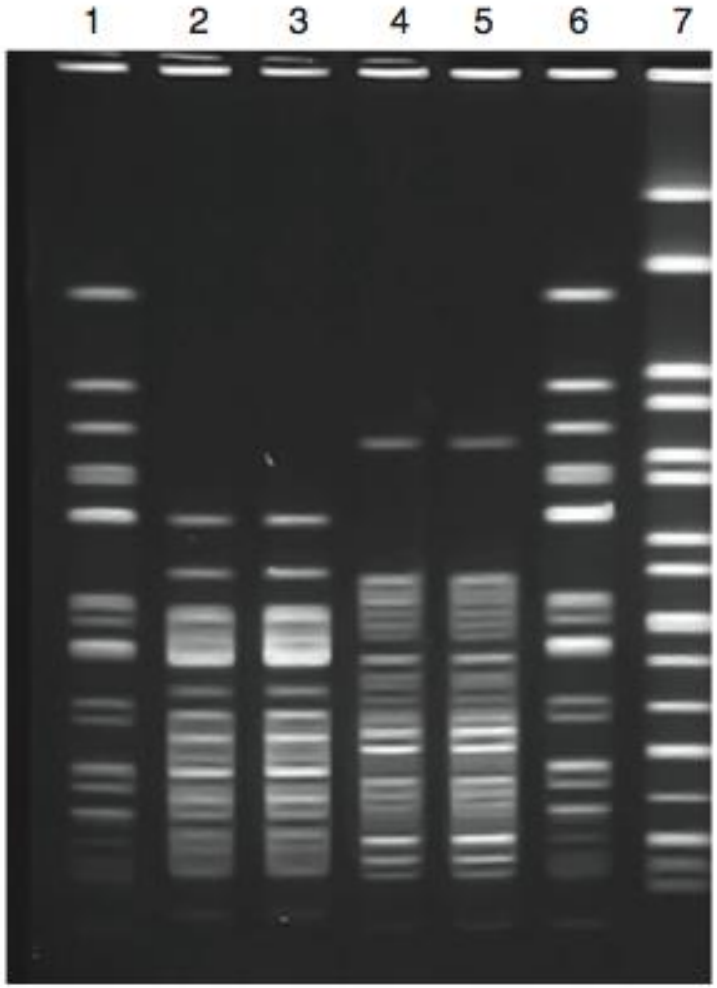


Figure 10.14 DNA fingerprints. DNA from seven different bacteria was digested with the same restriction enzyme. Each digest was put in a different well (origin) in the agarose gel. An electrical current was then applied to the gel to separate the fragments by size and electrical charge. The DNA was made visible by staining with a dye that fluoresces under ultraviolet light. Comparison of the lanes shows that DNA samples (and therefore the bacteria) in lanes 2 and 3; 4 and 5; and 1 and 6 are identical.

