AP Biology—Chapter 25 Lecture Notes

Phylogeny and Systematics

Phylogeny is the evolutionary history of a species or group of species
Systematics helps us understand phylogeny
--molecular systematics has been a powerful tool in recent years, showing relationships that scientists thought didn't exist (see figure 25.2)

Determining Phylogenies
--based on Darwin's assumption of common ancestry

1. Fossil Record
2. Homologous Anatomical Structures—be careful of convergent evolution and analogous structures!

   --analogous structures that have evolved independently are called *homoplasies*; an example is bird and bat wings
3. Homologous Molecular Structures (comparing DNA, RNA, and Amino Acid sequences)

Taxonomy
--allows organisms to be grouped according to their evolutionary similarity
--the taxonomic system put forth by Linnaeus has two main components:

1. It arranges organisms hierarchically: Kingdom, Phylum, Class, Order, Family, Genus, Species; sometimes kingdoms are called *Divisions* in plant classification; there are larger groupings called Domains as well—Eukarya, Archaea, and Bacteria
2. It uses binomial nomenclature—a system of two names for each organism that suggests the organism's relatedness

--Systematics allows scientists to construct *Phylogenetic Trees* which show branching points where species diverged from a common ancestor
--Phylogenetic Systematics looks at shared characters; the evolutionary tree based on these shared characters is called a *cladogram* (see p. 497); the science of constructing a cladogram is **Cladistics**
--groups of organisms sharing a common ancestor are called *clades*
--when looking at cladograms, there are three possible groupings of organisms (see fig.25.10):

1. Monophyletic—consists of the ancestral species and all of its descendents; this group represents a true clade
2. Paraphyletic—consists of the ancestral species and some, but not all, of its descendents
3. Paraphyletic—consists of a group of several species that lack a common ancestor

--characters looked at to produce cladogram are homologies
--scientists look at *shared derived* characters and *shared primitive* characters when producing a cladogram (see p. 498)
--*outgroup comparison* allows scientists to distinguish between shared derived and shared primitive characters by comparing the group in question to a species not in the group but related to the group; the "outgroup" would share its primitive characters with the "ingroup (see figure 25.11)"

Timing of Evolutionary Events

Phylograms—the length of a branch in this special cladogram represents the number of changes in a particular DNA sequence for that lineage (see figure 25.12)

Ultrameric Trees—place evolutionary relationships in the context of geologic time; branches that can be traced from common ancestor to present are of equal length

Maximum Parsimony

--assumes the simplest explanation for describing evolutionary relationships is the correct one (see p. 901)

--the principle of *maximum likelihood* say that given rules about how DNA changes over time, a tree can be found that represents the most likely evolutionary changes (see fig. 25.14)

***phylogenetic trees can be thought of as evolutionary hypotheses! (see p. 502-503)**

****Parsimony doesn't always work! (see fig. 25.16)**

Connection to Genomes

--evolutionary history can be seen in an organism's genome

--rates of gene mutations can be used to tell how long ago species diverged

--mitochondrial DNA has a higher rate of mutation than does ribosomal RNA

Gene Duplications and Gene Families (see fig. 25.17)

1. Orthologous genes—passed in a straight line from one generation to the next but ended up in different gene pools due to speciation; we share 50% of our genes with yeast→certainly suggests distant common ancestry!
2. Paralogous genes—result from gene duplication; are found in multiple copies in the same genome; even though duplications have occurred, there are not as many duplications as there are different phenotypes between different species

--orthologous genes can be used as *molecular clocks*; the number of substitutions is proportional to the amount of time they have been present in different species (see p. 507 for a molecular clock on the origin of HIV)

The Universal Tree of Life (see fig. 25.18)

--must use molecular clocks that mutate very slowly but can be sequenced to show differences between organisms (ribosomal RNA—rRNA)

--the tree of life contains three domains: Bacteria, Archaea, and Eukarya

--early history of these domains is not yet clear; there was likely substantial interchange of genes between these groups early on in their evolution→horizontal gene transfer (transposons, etc.)