

Lecture-13

Microbial classification

Content

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 - ❑ Taxonomy
 - ❑ Systematics
- ❑ Phenotypic Analysis
- ❑ Genotypic Analysis
- ❑ Classification and Nomenclature

Definitions

Taxonomy

- The science of identification, classification, and nomenclature

Systematics

- The study of the diversity of organisms and their relationships
- Links phylogeny with taxonomy

Definitions

The *polyphasic approach* to taxonomy uses three methods:

1. Phenotypic analysis
2. Genotypic analysis
3. Phylogenetic analysis

Approaches in taxonomy

The polyphasic approach to taxonomy uses three methods:

1. Phenotypic analysis



2. Genotypic analysis

3. Phylogenetic analysis

Examines the morphological, metabolic, physiological, and chemical characters of the cell

Approaches in taxonomy

The polyphasic approach to taxonomy uses three methods:

1. Phenotypic analysis

2. Genotypic analysis 

3. Phylogenetic analysis

Several methods of genotypic analysis are available:

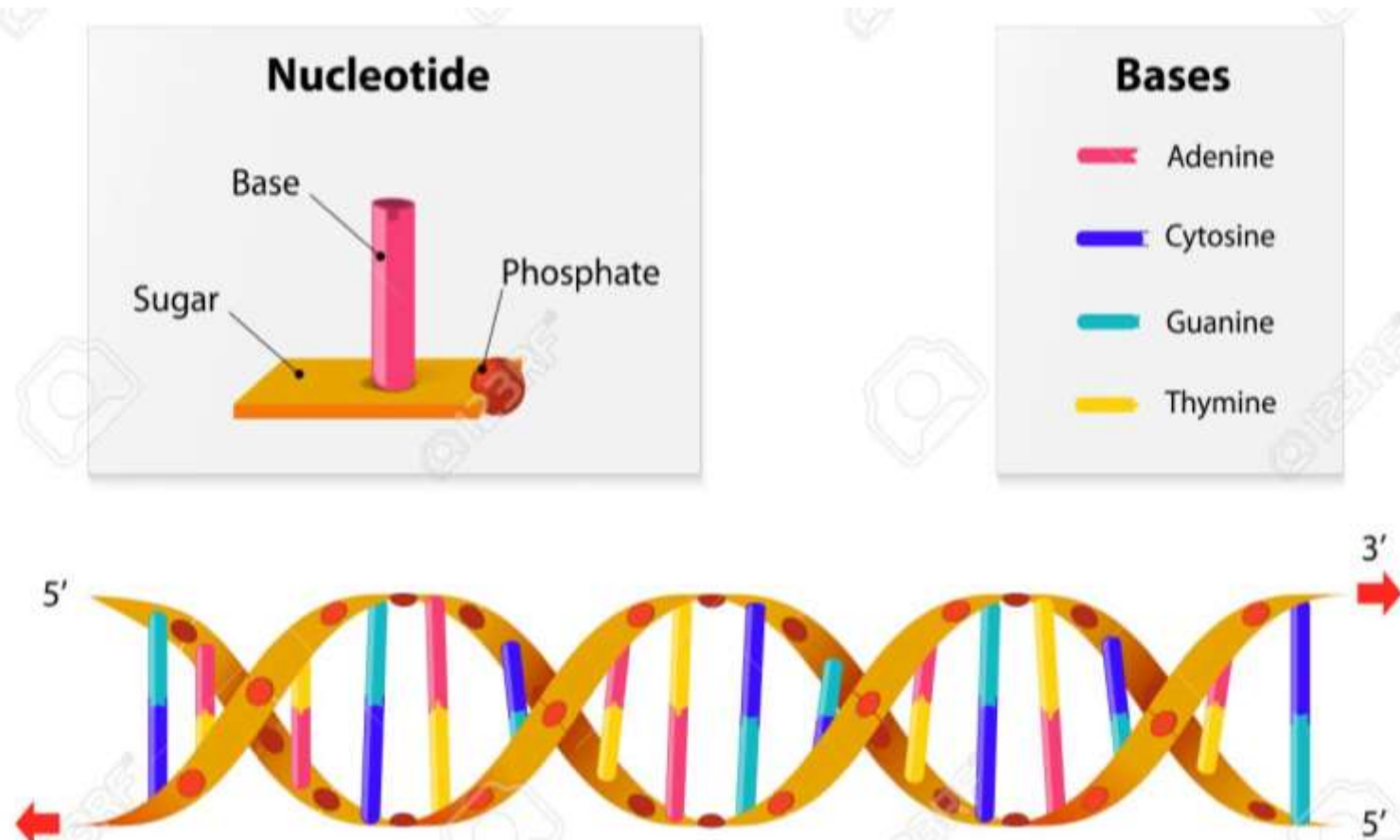
1. DNA–DNA hybridization

2. DNA profiling

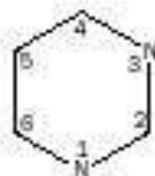
3. Multilocus sequence typing (MLST)

4. GC ratio

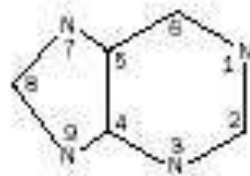
Genotypic analysis



BASES

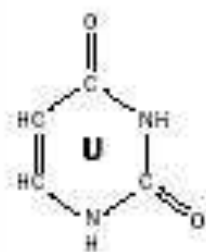


PYRIMIDINE

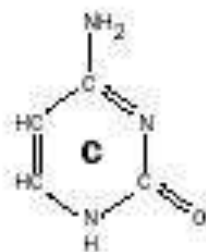


PURINE

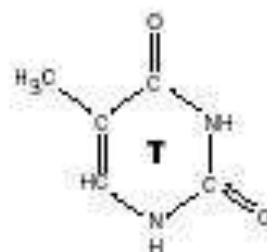
The bases are nitrogen-containing ring compounds, either purines or pyrimidines.



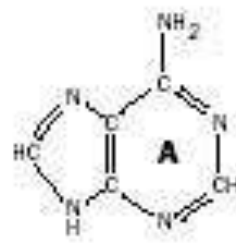
uracil



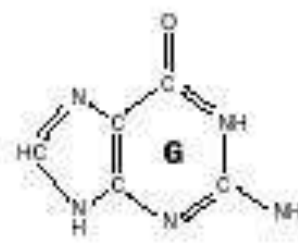
cytosine



thymine



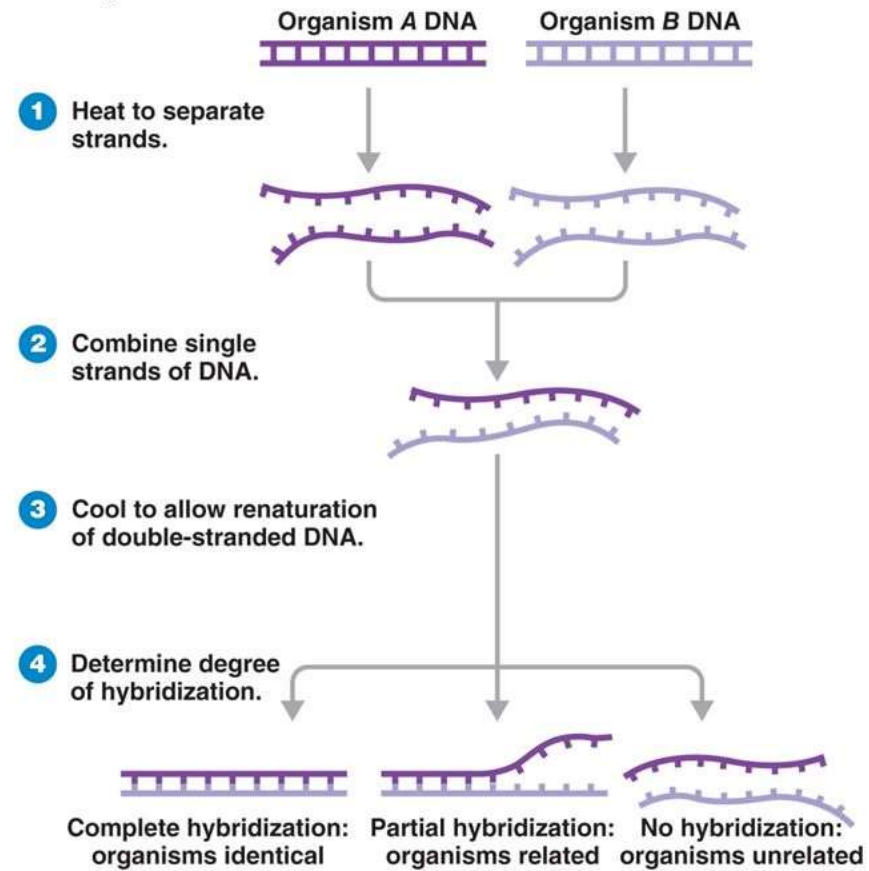
adenine



guanine

DNA-DNA hybridization

Figure 10.15 DNA-DNA hybridization.



