British Mycological Society promoting fungal science

2025

www.britmycolsoc.org.uk

BRITISH MYCOLOGICAL SOCIETY

ANNUAL SCIENTIFIC MEETING

15 - 17 JULY 2025

Royal Holloway, University of London, Egham, Surrey

WELCOME TO THE BRITISH MYCOLOGICAL SOCIETY'S ANNUAL SCIENTIFIC MEETING 2025!

On behalf of the organising committee, it is a great pleasure to welcome you to this year's Annual Scientific Meeting of the British Mycological Society. The Annual Scientific Meeting was first held - in its current format - at the University of Nottingham in 2004. It is our flagship scientific event, and is central to the society's mission of promoting fungal science internationally, furthering the understanding of fungal science, and inspiring future generations of mycologists.

This year we are hosting a delegation of 133 mycologists, including 42 postgraduate students and 91 researchers; from 12 different countries, and representing 32 universities, plus the Royal Botanic Gardens Kew, CABI, Rothamsted Research, the Natural History Museum, London, and National Institute of Agricultural Botany.

Over the next two days we will enjoy talks and posters that span a vast range of mycological science, including 8 invited and 3 prize lectures. We will learn more about the activities of the BMS, including funding opportunities, awards and publishing. We are delighted to be located at Royal Holloway, University of London, surrounded by beautiful grounds and in close proximity to the Royal Botanic Gardens Kew, a visit to which will be another highlight of the week, as will the BMS Conference dinner and auction.

In the current day, facing challenges of climate change, antifungal drug resistance and the demise of multiple fungal, plant and animal species, there is a greater need than ever before for mycologists having diverse interests to unite, exchange ideas, form new collaborations and collectively promote the visibility and growth of fungal science. The BMS, as one society for all mycology, is exceptional in its capacity to convene such diversity. We hope that you will find the programme enjoyable and invigorating, and we look forward to spending time with you all.

Elaine Bignell, President of the BMS, on behalf of the ASM 2025 organising committee.

Dan Bebber, University of Exeter

Elaine Bignell, University of Exeter

Alessandra da Silva Dantas, Newcastle University

Esther Garcia Cela, University of Hertfordshire

Ester Gaya, Royal Botanic Gardens Kew

Janet Quinn, Newcastle University

Jason Rudd, Rothamsted Research

SHARE YOUR EXPERIENCE #BMS2025

PROGRAMME - 15 July 2025

13:00	**Arrival and registration** *Windsor Building*
13:40	**Welcome and introductions** *Jason Rudd, Rothamsted Research, Chair of Fungal Biology Research Committee*
13:45	**Exploring the basis of cell cycle-associated development to understand disease caused by the rice blast fungus *Magnaporthe oryzae*** *Miriam Oses-Ruiz, University of Navarre, Spain*
14:15	**Entomopathogenic fungi of the British Isles: Past, present and future** *Harry Evans, CABI, UK*
14:30	**Cross kingdom warfare – investigations into the mode of action of the antifungal effector Tfe1 elicited by the *Serratia marcescens* Type VI Secretion System** *Janet Quinn, Newcastle University, UK*
14:45	**John Webster Award Lecture 2024: Fungal community ecology** *John Taylor, University of California at Berkeley, USA*
15:15	**Refreshments**
15:45	**Adaptation of *Candida albicans* to the human host** *Rebecca Hall, University of Kent, UK*
16:15	**Genomic analysis of the hyper branching C-variant phenotype in the Quorn mycoprotein fungus *Fusarium venenatum* A3/5** *Jordan Price, NIAB, UK*
16:30	**Monoclonal antibodies targeting the fungal cell surface: next generation antifungal therapeutics** *Stephen McPherson, University of Aberdeen, UK*
16:45	**Poster 1-minute flash talks, session 1:** *Poster no.s 1 - 23*
17:15	**Poster session**
18:15	**Break**
19:00	**Welcome BBQ and networking** *South Quad, Founder's Building*

PROGRAMME - 16 July 2025

08:30	**Arrival and refreshments** *Windsor Building*
09:00	**Responding to challenges: an insider's view of a fungal pathogen spatiotemporal organization** *Martine Bassilana, Université Côte d'Azur, France*
09:30	**Index Fungorum and Species Fungorum: Advancing through digital innovation** *Mounes Bakhshi, Royal Botanic Gardens, Kew, UK*
09:45	**Understanding interactions between plants and microbes, the role of mycorrhizal symbionts** *Timothy George, The James Hutton Institute, UK*
10:15	**Refreshments**
10:45	**Widespread tissue-specific gene expression during fruiting body development of *Coprinopsis cinerea* revealed by laser-capture microscopy coupled low-input RNA sequencing** *Torda Varga, Royal Botanic Gardens, Kew, UK*
11:00	**Testing novel anti-biofilm technologies** *Ellen Wikeley, University of Nottingham, UK*
11:15	**Visit to the Royal Botanic Gardens, Kew** *Pre-booked tickets only due to limited number of spaces available on the tours.*
	- Pick up your picnic before getting on the coach at Royal Holloway. - Coaches leave at 11:30 promptly. - Small group tours of the Fungarium to take place between 13:00 and 15:00. - You'll be allocated to a group and must join the tour at the correct time. - When not visiting the Fungarium, do enjoy the gardens. - Meet in the Jodrell Auditorium at 15:30 for refreshments. - At 16:00, we will hear from the Kew mycology team about the Fungarium Sequencing Project. - Coaches leave Kew at 17:15 promptly. ***Lost at Kew or need to get in touch? Call Sally on 07934 064002.***
19:00	**BMS Conference Dinner and Auction** *The Picture Gallery, Founder's Building*

