

CBS Symposium Fungi and Health

Amsterdam, 13 - 14 November 2008

This year it will be two hundred years since King Louis Napoleon (brother of Napoleon Bonaparte) founded the Royal Institute of Science, Letters and Fine Arts, the forerunner of the Royal Netherlands Academy of Arts and Sciences. The Academy is celebrating this landmark year (KNAW 200) by organizing a wide variety of different events. One of these events is that the Academy institutes will present their research in special symposia. The CBS Fungal Biodiversity Centre has chosen November 13 and 14 with the symposium "**Fungi and Health**", which will consist of six sessions each with a special topic. These symposia address the mycological research of the five CBS research groups.

During the CBS symposium two special awards will be presented: the Johanna Westerdijk Award for an individual who has made an outstanding contribution to the culture collection of the CBS Fungal Biodiversity Centre, marking a distinguished career and the Josef Adolf von Arx Award for an individual who has made an outstanding contribution to taxonomic research of fungal biodiversity, marking a distinguished career.

The Johanna van Westerdijk award

The van Westerdijk award, named after the first female professor in the Netherlands and an important initiator of the CBS culture collection, will be given on special occasions to an individual who has made an outstanding contribution to the culture collection of the CBS Fungal Biodiversity Centre, marking a distinguished career. The nominees for the award have been evaluated on the basis of quality, originality, and quantity of their contributions to the collection, and on the basis of associated mycology research in general.

The Josef Adolf von Arx Award

This award named after the famous Swiss mycologist, who was a director of CBS for more than 16 years and who contributed greatly to the taxonomy of ascomycetous fungi in the institute, will be given on special occasions to an individual who has made an outstanding contribution to taxonomic research of fungal biodiversity, marking a distinguished career. The nominees for the award have been evaluated on the basis of quality, originality, and quantity of their contributions in the field of fungal taxonomy.



CBS Fungal Biodiversity Centre

An Institute of the Royal Netherlands Academy of Arts and Sciences



CBS - Fungal Biodiversity Centre

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Studies in Mycology: www.studiesinmycology.org

Persoonia: www.persoonia.org

Deposit new names and data in **MycoBank:** www.mycobank.org

Registration and coffee

9.30 – 10.00

Welcome and Introduction – Prof. Dr Theo W. Mulder (Director Research KNAW) and Prof. Dr Pedro Crous (Director CBS)
Presentation of the CBS Progress Report to the President of the KNAW Prof. Dr Robbert H. Dijkgraaf

10.00 – 10.30

Session 1. Fungi and our health

Chair Sybren de Hoog

Nothing is closer to us than our own body. Billions of euros are spent each year to keep it healthy and free of microbes. This has worked well with bacteria, but fungi are much more difficult to combat. Some pathogenic fungi have a remarkable ability to evolve with their mammal hosts. In addition, humans made life easier for some nasty opportunists. We created polluted environments where some of these organisms proliferate better than in nature. Agricultural use of antifungal compounds, developed initially to treat infected patients, has led to lower degrees of fungal susceptibility, thereby weakening current therapeutic strategies. Scientists are now frantically analyzing fungal genomes, in order to understand infection processes and to find weak spots in the fungal defense apparatus.

How sequencing the *Aspergillus* genomes helps patients with aspergillosis

10.30 – 11.00

David Denning
School of Medicine, Education and Research Centre, University Hospital of South Manchester, Southmoor Road, Manchester M23 9LT, UK

There is more biodiversity amongst members of the *Aspergillus* genus than between fish and man. There are more allergens in *Aspergillus fumigatus* than any other living organism. *Aspergillus* is unique among microorganisms in being capable of infecting man, plants, insects, fish, coral and birds, and critically for human health in causing life-threatening infection in immunocompromised patients, lung and sinus disease in 'normal' people and severe allergic disease. Genome sequencing of more than 10 species has greatly expanded the understanding of this fungal genus, directly lead to opportunities for new drug development and diagnostic tests and provided an engine for numerous biotechnological products such as thermostable enzymes and antimicrobial agents. Unfortunately genome sequencing will not rid the world of this fungus, which in any case is critically important to the carbon and nitrogen cycles, but will provide mankind with better tools to combat infection and allergy."

Azole resistance in *Aspergillus fumigatus*: collateral damage of fungicide use?

11.00 – 11.30

Paul Verweij
Medical Microbiology, Radboud University, Nijmegen, The Netherlands

Azoles play an important and increasing role in the management of invasive aspergillosis, a generally lethal infection caused by the mold *Aspergillus*

fumigatus. Recently, emergence of resistance was observed in isolates cultured from patients failing to azole therapy. An epidemiologic study using the fungus culture collection of the UMC St Radboud showed that resistance has emerged recently in *A. fumigatus* and was due to a single highly dominant resistance mechanism. Resistance was also found in clinical isolates from all University hospitals in the Netherlands. The dominance of a single resistance mechanism suggests that resistance might be developing in the environment in addition to azole treated patients.

11.30 – 12.00

Dangerous black fungi are all around us – how come we are still alive?

Sybren de Hoog

CBS Fungal Biodiversity Centre, Utrecht, the Netherlands

Nothing is closer to us than our own body. Billions of Euros are spent each year to keep it healthy and free of microbes. This has worked well with bacteria, but fungi are much more difficult to combat. Some pathogenic fungi have a remarkable ability to evolve with their mammal hosts. In addition, humans made life easier for some nasty opportunists. We created polluted environments where some of these organisms proliferate better than in nature. Agricultural use of antifungal compounds, developed initially to treat infected patients, has led to lower degrees of fungal susceptibility, thereby weakening current therapeutic strategies. Scientists are now frantically analyzing fungal genomes, in order to understand infection processes and to find weak spots in the fungal defense apparatus.

12.00 – 12.30

Pneumocystis fungi and mammals: a unique model of parallel history

Jacques Guillot

Service de Parasitologie-Mycoologie, Ecole Nationale Vétérinaire d'Alfort, 94704 Maisons-Alfort Cedex, France

Fungal species have developed sophisticated strategies to survive in a very wide range of ecosystems. Many fungi evolved in close contact to plant or animal populations and for some of them, this long process clearly modified their phenotypic and genotypic characteristics. *Pneumocystis* are unculturable, highly diversified fungal organisms able to attach specifically to type-I alveolar cells and to proliferate in pulmonary alveoli of many mammalian species. Infection by *Pneumocystis jirovecii* (formerly *Pneumocystis carinii*) remains one of the most common and life-threatening infection occurring in immunocompromised individuals, especially HIV-infected patients. The outstanding narrow host-parasite specificity of *Pneumocystis* species suggested that they resulted from a long co-speciation process. A study on primate-related *Pneumocystis* showed that more than 60% of the homologous nodes of the respective host and parasite cladograms may be interpreted as resulting from co-divergence events. Similar observations were made for *Pneumocystis* from different bat species living in central and south America. Co-speciation between *Pneumocystis* and mammals may also occur at the population level as recently described within the rodent species *Apodemus sylvaticus*. The phylogeny of mammalian species is still a matter of controversy and the description of the genetic diversity of *Pneumocystis* organisms may be used as an original tool to participate to this complex debate.

