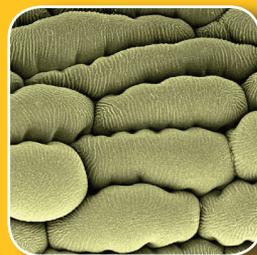
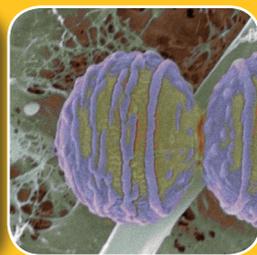
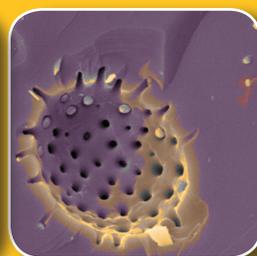
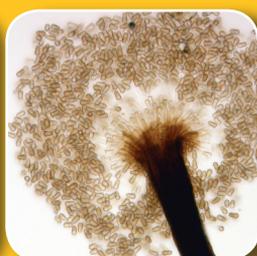


CBS - KNAW Fungal Biodiversity Centre



Progress Report

2014–2015



FUNGAL COLLECTIONS AND THE MYCOLOGICAL VALUE CHAIN

For more than 100 years the CBS-KNAW Fungal Biodiversity Centre has followed the motto “To Collect, Study and Preserve”, with the aim to globally advance mycology as science. We are all aware of the fact that the preservation of fungi is essential to improve quality of life, and that fungi play a major role in our everyday life and the global economy. Many species of fungi are very significant plant pathogens of important staple food crops, or are clinically important, having either positive or negative repercussions for our health, or have major industrial applications that could lead to novel products or processes. To help us understand these processes, it is essential to have access to a well-curated collection of accurately identified isolates supported by a solid genetic platform. Presently we know approximately 100–120,000 formally described species



of fungi, of which only around 20 % have been deposited in Biological Resource Centres. This means that even after 100 years of collecting and preserving fungi, our global task is far from complete, which also heralds a big challenge for the future.

With financial support from industry, various national and international research programmes, including the Royal Dutch Academy of Arts and Sciences (“KNAW”), the CBS was the first Biological Resource Centre that managed to generate DNA barcodes of its entire holdings. These DNA barcodes and the associated databases also play a vital role in enhancing quality of life, e.g. the Indoor Microbial Barcode of Life (Sloan foundation), and stimulating economic growth through trade, e.g. the Quarantine Barcode of Life (QBOL,

Q-Bank, Q-Collect). DNA data integrated in intelligent database networks represent a stable platform for the future of mycology, and will also give other scientists access to fungal data in biological systems.

The CBS consists of a fungal collection, infrastructure, and excellent research team, which make it quite a unique global resource. In 2015 the CBS also completed its 2020 strategy, which can be summarised in a few key points, namely to strengthen bioinformatics and its research network on Utrecht campus, and to launch two new groups, namely medical mycology and novel product discovery. In this regard our new research wing for industrial mycology has finally been approved, and we hope that we will be able to occupy this building at the end of the year. It also means that we will be establishing search committees for two new dynamic group leaders to help propel CBS into the future. An important point I want to highlight is that our new vision has chosen for growth, aiming to grow our business and budget to meet our ever-increasing needs.

To strengthen our research partnerships on campus, CBS also initiated a new strategy session on campus, formulating a plan for what will be known as the “Fungal Network Utrecht”. This will essentially be a collaboration of CBS with Utrecht University and the Utrecht Medical Centre, setting up a distributed pipeline on campus to effectively use fungal secondary metabolites to screen for novel antibiotics, linking to the Netherlands Centre for One Health, and sustainable crop protection, linking to Future Food as strategic initiative, the Dutch Top Sectors, and the National Scientific Agenda. If funded, this will give huge momentum to CBS, who will be positioned in the centre of this exciting new initiative.

Fungi occur everywhere, and influence our daily lives. In spite of being pathogens of crops, humans and animals, they also hold great promise and opportunity for the future. At CBS we preserve this asset, and strive to make it available to the scientific community to improve quality of life. If you want a career that has meaning and will make a difference, I invite you to join us on our journey: come to CBS, and think big!

A handwritten signature in black ink that reads "P.W. Crous". The signature is written in a cursive, slightly slanted style.

Prof. dr Pedro W. Crous
Director: CBS-KNAW



The primary aim of the CBS-KNAW Fungal Biodiversity Centre is to preserve the world's fungal biodiversity in a living collection. As one of the Academy institutes, our task is also to make this collection as widely available as possible for the international research community. Unlocking a collection implies that collection data should be accessible on different levels, namely the fungal cultures, but also the associated metadata. Since it was originally established, the CBS has always been closely linked to industry and service. As a result, there are numerous connections between the institute, industry, as well as governmental institutions.

