

21st Century Guidebook to Fungi, Second Edition of the online version, by David Moore, Geoffrey D. Robson and Anthony P. J. Trinci

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Chapter 16: Fungi as pathogens of animals, including humans

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Chapter 16: Fungi as pathogens of animals, including humans

In this Chapter we study fungi as pathogens of animals, including humans. There are many pathogens of insects amongst the fungi and fungus-like organisms: Microsporidia, Trichomycetes, Laboulbeniales, and entomogenous fungi. Inevitably, discussion of insect disease eventually turns to thoughts of the potential for biological control of arthropod pests. In other animals, cutaneous chytridiomycosis is an Emerging Infectious Disease (EID) of amphibians. We will discuss EIDs in this Chapter. In both animals and plants, an unprecedented number of fungal and fungus-like diseases have recently caused some of the most severe die-offs and extinctions ever witnessed of species in the wild, and they are jeopardising our food security. We have already mentioned some EIDs of plants, especially crop plants. Among animals, fungal EIDs have reduced population abundances in amphibians, bats and even corals across many species and over large geographical areas, and the most recently recognised fungal disease of snakes may have caused declines in some snake populations in the Eastern United States.

Our main concern, though, are the **mycoses** that are the *fungus diseases of humans*. We describe the clinical groupings set up for human fungal infections; fungi within the home, and their effects on health through production of allergens and toxins. In the penultimate Section we attempt a comparison of animal and plant pathogens and briefly discuss the essentials of

epidemiology. We finish the Chapter with a short discussion of mycoparasitic and fungicolous fungi; that is, fungi that are pathogenic on other fungi.

As with other Chapters, we will introduce you to some important and thought-provoking academic publications in this chapter; and here we will direct you to the Editorial published on 25th July 2017 in the journal *Nature Microbiology* [[VIEW THIS now](#)]. If you read no other reference, we suggest you read this. We are so keen on this Editorial because we believe the message of its content should be much more widely appreciated. And we like its title: ‘**Stop neglecting fungi**’. The following quotation will give you a flavour of its content:

‘...over 300 million people suffer from serious fungal-related diseases, ... fungi collectively kill over 1.6 million people annually, which is more than malaria and similar to the tuberculosis death toll. Fungi and oomycetes destroy a third of all food crops each year, which would be sufficient to feed 600 million people. Furthermore, fungal infestation of amphibians has led to the largest disease-caused loss of biodiversity ever recorded, while fungi also cause mass mortality of bats, bees and other animals, and decimate fruit orchards, pine, elm and chestnut forests...’

The report published by the Royal Botanic Gardens, Kew, *State of the World's Fungi 2018*, also coined a memorable phrase:

‘...when looking for nature-based solutions to some of our most critical global challenges, fungi could provide many of the answers’ (Willis, 2018).

16.1 Pathogens of insects

Arthropods are the most diverse group of animals on Earth; insects occurring in most terrestrial environments, though only a few species are found in marine habitats, as these are dominated by the crustaceans. Estimates of the number of arthropod species vary between 1,170,000 and 10 million, accounting for over 80% of all known living animal species; with the insects as the most species-rich subgroup in land and freshwater environments.

As arthropods were emerging as the (numerically) dominant animals they are today, fungi were also colonising the land. Over the past 400 million years or so, fungi and insects have evolved together in a wide array of intimate associations; including mutualistic endosymbiosis; using fungi as obligate food sources, such as those found in fungus-gardening ants ([Section 15.2](#)); sexually and behaviourally transmitted parasites, such as Laboulbeniales ([Section 16.4](#), below); and with fungi as the most common disease-causing agents of insects, and many entomologists believe that there may be more species of *insect pathogens* than there are species of insects (Lovett & St. Leger, 2017).

Insect species are infected by pathogenic viruses, bacteria, and protozoa, as well as two groups of organisms that have uncertain relationships, the microsporidia and the trichomycetes; all of these tend to cause infection after being *ingested by the insect*.

