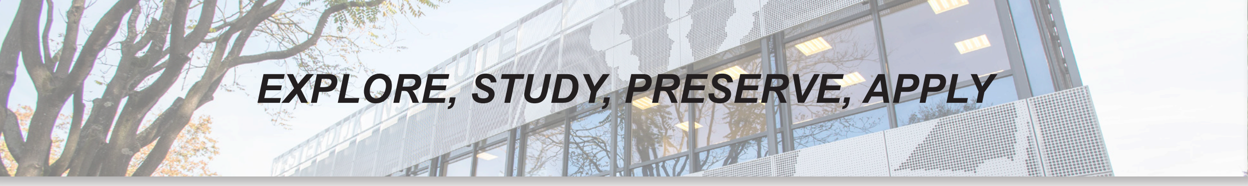
WESTERDIJK
FUNGALBIO
DIVERSITY
INSTITUTE

Progress Report

2021–2022

KONINKLIJKE NEDERLANDSE
AKADEMIE VAN WETENSCHAPPEN



EXPLORE, STUDY, PRESERVE, APPLY

Having successfully transgressed the Covid-19 pandemic, the institute could again proceed to a more “normal” workflow. Our postponed Spring Symposium “Rise of the Fungi” was finally held in April 2022 and will go down in the books as one of the most successful symposia ever. Despite the delay, our institute’s peer review could proceed as a hybrid review, with only some of the panel members physically being present in the institute. Regardless of these hurdles, the institute was rated as “excellent” and based on the recommendations, can now proceed to reposition itself, and start preparing, for the next review in 2027. Another implication of the pandemic was that the International Mycological Congress (IMC12) was postponed to 11–15 August 2024, and relocated to the MECC in Maastricht, as the RAI in Amsterdam could not accommodate these dates. We plan to open the call for symposia and workshops on the IMC12 website (www.IMC12.org) early in 2023.

The jointly organised workshop of the International Commission on Food Mycology (ICFM) and International Commission of Penicillium and Aspergillus (ICPA) was held at the WI from 17–19 July 2022. Studying the relation between food and fungi makes our food safer and reduces food loss and food insecurity. During the meeting, Jos Houbraken was elected chair of ICFM, while Ferry Hagen, our Executive Board member in the Netherlands Centre for One Health (NCOH), was appointed as professor (1 April 2022) in Fungal Functional Diversity at the University of Amsterdam (UvA).

BiodiversityXL, which is a new collaborative venture among the four biodiversity research institutes in the Netherlands (Naturalis Biodiversity Center, the Netherlands Institute of Ecology (NIOO-KNAW), the Royal Netherlands Institute for Sea Research (NIOZ-NWO), and the WI) strives to combat biodiversity loss in the Netherlands. Furthermore, plans are afoot to work together to significantly increase integral knowledge of Dutch biodiversity in all environments: on land, in fresh and saltwater, in the air, and from genes to ecosystems. This cooperation also builds on NWO’s recent investments in the National Roadmap for Large- Scale Scientific Infrastructure. Awards were made for the ARISE project (including Naturalis and the WI) for the construction of a globally unique infrastructure to map all multi-cellular species within the Netherlands and to provide NIOZ’s research fleet with innovative, large-scale scientific equipment. Finally, a Biodiversity Help desk (BiodiversiteitHelpdesk.nl) has been launched to provide a platform where citizens can ask biodiversity-related questions and be redirected to the experts in the various institutes to help them in this regard.

Following the national analysis of Dutch research institutes, a need was identified for the WI to collaborate more closely with NIOO-KNAW in soil microbiology. Our knowledge in fungal biodiversity together with the large number of soil fungi and their associated DNA data in the WI culture collection, as well as the current Citizen Science project, make us an ideal candidate for this collaboration. Although we presently have one such collaborative project (Bill and Melinda Gates Foundation), this has now been strengthened with projects on Asparagus root rot diseases, fungi that play a role in bioremediation, and synthetic ecology. Finally, plans are already proceeding for the next Spring Symposium, which is planned for 17–18 April 2023 in Amsterdam, having the catchy topic “Fungal Evolution”. I hope to see you there!

PWCrous

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

Scientific output		
Output type	**2021**	**2022**
Papers	98	87
Dissertations	1	6
Services		
Service type	**2021**	**2022**
Aquisition new strains	1795	2079
Identifications fungi	264	392
Deposition patent strains	58	48
Dispatch of strains*	3831	3616
Dispatch of DNA samples	197	109
MycoBank		
Internet visits	**2021**	**2022**
MycoBank unique visitors**	227K	482K***
*Fungi, bacteria/actinomycetes, yeasts.		
**Measuring software excludes crawlers and single page users.		
***In 2022 we welcomed users from 194 countries with regular peaks at 4000+ unique users/day.		

EVOLUTIONARY PHYTOPATHOLOGY

Prof dr Pedro Crous

Healthy soils and food security

Soil health is important for good food production. However, global climate change effects, linked to increases in CO_2 concentration, temperature and nitrogen (N) deposition, will affect fungal soil communities, resulting in a shift in disease problems. Correct pathogen diagnosis remains essential to mitigate effective management practices. Global trade in food and fibre will continue to result in unwanted pathogen introductions into areas where they are non-native and could jump over to other important native crops. To ensure global food security, we need to urgently understand soil biodiversity in the context of various human activities in the medium and long term, and how these data could be used to help predict soil health.

