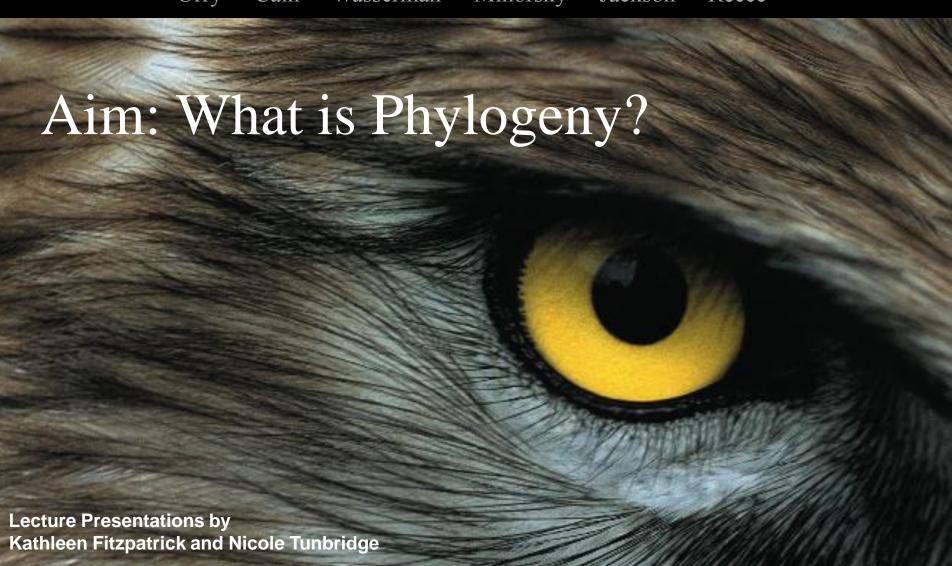
CAMPBELL BIOLOGY IN FOCUS

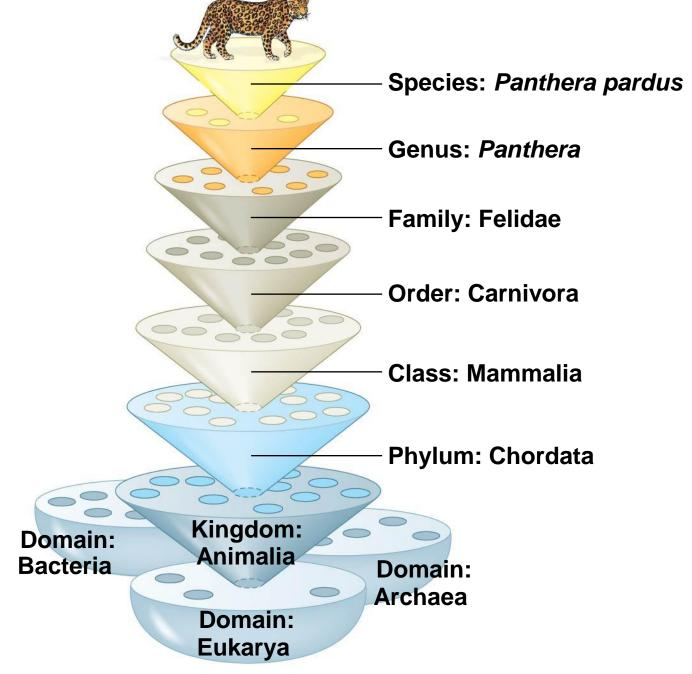
Urry • Cain • Wasserman • Minorsky • Jackson • Reece



- Phylogeny is the evolutionary history of a species or group of related species
- Taxonomy is the ordered division and naming of organisms

Binomial Nomenclature

- In the 18th century, Carolus Linnaeus published a system of taxonomy based on resemblances
- Two key features of his system remain useful today: two-part names for species and hierarchical classification
- Linnaeus introduced a system for grouping species in increasingly broad categories
- The taxonomic groups from narrow to broad are species, genus, family, order, class, phylum, kingdom, and domain