GC ratio

The diagram shows a hand-drawn calculation on a green grid background. At the top, the DNA sequence **CTTGGCCCGAGGGAC** is written in red and green. Below it, the number of G and C bases is counted as $G/C = 11$. The GC content is then calculated as a fraction: $GC \text{ content} = \frac{11}{15}$. Finally, this fraction is converted to a percentage: $= 73.33\%$. A hand holding a green marker is shown on the right side of the grid.

CTTGGCCCGAGGGAC

$G/C = 11$

$GC \text{ content} = \frac{11}{15}$

$= 73.33\%$

Approaches in taxonomy

The polyphasic approach to taxonomy uses three methods:

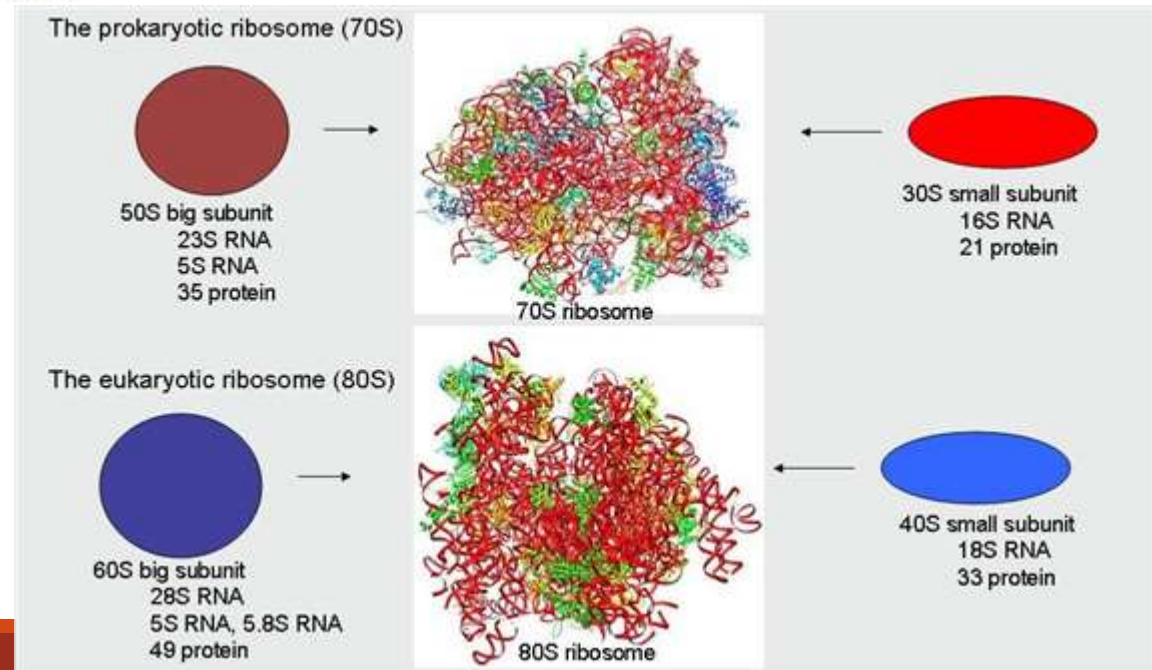
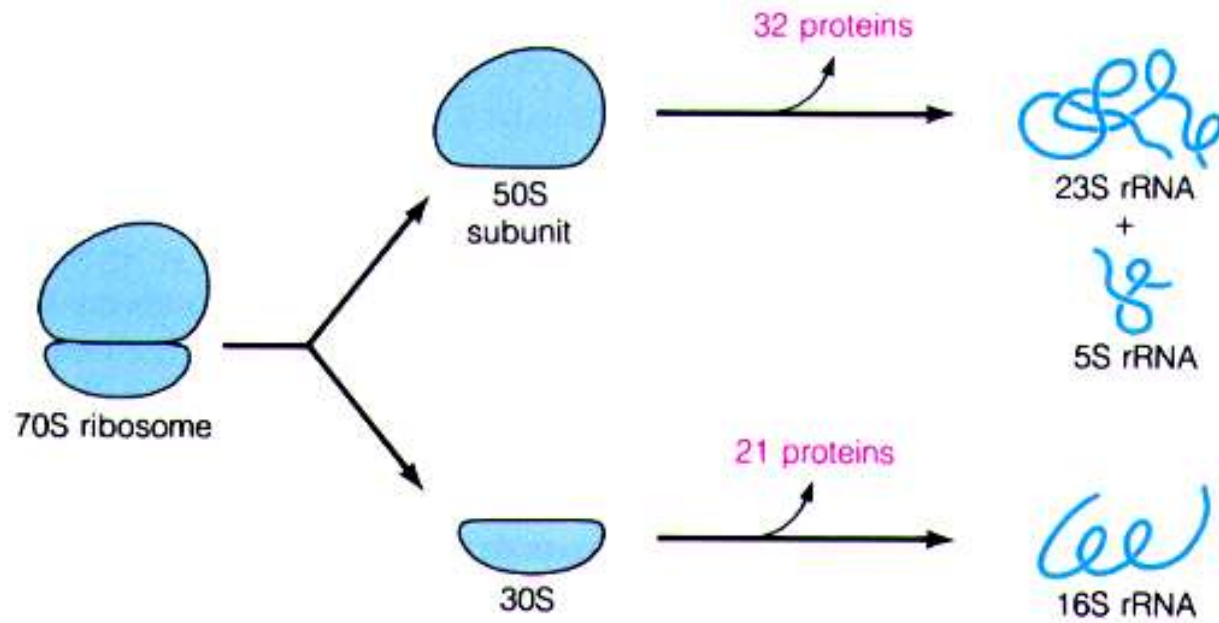
1. Phenotypic analysis
2. Genotypic analysis