HIGHLIGHTS

The *Nectriaceae* includes many lineages with a fusarioid morphology. However, species of *Fusarium s. str.* are characterised by *Gibberella* sexual morphs, asexual morphs with thin- or thick-walled macroconidia that have variously shaped apical and basal cells, and trichothecene mycotoxin production, which separates them from other fusarioid genera. The Wollenweber concept of *Fusarium* presently accounts for 20 segregate genera with clear-cut synapomorphic traits, of which the fusarioid macroconidia represent a character that has been gained or lost multiple times throughout the family. The present study represents the first step to generating a new online monograph of *Fusarium* and allied fusarioid genera (www.fusarium.org). Crous *et al*. (2021). *Fusarium*: more than a node or a foot-shaped basal cell. *Studies in Mycology* **98**: 100116.

This paper is the fourth contribution in the Genera of Phytopathogenic Fungi (GOPHY) series. The series provides morphological descriptions and information about the pathology, distribution, hosts and disease symptoms, as well as DNA barcodes for the taxa covered. Moreover, 12 whole-genome sequences for the type or new species in the treated genera are provided. The present paper in the GOPHY series covers 19 genera of phytopathogenic fungi and their relatives, including *Ascochyta*, *Cadophora*, *Celoporthe*, *Cercospora*, *Coleophoma*, *Cytospora*, *Dendrostoma*, *Didymella*, *Endothia*, *Heterophaeomoniella*, *Leptosphaerulina*, *Melampsora*, *Nigrospora*, *Pezicula*, *Phaeomoniella*, *Pseudocercospora*, *Pteridopassalora*, *Zymoseptoria*, and one genus of oomycetes, *Phytophthora*. This study includes two new genera, 30 new species, five new combinations, and 43 typifications of older names. Chen *et al*. (2022). Genera of phytopathogenic fungi: GOPHY 4. *Studies in Mycology* **101**: 417–564.

Circinotrichum, *Gyrothrix* and *Vermiculariopsiella* represent a complex of dematiaceous, setose, saprobic hyphomycetes that are commonly collected on plant litters in tropical, subtropical to temperate climates. Multi-locus analysis revealed that these genera are polyphyletic, and species belong to 10 genera grouping in three different clades within *Xylariales*, namely *Coniocessiaceae*, *Microdochiaceae* and *Gyrothricaceae*. Hernández-Restrepo *et al*. (2022). Phylogeny and taxonomy of *Circinotrichum*, *Gyrothrix*, *Vermiculariopsiella* and other setose hyphomycetes. *Persoonia* **49**: 99–135.

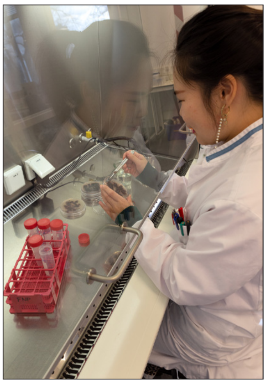
FUNGAL NATURAL PRODUCTS

Dr Jérôme Collemare

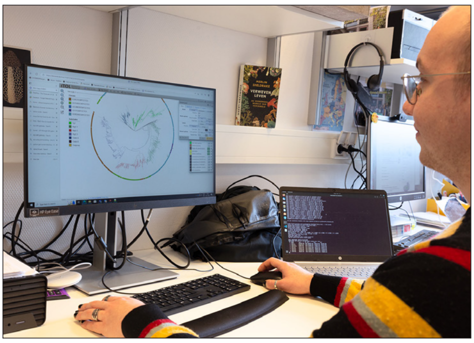
Understanding fungal evolution for the production of novel bioactive compounds

Fungi produce natural products known as secondary metabolites (SMs) that have 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. Although fungi have provided us with life-changing compounds, the fungal kingdom has remained underexploited. The Fungal Natural Products group identifies novel bioactive compounds and elucidates their biosynthesis in order to provide solutions to medicine, industry and agriculture. We generate new fundamental knowledge to identify, characterize and apply fungal natural products. The major objectives are (1) to exploit the biodiversity of the CBS fungal biobank and of fungal genomes to identify new compounds; (2) to elucidate how these molecules are synthesized; (3) to determine how their biosynthetic pathways evolve; and (4) to understand their biological functions. For these purposes, we are using two complementary strategies. On one hand, bioactivity-guided screenings identifies interesting biological activities from the CBS collection. On the other hand, evolution-informed discovery exploits the genomic diversity and synthetic biology tools to characterize and produce novel natural products. These multidisciplinary approaches combine bioinformatics, genomics, synthetic biology, microbiology, bioassays and analytical chemistry. The knowledge generated in the Fungal Natural Products group is serving the long-term objectives of engineering new-to-nature bioactive molecules and developing fungal cell factories for their sustainable fermentation-based production.