The true fungi that infect insects are *invasive pathogens*; that is, they can produce enzymes and hyphae that can penetrate the insect cuticle. These disease organisms often act as natural control agents by regulating the population size of insect pests. There is consequently considerable interest in harnessing this capability commercially to control insects that are pests because of their adverse effects on our agricultural activities or because they act as vectors of human diseases (Lacey *et al.*, 2015; Butt *et al.*, 2016; and see chapters 1 & 2 in *Ecofriendly Pest Management for Food Security*, Omkar, 2016 [[VIEW on Amazon](#)]; Blackwell, 2017; Lovett & St. Leger, 2017).

16.2 Microsporidia

Microsporidia comprise a phylum of over 1,400 species of fungal-related parasites that can infect nearly all animal hosts. **Microsporidia are the smallest of eukaryotes**: they have genomes in the same size range as bacterial genomes; they have unicellular spores; they lack mitochondria, peroxisomes and centrioles, but have several prokaryotic characteristics, such as 70S ribosomes, and fused 5.8S and 28S rRNAs. Nevertheless, they are highly specialised eukaryotic cells, living only as obligate intracellular parasites of other eukaryotes. Most are important pathogens of insects, but they are also responsible for common diseases of crustaceans and fish, and have been found in most other animal groups, including humans (probably transmitted through contaminated food and/or water) (Weiss & Becnel, 2014; Troemel, 2017).

Microsporidia have been subjected to the most dramatic taxonomic revisions over the years. They were traditionally thought to be a unique phylum of spore-forming protozoa. Then, on the basis of the earliest electron microscopy studies, they were presumed to be one of the most primitive eukaryotic lineages because of a remarkable absence of 'standard' eukaryotic features such as Golgi bodies, peroxisomes, mitochondria and the 9+2 arrangement of microtubules. They were placed with other protists lacking mitochondria in a kingdom called Archezoa, and microsporidia were postulated to be direct descendants of a primitive eukaryote that predated mitochondrial endosymbiosis.

Finally, genome sequencing and the discovery of microsporidian **mitosomes**, which are highly reduced (in both physical size and biochemical properties) **mitochondrial relics**, caused the re-classification of **microsporidia as fungi**. Microsporidia share several characteristics with fungi: nuclear division takes place within an intact nuclear membrane, they have the same mRNA capping mechanism, chitin and trehalose in their spores, and some gene structures present only in fungal opisthokonts (Corradi & Keeling, 2009; Capella-Gutiérrez *et al.*, 2012).

While the fungal nature of microsporidia is now accepted, their exact position in the fungal tree of life is still uncertain. They are now thought to be related to the Chytridiomycota and may be derived from a **reduced endoparasitic chytrid** (see [Section 2.8](#)) (Gill & Fast, 2006). In this case they are now presumed not to be the most primitive eukaryotes, but to be the most reduced and highly specialised fungi. Adaptations to an obligate intracellular lifestyle have modified their cell biology and genome by **severe selective reduction of cell structure, metabolism, and gene structure** as they separated from the main fungal lineage as a sister clade (see Fig. 10 in Chapter 2; [CLICK HERE](#) to view the page).

Microsporidian genomes, although they are always very small, **do have** multiple linear chromosomes with telomeres, but in other respects they resemble bacteria by having few introns and transposons, generally short intergenic regions, and few duplicated genes. The complement of genes encoded in microsporidian genomes is remarkably similar from one species to another, regardless of genome size, and it is evident that microsporidia have acquired specific genes from unrelated lineages through horizontal gene transfer (see [Section 17.15](#)); many of these genes playing a central role in microsporidian evolution (Keeling *et al.*, 2014; Corradi, 2015).

Although their taxonomic classification has evolved through time, understanding to which kingdom microsporidia belong is not an idle academic pastime. **Microsporidia cause diseases** and it is essential for the clinician to understand that **the disease organism is a fungus** and that the disease is likely to be controllable by **antifungal agents** rather than wasting time and resources trying the effects of **antibacterials** or **antiprotozoal** drugs.

The first microsporidian to be described, a disease of European silkworms studied in 1857, was shown to be a microscopic parasite that was named *Nosema bombycis* and was assigned to a new group of organisms called Microsporidia in 1882 (Keeling & Fast, 2002). The microsporidian