PROJECT SUMMARY

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Morphological and ecological diversification in the homobasidiomycetes:a molecular phylogenetic analysis.

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Homobasidiomycetes include the mushroom-forming fungi and their relatives. Approximately 13,500 species of homobasidiomycetes have been described, which is about 23% of all known species of fungi. The fruiting bodies of homobasidiomycetes include complex, developmentally integrated structures, such as mushrooms, as well as very simple forms, such as the resupinate, crustlike fruiting bodies of 'corticioid' fungi. Homobasidiomycetes play a major role in carbon cycling in terrestrial ecosystems; they comprise the majority of wood-decay fungi and ectomycorrhizal fungi, and also include mycoparasites, insect symbionts, lichens, and litter decomposers. Homobasidiomycetes have been studied intensively. Nevertheless, patterns of morphological and ecological evolution in homobasidiomycetes have been difficult to resolve, owing to the lack of a broad phylogenetic hypothesis for the group.

In recent years, considerable progress has been made in understanding homobasidiomycete phylogeny through the use of molecular sequence characters, particularly the genes encoding mitochondrial and nuclear ribosomal RNA (rDNA). In prior NSF-supported research, MJD and DSH developed a preliminary phylogenetic outline of the homobasidiomycetes as a whole, using rDNA sequence characters. The proposed research will test and expand upon this phylogenetic framework. Existing databases of nuclear and mitochondrial ribosomal DNA (rDNA) sequences will be expanded, and new datasets from protein-coding genes will be developed. Disparate datasets from the work of MJD and DSH and the literature will be integrated. This will be achieved through a combination of conventional 'simultaneous' phylogenetic analyses and 'supertree' approaches (which combine independent phylogenetic trees with overlapping sets of taxa to construct a composite phylogenetic hypothesis). Thus, the proposed research will generate detailed, comprehensive phylogenetic hypotheses for the homobasidiomycetes. These trees will be used to construct phylogenetic classifications and study historical patterns of evolution in selected morphological and ecological characters. Specific characters to be investigated include (i) corticioid vs. erect fruiting body forms; (ii) brown rot vs. white rot modes of wood decay; and (iii) ectomycorrhizal vs. saprotrophic and pathogenic nutritional modes. In addition to inferring the historical pattern of evolution in these characters, recently developed 'comparative methods' will be used to infer patterns of correlated evolution among characters, as well as general trends (evolutionary models) for individual characters. For example, the proposed research will address whether derivation of simple corticioid fruiting bodies from complex forms, such as mushrooms, is as likely as the derivation of complex forms from corticioid forms.

The proposed research will contribute to a comprehensive phylogenetic classification of homobasidiomycetes, and will facilitate studies at lower taxonomic levels by clarifying sistergroup relationships. This research will benefit all disciplines that use phylogenies, such as biogeography and conservation biology (two areas where fungi have not traditionally been prominent). Finally, the proposed research will infer patterns and identify possible causal factors in the evolution of fungal morphology and nutritional

modes (wood decay modes and mycorrhizal symbioses). The latter will contribute to an understanding of the role of fungi in the evolution of terrestrial ecosystems.