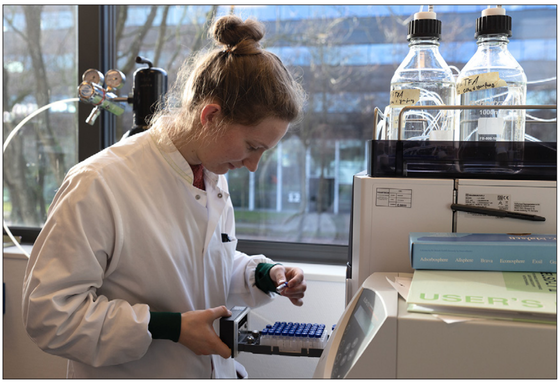
HIGHLIGHTS



After an initial 5-year period, the Fungal Natural Products group is fully established and tenured! Three postdocs, three PhD students, three technicians, and 15 students (MSc, BSc, MBO and HLO levels) have been trained and contributed to this success. The group is recognized internationally and attractive. Guest researchers from all over the world and from different backgrounds in mycology, molecular biology or chemistry visited us to learn about fungal genomics and heterologous expression. With its unique expertise, the group is now leader in genomics and evolution of fungal secondary metabolism in the Netherlands and Europe.



Proof-of-concept: evolution-driven discovery of new bioactive compounds. We have applied a phylogenetic dereplication and comparative genomics strategy to explore the genomes of lichenized fungi, and we identified two novel biosynthetic pathways. Using heterologous expression in *Aspergillus oryzae*, we found that one biosynthetic pathway was responsible for the production of naphthalenone polyketides in fungi (Mosunova *et al*. (2022). *mBio* **13(3)**: e0022322), and the second pathway produced new derivatives of orsellinic acid, one of which exhibited antibiotic activity and inhibited pigmentation of zebrafish embryos.



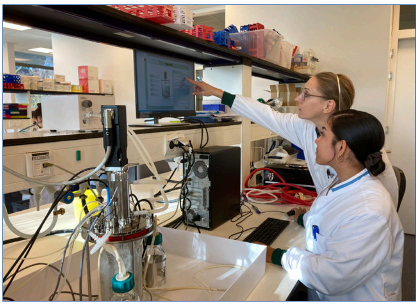
Drugs in the pipeline: secondary antimicrobial screenings of 93 fungal strains from the collection, including new culture conditions, resulted in a total of 33 extracts with antibiotic activities, for which we are elucidating chemical structures. Thanks to the use of *Bacillus subtilis* reporter strains, we obtain mode of action information while screening for activity: a few extracts that target RNA metabolism and cell envelope were identified, but the vast majority likely exhibit new modes of action.

FUNGAL PHYSIOLOGY

Prof dr ir Ronald de Vries

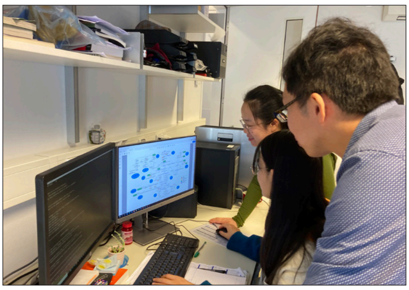
Unravelling the mechanisms of the carbon utilization abilities of fungi to facilitate the development of the biobased economy

Fungi have become major players in the establishment of the biobased economy, due to their wide range of extracellular and metabolic enzymes that are relevant for many different industrial applications. However, the success rate of implementing fungi or fungal enzymes is still too low due to a lack of detailed knowledge on these enzymes and metabolic pathways, and their regulation and diversity in fungi. The Fungal Physiology group aims to unravel the molecular mechanisms that affect fungal physiology on natural substrates and apply this knowledge to develop strains (*e.g.* cell factories) and enzymes for a wide range of applications, from the protein transition to production of biochemicals. We often team-up with other academic as well as industrial partners in complementary collaborations to enable a multidisciplinary approach in our research lines. By performing in-depth studies on a small number of model or reference species and use these results in comparative studies across the fungal tree of life we are able to elucidate novel functions and mechanisms as well as provide reference data for other scientists. 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 mature bioinformatics infrastructure of the group is the backbone of many of our research lines.

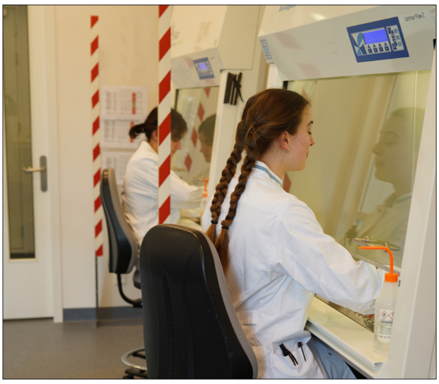


HIGHLIGHTS

During 2021/2022 five PhD students successfully defended their thesis and have moved on to new positions in academia or industry. With between 5 and 10 published papers within and additional papers outside the scope of their thesis, they generated a total of 37 publications over the last years and through this contributed significantly to the overall development and output of the group. Their theses also exemplify the diversity of topics studied in our group: aromatic (Ronnie Lubbers) and primary (Tania Chroumpi) metabolism, enzyme discovery (Xinxin Li), generation of fungal cell factories (Jiali Meng) and regulatory mechanisms (Roland Kun).