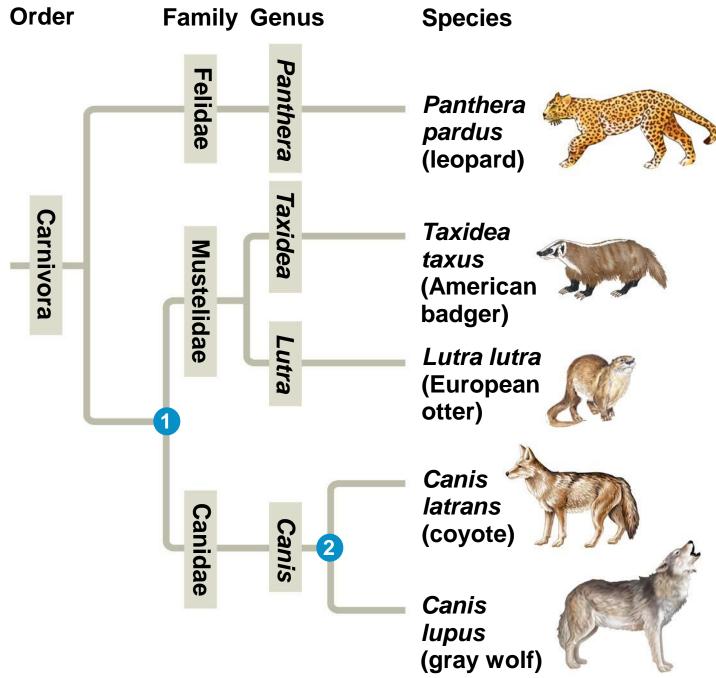


 A taxonomic unit at any level of hierarchy is called a taxon

Linking Classification and Phylogeny

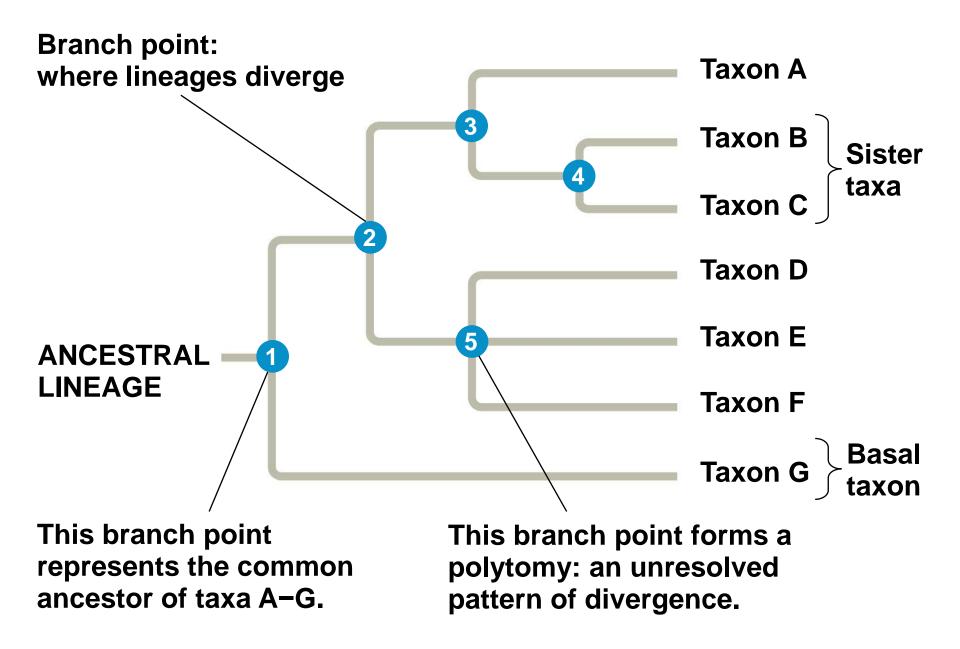
 Systematists depict evolutionary relationships in branching phylogenetic trees

Figure 20.4



- A phylogenetic tree represents a hypothesis about evolutionary relationships
- Each branch point represents the divergence of two taxa from a common ancestor
- Sister taxa are groups that share an immediate common ancestor

- A rooted tree includes a branch to represent the most recent common ancestor of all taxa in the tree
- A basal taxon diverges early in the history of a group and originates near the common ancestor of the group
- A polytomy is a branch from which more than two groups emerge



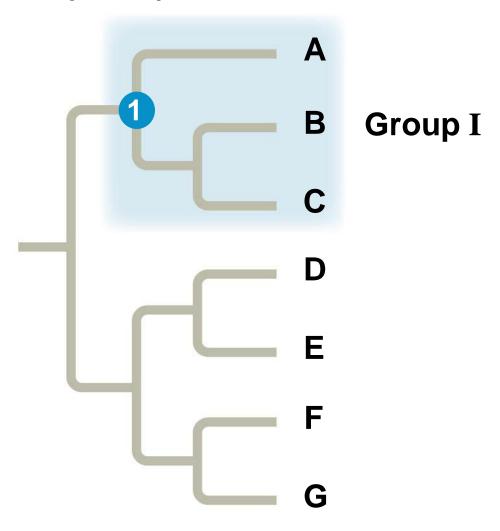
Sorting Homology from Analogy

- When constructing a phylogeny, systematists need to distinguish whether a similarity is the result of homology or analogy
- Homology is similarity due to shared ancestry
- Analogy is similarity due to convergent evolution

