**Chapter 26 - Phylogeny**

Phylogeny is the \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ of a species or group of related species

The discipline of \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ classifies organisms and determines their evolutionary relationships

Systematists use fossil, molecular, and \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ data to infer evolutionary relationships

**Concept 26.1: Phylogenies show evolutionary relationships**

Taxonomy is the ordered \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ and \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ of organisms

Binomial Nomenclature

In the 18th century, Carolus Linnaeus published a system of taxonomy based on \_\_\_\_\_\_\_\_\_\_\_\_\_

Two key features of his system remain useful today: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ for species and \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

The two-part scientific name of a species is called a \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

The first part of the name is the \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

The second part, called the specific epithet, is unique for each \_\_\_\_\_\_\_\_\_\_\_\_\_ within the genus

The \_\_\_\_\_\_\_\_\_\_\_\_\_ of the genus is capitalized, and the entire species name is \_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ together name the species (not the specific epithet alone)

Hierarchical Classification

Linnaeus introduced a system for grouping species in increasingly broad categories

The taxonomic groups from \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ are: domain, kingdom, phylum, class, order, family, genus, and species

A taxonomic unit at any level of hierarchy is called a \_\_\_\_\_\_\_\_\_\_\_

Linking Classification and Phylogeny

Systematists depict evolutionary relationships in branching \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

A phylogenetic tree represents a \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ about evolutionary relationships

Each \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ represents the \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ of two species

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ are groups that share an immediate common ancestor

 A \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ includes a branch to represent the last common ancestor of all taxa in the tree

A \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ is a branch from which more than two groups emerge

What We Can and Cannot Learn from Phylogenetic Trees

Phylogenetic trees do show \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Phylogenetic trees \_\_\_\_\_\_\_\_\_\_ indicate when species evolved or how much \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ occurred in a lineage

It shouldn’t be assumed that a taxon evolved from the taxon next to it

Applying Phylogenies

Phylogeny provides important information about \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ in \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Concept 26.2: Phylogenies are inferred from morphological and molecular data**

To infer phylogenies, systematists gather information about morphologies, genes, and biochemistry of living organisms

 Morphological and Molecular Homologies

Organisms with \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ or DNA sequences are likely to be more \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ than organisms with different structures or sequences

Sorting Homology from Analogy

When constructing a phylogeny, systematists need to distinguish whether a similarity is the result of \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ is similarity due to shared ancestry

 \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ is similarity due to convergent evolution

Convergent evolution occurs when similar environmental pressures and \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ produce similar (analogous) adaptations in organisms from different evolutionary lineages

Bat and bird wings are \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ as forelimbs, but analogous as functional wings

Analogous structures or molecular sequences that evolved independently are also called \_\_\_\_\_\_

Homology can be distinguished from analogy by comparing fossil evidence and the degree of complexity

The more \_\_\_\_\_\_\_\_\_\_\_ two similar structures are, the more likely it is that they are homologous

Evaluating Molecular Homologies

Systematists use computer programs & mathematical tools when analyzing comparable \_\_\_\_\_\_ segments from different organisms

It is also important to distinguish homology from analogy in molecular similarities

Mathematical tools help to identify molecular homoplasies, or coincidences

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ uses DNA and other molecular data to determine evolutionary relationships

**Concept 26.3: Shared characters are used to construct phylogenetic trees**

Once homologous characters have been identified, they can be used to infer a phylogeny

Cladistics

Cladistics groups organisms by common descent

A clade is a group of species that includes an ancestral species and all its descendants

Clades can be nested in larger clades, but not all groupings of organisms qualify as clades

A valid clade is \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_, signifying that it consists of the ancestor species and all its descendants

A \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ grouping consists of an ancestral species and some, but not all, of the descendants

A \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ grouping consists of various species that lack a common ancestor

*Shared Ancestral and Shared Derived Characters*

In comparison with its ancestor, an organism has both shared and different characteristics

A shared \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ character is a character that originated in an ancestor of the taxon

A shared \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ character is an evolutionary novelty unique to a particular clade

A character can be both ancestral and derived, depending on the context

*Inferring Phylogenies Using Derived Characters*

When inferring evolutionary relationships, it is useful to know in which clade a shared derived character first appeared

Phylogenetic Trees with Proportional Branch Lengths

In some trees, the length of a branch can reflect the number of \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ that have taken place in a particular DNA sequence in that lineage

In other trees, branch length can represent \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_, and branching points can be determined from the fossil record

**Chapter 27: Bacteria and Archaea**

Overview: Masters of Adaptation

Prokaryotes thrive \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_, including places too acidic, salty, cold, or hot for most other organisms

Most prokaryotes are \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_, but what they lack in size they make up for in \_\_\_\_\_\_\_

There are more in a handful of fertile soil than the number of people who have ever lived

They have an astonishing \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Prokaryotes are divided into two domains: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Concept 27.1: Structural and functional adaptations contribute to prokaryotic success**

