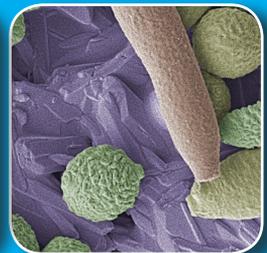
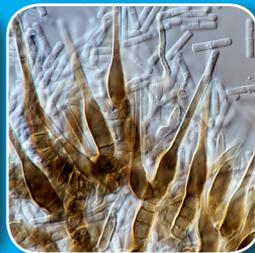
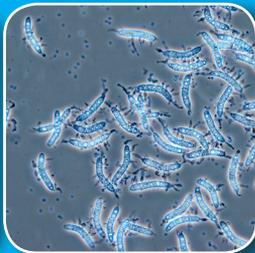
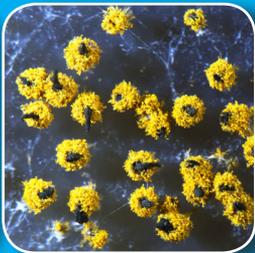
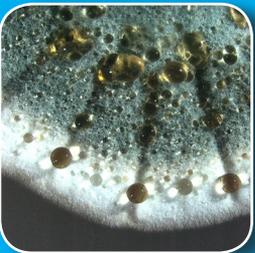
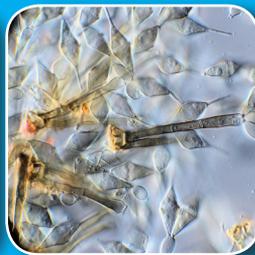


WESTERDIJK  
FUNGALBIO  
DIVERSITY  
INSTITUTE

# Progress Report

## 2016–2018



KONINKLIJKE NEDERLANDSE  
AKADEMIE VAN WETENSCHAPPEN

# EXPLORE, STUDY AND PRESERVE: FACILITATING FUNGAL FUTURES

The current reporting period was characterised by an extraordinary range of exciting activities. Three new group leaders were appointed, namely Jos Houbraken (Applied and Industrial Mycology), Ferry Hagen (Medical Mycology), and Jérôme Collemare (Fungal Natural Products). Houbraken took over the reins of Applied and Industrial Mycology from Rob Samson, while a new *Fungal Network* project was launched for Collemare, focusing on antibiotics and antifungals, and a *Clinical Mycology Utrecht* collaborative project was initiated by Hagen, working with the University Medical Center Utrecht and the Princess Máxima Center, focusing on rapid clinical diagnostics.

The past period also saw us rounding off the DNA barcoding project of the biobank, and releasing thousands of previously unpublished DNA barcodes to facilitate mycological research globally.

The Westerdijk year kicked off on February 10 (2017) at 14:00, which was exactly 100 years since Johanna Westerdijk (our first director, 1906–1959; 53 years!) was inaugurated as the first female professor in the Netherlands, and at the same time our name “Centraalbureau voor Schimmelcultures” changed to the Westerdijk Fungal Biodiversity Institute (WI). The Westerdijk year (with celebratory coffee mug, *Westerdijkella centenaria* sp. nov.), was characterised by numerous symposia, and a diverse range of public meetings and lectures. Using crowd funding, we were able to commission a bronze statue of Johanna Westerdijk, the unveiling of which coincided with the inauguration of the new research wing of the WI in August of the same year.

To complement our flagship journal *Studies in Mycology*, 2018 also saw the launch of a new open access journal, *Fungal Systematics and Evolution* (FUSE), with a clear focus on fungal systematics, aiming to expedite the naming of new fungal taxa, and further expand the fungal biobank. The past period also saw us strengthen our public engagement activities with the launch of a Citizen Science project whereby school children visiting a fungal exhibition in the Utrecht University Museum, received a kit to sample soil from their home gardens. Once the samples were received, all cultivatable fungi were isolated, and new taxa subsequently named after the schools, families or collectors, leading to extensive coverage on television, radio and other news media. Future initiatives are already afoot to generate whole genomes of these fungi, and to screen them for novel activities which could ultimately culminate in new products. These genomes provide valuable information to help understanding of fungal biology, diseases, treatments, the bioeconomy, novel metabolites, enzymes etc., and can contribute to solving some of the major health and food issues facing humanity. Now that we have DNA barcodes for the entire biobank, a major challenge for the WI



in the coming years will be to generate genomes of all species that are known to play a major role in agriculture, industry, or health. At the WI we preserve an incredibly valuable asset, but we also need to strive to unlock this resource in the best way possible, as only such a bold vision will help us to better understand life on this planet.

