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Molecular phylogeny of the Laboulbeniomyces (Ascomycota)

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Abstract A first molecular-based phylogeny is presented for the Laboulbeniomyces, a group of ascomycete fungi that utilize arthropods for nutrition and/or dispersal. Morphological diversification and life-history evolution has made it difficult to resolve relationships within the group, and to identify close relatives. Here, we infer a preliminary phylogeny based on acquisition of 51 new SSU rDNA sequences, representing a total of 65 taxa. The results of this study demonstrate that Laboulbeniomyces is monophyletic, and related to Sordariomycetes. The class could be divided into at least 4 or 5 orders, though we refrain from formally giving names to these at this stage. Further evidence for the occurrence of asexuality within the class is provided by the inclusion of the genera *Chantransiopsis* and *Tetrameronycha*, both known only as asexual taxa with thalli consisting of linearly superposed cells. The precise placement of the genus *Herpomycetes* (Herpomycetaceae), on cockroaches, remains unresolved in our analysis, but lies outside of the main clade of sexually reproducing Laboulbeniales. There is good support for this latter grouping, comprising taxa that are found on both aquatic and terrestrial hosts. Within this large assemblage, we recognize 5 distinct clades (clades E, F, G, H, I). Relationships among the so-called “aquatic genera” (\equiv Ceratomycetaceae + some Euceratomycetaceae) are poorly resolved in our analyses, accounting for 3 of these clades (E, F, G), with the remainder of the taxa (largely equivalent to Laboulbeniaceae) split into two major groupings (clades H, I). Across all taxa, antheridial characteristics, features on which the earliest classifications were based, are shown to be homoplastic. On the other hand, features of perithecial development show an overall

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