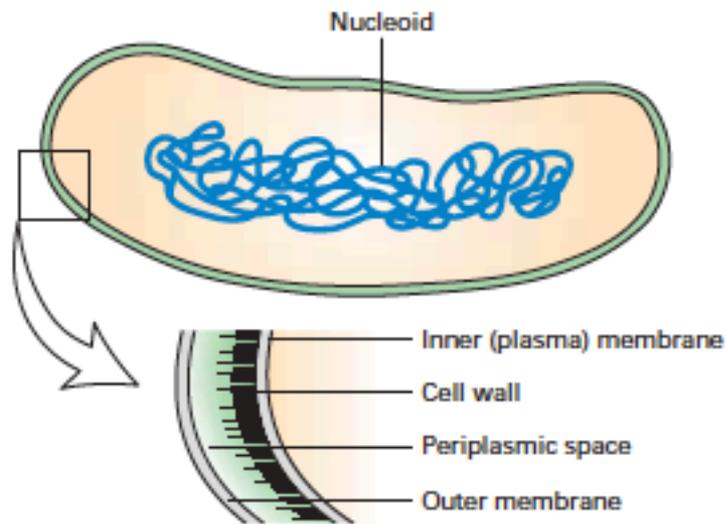
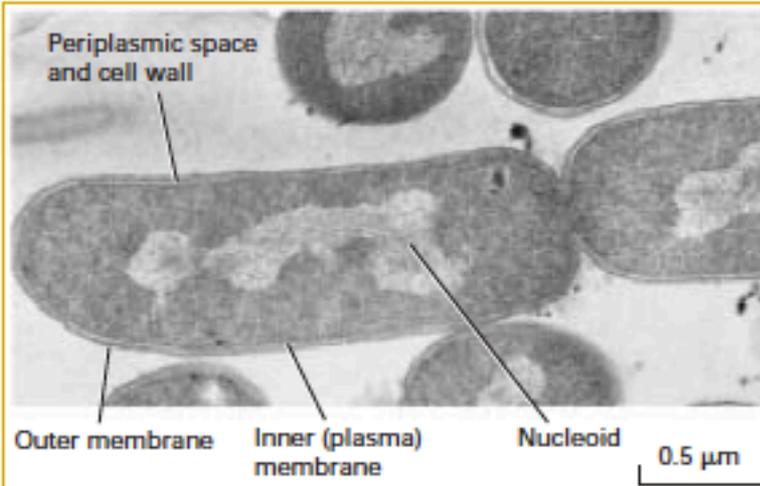
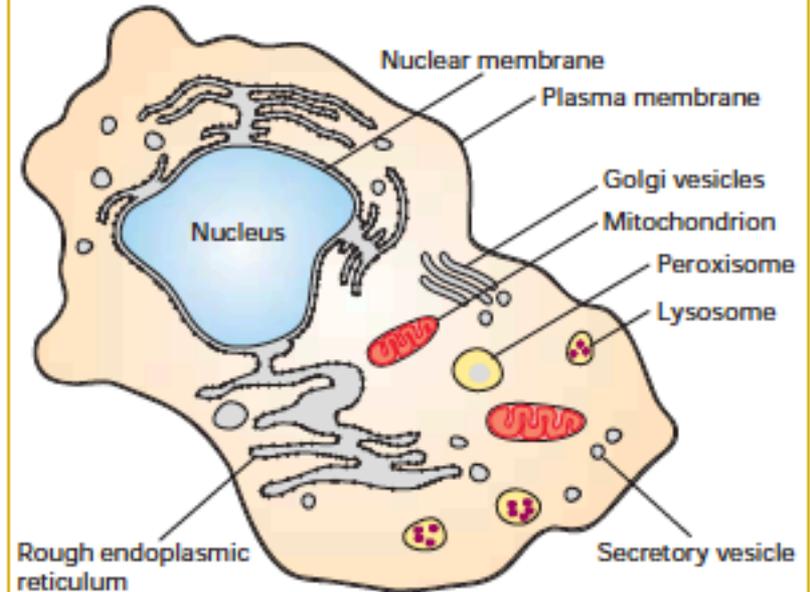
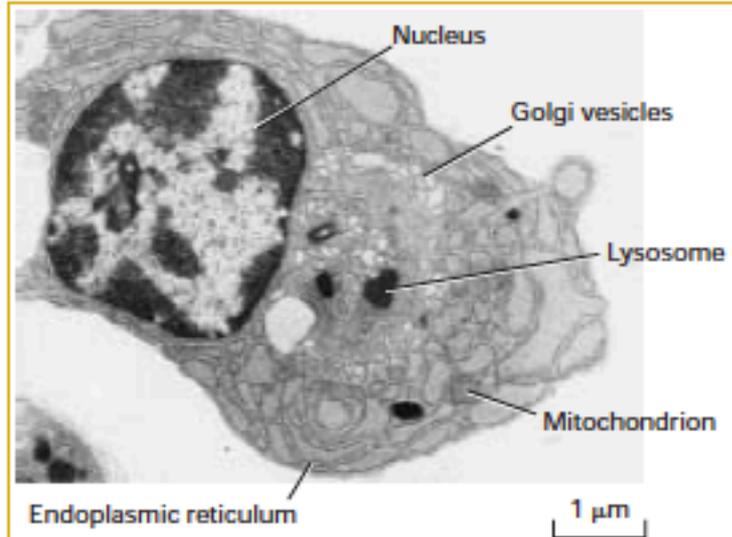


