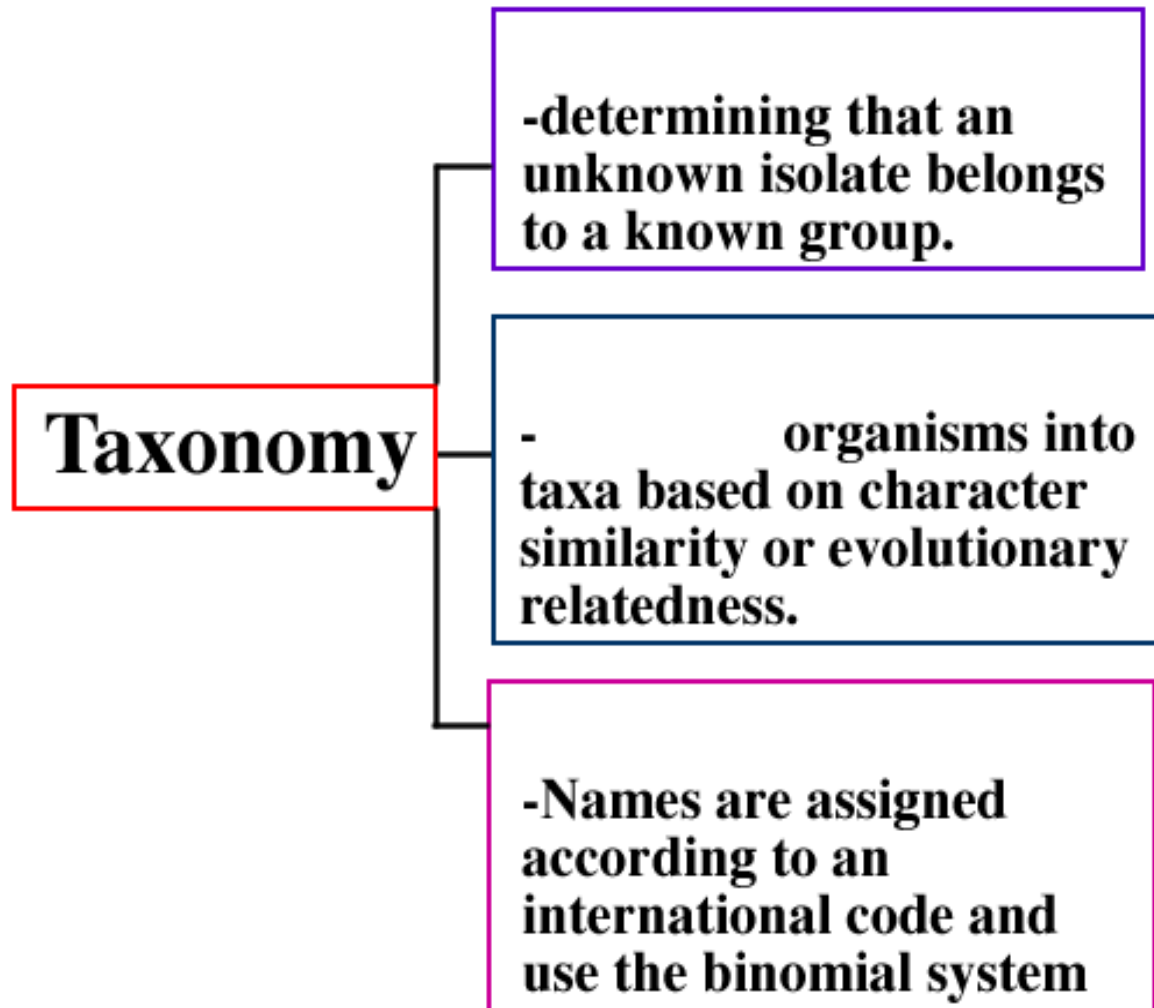


# Lecture 21: Microbial Taxonomy

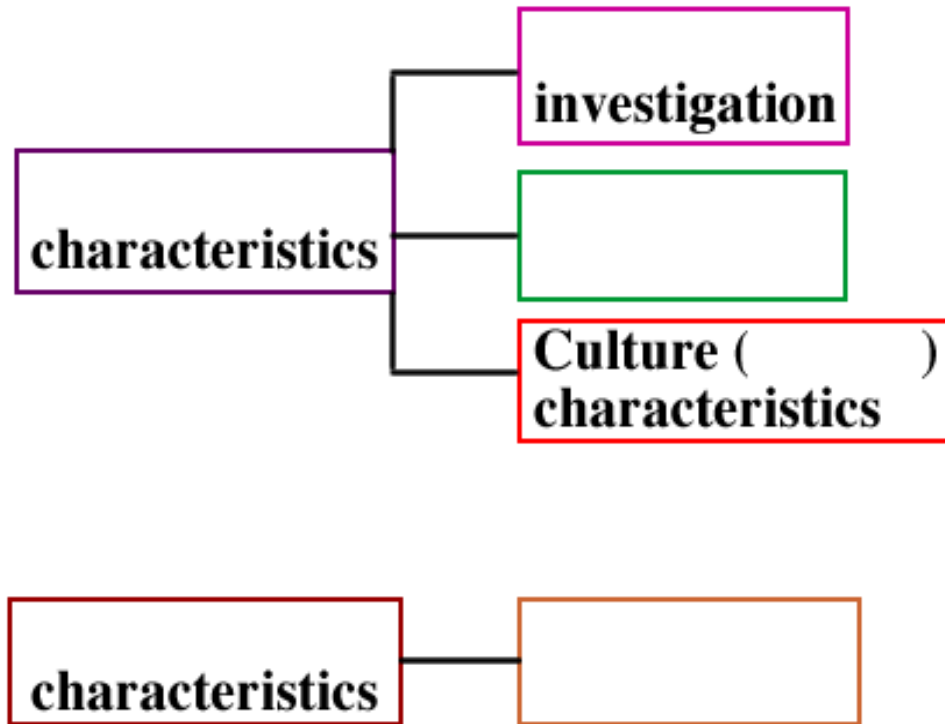
## Identification and Classification of Prokaryotes