Last but not least, we are incredibly happy to announce that our bid to host the International Mycological Congress (IMC12) of the International Mycological Association (25–29 July 2022) in Amsterdam was successful! Preparations are already underway for IMC12, which promises to be a life-changing experience. I hope to see you there!

*P.W. Crous*

Prof dr Pedro W. Crous  
Director: Westerdijk Fungal Biodiversity Institute

<b>Scientific output</b>			
Output type	2016	2017	2018
Papers	195	164	152
Chapters in books	8	6	13
Books	1	1	1
Dissertations	6	3	9
<b>Services</b>			
Service type	2016	2017	2018
Aquisition new strains	1796	1961	1958
Identifications	432	254	156
Deposition patent strains	173	81	134
Dispatch of fungal strains	5068	4990	5699
Dispatch of DNA samples	-	100	620
<b>MycoBank</b>			
Internet visits	2016	2017	2018
MycoBank unique visitors	318K	368K	437K

# EVOLUTIONARY PHYTOPATHOLOGY

Prof dr Pedro Crous

## Fungal pathogens pose a major threat to plant health

Current estimates indicate that by 2050 the largest explosion in the world's population growth will be occurring in Africa, which is already stricken by drought and famine. The increasing demand for food, linked to changing global climate patterns, also indicates that the fungal



diseases prevalent in certain regions will change along with the climate. We already see a shift in disease problems, as new diseases constantly emerge, either from previously less important pathogens, or from pathogens newly introduced into areas where they are non-native. To combat plant disease, it has become imperative that plant pathologists know exactly 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 results in pathogens getting introduced into areas where they are non-native. Rapid and accurate detection of plant pathogens remain paramount for global food security.



CBS symptoms on fruit in South Africa

### HIGHLIGHTS

*Phyllosticta citricarpa* is the causal agent of Citrus Black Spot (CBS) disease, and is a pathogen of quarantine concern in Europe. Although the pathogen affects fruits and leaves of several citrus hosts (*Rutaceae*), the present study showed that it could also be present as a harmless endophyte in citrus leaf litter collected in several European countries. This finding underlines the fact that simple visual inspections are no longer sufficient to determine presence or absence of quarantine organisms. Guarnaccia *et al.* (2017). *Studies in Mycology* **87**: 161–185.

Genera of Phytopathogenic Fungi (GOPHY) was introduced as a new series of publications in order to provide a stable platform for the taxonomy of phytopathogenic fungi. This first paper treated 21 genera of phytopathogenic fungi, providing primary and secondary DNA barcodes of the presently accepted species for each genus, and relevant literature. Marin-Felix *et al.* (2017). *Studies in Mycology* **86**: 99–216.



*Exserohilum* includes a number of plant pathogenic, saprobic and clinically relevant fungi, one of which has been linked to the death of several humans in the USA. In this study, *Exserohilum* was revised based on available ex-type cultures from worldwide collections, leading to the acceptance of 11 species, with the human pathogen being identified as *E. rostratum*. Hernández-Restrepo *et al.* (2017). *Persoonia* **41**: 71–108.