THE DIVERSITY  
OF GENOMES AND  
THE TREE OF LIFE

(a) Prokaryotic cell

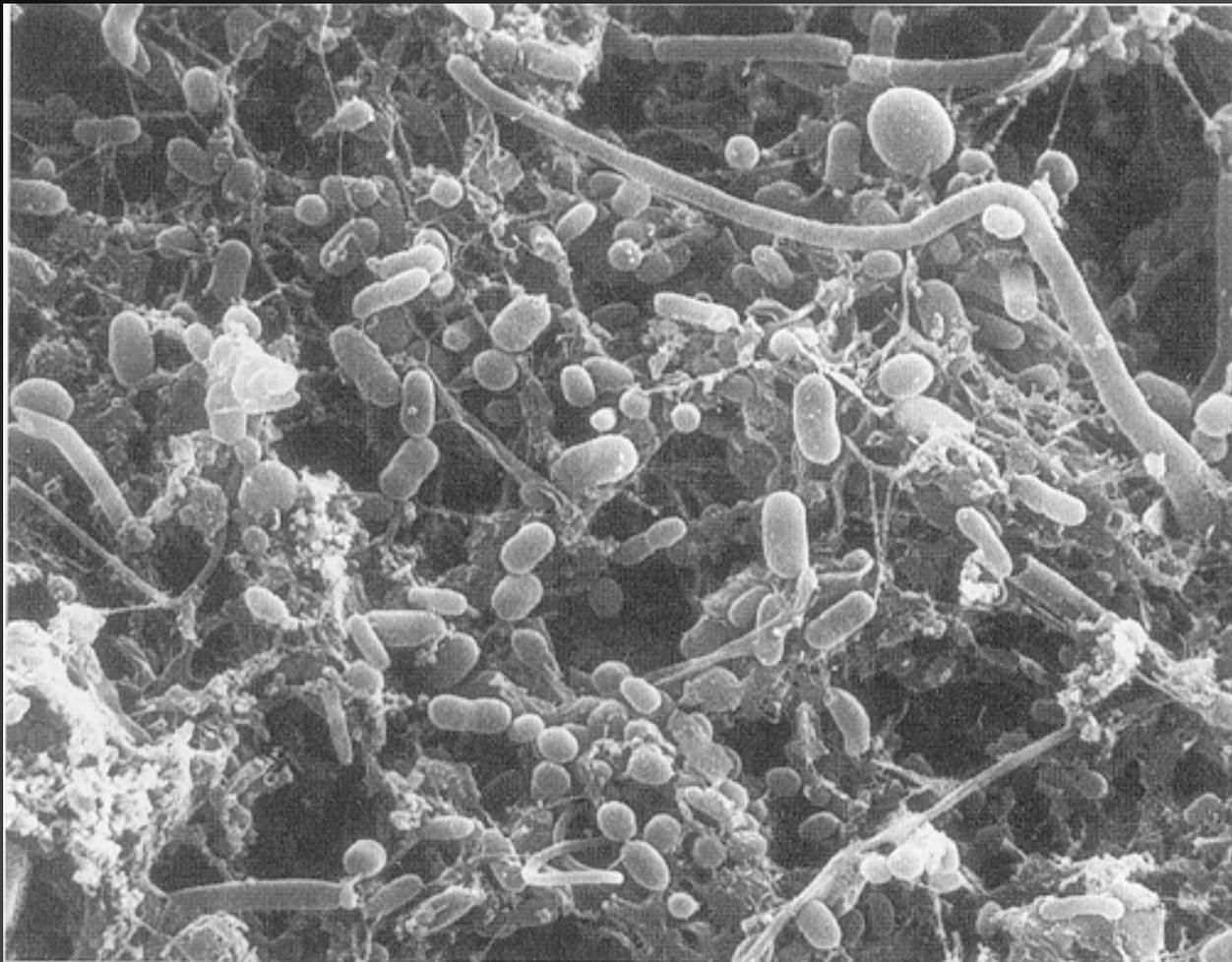


(b) Eukaryotic cell



Some Cells Fix Nitrogen and  
Carbon Dioxide for Others

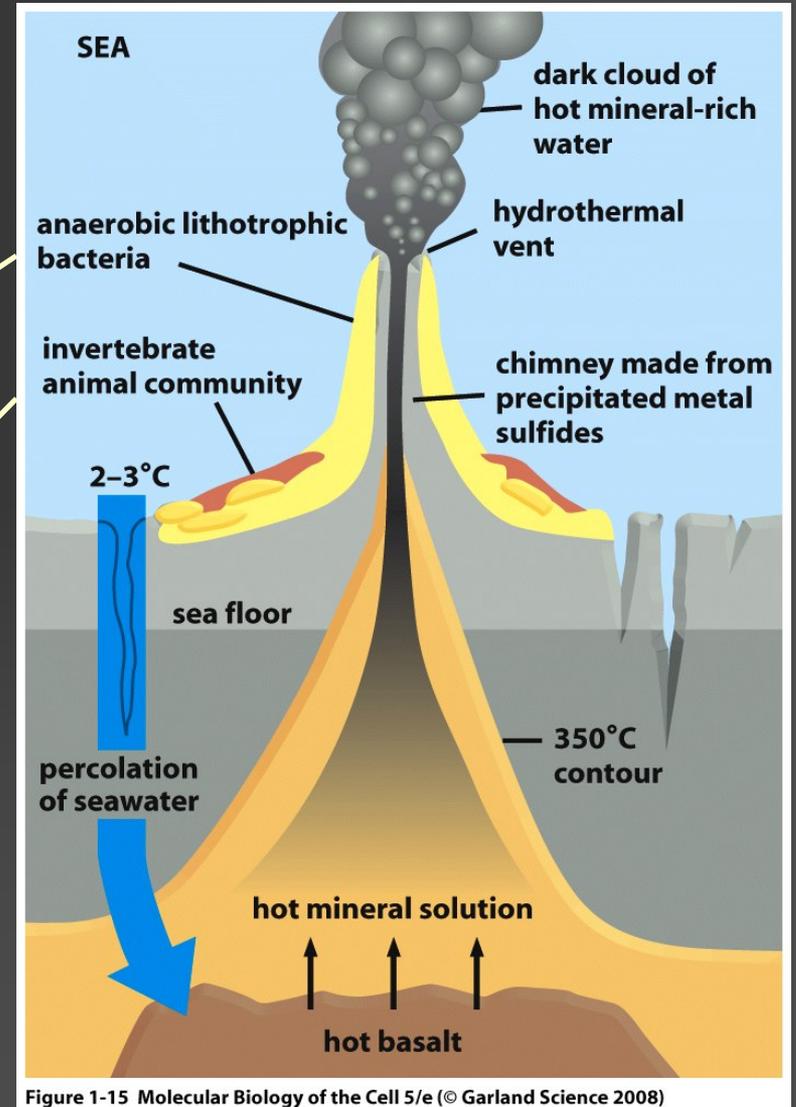
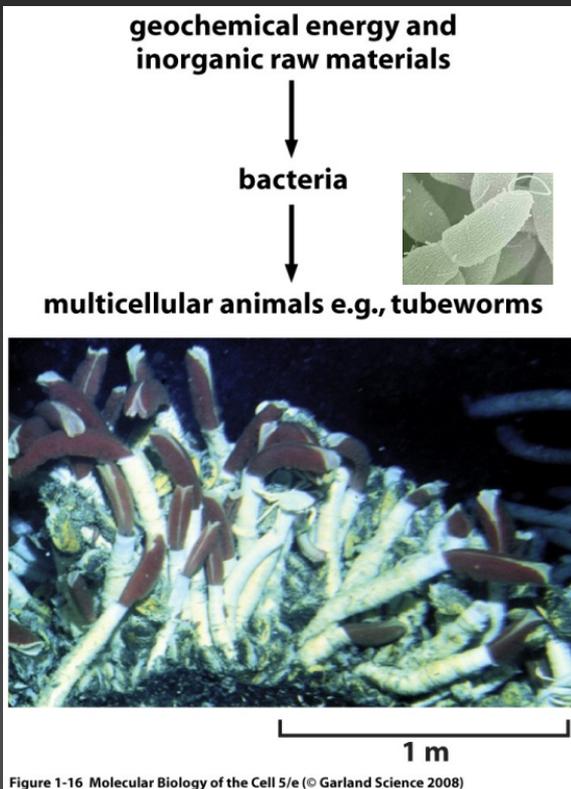
Cells Can Be Powered by a  
Variety of Free-Energy Sources

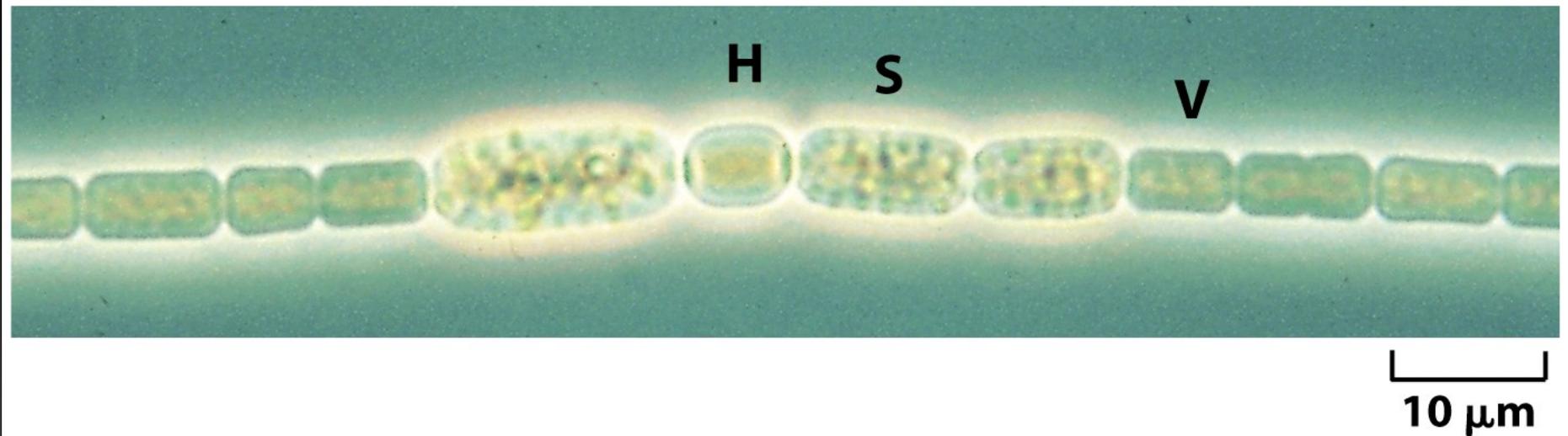


2 μm

**25.9 Chemoautotrophs** All of these archaea are chemoautotrophs that live near a hot-water vent along the Galapagos Rift in the eastern Pacific, where their fixing of carbon supports an entire community of organisms that thrives in total darkness.

# The geology of a hot hydrothermal vent in the ocean floor





The phototrophic bacterium *Anabaena cylindrica* viewed in the light microscope.

The cells of this species form long, multicellular filaments.

Most of the cells (labeled V) perform photosynthesis, while others become specialized for nitrogen fixation (labeled H) or develop into resistant spores (labeled S).



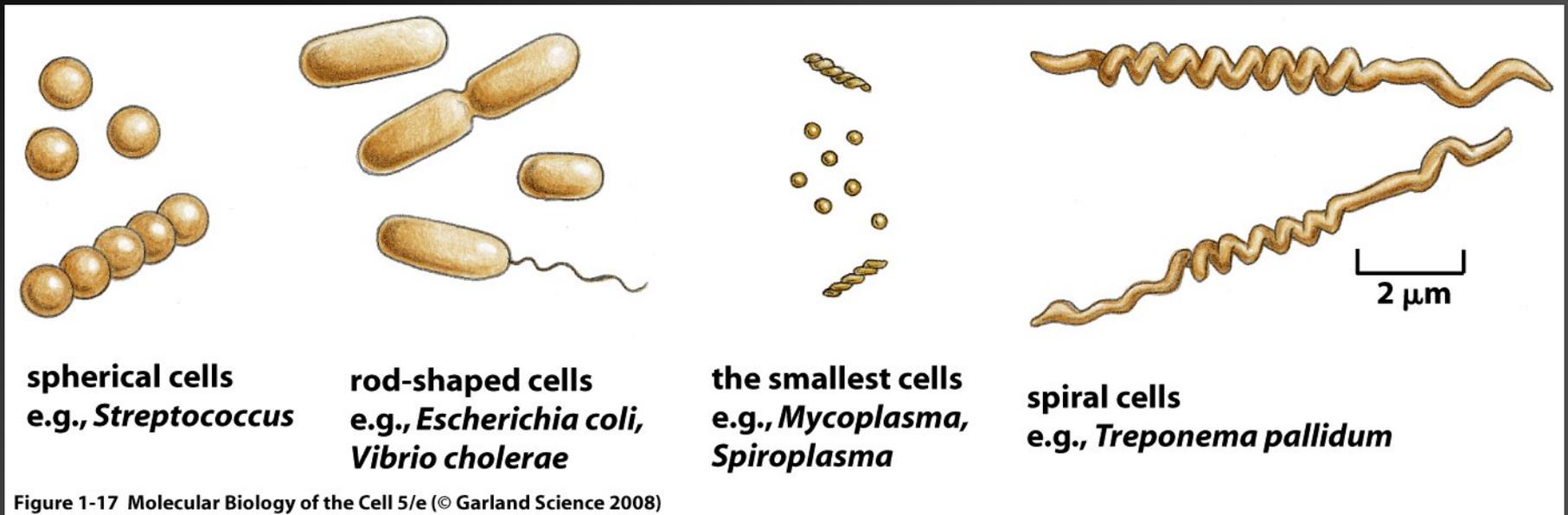
6  $\mu\text{m}$

A lithotrophic bacterium.