PROGRAMME - 17 July 2025

08:30	**Arrival and refreshments** *Windsor Building*
09:00	**Gene loss and evolutionary divergence in lipid biosynthesis and DNA repair pathways of arbuscular mycorrhizal fungi** *Alexandra Dallaire, RIKEN-Cambridge Joint Crop Symbiosis Research Team and RIKEN Center for Sustainable Resource Science, Japan*
09:30	**Fungal life aquatic** *Michael Cunliffe, University of Plymouth and Marine Biological Association, UK*
10:00	**Refreshments**
10:30	**Underpinning mycological research - culture collections of living fungi** *Matthew Ryan, CABI, UK*
10:45	**Investigating the role of histone post-translational modifications in antifungal resistance** *Takanori Furukawa, Teeside University, UK*
11:00	**Latent pathogens: The *Botryosphaeriaceae* in a changing world** *Bernard Slippers, University of Pretoria, South Africa*
11:30	**Enhancing the conservation status of Clavariaceae (Fairy Clubs, Spindles and Corals) in ancient grassland habitats by applying molecular phylogenetics** *Louise Tranter, Aberystwyth University, UK*
11:45	**Rhamnolipids, antifungals for mucormycosis?** *Jacob Hudson, University of Kent, UK*
12:00	**Poster 1-minute flash talks, session 2:** *Poster no.s 24 - 41*
12:30	**Poster session and lunch**

17 July 2025 continued

14:00	**Berkeley Award Lecture 2024:** **Fungal adaptation in the Anthropocene: optimism and obstacles** *Johanna Rhodes, University of Birmingham, UK*
14:30	**Fungal morphometrics: Correlating carbon source variations with mechanics and surface chemistry of fungal mycelia** *Juwon Samuel Afolayan, Nottingham Trent University, UK*
14:45	**Assessing the susceptibility of mycelium-based composite insulation materials to mould growth** *Joni Wildman, University of Bath, UK*
15:00	**Reconciling the rusts and the consequences of a complex life cycle** *Mary Catherine (Cathie) Aime, Purdue University, USA*
15:30	**Tony Trinci Award Lecture 2025** **The pangenome of *Aspergillus fumigatus* highlights the dynamics of gene gain-loss over evolutionary time-scales in a human fungal pathogen** *Harry Chown, Imperial College London, UK*
16:00	**Presentation of the Howard Eggins Early Career Mycologist Awards for best talks and best posters**
16:30	**Summary and close of conference** *Elaine Bignell, University of Exeter, President of the British Mycological Society*

POSTERS

Poster 1

Understanding interactions of fungicides, fungi and wheat to inform the restoration of degraded agricultural land

Alice Day, Imperial College London, UK

Poster 2

***Paradendryphiella salina* – a model marine fungus for investigating the biology, ecology and biotechnology potential of macroalgae (seaweed) fungal interactions**

Beth Tindall-Jones, The Marine Biological Association, UK, and University of Exeter, UK

Poster 3

Targeting Nutrient Sensing in a Hazardous Fungal Pathogen to Turn-Off Virulence and Mycotoxins

Diah Putri, University of Bath, UK

Poster 4

Dissecting the molecular mechanisms driving heightened antifungal stress resistance in aged *Candida albicans* population

Eloise Mitchell, Newcastle University, UK

Poster 5

Mechanisms behind virus-host interactions: how mycoviruses modulate fungal host phenotypes

Josephine Battersby, University of Hertfordshire, UK, and Imperial College London, UK

Poster 6

Investigating Fungal Spore Dispersal in UK Arable Crop Systems Under Current and Future Environmental Conditions

Patrick McClean, Rothamsted Research, UK

Poster 7

Fungi of Future Forests: do elevated CO_2 levels affect soil fungal community composition in oak woodland?

Rachel Calder, University of Birmingham, UK

Poster 8

Beware the air?: Exploring indoor airborne fungal communities and urban chemical pollutants

Sam Hemmings, Imperial College London, UK

Poster 9

Genome editing to induce genome rearrangements in a human fungal pathogen

Matthew Shaw, University of Kent, UK

Poster 10

Harnessing the Microbiome to Combat the Threat of Fungal Mycotoxins

Oly Grey Ascione, University of Bath, UK

POSTERS

Poster 11
Old Products, New Consumers: A Mycotoxin Exposure Concern
Esther Garcia-Cela, University of Hertfordshire, UK

Poster 12
Seeking Candidates for Diesel and Petrol Remediation
Esther Garcia-Cela, University of Hertfordshire, UK

Poster 13
Are Stressful Environments Driving Increasing Threats from Virulent, Toxic, Drug-Resistant *Fusaria*?
Neil Brown, University of Bath, UK

Poster 14
Elucidating the status of type specimens deposited in the Royal Botanic Gardens Kew's Fungarium
Matteo Gelardi, Royal Botanic Gardens, Kew, UK

Poster 15
Marine diatrypaceous fungi from mangroves in Egypt and Saudi Arabia
Ali H. A. Bahkali, King Saud University, Saudi Arabia

Poster 16
Fungarium Sequencing Project: Sampling Progress and Outputs
Emily Hodgson, Royal Botanic Gardens, Kew, UK

Poster 17
Cryptic Marine Fungi: Chlamydospore-Producing Taxa
E. B. Gareth Jones, King Saud University, Saudi Arabia

Poster 18
Improving Curation and Documentation of Fungal Types Alongside a Large-Scale Sequencing Project
Henry Miller, Royal Botanic Gardens, Kew, UK

Poster 19
Synthesis and Biological Activity of New Antifungal Prodrugs
Ondřej Štěpánek, Charles University, Prague, Czechia

Poster 20
Detecting fungicides in UK soils by LC-MS analysis
Rodrigo Leitao, Imperial College London, UK

POSTERS

Poster 21
Gene family expansion drives the evolution of medicinal Erinacine A biosynthesis
Josepha Becker, Royal Botanic Gardens, Kew, UK

Poster 22
Tracking the tuneability of fungal mycelium through chemotrophic and imaging studies: New approaches to study engineered living materials
Juwon Samuel Afolayan, Nottingham Trent University, UK

Poster 23
Fungarium Sequencing Project: Specimens of Particular Interest Housed by RBG Kew's Fungarium
Mikele Baugh, Royal Botanic Gardens, Kew, UK

Poster 24
Functionalizing mycelium for photosensing applications, a step closer to photoresponsive materials
Xin Zhang, Nottingham Trent University, UK

Poster 25
Fungi in Thai mangroves: Novel taxa, marine adaptations and phylogenetic insights
Carlo Chris S. Apurillo, Mae Fah Luang University, Thailand

