Tennessee State University
Department of Biological Sciences

2007 SPRING SEMINAR/ CHALK TALK FORUM SERIES

Frontiers in Ecology and Evolutionary Biology

January 25, 2008	Katja Schulz Managing Editor/Tree of Life Project University of Arizona tolweb.org	The Tree of Life: Biodiversity from a phylogenetic perspective

Seminar **Holland Hall Room 102** **11:30 – 12:30PM**

Currently, there are about 1.75 million species known to science. All estimates of species numbers are vague, because there is to date no comprehensive catalog of species. Scientists have described named only a fraction of existing species, and most species living on Earth today are still completely unknown to science. Available estimates of the total number of living species range widely from about 5 to 100 million species, and most of the undiscovered species are probably in insects, nematodes, fungi, protists, and bacteria.

Evidence from morphological, physiological and gene sequence data indicates that all organisms on Earth are genetically related, and the genealogical relationships of animals, plants, fungi, and microbes can be represented by a vast evolutionary tree, the "Tree of Life". The Tree of Life represents the phylogeny of organisms, i. e., the history of organismal lineages as they change through time. It implies that different species arise from previous forms via descent, and that all organisms are connected by the passage of genes along the branches of the phylogenetic tree that links all of life. The organisms that are alive today are but the leaves of this giant tree, and if we could trace their history back down the branches of the Tree of Life, we would encounter their ancestors, which lived thousands or millions, or hundreds of millions of years ago.

If we look closely at the history of life, we see that it consists of a series of speciation events. Speciation occurs, when a species splits into two separate lineages, which will then go on to evolve independently, splitting again over time into ever more independently evolving genetic lineages. Genes are passed on from ancestors to descendents in the form of DNA molecules. Over time, these molecules change through random mutations, and if a mutation spreads through a population and gets passed on to future generations, it constitutes an evolutionary novelty. Because different lineages evolve independently, their genes will diverge over time, i. e., their DNA molecules will become more dissimilar due to the accumulation of sequence changes. Each sequence change will uniquely characterize the descendents of a given lineage until that particular gene is modified by yet another mutation at the same site. The DNA molecules present in the cells of all organisms thus not only contain the molecular genetic instructions to build an organism, they also hold an extensive record of evolutionary ancestry and descent, and phylogenetic biologists can use this information to resconstruct the evolution of life.

Phylogenetic analyses infer the history of different groups of organisms by comparing their molecular sequences. The more closely related two species are, the more evolutionary novelties (shared derived characters, synapomorphies) they will share. However, sometimes, new mutations will also lead to uniquely shared characters in species that are not closely related. Shared characters that are not inherited from a common ancestor are called convergent mutations or homoplasies. Homoplasies are quite common in the DNA of organisms, and in order to reconstruct the evolution of life, phylogenetic analyses have to sort out the homoplasies from the shared derived characters that constitute the true record of evolutionary history. Every phylogenetic study creates a hypothesis of relationships that needs to be tested and refined by subsequent research. Biologists continually add new data to the picture, they develop better methods of analysis, and they come up with improved models of evolution. In order to explain similarities and differences between organisms, we need to understand the history that has produced them. Reconstructing the genealogical relationships between organisms, is the basis for any such understanding. Knowledge about phylogenetic relationships can improve human health, it can help us control the spread of pest and invasive species, and it should guide the management of our natural resources.

In addition to its great explanatory and predictive potential, the tree of life is also an ideal model for the organization of biological knowledge, and this is the focus of our work at the Tree of Life Web project (ToL, http://tolweb.org). The ToL is a collaborative effort of more than 500 biologists from around the world. On more than 9000 World Wide Web pages, the project provides information about the diversity of organisms on Earth, their evolutionary history, and characteristics. One of the most important characteristics of the ToL is that the navigational structure and architecture of the site is based upon the phylogenetic relationships between the organisms it describes. The project presents biodiversity from a phylogenetic perspective, and the content management system is highly customized to meet the special demands of biological data. Because the documentation of biodiversity is a vast endeavor, one of the most important aspects of our current work is to achieve better interoperability with other, related biodiversity projects. In collaboration with the emerging Encyclopedia of Life (http://eol.org), we hope to attain our goal to assemble a comprehensive, authoritative online resource documenting all that is known about life on Earth.

Chalk Talk **Holland Hall Room 124** **2:00 – 5:00PM**