*Beggiatoa*, which lives in sulfurous environments, gets its energy by oxidizing  $\text{H}_2\text{S}$  and can fix carbon even in the dark.

Note the yellow deposits of sulfur inside the cells.

The Greatest Biochemical  
Diversity Exists Among  
Prokaryotic Cells



Most prokaryotic cells are small and simple in outward appearance. They live mostly as independent individuals or in loosely organized communities, rather than as multicellular organisms. They are typically spherical or rod-shaped and measure a few micrometers in linear dimension.

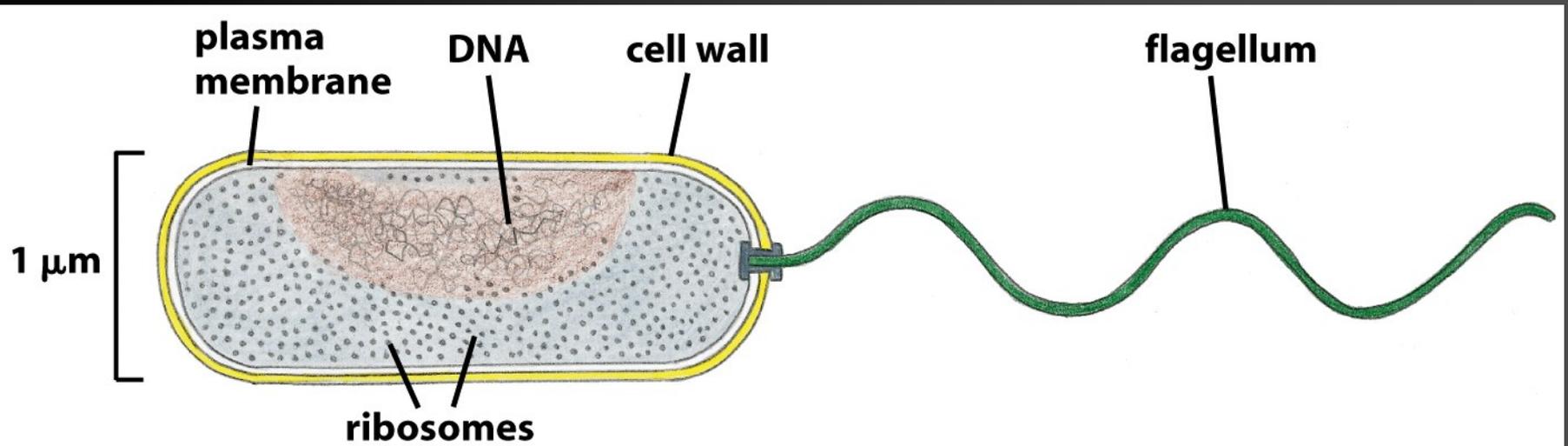


Figure 1-18a Molecular Biology of the Cell 5/e (© Garland Science 2008)

## Vibrio cholerae

In the electron microscope, cell interior of bacteria appears as a matrix of varying texture without any discernible organized internal structure

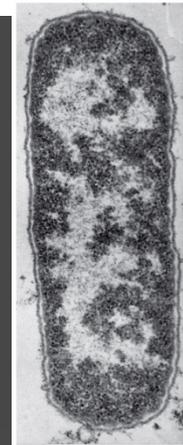
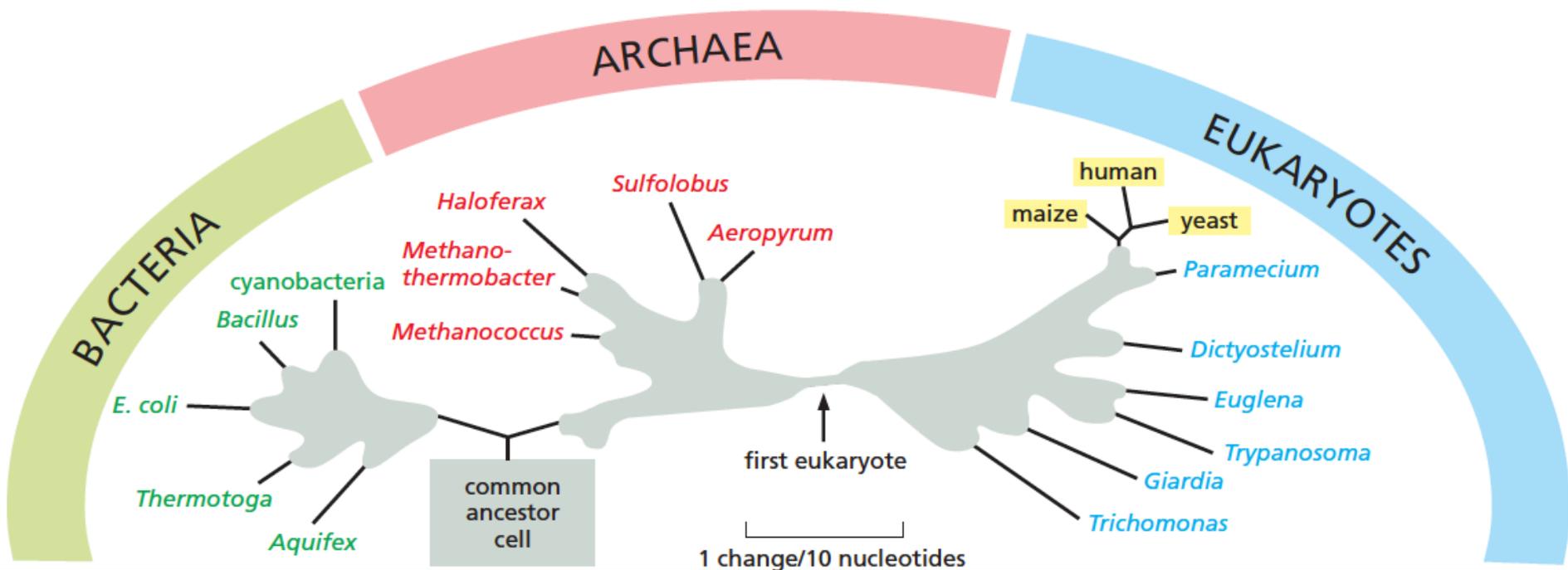


Figure 1-18b Molecular Biology of the Cell 5/e (© Garland Science 2008)

# The three major divisions (domains) of the living world



The tree shown here is based on comparisons of the nucleotide sequence of a ribosomal RNA (rRNA) subunit in the different species, and the distances in the diagram represent estimates of the numbers of evolutionary changes that have occurred in this molecule in each lineage

Some Genes Evolve Rapidly;