Poster 26
Study on the Antimicrobial Efficiency of Lichen Extract Combined with Metal Nanoparticles
Ek Sangvichien, Ramkhamhaeng University, Thailand

Poster 27
Call off the dogs! Sniffing out *Hymenogaster* with distribution modelling
Alexandra Dombrowski, University of Gothenburg, Sweden

Poster 28
The UK Crop Microbiome Cryobank: a national resource for research and development
J. Miguel Bonnin, CABI, UK

Poster 29
Fungarium Sequencing Project: Sampling Methods from the Royal Botanic Gardens, Kew's Fungarium
Lawton Riness, Royal Botanic Gardens, Kew, UK

Poster 30
Inter-cladal variation in the response to environmental stress in the emerging fungal pathogen *Candida auris*
Alison Day, Newcastle University, UK

POSTERS

Poster 31
From Fungal Chemistry to crop security: decoding sex hormones and their biosynthetic pathways
Lisa Humbert, University of Nottingham, UK

Poster 32
Developing large-scale lab methodologies for whole genome sequencing of ancient and historical fungal material
Charlotte Goodman, Royal Botanic Gardens Kew, UK

Poster 33
Fungal FLC proteins that are essential for cell wall integrity and Ca^{2+} homeostasis belong to a novel transmembrane protein superfamily
Rachael Murray, University of Edinburgh, UK

Poster 34
Rezafungin for Treating a Complex *Candida* Infection
Dev Patel, University Hospitals of North Midlands NHS Trust, UK

Poster 35
Novel-to-Nature NRPS-Like Benzoquinone Products
Nicholas R. Moody, University of Nottingham, UK

Poster 36
Building a scalable bioinformatics strategy for sequencing historical fungal collections
Wu Huang, Royal Botanic Gardens Kew, UK

Poster 37
Physicochemical and Metagenomic Characterization of Desert Soil: Advancing Desert Truffle Cultivation in Saudi Arabia
Sakhr Alhuthali, King Abdulaziz University, Saudia Arabia

Poster 38
Natural Occurrence of Fumonisins in Pre-Harvest and Post-Harvest Maize in South Africa: A South African Maize Trust Project
Oluwasola Abayomi Adelusi, University of Johannesburg, South Africa

Poster 39
The genetics of speciation in *Saccharomyces*
Jasmine Ono, University of Nottingham, UK

Poster 40
A standardised fungal collection framework for the Darwin Tree of Life Project
Ester Gaya, Royal Botanic Gardens Kew, UK

Poster 41
Defining the antifungal mode of action of miltefosine to unlock its potential in targeting eukaryotic pathogens
Tanmoy Chakraborty, Newcastle University, UK

VISIT TO THE ROYAL BOTANIC GARDENS, KEW

Please note: This visit is for those with pre-booked tickets only as spaces are limited.

During this afternoon session at Kew on **Wednesday 16 July**, attendees will receive a guided tour of the Fungarium and hear from Ester Gaya and the Kew mycology team about the Fungarium Sequencing Project, an ambitious initiative to obtain the whole genome sequences of Kew's reference species collection, funded by the UK government's Department for Environment, Food & Rural Affairs. There will also be time to chat with the team, and enjoy a picnic in the gardens!

The Fungarium at Kew Gardens is the world's largest collection of fungal specimens, holding over 1.25 million samples from across the globe. This historic collection, which dates back to 1879, is a cornerstone for mycological research, offering valuable insights into the taxonomy, biodiversity, and ecological roles of fungi. It provides a reference library of fungal species, enabling scientists to classify and understand fungal evolution and distribution. This collection is crucial for both scientific and practical applications.

By preserving fungal biodiversity, the Fungarium supports essential research into the role of fungi in ecosystems, including decomposition, plant health, and potential biotechnological uses in medicine, agriculture, and industry. It also aids in identifying rare or endangered species, contributing to conservation efforts and ecological assessments that inform sustainable practices and biodiversity policies.

Ester Gaya
Royal Botanic Gardens Kew, UK

Ester Gaya discovered her passion for fungi during her undergraduate degree and PhD at the University of Barcelona, where she focused on lichen taxonomy and systematics and, at Duke University, she developed an interest in evolutionary biology and phylogenetic methods. At Kew, Ester has expanded her area of research to almost all major groups of fungi and has transitioned into phylogenomics and comparative genomics approaches which she applies to her favourite group of organisms.

INVITED SPEAKERS

Miriam Oses-Ruiz
University of Navarre, Spain

I completed my PhD with Prof. Nick Talbot FRS at the University of Exeter (UK) as a Marie Curie Fellow. I specialised in cell cycle regulation and transcriptional responses during infection associated development in the ascomycete fungus *Magnaporthe oryzae*. Afterwards I moved to The Sainsbury Laboratory (Norwich, UK) as a senior postdoctoral fellow, specializing in phosphoproteomics. In 2021, I obtained an independent research grant "Retos de Investigación JIN," from the Agencia Estatal de Investigación from the Spanish government to conduct my own research in DNA Damage response at Public University of Navarre (UPNA) (Spain). In 2022 I obtained a Ramon y Cajal fellowship to set up my own lab and currently I lead the group of Molecular Biology of Fungi at UPNA. My research program aims to investigate three main areas: cell cycle related development, cel-to-cell communication and cellular heterogeneity and, hierarchical transcriptional networks.

Exploring the basis of cell cycle-associated development to understand disease caused by the rice blast fungus *Magnaporthe oryzae*

The filamentous fungus *Magnaporthe oryzae* causes a devastating disease in cultivated rice that destroys enough rice to feed 60 million people in the world. *M. oryzae* it is widely known for being highly variable, undergoing host jumps and causing new outbreaks, constituting a threat to global food security. *M. oryzae* causes infection thanks to the formation of a specialised cell called the appressorium. The appressorium develops from a three-celled spore upon contact with the surface of a leaf. During appressorium development the apical cell of the spore undergoes a round of mitosis, whilst the other two undergo autophagy-mediated cell death. It is unknown how the mitotic cell cycle operates coordinated with appressorium development. In the lab we are dissecting the molecular mechanisms associated to cell cycle- to understand how it is intertwined with other pathways to drive appressorium development and infection. We use a combinatory approach of phosphoproteomics, cell biology, transcriptomics and genetics for it.

