

Fungal Pathogen Epidemiology in Animals and Plants

Matteo Brunelli*

Department of Pathology and Public Health, University of Verona, Verona, Italy

*Corresponding author: Dr. Matteo Brunelli, Department of Pathology and Public Health, University of Verona, Verona, Italy, E-mail: matteo.brunelli@univr.it

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About the Study

The advent of molecular markers offers great tools for studying key processes of parasite biology, such as dispersal, mating systems, host adaption and patterns of speciation. Population genetics studies have also valuable practical applications, for instance, for studying the evolution of drug resistance or new virulence. Another reason to study epidemiology and evolution in parasites is that they display a huge diversity of life cycles, thus providing great opportunity for comparative studies to test pathogen-specific questions or general issues about evolution. About 10,000 species of fungi have been described so far of which a high percentage obtain nutrients by living in close association with other organisms, mainly plants. Many fungi are pathogenic and can have important impact on human health or lead to severe economic losses due to infected crops or to animal diseases. Fungal species parasitizing animals and plants are found interspersed with saprophytes and mutualists in fungal phylogenies, suggesting that transistors between these life-history strategies have occurred repeatedly within the fungal kingdom.

The two major groups that have been traditionally recognized among the true fungi are the Ascomycota, including the yeasts and filamentous fungi, with several important model species e.g. *Saccharomyces cerevisiae* and *Neurospora crassa* and the Basidiomycota, including the conspicuous mushrooms, the rusts and the smuts. Ascomycota and Basidiomycota have been resolved as sister taxa and they have been called the *Dicaryomycota*. Basal to the Dikarya branch several other fungal groups. The *Chytridiomycota*, for instance, are defined as fungi with flagellated cells and were long thought to be sister group of all the other true fungi, nonflagellated. Phylogenies since mid-2000s however have suggested that the

chytrids may in fact be polyphyletic, representing early diverging lineages having retained the ancestral flagellum. Chytrids also encompass plant and animal pathogens. Oomycetes have long been considered as fungi but were recognized during mid-2000s to belong to the distant Stramenophiles. These filamentous organisms, however share many morphological and physiological characteristics with fungi and continue to be studied with mycologists.

Most fungi have been dependent on other organisms for their resources through much of their evolutionary history, in particular fungal pathogens. During the 20th century however, many new fungal diseases have emerged. This is probably due to human activities that have completely modified the ecosystems on earth at a global scale e.g. climate warming, widespread deforestation, habitat fragmentation and urbanization, changes in agricultural practices and global trade. Of these, the intensification and globalization of agriculture as well as the increase in international trade and travel have broken many natural barriers to dispersal causing an unprecedented redistribution of many organisms. Concomitantly, there is growing evidence that these global changes play a key role in the emergence of infectious diseases in humans, wildlife, domestic animals and plants.

To understand how new diseases emerge and more generally to understand the spread and maintenance of diseases, it is essential to study dispersal, mating systems, host adaption and mechanisms of speciation. The advent of molecular markers offers great tools for studying these key processes of parasite biology. The development of full-genome sequencing since mid-2000s, especially among fungi because they have small genomes, has allowed comparative genomics to begin drawing inference on the mechanisms of pathogenicity.