CHAPTER 26:
PHYLOGENY AND THE TREE OF LIFE

AP Biology 2013

PHYLOGENY AND SYSTEMATICS

- Phylogeny - evolutionary history of a species or group of related species
- Systematics - analytical approach to understanding the diversity and relationships of organisms both present-day and extinct
  - Systematists use morphological, biochemical, and molecular comparisons to infer evolutionary relationships

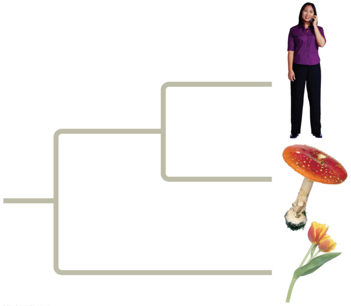
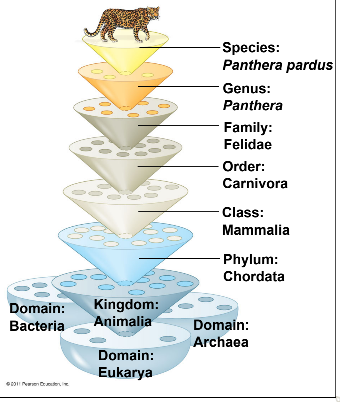


Fig. 26.2

TAXONOMY

Fig. 26.3

- Taxonomy - ordered division and naming of organisms
- 18th century - Linnaeus published a system of taxonomy based on resemblances
  - Binomial Nomenclature - first part is the genus, second part is the species
  - Hierarchical Classification - grouping system (domain, kingdom, phylum, class, order, family, genus, species)



PHYLOGENETIC TREES

- Systematists depict evolutionary relationships in a branching phylogenetic trees
- Each branch represents the divergence of two species
- Deeper branch points represent progressively greater amounts of divergence
- Sister taxa - groups that share an immediate common ancestor

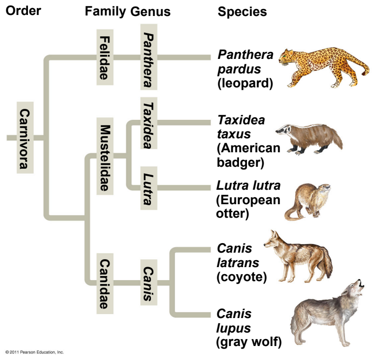


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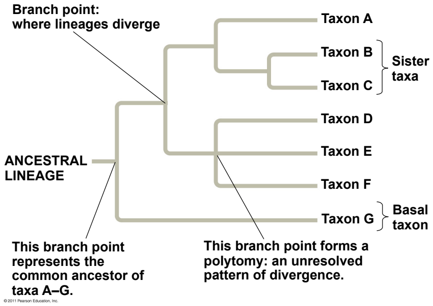
Fig. 26.4

USES OF PHYLOGENETIC TREES

- Show patterns of descent, not phenotypic similarity
- Do not indicate when species evolved or how much change occurred in a lineage
- Provides information about similar characteristics in closely related species



This branch point represents the common ancestor of taxa A–G.

This branch point forms a polytomy: an unresolved pattern of divergence.

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Fig. 26.5

MORPHOLOGICAL AND MOLECULAR HOMOLOGIES

- In addition to fossil organisms, phylogenic history can be inferred from certain morphological and molecular similarities among living organisms
- In general, organisms that share very similar morphologies or similar DNA sequences are likely to be more closely related than organisms with vastly different structures or sequences
- Similarity due to convergent evolution is called **analogy** rather than shared ancestry

CONVERGENT EVOLUTION

- Occurs when similar environmental pressures and natural selection produce similar (analogous) adaptations in organisms from different evolutionary lineages
- Analogous structures or molecular sequences that evolved independently are also called **homoplasies**

Figure 26.7

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Fig. 26.7

EVALUATING HOMOLOGIES

- Systematists use computer programs and mathematical tools when analyzing comparable DNA segments from different organisms

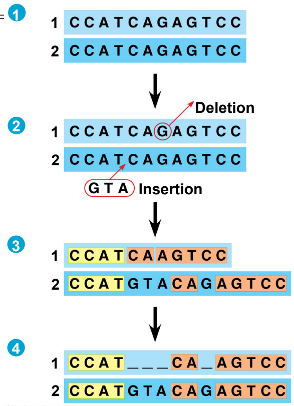

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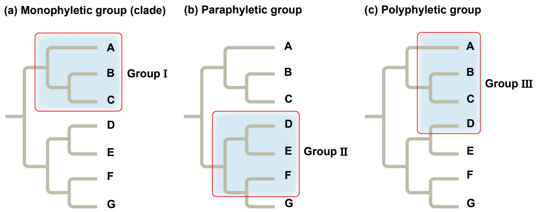
Fig. 26.8

CLADOGRAM

- Depiction of patterns of shared characteristics among taxa
- A **clade** is a group of species that includes an ancestral species and all of its descendants (monophyletic)
- Cladistics - study of resemblances among clades



