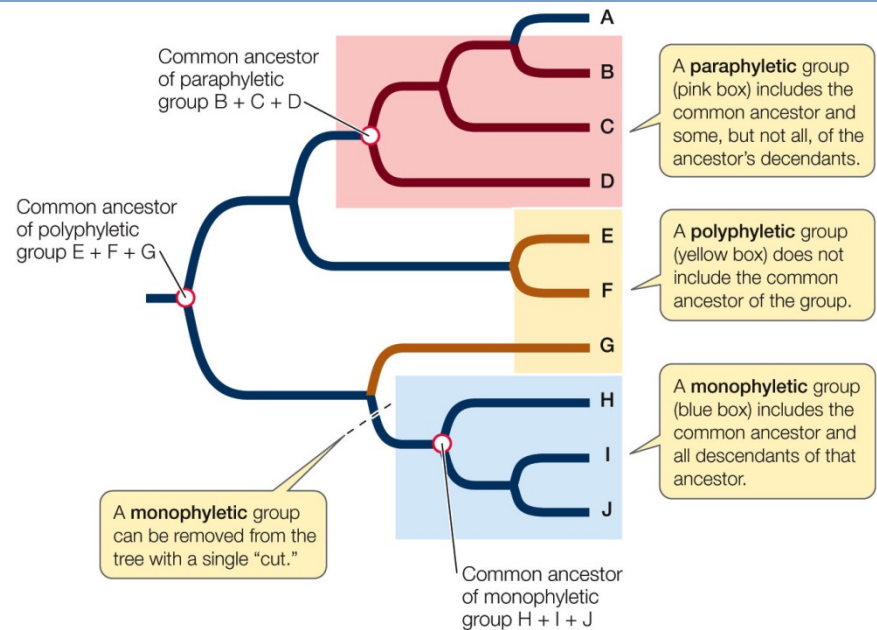


General Biology I (101-NYA)

Phylogeny Concepts & Learning Outcomes

Topic	Chapter 27 pages*	Concept	Learning Outcomes
What is phylogeny?	p. 521-522	<ol style="list-style-type: none"> 1. Phylogeny is the evolutionary history of relationships among organisms. 2. Phylogeny is represented in a phylogenetic tree: <ol style="list-style-type: none"> a. Root: common ancestor. b. Node: point of divergence. c. Taxon: group of species within a clade (e.g., primates). d. Clade: taxon consisting of all the descendants of a common ancestor 3. Phylogenetic trees have a time scale where the root is the oldest event and nodes are more recent events in time. Branches can be rotated around nodes without changing the meaning of the tree and therefore the order of taxa (species) is arbitrary and does not reflect evolutionary relationships. 4. Tree of life: complete, 4-billion-year history of life, depicting that all life forms are connected through related evolutionary history (greatest unifying concepts in biology). 	<ol style="list-style-type: none"> 1. Define phylogeny, taxon, and clade 2. Analyze evolutionary relationships based on the interpretation of cladograms, describing the meaning of nodes and branches
Types of phylogeny		<ol style="list-style-type: none"> 5. A taxon could be: <ol style="list-style-type: none"> a. Monophyletic: all species share a single common ancestor b. Polyphyletic: species are derived from more than one common ancestor. c. Paraphyletic: all of a particular clade's members share a common ancestor but not all taxa that share that common ancestor are included in that group 	<ol style="list-style-type: none"> 5. Compare and contrast monophyletic, paraphyletic, and polyphyletic taxa



Phylogeny and species comparison

p. 522-524

- 6. Knowledge of evolutionary relationships is essential for making comparisons in biology. In trait comparison, differences within a group of interest determine when traits evolved.
- 7. Traits can be homologous or homoplastic (analogous).
 - a. Homology: similarities due to common descent; eg, vertebral column in all vertebrates is a derived trait (synapomorphy) that evolved from a notochord (ancestral trait) or body segmentation and location of body parts.
 - b. Homoplasy: similarities in traits that are *not* inherited from a common ancestor, but caused by convergent evolution (natural selection leads to similar solutions to the challenges posed by a particular habitat); eg, evolution of the eye in insects and vertebrates.

- 9. Compare convergent and divergent evolution, and distinguish by giving examples between homologous and analogous traits

Data used to construct phylogenetic trees

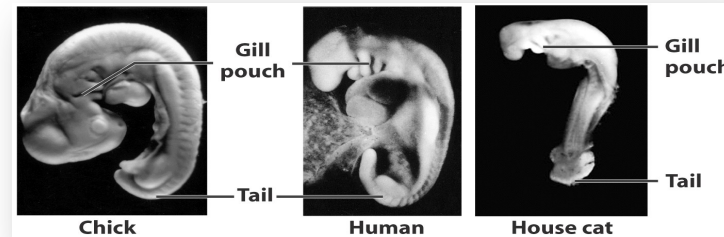
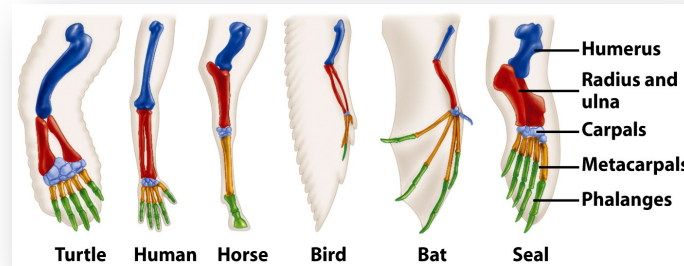
p. 524-527