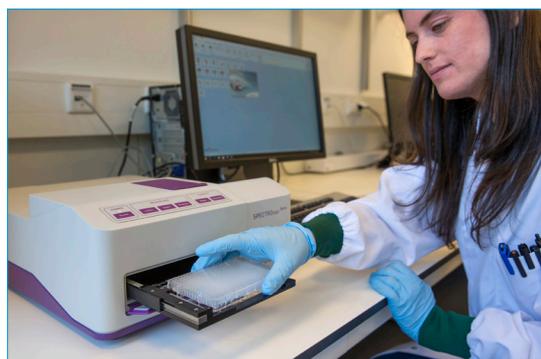


# FUNGAL NATURAL PRODUCTS

Dr Jérôme Collemare

## The fungal kingdom is an underexploited resource of bioactive molecules

Fungi produce natural products known as secondary metabolites (SMs) that have had significant impact on human societies. The most famous fungal SM is the broad-spectrum antibiotic penicillin, which provided the first effective treatment of bacterial infection and revolutionized modern medicine. Fungal SMs play important roles not only in healthcare, but also in agriculture and industry. These small molecules can also be harmful to human and cattle as many plant pathogenic fungal species produce SM mycotoxins that are responsible for acute intoxications. Although fungi have provided us with life-changing compounds, the fungal kingdom has remained underexploited. The genomic era has revealed that fungal genomes encode many more biosynthetic pathways than the number of known SMs. This is due to the tight regulation of the expression of these pathways under very specific conditions that are difficult to reproduce in the laboratory. The Fungal Natural Products group aims to identify novel compounds and understand their biosynthesis in order to provide solutions for healthcare, industry and agriculture. More specifically, the objectives are to (i) exploit the biodiversity of the Westerdijk fungal bioresource and of fungal genomes to identify new compounds; (ii) elucidate their biosynthesis; (iii) determine the evolution of biosynthetic pathways; and (iv) characterize the role of SMs in fungal biology.



For these purposes, we employ a multi-disciplinary approach that combines bioinformatics, genomics, molecular biology, bioassays and chemistry. The group also actively collaborates with other national and international research groups, in particular with experts in bioinformatics and organic chemistry of fungal SMs. The research focuses on fundamental questions with potential societal applications, such as developing new antibacterials, antifungals or dyes of fungal origin.

### HIGHLIGHTS

August 1<sup>st</sup> 2017 was the start of the new Fungal Natural Products group, which is now composed of experts in bioinformatics (notably Dr Jorge Navarro, Odo van Vloten postdoc) and molecular biology. The group has invested in an analytical HPLC-MS system, jointly with the group of Prof dr J. den Hertog from the Hubrecht Institute. The two groups further collaborate, together with Utrecht University, on the search for new antifungal compounds by screening a collection of more than 10 000 fungal extracts against human and plant pathogens of importance.

The Fungal Natural Products group obtained the joint KNAW Research Fund in 2017 to identify and engineer novel antimicrobials. In March 2018 the group welcomed its first PhD student to work on this project. The *Lecanoromycetes* is a class of fungi that are not extensively studied, yet their genome contains a high number of unknown SM biosynthetic pathways. Using a comparative genomic approach, novel biosynthetic pathways have been identified and will be expressed in the heterologous host *Aspergillus oryzae* to produce new compounds.



Fungi produce SM pigments for protection against environmental stresses, including UV light and cold temperatures. The production of melanin is conserved in many fungal species, but the assignment of the biosynthetic pathway was not clear in a few fungi. A comparative genomics study revealed the accurate pathway assignment in these fungal species, highlighting the importance of combining phylogenetic analyses and heterologous expression for accurate assignment of biosynthetic genes to compound production. Griffiths *et al.* (2018). *PLoS One* **13**(12): e0209600.

# FUNGAL PHYSIOLOGY

Prof dr ir Ronald de Vries

## ***We aim to understand molecular mechanisms of fungi to support the biobased economy***

**T**he Fungal Physiology group aims to unravel the molecular mechanisms that affect fungal physiology on natural substrates (focussing on extracellular enzymes, regulatory systems and metabolism) and apply this knowledge to develop strains and enzymes to support the biobased economy. By answering fundamental questions of fungal biology we generate insights that provide the basis for more applied projects, such as improving enzyme production, discovery of novel enzymes, or metabolic engineering. This is often performed in close collaboration with industrial partners. Our in-depth studies focus on a small number of model or reference species (*Aspergillus niger*, *Aspergillus nidulans*, *Trichoderma reesei*, *Dichomitus squalens*, *Penicillium subrubescens*) and results from those studies are subsequently used in comparative studies across the fungal tree of life. We use diverse methodologies, including comparative genomics, transcriptomics and proteomics, as well as traditional and cutting edge (e.g. CRISPR/Cas9) 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.