### I. Principles of taxonomy

= a science that studies organisms in order to



A.



\*In a clinical setting, a  can also help to narrow down the possibilities of the organism responsible.

B. : based on phenotypic and genotypic differences

- Complicated by and inability to

(e.g species can not be defined as groups of interbreeding or potentially interbreeding populations).

- Because of these difficulties, the use of genotypic similarities and

is extremely useful in

prokaryotic classification.

# 1. Taxonomic hierarchies

**A collection of similar phyla.**

**A collection of similar classes.**

**A collection of In prokaryotic nomenclature, class name**

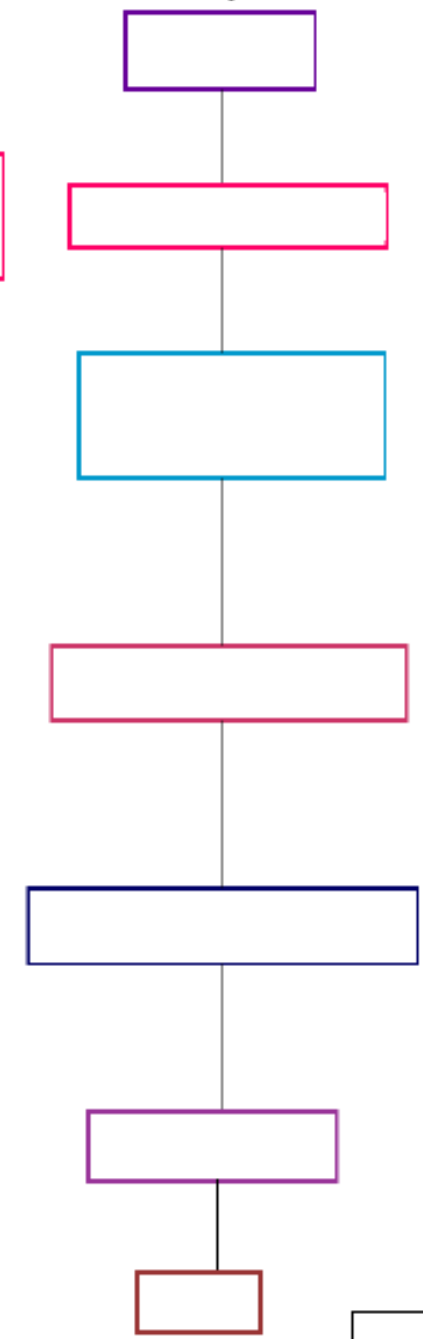
**A collection of similar families. In prokaryotic nomenclature, order name**

**A collection of In prokaryotic nomenclature, family name**

**= A collection of**

**= a group of related**

*Example:*



\*Note- sometimes informal groupings are used (e.g. The or the ).

## 2. Classification systems

In 1970, Carl Woese and colleagues proposed a classification system based on rRNA sequences. The domains archaea and bacteria diverged first and the eukaryotic cell is thought to have arose ~

II. (based on similarity of phenotypic characteristics):

Numerical taxonomy

A. Determines relatedness based on the percentage of (e.g. motility, ability to degrade lactose etc..)

B. Between 50 and several hundred characteristics are tested and a ( $S_{SM}$ ) is calculated:

$$S_{SM} = \frac{\text{Total number of characteristics compared}}{\text{Total number of characteristics compared}}$$

B. Simple matching coefficients are arranged to construct a

**Example adapted from Prescott's Microbiology**

|           |   | Bacterium |      |      |      |      |     |
|-----------|---|-----------|------|------|------|------|-----|
|           |   | 1         | 2    | 3    | 4    | 5    | 6   |
| Bacterium | 1 | 1.0       |      |      |      |      |     |
|           | 2 | 0.92      | 1.0  |      |      |      |     |
|           | 3 | 0.81      | 0.77 | 1.0  |      |      |     |
|           | 4 | 0.27      | 0.31 | 0.29 | 1.0  |      |     |
|           | 5 | 0.43      | 0.41 | 0.45 | 0.30 | 1.0  |     |
|           | 6 | 0.38      | 0.42 | 0.44 | 0.32 | 0.72 | 1.0 |