Others Are Highly Conserved



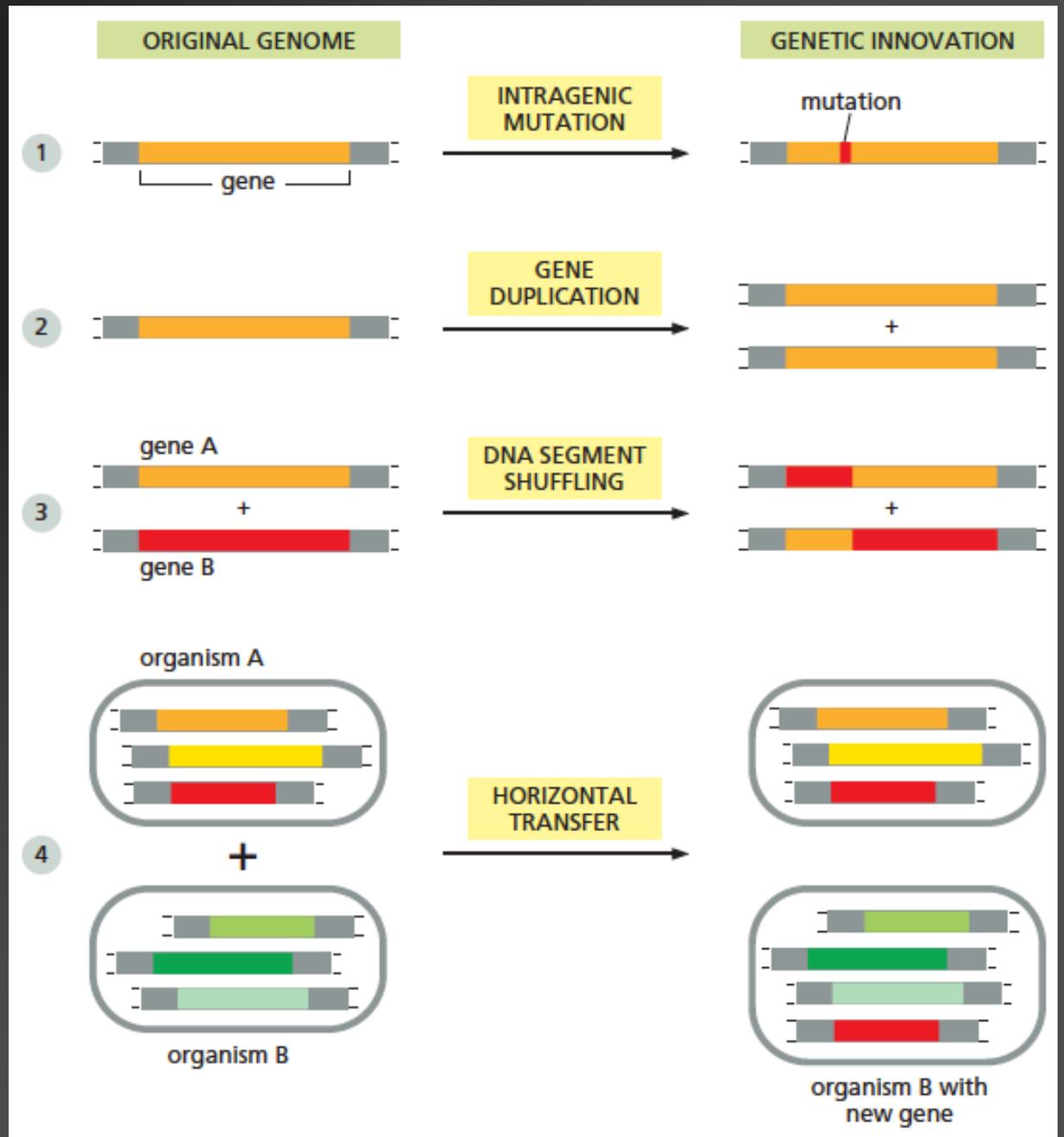
Most Bacteria and Archaea  
Have 1000-6000 Genes

| EUBACTERIA                                      | info  | habitat                                  | X1000(kb) genome | genes   |
|---|---|--|------------------|---------|
| <i>Mycoplasma genitalium</i>                    | smallest genome of any known cell                             | human genital tract                      | 580              | 468     |
| <i>Synechocystis</i> sp.                        | photosynthetic, oxygen-generating (cyanobacterium)            | lakes and streams                        | 3573             | 3168    |
| <i>Escherichia coli</i>                         | laboratory favorite   | human gut                                | 4639             | 4289    |
| <i>Helicobacter pylori</i>                      | causes stomach ulcers and predisposes to stomach cancer       | human stomach                            | 1667             | 1590    |
| <i>Bacillus subtilis</i>                        | bacterium   | soil                                     | 4214             | 4099    |
| <i>Aquifex aeolicus</i>                         | lithotrophic; lives at high temperatures                      | hydrothermal vents                       | 1551             | 1544    |
| <i>Mycobacterium tuberculosis</i>               | causes tuberculosis   | human tissues                            | 4447             | 4402    |
| <i>Treponema pallidum</i>                       | spirochaete; causes syphilis                                  | human tissues                            | 1138             | 1041    |
| <i>Rickettsia prowazekii</i>                    | bacterium most closely related to mitochondria; causes typhus | lice and humans (intracellular parasite) | 1111             | 834     |
| <i>Thermotoga maritima</i>                      | organotrophic; lives at high temperatures                     | hydrothermal vents                       | 1860             | 1877    |
| ARCHAEA   |   |  |                  |         |
| <i>Methanococcus jannaschii</i>                 | lithotrophic, anaerobic, methane-producing                    | hydrothermal vents                       | 1664             | 1750    |
| <i>Archaeoglobus fulgidus</i>                   | lithotrophic or organotrophic, anaerobic, sulfate-reducing    | hydrothermal vents                       | 2178             | 2493    |
| <i>Aeropyrum pernix</i>                         | aerobic, organotrophic hot-steam vents                        | coastal volcanic                         | 669              | 2620    |
| EUCARYOTES                                      |   |  |                  |         |
| <i>Saccharomyces cerevisiae</i> (budding yeast) | minimal model eucaryote                                       | grape skins, beer                        | 12,069           | ~6300   |
| <i>Arabidopsis thaliana</i> (wall cress)        | model organism for flowering plants                           | soil and air                             | ~142,000         | ~26,000 |
| <i>Caenorhabditis elegans</i> (nematode worm)   | simple animal with perfectly predictable development          | soil                                     | ~97,000          | ~19,000 |
| <i>Drosophila melanogaster</i> (fruit fly)      | key to the genetics of animal development                     | rotting fruit                            | ~137,000         | ~14,000 |
| <i>Homo sapiens</i> (human)                     | most intensively studied mammal                               | houses                                   | ~3,200,000       | ~30,000 |

# New Genes Are Generated from Preexisting Genes

1. **Intragenic mutation:** an existing gene can be randomly modified by changes in its DNA sequence, through various types of error that occur mainly in the process of DNA replication.
2. **Gene duplication:** an existing gene can be accidentally duplicated so as to create a pair of initially identical genes within a single cell; these two genes may then diverge in the course of evolution.
3. **DNA segment shuffling:** two or more existing genes can break and rejoin to make a hybrid gene consisting of DNA segments that originally belonged to separate genes.
4. **Horizontal (intercellular) transfer:** a piece of DNA can be transferred from the genome of one cell to that of another—even to that of another species. This process is in contrast with the usual vertical transfer of genetic information from parent to progeny.

Four modes of genetic innovation and their effects on the DNA sequence of an organism.



Gene Duplications Give Rise to  
Families of Related Genes  
Within a Single Cell

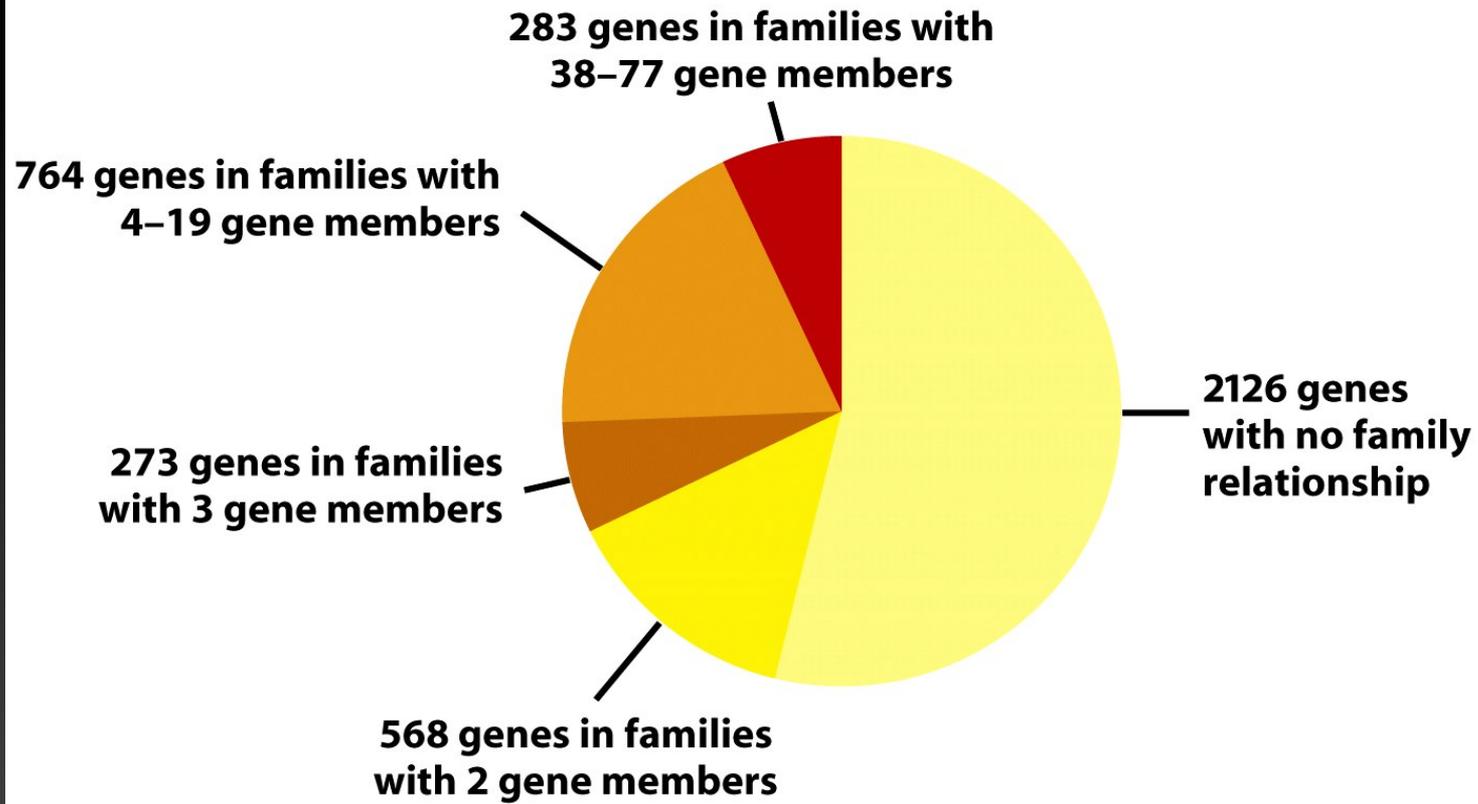
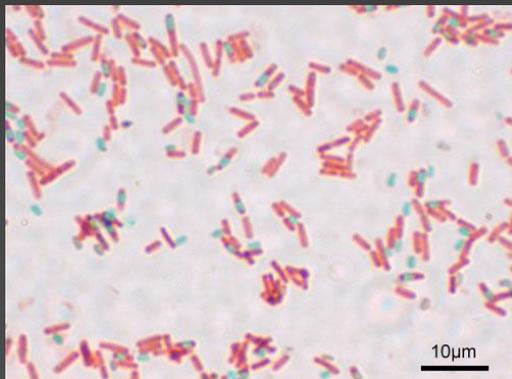