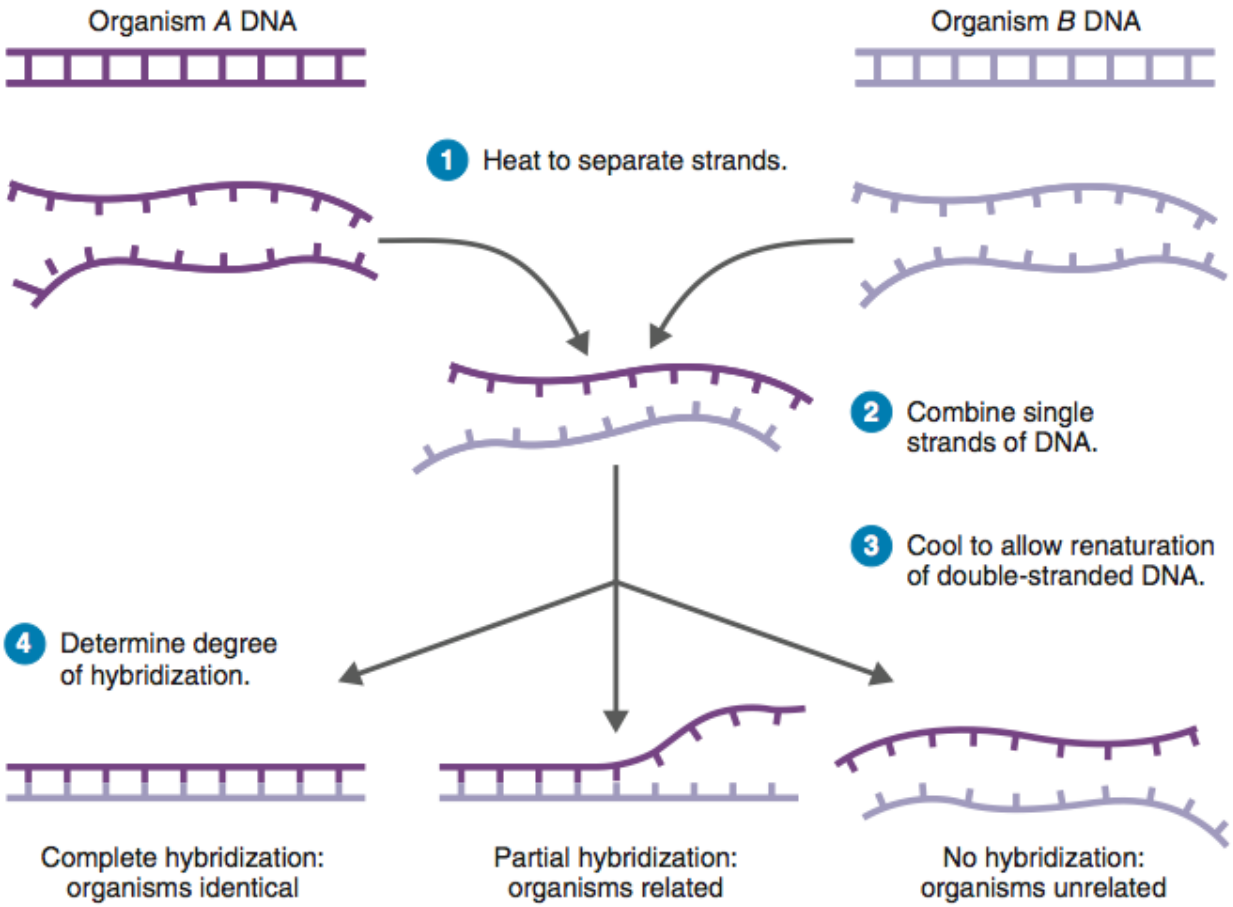
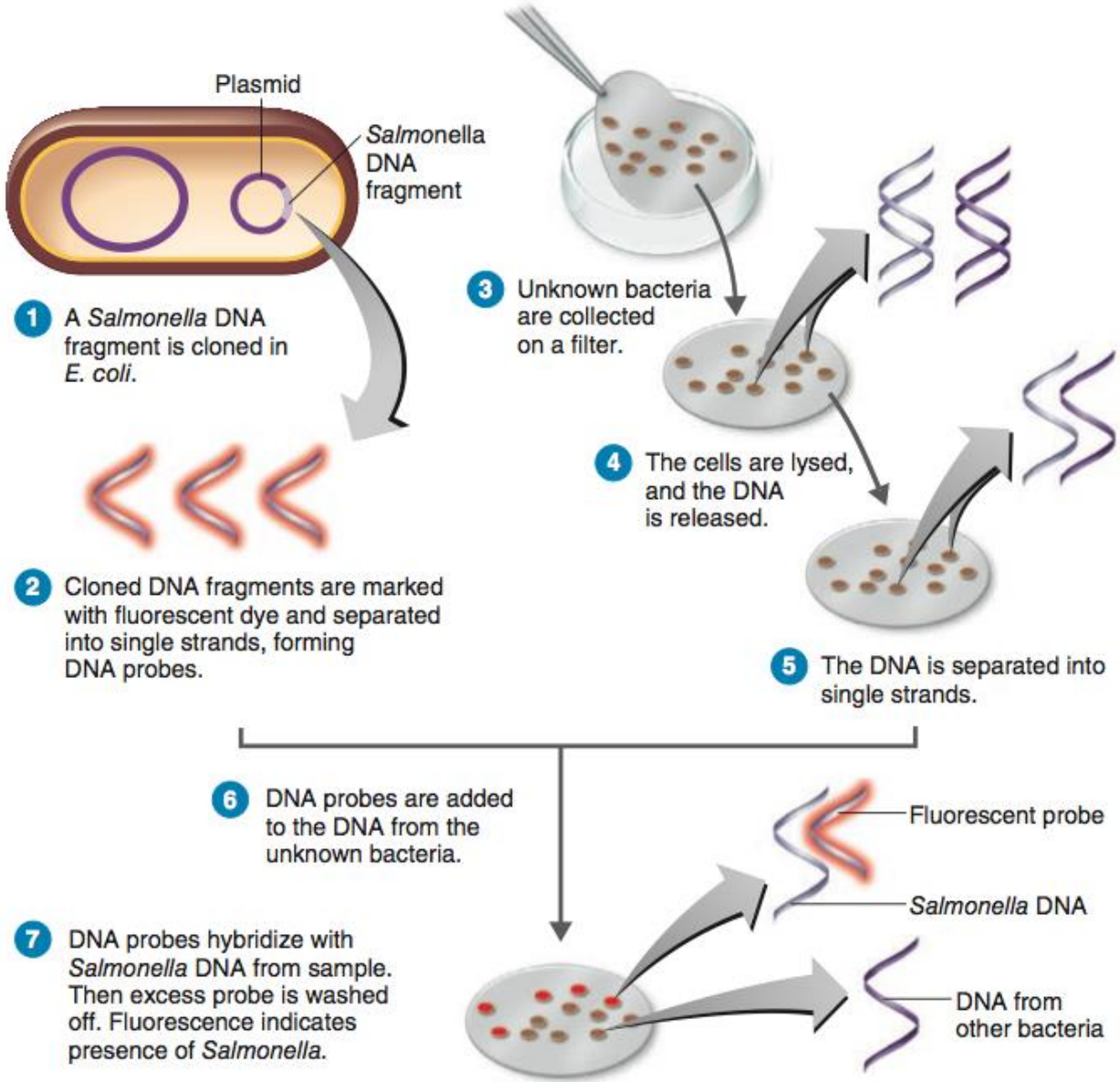