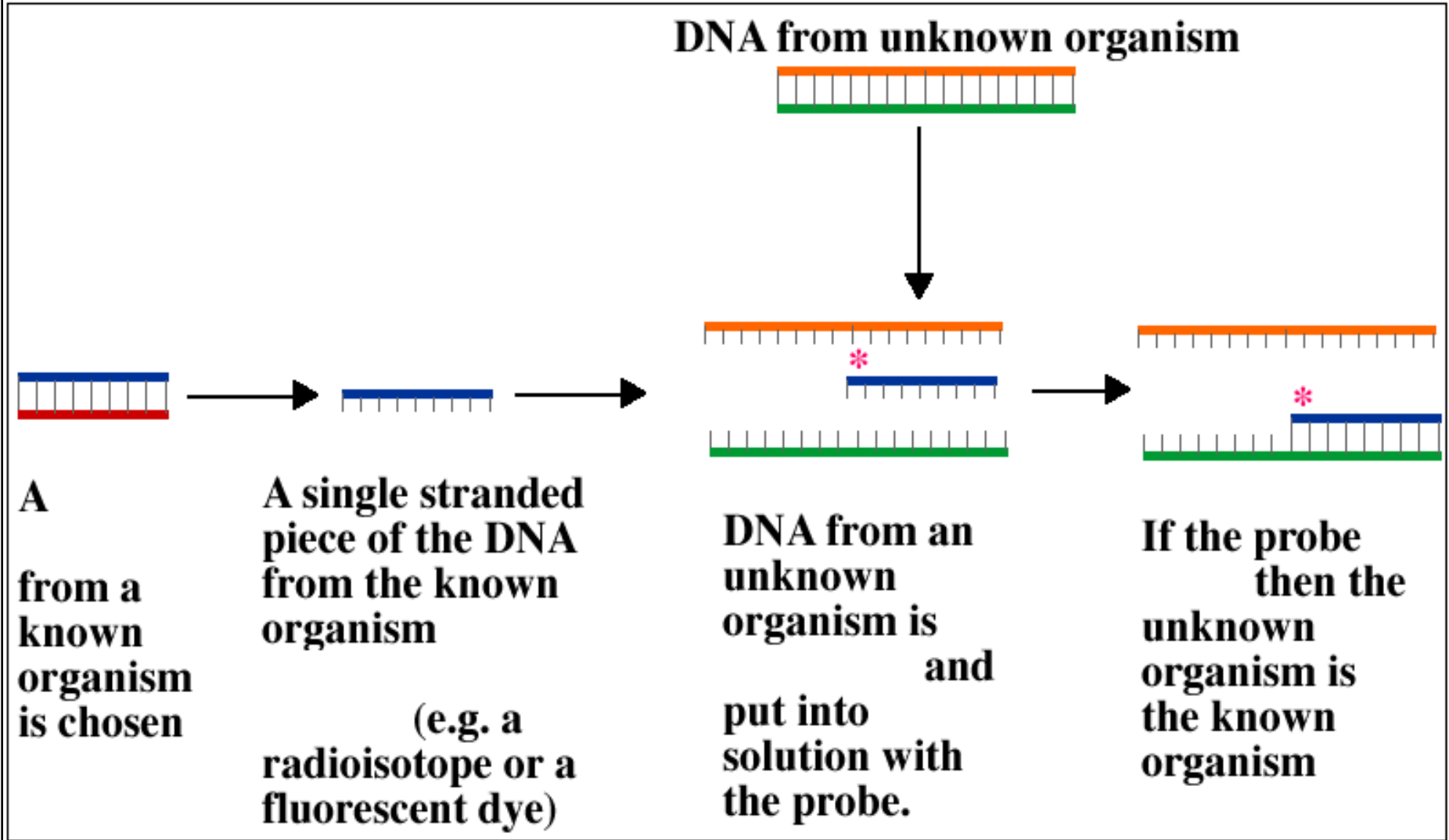
Which two strains are the most similar?

### III. methods (use of genotypic characteristics)

\*Makes it possible to identify organisms that \_\_\_\_\_ in the lab.