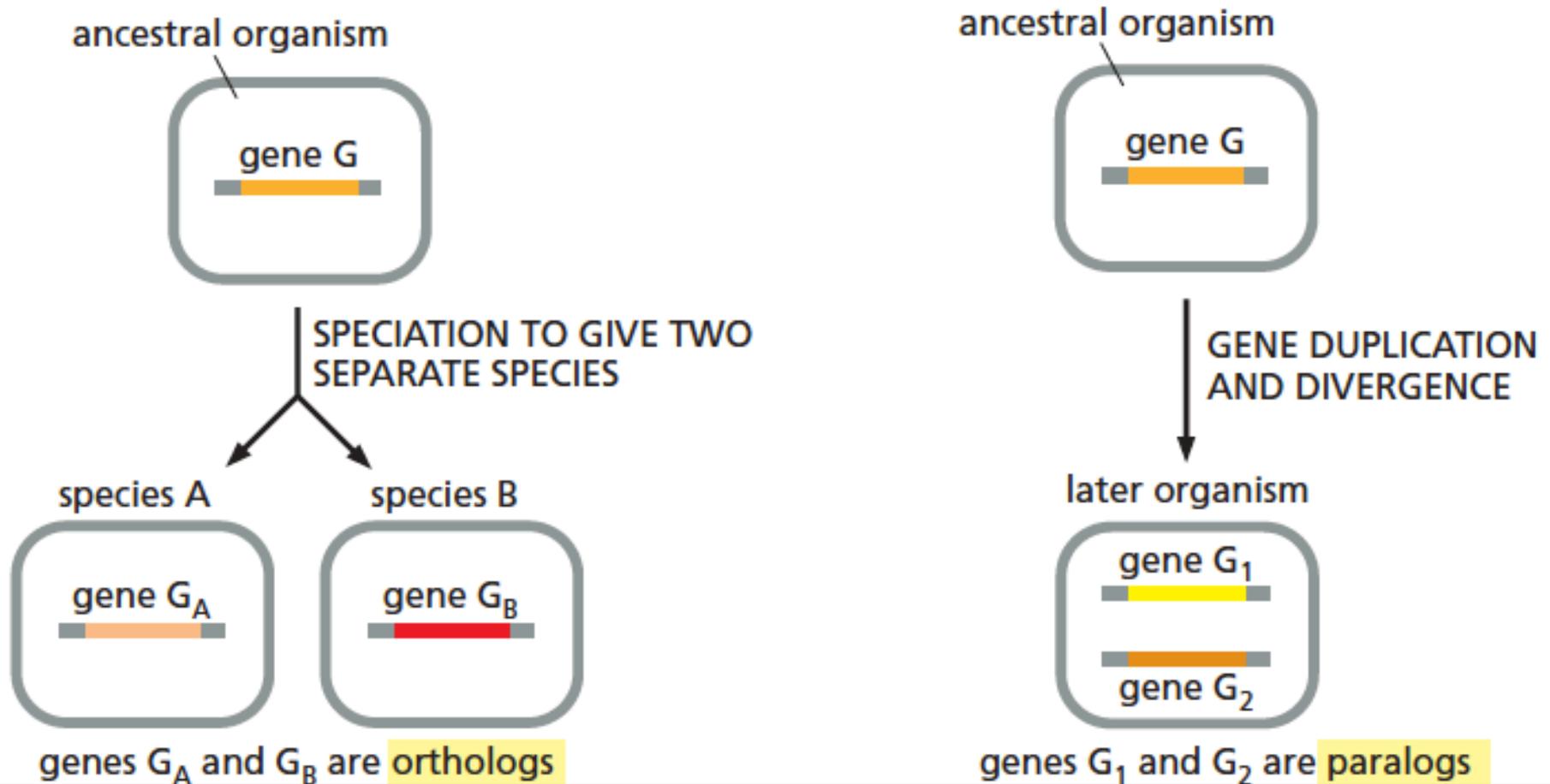
Figure 1-24 Molecular Biology of the Cell 5/e (© Garland Science 2008)



Families of evolutionarily related genes in the genome of *Bacillus subtilis*. The largest gene family in this bacterium consists of 77 genes coding for varieties of ABC transporters—a class of membrane transport proteins found in all three domains of the living world.

# Ortholog vs Paralog Homology

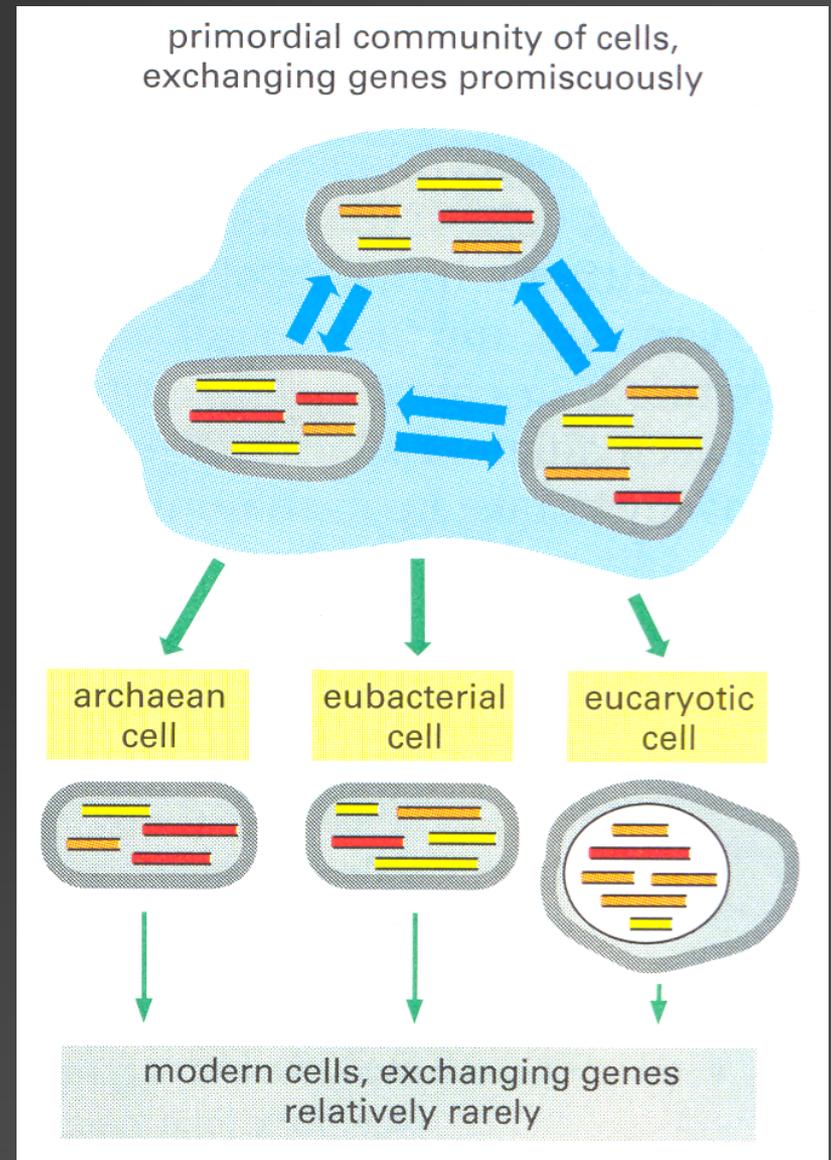
## Formation of new genes and gene families



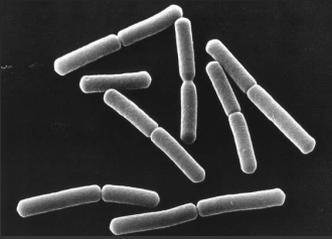
## Horizontal gene transfers in early evolution.