The CBS acquires around 1,700–3,000 new strains for the collection per annum, while 4,000–5,000 strains get dispatched for research purposes (nationally and internationally). The CBS also has a Service Unit that specifically deals with routine identification of fungal isolates, and does projects for industry upon request. Furthermore, the CBS publishes two book series (*CBS Biodiversity Series*, *CBS Laboratory Manual Series*) and three journals (*Studies in Mycology*, *Persoonia* and *IMA Fungus*). In recent years a lot of attention has been devoted to maintaining numerous databases for the international community, namely MycoBank (for the International Mycological Association), as well as strain databases, specific fungal databases, and websites, which together generate thousands of downloads or page views per hour.

CBS staff have also been highly successful in the competitive international and European research arena, and presently we are actively involved in several major EU, national and regional grants (FES: Making the Tree of Life Work; NWO: Biofuel production, in collaboration with CAS; Eurotransbio: CandIDazol project; SLOAN: indoor fungi; NUFFIC, KNAW/Chinese Academy: Bye-TOL project funded by KNAW and NSFC; barcoding medical fungi, one VENI- and VICI-grant, respectively; two NWO-JSTP grants with China; KNAW-SPIN project with Indonesia; Zon/MW: Bioprospecting for novel antibiotics; CRI: Citrus Black Spot disease; Qatar Foundation: Improved diagnostics of fungi-related infections in Qatar, and Mapping the microbial

diversity in the Arabian Gulf surrounding Qatar using genomic and metagenomic approaches; EMSL: Visualizing plant biomass degradation by *Aspergillus niger*; JGI: Selective and non-selective lignin degradation life styles of white rot fungi, and dissecting the approaches used by ascomycete fungi to degrade plant biomass; JGI-EMSL: Dissecting intraspecies diversity in fungal wood decay; NWO/STW VICI: Harvesting nature's bounty; NWO/ALW: Dissecting the differences in hardwood and softwood degradation by the basidiomycete white-rot fungus *Dichomitus squalens*; EMBO: Exploring new proteases for proteomics (with UU); BEBASIC: Regulation of enzyme production in fungal cell factories; BEBASIC: Assessment of establishing a sexual cycle in *Myceliophthora thermophila*; JGI:). We also participate in several major 7th Framework Programmes (e.g. Q-Collect, i4Life, EMbaRC, MIRRI, Cornucopia, NH&MRC: DNA Barcoding, OPTIBIOCAT, SUBICAT), ensuring that the institute and its collection remains well positioned for exciting new developments and research initiatives. The CBS has always been actively involved in numerous projects with diverse industries. The CBS Service Unit provides advice on fungal identification in relation to moulds in the indoor environment, new plant and human diseases, food spoilage by a range of fungal organisms, as well as fungal problems in factories and production lines.

Additional information about the programmes and their projects can be found on the CBS website, www.cbs.knaw.nl/research.

Since the last progress report (2012–2013), the CBS has managed to maintain its high research output, which is a result of new policy and research infrastructure. The institute has an active national and international research network, and the majority of the papers are published in international collaboration. Of the papers published during 2014–2015, 40 % are in a journal with an impact factor above 3 (49 % in 2012–2013), and 9–16 papers above impact factor 10 (2–10 in 2012–2013), which is considerable, considering that the average of the field "mycology" is 2.198 (JCR 2014).

Scientific output

ISI papers in CBS database	# IF > 3*	# IF > 10
2014	62	16
147 papers		
1 book		
4 book chapters and proceedings		
2015	50	9
133 papers		
1 book		
7 book chapters and proceedings		

* Average impact factor of the field "mycology" = 2.198 (JCR 2014).

Services

Strains	2014	2015
Identifications	230	298
Patent depositions	50	76
Deliveries	4602	3980
Aquisitions	3141	1701

EVOLUTIONARY PHYTOPATHOLOGY

Prof. dr Pedro Crous

“Fungal pathogens cause huge losses to food and fibre crops globally”

Can we feed an estimated 9.7 billion people by 2050? Other than the increasing demand for food and fibre, changing global climate patterns may mean that certain crops will have to be planted in other areas, and that many former agricultural regions will suffer severe climate shifts in coming years. Linked to this we are also seeing a shift in disease problems, as new diseases emerge, some being caused by fungi that are now better suited to attack these host plants, or are introduced to new environments on non-native hosts. To combat plant disease without simply applying huge amounts of broad-spectrum fungicides, it is paramount to know which pathogens are present, how they interact with one another, and to which fungicides they are sensitive. Global trade remains essential for the world economy, but linked to this is the concern of protecting markets from alien pathogens, and monitoring the spread of mating types and clones of known plant pathogens. Rapid detection, based on data obtained from curated databases linked to strains authentic for the organism, and accurate identification of pathogens of quarantine concern, remain important pillars for global food security.



