Phylogeny

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- Phylogenetic trees may be constructed through analysis of fossils or comparison of DNA proteins.
- In Analogous Structures Convergent evolution occurs when similar environmental pressures produce similar (analogous) adaptations in different animals
- Phylogenetic Tree vs. Cladogram In a Phylogenetic tree, the length of branches matters, while, in a cladogram, the length does not. A cladogram depicts patterns of shared characteristics among taxa.
- A clade is a group of species that includes an ancestral species and all of its descendants
- A valid clade is monophyletic
- A shared primitive character is a character that is shared beyond the taxon we are trying to define
- A shared derived character is an evolutionary novelty unique to a particular clade
- An outgroup is a group of organisms not belonging to the group whose evolutionary relationships are being compared
- Parsimony The principle of parsimony implies that we should prefer the phylogeny that requires the fewest evolutionary changes
- How do new species form?
 - 1. Isolation (allopatric or sympatric)
 - (a) Allopatric Geographic separation (other country)
 - (b) Sympatric Still live in same area, but different parts (same country)
- Barriers to Reproduction:
 - 1. Geographic Isolation (Being in different areas)

- 2. Ecological Isolation (Being in different environments)
- 3. Temporal Isolation (Mating in different seasons)
- 4. Behavioral Isolation (Bird songs)
- 5. Mechanical Isolation (Unable to reproduce)
- 6. Gametic Isolation (Gametes reject)

• Post-Reproduction Barriers:

- 1. Reduced Hybrid Viability (Survive worse due to combination of parents)
- 2. Reduced Hybrid Fertility (Offspring unable to reproduce)
- 3. Hybrid Breakdown

• Rate of Speciation:

- 1. Gradualism Gradual accumulation of small changes over a long time
- 2. Punctuated Equilibrium Rapid bursts of change mixed with long periods of little or no change

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