12.30 – 13.30

Lunch and poster session

Fungi can be used for useful food products such as bread and alcoholic beverages, but they can also spoil our food and produce dangerous toxins. These mycotoxins are now found in food products and beverages which have never been suspected to contain these toxins. Regulations of mycotoxins are important and the strategies are often not a balance of scientific and economical arguments.

Innovative molecular methods for monitoring toxigenic fungi and mycotoxin in food

13.30 – 14.00

Giancarlo Perrone

Institute of Sciences of Food Production- National Research Council (ISPA-CNR), Via Amendola 122/O, 70126 Bari, Italy

It is estimated that 25 to 50 % of the crops worldwide are contaminated with mycotoxins. In the last decade, to tackle this problem considerable attempts have been carried out to develop fast and precise molecular tools and a lot of methods based on the use of DNA markers and PCR techniques, has been widely studied and implemented. Recently, various genes of the biosynthetic pathways of the most important mycotoxins have been characterized and molecular detection methods have been developed using single or multiple biosynthesis genes. In this respect, Reverse Transcriptase PCR (RT-PCR) or Reverse Transcriptase Real Time PCR (RT Real Time PCR) are approaches to detect the level of mRNA in a cell instead of DNA. They aim at monitoring expression of key enzymes of mycotoxin biosynthetic pathways before the mycotoxin can be measured by analytical methods like TLC or HPLC. These systems can be used to identify molecular critical control points (MCCP's). In this respect the microarray technology can be regarded as a preventive approach to avoid mycotoxin production and to ensure food safety, while the official analytical methods are used to assess the level of mycotoxins in relation to statutory limits. First promising results have been recently achieved by the implementation of a microarray for monitoring the production of mycotoxins in food. As a consequence, future studies should be focused on the employment of molecular methods in rapid, robust and user friendly applications and their implementation in HACCP concepts for the food and feed industry in order to keep mycotoxin contamination at a minimum during storage and processing of food and feed raw materials.

Regulation of mycotoxins

14.00 – 14.30

Manfred Gareis

Max-Rubner-Institut (MRI) Bundesforschungsinstitut für Ernährung und Lebensmittel Institut für Mikrobiologie und Biotechnologie - Standort Kulmbach - E95326 Kulmbach, Germany

Until recently, harmonized regulations within the European Union concerning mycotoxins were focused on maximum levels for aflatoxins, ochratoxin A, and patulin, respectively. Aflatoxins and ochratoxin A were also used as model substances to establish regulations dealing with aspects of sampling, sample size, and quality criteria of analytical methods for mycotoxins. In the last few years, Fusarium toxins (deoxynivalenol, zearalenone, fumonisins, T-2 toxin/HT-2 toxin) dominated the agenda of authorities involved in regulatory activities. Toxicological evaluations, for example those published as "Opinions of the Scientific Committee on Food of the European Commu-

nity”, are available for several *Fusarium* toxins for years now. In response to the demands arising from scientific assessments on mycotoxins, the discussion concerning harmonized maximum values within the European Union intensified in recent years.

This contribution will primarily summarize present regulations on maximum levels for mycotoxins, will inform about the background for these regulations and will give an outlook on the possible level for some mycotoxins for which regulations can be expected soon. However, present (and future) maximum values have to be seen in the light of a controversial debate, in which aspects of consumers protection, the potential economic impact of regulations on food and feed industry, as well as regional differences in aspects of relevance of certain mycotoxins on agricultural production and aspects of the international trade may influence the individual point of view.

14.30 – 15.00

***Aspergillus niger* genomics and biotechnology: a healthy combination**

Noël van Peij, Peter van de Vondervoort, Hans Roubos, Hein Stam, Piet van Dijck and Herman Pel

DSM Food Specialties, P.O. Box 1, 2600 MA, Delft, The Netherlands

The filamentous fungus *Aspergillus niger* has been used for decades in the safe production of food enzymes and citric acid. These *A. niger* products have been affirmed the GRAS (Generally Regarded As Safe) status by the FDA. It is known that fungi can have the capability to produce mycotoxins. Consequentially, production strains and industrial fermentation products of DSM have been analyzed for mycotoxin production, confirming the safe and toxin-free production. Recently, genome sequences have been generated for *A. niger* strains. This allowed the development of Genomics analysis tools such as bio-informatics, transcriptomics, proteomics and metabolomics. Examples will be given how these Genomics technologies are used within DSM with the implications for safe enzyme production.

15.00 – 15.30

Domesticated microorganisms as new food biopreservatives

Johan Schnurer

Department of Microbiology, Swedish University of Agricultural Sciences (SLU), Box 7025, SE-750 07 Uppsala, Sweden

Biopreservative yeasts or lactic acid bacteria may inhibit growth of spoilage moulds that commonly destroy food and feed during storage. Their practical biotechnical application requires a thorough evaluation of safety aspects with regard to both the environment and human health, as well as the development of suitable formulations with long shelf life.

The large Swedish research program “Domestication of Microorganisms” has developed fermentation and formulation technology, as well as safety assessment systems, addressing these issues. Although nationally funded, the Domestication program welcomes international collaboration with both academia and industry, in particular on new applications of non-conventional microorganisms.

15.30 – 16.00

Coffee break

Fungi in indoor environments is attracting increasing interest of the public. Much information is now available about living or working in mouldy environments. In many countries the fungal problems are still rising and the scientific data about the adverse health implications are often in contrast with information supplied by consultants and companies who have merely an economical interest.

Being at home with fungi: progress in understanding the impact of fungi in indoor environments on health

16.00 – 16.30

James Scott and Brian Flannigan

Dalla Lana School of Public Health, University of Toronto, Canada and Scottish Centre for Pollen Studies, Napier University, Edinburgh, UK

The scientific investigation of microorganisms in indoor air really dates back to an 1887 paper by Carnelley, Haldane and Anderson that has been described in a US Environmental Protection Agency publication as “ground breaking in the field of indoor air quality”. Since then, a large number of investigators have repeatedly gone over this ground using improved methodology and confirming the basic findings of that early study. Over the last 120 years, however, much more has been learned about the identity of the fungi and bacteria in the airborne microbiota, and about their allergenic and toxic characteristics that may impact on the respiratory health of building occupants. Traditionally, the emphasis in sampling has been on the numbers and types of spores in the air, but it is now recognized that considerably greater numbers of biologically active hyphal fragments and other subcellular particles may be released into the air than spores of the same fungi, and these must therefore be taken into account when assessing human exposure to allergenic/toxigenic fungi. Because of difficulties in assessing exposure due to the large temporal variation in airborne fungi indoors, analysis of settled dust for the fungal component 1-3- β -D-glucan, which may interact with allergens and bacterial endotoxin, and/or ergosterol, has become the non-specific method of choice for epidemiological studies. Other techniques, such as polymerase chain reaction (PCR) methods for assessing exposure are being developed in various laboratories, but it will be some time before their use is widely adopted.