HIGHLIGHTS

The genera *Alternaria*, *Bipolaris*, *Ceratocystis*, *Colletotrichum*, *Pestalotiopsis*, and *Pyricularia* are linked to devastating diseases of staple food crops globally, several of them also representing important quarantine organisms. Furthermore, from these studies we concluded that many important genera of plant pathogenic fungi are paraphyletic, while many common pathogens still have numerous unnamed lineages, some restricted to specific continents, appearing to be distinct cryptic species. Crous & Groenewald (2014). *Studies in Mycology* **79**: 1–288.



The *Hypocreales* contains many important plant pathogenic fungal genera. One of these is *Calonectria*, which represents a serious threat to the growth and sustainability of plantation forestry of *Eucalyptus* in tropical and subtropical regions of the world. Another genus is *Fusarium*, which is associated with numerous plant diseases, including pitch canker disease of *Pinus* spp. The genus *Fusarium* is however polyphyletic, and represents several genera within *Nectriaceae*. Lombard *et al.* (2015). *Studies in Mycology* **80**: 1–245.

Naming species of plant pathogenic fungi has always represented a major challenge, especially as the evolutionary units evolve at different rates in different genera and families, but still could operate as distinct species units in nature. These issues are addressed in *Alternaria*, *Cladosporium*, as well as several genera in *Didymellaceae* and *Pleosporales*. Crous & Groenewald (2015). *Studies in Mycology* **82**: 1–217.



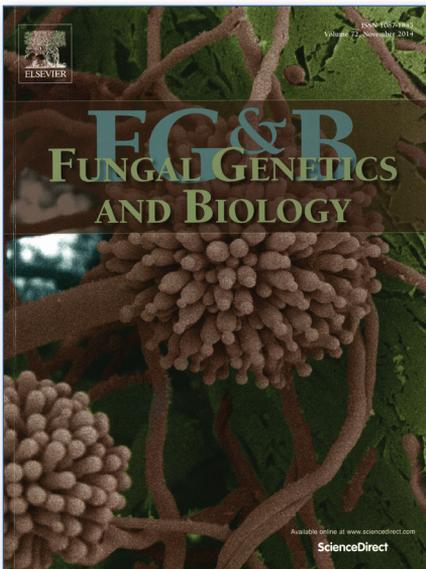
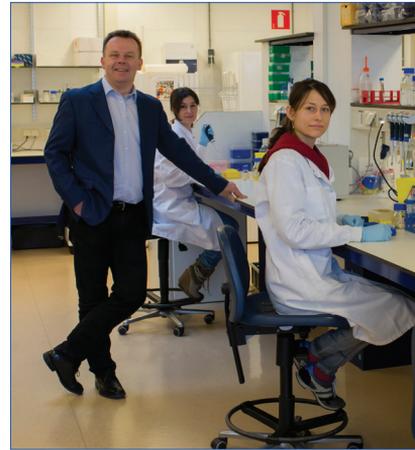
FUNGAL PHYSIOLOGY

Prof. dr ir Ronald de Vries

“We work in close collaboration with other academic institutions and with industry”

The Fungal Physiology group aims to unravel the molecular mechanisms that affect fungal physiology on natural substrates (extracellular enzymes, regulatory systems, metabolism) using a limited number of model species (*Aspergillus niger*, *Aspergillus nidulans*, *Trichoderma reesei*, *Dichomitus squalens*, *Myceliophthora thermophila*). These insights are subsequently used to perform comparative studies on a larger group of species covering the *Ascomycota*, *Basidiomycota* and *Zygomycota*. Comparative genomics, transcriptomics and proteomics have become valuable tools in our studies alongside more traditional methods in molecular biology, genetics and biochemistry. The expertise of the group is further strengthened through strategic collaborations with researchers from several other academic institutions.

Part of our research focuses on fundamental questions of fungal biology while other projects are more closely linked to industrial applications, such as improving enzyme production, enzyme discovery using a combination of comparative genomics and growth profiling, or improving mushroom production. In the latter projects we work in close collaboration with industry.



HIGHLIGHTS

In 2014 a Special Issue of the journal *Fungal Genetics & Biology* on Biomass Degradation by Fungi was edited by Ronald de Vries, Dr. Miia Mäkelä from University of Helsinki (Finland) and Dr. Nicole Donofrio of University of Delaware (USA). This issue highlighted the current state and width of this field of research with papers on ascomycetes, basidiomycetes and oomycetes, including model fungi, saprobes and plant pathogens. *Fungal Genetics and Biology* (2014) Vol. 72.