Figure 10.15 DNA-DNA hybridization. The greater the amount of pairing between DNA strands from different organisms (hybridization), the more closely the organisms are related.

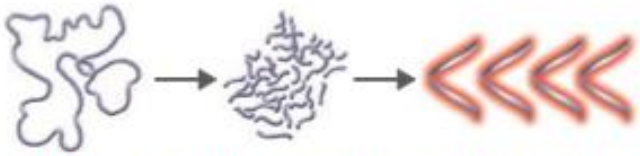
Q What is the principle involved in DNA probes?

Figure 10.16 A DNA probe used to identify bacteria. Southern blotting is used to detect specific DNA. This modification of the Southern blot is used to detect *Salmonella*.

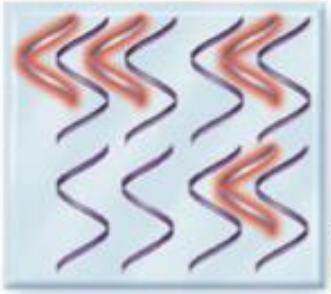
Q Why do the DNA probe and cellular DNA hybridize?



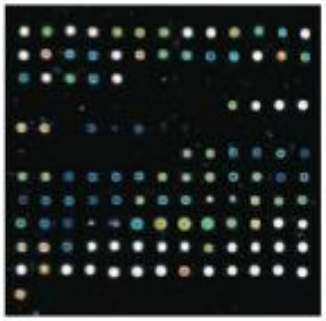
(a) A DNA chip can be manufactured to contain hundreds of thousands of synthetic single-stranded DNA sequences. Assume that each DNA sequence was unique to a different gene.



(b) Unknown DNA from a sample is separated into single strands, enzymatically cut, and labeled with a fluorescent dye.



(c) The unknown DNA is inserted into the chip and allowed to hybridize with the DNA on the chip.



(d) The tagged DNA will bind only to the complementary DNA on the chip. The bound DNA will be detected by its fluorescent dye and analyzed by a computer. In this *Salmonella* antimicrobial resistance gene microarray, *S. typhimurium*-specific antibiotic resistance gene probes are green, *S. typhi*-specific resistance gene probes are red, and antibiotic-resistance genes found in both serovars appear yellow/orange.

