Molecular phylogeny of the Entomophthoromycota.


Abstract

The Entomophthoromycota is a ubiquitous group of fungi best known as pathogens of a wide variety of economically important insect pests, and other soil invertebrates. This group of fungi also includes a small number of parasites of reptiles, vertebrates (including humans), macromycetes, fern gametophytes, and desmid algae, as well as some saprobic species. Here we report on recent studies to resolve the phylogenetic relationships within the Entomophthoromycota and to reliably place this group among other basal fungal lineages. Bayesian Interference (BI) and Maximum Likelihood (ML) analyses of three genes (nuclear 18S and 28S rDNA, mitochondrial 16S, and the protein-coding RPB2) as well as non-molecular data consistently and unambiguously identify 31 taxa of Entomophthoromycota as a monophyletic group distinct from other Zygomycota and flagellated fungi. Using the constraints of our multi-gene dataset we constructed the most comprehensive rDNA phylogeny yet available for Entomophthoromycota. The taxa studied here belong to five distinct, well-supported lineages. The Basidiobolus clade is the earliest diverging lineage, comprised of saprobe species of Basidiobolus and the undescribed snake parasite Schizangiella serpentis nom. prov. The Conidiobolus lineage is represented by a paraphyletic grade of tropically diverse species that include saprobes, insect pathogens, and facultative human pathogens. Three well supported and exclusively entomopathogenic lineages in the Entomophthoraceae center around the genera Batkoa, Entomophthora and Zoophthora, although several genera within this crown clade are resolved as non-monophyletic. Ancestral state reconstruction suggests that the ancestor of all Entomophthoromycota was morphologically similar to species of Conidiobolus. Analyses using strict, relaxed, and local molecular clock models documented highly variable DNA substitution rates among lineages of Entomophthoromycota. Despite the complications caused by different rates of molecular evolution among lineages, our dating analysis indicates that the Entomophthoromycota originated 405±90 million years ago. We suggest that entomopathogenic lineages in Entomophthoraceae probably evolved from saprobic or facultatively pathogenic ancestors during or shortly after the evolutionary radiation of the arthropods.

Involved Units and Groups

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