Fungal Allergy and Pathogenicity
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Volume Editors

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Foreword

Fungal organisms (yeasts and molds) are an increasing public health problem (Chiu and Fink) worldwide for several reasons. After transplantation surgery immunosuppressed patients frequently suffer from fungal infections which can become fatal; the AIDS pandemic, which is still on the increase, also leads to fungal infections that are difficult to treat and there is an increase in real and perceived allergic diseases which, in some developed countries, involve 20–30% of the population; a proportion of these allergies is due to inhaled fungal spores and other fungal material. Some of the older patients suffering from allergic or ‘nonallergic’ asthma are particularly prone to fungal infections of the lung. Moreover, fungal toxins (Bhatnagar et al.) still represent an important health problem both in humans and farm animals.

Exposure to fungal spores is ubiquitous and, therefore, of pivotal importance for the development of mycoses acquired via the respiratory tract. This situation has also led to increased public awareness of the importance of indoor air quality and to the emergence of aerobiology, which has established itself as a major environmental academic discipline (Levetin and Horner).

Fungal infections have led to an increasing demand for antifungal drugs. Compared to the well-known antibacterial antibiotics, these are generally less than satisfactory, because it is more difficult to combat eukaryotic than procaryotic pathogens, and severe side effects are still frequent. It is expected that fungal whole genome sequences (Breitenbach et al.), which are now being determined, will be very helpful in devising new antifungal drugs. Fungal genetics plays an increasing role in the study of clinically relevant fungi. Genome sequences will also lead the way to the discovery of new virulence factors which are important as drug targets. There are good reasons for hope, but at present no antifungal drug developed on the basis of fungal genomics is yet on the market.

Fungi are different from bacterial pathogens also because they are mostly opportunistic, that is they are present all the time in healthy individuals (for instance, on the skin), and only become dangerous in certain situations. A variety
of pathological conditions, including impaired immune function, are believed to cause host susceptibility to fungal infections. The major reason for the increase in systemic mycoses is undoubtedly related to an increased number of patients with congenital or acquired immunodeficiency. Therefore, it is important to study not only the fungal pathogens but also the host factors that contribute to fungal infectivity (Kauffman and Tomee, and Monod and Borg-von Zepelin).

Until recently, the study of fungal allergy was still in its infancy. It is no exaggeration to say that modern cDNA cloning techniques caused a major breakthrough in this field. Before the advent of allergen cloning, it was difficult, for several reasons, to identify the relevant fungal allergens unequivocally. Commercially available fungal extracts were for the most part not satisfactory for a reliable diagnosis and were not authorized for specific immune therapy (‘hyposensitization’) in many countries. This situation will improve with the advent of well-defined pure recombinant fungal allergens (Helbling et al., Breitenbach and Simon-Nobbe, and Crameri).

Nearly all major systematic groups of fungi are now known to contain allergenic and/or pathogenic species (Prillinger et al.). Among the Ascomycota, the new sequence-based phylogeny defines three large groups: the Hemiascomycetes, the Protomycetes (Archiascomycetes) and the Euascomycetes. Presently there is some debate on whether the Protomycetes are primitive Ascomycota (Archiascomycetes) or a derived group of Ascomycota with similarities to the Basidiomycota (Prillinger et al.). Until recently, some Ascomycota (Aspergillus, Alternaria, Cladosporium, Penicillium, Candida and others) were called ‘fungi imperfecti’ (Deuteromycota), but are now recognized as close relatives of ‘perfect’ Ascomycota based on molecular systematics.

The Hemiascomycete, Candida albicans, is a very important pathogen and allergen, aspects of which are treated by Monod and Borg-von Zepelin. Among the Euascomycetes, Trichophyton rubrum causes superficial skin infections (Hawranek); Histoplasma capsulatum is an intracellular parasite of the monocyte/macrophage system occasionally causing fatal infections, and Aspergillus fumigatus is a very important allergen and pathogen that is able to colonize the human lungs. Some aspects of Aspergillus infections are the topic of the chapters by Crameri, and Kauffman and Tomee. Cladosporium herbarum and Alternaria alternata (Breitenbach and Simon-Nobbe) are Euascomycetes. They are important causes worldwide of allergies. Pneumocystis carinii, an important pathogenic member of the Protomycetes, is the most common cause of lung infection in AIDS patients.

Among the major groups of the Basidiomycota, only the Uredinomycetes contain practically no known pathogens and/or allergens. Rhodotorula mucilaginosa and Rhodotorula glutinis have occasionally been isolated from patients. Interestingly, Malassezia (previously called Pityrosporum) furfur, a human
pathogen infecting the skin and hair follicles (Hawranek), is a member of the Ustilaginomycetes, a large group of plant pathogens. The most highly developed group of the Basidiomycota, the Hymenomycetes, contain a number of recently recognized important allergy-causing fungi: *Coprinus cinereus*, *Psilocybe cubensis*, and puffballs of the genus *Calvatia*, among others (Helbling et al.). Another Hymenomycete, *Cryptococcus neoformans*, is an important human pathogen causing the often fatal cryptococcosis of the lung and meningitis.

This volume clearly shows the importance of correct fungal systematics to understand the clinically relevant fungi. For this reason, we have included an extensive chapter on the new molecular fungal systematics. This chapter (Prillinger et al.) should be consulted whenever questions appear as to the correct systematic nomenclature and the older synonyms of a fungal organism. We are including a glossary because we feel that the highly specialized terminology, especially of clinical mycology and of systematic mycology, should be explained for nonspecialists.

This book addresses not only clinicians who want to learn more about clinically important fungi, but also allergologists, mycologists, biologists and lawyers concerned with the increasing number of lawsuits because of fungal spores in indoor air, which are claimed to be a major reason for ‘sick building syndrome’.

We are very grateful to Thomas Nold and the members of the team of Karger (Basel, Switzerland) for their excellent cooperation and patience during the time of collecting and editing the chapters of this book. We are also very grateful to the authors of this book who have spent many days checking and rechecking every chapter, especially to Birgit Simon-Nobbe and to Hansjörg Prillinger. Finally, we thank our families for their support and confidence in the final success of this project.

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