From Lascaux to Kyoto / moulds indoors and climate change

16.30 – 17.00

Thomas Warscheid

LBW – Bioconsult, 26215 Wiefelstede, Germany

In the course of extensive energy saving regulations motivated by the climate change, the rapid and insufficiently ventilated construction of buildings caused by economical constraints, the preferred application of organic modified building materials facilitating the building practice as well as insufficient maintenance and care in the course of individualized living conditions have created in the recent years an increasing problem of indoor mold infestations. Due to the growing allergenic predisposition and immunodeficiency of people this development has found also special attention in the health-related evaluation of referring damages in private and public buildings and construction especially in industrial countries. While in the past the importance of microbial induced impacts on building materials have been mostly neglected or minimized, today a partly exag-

generated sensibilisation for biogenic aerosols and cell compounds as well as their possible health-related effects disconcert building companies and craftsmen, consultants and lawyers, health authorities and physicians as well as the directly concerned owners, land lords and tenants. Especially in Germany tremendous efforts have been made to develop new guidelines for the understanding of possible causes for mold infestations indoors and their qualitative and quantitative evaluation. These guidelines represent a first attempt to handle the referring problem, however they are lacking of profound scientific data on the ecology of indoor mould, their metabolic behaviour and the real health-related impacts they might cause. In this presentation the complex interaction of building physics, building material composition and microbial growth conditions will be elucidated from the prehistoric cavern to Lascaux to modern buildings respecting the Kyoto protocol, the possibilities of an interdisciplinary and practice-related analysis will be presented, the possible health-and material-related microbial impacts will be explained and adequate countermeasures for a sustainable sanitation and control of the microbial infestations indoors will be explained.

17.00 – 17.30

Indoor fungi: a multidisciplinary challenge

Olaf Adan

Eindhoven University of Technology, TNO Built Environment and Geosciences, Delft, The Netherlands

The mere fact that some 25% of social dwellings, (i.e. more than 14 million units) in the 27 member states of the European Union is suffering from disfigurement due to fungi, underlines that mould problems should be considered as a widespread and profound problem. Recent studies show that the economic impact of fungi on public health in Europe is in the order of billion € annually. It is without doubt that there is no fungal growth without water. However, that relationship is much more complex than commonly assumed. Basically, a multidisciplinary approach, bringing together microbiology, materials science and physics is required to yield understanding of this relationship and to make a true step forward in control strategies.

17.30 – 18.00

Biodiversity of indoor moulds and climate change

Robert A. Samson

Applied and Industrial Mycology, CBS Fungal Biodiversity Centre, Utrecht, the Netherlands

The mycobiota occurring indoors consists of about 120 species of common genera such as *Penicillium*, *Aspergillus* and *Cladosporium*. The composition of these species seemed to be comparable in indoor environment in moderate climates. Little data are available from studies of the mycobiota from tropical indoor environments. In our studies in the Netherlands and other European countries we usually found a presumably stable mycobiota. However in the last three years there has been a remarkable shift to species rarely seen or representatives of the genus *Aspergillus*, which have preference for higher temperatures. The studies on the indoor mycobiota have also been influenced by new taxonomic concepts using a polyphasic approach. For identification a further step will be the barcoding of the common taxa in moderate and tropical climates. This will be an important step to allow rapid and accurate routine identification.

The Johanna van Westerdijk and Josef Adolf von Arx Awards

9.30 – 10.00



Johanna van Westerdijk



Josef Adolf von Arx

Session 4. Culture collection, DNA Barcoding and biosecurity

Chair: Ulf Thrane

This session focuses on developments in strain identification/validation of microorganisms that are key issues for biological resource collections in quality assessment and control. Secondly, it addresses the question how current community safety and security issues can affect biological resource collections in the future, and which strategies and management policies will have to be implemented in order to comply with current and expected legislation. Thirdly, it will show how genetic resources can be employed in the quest for novel bioactive compounds.

The culture of working with cultures for society

10.00 – 10.30.

Erko Stackebrandt

DSMZ-German Collection of Microorganisms and Cell Cultures GmbH, Braunschweig, Germany

For more than 120 years collections of microorganisms (CM) are a component of the scientific landscape: centers for taxonomic descriptions and identification, repositories of patent strains and safe deposits, providers of resources and keepers of diversity. Though the range of expertise differs widely among CMs, they have in common the goal to serve the community with the best of their capabilities. Despite their acknowledged economic and scientific value for a broad range of disciplines, most collections battle for their recognition, hence for their existence. Except for a few large centers the vast majority of CMs are in constant obligation to justify their existence, being dependent on granting and policy strategies in the academic and research environment. The recent OECD publications on the necessity of collections to strengthen their role by increasing excellence and quality have indeed resulted in an increasing awareness among policy makers. It is, nevertheless, difficult to pass on the message that the collection and provision of living resources is an ongoing process, especially in the light of how little is known about the extent of biodiversity. Not only need new collections (OECD definition) be established – especially in the Southern hemi-

sphere- but, in the light of frozen or reduced budgets, well established collections should feel the obligation to cooperate with small and emerging CMs and to build networks in order to increase expertise and recognition, to reduce redundancies and to explore new markets.

10.30 – 10.50

FT-IR based identification and classification of yeasts

Gianluigi Cardinali¹, Vincent Robert², Paolo Rellini¹, Laura Corte¹ and Fabrizio Fatichenti¹

¹*Department of Applied Biology, University of Perugia and* ²*CBS Fungal Biodiversity Centre, Yeast Collection and Bioinformatics, Utrecht, The Netherlands*

The Fourier Transform Infra Red Spectroscopy (FT-IR) has been proposed in the last years as a tool to characterize and identify microorganisms, including yeast. FT-IR is a consumables non-intensive technique, the sample is prepared in less than one hour and read in a couple of minutes; further mathematical and statistical treatments of the spectra can be carried out automatically. Algorithms and procedures have been developed for a rapid individuation of spectral regions more coherent with current taxonomic data. This or other similar tools can facilitate the efforts of using FT-IR within the framework of an accepted classification for rapid identification, such as those in the control procedures of microbial collections.

10.50 – 11.10

Antifungal susceptibility profiles of yeasts type strains

Marie Desnos-Ollivier, Dorothée Raoux, Damien Hoinard, Vincent Robert, Françoise Dromer

Institut Pasteur, Molecular Mycology Unit, National Reference Center for Mycoses and Antifungals; CNRS URA3012, Paris, France. CBS Fungal Biodiversity Centre, Yeast Collection and Bioinformatics, Utrecht, The Netherlands

Knowledge on the antifungal susceptibility of fungi is usually limited to pathogenic fungi and to the most common species recovered during human and animal infections. We thus decided to assess the antifungal susceptibility profiles of yeasts type strains in order to analyze whether drug resistance extended beyond known intrinsically resistant species. A total of 1779 type strains were studied of which 1641 were analyzed due to lack of growth in both test media even at 30°C (in addition 99 strains failed to grow in RPMI1640 and 11 in AM3 medium). This included a total of 102 genders (63 ascomycetes and 38 Basidiomycetes and 1 Eumycete) and 956 species (626 Ascomycetes and 330 Basidiomycetes). Overall, known intrinsic resistance was identified for the few pathogenic species tested, but a few unusual profiles were detected among some type strains synonyms of pathogenic species which will prompt checking of their identification. This is the first study analyzing the antifungal susceptibility profiles of a broad collection of yeasts type strains. It clearly shows that Basidiomycetes have decreased susceptibility to the 5 classes of antifungal drugs designed so far. Our results suggest that analysis of antifungal drug resistances including nucleotide sequences of the target genes could provide further insights into species lineages.