### **HIGHLIGHTS**

In 2017 a paper on a genomic comparison of 17 *Aspergilli* was published in *Genome Biology*. This 45-page paper included 117 authors from 73 Institutions and was the result of a Community Sequence project of the Joint Genome Institute of the Department of Energy of the USA, coordinated by Ronald de Vries. It contained a detailed genomic comparison of these species, supported by an unprecedented amount of experimental data, providing a unique reference for the diversity of fungi on many different important topics, such as secondary metabolism, carbon utilization and stress response. This paper was followed in 2018 by a special issue of *Studies in Mycology*, in which five topics were addressed in more detail. de Vries *et al.* (2017). *Genome Biology* **18**: 28. *Studies in Mycology* (2018) **91**.

In 2017 and 2018, five PhD students of the group (Joanna Kowalczyk, Claire Khosravi, Sara Casado López, Tiziano Benocci, Maria Victoria Aguilar Pontes) successfully defended their thesis. Four of these students were part of the NWO/STW-VICI project awarded to Ronald de Vries in 2013 that addressed the differences in plant biomass degradation of fungi that are either generalists or specialists with respect to their range of substrates. The fifth student (Sara) worked on a project that was a collaboration with Dr Miia Mäkelä of the University of Helsinki and the JGI and EMSL institutes of the Department of Energy, USA, to address the strain-specific genomics, transcriptomics, proteomic and metabolomic differences of the white rot fungus *Dichomitus squalens*. In addition to their theses, the PhD students together produced 30 peer-reviewed papers, with several more still to come.



Ronald de Vries is a PI in a project to genome sequence the entire *Aspergillus* genus, of which the first paper was published in 2018, demonstrating inter- and intra-species variation on several biological aspects in these fungi. This is the first time that a complete genus of filamentous fungi will become available for genome-based comparative projects. Vesth *et al.* (2018). *Nature Genetics* **50**: 1688–1695.

# APPLIED AND INDUSTRIAL MYCOLOGY

Dr Jos Houbraeken

## ***We generate and apply knowledge of fungi in the food and indoor environment***

**T**he relevance of fungal food contaminants and their mycotoxins is ever increasing. They cause food losses worldwide, affect health via the production of numerous mycotoxins, and are responsible for food insecurity in developing countries as they affect food quality. Fungi are also present in the indoor environment, where people spend the major part of their life. Fungal growth causes material deterioration when moisture is available. They affect health as they cause allergic reactions and even can be pathogenic to immunocompromised patients. The species that live on and in food and indoor environments (the mycobiota) are partially the same. Our group studies the taxonomy of the species and genera that occur in these environments, such as *Aspergillus*, *Penicillium*, *Talaromyces*, *Chaetomium* and *Scopulariopsis*. A complete and consistent classification and taxonomy of these important genera is essential for all researchers working in food- and indoor related branches. We also study the effect of various stress factors (e.g. temperature, wateractivity, preservatives) on food- and indoor fungi at a fundamental and applied level. Unique for our research group is the close interaction with industry, where the generated fundamental knowledge is continuously applied via various (tailor made) projects.



### **HIGHLIGHTS**

#### **Biodiversity of food and indoor fungi**

We used a polyphasic taxonomic approach to precisely describe genera and species occurring in foods and indoor environments. These studies resulted in two dedicated volumes in *Studies in Mycology* (84, 88) and numerous publications. In those volumes, the taxonomy of *Microascaceae* (*Scopulariopsis*, *Microascus*, *Cephalotrichum*), *Chaetomiaceae* (*Chaetomium* and chaetomium-like) and *Aspergillaceae* (*Aspergillus* sections *Aspergillus*, *Restricti*, *Nidulantes*) was addressed. These studies generated reference material such as cultures and DNA barcodes for other scientists studying the genomics and metagenomics (including metabarcoding) in these environments.

