Chapter 25- Tracing Phylogeny

(Key Concepts are <u>Underlined</u>)

Phylogeny- the evolutionary history of a species or group of related species
Systematics- the study of biological diversity in an evolutionary context

The Fossil Record and Geological Time

Fossil record- the ordered array in which fossils appear within layers (or strata) of sedimentary rocks marking the passing of geological time
<u>Sedimentary rocks are the richest sources of fossils</u>
- most fossils are mineralized remnants
- some fossils are imprints, or molds
- rare fossil finds retain organic material, which could be researched
- even fewer, fossils may include preserved corpses (where decomposers were absent)

<u>Paleontologists use a variety of methods to date fossils</u>
Relative Dating:
Index fossils- similar fossils found in strata layers in different locations (usually shells of sea animals)
Geological time scale- geologic time sequenced into historical periods determined by boundaries of explosive radiation and mass extinction recorded in rocks
Absolute Dating:

1) **Radiometric dating-** using the radioactive decay of radioactive isotopes accumulated during the fossil organism's lifetime

Half-life- the number of years for 50% of the original radioisotope sample to decay (e.g. ^{14}C for young fossils and ^{238}U for older ones)

2) *Rate of racemiztion of L- and D- amino acids*- L amino acids are converted into D-amino acids after an organism dies, but it is a little less reliable since it is temperature sensitive

<u>The fossil record is a substantial, albeit incomplete, chronicle of evolutionary history</u>

"A substantial fraction of species that have lived probably left no fossils, most fossils that have formed have been destroyed, and only a fraction of the existing fossils has been discovered."

- "…the fossil record is a remarkably detailed document of phylogeny over a vast scale of geological time."

<u>Phylogeny has a **biogeographical basis** in continental drift</u>

- continental plates drift on the hot mantle (driven by convection currents)

Pangea- a supercontinent formed near the end of the Paleozoic era about 250 million years ago and began to break up during the Mesozoic era about 180 million years ago; believed to be a traumatic period in evolutionary history

- explains the distribution of similar flora, fauna, and fossils on different continents

<u>The history of life is punctuated by mass extinctions followed by adaptive radiations of the survivors</u>

Major Adaptive Radiations

Adaptive zone- a set of new living conditions and resources which present many previously unexploited opportunities (as the result of various evolutionary novelties or mass extinctions)

Mass Extinctions

- extinction is inevitable in a changing world, and there have been crisis in the history of life when global environmental changes have been so rapid and disruptive that a majority of species are wiped away

<u>2 Major Exinctions</u>:

1) *Permian*- the boundary between the Paleozoic and Mesozoic eras about 250 million years ago; claimed about 90% of marine animals; occurred in less than 5 million years (possibly much less) and about the time the continents merged to form Pangea

2) *Cretaceous*- boundary between the Mesozoic and Cenozoic eras about 65 million years ago; nearly all dinosaur lineages wiped out; there are a few hypotheses for the extinction, including the impact hypothesis (Chicxulub impact)

Phylogeny and Systematics

Phylogenetic trees- diagrams tracing evolutionary relationships of genealogies of organisms

<u>Taxonomy employs a hierarchial system of classification</u>

- systematists use taxonomy in their attempts to arrange organisms in categories reflecting phylogeny
- **binomial** system: ***G**enus* (plural, **genera**) *species* (**specific epithet**)
- scientific names (binomials) avoid ambiguity
- Taxonomic Levels: Domains, K, P, C, O, F, G, S (not including subcategories)

Taxon (plural, **taxa**)**-** taxonomic unit at any level (e.g. Reptilia is the taxon at the *Class* level and includes many *orders* of reptiles)

<u>The branching pattern of a phylogenetic tree represents the taxonomic hierarchy</u>

- the position of tree branches indicate the relative age of the evolutionary divergences (the topmost branches represent recently derived taxa)

- systematists use comparative anatomy, fossil records, and DNA comparisons (when possible) to construct these "trees"