Figure 10.17 DNA chip. This DNA chip contains probes for antibiotic-resistance genes. It is used to detect antibiotic-resistant bacteria in samples collected from animals on a farm or in slaughter facilities.

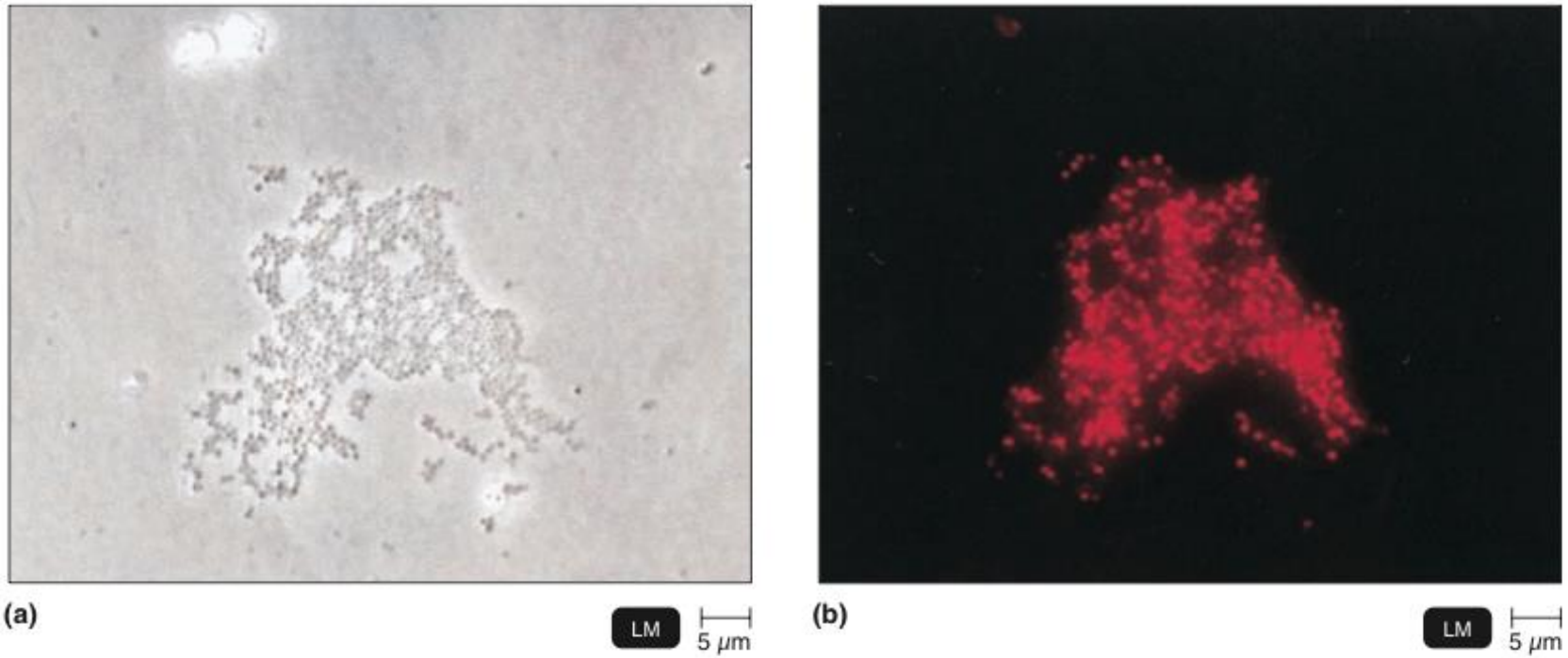


Figure 10.18 FISH, or fluorescent in situ hybridization. A DNA or RNA probe attached to fluorescent dyes is used to identify chromosomes. Bacteria seen with phase-contrast microscopy (**a**) are identified with a fluorescent-labeled probe that hybridizes with a specific sequence of DNA in *Staphylococcus aureus* (**b**).