11.10 – 11.30

Biological Resource Collections and Biosecurity

Joost Stalpers

CBS Fungal Biodiversity Centre, Utrecht, the Netherlands

Due to experiments with Ebola virus and intentional poisoning with *Bacillus anthrax* bioterrorism has become a political focal point. The realization that crops, stock and environment are also possible terrorist targets, while they were not included in specific security regulations disquieted policymakers and caused overreactions. These can seriously affect microbial culture collections. However, such collections do have the responsibility for a risk assessment, for which at the moment the necessary elements may not be in place.

The CBS Collections – a major resource for DNA barcode reference data

11.30– 12.00

Ursula Eberhardt

CBS Fungal Biodiversity Centre, Utrecht, the Netherlands

The success of DNA barcoding, like that of any other identification system, depends largely on the quality of the body of available reference data. For overcoming the shortcomings of GenBank, the at present most widely used DNA sequence reference database, sequence information has to be securely linked to specimens/strains which in turn must be of known origin and available for re-examination. Collections do not only provide an ample resource of such specimens, they are also the only sound way of connecting DNA barcoding data with taxonomic information through types. With its over 50.000 strains including about 7400 types, all digitized, available taxonomic resources such as MycoBank and active research groups in socially relevant groups of fungi, CBS is an excellent source of DNA barcoding reference data. As a living resource, the CBS collections, as opposed to herbaria or museum collections, give additional scope for relating organismic to functional diversity. Current DNA barcoding activities and plans will be presented.

Lunch and poster session

12.00-13.00

Session 5. Yeasts and health

Chair: Teun Boekhout

Yeasts play a prominent role causing disease to humans and animals. In this symposium we will address some key issues related to fungal virulence. Among these are interactions with macrophages, melanization, adaptation to the human skin as revealed by a comparative genomics approach, and important features of the yeast cell wall, which is involved in adhesion to the human host.

Mechanisms of virulence in the human pathogenic fungus *Cryptococcus*

13.00 – 13.30

Robin C. May

Department of Molecular Pathobiology, School of Biosciences, University of Birmingham, Birmingham B15 2TT, United Kingdom

Cryptococcus neoformans and the related species *Cryptococcus gattii* are the causative agents of cryptococcosis, a fatal infection of the central nervous system. Since other *Cryptococcus* species are non-pathogenic, it is important to understand how and why pathogenicity has evolved in these two species. Cryptococci infect people via the lung, where they are engulfed by phagocytic cells of the innate immune system. Unlike other pathogens, however, *Cryptococcus* is not destroyed but rather parasitises upon the host cell, proliferating within and then exiting from the cell using a novel mech-

anism that we have termed 'vomocytosis'. I will discuss our work on investigating the molecular basis of intracellular parasitism and also our recent findings that suggest that sudden evolutionary 'shifts' in this process may lead to cryptococcosis outbreaks, such as that which is currently occurring on Vancouver Island.

13.30 – 14.00

New insights into the biology and virulence of *Cryptococcus neoformans*

Arturo Casadevall

Department of Microbiology and Immunology, Albert Einstein College of Medicine, New York, USA

This talk will present the intracellular pathogenic strategy of *Cryptococcus neoformans* and recent findings on the mechanism for capsular enlargement. A remarkable aspect of *C. neoformans* intracellular replication is its ability for non-lytic exocytosis whereby yeast cells are released leaving the host cell alive and capable of replication. This phenomenon appears to involve actin rearrangement. Non-lytic exocytosis appears to be a mechanism that may have evolved for escape from phagocytic predators in the environment. In addition, the talk will present recent unpublished evidence that the capsule enlarges by the presence of single molecules that can span the breadth of the capsule.

14.00 – 14.30

Human scalp and hair health – an eight year collaboration between CBS and P&G reveals the role of a human skin commensal

Tom Dawson

The Procter & Gamble Company, Cincinnati, OH, USA

Commensal yeasts play a role in the overall process of human skin and hair biology. Over the last eight years we have investigated the role of *Malassezia* yeasts in dandruff and seborrheic dermatitis. Collaboration between the CBS and the Procter & Gamble Company has enabled significant improvement in our understanding of the metabolic processes that result in a human skin (scalp) disorder. We have identified the *Malassezia* species most closely correlated to dandruff, identified specific *Malassezia* metabolic processes contributing to the disorder, and have now completed sequencing of the *Malassezia globosa* genome and assessed a significant part of the *Malassezia restricta* genome. We now have the ability to further develop our understanding of human skin metabolism, in normal and abrogated skin, and begin to unravel the metabolic activity taking place in the complex interaction of a commensal microbe and its host.

14.30 – 15.00

Towards quantitative cell wall proteomics, a new era in fungal cell wall research

Piet de Groot

SILS – Biomolecular Mass Spectrometry, University of Amsterdam, The Netherlands.

Cell walls of pathogenic fungi play an important role in the host-pathogen interactions that underlie the establishment of mycoses. In many fungi, the cell wall consists of a network of stress-bearing polysaccharides, which serves as a scaffold for a dense external layer of glycoproteins. The functions of covalently linked fungal cell wall proteins (CWPs) are manifold, ranging from general functions like limiting cell wall porosity, water retention, and immunomodulation by masking the underlying polysaccharide layer, to more specific roles in cell wall biosynthesis, adhesion and viru-

lence. Based on a rigorous procedure to isolate cell walls combined with gel-independent tandem mass spectrometry, we have developed a sensitive and versatile method to identify and characterize covalently bound CWPs. This method was successfully applied to various fungi including the ascomycetes *S. cerevisiae*, *C. albicans*, *C. glabrata*, *S. pombe*, *A. gossypii* and *A. nidulans*. I will discuss results obtained with our methodology as well strategies to enable absolute and relative quantification of CWPs under various growth conditions that relate to the infection process.

Coffee break

15.00 – 15.30

Session 6. Fungi and healthy Plants

Chair: Pedro Crous

According to estimates of the World Health Organization, one-third of the world's population is well-fed, one-third is under-fed, and one-third is starving. Every year 15 million children die of hunger, while 800 million people suffer from hunger and malnutrition. Although there are several causes for this, fungi play an important role as causal agents of plant disease. Furthermore, inadvertent introductions of phytopathogenic fungi have dire consequences to nature and cultivated crops. To combat these diseases on an international scale, it is important to clarify whether the same species and genotypes occur in various countries, since each different species and genotype can be expected to have different patterns of attack, as well as different responses to fungicides and to climatological conditions. With such pathogens, it is also important to know what their host ranges and mating strategies are, and how this relates to different disease control mechanisms.