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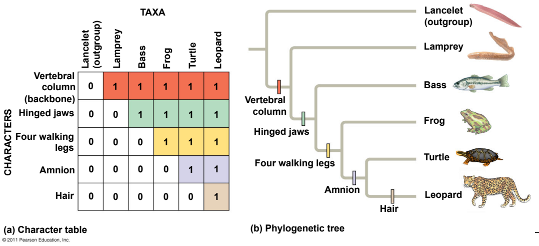
SHARED CHARACTERISTICS

- Cladistic analysis - clades are defined by evolutionary novelties
- Shared ancestral character - character that originated in an ancestor of the taxon
- Shared derived character - evolutionary novelty unique to a particular clade



CHARACTERS	Lancelet (outgroup)	Lamprey	Bass	Frog	Turtle	Leopard
Vertebral 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

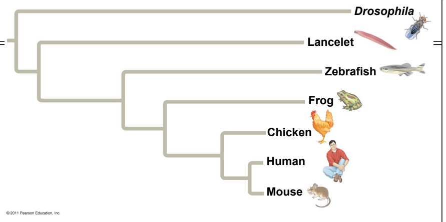
Fig. 26.11

OUTGROUPS

- Used to differentiate between shared derived and shared primitive characteristics
- Outgroup needs to be closely related to the ingroup (the species being studied)
- Outgroup comparison - based on the assumption that homologies present in both the outgroup and ingroup must be primitive characters that predate the divergence of both groups

TREES

Fig. 26.12



- Phylogram - Length of a branch in a cladogram reflects the number of genetic changes that have taken place in particular DNA or RNA sequence in that lineage
- Ultrametric trees - branching pattern is the same as in a phylogram, but all the branches that can be traced from the common ancestor to the present are of equal length

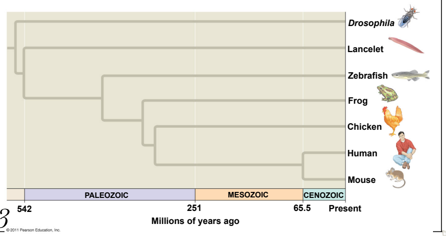


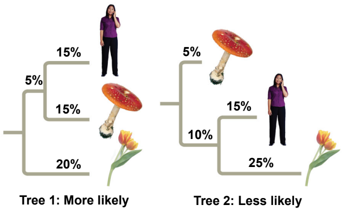
Fig. 26.13

PARSIMONY

- Most parsimonious tree is the one that requires the fewest evolutionary events to have occurred in the form of shared derived characters

	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

(a) Percentage differences between sequences



Tree 1: More likely

Tree 2: Less likely

(b) Comparison of possible trees

Fig. 26.14

PHYLOGENETIC TREE HYPOTHESES

- Phylogenetic bracketing allows us to predict features of an ancestor from features of its descendants
- Ex. Birds and crocodiles share features like: four-chambered hearts, nest building, and brooding
  - These characteristics likely evolved in a common ancestor

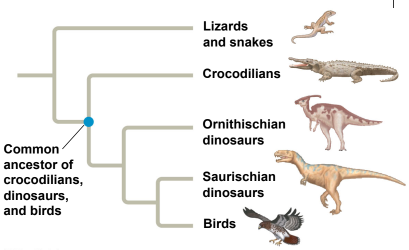


Fig. 26.16

EVOLUTIONARY TIME

- Molecular clock - measures absolute time of evolutionary change based on the observation that some genes and other regions of the genomes appear to evolve at constant rates

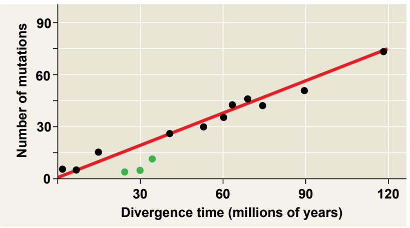
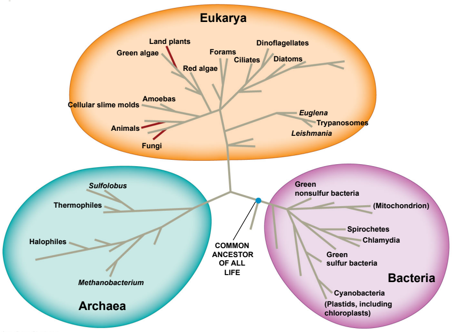


Fig. 26.19

UNIVERSAL TREE OF LIFE



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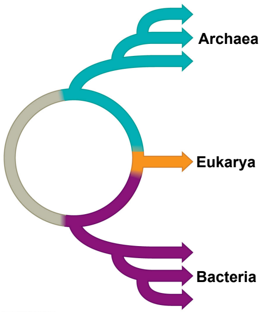
Figs. 26.21 & 26.23



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- Divided into the three major clades (domains): Bacteria, Archaea, and Eukarya