#### IDENTIFICATION

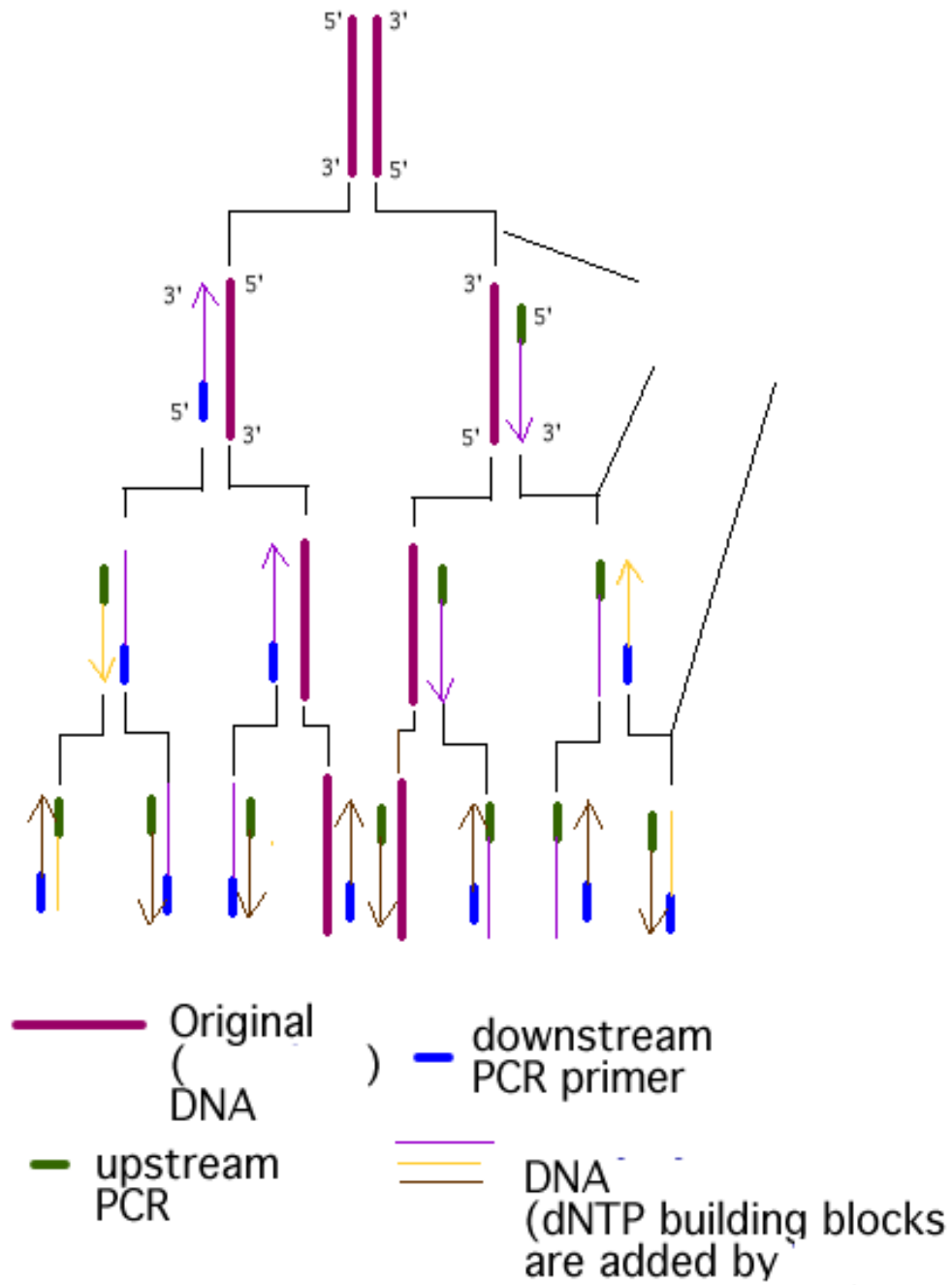
Nucleic acid probing:



\*To use probing methods, it's often necessary to \_\_\_\_\_ the DNA.



B. Amplifying specific DNA sequences using PCR  
 \*PCR can be used to amplify DNA samples from ect..



\* of PCR can amplify a sequence

## C. Sequencing rRNA genes

### **rRNAs**

**-Have essential functions so they contain**

**-Because of the high conservation of these sequences, the  
in order to**

**5S**

**16S**

**23S**

**Because of its ,  
16S rDNA is most often sequenced  
for identification. Extensive  
of 16S rDNA  
sequences are available.**

## CLASSIFICATION

### A. DNA base ratio ( )

1. The relative amount of A, T, G and C can be used to

of different bacteria => expressed as the

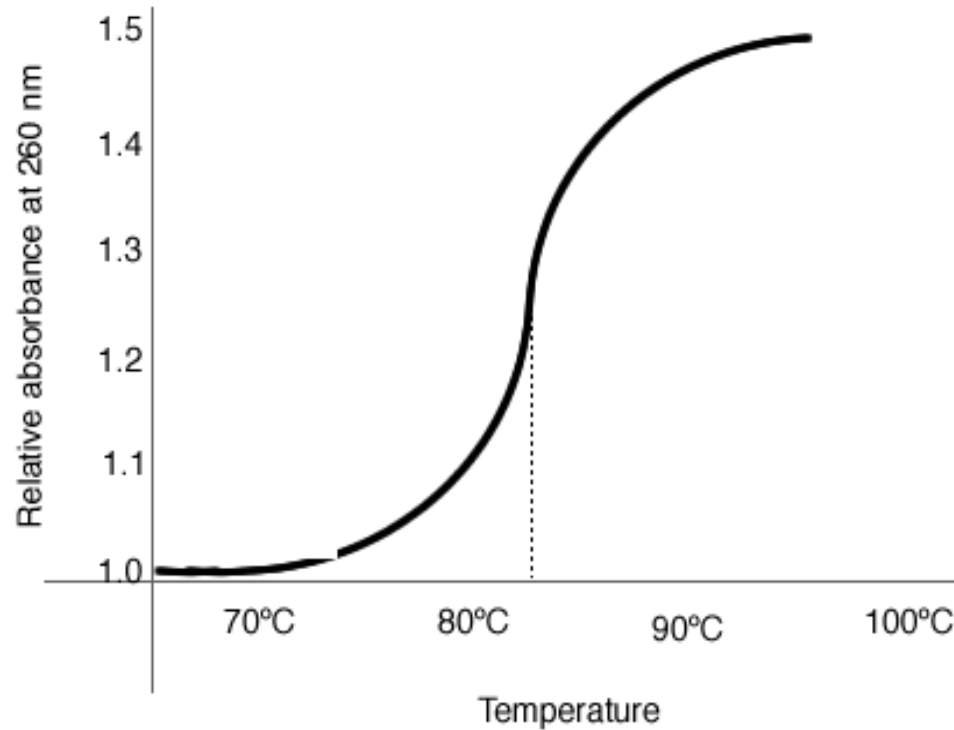
(G + C or simply GC).

\*If GC content = , then the AT content must be .