Invasive Species and Biosecurity: The importance of collections, databases and taxonomists for understanding biological invasions

15.30 – 16.00

Keith A. Seifert

Biodiversity (Mycology & Botany) Eastern Cereal and Oilseed Research Centre, Agriculture & Agri-Food Canada, Ottawa, Ontario K1A 0C6, Canada

Invasive alien species are a hot topic in the news all over the world. They are presented as real-life horror stories, exploiting deep human fears of horrible monsters (ugly insects) and disfiguring, painful diseases (invisible and deadly microbes). But how do we know when a species is an alien in the first place? How much of our fear is biological xenophobia, and how much can be supported by hard science? The science of biological invasions interfaces with the national interests inherent in plant quarantine and extends to basic questions of geographical and temporal occurrence of species. How much do we actually know about the distribution of even very common microorganisms? This presentation will consider several recent and anticipated future events involving plant quarantine, including the possible consequences of a hypothetical 'invasion' of a fictional country by one of the commonest moulds on Earth. Standards of proof for fungal identification will be discussed, and an emphasis will be placed on the critical role that biological collections play in the detection, monitoring and risk assessment of putative biological invasions. International initiatives, such as DNA barcoding, have the potential to enhance coordination and consistency of response between cooperating countries. Open access to biological data will ensure that all parties use the same information, reducing putative quarantine incidents based on faulty scientific assumptions, and ensure that scarce remediation resources are effectively deployed.

DNA barcoding of phytopathogens at ports of entry: a workable solution?

Peter Bonants

Plant Research International, Wageningen

Development of accurate identification tools for plant pathogens and pests is vital to support European Plant Health Policies. For this project Council Directive 2000/29/EC is important, listing some 275 organisms for which protective measures against introduction into and their spread within the Community needs to be taken. Those threats are now greater than ever because of the increases in the volumes, commodity types and origins of trade, the introduction of new crops, the continued expansion of the EU and the impact of climate change.

Currently identifying pathogens (in particular new emerging diseases) requires a staff with specialised skills in all disciplines (mycology, bacteriology, etc.); which is only possible within big centralised laboratory facilities. Taxonomy, phytopathology and other fields which are vital for sustaining sound public policy on phytosanitary issues are threatened with extinction. Modern molecular identification/detection techniques may tackle the decline in skills since they often require much less specialist skills to perform, are more amenable for routine purposes and can be used for a whole range of different target organisms. Recently DNA barcoding has arisen as a robust and standardized approach to species identification. QBOL wants now to make DNA barcoding available for plant health diagnostics and to focus on strengthening the link between traditional and molecular taxonomy as a sustainable diagnostic resource.

Within QBOL collections harbouring plantpathogenic Q-organisms will be made available. Informative genes from selected species on the EU Directive and EPPO lists will be DNA barcoded from vouchered specimens. The sequences, together with taxonomic features, will be included in a new internet-based database system. A validation procedure on developed protocols and the database will be undertaken across worldwide partners to ensure robustness of procedures for use in a distributed network of laboratories across Europe.

Organic Food Production and Fungal Pathogens

Ariena H.C. van Bruggen and Aad J. Termorshuizen

Biological Farming Systems, Wageningen University and Blgg, Wageningen

The organic food production chains differ in many respects from the conventional chains. At the farm level, differences in management practices are not only characterized by the presence versus absence of the use of synthetic pesticides and fertilizers, but also by a greater care for the maintenance of soil and agro-ecosystem health at organic than at conventional farms. In the food processing and marketing phases of the chains organic and conventional products need to be kept strictly separate. Synthetic preservatives and other additives are generally not allowed in the organic food chain, unless specific exemptions are granted. Yet, there are large differences among organic farms and production chains, similar to the wide variety of farms and chains in the conventional production system. For example, organic farms may have crop rotations ranging from only 1:2 (e.g. in greenhouses) to 1:8 (e.g. in mixed farming systems).

On the one hand, the absence of pesticides may lead to more disease, especially some foliar diseases, on the other hand the lack of negative side effects of pesticide use, enhanced biodiversity and the use of cultural con-

Control practices may result in less disease. In experiments and surveys where organic farming is compared with conventional farming the following differences are commonly observed: Root diseases are generally less severe in organic than in conventional farms. The reasons for reduced root disease have seldom been investigated, although relations with microbial activity and diversity have sometimes been found. Cultural practices like a longer rotation (resulting in decline in soil inoculum levels) and organic amendments contribute to soil health and disease suppression in organic farms. Foliar diseases may be similar, increased or reduced in organic compared to conventional farming systems, depending on, a.o., the plant nitrogen content and the sensitivity of the pathogen to microbial competition. Potential differences between biotrophic and necrotrophic fungal pathogens will be discussed. Post-harvest diseases and mycotoxin contents may also be more or less problematic on organic than on conventional products, depending a.o. on the time of infection (in the field or in storage) and the moisture content during storage.

As biodiversity is usually greater at organic than at conventional farms, potential pathogen and disease suppression will be discussed in relation to microbial interactions on the plant surface and inside the plant.

Climate change and emerging diseases

17.00 – 17.30

Bruce Fitt

Rothamsted Research, Harpenden, Herts AL5 2JQ, UK

Worldwide climate change is affecting agricultural crops and the diseases which attack them. For example, by combining a weather-based disease forecasting model with climate change scenarios, it is predicted that global warming will increase the range and severity of UK epidemics of phoma stem canker on winter oilseed rape, caused by *Leptosphaeria maculans*. This pathogen is more damaging than the related *L. biglobosa* and is spreading globally; it currently threatens 8M ha of susceptible crops in China. The 160 year archive of samples from the Broadbalk experiment at Rothamsted, started by John Bennet Lawes in 1843, has been used to study the relationships between *Septoria nodorum* (*Phaesphaeria nodorum*) and *Septoria tritici* (*Mycosphaerella graminicola*) on UK winter wheat. The increase in abundance of *S. nodorum* on wheat leaves was linked to increasing concentrations of SO₂ pollution. These results provide a stimulus to predict effects of climate change and pollution on other plant diseases in agricultural and natural ecosystems