John Webster Award Lecture

John Taylor

University of California at Berkeley, USA

I am a professor at UC Berkeley studying fungal evolution and ecology. Development of DNA amplification and sequencing in the late 1980s allowed me to study fungal phylogeny and phylogenomics, as well as fungal population genetics and population genomics. Over the past decade, I have used DNA sequencing of environmental samples to investigate fungal community ecology of indoor air, forest soils, desert soils and agriculture. In addition to teaching about and researching fungi, I have served in the leadership of my department at Berkeley, as well as for national and international mycological associations. My publications can be seen here.

Fungal community ecology

In natural and managed systems the importance of fungi has been overlooked or understudied compared to that of plants and bacteria. Recent community ecology research will be presented that addresses the importance of fungi in, for example, response of crop plants to drought stress, estimation of carbon storage in forests, and shaping bacterial community composition in grasslands.

Rebecca Hall
University of Kent, UK

I am interested in understanding how microbes adapt to their environment. After completing my PhD thesis on understanding how the nematode *C. elegans* adapts to environmental pH, I became a fungal biologist and have contributed to our understanding of how human pathogenic fungi respond to carbon dioxide, a key host environmental signal that triggers fungal pathogenesis, and how the fungal cell wall is synthesised. I started my independent research career through the award of an MRC career development fellowship and I'm currently a Senior Lecturer in Microbial Adaptation at the University of Kent. My research group focuses on understanding how adaption of fungi to their environment affects the synthesis of the fungal cell wall, and the implications this has on the host-pathogen interaction. My group is also interested in interkingdom interactions and their role in antimicrobial resistance in biofilms, mucormycosis and the development and identification of novel antifungals. Outside of research, I'm passionate about supporting postgraduate wellbeing and supporting ECRs

Adaptation of *Candida albicans* to the human host

Candida albicans is a commensal fungus of the oral, genital, and gastrointestinal tracks of humans. However, under specific environmental conditions and immune deficiencies, *C. albicans* can become pathogenic causing 400,000 life-threatening systemic infections, and 150 million mucosal infections worldwide each year. The balance between commensalism and infection is tightly regulated by actions of the microbiome and the innate immune system. The cell wall of *C. albicans* is a highly dynamic organelle, with the structure and composition changing in response to environmental adaptation. These changes in cell wall organisation lead to an altered host-pathogen, and can either promote pro-inflammatory responses, or can enable the pathogen to evade detection by the innate immune system, with both outcomes promoting disease. This talk will cover our most recent research on understanding how *C. albicans* adapts to host-induced environmental conditions, and the impact this adaptation has on the host-pathogen interaction.

Martine Bassilana
Université Côte d'Azur, France

I am a Research Director at the French national research organization CNRS, working on fungal biology for more than 20 years at the University Côte d'Azur. My work is aimed at understanding how cell shape changes are regulated, which is critical for a range of biological processes and the virulence of a variety of plant and human fungal pathogens. The main focus of our research is the study of key regulators in cell polarity and membrane traffic during the switch from budding to hyphal growth, and further branching, of the opportunistic human fungal pathogen *Candida albicans*. Specifically, we have generated a number of mutants and fluorescent reporters to follow the spatiotemporal dynamics of small GTPases and lipids, as well as to determine their role in growth and virulence. We have also used different approaches, such as optogenetics, synthetic physical interactions and polymer microfabrication, to investigate how *C. albicans* responds to distinct challenges. More recently, we have become interested in the link between the physical properties of the cytoplasm and *C. albicans* growth in different conditions, including antifungal drugs.

Responding to challenges: an insider's view of a fungal pathogen spatiotemporal organization

In response to a changing environment, many fungal pathogens adapt their morphology to disseminate, acquire nutrients, and escape the immune system. The human fungal pathogen *Candida albicans* can switch in a few hours from an ovoid shaped cell of approximately five microns to filamentous cells hundreds of microns long with multiple branches, a process critical for virulence. How are such shape changes initiated and sustained? To decipher the cellular, physical and biochemical mechanisms that underly these changes, we use a combination of molecular genetics and live cell microscopy. I will discuss our findings, including the role of key components of cell polarity and membrane traffic, at different temporal and spatial scales, during *Candida albicans* growth in distinct environments. Furthermore, this talk will cover the relationship, and causality, between developmental states and physical properties of the cytoplasm.

Timothy George
The James Hutton Institute, UK

I am a rhizosphere scientist at the James Hutton Institute and the Deputy Director of the International Barley Hub. I got my BSc from the University of Newcastle-upon-Tyne in 1996 and PhD in Soil Science from the University of Reading in 2000 and currently hold Honorary Professorships at the University of Aberdeen and the University of Nottingham. I have specific expertise in understanding how the external environment mitigates plant physiological and genetic responses to a lack of resources in the rhizosphere. I have published >140 papers and currently coordinate an EU Horizon Europe to develop root phenotyping and genetic improvement for crops resilient to environmental change. In addition, I am actively involved in promoting plant and soil science as Marschner Editor for Plant and Soil, UK coordinator of Fascination of Plants Day, Board member of EPSO and Chair of the EPSO Plant Science Seminar series and the Dundee Root Medal.

Understanding interactions between plants and microbes, the role of mycorrhizal symbionts

Arbuscular mycorrhizal (AM) fungi-associated hyphosphere microbiomes can be considered as the second genome of plants. Their composition can be thought of as a stably recurring component of a holobiont, defined by the hyphosphere core microbiome, which is thought to benefit AM fungal fitness and that of the associated plant. I will review evidence indicating the existence of the hyphosphere core microbiome, highlight its functions linked to those functions lacking in AM fungi and associated plants, and further explore the mechanisms by which different core members ensure their stable coexistence. I will suggest that deciphering and utilising the hyphosphere core microbiome provides an entry point for understanding the complex interactions among plants, AM fungi and bacteria.