2. Often measured by determining the temperature at which the

double-stranded DNA . The the GC content, the

the melting temperature ( ).



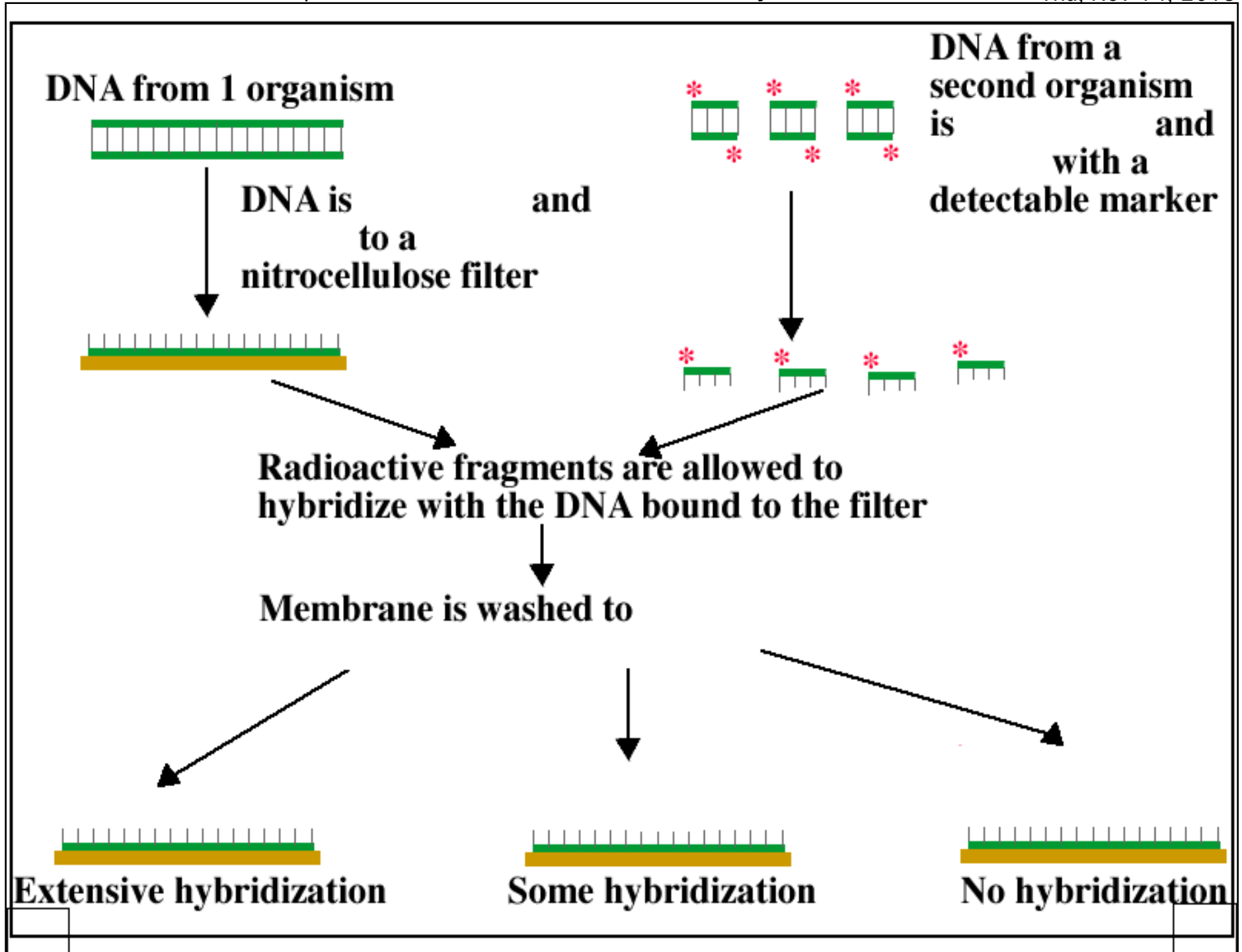
3. If the GC content varies by greater than  $\sim 10\%$ , the organisms

\*Note-two organisms with the same GC content

(*Bacillus subtilis* and *Staphylococcus aureus* both have 40% GC).

## B. DNA hybridization

The  between two organisms can be determined by measuring how well single strands of their DNA will  to each other.