Poster presentations

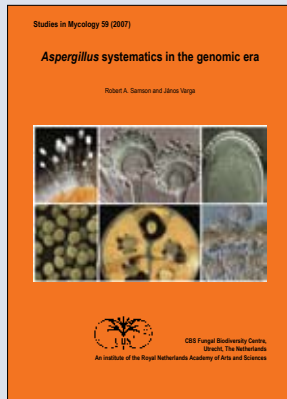
1. Analysis of volatile metabolites by common indoor moulds - Viviana Polizzi
2. Where is the origin of the Vancouver Island *Cryptococcus gattii* outbreak? - Ferry Hagen
3. *Malassezia* and *Candida* colonization on glans penis of circumcised men - Atilla Aridogan
4. Performance of chromogenic media, Chromogenic Candida agar and CHROMagar Candida, in recovery and presumptive identification of mono-fungal and polyfungal vaginal isolates - Mehmet Macit Ilkit
5. Fungi in Archives: Human and Cultural Heritage Threat - Ana Catarina Pinheiro
6. CandIDazol: Innovative Diagnostics for the Rapid Identification and Detection of Azole Resistant Candida Yeasts - Rolf Boesten
7. Fumonisin from *Aspergillus niger* - a new health risk?" - Jesper Mølgaard Mogensen
8. Polyphasic analysis of *Phoma* section *Peyronellaea*" - Jens Laurids Sørensen
9. Antifungal susceptibility in dermatophytes isolated from patients of a health-care center in Lisbon (Portugal) - Rogério Tenreiro
10. Control of *Fusarium* sp and *Pythium* sp in tomato culture at Songon - Dabou (Côte d'Ivoire) - Soro Sibirina
11. Microbial ecology and functionality of Chinese food fermentations - B - Z.Han and M.J.R.Nout
12. Ergosterol rich cap in membrane of germinating conidia - Richard van Leeuwen
13. *Dekkera bruxellensis* - a new ethanol production yeast - Volkmar Passoth
14. Chemical and microbiological studies on Daqu - Xiao - Wei Zheng, Minoo R. Tabrizi, Xiao - He Wu, Jing - Yu Chen, Teun Boekhout, Robert Samson, Bei - Zhong Han, M.J. Robert Nout - Mrs. Xiaowei Zheng
15. The CBS Collections – preserving the world's microbial diversity for science, education and industry - Gerard Verkley
16. Good Chemistry between DTU (Lyngby, Denmark) and CBS (Utrecht, The Netherlands) - Jens Frisvad, Ulf Thrane, Birgitte Andersen, Robert A. Samson, Jos Houbraken
17. Cork fungi diversity and characterization - Carmo Basilio
18. Cooperations between SLU (Uppsala, Sweden) and CBS (Utrecht, The Netherlands): Three leads of common research in applied mycology - Jennifer Jenessen, Mathilda Ostorpe, Olga Vinerre, Su-lin Leong, Johan Schnürer, Robert A. Samson, Jos Houbraken and Jan Dijksterhuis
19. Distinguishing varieties within the *Phoma exigua* complex using DAF-based DNA barcodes - M.M. Aveskamp, E. Turco, J. de Gruyter, J.Z. Groenewald, and P.W. Crous
20. A comparative study of *Phytophthora* species - Henk Brouwer, Arthur W.A.M. de Cock, Collin H.A. Gerritzen, Peter J.M. Bonants, C. André Lévesque, Pedro W. Crous
21. Multilocus sequence typing (MLST) of the pathogenic genus *Fonsecaea* - M.J.Najafzadeh, C.GUEIDAN, G.S.de Hoog, A.H.G.Gerrits van den Ende and H.Badali
22. Molecular identification of mycorrhizal fungi of dipterocarp seedlings in Indonesian rubber agroforests - Hest L. Tata, G.S. de Hoog, R.C. Summerbell, M. van Noordwijk and M.J.A. Weger
23. Polyphasic taxonomy of *Penicillium citrinum* and related species - Jos Houbraken, Jens C. Frisvad, Martin Meijer, Robert A. Samson
24. Subclinical Investigation for the Presence of Allergenic Mould - Josef Dumanov
25. DNA barcoding at CBS - Ursula Eberhardt

Studies in Mycology 60: Neotropical Hypocrella (anamorph Aschersonia), Moelleriella, and Samuelsia

Chaverri P, Liu M, Hodge KT (2008). . 68 pp., € 40.00

The present taxonomic revision deals with Neotropical species of three entomopathogenic genera that were once included in *Hypocrella* s. l.: *Hypocrella* s. str. (anamorph *Aschersonia*), *Moelleriella* (anamorph *aschersonia*-like), and *Samuelsia* gen. nov. (anamorph *aschersonia*-like). Species of *Hypocrella*, *Moelleriella*, and *Samuelsia* are pathogens of scale insects (Coccidae and Lecaniidae, Homoptera) and whiteflies (Aleyrodidae, Homoptera) and are common in tropical regions. Phylogenetic analyses of DNA sequences from nuclear ribosomal large subunit (28S), translation elongation factor 1- α (TEF 1- α), and RNA polymerase II subunit 1 (RPB1) and analyses of multiple morphological characters demonstrate that the three segregated genera can be distinguished by the disarticulation of the ascospores and shape and size of conidia. *Moelleriella* has filiform multi-septate ascospores that disarticulate at the septa within the ascus and *aschersonia*-like anamorphs with fusoid conidia. *Hypocrella* s. str. has filiform to longfusiform ascospores that do not disarticulate and *Aschersonia* s. str. anamorphs with fusoid conidia. The new genus proposed here, *Samuelsia*, has filiform to longfusiform ascospores that do not disarticulate and *aschersonia*-like anamorphs with small allantoid conidia. In addition, the present study presents and discusses the evolution of species, orphology, and ecology in *Hypocrella*, *Moelleriella*, and *Samuelsia* based on multigene phylogenetic analyses.

68 pp., fully illustrated with colour pictures (A4 format), paperback, 2008. € 40



Studies in Mycology 59: Aspergillus systematics in the genomic era

editors Robert A. Samson and János Varga

Since Pier Antonio Micheli described *Aspergillus* in his *Nova Plantarum Genera* in 1729 the genus attracted an immense interest. Many species were found as spoilage agents, or responsible for human and animal diseases. On the other hand *Aspergilli* were also found as beneficial micro organisms in the fermentation of Asian food and beverages. With the discovery of aflatoxins, the interest and research of the *Aspergilli* increased even more. In the present days *Aspergillus* research has grown to such a level, that it could be stated that *Aspergilli* might be the most studied fungi.

This issue comprises 14 papers and is a summary of presentations and discussions of the international workshop entitled “*Aspergillus* systematics in the genomics era” with a multidisciplinary audience held in Utrecht, The Netherlands (12-14 April, 2007). The papers discuss topics such as the current species concept; what can comparative genomics tell us about species concepts in *Aspergillus*; sexual and vegetative compatibility genes in the *aspergilli*; secondary metabolite (including mycotoxins) profiling, growth profiles and other tools for species recognition; identification in the clinical setting; *Aspergillus* strain typing in the genomics era and the biodiversity of *Aspergillus* species in some important agricultural products. Nomenclatural considerations in naming species of *Aspergillus* and its teleomorphs were discussed in a separate paper, while the recommendations of an international panel are included. Additionally, the polyphasic methods applied recently on *aspergilli* resulted in four monographs included in this issue:

Aspergillus sections *Candidi*, *Clavati*, *Fumigati* and *Usti*. Diagnostic tools developed for the identification of the economically extremely important but taxonomically problematic black *aspergilli* (*Aspergillus* section *Nigri*) are also covered in a separate paper. This issue contains many colour illustrations, particularly in the four monographs.

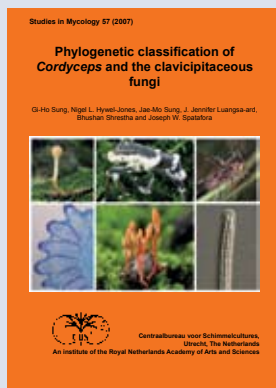
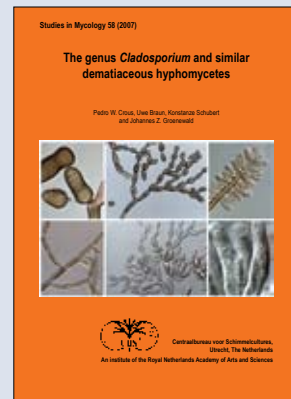
206 pp., fully illustrated with colour pictures (A4 format), paperback, 2007. € 65

Studies in Mycology 58: The genus Cladosporium and similar dematiaceous hyphomycetes

Pedro W. Crous, Uwe Braun, Konstanze Schubert and Johannes Z. Groenewald

Species of *Cladosporium* are common and widespread, and interact with humans in every phase of life, from producing allergens in the indoor environment, to causing fruit decay and plant disease, or being associated with human mycoses. Although *Cladosporium* is one of the largest and most heterogeneous genera of hyphomycetes, only a mere fraction of these species are known from culture, and few have been characterised based on molecular data. The present volume consists of nine research papers, and introduces 71 new combinations, 53 new species, 15 genera, and one family. Specific conditions and media are recommended to study *Cladosporium* and allied genera, while the genus is circumscribed, and separated from morphologically similar taxa with which it has been confused in the past. Generic issues related to the anamorph genera and associated *Dothideomycete* teleomorph genera (*Davidiella*, *Mycosphaerella*, *Venturia*) are addressed, and multi-allelic data sets provided to facilitate species recognition. The volume is richly illustrated, with more than 100 colour plates, numerous line drawings, and scanning electron micrographs.