Isabelle Benoit and Ad Wiebenga, together with other group members and external collaborators, demonstrated that, despite high similarity in their genome content, eight *Aspergillus* species use highly different enzymatic approaches for the degradation of plant biomass. These insights will help the design of better commercial enzyme cocktails for biofuel production. Benoit *et al.* (2015). *Biotechnology for Biofuels* 8: 107.

In 2014 Ronald de Vries was appointed as Professor in Fungal Molecular Physiology at Utrecht University and on February 27th,

2015 his inaugural lecture was linked to the first Symposium on Plant Biomass Utilization by Fungi. The symposium was attended by over 150 people with more than 1/3 of them from abroad, and featured seven of the top scientists of the field. The symposium will likely become a biennial event.



APPLIED AND INDUSTRIAL MYCOLOGY

Prof. dr dr h c Rob Samson

“Fungi in the food we eat and in the air we breathe”

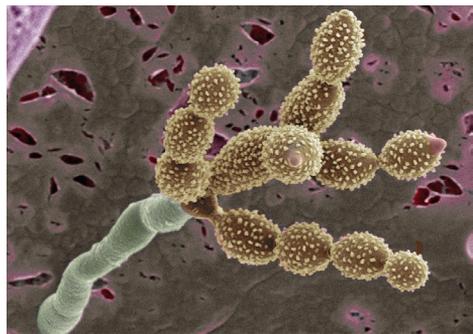
A large part of food on the world is degraded by fungi before consumption. These fungi are also a threat for health as producers of mycotoxins. In addition, fungi also grow indoor on building materials after water damage or in bathrooms. Food- and indoor fungi can sometimes be pathogenic to immunocompromised patients or can be the cause of allergic reactions. Our group studies food-spoiling and indoor fungi including the taxonomy of the genera *Aspergillus*, *Penicillium*, *Talaromyces* and *Paecilomyces*. These genera contain species that can cause a lot of damage to food crops, but also are used as industrial work horses in food fermentation, and as producers of many metabolites and enzymes. A stable classification and taxonomy is essential for all those applied researchers working in these fields. In our group we do research on all aspects discussed above (food fermentation, spoilage, stress resistance, indoor growth and novel metabolites) on a fundamental and applied level.



HIGHLIGHTS

New taxonomic insights in *Aspergillus*, *Penicillium* and *Talaromyces*

The taxonomic studies on the important genera were continued and with the polyphasic taxonomic concept we demonstrate that these common genera show a high biodiversity. Important papers on the species concept, methods for taxonomic classification and identifications have been published. Lists of names following the single nomenclature were proposed and this will help the user in applied mycology to use a stable naming of the many species. Although in many taxa the phylogenetic distinction between species can be supported by phenotypic differentiation, in some groups or complexes this is more troublesome. Much attention will be given to discover if morphological and physiological differences can be found to facilitate a correct identification.



Fungal biodiversity of indoor fungi

Much research has been performed together with the Biodiversity (Mycology and Microbiology) Centre of Agriculture and Agri-Food Canada (Ottawa) to elucidate the biodiversity of fungi in indoor environments supported by a generous grant of the US Alfred Sloan Foundation. The aim is to put names on new species, genera and families of fungi occurring in the built environment, and to generate reference material for other scientists studying genomics and metagenomics (including metabarcoding) in the built environment. The reference material includes both cultures and DNA barcodes. In addition much emphasis is given to the xerophilic nature of common indoor fungi and the first results show that xerophily is very common among these fungi.

Segers *et al.* (2015). Xerotolerant *Cladosporium sphaerospermum* are predominant on indoor surfaces compared to other *Cladosporium* species. *PLoS ONE* **10** (12): 1–15.

Samson *et al.* 2014. Phylogeny, identification and nomenclature of the genus *Aspergillus*. *Studies in Mycology* **78**: 141–173.

Visagie *et al.* 2014. Identification and nomenclature of the genus *Penicillium*. *Studies in Mycology* **78**: 343–371.