Further development of our bioinformatics infrastructure by Mao Peng now also includes pipelines for machine learning which have been applied for the identification of genes of interest. These pipelines combine various features (gene domains, transcriptomics, proteomics, phylogeny, *etc.*) to obtain a high-confidence prediction of genes involved in a specific biological process. In the first publication on such a pipeline the focus was on the identification of novel enzymes involved in pectin degradation, but these pipelines can be used for any process, as long as sufficient relevant data is available. Peng & de Vries (2021). *Microbial Genomics* **7**: 000674.



Building on our previous *in silico* model of primary carbon metabolism in *Aspergillus niger*, Tania Chroumpi validated this model by deleting all the genes predicted to be involved and demonstrated that multiple enzymes encode most steps of the pentose catabolic pathway. Jiali Meng continued on this and demonstrated that metabolic engineering can be used to generate fungal cell factories that can directly produce xylitol from wheat bran. Chroumpi *et al*. (2021) *Microbial Biotechnology* **14**: 2525–2537, Chroumpi *et al*. (2021) *Frontiers in Bioengineering and Biotechnology* **9**: 644216, Meng *et al*. (2021) *Bioresource Technology* **344**: 126199.

FOOD AND INDOOR MYCOLOGY

Dr Jos Houbraken

Fungi that cause food safety and security concerns, and pose health threats

A substantial portion of the world's food supply is subject to degradation by fungi prior to consumption, with many species presenting potential health hazards due to their production of mycotoxins. Additionally, fungi can proliferate in indoor environments, such as in the aftermath of water damage or in bathrooms, where they can pose a threat to immunocompromised individuals or cause allergic reactions. Our research group studies food spoilage and indoor fungi, with a focus on the taxonomy of the genera *Aspergillus*, *Penicillium*, *Talaromyces*, and *Paecilomyces*. These genera encompass species that can cause significant damage to food crops, but also serve as crucial industrial workhorses in food fermentation and as producers of a wide range of metabolites and enzymes. A robust classification and taxonomy is critical for the successful application of research in these fields. Our research program encompasses a broad range of topics, including food fermentation, spoilage, stress resistance and indoor growth, with a focus on both fundamental and applied research.


ICFM/ICPA meeting 2022

HIGHLIGHTS

The research group activities and highlights are centered on three main themes:

1. **Taxonomy and biodiversity**: In 2021–2022, systematic studies on the classification of genera and species associated with food and indoor environments continued. Even though many taxa in *Aspergillus* are well supported by phenotypic characters and/or phylogenetic markers, the taxonomy of some species remained troublesome. The taxonomy of these species was elucidated by studying large strain sets in combination with multispecies coalescence models, surprisingly resulting in a reduction of the number of accepted species. A notable accomplishment was the development of a comprehensive list of accepted species within the family *Chaetomiaceae*, which underwent substantial taxonomic revision in recent years. This list provides a useful reference for accurate species identification and consistent nomenclature within the field.
2. **Fundamental projects**: The biology of food and indoor fungi is studied with the aim to find novel solutions for prevention of food spoilage and fungal growth in the harsh indoor environment. Within the "Fungal food spoilers" project funded by TiFN, studies on the intraspecific variation within *Aspergillus niger*, *Paecilomyces variotii* and *Penicillium roqueforti* were performed using genomic and physiological techniques, with the aim to get insight in the variation of resistance to preservatives and heat. Within the project, Tom van den Brule successfully defended his Ph.D. thesis: "Heterogeneity in stress resistance of *Paecilomyces variotii* and related food spoilage fungi" on September 21 2022.
3. **Applied projects for industry and government**: The Service Unit conducted over 400 small and large projects for a diversity of clients (government, industrial, pharmaceutical, food and beverage, and commercial sectors), covering a wide spectrum of mycological issues. Tailor made trainings for specific industries were organised and our highly regarded annual course on food and indoor fungi was taught with great success.

Organisation of the international symposium of the ICFM (International Commission on Food Mycology) and ICPA (International Commission of *Penicillium* and *Aspergillus*). "Taxonomy, Spoilage and Mycotoxins", July 17–19 2022, Utrecht, the Netherlands.

Van den Brule *et al*. (2022). Intraspecific variability in heat resistance of fungal conidia. *Food Research International* **156**: 111302.

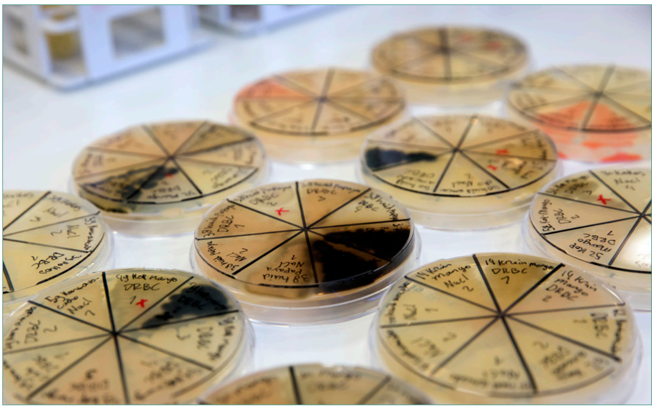
Wang *et al*. (2022). Taxonomy, phylogeny and identification of *Chaetomiaceae* with emphasis on thermophilic species. *Studies in Mycology* **101**: 121–243.