Most prokaryotes are \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_, although some species form \_\_\_\_\_\_\_\_\_\_\_\_\_\_

Most prokaryotic cells are 0.5–5 µm, much smaller than the 10–100 µm of many eukaryotic cells

Prokaryotic cells have a variety of \_\_\_\_\_\_\_\_\_\_\_\_\_

The three most common shapes are \_\_\_\_\_\_\_\_\_\_\_\_\_ (cocci), rods (bacilli), and \_\_\_\_\_\_\_\_\_\_\_\_\_\_

Cell-Surface Structures

An important feature of nearly all prokaryotic cells is their \_\_\_\_\_\_\_\_\_\_\_\_, which maintains cell \_\_\_\_\_\_\_\_\_\_\_, provides physical \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_, and prevents the cell from bursting in a hypotonic environment

Eukaryote cell walls are made of cellulose or chitin

Bacterial cell walls contain **\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**, a network of sugar polymers cross-linked by polypeptides

Archaea contain polysaccharides and \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ but lack peptidoglycan

Using the **\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**, scientists classify many bacterial species into **\_\_\_\_\_\_** and **\_\_\_\_\_** groups based on cell wall composition

Gram-negative bacteria have \_\_\_\_\_\_\_\_ peptidoglycan and an outer membrane that can be \_\_\_\_\_\_\_\_\_\_\_, and they are more likely to be \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Many antibiotics target peptidoglycan and damage bacterial \_\_\_\_\_\_\_\_\_\_\_\_\_

A polysaccharide or protein layer called a **\_\_\_\_\_\_\_\_\_\_\_** covers many prokaryotes

Some prokaryotes have **\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_** (also called *attachment pili*), which allow them to stick to their substrate or other individuals in a colony

**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_** are longer than fimbriae and allow prokaryotes to exchange \_\_\_\_\_\_

Motility

Most motile bacteria propel themselves by flagella that are structurally and functionally different from eukaryotic flagella

In a heterogeneous environment, many bacteria exhibit **taxis**, the ability to move toward or away from certain stimuli

Internal and Genomic Organization

Prokaryotic cells usually lack complex compartmentalization

Some prokaryotes do have specialized membranes that perform metabolic functions

The prokaryotic genome has less DNA than the eukaryotic genome

Most of the genome consists of a circular chromosome

Some species of bacteria also have smaller rings of DNA called **plasmids**

The typical prokaryotic genome is a ring of DNA that is not surrounded by a membrane and that is located in a **nucleoid region**

Reproduction and Adaptation

Prokaryotes reproduce quickly by binary fission and can divide every 1–3 hours

Many prokaryotes form metabolically inactive **endospores**, which can remain viable in harsh conditions for centuries

Prokaryotes can evolve rapidly because of their short generation times

**Concept 27.2: Rapid reproduction, mutation, and genetic recombination promote genetic diversity in prokaryotes**

Prokaryotes have considerable genetic variation

Three factors contribute to this genetic diversity:

Rapid reproduction

Mutation

Genetic recombination

Rapid Reproduction and Mutation

Prokaryotes reproduce by binary fission, and offspring cells are generally identical

Mutation rates during binary fission are low, but because of rapid reproduction, mutations can accumulate rapidly in a population

High diversity from mutations allows for rapid evolution

Genetic Recombination

Additional diversity arises from genetic recombination

Prokaryotic DNA from different individuals can be brought together by transformation, transduction, and conjugation

*Transformation and Transduction*

A prokaryotic cell can take up and incorporate foreign DNA from the surrounding environment in a process called **transformation**

**Transduction** is the movement of genes between bacteria by bacteriophages (viruses that infect bacteria)

*Conjugation and Plasmids*

**Conjugation** is the process where genetic material is transferred between bacterial cells

Sex pili allow cells to connect and pull together for DNA transfer

A piece of DNA called the **F factor** is required for the production of sex pili

The F factor can exist as a separate plasmid or as DNA within the bacterial chromosome

The F Factor as a Plasmid

Cells containing the **F plasmid** function as DNA donors during conjugation

Cells without the F factor function as DNA recipients during conjugation

The F factor is transferable during conjugation

The F Factor in the Chromosome

A cell with the F factor built into its chromosomes functions as a donor during conjugation

The recipient becomes a recombinant bacterium, with DNA from two different cells

It is assumed that horizontal gene transfer is also important in archaea

You should now be able to:

Distinguish between the cell walls of gram-positive and gram-negative bacteria

State the function of the following features: capsule, fimbriae, sex pilus, nucleoid, plasmid, and endospore

Explain how R plasmids confer antibiotic resistance on bacteria

Distinguish among the following sets of terms: photoautotrophs, chemoautotrophs, photoheterotrophs, and chemoheterotrophs; obligate aerobe, facultative anaerobe, and obligate anaerobe; mutualism, commensalism, and parasitism; exotoxins and endotoxins