3. Phylogenetic analysis

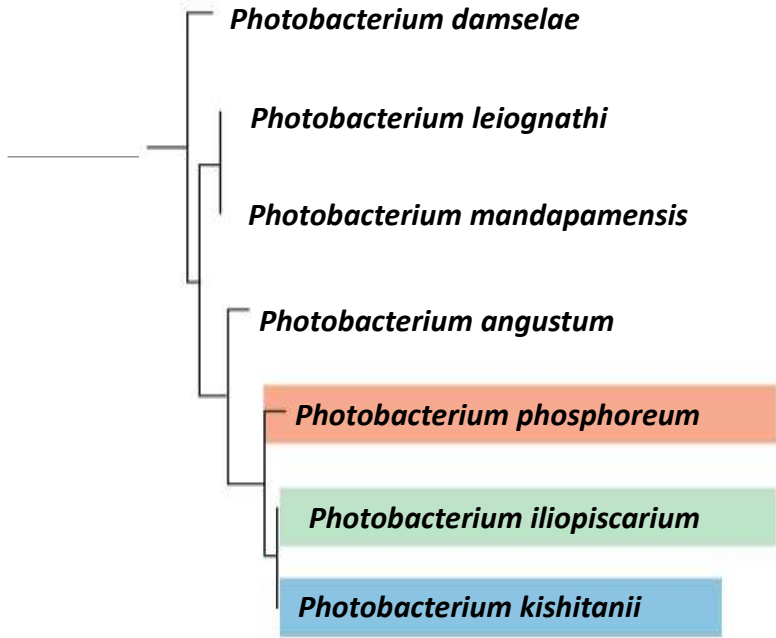


The means of estimating the relationships between microorganisms

- 16S rRNA gene sequences are useful in taxonomy; serve as “gold standard” for the identification and description of new species
- Whole-genome sequence analyses are becoming more common
 1. Genome structure: size and number of chromosomes, GC ratio, etc.
 2. Gene content
 3. Gene order