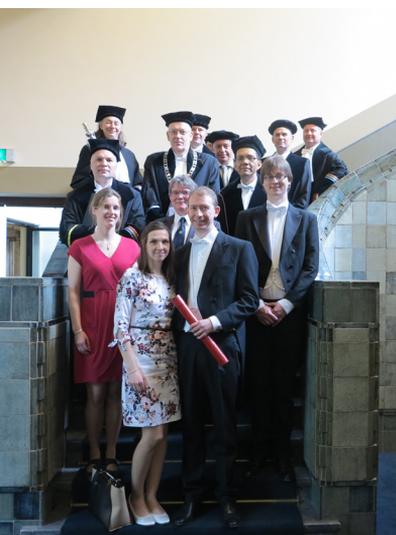


#### **Stress of indoor fungi**

Without water no fungal growth occurs. In a research project in collaboration with Prof O. Adan and Dr H. Huinink (Technical University of Eindhoven) we studied the presence and behaviour of the indoor fungus *Cladosporium halotolerans*. Variations in humidity are characteristic for many indoor environments as a result to human activity. Interestingly, *C. halotolerans* was able to survive variation in humidity markedly better than other fungi, while the lower limit of growth did not differ. Frank Segers defended his Ph.D. thesis on this topic entitled: "Growth of indoor fungi under changing water conditions" on 17<sup>th</sup> May 2017.

Segers *et al.* 2016. The indoor fungus *Cladosporium halotolerans* survives humidity dynamics markedly better than *Aspergillus niger* and *Penicillium rubens*, despite less growth at lowered steady state water activity. *Applied and Environmental Microbiology* **82**: 5089–5098.

Chen *et al.* 2017. Polyphasic taxonomy of *Aspergillus* section *Aspergillus* (formerly *Eurotium*), and its occurrence in indoor environments and food. *Studies in Mycology* **88**: 37–135.



# MEDICAL MYCOLOGY

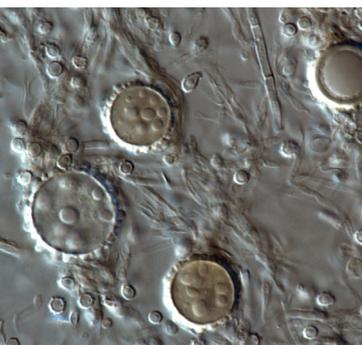
Dr Ferry Hagen

## **Fungal infections have a high mortality rate and we strive to improve diagnostics**

**F**ungal infections are a serious health concern at a global scale. Worrying is that invasive fungal infections affect over 1.5 million individuals annually and have a high mortality rate. Globally, the fungal pathogens belonging to *Aspergillus*, *Candida*, *Cryptococcus*, *Pneumocystis* and *Mucorales* cause the majority of invasive fungal infections. The geographically restricted fungal pathogens that belong to *Coccidioides*, *Histoplasma* and *Paracoccidioides* are also involved in serious fungal infections, often linked to outbreaks. Molecular epidemiology and novel routine diagnostics approaches have increased our insights into these pathogens. Outbreaks with new or otherwise rare fungal species seem to occur more often, including the rise of antifungal (multi)resistant pathogens such as *Candida auris*. There is a need for better conventional and molecular diagnostics to identify these pathogens and understand their antifungal susceptibility. We investigate these emerging novel pathogens using comparative genomics. To reach our goal to improve fungal diagnostics we collaborate with diagnostic laboratories worldwide.



### **HIGHLIGHTS**



*Cryptococcus* is one of the major fungal pathogens. While it has been extensively studied, there is relatively little known about the genetic diversity and antifungal susceptibility of the involved cryptococcal species. We further unraveled the host-pathogen relationship by combining phenotypic and genotypic characteristics, including a new approach to genotype *Cryptococcus* from clinical material.

Herkert *et al.* (2018). Molecular characterization and antifungal susceptibility testing of *Cryptococcus neoformans sensu stricto* from southern Brazil. *Journal of Medical Microbiology* **67**(4): 560–569. doi: 10.1099/jmm.0.000698.

Nyazika *et al.* (2018). Epidemiology and aetiologies of cryptococcal meningitis in Africa, 1950–2017: protocol for a systematic review. *BMJ Open* **8**(7): e020654. doi: 10.1136/bmjopen-2017-020654.

Bauer *et al.* (2018). Case report: A fatal case of cryptococcosis in an immunocompetent patient due to *Cryptococcus deuterogattii* (AFLP6/VGII). *JMM Case Reports* **5**(10): e005168. doi: 10.1099/jmmcr.0.005168.

Hagen *et al.* (2017). Importance of resolving fungal nomenclature: the case of multiple pathogenic species in the *Cryptococcus* genus. *mSphere* **2**(4). pii: e00238-17. doi: 10.1128/mSphere.00238-17.



