Chapter 25

Phylogeny and Systematics

PowerPoint Lectures for
***Biology*, Seventh Edition**
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Tracing phylogeny

- Phylogeny:
  - The evolutionary history of a species or group of related species
- Gathering data:
  - The fossil record
    - Shows ancestral characteristics that may have been lost over time
  - Morphological, biochemical, and molecular comparisons
  - Systematics
    - An analytical approach to understanding the diversity and relationships of organisms, both present-day and extinct

Systematics

- Evolutionary relationships

Figure 25.2

- Though sedimentary fossils are the most common
  - Paleontologists study a wide variety of fossils

(a) Dinosaur bones being excavated from sandstone
(b) Petrified tree in Arizona, about 190 million years old
(c) Leaf fossil, about 40 million years old
(d) Casts of ammonites, about 375 million years old
(e) Boy standing in a 150-million-year-old dinosaur track in Colorado
(f) Insects preserved whole in amber
(g) Tusks of a 23,000-year-old mammoth, frozen whole in Siberian ice

Figure 25.4a–g

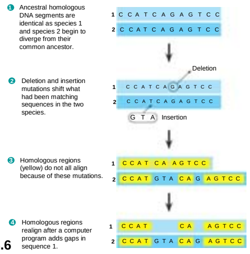
Careful of convergent evolution

- Convergent evolution occurs when similar environmental pressures and natural selection produce similar (analogous) adaptations in organisms from different evolutionary lineages

Figure 25.5

Evaluating Molecular Homologies

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



① Ancestral homologous DNA segments are identical as species 1 and species 2 begin to diverge from their common ancestor.

② Deletion and insertion mutations shift what had been matching sequences in the two species.

③ Homologous regions (yellow) do not all align because of these mutations.

④ Homologous regions realign after a computer program adds gaps in sequence 1.

Figure 25.6

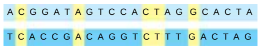


Figure 25.7

Hierarchical Classification

- Linnaeus developed binomial nomenclature
- Linnaeus introduced a system for grouping species in increasingly broad categories

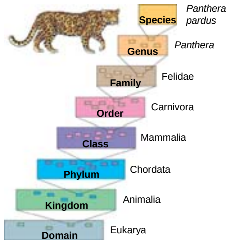


Figure 25.8

Linking Classification and Phylogeny

- Systematists depict evolutionary relationships
  - In branching phylogenetic trees

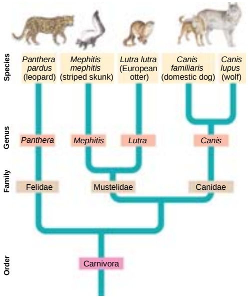
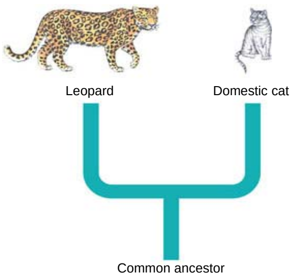
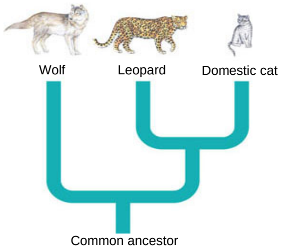


Figure 25.9

- Each branch point
  - Represents the divergence of two species



- “Deeper” branch points
  - Represent progressively greater amounts of divergence



Phylogenetic systematics

- Construction of phylogenetic trees based on shared characteristics
- A cladogram
  - patterns of shared characteristics among taxa
- A clade within a cladogram
  - A group of species that includes an ancestral species and all its descendants
- Cladistics
  - Is the study of resemblances among clades

Cladistics

- Clades
  - Can be nested within larger clades, but not all groupings or organisms qualify as clades

- A valid clade is monophyletic
  - Signifying that it consists of the ancestor species and all its descendants

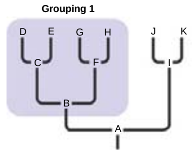


Figure 25.10a

(a) Monophyletic. In this tree, grouping 1, consisting of the seven species B–H, is a monophyletic group, or clade. A monophyletic group is made up of an ancestral species (species B in this case) and *all* of its descendant species. Only monophyletic groups qualify as legitimate taxa derived from cladistics.

- A paraphyletic clade
  - Is a grouping that consists of an ancestral species and some, but not all, of the descendants

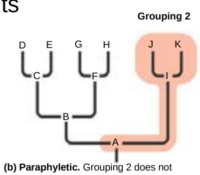


Figure 25.10b

(b) Paraphyletic. Grouping 2 does not meet the cladistic criterion: It is paraphyletic, which means that it consists of an ancestor (A in this case) and *some*, but not all, of that ancestor's descendants. (Grouping 2 includes the descendants I, J, and K, but excludes B–H, which also descended from A.)

