

CHAPTER 16:

PHYLOGENY: THE UNITY AND

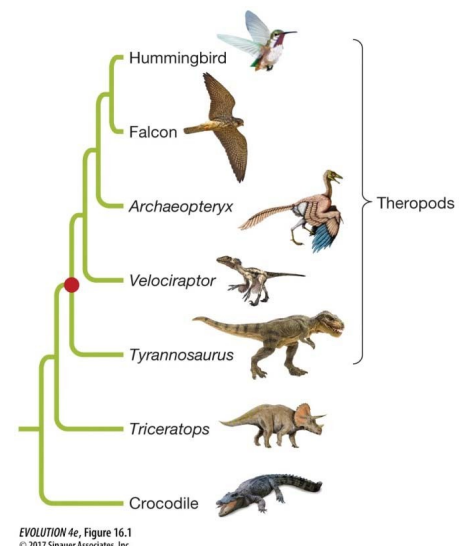
DIVERSITY OF LIFE

DEFINITIONS

1. **Derived characters:** acquired by the most recent common ancestor of the taxa under consideration (absent in the last common ancestor)
2. **Ancestral characters:** inherited from the common ancestor of a clade and has undergone little change since.
3. **Synapomorphy:** a characteristic present in an ancestral species and shared exclusively (in more or less modified form) by its evolutionary descendants.
4. **Monophyletic group/clade:** The set of species that have descended from a common ancestor.
5. **Most recent common ancestor (MRCA):** the **most recent** individual from which all the organisms from such set are directly descended.
6. **Outgroups:** species more distantly related to the members of a certain clade than species within the clade are to each other.
7. **Parsimony:** Follows the simple rule of choosing the tree that requires the fewest evolutionary changes.
8. **Homoplasy:** the independent evolution of similar traits. Results from convergent evolution, parallel evolution and evolutionary reversal.
9. **Evolutionary reversal:** return to an earlier, ancestral character state.
10. **Radiation:** If several species arise from a common ancestor over a short period of time, it can be difficult to determine the phylogenetic relationship among them.
11. **Phylogeny:** the evolutionary relationships among species
12. **Gene tree:** The genealogical history of a group of gene copies at the same locus
13. **Introgression:** the transfer of genetic information from one species to another as a result of hybridization between them and repeated backcrossing.
14. **Comparative method:** comparing sets of species to test hypotheses about adaptation
15. **Paraphyletic taxon:** Includes an ancestor and some, but not all, of its descendants.
16. **Polyphyletic taxon:** Species from 2 or more different ancestors, but excludes other descendants that are placed in different taxa.
17. **Crown group:** living members of a group+ last common ancestor
18. **Stem group:** larger clade of related extinct lineages

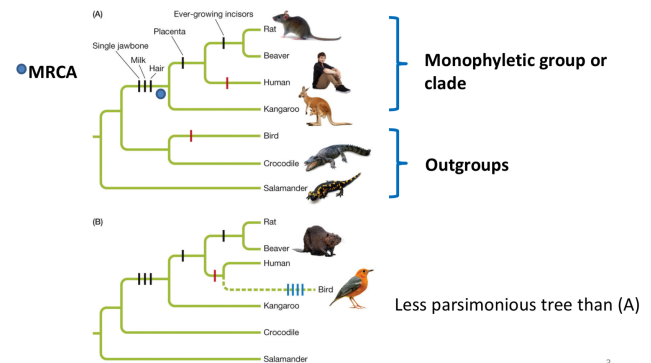
2 sources of information inform us about the past:

1. Fossils
 2. Living organisms
- Behaviour, physiology, life history and genome structure cannot be ascertained through fossils – determined through analyzing phylogenetic trees and the history of how different species have arisen.



INFERRING PHYLOGENIES

- Phylogenetic relationships among species are estimated from similarities and differences.
- Vertebrae = **derived** character state in contrast to the **ancestral** state which is absence of vertebrae.
- A derived character that is shared by a group of species (**synapomorphy**) is evidence that the species evolved from a common ancestor.
- Mammals are a clade of species with synapomorphic characteristics that distinguish them from reptiles and amphibians (eg hair, milk, lower jaw etc)
- Outgroups help us to determine the direction of evolutionary change.
- Diagram to the right:* Humans and birds are bipedal due to independent convergent evolution
- Parsimony uses derived traits as evidence for common ancestry, it does not use shared traits that are ancestral.



WHY ESTIMATING PHYLOGENIES CAN BE HARD?

- Many characteristics evolve repeatedly.
- Repeated independent mutations and several other evolutionary phenomena can make it difficult to determine relationships and phylogenetic history.
- Homoplasy creates problems for estimating phylogenies because the similarity is not caused by shared ancestry or homology
- Diagram right:* Insect wings illustrate how Homoplasy complicates building the phylogeny for a group of species. Bristletails and silverfishes are wingless and branched off from the lineage that later evolved wings. Some orders lost their wings secondarily and some orders have no winged species (lice and fleas) – undergo reversal to a wingless state.
- Size, shape and coloration undergo convergent evolution in diverse lineages.
- Same holds for mutations: Only 4 possible states of a particular site in a DNA sequence, exactly the same mutation will occur repeatedly over sufficiently long periods of evolutionary time – some mutations can be reversed to the ancestral state.
- Single base pair difference among species provides little reliable evidence about their phylogeny.
- Diagram to the right:* sequence differences evolved more rapidly at 3rd positions and more slowly at 2nd positions within codons.
- Divergence at 3rd position increases rapidly at first then levels off due to multiple subs at the same sites.
- Thus –provides no phylogenetic information for taxa that diverged about 75 Mya.