In collaboration with our global network of reference laboratories, we investigate the fungal epidemiology using molecular and phenotypic approaches to identify new emerging fungal pathogens. The Medical Mycology research group is actively involved in the Clinical Mycology Utrecht network, together with other Westerdijk Institute research groups, the University Medical Center Utrecht, the Princess Máxima Center for Pediatric Oncology, and the Hubrecht Institute. Together with the Clinical Mycology Utrecht network, national and international research, hospital and industry partners, we are improving fungal diagnostics and contribute to the development of guidelines.

# COLLECTION

Dr Gerard Verkley

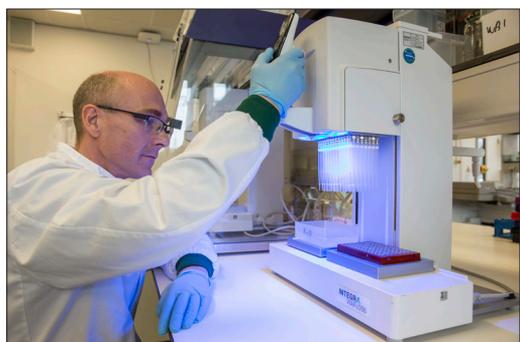
## Trusted and high-quality resources for research, development and education

The Biological Resource Centre (BRC) of the Westerdijk Institute maintains the CBS collection of living fungi (established 1904), and the NCCB Collection, which resulted from a merger in 1998 of unique Dutch collections of wild-type and mutant bacteria, plasmids and phages. In the period 2016–2018 the BRC acquired 5 700 new cultures and supplied 15 800 strains to scientists in 70 countries. The number of type-strains in the CBS collection (see Table) increased by 1 800 in 2016–2018, by means of new deposits and the selection of earlier deposited strains as epi-type or neotype. In addition, the BRC frequently incorporates orphaned research collections. In 2016 a valuable collection of 1 800 yeast strains isolated from insects, was received from Meredith Blackwell. Incorporation of these strains in the CBS yeast collection is ongoing at the moment. 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. The BRC also maintains a closed collection for the deposit of microorganisms for the purpose of patent procedures under the Budapest Treaty, and safe deposits. The BRC is ISO 9001:2015 certified.



### Thousands of DNA Barcodes publically released for type- and other reference strains of fungi and yeast in the CBS collection

With a high throughput DNA-barcoding pipeline including an in-house sequencing facility and LIMS system the BRC produced DNA barcode sequences (ITS and LSU nrDNA) of all fungal and yeast strains in the CBS collection. Two important barcoding papers were published in 2016 and 2018, marking the release of in total 8 700 sequences of 4 730 CBS yeast strains of 1 351 accepted yeast species (80 % of total accepted species), and 24 000 sequences of 7 300 filamentous fungal species, respectively, to the Westerdijk website and GenBank. These released sequences constitute a huge step forward in the coverage of reference sequences of fungal biodiversity. They not only are of great value for strain identification, but also facilitate the selection of strains



### Number of strains preserved in the BRC by the end of 2018

CBS strains	
Filamentous fungi	72 630
Yeasts	12 210
Oomycota	1 894
NCCB strains	
Bacteria	8 810
Actinobacteria	1 283
Plasmids	563
<b>Total</b>	<b>97 390</b>
Type strains	
Filamentous fungi	9 697
Oomycota	263
Yeasts	2 737
<b>Total</b>	<b>12 497</b>

for whole genome sequencing projects, for which the CBS collection is an increasingly important source of material.



### International collaboration

The BRC staff has been involved from the start in building the Microbial Resource Research Infrastructure (MIRRI, [www.mirri.org](http://www.mirri.org)), a pan-european RI of microbial BRCs. The consortium of partners has recently completed a first step submission for an ERIC legal status. The BRC staff were also involved in the Preparatory Action for Plant and Animal Genetic Resources (2014–2016) and CORBEL (2015–2019), an 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.

