EVOLUTION, LECTURE 8: PHYLOGENY & SYSTEMATICS (536–543, 547–553)

The **tree of life** is a familiar motif in many cultures, and the western scientific version of the tree of life developed from earlier traditions. Ernst Haeckel was one of the first scientists to depict life's diversity on the skeleton of an old tree, and he ushered in an era of depicting living forms on a branching **phylogeny** (Haeckel coined the term).

Of course, Linnaeus had established his system of **binomial nomenclature** much earlier, and the **Linnaen system** of ranking taxa based on similarities of essential characters had been widely adopted. Darwin showed that the hierarchical Linnaen system was consistent with an evolutionary history of branching events, and Linnaeus's system survived intact for another hundred years.

In the 1960s, **Willi Hennig** sparked a revolution in the science of systematics (the science of collecting, describing, naming, and classifying organisms) by founding the new field of **cladistics** (or **phylogenetic systematics**).

Cladistic analysis classifies organisms according to their evolutionary relationships: taxa are ***defined*** by ancestral relationships, and they are ***diagnosed*** by shared, derived characters (**synapomorphies**). A **cladogram** is a branching diagram of hypothetical evolutionary relationships.

Please become familiar with the cladistic terminology from your book and the lab manual, e.g., **homology**, **homoplasy**, **monophyly** (and **paraphyly** and **polyphyly**), **synapomorphy**, **symplesiomorphy**, **parsimony** (Occam's Razor), **outgroup**, and so forth. Also, please know the difference between **orthologous** and **paralogous** genes.

You should also be familiar with the basic methods of **cladogram construction**, and the critical role of molecular data in building phylogenies. In order to establish dates of divergence between lineages, investigators sometimes rely on a **molecular clock**, in combination with fossil data.

The application of molecular phylogenetic analysis has greatly refined our understanding of organismal relationships and revealed the evolutionary histories of many taxa that were previously poorly understood. Broad scale, synthetic studies of the diversity of life are now underway for many organismal groups.

Armed with a robust phylogeny for a particular clade, it is possible to rigorously investigate a wide range of questions in ecology, biomechanics, biogeography, and more. We looked at several examples, including the evolution of wings in stick insects, the geography of bat diversification, and the evolution of body lice and human clothing.

The **extant phylogenetic bracket** is a method that infers the natural history features of extinct lineages based on cladograms that include both extinct and extant lineages. We looked at the example of parental care and vocalization in dinosaurs based on our understanding of the biology and phylogenetic relationships of crocodiles and birds.

The precise branching relationships among the three great **domains** of life—**Archaea**, **Eukarya**, and **Bacteria**—are difficult to establish, in part, because of **horizontal gene transfer** early in earth history. Given the apparent reticulation of lineages at the base of the phylogenetic tree, some investigators prefer a **ring of life** metaphor to the more familiar branching tree.