The the degree of hybridization, the the similarity. Strains

that show are often considered the

C. Because of the high level of conservation in 16S rRNA, comparisons

between these sequences can show by

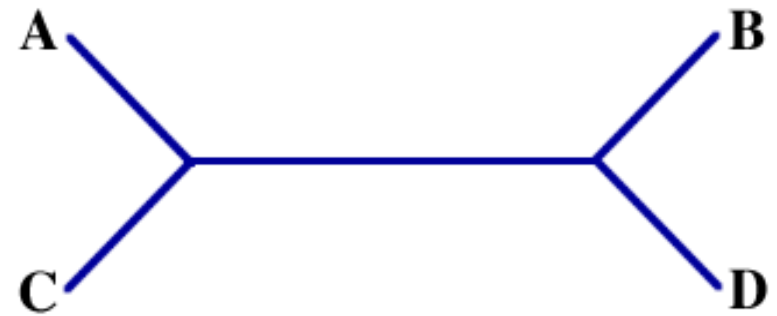
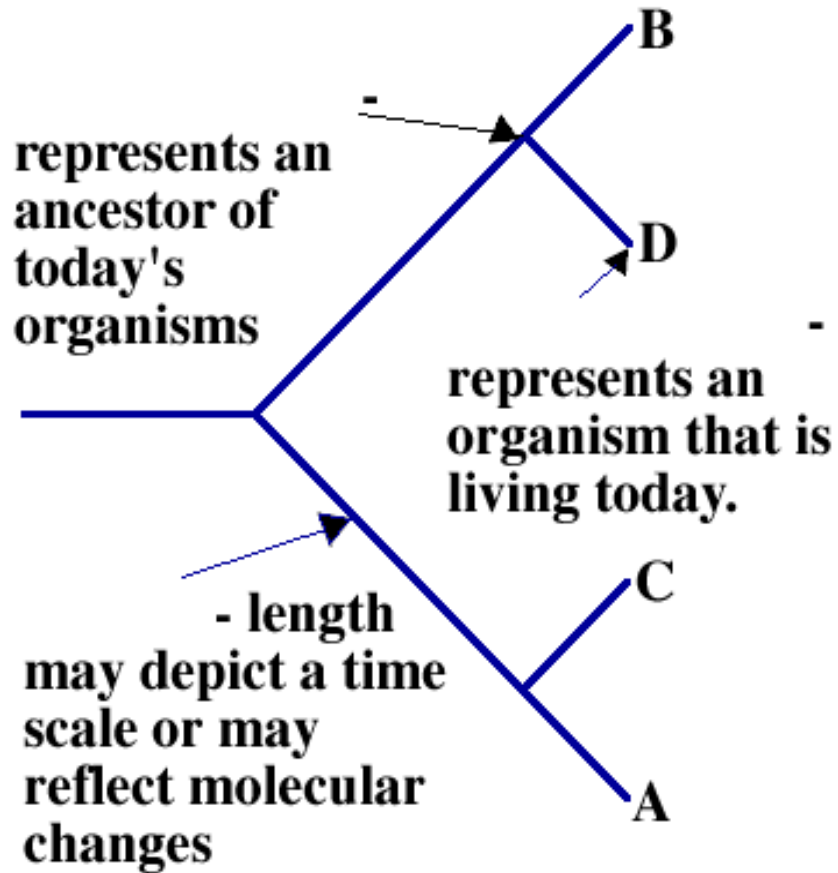
giving a measure of the time elapsed since the organisms

. That is, 16S rRNAs make good

! In this way, rRNA sequences help with the

construction of .

## Phylogenetic Trees: A graph made from branches and nodes



Shows existing species but between

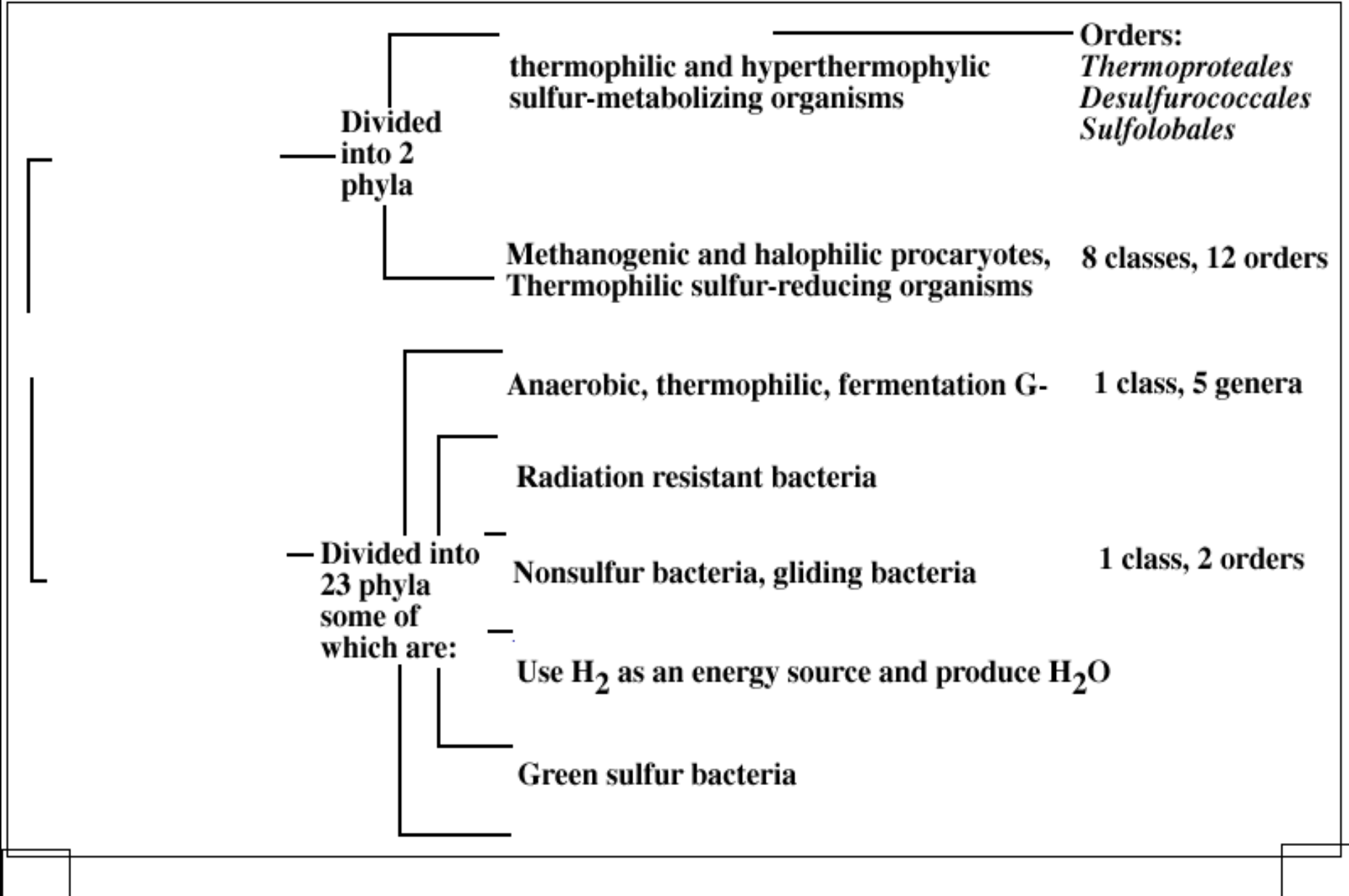
Has a node that represents a ; shows development