MEDICAL MYCOLOGY

Prof dr Ferry Hagen

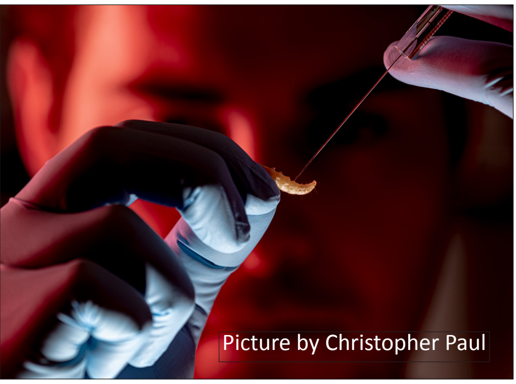
Novel pathogens are on the rise in the clinic

Fungal infections impact the quality of life of over a billion individuals, ranging from cosmetic issues like skin and nail infections to serious life-threatening invasive infections that result each year in more than 1.5 million hospitalizations. Optimal treatment is increasingly complicated by the emergence of antifungal resistance. Novel pathogens are on the rise in the clinic, being the multidrug-resistant yeast *Candida auris* the most notorious example. We investigate how these novel pathogens emerge in clinical environments and how they can be better detected and identified. Genomic data for these emerging pathogens is indispensable to setup molecular typing tools and rapid diagnostic assays. Therefore, we have implemented long-read nanopore sequencing and downstream analysis tools to perform de novo genome assembly and variant calling analyses to investigate outbreaks. Genetic characterization is supplemented with phenotypic data, next to screening for enzymatic activity and stress-related compounds, we use greater wax moth larvae (*Galleria mellonella*) to study host-pathogen interactions.



HIGHLIGHTS

To study the virulence potential of fungal pathogens a wide variety of model organisms are used, well-known examples are fruit flies, nematodes and mice. A fourth model organism that gained interest is the greater wax moth (*Galleria mellonella*) of which the larvae have the advantage that they can be easily reared, can be maintained at human body temperature, and can be injected with a precise dose of fungal cells. So far, there has been no standardized protocol to perform virulence studies with this promising model organism. In collaboration with the team of Prof. dr. Astrid Groot (University of Amsterdam, NL) we have setup guidelines for standardization.



Picture by Christopher Paul

de Jong *et al*. (2022) Standardized methods to rear high-quality *Galleria mellonella* larvae for the study of fungal pathogens. *Entomologia Experimentalis et Applicata* **170**: 1073–1080. https://doi.org/10.1111/eea.13237.

Extraordinary fungal infections, or those caused by atypical species, are part of our routine identification activities. Besides standard identification tools, like ITS barcoding, our team has implemented long-read nanopore sequencing. With this state-of-the-art technology we generate genomic data for rare and emerging fungal pathogens to setup molecular diagnostics and typing tools.

Boden *et al*. (2022) De novo nanopore genome sequencing of the clinical *Diutina catenulata* type-strain CBS565. *Mycopathologia* **187**: 417–420. doi: 10.1007/s11046-022-00632-x.

de Jong *et al*. Nanopore genome sequencing and variant analysis of the susceptible *Candida auris* strain L1537/2020, Salvador, Brazil. *Mycopathologia* **186**: 883-887. doi: 10.1007/s11046-021-00593-7.

Endemic mycoses due to *Histoplasma*, *Paracoccidioides*, and *Sporothrix* are increasingly encountered in Latin America. These fungal infections have a severe health impact, but the availability of rapid detection and identification tools remain a diagnostic gap. To overcome this, our team collaborates with that of teams of Prof. dr. Anderson Rodrigues (Federal University of São Paulo, Brazil) and Prof. dr. Rosane Hahn (Universidade Federal de Mato Grosso, Brazil).

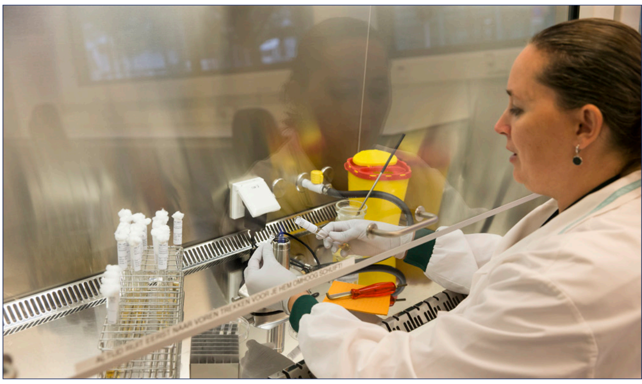
Hahn *et al*. (2022) Paracoccidioidomycosis: Current status and future trends. *Clinical Microbiology Reviews* **35**: e0023321. doi: 10.1128/cmr.00233-21.

COLLECTION

Dr Gerard Verkley and Dr Marizeth Groenewald

Fifteen years of certified quality management

The Biological Resource Centre (BRC) of the Westerdijk Institute has been ISO 9001 certified since 2007. Scope of our certificate includes the accession, preservation, storage and supply of micro-organisms (public deposits, safe deposits and patent deposits) and their DNA, and related information in the public WI databases. The public CBS collection of living fungi was established 1904. The NCCB Collection of wild-type and mutant bacteria, plasmids and phages was incorporated in 1998. In 2021–2022, 3 874 new strains were deposited and 7 447 supplied to scientists worldwide. The CBS collection is a reference collection for fungal and yeast biodiversity, and very rich in type-strains (1 130 new types accepted this period). The collection is rich in clinical (up to risk group 3), quarantine and soil fungi, and strains for food and biotechnological applications. The online strain catalogue i.a. presents information relevant for access and benefit sharing under the CBD and Nagoya Protocol. The closed CBS Collection is an International Depository Authority under the Budapest Treaty for patent strains, and also accepts safe deposits.