# BIOINFORMATICS, SOFTWARE DEVELOPMENT AND DATABASING

Dr Vincent Robert

## ***Our databases and algorithms allow fast and reliable identifications and data analyses of large datasets***

The bioinformatics, software development and databasing group works on the creation and the maintenance of reference databases and websites including CBS collections, ISHAM Barcoding and MLST, MycoBank, MIRRI, Q-Bank and other fungal molecular databases. Specific software has been created for the management, the analysis and the publication of large and complex collections of scientific data that is being used at the Westerdijk Institute as well as in many research groups or companies distributed all around the world. We also develop algorithms that allow fast and reliable identifications and data analyses of large datasets. We create new clustering and comparison algorithms that are much faster and accurate than the existing ones. Currently we are developing new methods to store and analyze large amounts of data, including Maldi-Tof profiles or complete genomes. These are huge challenges given the complexity and the diversity of fungal genomes. We are working on the establishment of a new workflow management system and the integration of data analyses pipelines. We are actively participating in several international initiatives and projects. One of them is the EOSC-Life project (25 million Euros) that intends to create an open collaborative digital space for life science in the European Open Science Cloud (EOSC).



### **HIGHLIGHTS**

Vu *et al.* (2019). Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. *Studies in Mycology* **92**: 135–154.

de Vries *et al.* (2017). Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus *Aspergillus*. *Genome Biology* **18**: 28.

Pigmentation is a fundamental characteristic of living organisms that is used to absorb radiation energy and to regulate temperature. Since darker pigments absorb more radiation than lighter ones, they stream more heat, which can provide an adaptive advantage at higher latitudes and a disadvantage near the Tropics, because of the risk of overheating. This intuitive process of color-mediated thermoregulation, also known as the theory of thermal melanism (TTM), has only been tested in ectothermic animal models. We report an association between yeast pigmentation and their latitude of isolation, with dark-pigmented isolates being more frequent away from the Tropics. To measure the impact of microbial pigmentation in energy capture from radiation, we generated 20 pigmented variants of *Cryptococcus neoformans* and *Candida* spp. Infrared thermography revealed that dark-pigmented yeasts heated up faster and reached higher temperatures (up to 2-fold) than paler ones following irradiation. Melanin-pigmented *C. neoformans* exhibited a growth advantage relative to non-melanized yeasts when incubated under the light at 4 °C but increased thermal susceptibility at 25 °C ambient temperatures.



Cordero *et al.* (2018). Impact of yeast pigmentation on heat capture and latitudinal distribution. *Current Biology* **28** (16): 2657–2664. e3.



## Our goal is to guide clinicians in choosing the right treatment

**Y**east biodiversity is economically important. Novel species may exhibit unknown properties that may be of interest in biotechnology, fermentations, and so on. On the negative side, we also witness the emergence of hitherto unknown yeast pathogens. *Candida auris* is a very prominent example of this. In the context of the Opathy ITN (<https://www.opathy.eu/>), a European Training Network in the Horizon 2020 Marie Skłodowska Curie Actions including academia, clinical centres and companies, 13 PhD students are working in seven European countries to improve diagnosis of such yeasts infections. Two students work at the Westerdijk on the improvement of molecular diagnostics of yeast infections, including resistance to commonly used antifungal drugs. For several pathogens, including *C. auris*, PCR protocols and MALDI-TOF MS techniques were developed and tested, including those targeting resistant isolates (see Highlights). In addition, a correlation was found between the phylogenetic affiliations of species and their intrinsic susceptibility profiles that will be further explored to develop diagnostics targeting resistance profiles. During the project, a Winter school was organized together with the SME QVQ on how to valorise the outcome of the Opathy ITN (<https://youtu.be/BhpzZunLa5s>).



### HIGHLIGHTS

To further enhance dissemination of biodiversity-related information on yeasts, an open access platform 'The Yeasts' is in development ([www.theyeasts.org](http://www.theyeasts.org)) with global collaborators and support of International Union of Microbiological Societies (IUMS), Foundation Antonie van Leeuwenhoek and Health-Holland. Next to morphological information and growth profiles, this open access system will also contain molecular barcodes, MALDI-TOF MS spectra and resistance-related sequences to guide clinicians in making the right choice of treatment.

Vatanshenassan *et al.* (2018). *Candida auris* identification and rapid antifungal susceptibility testing against echinocandins by MALDI-TOF MS. *Frontiers in Cellular and Infection Microbiology* (in press).

Arastehfar *et al.* (2018). Novel multiplex real-time quantitative PCR detecting system approach for direct detection of *Candida auris* and its relatives in spiked serum samples. *Future Microbiology* **14**: 33–45. doi: 10.2217/fmb-2018-0227.