Alexandra Dallaire

RIKEN-Cambridge Joint Crop Symbiosis Research Team and RIKEN Center for Sustainable Resource Science, Japan

I am a molecular biologist and biochemist by training, and I further specialised in genomics and evolutionary biology, particularly in non-model fungi of ecological interest. I studied the function of small non-coding RNAs in the nematode *C. elegans* during my PhD in Canada. During my postdoc in Cambridge, I investigated the role of small RNAs et DNA methylation in the regulation of transposable elements of arbuscular mycorrhizal (AM) fungi. As an independent fellow at Kew Gardens, I developed a comparative genomics tool to discover gene families associated with transposable elements. Now I'm deputy leading the Japanese division of the Crop Symbiosis team at RIKEN, where we develop single-cell sequencing and a transformation method for diverse species of AM fungi.

Gene loss and evolutionary divergence in lipid biosynthesis and DNA repair pathways of arbuscular mycorrhizal fungi

Arbuscular mycorrhizal fungi (AMF) form nutritional symbioses within the roots of most land plants and influence plant productivity, survival, and composition. Their cell biology is unique but poorly understood, and as part of our efforts to understand the diversity and dynamics of individual cells during symbiosis, we developed a phylogenomics framework for comparative transcriptome analyses. The highly divergent protein sequences found in AMF render functional inferences difficult such that roughly half of their genes have no predicted function. Here, I will describe our efforts using sequence and structural similarity approaches to improve the functional annotation of AMF genes, using comparisons to Mucoromycota and Dikarya species. Focusing on lipid biosynthesis and DNA repair pathways, I will illustrate specific examples where structural predictions allow to distinguish gene losses from extreme sequence divergence. This effort to identify and curate orthologous groups will enhance the meaningfulness of omics applied to AMF and other fungi.

Michael Cunliffe

University of Plymouth and Marine Biological Association, UK

At the Marine Biological Association (MBA) I am the Director of Science and a Senior Research Fellow, as well as Professor of Marine Microbiology at the University of Plymouth. My research covers the biology, ecology and evolution of aquatic fungi, with a global reach from the coastal waters around Plymouth to the open ocean and polar ecosystems. I led the establishment of the MBA Marine Fungi Culture Collection – a culture collection with over 500 fungal strains from seawater, sediments and seaweeds, including from the open Atlantic Ocean, Antarctic and Arctic.

Fungal Life Aquatic

Fungi are prevalent in aquatic ecosystems, from freshwater ponds and streams to the open ocean and frozen polar regions. Relative to their terrestrial counterparts, we have a limited understanding of the biology, ecology and evolution of aquatic fungi. What are the underpinning mechanisms used by fungi to survive and sometimes thrive in aquatic ecosystems? How did such mechanisms evolve and to what extent are they specific to aquatic fungi? Our approach to address these questions has been to study aquatic fungi in their natural habitats as well as with model representatives in the laboratory. Using specific examples from our recent work, I will cover how some fungi from the open ocean use cell morphological plasticity as and adaptive strategy to changing resource ability, how some marine fungi utilise associations with other organisms to survive the harsh environment of the intertidal zone and the evolutionary processes involved in the niche expansion of an enigmatic group of aquatic saprotrophs.

Bernard Slippers
University of Pretoria, South Africa

I am the Director of the Forestry and Agricultural Biotechnology Institute (FABI), and Professor in the Department of Biochemistry, Genetics and Microbiology at the University of Pretoria. I study the interactions between organisms that affect plant health in a changing global context, and use molecular, chemical and sensor technologies to develop precision pest management tools for them. I have published more than 330 papers and have trained more than 100 PhD and MSc candidates and postdoctoral fellows.

Latent pathogens: The *Botryosphaeriaceae* in a changing world

In this talk, I will reflect on the transformation in our understanding of the *Botryosphaeriaceae* driven by advances in molecular ecology and evolution studies, and genomics. I will highlight emerging questions surrounding their interactions within microbiomes and with host organisms, as we seek new strategies to manage these widespread, often inconspicuous, and increasingly significant tree pathogens in a changing world.

Berkeley
Award Lecture

Johanna Rhodes

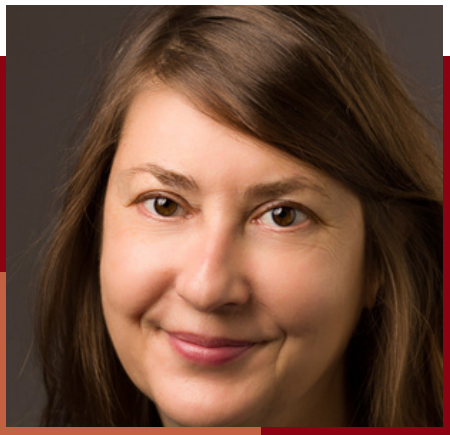
University of Birmingham, UK

After completing my PhD in host gene regulatory networks activated in response to fungal infection at the University of Warwick, I moved to Imperial College London to research the pathogen itself, and focus on human infection. My research has focused on three of the four WHO Critical Priority Group fungal pathogens: *Cryptococcus neoformans, Candida auris* and *Aspergillus fumigatus*. As an assistant professor at the University of Birmingham, the Rhodes Group uses a One Health approach to balance and optimise the health of humans, animals and the environment.

Fungal adaptation in the Anthropocene: optimism and obstacles

Fungi play critical roles in ecological resilience, from nutrient cycling to supporting biodiversity. Fungi are master adaptors, and utilise a variety of adaptive strategies to climate change and human activity in the Anthropocene, highlighting their remarkable capacity for survival and innovation. While fungal resilience offers reasons for optimism, significant obstacles, such as habitat loss, shifting symbiotic relationships, and emerging fungal pathogens, present challenges to plant, wildlife and human health. By examining these dynamics, we aim to shed light on the intricate interplay between fungi and a rapidly changing world.