- A polyphyletic grouping
  - Includes numerous types of organisms that lack a common ancestor

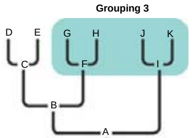


Figure 25.10c

(c) Polyphyletic. Grouping 3 also fails the cladistic test. It is polyphyletic, which means that it lacks the common ancestor of (A) the species in the group. Furthermore, a valid taxon that includes the extant species G, H, J, and K would necessarily also contain D and E, which are also descended from A.

Shared Primitive and Shared Derived Characteristics

- In cladistic analysis
  - Clades are defined by their evolutionary novelties

- A shared derived character
  - An evolutionary novelty unique to a clade
- A shared primitive character
  - A homologous structure that predates the branching of a particular clade from other members of that clade
  - Is shared beyond the taxon we are trying to define

Outgroups

- Systematists use a method called outgroup comparison
  - To differentiate between shared derived and shared primitive characteristics

- As a basis of comparison we need to designate an outgroup
  - which is a species or group of species that is closely related to the ingroup, the various species we are studying
- Outgroup comparison
  - Is based on the assumption that homologies present in both the outgroup and ingroup must be primitive characters that predate the divergence of both groups from a common ancestor

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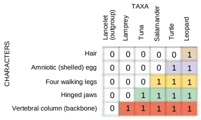
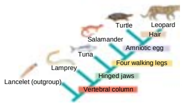
- The outgroup comparison
  - Enables us to focus on just those characters that were derived at the various branch points in the evolution of a clade



CHARACTERS \ TAXA	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Hair	0	0	0	0	0	1
Amniotic (shelled) egg	0	0	0	0	1	1
Four walking legs	0	0	0	1	1	1
Hinged jaws	0	0	1	1	1	1
Vertebral column (backbone)	0	1	1	1	1	1

(a) Character table. A 0 indicates that a character is absent; a 1 indicates that a character is present.



(b) Cladogram. Analyzing the distribution of these derived characters can provide insight into vertebrate phylogeny.

Figure 25.11a, b

Phylogenetic Trees and Timing

- Any chronology represented by the branching pattern of a phylogenetic tree
  - Is relative rather than absolute in terms of representing the timing of divergences

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Phylograms

- In a phylogram
  - The length of a branch in a cladogram reflects the number of genetic changes that have taken place in a particular DNA or RNA sequence in that lineage

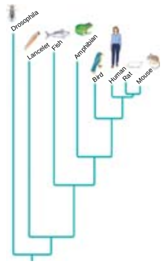

Figure 25.12

Ultrametric Trees

- In an ultrametric tree
  - The 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

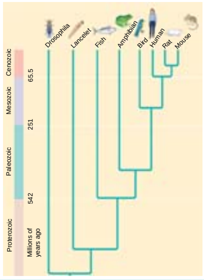

Figure 25.13

Maximum Parsimony and Maximum Likelihood

- Systematists
  - Can never be sure of finding the single best tree in a large data set
  - Narrow the possibilities by applying the principles of maximum parsimony and maximum likelihood

- Among phylogenetic hypotheses
  - The most parsimonious tree is the one that requires the fewest evolutionary events to have occurred in the form of shared derived characters

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- Applying parsimony to a problem in molecular systematics

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

Figure 25.14

(a) Percentage differences between sequences

- Applying parsimony to a problem in molecular systematics

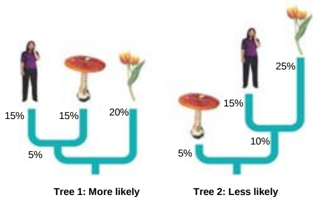


Figure 25.14

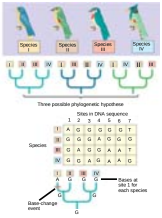
(b) Comparison of possible trees

- The principle of maximum likelihood
  - States that, given certain rules about how DNA changes over time, a tree can be found that reflects the most likely sequence of evolutionary events

APPLICATION In considering possible phylogenies for a group of species, systematists compare molecular data for the species. The most efficient way to study the various phylogenetic hypotheses is to begin by first considering the most parsimonious—that is, which hypothesis requires the fewest total evolutionary events (molecular changes) to have occurred.

TECHNIQUE Follow the numbered steps as we apply the principle of parsimony to a hypothetical phylogenetic problem involving four closely related bird species.

1. First, draw the possible phylogenies for the species (only 3 of the 15 possible trees relating these four species are shown here).
2. Tabulate the molecular data for the species (in this simplified example, the data represent a DNA sequence consisting of just seven nucleotide bases).
3. Now focus on site 1 in the DNA sequence. A single base-change event, marked by the crossbar in the branch leading to species I, is sufficient to account for the site 1 data.