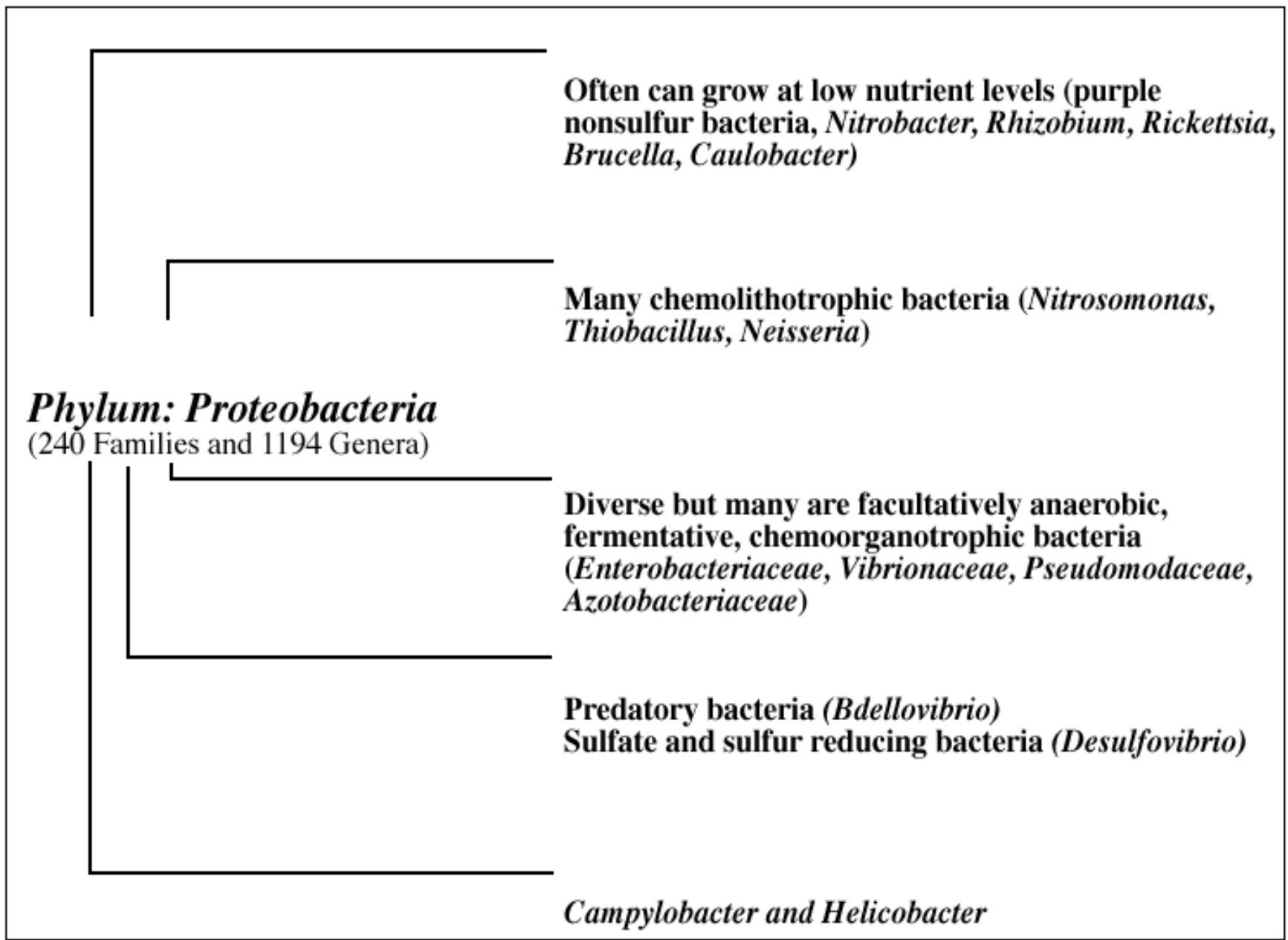


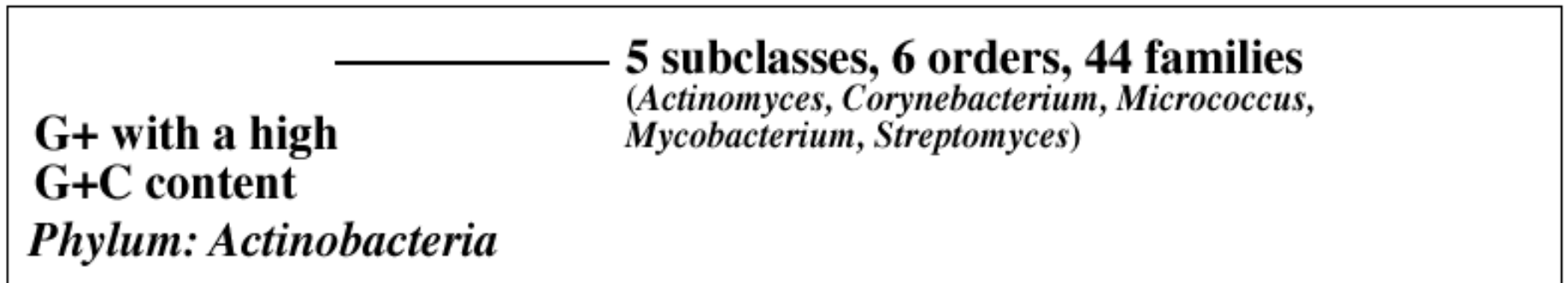
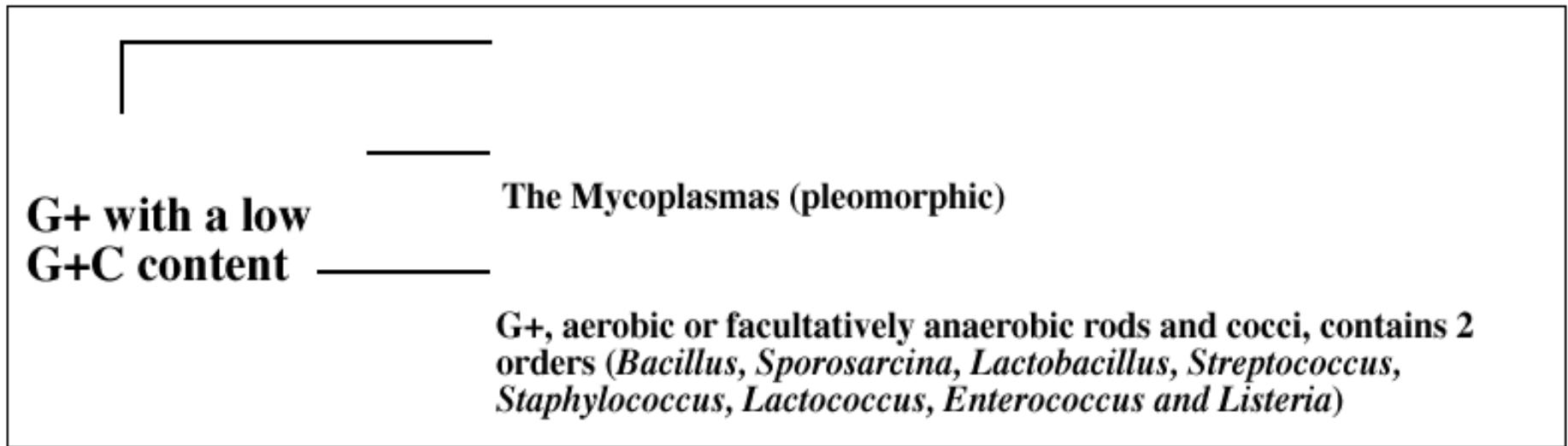
IV.

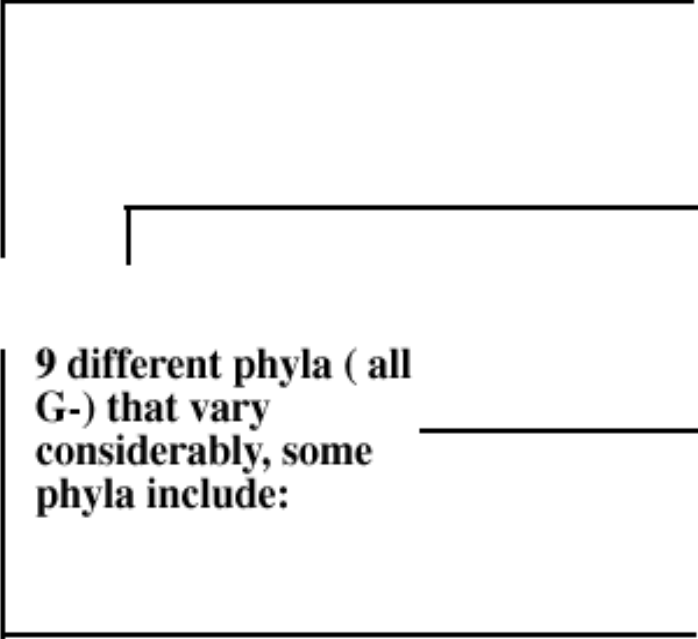
-5 volumes that

according to phylogenetic data









**Coccoid to ovoid or pear-shaped, lack peptidoglycan, some have a membrane-enclosed nucleoid, many are aquatic and often have appendages**

**Coccoid organisms with no appendages, lack peptidoglycan (*Chlamydia*)**

**9 different phyla ( all G-) that vary considerably, some phyla include:**

**(*Treponema and Borrelia*)**