ECOLOGY OF CLINICAL FUNGI

Prof. dr Sybren de Hoog

“Human-pathogenic fungi may show epidemic behaviour, with large consequences for public health”

Until recently it was thought that most fungal infections are coincidental, single-event inoculations. However, spatial and temporal distances between infections have masked epidemic behaviour. Some epidemics, such as sporotrichosis are even enormous, with several thousands of patients within a few years. Large differences in epidemic patterns can be observed even between closely related species. *Sporothrix brasiliensis* in southeast Brazil is a zoonosis transmitted by cats, while in China the thousands of cases caused by *S. globosa* are a sapronosis, probably originating from fermenting plant debris. Clonal expansions may have very different public health implications, because plant debris can be removed, while it is not possible to kill all stray cats of Rio de Janeiro. Pathogens may emerge within a very short time span: the Brazilian *Sporothrix* species is known only since a few decades. Similarly a sudden emergence of emmonsia-like systemic pathogens is observed causing a striking disease with pulmonary symptoms and a high case fatality rate. The first of these cases were seen only three decades ago and now have taken epidemic proportions in South Africa with several dozens of deaths. Early recognition and appropriate therapy of these new and emerging pathogens has to be developed with high priority.



HIGHLIGHTS

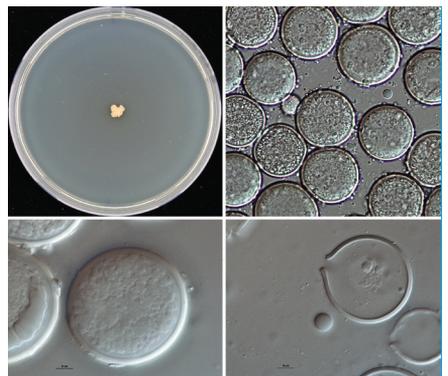


Using the epidemic distribution patterns of *Sporothrix* species it was possible to identify historical cases with high confidence even in the absence of live specimens, and to reconstruct epidemics by these species in the past. Epidemic expansion is characteristic for all *Sporothrix* species.

Zhang *et al.* (2015). Phylogeography and evolutionary patterns in *Sporothrix* species with a pathogenic potential. *Persoonia* **35**: 1–20; Teixeira *et al.* (2015). Asexual propagation of a virulent clone complex in a human and feline outbreak of sporotrichosis. *Eukaryotic Cell* **14**: 158–169.

Several emmonsia-like systemic pathogens are emerging since three decades, while *Emmonsia* earlier was just known from insignificant pulmonary colonization of small terrestrial mammals. It is the first time that not just species, but entire genera of human pathogens are emerging.

Schwartz *et al.* (2015). 50 years of *Emmonsia* in humans: the dramatic emergence of a cluster of novel fungal pathogens. *Plos Pathogens* **11**(11):e1005198; Feng *et al.* (2015). Disseminated infections caused by *Emmonsia pasteuriana* in a renal transplant recipient: A case report and review of literature. *The Journal of Dermatology* **42**: 1179–1182.



Asian fermented food is prepared with the aid of mucoralean fungi, of which 11% carry intracellular bacteria which produce rhizoxin, a carcinogenic toxin. It is recommended to verify if soy-based products are free of these toxins.

Dolatabadi (2015). *Mucorales* between food and infection. PhD Thesis, Amsterdam.

COLLECTION

Dr Gerard Verkleij

“Fungal genetic resources for research, development and education”

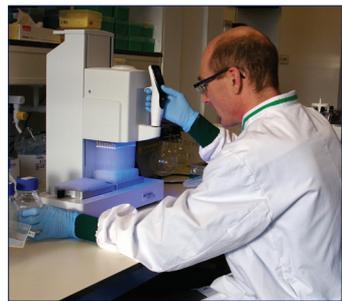
The CBS Collection is the largest public service collection of living fungi in the world. It was established in 1904. Today the collection is a Biological Resource Centre (BRC) holding 69,000 strains of filamentous fungi and 10,500 yeasts strains. The BRC also preserves 10,000 strains of the NCCB Collection of bacteria, plasmids and phages. In the period 2014–2015, CBS acquired near 4,850 new cultures, and supplied 8,600 strains to scientists in 70 countries. CBS also accepts safe deposits of microorganisms and deposits for the purpose of patent procedures under the Budapest Treaty. The online strain catalogue provides access to information on available cultures, as well as tools to identify fungi and yeasts by sequence BLAST and phenotypic analyses. All these services are ISO 9001:2008 certified.



HIGHLIGHTS

DNA Barcodes for all fungi and yeast strains – a milestone in the history of CBS

In the DNA Barcoding project financed by the Dutch Ministry of Education, Culture and Science, and the KNAW, a high throughput DNA-barcoding pipeline including an in-house sequencing facility and LIMS system was set up that now has produced DNA barcode sequences (ITS and LSU nrDNA) of all fungal strains in the CBS Collection. By the end of 2015, over 90,000 strains had been extracted and sequenced. Thus, an invaluable body of data has been created which will be used for quality control by the Collection and selection of strains relevant to the field of applied genomics. Activities will continue for some time to validate all barcodes generated in this project, and new ones will be continuously added as new accessions go through the pipeline for quality control purpose. The barcode sequences of public strains will be made available to the scientific community as reference sequences and for strain identification. The number of CBS strains for which full genome sequences are available is also rapidly growing. In collaboration with the CBS Yeast research group seven gene regions of all ascomycetous yeast type strains are being sequenced. One of the main purposes of this project is to revise the taxonomic classification of *Candida* species.



