New England Botanical Club - Minutes of the 1011th Meeting
4 November 2005
Karen Lombard, *Recording Secretary*

The 784th meeting of the New England Botanical Club, being the 1011th since its original organization, was held on Friday, November 4, 2005, in the Lecture Room of the Fairchild Biochemistry Building, Divinity Avenue, Cambridge MA.. There were 33 members and guests in attendance.

Karen Searcy introduced Dr. David Hibbett of Clark University in Worcester, Massachusetts, who gave a talk titled "Morphological Evolution in Mushroom-Forming Fungi." Dr. Hibbett's research focuses on the phylogeny and diversity of cap-forming fungi, as well as the evolution of aquatic Basidiomycetes and fungal paleontology.

Dr. Hibbett began his presentation with background on the morphological diversity in the Agaricomycetes, also known as Homobasidomycetes or mushroom-forming fungi, a group that includes 17,000 species and is one of the major clades of the Basidiomycota. This group includes the major wood-decay fungi as well as ectomycorrhizal fungi associated with tree species. The fruiting body diversity in this group is extensive, and includes polypores, agarics, coralloid taxa, resupinate forms, and gasteroid taxa. For the lay person, these include groups such as bracket fungi, cap-forming or gill mushrooms, coral fungi, crust-like fungi, and the puffballs, earth-stars and bird's-nest fungi. Former taxonomy has focused on similarities in morphology, however, work over the last 15 years in phylogenetics is causing significant changes in the understanding of evolution in this group. Comprehensive molecular data sets now allow researchers to address larger patterns of evolution. David summarized the work of a number of researchers, including himself, that have laid the foundation for a new taxonomy of the Agaricomycetes. This new work has resolved approximately 12 major clades that make up the Agaricomycetes. One surprise was the apparently close relationship of several formerly disparate groups in the "Gomphoid-Phalloid clade," including stinkhorns, coral fungi, earth-stars, and cannonball fungi. Several new major clades have also been discovered in the resupinate (crust-forming) fungi.

The second part of the presentation focused on trends in morphological evolution of the Agaricomycetes. A trend in morphological evolution is a general tendency in evolution that is manifested in a repeated pattern of forms. Trends can be hard to detect, and Dr. Hibbett gave as an example the hypothesis that evolution favors an increase in size and complexity of organisms. However, there could be alternate explanations for increases in size and complexity over time; other scientists have hypothesized that increases in complexity could also occur in a passive-diffusive process, since there is no chance of developing an organism with less than one cell.

Dr. Hibbett has tested several hypotheses regarding trends in morphological evolution in the Agaricomycetes. One hypothesis is that, because the resupinate fungi are simple compared to other types in this group, there could be a trend towards more complex forms. A second is that cap-forming mushrooms have evolved repeatedly as they are very common, and even exist in the fossil record. The third is that evolution of fungi of the gasteroid forms is irreversible. David and his colleagues used methods developed by Mark Pagel and others that reduce evolution to a simple model so that rates of change between various states can be estimated. Modeling tests progressively restricted parameters in an attempt to find the model with the fewest free parameters that adequately explained the data. The results suggested that resupinate forms do not necessarily evolve to more complex forms, but that cap-forming mushrooms may be a particularly stable form and that transitions to gasteroid forms might be irreversible. This modeling approach is useful because it allows testing of specific hypotheses about evolutionary trends. However, some may consider the models too simple or the assumptions too controversial to adequately test hypotheses about complex evolutionary processes.

The final third of the talk focused on new directions in the phylogenetics of the Agaricomycetes. Understanding of the phylogeny of fungi is currently developing very rapidly. Because data on new species are pouring in faster than they can be processed, and print articles can not keep changes in this field up-to-date, phylogenetic trees are now being developed by computers. New gene sequences are obtained from GenBank, analyzed by computer programs on an automated basis (an example is a program called *mor*, which was developed in Hibbett's laboratory; http://www.clarku.edu/faculty/dhibbett/), and used to construct an ever-growing fungal phylogenetic tree.