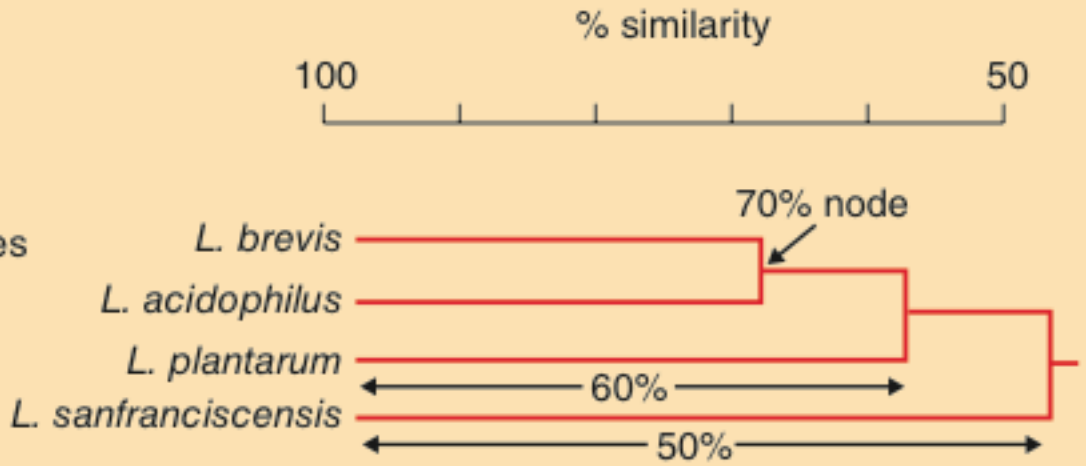
1. Determine the sequence of bases in an rRNA molecule for each organism. Only a short sequence of bases is shown for this example.

Lactobacillus brevis	AGUCCAGAGC
L. sanfranciscensis	GUAAAAGAGC
L. acidophilus	AGCGGAGAGC
L. plantarum	ACGUUAGAGC

2. Calculate the percentage of similarity in the nucleotide bases between pairs of species. For example, there is a 70% similarity between the sequences for *L. brevis* and *L. acidophilus*.

	Percent similarity
L. brevis → *L. sanfranciscensis*	50%
L. brevis → *L. acidophilus*	70%
L. brevis → *L. plantarum*	60%
L. sanfranciscensis → *L. acidophilus*	50%
L. sanfranciscensis → *L. plantarum*	50%
L. plantarum → *L. acidophilus*	60%

3. Construct a cladogram. The length of the horizontal lines corresponds to the percent similarity values. Each branch point, or node, in the cladogram represents an ancestor common to all species beyond that node. Each node is defined by a similarity in rRNA present in all species beyond that branch point.