Mary Catherine (Cathie) Aime
Purdue University, USA



I am a Professor of Mycology in the Department of Botany & Plant Pathology and Director of the Arthur Fungarium and Kriebel Herbarium at Purdue University. I received my M.S. and Ph.D. in Biology at Virginia Polytechnic Institute and State University under the guidance of Orson K. Miller, Jr., and conducted post-doctoral research at the University of Oxford under Lorna Casselton. My research combines expeditionary field work and traditional approaches with molecular genetics and multi-omics approaches to understand fungal diversity and evolution. I am a past Managing Editor of the journal Mycologia and Past President of the Mycological Society of America, President of the International Commission on the Taxonomy of Fungi, and President Elect of the International Mycological Association, and a fellow of the Mycological Society of America, the American Association for the Advancement of Science, the Explorer's Club, and the Linnean Society of London.

Reconciling the rusts and the consequences of a complex life cycle

In terms of species numbers, the rust fungi (Pucciniales) are an incredibly successful lineage. Together, the more than 7000 described species form the largest known monophyletic group of plant pathogens, and the 2nd largest order of Fungi. All are obligate parasites of vascular plants including agricultural, forest and ornamental crops resulting in billions of dollars of damage worldwide each year. An intriguing aspect of rust biology is that many species are heteroecious, i.e., require alternation between two unrelated hosts in order to complete their life cycle. Whether the character of heteroecism is ancestral or derived within the rusts has never been satisfactorily resolved. Most classical treatments of rust classification were based on the hypothesis that "primitive" hosts (e.g., ferns) harbored "primitive" rusts (e.g. *Uredinopsis, Hyalopsora*) that alternate on members of the Pinaceae. However, alternative hypotheses of rust evolution have proposed various short-cycled primarily tropical rusts as ancestral, with the defining characteristic of heteroecism thus being derived within the group. Molecular studies based on rDNA genes have since disproved the fern rust hypothesis, but the second hypothesis remains. This study analyzes loci from multiple genes and taxa selected from all known families to resolve the base of the rust fungi and infer ancestral characters including the origins of heteroecism for the order, and the implications for how this strategy may have been adaptive for the lineage.

Harry Chown

Imperial College London, UK

Tony Trinci Award Lecture

I obtained a bachelor's degree from the University of Exeter and a master's degree and PhD from the University of Manchester. During my doctoral studies, I was based within the Manchester Fungal Infection Group, and focussed on the development, interrogation, and application of pangenomics in the fungal pathogen *Aspergillus fumigatus*. My research contributed to a deeper understanding of the genetic diversity within *A. fumigatus* populations and the implications of genome variability in fungal antimicrobial resistance (fAMR).

Following my PhD, I joined Matthew Fisher's group at the MRC Centre for Global Infectious Disease Analysis, Imperial College London, as a research assistant. My current work builds upon the initial pangenome of *A. fumigatus,* and leverages comparative genomics, population genetics, and bioinformatics to explore the ecological, environmental, and evolutionary drivers of fAMR. By integrating large-scale genomic datasets with environmental and clinical metadata, I aim to elucidate the mechanisms underlying the emergence and spread of antifungal resistance, with the long-term goal of informing surveillance strategies and fAMR mitigation efforts.

The pangenome of *Aspergillus fumigatus* highlights the dynamics of gene gain-loss over evolutionary time-scales in a human fungal pathogen

Each year over 6.5 million individuals acquire an invasive fungal infection, and approximately half will die as a result. Morbidity rates from fungal infections are higher than malaria, HIV and tuberculosis, combined. Additionally, the number of antifungal compounds are extremely limited, with only a handful of drug classes commonly used. In contrast, there is a much wider range of fungicides - chemicals used to kill fungi in agriculture – available on the market, often with the same mechanism of action as antifungal drugs. As a result, soil dwelling pathogenic fungi, such as *Aspergillus fumigatus*, have developed antifungal resistance through exposure to fungicides. Large-scale application of fungicides has led to an increased prevalence of antifungal resistant isolates. The mechanisms of resistance vary amongst populations with different genetic factors contributing towards the phenotype. To assess genetic variation at the population level we constructed the largest filamentous fungal pangenome, to-date, incorporating over 1,000 isolates over a 100-year period, spanning 34 countries. We then investigated contributions from the accessory genome towards drug resistance, highlighting either novel mechanisms of resistance or traits associated with other environmental conditions that have been selected for. Furthermore, using the temporal breadth of sampling, we have been able to calculate a time-corrected phylogeny that identifies the rate of gene gain and loss and how this varies across the population. Additionally, we reveal that specific cohorts of genes undergo differential rates of gain and loss, over evolutionary time periods, revealing the dynamics of the pangenome in *A. fumigatus*. These results highlight the ability of the species to acquire or lose genetic material, which may enable survival under new selection pressures.

OFFERED TALK

Entomopathogenic fungi of the British Isles: Past, present and future

Harry C Evans

CABI, UK

Entomopathogenic fungi *sensu lato* infect, colonise and kill their arthropod hosts using a range of mechanisms and a cascade of metabolites to breach the exoskeleton and to colonise the haemocoel. Historical records of entomopathogenic fungi from the British Isles, especially those compiled by Tom Petch in the 1940s, are summarised and discussed. Subsequent records of EPF have been sporadic and predominantly made by amateur collectors and published in the reports of local natural history societies. However, they reveal a surprisingly diversity of pathogens, often in such numbers as to suggest local epizootics,as exemplified in the Fens of East Anglia. More recent records over the past decade show that there is a cryptic but rich vein to be tapped with new records and species on diverse arthropod hosts. Notable examples are new taxa in the *Hypocreales* (*Ophiocordycipitaceae*) on the red ant, *Myrmica rubra*, which are most closely-related to ant pathogens previously collected in the humid tropics,as well as new species of *Gibellula, Samsoniella* (both *Cordycipitaceae*) and *Harposporium* (*Clavicipitaceae*) on spider, moth and beetle hosts, respectively. The former two genera, collected on troglodyte hosts in cave systems on the island of Ireland, are highlighted in relation to behavioural changes in infected arthropods. A case study of a newly-discovered *Ophiocordyceps* species infecting leafhoppers on beech trees is presented and the implications for natural control are discussed. Recent collections have prioritised *in vitro* cultivation of EPF with the aim of screening these for potentially-useful secondary metabolites. There is increasing evidence that EPF produce an array of metabolites , including antibiotics and immuno-suppressants, in order to occupy their unique ecological niche which may offer new sources of products for the pharmaceutical industry. EPF in the British Isles, therefore, could have a pivotal role in the development of novel medicines with no underlying legislative issues.