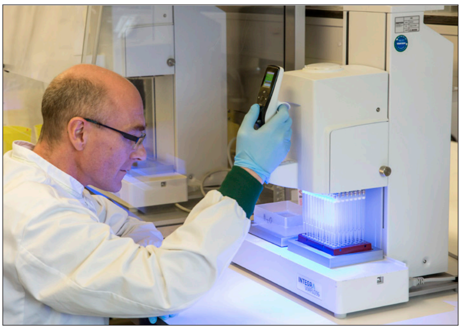
Number of strains preserved in the BRC	
CBS strains	
Filamentous fungi	76 824
Yeasts	14 812
Oomycota	2 050
NCCB strains	
Bacteria	8 869
Actinobacteria	1 474
Plasmids	564
Total	**104 593**
Type strains	
Filamentous fungi	11 336
Yeast	2 966
Oomycota	378
Total	**14 680**

International collaboration

In 2022, Gerard Verkley was re-elected President of the European Culture Collections' Organization (ECCO, https://www.eccosite.org), of which presently 82 collections of microorganisms and cell-cultures from 25 European countries are member. After having served as secretary on the board of the World Federation of Culture Collections (WFCC, https://wfcc.info) for six years, Marizeth Groenewald stepped down in 2021. From the start we have been involved in building the Microbial Resource Research Infrastructure (MIRRI, www.mirri.org), a pan-european RI of microbial BRCs, which managed to reach ERIC status in 2022. In collaboration with partners in the IS_MIRRI21 project (2020–2023), https://ismirri21.mirri.org, the CBS curators organised two international workshops in Louvain-la-Neuve, Belgium, in June 2022, one dealing with biosecurity and another one on access and benefit sharing (Nagoya protocol).

The BRC delivering for biodiversity research and sustainable bio-economic development

For all CBS strains ITS and LSU rDNA sequences are generated, validated by the curators and used for verifying of authenticity and quality control. Validated sequences are published in GenBank. Value of the data is also demonstrated by a series of highly cited papers by Duong Vu of WI in collaboration with the curators, such as the recent paper presenting DNAbarcoder as an open-source software for analysing and predicting DNA sequence similarity cut-offs for fungal species identification. On 29 November 2022, the dataset was awarded with the Dutch Data Price in the category Life sciences and Health. The data and software help to improve analyses of eDNA and metabarcoding datasets and help to better understand the composition and function of microbial communities, and how such communities respond to climate change. The number of strains for which genomes are available is rapidly increasing. In the past two years, we have seen a further strong increase in interest from industry to use our strains for screening on bioactive properties, biodegradation and other enzymatic capabilities.



YEAST RESEARCH

Prof dr Teun Boekhout

Retirement of Prof dr Teun Boekhout: the end of an era

With the retirement of Teun Boekhout as head of the Yeast Research Group, Westerdijk Institute loses a world-renowned yeast expert. Teun was editor of the last printed version of "The Yeasts, A Taxonomic Study", the go-to reference work on yeast taxonomy, and has been the driving force behind the transition to a more flexible and interactive online platform https://theyeasts.org/. One of Teun's interests is the application of yeasts in food and beverage production, resulting in his very own retirement beer "Teuntje" (see illustration *). He has always stimulated growth opportunities for team members, resulting in the continuation of some of his main research themes. Leading up to his retirement, he handed over the *Malassezia* research program to Bart Theelen, former research technician and currently PhD-student. Fortunately, Teun is still involved in some ongoing projects, such as the descriptions of novel species encountered on various antiques.

Ingrediënten: Water, **Gerstemout** (Pils, Maris Otter, Munich, Caramunich 1, Special B), Hop (Amarillo, Styrian Goldings, Saaz), Gist (CBS 1171). *Batchcode 23.03.001.X.* Ten minste houdbaar tot 31-03-23

TEUNTJE is gebrouwen met CBS 1171, de referentiestam van biergist *Saccharomyces cerevisiae*. Dit goudkleurige bier is vol-gistend en complex. Fris en gul, met een mild bittere uitvloeiing.

TEUNTJE
BLOND BIER

TEUNTJE Blond werd met zorg gebrouwen ivm het afscheid van Teun Boekhout van het Westerdijk Instituut.