3. Nomenclature

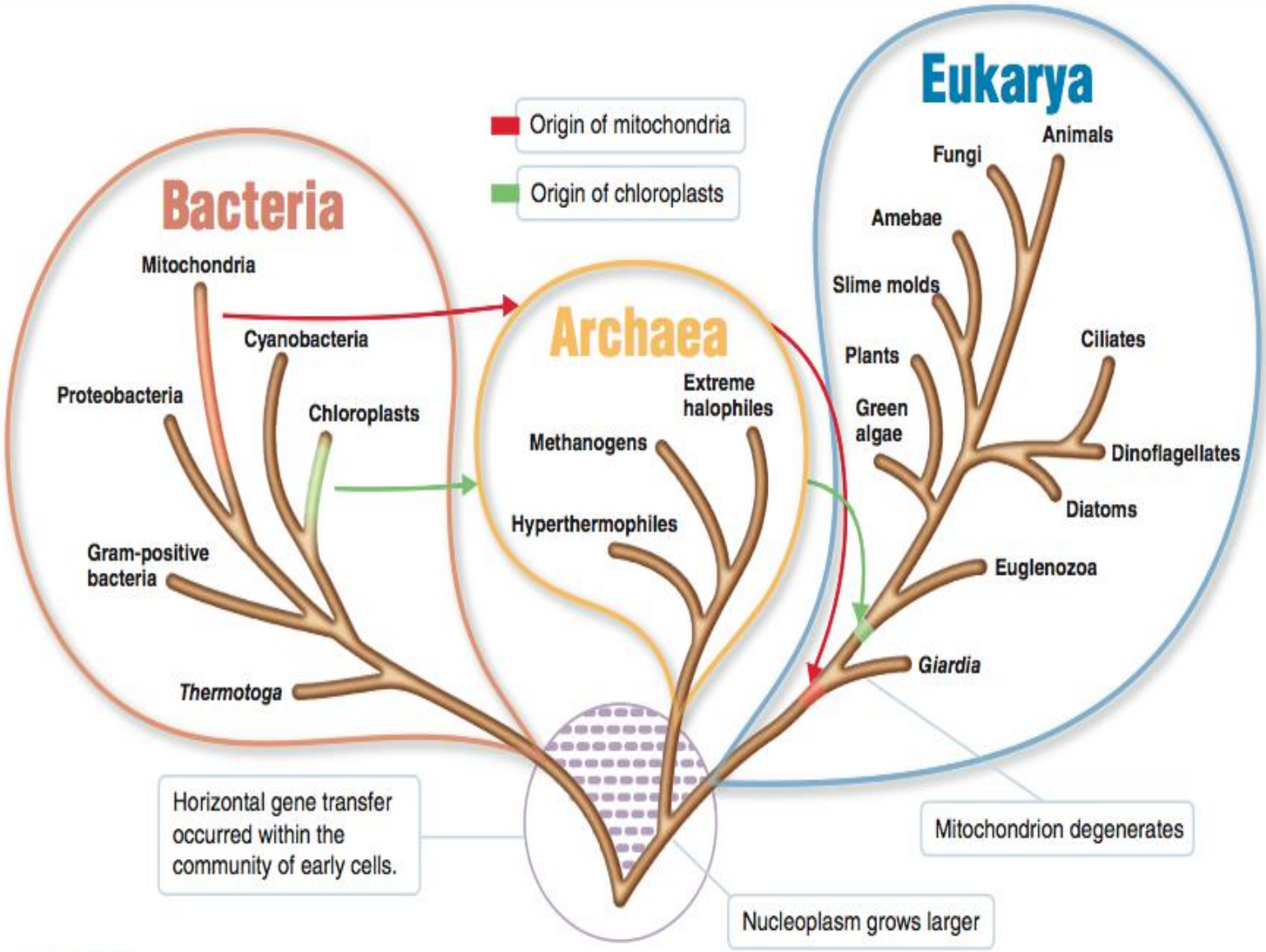
Sceintific classification is made up of 2 words:

GENUS + SPECIES

Bacillus anthracis	*Bac. anthracis*	*B. anthracis*
Staphylococcus aureus	*Staph. aureus*	*S. aureus*
Streptococcus pyogenes	*Str. pyogenes*	*S. pyogenes*