International collaboration

CBS is partner to the EU funded project Microbial Resource Research Infrastructure (MIRRI), a “Preparatory Phase” project under ESFRI (2012–2015). CBS led Workpackage 9, which focused on the preparation of a legal operational framework for collections and biosecurity. To implement the Nagoya Protocol on Access and Benefit Sharing (ABS) and the EU Regulation 511/2014 in mBRCs, workshops were organised

and a Policy and Best Practice developed. The MIRRI Consortium is preparing for a legal ERIC status. Other EU-funded projects where CBS is involved include the Preparatory Action for Plant and Animal Genetic Resources (2014–2016) and CORBEL (2015–2019), a new initiative of eleven biological and medical RIs, to create a platform for harmonised user access to technologies, biological samples and data services for cutting edge biomedical research.

Securing high-impact research collections

In 2014–2015 CBS incorporated many strains from the marine yeast collections of Jack Fell and the collection of dematiaceous hyphomycetes of the late Emory Simmons, to ensure their availability for future reference and research.

“Fungal thermal tolerance and climate change”

In terms of fungal virulence in mammals, thermal tolerance can be defined as the ability to grow in the 35°C to 40°C range. We used archival information in a fungal collection to analyze the relationship between thermal tolerance and genetic background for over 4,289 yeast strains belonging to 1,054 species. Fungal genetic relationships were inferred from pairwise alignments using ITS and LSU sequences. Thermal tolerance for growth at mammalian temperatures was not monophyletic, with thermally tolerant species being interspersed among families that include closely related species that are not thermal tolerant. Thermal tolerance and resistance to antifungal drugs were not correlated, suggesting that these two properties evolved independently. Nevertheless, the ability to grow at higher temperatures did correlate with origin from lower geographic latitudes, capacity for fermentation and assimilation of certain carbon sources. Thermal tolerance was significantly more common among ascomycetous than basidiomycetous yeasts, suggesting an explanation for the preponderance of ascomycetous yeasts among human pathogenic fungi. Analysis of strain maximum tolerable temperature as a function of collection time suggested that basidiomycetous yeasts are rapidly adapting to global warming. The analysis identified genera with a high prevalence of the thermal-tolerant species that could serve as sources of emerging pathogenic fungi.



HIGHLIGHTS

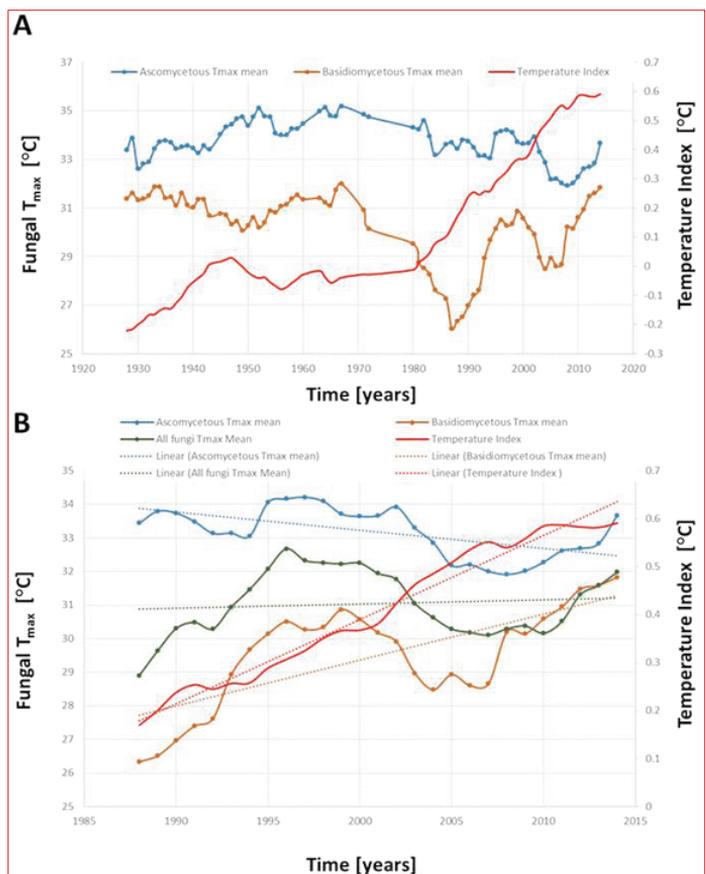
Vu *et al.* (2014). Massive fungal biodiversity data re-annotation with multi-level clustering. *Scientific Reports* 4, Article number: 6837. doi:10.1038/srep06837.

