

Lecture Outline: Phylogeny

I. Classification Based on Shared Ancestry

A. Phylogeny

1. Classifying organisms based on shared ancestry, moving beyond classification based solely on appearance.

B. Phylogenetic Trees (Cladograms)

1. Diagrams illustrating evolutionary relationships.
2. **Rooted Trees:** Indicate a common ancestor at the base.
3. **Sister Taxa:** Groups that share an immediate common ancestor.
4. **Polytomy:** An unresolved pattern where multiple lineages diverge from the same point.

C. Grouping Taxa

1. **Clade (Monophyletic Group):** A common ancestor and **all** of its descendants.
2. **Paraphyletic Group:** A common ancestor but **not all** its descendants.
3. **Polyphyletic Group:** Distantly related species without a common ancestor.

II. Distinguishing Evolutionary Similarity

A. Homology vs. Analogy

1. **Homology:** Similarity due to shared ancestry (e.g., bone structure).
2. **Analogy:** Similarity due to convergent evolution (independent adaptation).

B. Cladistics (Classification by Common Descent)

1. **Shared Ancestral Character:** Trait that originated in an ancestor of the clade.
2. **Shared Derived Character:** Trait unique to a specific clade.
3. **Outgroup:** A species related to the study group but diverged before the group's lineage.

III. Reconstructing Phylogenetic Trees

A. Principle of Maximum Parsimony

1. The simplest explanation, requiring the fewest evolutionary events, is most likely correct.

B. Gene Transfer in Evolution

1. **Vertical Gene Transfer:** Genes passed from parent to offspring.
2. **Horizontal Gene Transfer (HGT):** Gene transfer between organisms that are not parent and offspring (e.g., virus to plant).
3. HGT complicates and obscures true evolutionary relationships on phylogenetic trees.