Cladistics

- Cladistics classifies organisms by common descent
- A clade is a group of species that includes an ancestral species and all its descendants
- Clades can be nested in larger clades, but not all groupings of organisms qualify as clades
- A valid clade is monophyletic, signifying that it consists of the ancestor species and all its descendants

(a) Monophyletic group (clade)

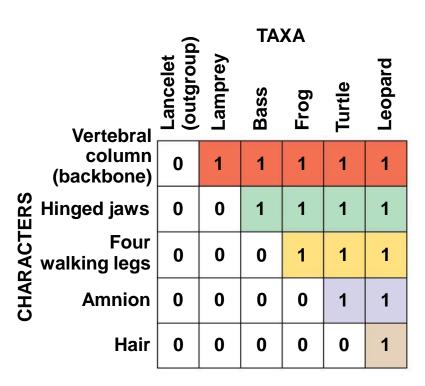


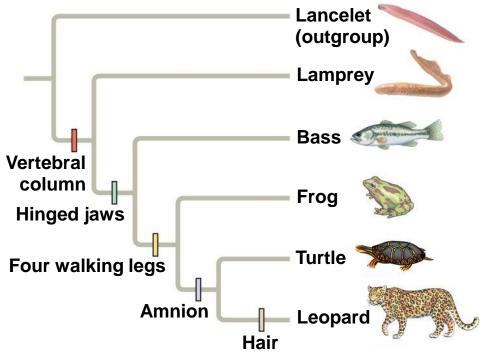
Shared Ancestral and Shared Derived Characters

 In comparison with its ancestor, an organism has both shared and different characteristics

Inferring Phylogenies Using Derived Characters

- When inferring evolutionary relationships, it is useful to know in which clade a shared derived character first appeared
- A shared ancestral character is a character that originated in an ancestor of the taxon
- A shared derived character is an evolutionary novelty unique to a particular clade
- A character can be both ancestral and derived, depending on the context



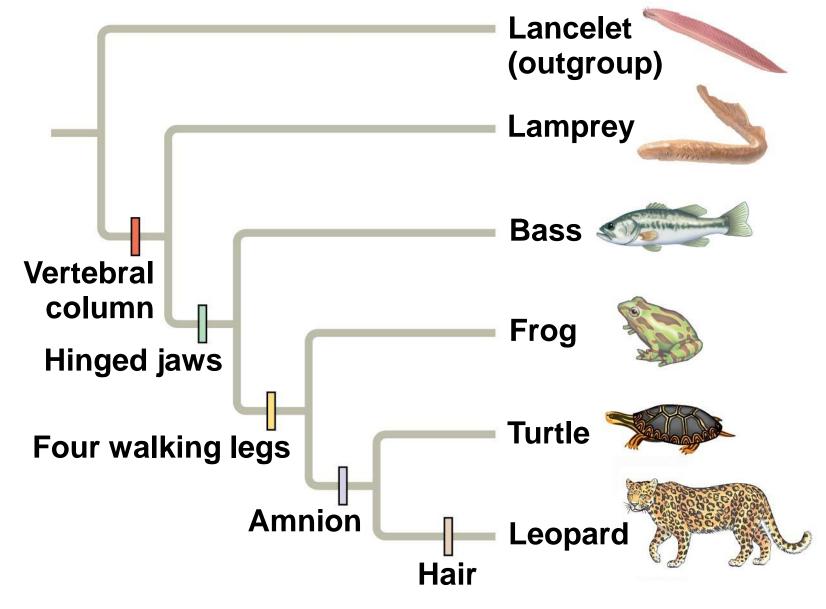


(a) Character table

(b) Phylogenetic tree

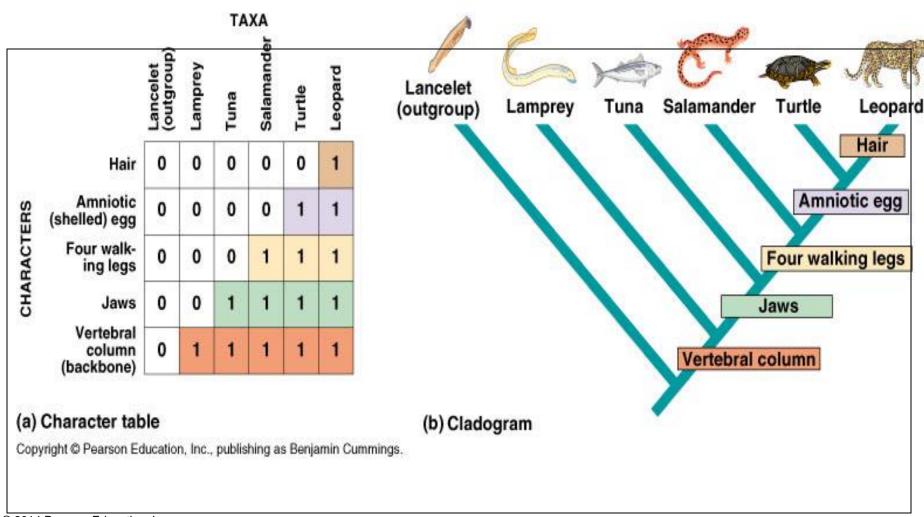
		⊙ TAXA					
Vertebral		Lancelet (outgroup)	Lamprey	Bass	Frog	Turtle	Leopard
CHARACTERS	column (backbone)	0	1	1	1	1	1
	Hinged jaws	0	0	1	1	1	1
	Four walking legs	0	0	0	1	1	1
	Amnion	0	0	0	0	1	1
	Hair	0	0	0	0	0	1