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FOTO: COLL.IAV-ATRIA © N.SCHUITVLOT, 1912

GEBROUWEN BIJ K.E.G.S.
SOLOSTRAAT 31, AMSTERDAM

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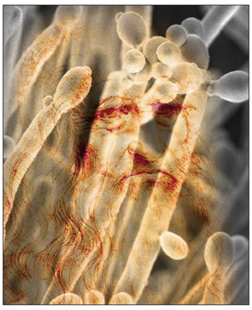
HIGHLIGHTS

***Blastobotrys* yeasts have a neck for antiquity**



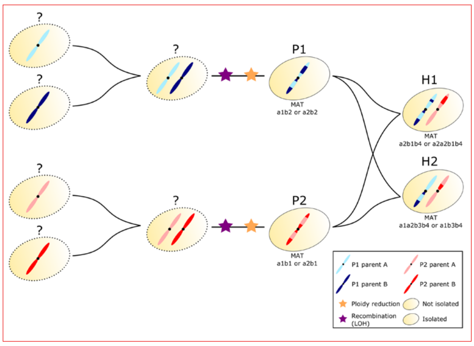
A collaboration with former colleagues Cobus Visagie and Neriman Yilmaz led to the description of novel species *Blastobotrys davincii*, detected from diverse substrates, including cave wall paintings, mummies, and the iconic self-portrait of Leonardo da Vinci from *ca*. 1512. Currently, we are working on the description of yet another novel *Blastobotrys* species, isolated from a Roman shipwreck in The Netherlands.

Visagie CM *et al*. (2022) Da Vinci's yeast: *Blastobotrys davincii f.a., sp. nov.* YEAST. Accepted. https://doi.org/10.1002/yea.3816

***Malassezia* research: Do various genotypes and hybrid lineages differ in virulence?**

Malassezia is the most abundant fungal genus on healthy human skin but may also cause various skin disorders. It is increasingly implicated in bloodstream infections, gut health/disease, and may promote pancreatic oncogenesis, highlighting the need for a better understanding of *Malassezia* evolution and pathobiology. Hybridization has been suggested as a biological mechanism of adaptation to new hosts and increased pathogenicity and many examples of hybrid yeast pathogens exist. In a recent mBio publication, we identified and explored hybridization events in *Malassezia furfur* with comparative genomics and mating type analysis, adding to our understanding of the evolutionary trajectory of this species and providing valuable resources for exploring the role of hybridization in pathogenicity and adaptation. Another study in FEMS Yeast Research focused on mitochondrial genomics in this species, further confirming significant intraspecies genetic diversity. In a follow-up project, virulence factors are explored for all genotypes, including hybrid lineages.

Theelen *et al*. (2022). Multiple hybridization events punctuate the evolutionary trajectory of *Malassezia furfur*. *mBio* **13(2)**: e0385321. https://doi.org/10.1128/mbio.03853-21 **



Theelen *et al*. (2021). Comparative analysis of *Malassezia furfur* mitogenomes and the development of a mitochondria-based typing approach. *FEMS yeast research* **21(7)**: foab051. https://doi.org/10.1093/femsyr/foab051

* ↑ Beer label designed by Ruud Willems.

** ← Figure from Theelen *et al*. (mBio, 2022) representing the proposed evolutionary trajectory of *Malassezia furfur* hybrids.

OUR GRADUATES 2021–2022

Ronnie
Lubbers

20
21

Exploration and application of aromatic metabolic pathways from *Aspergillus niger* for the production of aromatic compounds

Virtual Senate Hall PhD Defense Ronnie Lubbers

Ronnie Lubbers
7 June 2021

Aimi Stavrou
10 February 2022

EMERGING SACCHAROMYCOTINA YEAST PATHOGENS: DETECTION AND SUSCEPTIBILITY PROFILES

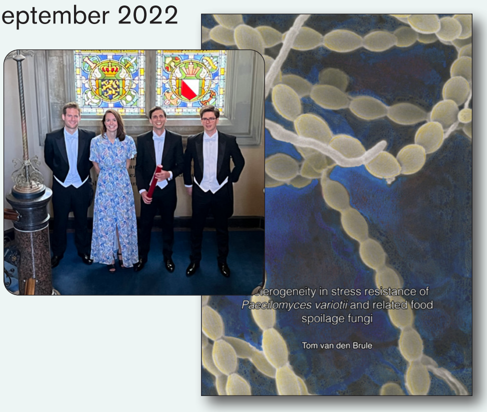
AIMILIA AIKATERINI STAVROU

Unraveling the Genetic Complexity and Redundancy of *Aspergillus niger* Sugar Metabolism

Tania Chroumpi

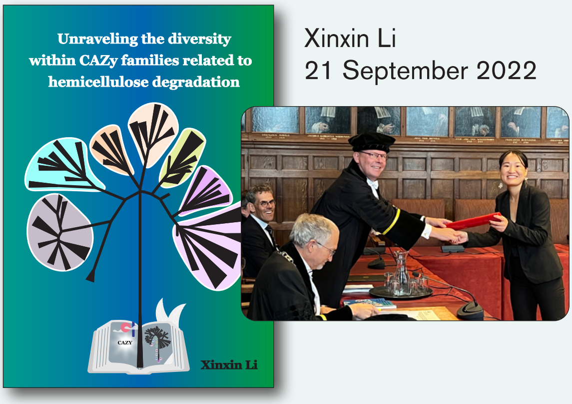
Tania Chroumpi
28 March 2022

Tom van den Brule
21 September 2022



terogeneity in stress resistance of *Paecilomyces variotii* and related food spoilage fungi

