General Biology: Phylogeny

AI-Generated Study Guide

(Based on lectures delivered by Dr. Ty C.M. Hoffman)

I. Classification and Phylogeny

Phylogeny is a method of classifying organisms based on **shared ancestry**. Historically, classification relied on how organisms appeared, which can be misleading regarding actual evolutionary relatedness. For example, the limbless Eastern Glass Lizard appears snake-like but is phylogenetically closely related to other lizards, not true snakes.

Taxonomy refers to the classification of organisms into **taxa** (groups). Classification uses a **hierarchical** or nested arrangement:

- **Domains:** The largest and most inclusive taxa. There are three domains: **Eukarya, Bacteria, and Archaea**.
- **Kingdom, Phylum, Class, Order, Family, Genus, Species.**

Although there is a **dichotomy of cell type** (prokaryotic vs. eukaryotic), prokaryotes are divided into two domains (**Bacteria and Archaea**). The domain Eukarya contains all eukaryotic organisms.

Binomial Nomenclature (two-name naming system) identifies organisms by their **scientific name**, consisting of the **genus** and the **species** (e.g., *Panthera pardus*). The genus name is always capitalized and italicized; the species name is only italicized.

II. Evolutionary Concepts

Origin of Traits Traits are determined indirectly by genes (via RNA and proteins). The appearance of a new trait is caused by **mutation** (random accidents in DNA), which is the original source of all genetic variation. If a random mutation produces a trait that increases an organism's **fitness** (survival and reproductive success), it can become incorporated into the population through **adaptive evolution**.

Convergent Evolution Convergent evolution occurs when evolution proceeds independently in two different populations because they experience similar environmental **selection pressures**. This process leads to the development of **analogous structures**—similarities that are **not** based on shared ancestry. Examples include the independent evolution of limblessness in snakes and the Eastern Glass Lizard, or burrowing adaptations (eyelessness, stout limbs) in unrelated marsupial and eutherian moles.

The presence of analogous structures complicates phylogeny construction because they can be misinterpreted as evidence of close shared ancestry. In contrast, **homologous structures** are similarities based on shared ancestry.

III. Phylogenetic Trees (Phylogenies)

A phylogenetic tree is a visual representation of evolutionary relationships that serves as a **hypothesis** about how organisms came about.

Tree Components:

- **Lineage:** A line representing a succession of organisms.
- **Node (Branch Point):** Represents a **speciation event** or the **divergence** (split) of one lineage into two separate species. Nodes can swivel without changing the underlying evolutionary relationships represented by the tree.
- **Most Recent Common Ancestor (MRCA):** The node that represents the ancestor shared by a specific group of descendants most recently.
- **Sister Taxa:** Two lineages that spring directly from the same node.
- **Basal Taxon:** A lineage that springs from the ancestor of the entire tree shown but does not subdivide further. It is likely the most similar lineage to that shared ancestor.
- **Polyotomy:** A branch point where a lineage splits simultaneously into three or more separate lineages. This is problematic because a simultaneous split is considered astronomically unlikely; a polyotomy is usually an admission that there is insufficient data to **resolve** the exact order of branching.

Shared Characters: The characteristics used to construct phylogenies are defined relative to the group being studied:

- **Shared Derived Character (Synapomorphy):** A character that evolved recently and defines the specific taxon being studied.
- **Shared Ancestral Character (Plesiomorphy):** A character that evolved farther back in the past, appearing one or more nodes prior to the node defining the specific taxon.
- The terms ancestral and derived are **relative** and depend entirely on the focus group.

IV. Defining Phylogenetic Groups

Phylogenetic groups are categorized based on whether they fully capture an ancestral lineage:

- **Monophyletic Group (Clade):** A group containing the most recent common ancestor and **all** of its descendants. These groups are the most useful for discussion.
- **Paraphyletic Group:** A group containing the most recent common ancestor and **some** but **not all** of its descendants.
- **Polyphyletic Group:** A group that **does not** include the most recent common ancestor of all members in the group.

V. Tree Construction and Time

Principle of Parsimony When choosing between multiple possible hypotheses (trees), scientists favor the most **parsimonious** explanation—the one that is the least complicated. This means selecting the tree that requires the **fewest required evolutionary events** (mutational changes) to explain the observed differences in characteristics.

DNA Analysis Identical DNA sequences suggest a very recent divergence. When DNA sequences differ, the differences are due to mutations: substitutions, insertions, and deletions (indels).

- Substitutions are easier to analyze because they do not change the sequence length.
- Indels change the sequence length, making **alignment** (matching nucleotides column by column) difficult. Sophisticated computer software is needed to identify masked similarities

caused by indels and to distinguish true ancestral matches from **random matches** that occur merely by chance.

Molecular Clock Mutations occur randomly but at an average frequency over time. By plotting the number of mutations against known divergence time, a **linear relationship** can be established. This relationship acts as a **molecular clock**, allowing scientists to estimate how long ago two lineages separated based on the differences observed in their DNA.

Reading Timelines Unless a phylogenetic tree explicitly includes a timeline (often listed along the x-axis), assumptions should not be made about the passage of time. In some trees, the length of the lineage represents the amount of **mutational change** that has occurred since the previous node, rather than time.

Horizontal Gene Transfer (HGT) Vertical gene transfer is the standard transfer of genes from parent to offspring. **Horizontal gene transfer** is the transfer of genes between organisms that are not parent and offspring (e.g., via viruses). HGT occurs naturally and complicates tree construction by making relationships appear confusingly close or distant, resulting in a messier phylogeny.

Overall Tree of Life Phylogenetic analysis of the three domains reveals that **Bacteria** is the basal lineage, having split earliest. **Archaea** is more closely related to **Eukarya** than either is to Bacteria.