Early cells may have been less capable of maintaining their separate identities and exchanging genes more readily than now.

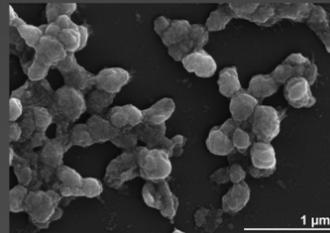
Three main lineages may have inherited different but overlapping subsets of gene from primordial community of cells.



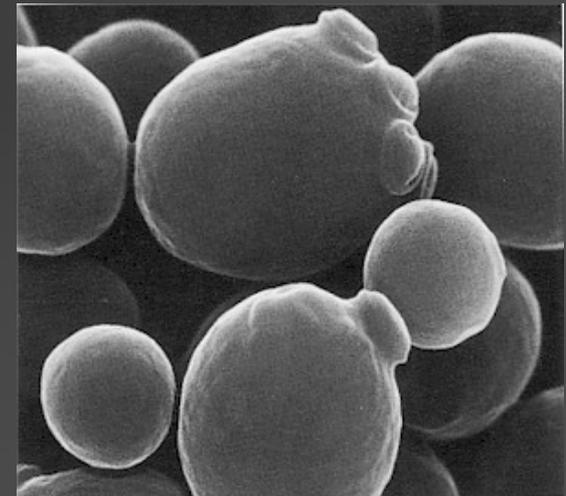
# More Than 200 Gene Families Are Common to All Three Primary Branches of the Tree of Life



bacteria



archaea



eukaryotes

## The Number of Gene Families, Classified by Function, Common to All Three Domains of the Living World

| Information processing  |    | Metabolism   |    |
|---|----|--|----|
| Translation   | 63 | Energy production and conversion   | 19 |
| Transcription   | 7  | Carbohydrate transport and metabolism                                    | 16 |
| Replication, recombination, and repair                        | 13 | Amino acid transport and metabolism                                      | 43 |
| Cellular processes and signaling                              |    | Nucleotide transport and metabolism                                      | 15 |
| Cell-cycle control, mitosis, and meiosis                      | 2  | Coenzyme transport and metabolism  | 22 |
| Defense mechanisms  | 3  | Lipid transport and metabolism   | 9  |
| Signal transduction mechanisms                                | 1  | Inorganic ion transport and metabolism                                   | 8  |
| Cell wall/membrane biogenesis                                 | 2  | Secondary metabolite biosynthesis, transport, and catabolism             | 5  |
| Intracellular trafficking and secretion                       | 4  | Poorly characterized   |    |
| Post-translational modification, protein turnover, chaperones | 8  | General biochemical function predicted; specific biological role unknown | 24 |

For the purpose of this analysis, gene families are defined as “universal” if they are represented in the genomes of at least two diverse archaea (*Archaeoglobus fulgidus* and *Aeropyrum pernix*), two evolutionarily distant bacteria (*Escherichia coli* and *Bacillus subtilis*), and one eukaryote (yeast, *Saccharomyces cerevisiae*).

# The Function of a Gene Can Often Be Deduced from Its Sequence

| No. | Exon / Intron                      | Start     | End       | Start Phase | End Phase | Length | Sequence   |
|-----|------------------------------------|-----------|-----------|-------------|-----------|--------|--|
|     | 5' upstream sequence               |           |           |             |           |        | .....gcaggagccagggtggtggccataaaaagtcagggcagagccatctattgctt   |
| 1   | <a href="#">ENSPTR00000032829</a>  | 4,978,050 | 4,977,909 | -           | 2         | 142    | ACATTTCCTTCTGACACAACCTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACC<br>TGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAG<br>TTGGTGGTGAGGCCCTGGGCAG  |
|     | <a href="#">Intron 1-2</a>         | 4,977,908 | 4,977,779 |             |           | 130    | gttggtatcaagggtacaagacagg.....tattgggtattttcccaccccttag  |
| 2   | <a href="#">ENSPTR00000032833</a>  | 4,977,778 | 4,977,556 | 2           | 0         | 223    | GCTGCTGGTGGTCTACCCITGGACCCAGAGGTTCTTTGAGTCCCTTTGGGGAICTGTCCAC<br>TCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTCTCGGTGC<br>CITTAGTGATGSCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACTGAGTGA<br>GCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGG                                  |
|     | <a href="#">Intron 2-3</a>         | 4,977,555 | 4,976,706 |             |           | 850    | gtgagtctatgggacccttgatgtt.....catacctcttgtcttctcccacag   |
| 3   | <a href="#">ENSPTR000000405718</a> | 4,976,705 | 4,976,444 | 0           | -         | 262    | CTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCATCACTTTGGCAAAGAAITCACCOC<br>CCAGTGCAGGCTGCCATCAGAAAGTGGTGGCTGGTGGCTAATGCCCTGGCCACAAAG<br>TATCACTAAGCTCGCTTTCTGCTGTCCAATTCTATTAAAGGTTCCCTTGTCCCTAAG<br>TCCAACTACTAAACTGGGGGATATTGAAGGGCCTTGAGCATCTGGATTCTGCCTAATA<br>AAAAACATTTATTTTCATTGCA |
|     | 3' downstream sequence             |           |           |             |           |        | atgggtgatttaaattatctgaatattttactaaaaaggaatgtggg.....   |

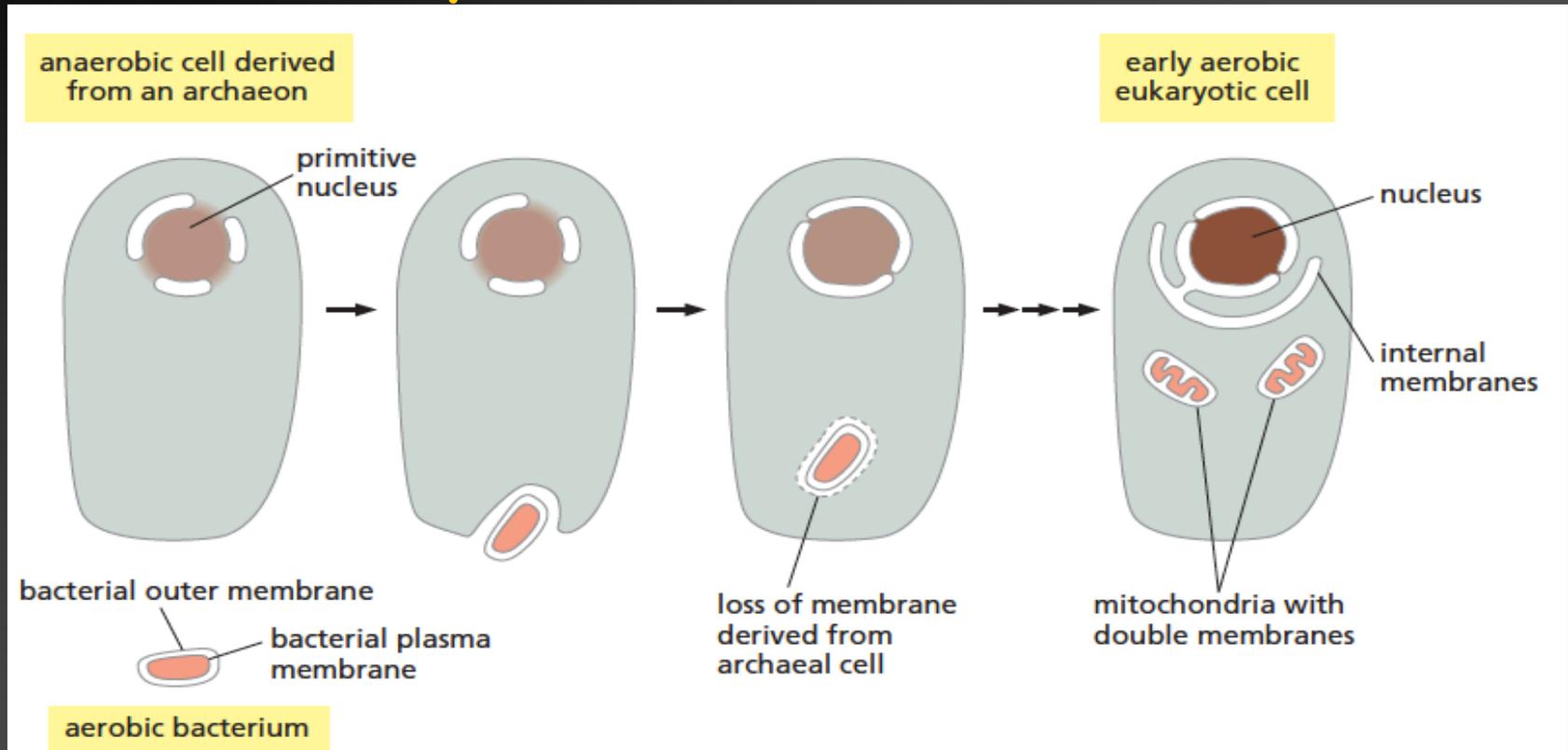
## Hb beta Gene cluster

```
ce
.....gcaggagccagggctgggcataaaaagt cagggcagagccatctattgctt
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TTGGTGGTGAGGCCCTGGGCAG
gttggtatcaaggttacaagacagg.....tattgggctatthtcccacccttag
GCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCTGTCCAC
TCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTCTCGGTGC
CTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACTGAGTGA
GCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGG
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CTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCAACCCCA
CCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCACAAG
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TCCAACACTAAACTGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATA
AAAAACATTTATTTTCATTGCA
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```