Robert *et al.* (2015). Distribution and impact of yeast thermal tolerance permissive for mammalian infection. *BMC Biology* 13: 18 DOI: 10.1186/s12915-015-0127-3.

Stielow *et al.* (2015). One fungus, which genes? Development and assessment of universal primers for potential secondary fungal DNA barcodes. *Persoonia* 35(1): 242–263.

Data storage and analysis

Our group has been and will continue to work on the creation and the maintenance of reference databases (including all possible meta data and genomes) and algorithms that allow fast and reliable identifications and data analyses of large datasets. We have developed new clustering algorithms that are much faster and accurate than the existing ones. We are now developing new methods to store and analyses large amounts of data, including complete genomes. These are huge challenges given the complexity and the diversity of fungal genomes.



Trends in strain Tmax over time. (A) Trend of fungal maximum temperature of growth Tmax during the last century, compared with the global temperature index. The fungal Tmax reported was calculated from a 10-year mobile mean. The temperature index is the global mean land-ocean temperature index, 1880 to present, with the base period 1951 to 1980. (B) Regression analysis of fungal Tmax and the global temperature index during the last 30 years.

YEAST RESEARCH

Dr Teun Boekhout

“An updated new classification for the basidiomycetous yeasts”

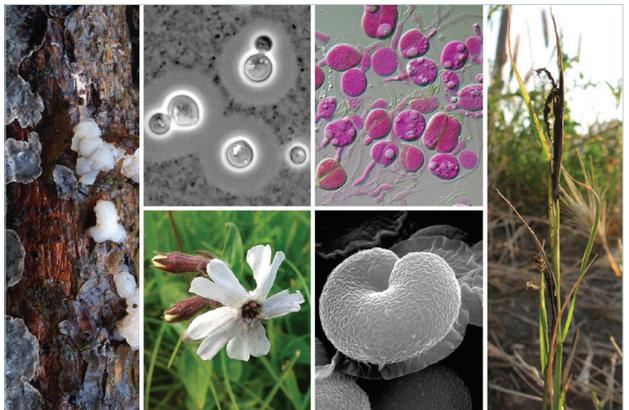
Yeast biodiversity is expanding rapidly. Due to the existing molecular barcoding databases, novel isolates can be readily identified. Also species new to science are being described with an increasing pace (Kurtzmann *et al.* 2015, FEMS Yeast Research 15(6). pii: fov050. doi: 10.1093/femsyr/fov050. Epub 2015 Jun 30). Yet we have to realize that many areas and habitats on earth have not been explored. Yeasts bring many benefits to mankind, e.g. as they are involved traditional and modern fermentations, production of highly valuable compounds, biofuels, roles in biocontrol, and bioremediation. In contrast, some yeast species are also known as important human pathogens. The taxonomy of yeasts was largely based on phenotypic traits and this has resulted in a largely artificial classification. Together with colleagues from the Institute of Microbiology, Chinese Academy of Sciences, we performed a multigene-based phylogenetic study of almost all basidiomycetous yeasts, including some of their filamentous growing relatives [projects KNAW 10CDP019 and NSFC 31010103902].



HIGHLIGHTS

New updated taxonomy for the basidiomycetous yeasts and the *Cryptococcus neoformans* / *C. gattii* species complex

The taxonomy of the basidiomycetous yeasts was revised based on a phylogenetic analysis of multiple genes. Several traditionally recognized genera of basidiomycetous yeasts were highly polyphyletic, e.g. *Cryptococcus* and *Rhodotorula*. In *Tremellomycetes* (*Agaricomycotina*) five orders contain yeast taxa, namely *Cystofilobasidiales*, *Filobasidiales*, *Holtermanniales*, *Tremellales* and *Trichosporonales*. The polyphyletic mushroom-forming genus *Tremella* is also reclassified in part. Within *Pucciniomycotina* five classes contain taxa with a dominant yeast stage, namely *Agaricostilbomycetes*, *Cystobasidiomycetes*, *Microbotryomycetes*, *Mixiomycetes* and the newly recognized class *Spiculogloeomycetes*. Within *Ustilaginomycotina* yeast and yeast-like taxa occur in four classes: *Exobasidiomycetes*, *Malasseziomycetes*, *Moniliellomycetes* and *Ustilaginomycetes*. In total 46 new genera and 325 new combinations have been proposed.



Cover picture from *Studies in Mycology* 81. Photo's courtesy Ibai Olariaga, Ferry Hagen, Ana Millanes, Andrey Yurkov and Jack Fell.