OFFERED TALK

Cross kingdom warfare – investigations into the mode of action of the antifungal effector Tfe1 elicited by the *Serratia marcescens* Type VI Secretion System

Maisie Palmer[1], Genady Pankovs[2], Pantelitsa Papakyriacou[3], Katharina Trunk[1], Amy Milburn[4], Ian Leaves[5], Christian Hacker[5], Neil Gow[5], Chris MacDonald[4], Colin Rickman[3], Sarah Coulthurst[2], Janet Quinn[1*]

[1] Biosciences Institute, Faculty of Medical Sciences, Newcastle University, UK
[2] Molecular Microbiology, School of Life Sciences, University of Dundee, UK
[3] Institute of Biological Chemistry, Biophysics and Bioengineering, Heriot-Watt University, UK
[4] Department of Biology, University of York, UK
[5] MRC Centre for Medical Mycology, University of Exeter, UK

Recent studies have revealed that gram-negative bacteria can deploy their Type VI Secretion System (T6SS) as a potent antifungal weapon via the secretion of specific antifungal toxins. This secretion system is a contractile nano-syringe which rapidly punctures neighbouring cells releasing effector toxin proteins. Although primarily considered to function in interbacterial competition through the secretion of antibacterial effectors, the identification of antifungal effectors illustrates an additional role for the T6SS in shaping polymicrobial communities and we are interested in the role of the T6SS in modulating the fungal composition of polymicrobial communities such as the gut microbiome.

We have amassed evidence that the use of the T6SS against fungal competitors is widespread. The *Serratia marcescens* T6SS secretes two potent antifungal effectors Tfe1 and Tfe2, and homologues of such effectors are found in a range of gram-negative bacterial species. Tfe1 displays potent activity against model (*Saccharomyces cerevisiae*) and pathogenic (*Candida albicans, Candida auris*) yeasts, and high resolution microscopy revealed that this effector accumulates at distinct loci at the plasma membrane. Our structure-function analyses, together with non-biased approaches, have provided a global overview of the impact of Tfe1 on yeast cell biology, with recent biochemical approaches defining the mode of action of this potent antifungal effector. As fungal pathogens cause an estimated 1.5 million deaths and destroy a third of global crop yields each year, can we exploit the mode of action of these potent antifungal effectors to identify new strategies to combat pathogenic fungi?

OFFERED TALK

Genomic analysis of the hyper branching C-variant phenotype in the Quorn mycoprotein fungus *Fusarium venenatum* A3/5

Jordan Price[1*], Ivey Geoghegan[2], John Connell[1], Helen Bates[1], Fiona Wilson[1], Richard Harrison[3]

[1] NIAB, UK
[2] Marlow Ingredients, UK
[3] Wageningen University and Research, The Netherlands

Quorn mycoprotein, a protein rich meat alternative, is produced through large scale fermentation of the fungus *Fusarium venenatum* A3/5. The A3/5 isolate was originally selected, in part, for its sparsely branched mycelium that enables processing into a meat-like texture. Maintaining fungal morphology is critical for consistent texture and production efficiency. However, each fermentation campaign can only be run for a few weeks before hyperbranched mutants, known as C-variants, appear within the population. These highly branched C-variants negatively affect the texture of the final product, ultimately limiting production capacity. We have isolated 12 C-variants and 12 post-fermentation WT-like strains from commercial mycoprotein fermentations and confirmed differences in morphology using radial growth assays. Whole genome sequencing identified mutations in the *FvLRG1* gene in 11 out of 12 C-variant isolates, which were not observed in the wild type isolates. *FvLRG1* encodes a Rho-GTPase activating protein that coordinates PKC and TOR pathway signalling through negative regulation of Rho1, and has been implicated in hyphal branching in other filamentous fungi. To confirm the role of these mutations, we used CRISPR/Cas9-mediated homology directed recombination (CRISPR-HDR) to separately introduce two of the C-variant mutations into the wild-type A3/5 isolate, which successfully recapitulated the characteristic C-variant morphology. This work has identified *FvLRG1* as the causal gene for C-variant formation during mycoprotein production. Ongoing investigation into the mechanisms of aberrant hyphal branching aims to prevent or delay C-variant appearance, extending the production cycle, reducing costs, and enhancing sustainability to meet growing demand for alternative proteins.

OFFERED TALK

Monoclonal antibodies targeting the fungal cell surface: next generation antifungal therapeutics

Steven McPherson[1,2], Yixin Zhao[2,1] ,Sami Alawfi[1*], Mark Mawer[1,2], Donna MacCallum[1], Soumya Palliyil[2], Carol Munro[1]

[1]Aberdeen Fungal Group, Institute of Medical Sciences, University of Aberdeen, UK
[2]Scottish Biologics Facility, Institute of Medical Sciences, School of Medicine, Medical Sciences and Nutrition, University of Aberdeen, UK

Invasive fungal infections are responsible for over 2.5 million global deaths annually. Currently there are several major challenges complicating the treatment of fungal infections. These include a concerning rise in antifungal drug resistance, the emergence of multidrug-resistant species, drug toxicities and drug-drug interactions. In parallel there is an ever-increasing number of immunocompromised patients and those at high risk of invasive infections. As a result, there is an unacceptably high mortality rate associated with these infections, reaching in excess of 40% even with treatment. Therefore, novel antifungal treatment approaches are being investigated, these include monoclonal antibodies and vaccines.