```
ce
.....gcaggagccagggctgggcataaaaagt cagggcagagccatctattgctt
ACATTTGCTTCTGACACAACCTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCATC
TGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAG
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GCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCTGTCCAC
TCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTCTCGGTGC
CTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACTGAGTGA
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TCCAACACTAAACTGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATA
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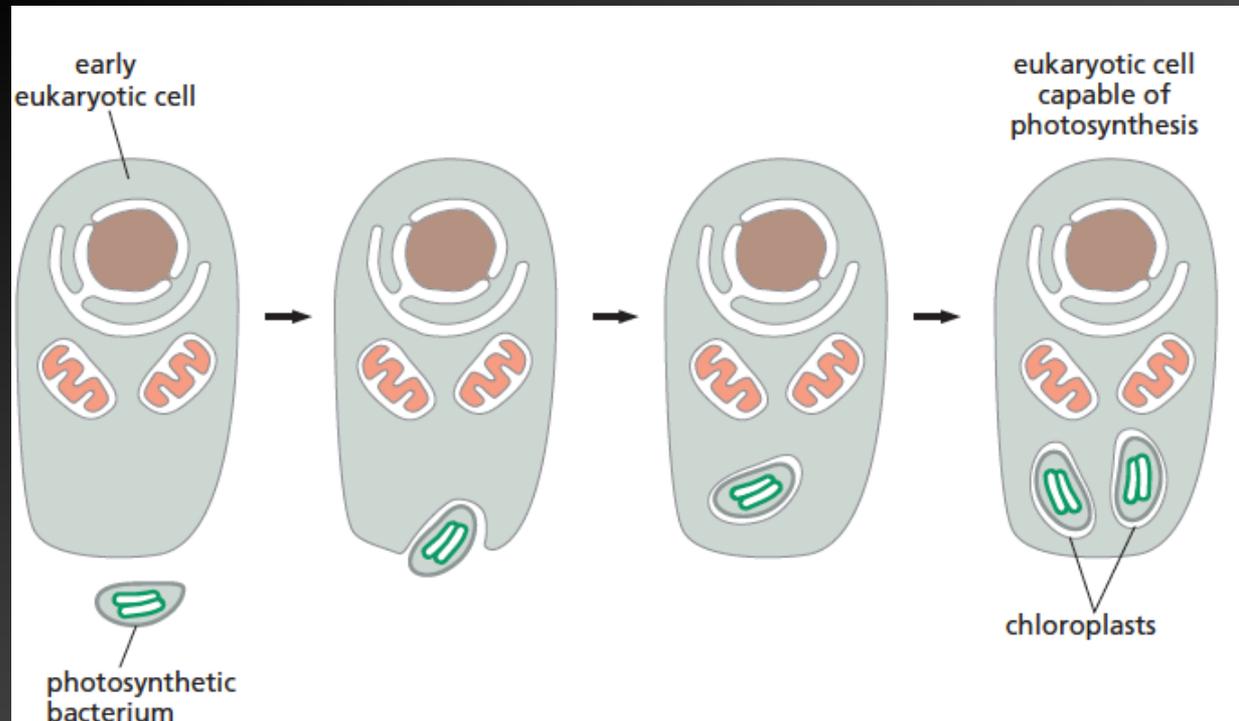


# Eukaryotes Have Hybrid Genomes



## The origin of mitochondria.

An ancestral anaerobic predator cell (an archaeon) is thought to have engulfed the bacterial ancestor of mitochondria, initiating a symbiotic relationship. Clear evidence of a dual bacterial and archaeal inheritance can be discerned today in the genomes of all eukaryotes.



## The origin of chloroplasts.

An early eukaryotic cell, already possessing mitochondria, engulfed a photosynthetic bacterium (a cyanobacterium) and retained it in symbiosis. Present-day chloroplasts are thought to trace their ancestry back to a single species of cyanobacterium that was adopted as an internal symbiont (an endosymbiont) over a billion years ago.

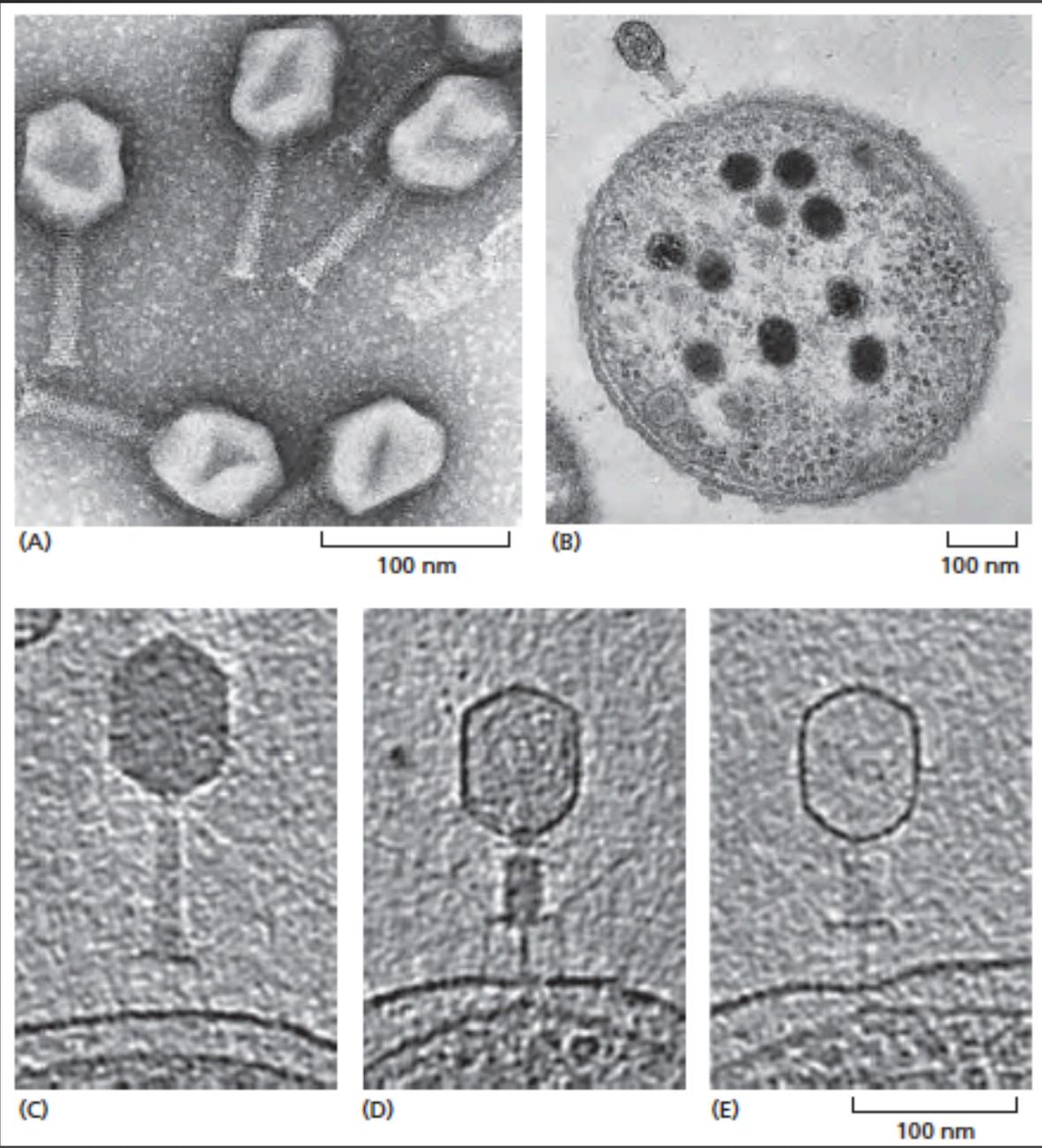
Genes Can Be Transferred  
Between Organisms, Both in the  
Laboratory and in Nature