Studies in Mycology 81 (2015). Multigene phylogeny and reclassification of yeasts and related filamentous taxa in *Basidiomycota*, T. Boekhout, F.-Y. Bai (Eds).

In addition, the taxonomy of the pathogenic species complex *Cryptococcus gattii* / *Cryptococcus neoformans* species complex was revised. Seven species have been recognized. The type strain of *C. neoformans* CBS132 represents a *C. neoformans* × *C. deneoformans* hybrid and is replaced. The newly delimited species differ in aspects of pathogenicity, prevalence for patient groups, as well as biochemical and physiological aspects, such as susceptibility to antifungals. MALDI-TOF mass spectrometry readily distinguishes the newly recognized species.

Hagen *et al.* (2015). Recognition of seven species in the *Cryptococcus gattii* / *Cryptococcus neoformans* species complex. *Fungal Genetics and Biology* 78: 16–48.

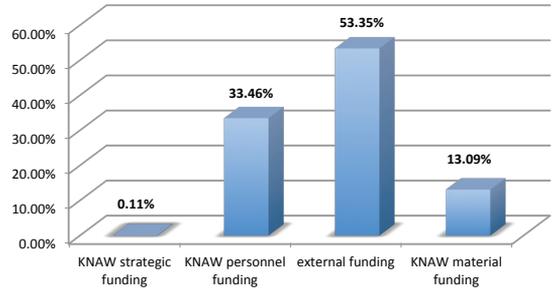
FINANCES AND STAFF

“75 % of CBS total expenditure is spent on direct research costs”

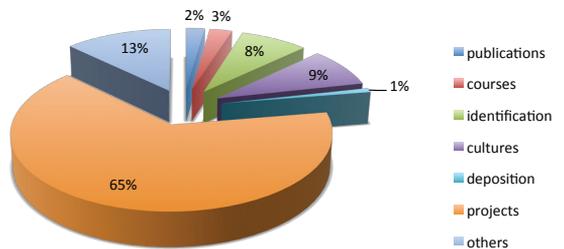
INCOME

The CBS-KNAW Fungal Biodiversity Centre has a total income of 6,46 million Euros. Approximately 50 % of this amount is funded by the KNAW. The subsidy of KNAW strategic funds is used for initiating innovative research projects.

income 2014 (x €1000)



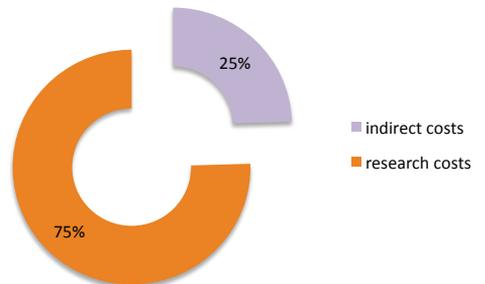
The external funding - 3,26 million Euros - is generated mainly from (applied) research projects and regular activities, such as book sales, training and courses, identification/sales of fungi and bacteria. The “Odo van Vloten” Foundation finances one Postdoc research project.



EXPENDITURES

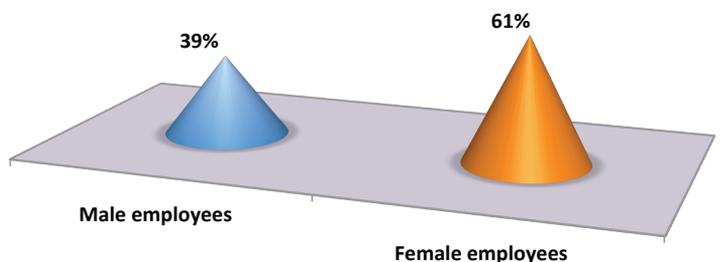
The total expenditure of the CBS consists mainly of salaries (67 %). Non-personnel costs are costs of materials, housing, depreciation of durable equipment, and intangible assets e.g. software.

Three-quarters of expenditures can be indicated as direct research costs. Indirect costs are for management and for the collective support division of the CBS and the Hubrecht Institute (HI).



STAFF

The CBS had 64 employees on December 31, 2014, with an equivalent of 58 fulltime staff (fte): both researchers and support staff (analytical/technical/administrative). A considerable part of the support staff is involved in the applied research division and preservation and digitalisation of the collection. Approximately 50 students and guest researchers (researchers with an official appointment other than the CBS) have been working at the CBS in 2014 for > 1 month.



In total, 61 % of the employees are female, and 39 % are male. On average female employees are working four days, while male employees work five days a week.

The collective support division CBS/HI employs 32 people with a fulltime equivalent of 30.3 fte, with approximately 8 fte effectively working for the CBS.



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