(a) Character table



(b) Phylogenetic tree

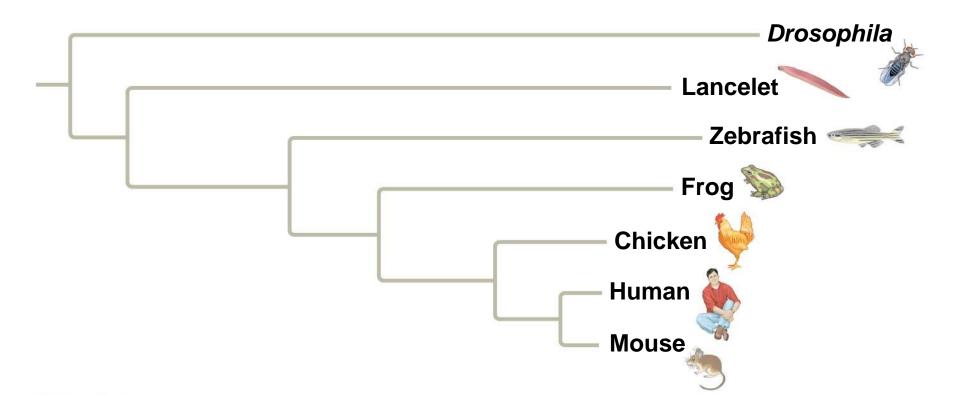
A Cladogram

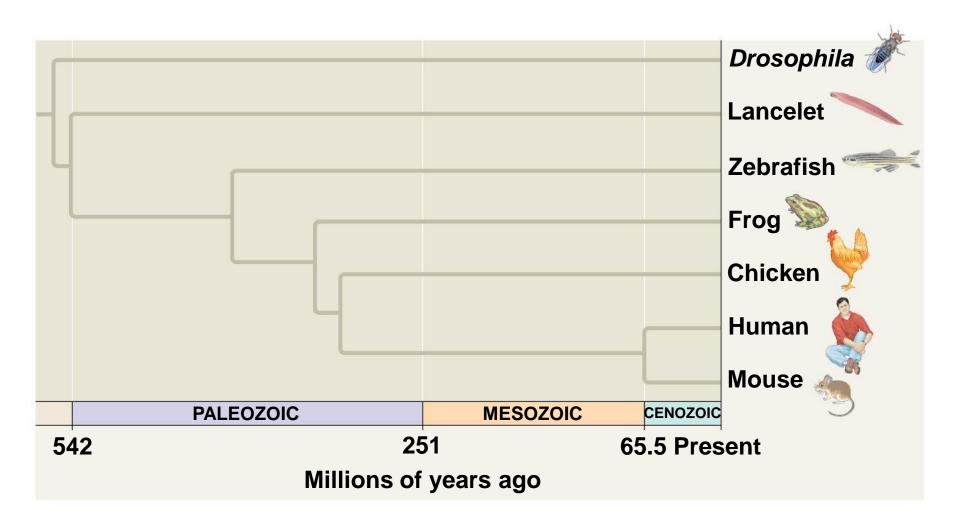


- An outgroup is a species or group of species that is closely related to the ingroup, the various species being studied
- The outgroup is a group that has diverged before the ingroup
- Systematists compare each ingroup species with the outgroup to differentiate between shared derived and shared ancestral characteristics

Phylogenetic Trees with Proportional Branch Lengths

- In some trees, the length of a branch can reflect the number of genetic changes that have taken place in a particular DNA sequence in that lineage
- In other trees, branch length can represent chronological time, and branching points can be determined from the fossil record





Phylogenetic Trees as Hypotheses

- The best hypotheses for phylogenetic trees fit the most data: morphological, molecular, and fossil
- Phylogenetic hypotheses are modified when new evidence arises

Molecular Clocks

- A molecular clock uses constant rates of evolution in some genes to estimate the absolute time of evolutionary change
- The number of nucleotide substitutions in related genes is assumed to be proportional to the time since they last shared a common ancestor



Plantao Animalia

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