Sites in DNA sequence

Species	1	2	3	4	5	6	7
I	A	G	G	G	G	G	T
II	G	G	G	A	G	G	G
III	G	A	G	G	A	A	T
IV	G	G	A	G	A	A	G

Figure 25.15a

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4. Continuing the comparison of bases at sites 2, 3, and 4 reveals that each of these possible trees requires a total of four base-change events (marked again by crossbars). Thus, the first four sites in this DNA sequence do not help us identify the most parsimonious tree.
5. After analyzing sites 5 and 6, we find that the first tree requires fewer evolutionary events than the other two trees (two base changes versus four). Note that in these diagrams, we assume that the common ancestor had GG at sites 5 and 6. But even if we started with an AA ancestor, the first tree still would require only two changes, while four changes would be required to make the other hypotheses work. Keep in mind that parsimony only considers the total number of events, not the particular nature of the events (how likely the particular base changes are to occur).
6. At site 7, the three trees also differ in the number of evolutionary events required to explain the DNA data.

RESULTS To identify the most parsimonious tree, we total all the base-change events noted in steps 3–6 (don't forget to include the changes for site 1, on the facing page). We conclude that the first tree is the most parsimonious of these three possible phylogenies. (But now we must complete our search by investigating the 12 other possible trees.)

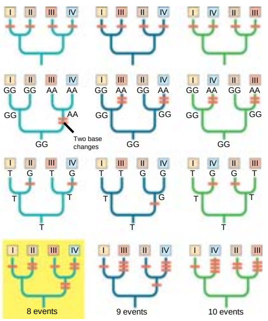
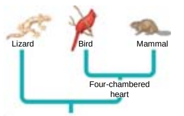


Figure 25.15b

Phylogenetic Trees as Hypotheses

- The best hypotheses for phylogenetic trees
  - Are those that fit the most data: morphological, molecular, and fossil

- Sometimes there is compelling evidence
  - That the best hypothesis is not the most parsimonious



(a) Mammal-bird clade

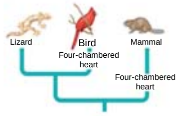


Figure 25.16a, b (b) Lizard-bird clade

- Much of an organism's evolutionary history is documented in its genome
- Comparing nucleic acids or other molecules to infer relatedness
  - Is a valuable tool for tracing organisms' evolutionary history

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Gene Duplications and Gene Families

- Gene duplication
  - Is one of the most important types of mutation in evolution because it increases the number of genes in the genome, providing further opportunities for evolutionary changes

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- Orthologous genes
  - Are genes found in a single copy in the genome
  - Can diverge only once speciation has taken place

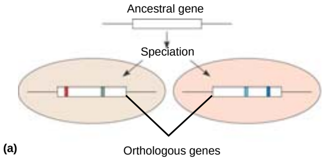

Figure 25.17a

- Paralogous genes
  - Result from gene duplication, so they are found in more than one copy in the genome
  - Can diverge within the clade that carries them, often adding new functions

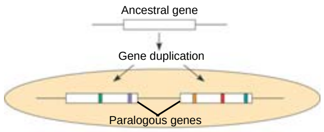

Figure 25.17b (b)

Genome Evolution

- Orthologous genes are widespread
  - And extend across many widely varied species
- The widespread consistency in total gene number in organisms of varying complexity
  - Indicates that genes in complex organisms are extremely versatile and that each gene can perform many functions

- Concept 25.5: Molecular clocks help track evolutionary time

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Molecular Clocks

- The molecular clock
  - Is a yardstick for measuring the absolute time of evolutionary change based on the observation that some genes and other regions of genomes appear to evolve at constant rates

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Neutral Theory

- Neutral theory states that
  - Much evolutionary change in genes and proteins has no effect on fitness and therefore is not influenced by Darwinian selection
  - And that the rate of molecular change in these genes and proteins should be regular like a clock

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Difficulties with Molecular Clocks

- The molecular clock
  - Does not run as smoothly as neutral theory predicts

Applying a Molecular Clock: The Origin of HIV

- Phylogenetic analysis shows that HIV
  - Is descended from viruses that infect chimpanzees and other primates
- A comparison of HIV samples from throughout the epidemic
  - Has shown that the virus has evolved in a remarkably clocklike fashion

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The Universal Tree of Life

- The tree of life
  - Is divided into three great clades called domains: Bacteria, Archaea, and Eukarya
- The early history of these domains is not yet clear

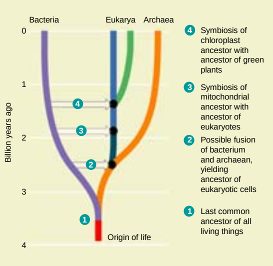

Figure 25.18