253 pp., illustrated with colour pictures (A4 format), paperback, 2007. € 65



Studies in Mycology 57: Phylogenetic classification of Cordyceps and the clavicipitaceus fungi

Gi-Ho Sung, Nigel L. Hywel-Jones, Mae-Mo Sung, J. Jennifer Luangsa-ard, Bhusan Shrestha and Joseph W. Spatafora

The taxonomy of *Cordyceps* and the *Clavicipitaceae* is revised based on a multi-gene phylogeny. The phylogenetic relationships of 162 taxa were estimated based on analyses consisting of five to seven loci, which strongly support the existence of three clavicipitaceus clades and reject the monophyly of both *Cordyceps* and *Clavicipitaceae*. Most diagnostic characters used in current classifications of *Cordyceps* (e.g., arrangement of perithecia, ascospore fragmentation, etc.) were not supported as being phylogenetically informative; the characters that were most consistent with the phylogeny were texture, pigmentation and morphology of stromata. The family *Cordycipitaceae* is validated based on the type of *Cordyceps*, *C. militaris*, and includes most *Cordyceps* species with brightly coloured, fleshy stromata. The new family *Ophiocordycipitaceae* is proposed and based on *Ophiocordyceps* Petch. The majority of species in this family produce darkly pigmented, tough to pliant stromata that often possess aperithecial apices. The new genus *Elaphocordyceps* is proposed for all species of *Cordyceps* that parasitise the *Elaphomyces* and arthropods. The family *Clavicipitaceae* s. s. is emended and includes grass symbionts and the entomopathogenic genus *Hypocrella* and relatives. In addition, the new genus *Metacordyceps* is proposed which are closely related to the grass symbionts in the *Clavicipitaceae* s. s. Two new species are described, and lists of accepted names for species in *Cordyceps*, *Elaphocordyceps*, *Metacordyceps* and *Ophiocordyceps* are provided.

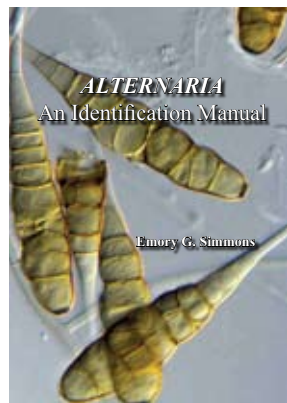
63 pp., illustrated with colour pictures (A4 format), paperback, 2007. € 40

No. 7: Microfungi occurring on Proteaceae in the fynbos

Seonju Marinowicz, Pedro W. Crous, Johannes Z. Groenewald and Michael J. Wingfield

The fynbos is a shrubland characterised by a fire-prone ecosystem and Mediterranean climate. Although it is extremely rich in plant species, and has a high degree of floral endemism, very little is known regarding the fungi in this unique and fascinating environment. The present study investigated the saprobic microfungi that colonise and utilise leaf and twig litter and senescent flower heads of Proteaceae. A total of 29 species and sub-species belonging to four genera of Proteaceae were sampled from 12 sites in the Western Cape Province of South Africa spanning a period of two years (2000–2001). Thirty-eight species reflected new records for South Africa, and 48 species were new reports on Proteaceae. Two new genera and one new combination were also introduced. The fungal community found on twig litter had the highest species richness, while flower head-styles yielded the highest percentage (100 %) of unique species. The percentage of new fungal taxa (43 % of the total species) was exceptionally high, and most of these probably host-specific. More than 80 % of the fungi collected in this study had hard and closed fruiting structures, indicating an adaptation to the constraints of the harsh fynbos environment. Other than providing a foundation for further studies, this investigation highlights a disturbing paucity of knowledge regarding the fynbos Mycota in one of the world's most threatened and unusual floral Kingdoms

166pp., 93 colour plates, 6 black & white plates; Hardcover 2008. € 50



No. 6: Alternaria An Identification Manual

Emory G. Simmons

This book will fill a very large void in the scientific literature and it is quite certain that the volume will become the standard reference for those needing to have critical access to *Alternaria* literature and taxonomic information. There are many scientists, both research and regulatory, who are in desperate need of resources like this book to facilitate routine identification. More than 1 100 published names are associated with taxa that must be considered in the *Alternaria* context. Of these, 276 species with validly published names are maintained here as currently identifiable; these are keyed in the main text of the volume. An additional 16 named taxa, although requiring expanded information and comparison, also are accepted. A few species that have been associated with the genus for years but which now are considered anomalous in the genus have been removed to other genera. Chapters of species and genus characterisations are followed by a comprehensive list of all the nearly 1 200 names involved historically with *Alternaria* taxonomy in the period 1796-2007. Each name is listed with its source, type, and an opinion on its validity and taxonomic disposition. A host index to all accepted species is followed by a comprehensive list of literature cited and a general index. Within the context of the manual, 88 names are assigned to newly described species and genera and to taxa whose epithets appear in new combinations.

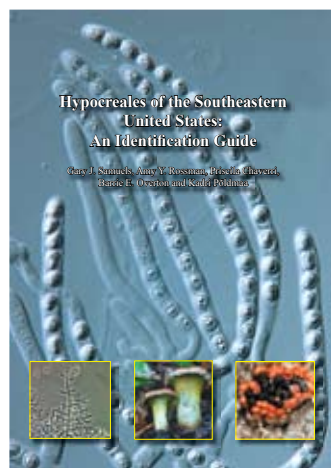
775 pp., with more than 288 line drawings (A4 format). Hardbound, 2007. € 170

No. 5: Mycosphaerella and its anamorphs: 2. Conspectus of Mycosphaerella

André Aptroot

A revision of the species described in *Mycosphaerella* and *Sphaerella* is presented, together with observations on the types of most species or their disposition. The genus *Stigmidium* is expanded to encompass fungicolous species and internal parasites of algae, and includes the genus *Mycophycias*.

173 pp., 115 plates (A4 format), paperback with spiral binding, 2005. € 50



No. 4: Hypocreales of the Southeastern United States: An Identification Guide

Gary J. Samuels, Amy Y. Rossman, Priscila Chaverri, Barrie E. Overton and Kadri Põldmaa

An illustrated guide is presented to the members of the ascomycete order Hypocreales that are known to occur in the southeastern states of the United States, including North and South Carolina, Tennessee and Georgia. Species were selected mainly based on records in the United States National Fungus Collections (BPI). These states include or surround the Great Smoky Mountains National Park. Species of the Hypocreales are among the most numerous, and certainly most conspicuous, of the microfungi. The order also includes some of the most economically important fungi. This guide is intended for individuals who are participating in All Taxa Biological Diversity studies of the Great Smoky Mountains National Park as well as other interested professionals and amateurs. Short descriptions and colour illustrations of one-hundred and one species and two varieties in twenty genera are provided. Keys to genera and species are included. The new combination *Neonectria ditissima* is proposed.