# The viral transfer of DNA into a cell.

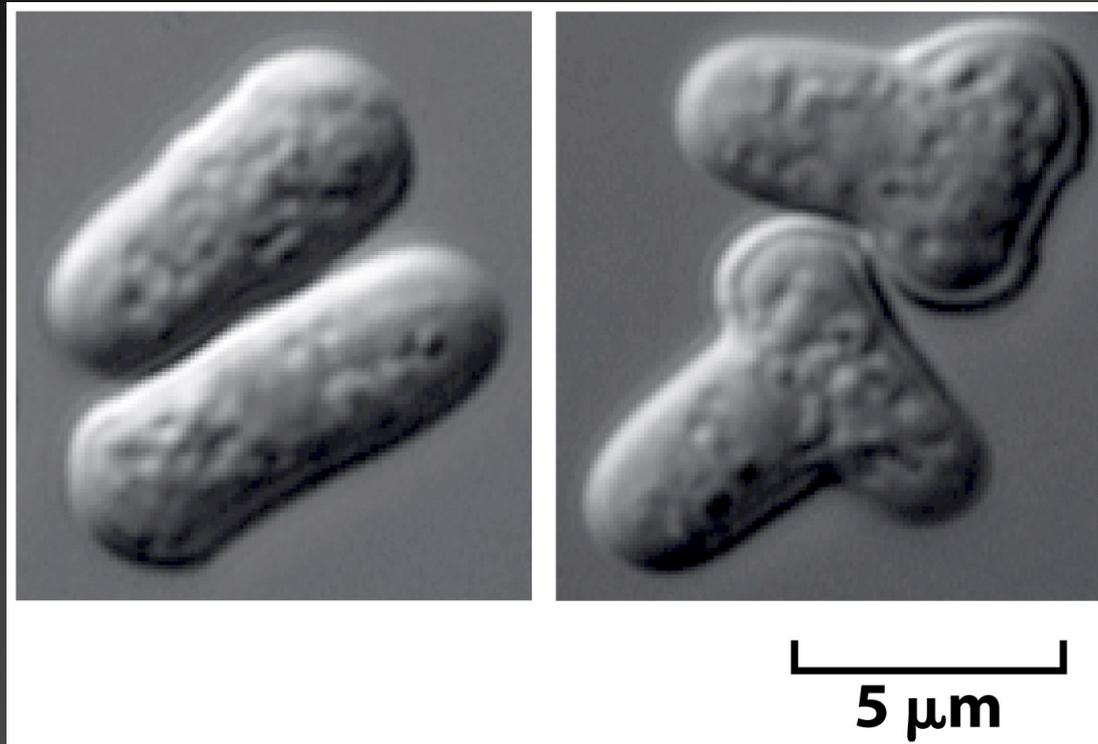
(A) An electron micrograph of particles of a bacterial virus, the T4 bacteriophage.

(B) A cross section of an *E. coli* bacterium with a T4 bacteriophage latched onto its surface.

(C-E) The process of DNA injection into the bacterium

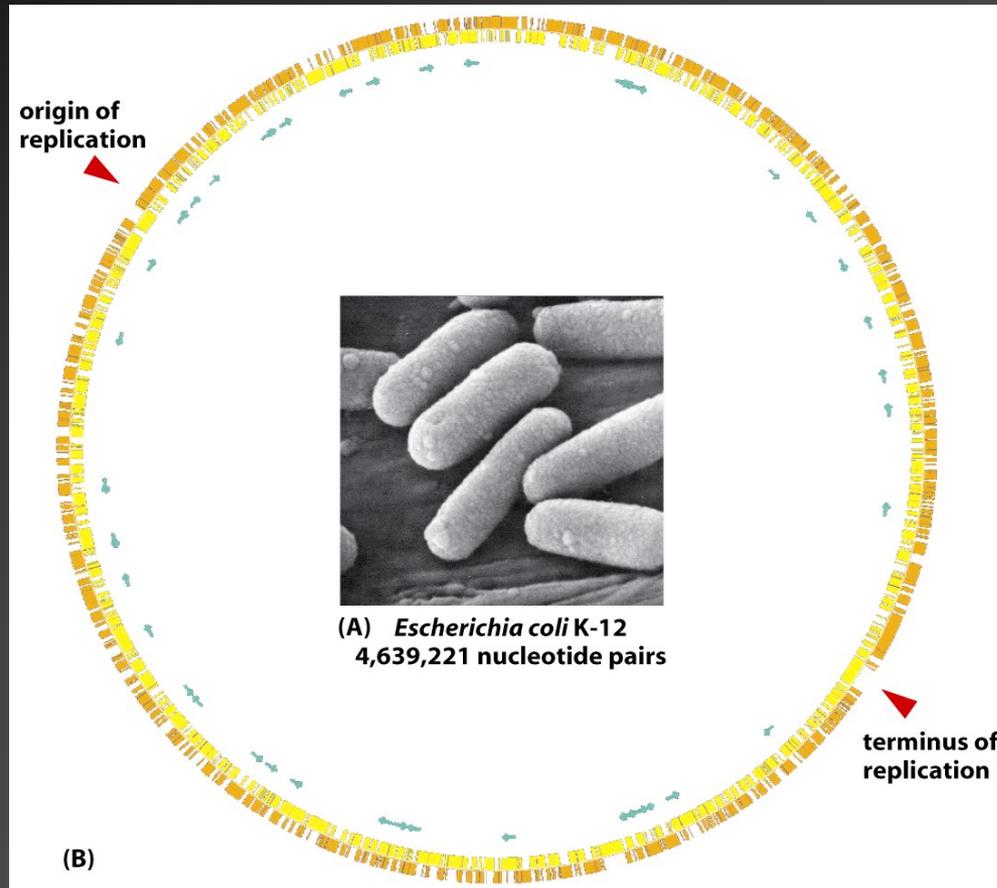


# Mutations Reveal the Functions of Genes



A mutant phenotype reflecting the function of a gene. A normal yeast (of the species *Schizosaccharomyces pombe*) is compared with a mutant in which a change in a single gene has converted the cell from a cigar shape (left) to a T shape(right).

# Molecular Biology Began with a Spotlight on *E. coli*



# MODEL ORGANISMS



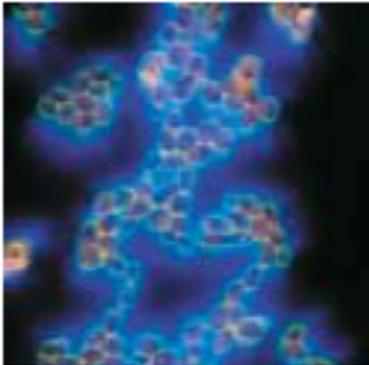
## Viruses

Proteins involved in DNA, RNA, protein synthesis  
Gene regulation  
Cancer and control of cell proliferation  
Transport of proteins and organelles inside cells  
Infection and immunity  
Possible gene therapy approaches



## Bacteria

Proteins involved in DNA, RNA, protein synthesis, metabolism  
Gene regulation  
Targets for new antibiotics  
Cell cycle  
Signaling



## Yeast (*Saccharomyces cerevisiae*)

Control of cell cycle and cell division  
Protein secretion and membrane biogenesis  
Function of the cytoskeleton  
Cell differentiation  
Aging  
Gene regulation and chromosome structure



## Roundworm (*Caenorhabditis elegans*)

Development of the body plan  
Cell lineage  
Formation and function of the nervous system  
Control of programmed cell death  
Cell proliferation and cancer genes  
Aging  
Behavior  
Gene regulation and chromosome structure



**Fruit fly (*Drosophila melanogaster*)**

Development of the body plan  
Generation of differentiated cell lineages  
Formation of the nervous system, heart, and musculature  
Programmed cell death  
Genetic control of behavior  
Cancer genes and control of cell proliferation  
Control of cell polarization  
Effects of drugs, alcohol, pesticides



**Zebrafish**

Development of vertebrate body tissues  
Formation and function of brain and nervous system  
Birth defects  
Cancer



**Mice, including cultured cells**

Development of body tissues  
Function of mammalian immune system  
Formation and function of brain and nervous system  
Models of cancers and other human diseases  
Gene regulation and inheritance  
Infectious disease



**Plant (*Arabidopsis thaliana*)**

Development and patterning of tissues  
Genetics of cell biology  
Agricultural applications  
Physiology  
Gene regulation  
Immunity  
Infectious disease

**TABLE 1–2 Some Model Organisms and Their Genomes**

| Organism                                     | Genome size*<br>(nucleotide pairs) | Approximate number<br>of genes |
|--|------------------------------------|--------------------------------|
| <i>Escherichia coli</i> (bacterium)          | 4.6 x 10 <sup>6</sup>              | 4,300                          |
| <i>Saccharomyces cerevisiae</i> (yeast)      | 12.1 x 10 <sup>6</sup>             | 6,600                          |
| <i>Caenorhabditis elegans</i><br>(roundworm) | 100 x 10 <sup>6</sup>              | 20,222                         |
| <i>Arabidopsis thaliana</i> (plant)          | 119 x 10 <sup>6</sup>              | 25,000                         |
| <i>Drosophila melanogaster</i> (fruit fly)   | 137 x 10 <sup>6</sup>              | 17,660                         |
| <i>Danio rerio</i> (zebrafish)               | 1.4 x 10 <sup>9</sup>              | 25,592                         |
| <i>Mus musculus</i> (mouse)                  | 2.7 x 10 <sup>9</sup>              | 22,619                         |
| <i>Homo sapiens</i> (human)                  | 3.1 x 10 <sup>9</sup>              | 20,418                         |

\*Genome size includes an estimate for the amount of highly repeated DNA sequence not in genome databases.