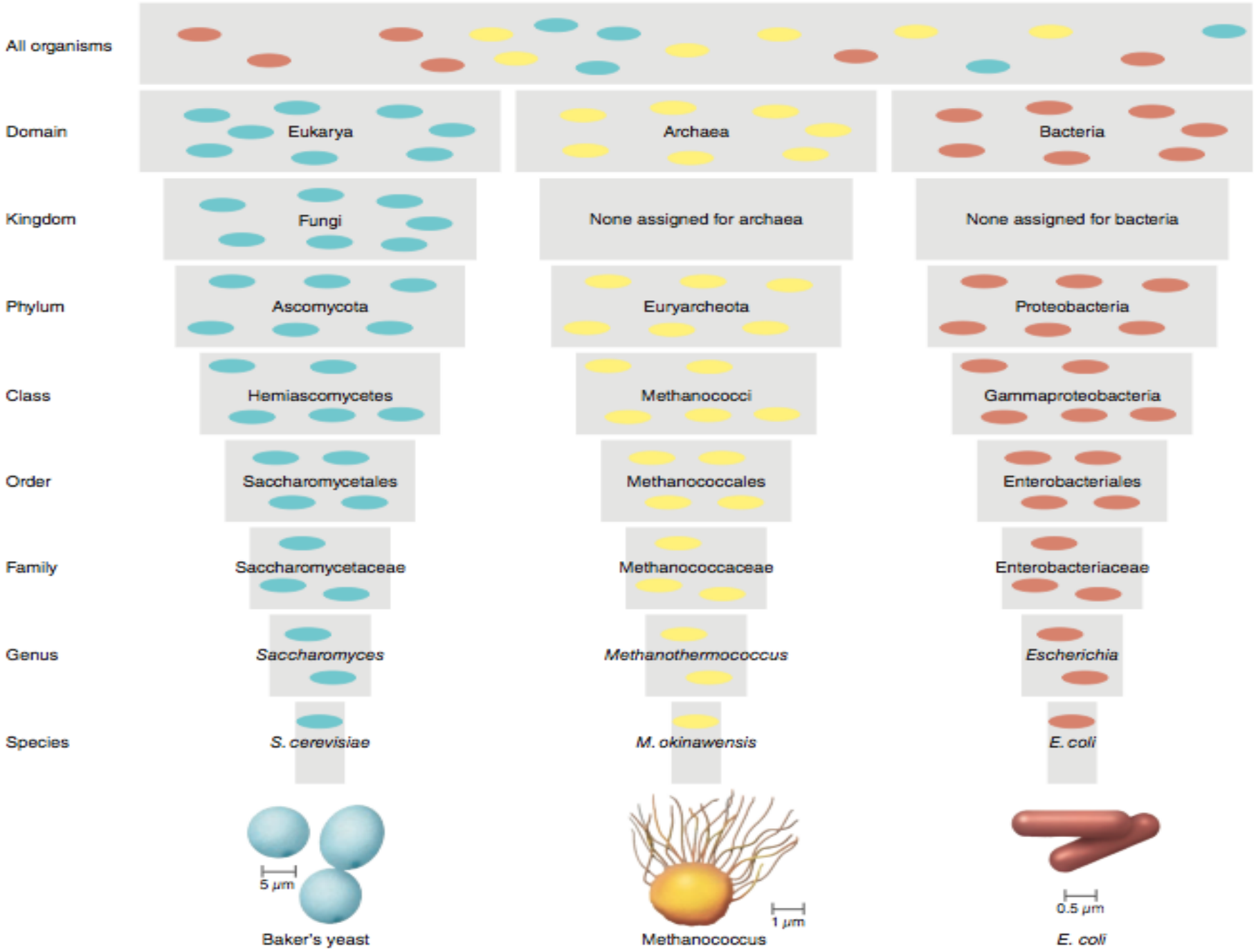
3. Nomenclature

- In the process of identification of bacteria, it is aimed to define the microorganism, honor the finder of the bacteria or describe the habitat in which these species are involved.
- Example: *Staphylococcus aureus*
- Staphylo (bunch of grapes) / coccus (globular) / aureus (means gold in Latin)
- *Escherichia coli*
- Theodor Escherich (finder/ coli (colon; where factor found)



KEY CONCEPTS

- All organisms evolved from cells that formed over 3 billion years ago.
- The DNA passed on from ancestors is described as *conserved*.
- The Domain Eukarya includes the Kingdoms Fungi, Plantae, and Animalia, as well as protists. The Domains Bacteria and Archaea are prokaryotes.


All organisms
Domain
Eukarya
Archaea
Bacteria
Kingdom
Fungi
None assigned for archaea
None assigned for bacteria
Phylum
Ascomycota
Euryarcheota
Proteobacteria
Class
Hemiascomycetes
Methanococci
Gammaproteobacteria
Order
Saccharomycetales
Methanococcales
Enterobacteriales
Family
Saccharomycetaceae
Methanococcaceae
Enterobacteriaceae
Genus
Saccharomyces
Methanothermococcus
Escherichia
Species
S. cerevisiae
M. okinawensis
E. coli
5 µm
1 µm
0.5 µm
Baker's yeast
Methanococcus
E. coli

REGNUM (KINGDOM)	: Eubacteria
DIVISION (PHYLUM)	: Proteobacteria
CLASS (CLASSIO)	: Gamma Proteobacteria
TRIBE	: Enterobacteriales
FAMILY (FAMILIA)	: Enterobacteriaceae
GENUS	: *Escherichia*
SPECIES	: *Echerichia coli*
SUBSPECIES	