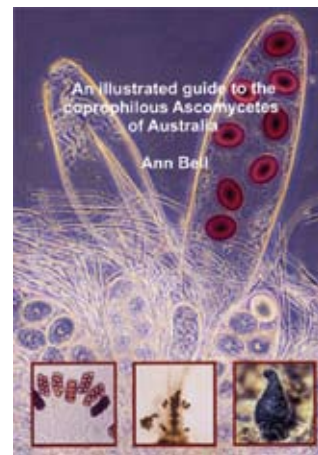
145 pp., over 120 colour pictures (A4 format), paperback with spiral binding, 2006. € 70

No. 3: An illustrated guide to the coprophilous Ascomycetes of Australia

Ann Bell

Descriptions, keys and illustrations (many in colour). Ann Bell's observations of her own collections and some 2 000 microscope slides and assorted notebooks on Australian coprophilous fungi made by the late Major Harry Dade during his retirement years in Victoria.

173 pp., 115 plates (A4 format), paperback with spiral binding, 2005. € 55

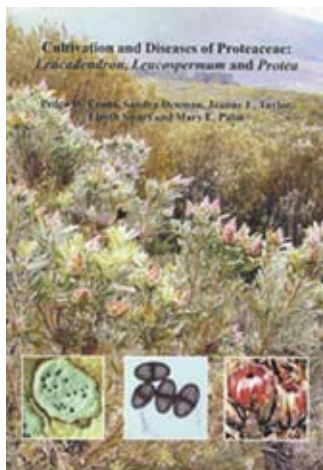


No. 2: Cultivation and Diseases of Proteaceae: Leucadendron, Leucospermum and Protea

Pedro W. Crous, Sandra Denman, Joanne E. Taylor, Lizeth Swart and Mary E. Palm

The Proteaceae represent one of the Southern Hemisphere's most prominent flowering plant families, the cultivation of which forms the basis of a thriving export industry. Diseases cause a loss in yield and also limit the export of these flowers due to strict phytosanitary regulations. In this publication the fungi that cause leaf, stem and root diseases on Leucadendron, Leucospermum and Protea are treated. Data are provided pertaining to the taxonomy, identification, host range, distribution, pathogenicity and control of these pathogens. Taxonomic descriptions and illustrations are provided and keys are included. Disease symptoms are illustrated with colour photographs.

510 pp., (17 x 25 cm), paperback, 2004. € 55

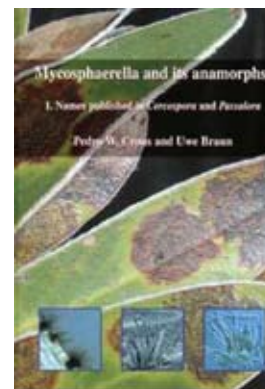


No. 1: Mycosphaerella and its anamorphs: 1. Names published in Cercospora and Passalora

Pedro W. Crous and Uwe Braun

This book contains a compilation of more than 3000 names that have been published or proposed in *Cercospora*, of which 659 are presently recognised in this genus, with a further 281 being referred to *C. apii* s.lat. Approximately 550 names of *Passalora* emend. (incl. *Mycovellosiella*, *Phaeoramularia*, *Tandonella* and *Phaeoisariopsis* p.p.) are treated in a second list. In total 5720 names are treated. 553 taxonomic novelties are proposed.

571 pp., 31 figures (17 x 25 cm), hard cover, 2003. € 80



Selection of other CBS publications

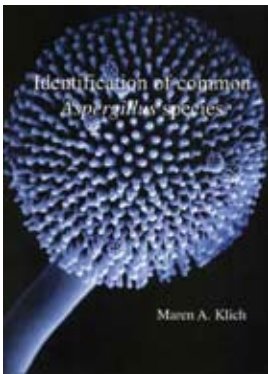


Introduction to food- and airborne fungi

Robert A. Samson, Ellen S. Hoekstra and Jens C. Frisvad

Seventh edition with updated taxonomy and addition of some important species. The keys to the taxa were improved. The taxonomy and the nomenclature of *Fusarium* is revised and the number of *Penicillium* species has been increased because they are frequently encountered on food and indoor environments. The identification of *Penicillium* based on morphological characters remains difficult and therefore synoptic keys and tables are added to assist with the identification.

389 pp., 120 plates (A4 format), paperback, 2004. € 55

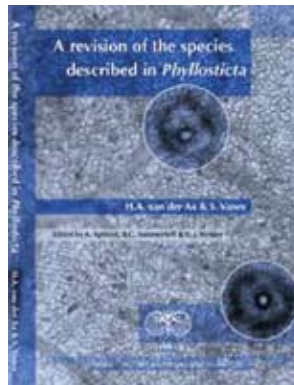


Identification of Common Aspergillus Species

Maren A. Klich

Descriptions and identification keys to 45 common *Aspergillus* species with their teleomorphs (*Emericella*, *Eurotium*, *Neosartorya* and *Sclerocleista*). Each species is illustrated with a one page plate and three plates showing the most common colony colours.

116 pp., 45 black & white and 3 colour plates (Letter format), paperback, 2002. € 45

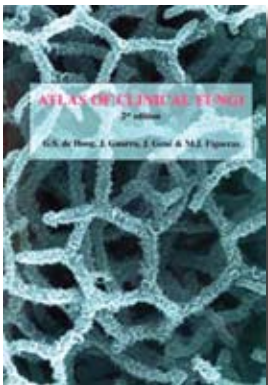


A revision of the species described in Phyllosticta

Huub A. van der Aa and Simon Vanev

2936 taxa are enumerated, based on the original literature and on examination of numerous herbarium (mostly type) specimens and isolates. 203 names belong to the genus *Phyllosticta* s.str., and are classified in 143 accepted species. For seven of them new combinations are made and for six new names are proposed. The great majority, 2733 taxa, were redispersed to a number of other genera. A complete list of these novelties, as included in the book's abstract, can also be consulted on the web-site of CBS.

510 pp. (17 x 25 cm), paperback, 2002. € 55



Atlas of Clinical Fungi

G.S. de Hoog, J. Guarro, J. Gené and M.J. Figueras (eds)

The second fully revised and greatly expanded edition of the Atlas of Clinical Fungi appeared in 2000. The modest and very competitive price of this standard work has certainly contributed to the popularity of the first edition. In recent years the application of molecular biology has become within reach for many routine laboratories. The new Atlas will provide ample molecular data for the majority of clinically relevant fungi. It will set a standard for innovative techniques in medical mycology. In addition, antifungal susceptibility data will be given for most species, which will provide essential knowledge for the clinician in view of adequate therapy.

1126 pp., fully illustrated with line drawings and black & white photo plates (A4 format), hard cover, 2004. € 140.

Interactive CD-ROM v. of the Atlas € 65, Book plus CD-ROM € 180