<u>Determining monophyletic taxa is key to classifying organisms according to their evolutionary history</u>

Monophyletic- a single ancestor gave rise to all species in that taxon

Polyphyletic- a taxon where its members are derived from two or more ancestral forms, not common to all members

Convergent evolution- species from different evolutionary branches may come to resemble one another if they have similar ecological roles and natural selection has shaped analogous adaptations (analogy, not homology)

Homologies- used to classify organisms (not analogies); the greater the numbers of homologous parts between two species, the more closely the species are related and should be reflected in their classification

- the more complex two similar structures are, the less likely it is they evolved independently (e.g. skulls of chimps and humans)

Molecular biology provides powerful tools for systematics

- species phylogenetically closely related have more similar nucleotide *sequences in their nucleic acids* and a greater number of *similar amino acid sequences* in their proteins than do distantly related species

- an increase number of genomes are in electronic data bases and available via the Internet for comparative studies

DNA and RNA Comparisons:

1) **DNA-DNA hybridization-** looks at the degree of hydrogen bonding between DNA of different species
2) **Restriction maps-** compares the distributions of restriction sites and size of restriction fragments of genomes of different species
    a) smaller DNA segments work best
    b) *mitochondrial DNA (mtDNA)* comparisons work well with closely related species, of populations within species due to its increased mutation rate; mtDNA mutates 10 faster than does nuclear DNA
    c) **DNA sequence analysis-** compares the actual nucleotide sequences of DNA segments
    d) *rRNA sequencing*- since DNA coding for rRNA changes more slowly than most other DNA, it is useful to trace earlier phylogenetic branching

Identifying and Comparing Homologous DNA Sequences:

- potential homologous sequences of two species are generally evaluated according to the number of differences they exhibit per unit length of nucleotide segment (also factoring in how genomes change over time); once identified, their differences can be evaluated to aid in the development of a phylogenetic hypotheses, or trees

Molecular Clocks:

- if we assume the mutation rates of some proteins and nucleic acids are constant over time, we can estimate the time of divergence for species and higher taxa from a graph comparing amino acid or nucleic acid sequence differences against times of evolutionary branch points (may be affected by differences in generation time and metabolic rates)

<u>The search for fossilized DNA continues despite recent setbacks</u>

- the most reliable fossil DNA is from organisms fossilized in extremely dry or cold places, where organic material tends to be preserved (less contamination by decomposers- bacteria and/or fungi)

The Science of Phylogenetic Systematics

<u>Phenetics increased the objectivity of systematic analysis</u>

Phenetics- bases taxonomic affinities entirely on measurable similarities and differences- "phenotype" (does not sort between homology and analogy); few proponents today

<u>Cladistic analysis uses novel homologies to define branch points on phylogenetic trees</u>

Cladistic analysis- synonymous with phylogenetic systematics

Clade- evolutionary branch in a phylogenetic tree

- cladisitic analysis classifies organisms according to the order in time branches arose along dichotomous phylogenetic trees, considering *only novel homologies*

Outgroup Comparison:
- a group of species relatively closely related to the study group (called an **outgroup**) to help identify primitive characters of the study group; defines the root, or establishes a starting point, of a phylogenetic tree
Use of ***Synapomorphies (Shared Derived Characters)*** *and Parsimony:*
- comparative data (i.e. *synapomorphies*) helps researchers construct phylogenetic trees; the more the syanpomorphies between species within a study group, the closer the branch point between the two
Parsimony- the simplest tree consistent with the comparative data is most likely the correct one
Acceptance of Only Monophyletic Taxa:
- in the strictly cladistic view, only monophyletic taxa reflect phylogeny; does not always work (e.g. birds and reptiles should be in the same taxon according to strict cladistic analysis)

<u>Phylogenetic systematics relies on **both** morphology and molecules</u>
Phylogenetic biology- the application of cladistic analysis in the study of evolutionary history and its relations to all aspects of life