Arastehfar *et al.* (2018). YEAST PANEL Multiplex PCR for identification of yeast pathogens: Stepwise diagnostic strategy, useful for developing countries. *Diagnostic Microbiology and Infectious Disease* doi:10.1016/j.diagmicrobio.2018.09.007.

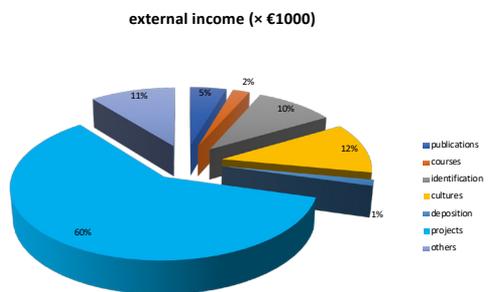
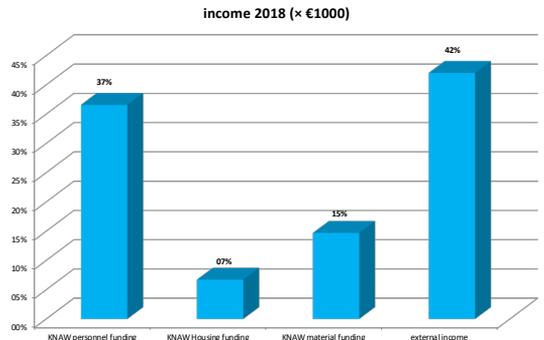
# FINANCES AND STAFF

*The low rate of absenteeism in the institute proves that it is a positive environment in which to work*

## INCOME

The Westerdijk Fungal Biodiversity Institute has a total income of € 6,57 M. Of this amount, 58 % is funded by the KNAW (€ 3,8 M).

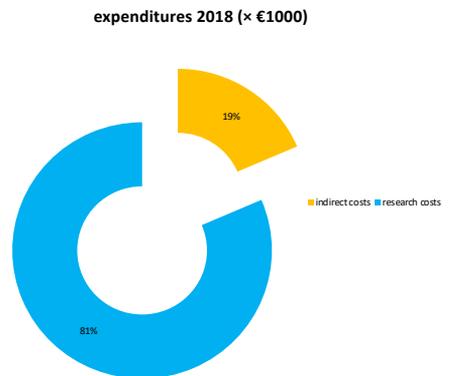
Of the external income, 60 % is related to projects (€ 1,6 M). 29 % (€ 812 K) of the external income is directly or indirectly derived from the collections, and activities such as book sales, training and courses, identification/sales of fungi and bacteria. The “Odo van Vloten” Foundation finances one Postdoc research project.



## EXPENDITURES

The total expenditure of the Westerdijk Fungal Biodiversity Institute (€ 6,8 M) consists mainly of salaries (57 %). Non-personnel costs are costs of materials, housing, and depreciation of durable equipment and intangible assets e.g. software.

81 % of expenditures can be indicated as direct research costs. Indirect costs are for management and for the collective support division of the Westerdijk Fungal Biodiversity Institute and the Hubrecht Institute (HI).



## STAFF

On December 2018 the Westerdijk Institute employed 56,58 FTE in total. Of all employees 28,06 FTE was research staff. 23,83 FTE are analytical and technical support for the research division and preservation and digitalization of the collection. Administrative support is 4,69 FTE. 30,4 FTE (53,2 %) are employed with an appointment for an indefinite period of time.



The gender division of the staff was: female 24,11 FTE. (42,61 %) and male 32,47 FTE (57,39 %). In headcount: female 30 (46,88 %), male 34 (53,12 %).

The Institute employs 3 professors. Ultimo 2018 the Westerdijk Institute employed 8 promovendi and hosted 17 promovendi on a guest status.

The Westerdijk Institute is a good place to work looking at the low rate of sick leave: with 2,28 % annually, it is one of the lowest rates within the Royal Academy.



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“Studies in Mycology” online via Elsevier ([www.studiesinmycology.org](http://www.studiesinmycology.org))

“Fungal Systematics and Evolution” online via Ingenta (<http://fuse-journal.org/>)

Pictures by Westerdijk Fungal Biodiversity Institute & Photographer Thijs Roomans