- 8. Phylogenetic trees are typically constructed using and comparing hundreds or thousands of traits that can be grouped as:
 - a. Morphological: **structural homologies** (similarity of morphological traits)
 - b. Fossil: provide information about the morphology of past organisms, and where and when they lived
 - c. Developmental: homologies in embryo morphology and/or pattern of tissue differentiation
 - d. Molecular: now most widely used data for constructing phylogenetic

- 10. List, describe, and give examples of the different categories of homologies used in the construction of phylogenetic trees

trees (sequence of mtDNA, chloroplast DNA, nuclear DNA, amino acid sequences in proteins)

- e. Behavioral: behavior can be inherited; eg, frog calls are genetically determined and therefore can be used in phylogenetic trees



Gene: Amino acid sequence (single-letter abbreviations):
Aniridia (Human) LQRNRTSFTQEIEALEKEFERTHYPDVFARERLAAKIDLPEARIQVWFSNRRAKWRREE
eyeless (Fruit fly) LQRNRTSFTNDQIDSLEKEFERTHYPDVFARERLAGKIGLPEARIQVWFSNRRAKWRREE

Only six of the 60 amino acids in these sequences are different. The two sequences are 90% identical.

How we construct phylogenetic trees

p. 468-470

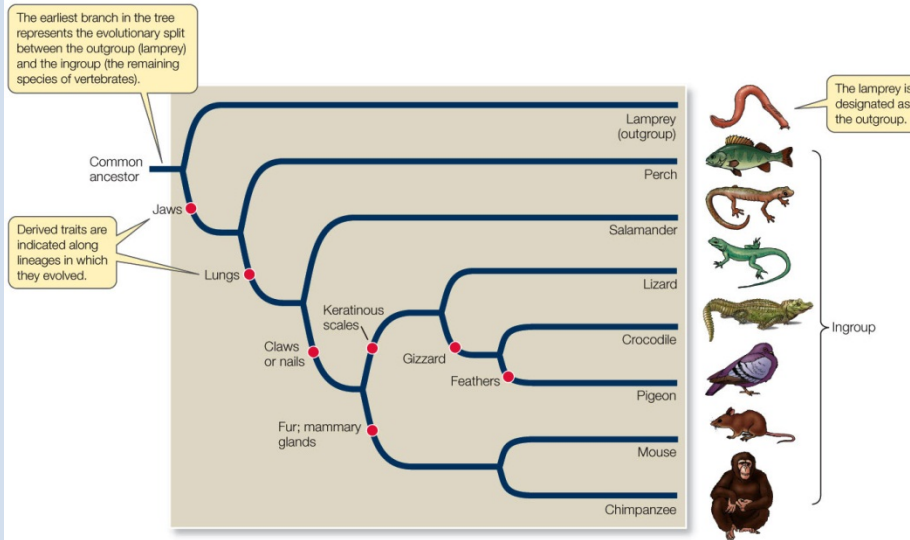
- 9. Information about the synapomorphies is used in constructing phylogenetic trees.
- 10. The principle of parsimony is applied: simplest explanation; assuming no or fewest homoplasies, no convergent evolution, and no derived traits have been lost
- 11. Comparison with the outgroup shows which traits of the ingroup are derived

- 11. Apply the concept of parsimony and comparison of shared synapomorphies to the classification of organisms and the construction of phylogenetic trees

and which are ancestral.

TABLE 22.1								
Eight Vertebrates Ordered According to Unique Shared Derived Traits								
TAXON	DERIVED TRAIT ^a							
	JAWS	LUNGS	CLAWS OR NAILS	GIZZARD	FEATHERS	FUR	MAMMARY GLANDS	KERATINOUS SCALES
Lamprey (outgroup)	-	-	-	-	-	-	-	-
Perch	+	-	-	-	-	-	-	-
Salamander	+	+	-	-	-	-	-	-
Lizard	+	+	+	-	-	-	-	+
Crocodile	+	+	+	+	-	-	-	+
Pigeon	+	+	+	+	+	-	-	+
Mouse	+	+	+	-	-	+	+	-
Chimpanzee	+	+	+	-	-	+	+	-

^aA plus sign indicates the trait is present, a minus sign that it is absent.



Taxonomic levels

p. 8-9

12. Linnaeus' system of classification is binomial and hierarchical with nested taxa.

13. Taxonomic levels from least to most specific: domain (Eukarya), kingdom (Animalia), phylum (Chordata), class (Mammalia), order (Primates), family (Hominidae), genus (*Homo*), and species (*sapiens*).

12. Describe the binomial system of naming organisms and arrange taxonomic categories in hierarchical fashion from most inclusive to least inclusive

* Textbook: *Biological Science*, Freeman, S. *et al.*, 2nd Canadian ed., 2014