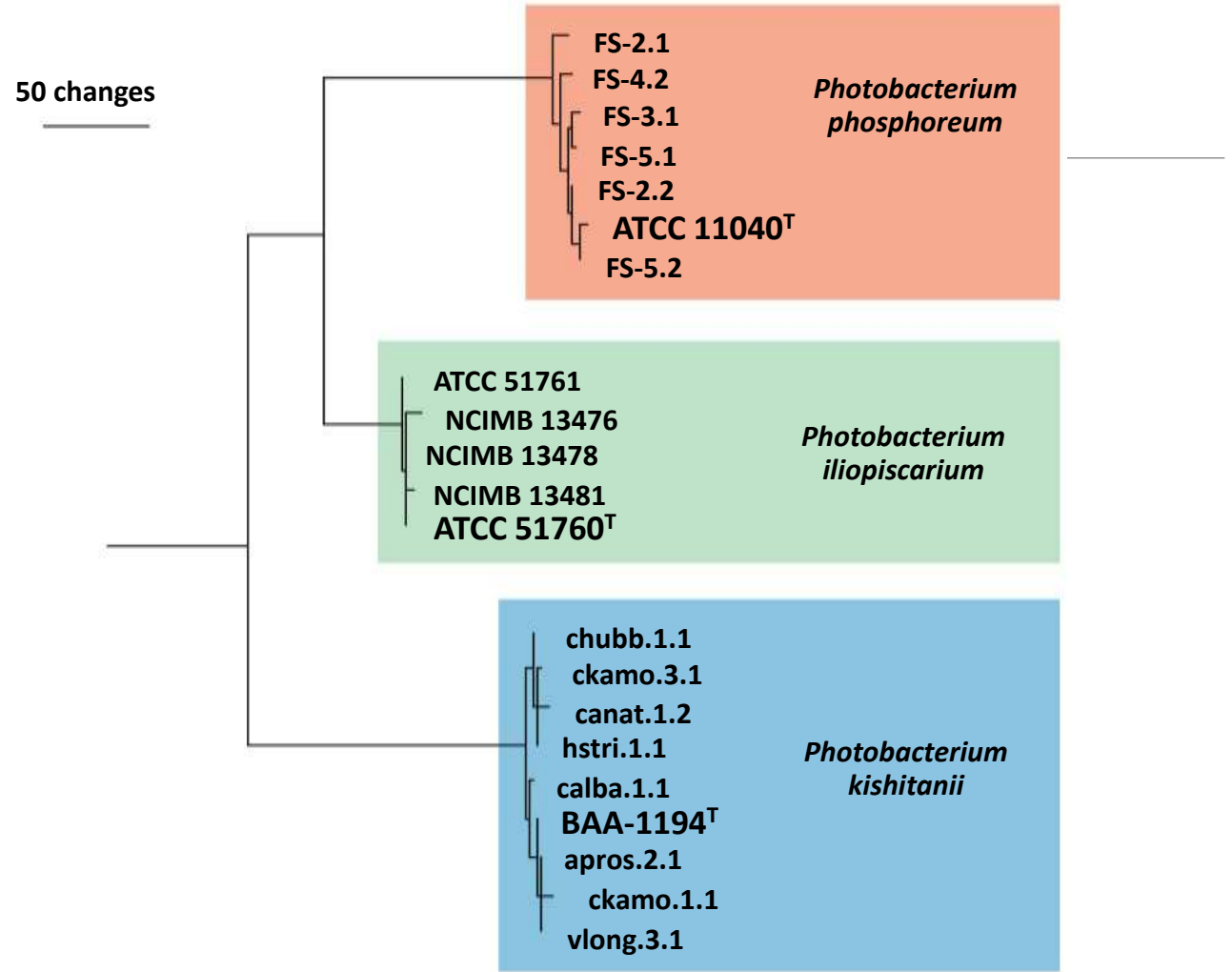


16S rRNA Gene Tree



(a)

Multigene Tree



(b)

Classification and Nomenclature

Classification

Organization of organisms into groups on the basis of either phenotypic similarity or evolutionary relationship

- Prokaryotes are given descriptive genus names and species epithets following the binomial system of nomenclature used throughout biology
- Assignment of names for species and higher groups of prokaryotes is regulated by the *International Code of Nomenclature of Bacteria*
- Major references in bacterial diversity:
 - *Bergey's Manual of Systematic Bacteriology*
 - *The Prokaryotes*