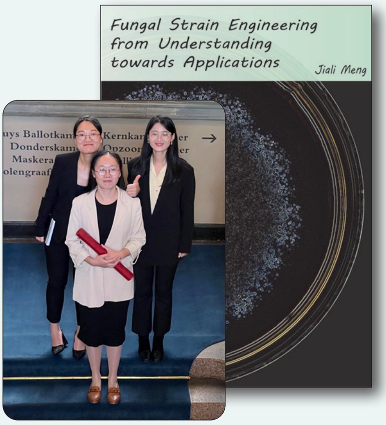
Tom van den Brule



Unraveling the diversity within CAZy families related to hemicellulose degradation

Xinxin Li

Xinxin Li
21 September 2022



Fungal Strain Engineering from Understanding towards Applications

Jiali Meng

Jiali Meng
28 September 2022

Harnessing the CRISPR/Cas9 system to study the regulatory network of plant biomass degradation in *Aspergillus niger*

Roland S. Kun
2022

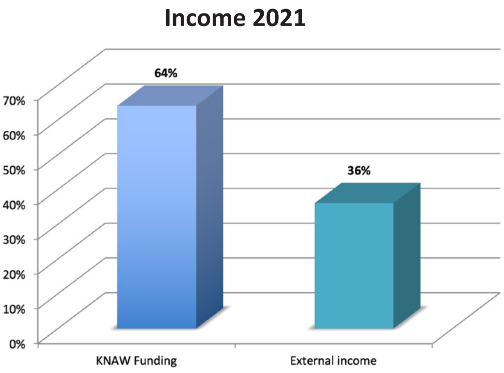
Roland Kun
17 October 2022

FINANCES AND STAFF

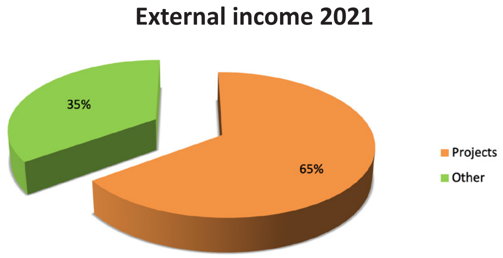
A healthy workplace environment

INCOME

The Westerdijk Institute has a total income of € 6.29 M. Of this amount, 64% is funded by the KNAW (€4.0 M).



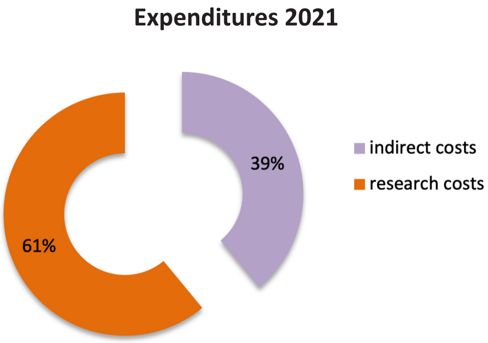
Of the external income, 65% is related to projects (€ 1.5 M). 35% (€ 805 K) of the external income is directly or indirectly derived from the collections and activities such as book sales, training and courses, as well as identification/sales of fungi and bacteria. The Odo van Vloten Foundation finances one postdoc research project.



EXPENDITURES

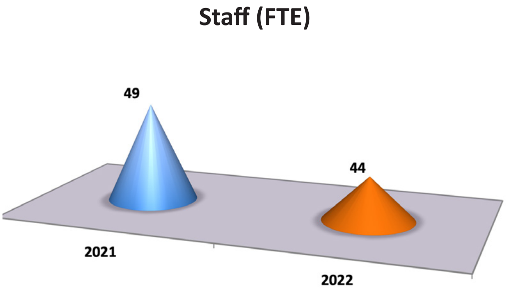
The total expenditure of the Westerdijk Institute (€ 6.6M) consists mainly of salaries (65%). Non-personnel costs are costs of materials, housing, and depreciation of durable equipment and intangible assets, e.g. software.

61% of the expenditures can be indicated as direct research costs. Indirect costs (39%) are for management, maintenance of the collection and for the collective support division of the Westerdijk Institute and the Hubrecht Institute.



STAFF

In December 2022 the Westerdijk Institute employed 44 FTE. The number of FTEs decreased by 5 FTE compared to 2021. However, relatively speaking more employees have received a permanent contract compared to 2021 due to the new collective labor agreement rules concerning contract extensions. Upon proven suitability and if an employee performs work of a structural nature, a permanent employment contract is entered into immediately after 12 months.



The Westerdijk Institute employs three full professors. Ultimo 2022 the Westerdijk Institute hosted 17 promovendi.

The Westerdijk Institute has a happy working environment with a low rate of sick leave: The average rate of sick leave increased with 1 percent compared to 2021, but is still far below the average sick leave percentage of the KNAW (4.49%) and the national absenteeism rate of 5.4%.

Westerdijk Fungal Biodiversity Institute

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@_Westerdijk_ Westerdijk Fungal Biodiversity Institute @WesterdijkInstitute

“Studies in Mycology” online via Ingenta (www.studiesinmycology.org)
“Fungal Systematics and Evolution” online via Ingenta (http://fuse-journal.org)
"Persoonia" online via Ingenta (https://www.persoonia.org)

Pictures by Westerdijk Fungal Biodiversity Institute, Thijs Rooimans and Annick Elzenga