Here we investigate monoclonal antibodies (mAbs) specifically targeting the surface exposed regions of two key cell wall proteins (CWPs), Pga31 and Utr2 of the major human fungal pathogen *Candida albicans*. These mAbs were isolated from a human antibody library through phage display technology. Previous studies in our laboratory have shown these CWPs play a key role in cell wall remodelling and the maintenance of wall integrity when exposed to antifungal agents. The mAbs have demonstrated protection in a mouse model of systemic candidiasis, with our lead mAb achieving 83% survival. Importantly, our mAbs have demonstrated recognition of several clinically significant *Candida* species, including drug-resistant and drug-susceptible isolates of *C. albicans, C. auris, C. parapsilosis* and *C. tropicalis*. Furthermore, antibody binding assessed through *Candida* whole-cell ELISA and fluorescence microscopy has demonstrated preferential binding to the hyphal morphology when compared to yeast cells, suggesting these mAbs could be effective in the treatment of disseminated infection. To further interrogate the mechanisms of protection offered by our mAbs, immune cell interaction assays have been performed, showing enhanced phagocytosis by macrophages following pre-incubation with mAbs. Taken together, this initial promising data demonstrates the potential of our mAbs as a novel first-in-class therapy for invasive and drug-resistant fungal infections.

OFFERED TALK

Index Fungorum and Species Fungorum: Advancing through Digital Innovation

Mounes Bakhshi[1]*, Paul M. Kirk[1], Michelle Shackleford[1], Irina S. Druzhinina[1]

[1] Royal Botanic Gardens, Kew, UK

The ability to access quick, reliable, and up-to-date nomenclatural information is crucial for mycological research, biotechnology, biodiversity assessment, and regulatory decision-making. Unlike other eukaryotic groups, mycology is at the forefront of nomenclatural standardization, owing to the long-established public availability of fungal name resources and the mandatory registration of new fungal names before publication. This structured approach has significantly enhanced the stability and accessibility of fungal taxonomy, facilitating global collaboration.

Index Fungorum and Species Fungorum are globally recognized databases of fungal names and websites, launched in the late 1990s. They were based originally at International Mycological Institute (IMI) and were transferred to the Royal Botanic Gardens, Kew, on 30th June 2013. Currently, Index Fungorum, is one of the three officially recognized repositories, mentioned in International Code of Nomenclature for algae, fungi, and plants (ICNafp, Article F.5.1.), serves as the authoritative platform for the registration of fungal names. Species Fungorum is a platform, to produce an effectively complete global checklist of organisms belonging to the kingdom Fungi, and fungal-like taxa. These databases play a pivotal role in supporting researchers, policymakers, and conservationists by promoting standardized fungal nomenclature and fostering global collaboration in mycological studies. In 2024, Fungal Diversity & Systematics team at Kew initiated a new project to further develop and maintain these essential fungal name resources. The primary goal for 2025/2026 is to accelerate the curation and completion of database entries, ensuring the most accurate and up-to-date nomenclatural and taxonomic information is available. In partnership with Kew's Digital Revolution team, we are enhancing the website and optimising database management by improving accessibility, functionality, cybersecurity, and automation of data processing. During this presentation, we will outline the progress made towards these objectives and invite feedback from the scientific community, gathering ideas for further improvement.

OFFERED TALK

Widespread tissue-specific gene expression during fruiting body development of *Coprinopsis cinerea* revealed by laser-capture microscopy coupled low-input RNA sequencing

Torda Varga[1,2]*, Balázs Bálint[1], Xiao-Bin Liu[1], Hongli Wu[1], Zhihao Hou[1], Máté Virágh[1], Csenge Földi[1], Árpád Csernetics[1], Nikolett Miklovics[1], Zsolt Merényi[1], László G. Nagy[1]

[1] Synthetic and Systems Biology Unit, Institute of Biochemistry, HUN-REN Biological Research Centre, Hungary
[2] Royal Botanic Gardens Kew, UK

The fate of cells in a developing organism has always been a central question for biologists. While elaborate cell fate maps exist in animal and plant model systems, we have little knowledge about how the main tissue types are formed during multicellular development in fungi. Here we explore tissue differentiation of *Coprinopsis cinerea* using laser-capture microdissection (LCM) coupled with low-input RNA sequencing and compare temporal and spatial mRNA expression changes in different cell populations of six primordial developmental stages and 26 tissue types to understand fine-scale patterns of early fruiting body development.

Gene expression showed a high level of tissue-specificity within the primordium, implying significant spatial variation in the transcriptome. For example, defense-related and cell surface-protein encoding genes showed increased expression in tissues close to the environment (e.g., universal veil or cap) relative to inner fruiting body structures (e.g., nodulus, stipe). GO enrichment analyses identified higher activity of methyl transferases in stipe-, cap- and gill-related tissues, suggesting tissue-specific protein modifications. The conserved biogenesis of the pheromone mating factor in fungi involves methylation of the protein's CAAX motif, therefore, we further investigated the tissue-specific expression of pheromones and proteins harboring CAAX motif. To validate the role of candidate proteins controlling fruiting body development, we generated knock-out and overexpression mutants, supporting our hypothesis that small proteins with a CAAX motif play a role in tissue differentiation.

In summary, we showed that cell populations during the early development of the fruiting body follow a strict genetic program and gene expression exhibits a high tissue-specificity even at the early phases of cell differentiation. Our work could further extend our knowledge on the genetics of fruiting development and could generate new hypotheses for gene functions.

OFFERED TALK

Testing Novel Anti-biofilm Technologies

Ellen Wikeley[1], Joanne O'Keefe[2], Matthias Brock[1]

[1] School of Life Sciences, University of Nottingham, UK
[2] Unilever, UK

Biofilms are structured surface-adherent microbial communities embedded in a self-made extracellular polymeric matrix. Fungi commonly form biofilms, often synergistically with bacteria, causing issues across multiple sectors including healthcare, textiles, and marine environments. However, removing biofilms is hampered by increased resistance to most of the currently applied methods. The project partner Unilever has developed variations of an organic lactam compound that could be suitable as a novel antibiofilm technology. The lead structure is derived from furanones that are produced by the red seaweed *Delisea pulchra* to block microbial colonisation on its surface. We are focussing on the mechanistic understanding of the effects of lactams on fungal and polymicrobial biofilms. Thereby, we investigate both fungal-specific targets and potential targets that may be commonly shared between fungi and bacteria. Thus, we combine techniques of gene expression analyses, generation of fungal deletion and overexpression strains, and high-performance liquid chromatography. First results confirmed that various lactam derivatives delayed or inhibited fungal spore germination in a concentration and species-dependent manner. By contrast, the mycelium of some filamentous fungi converts lactams into novel products with reduced toxicity. Conversion of lactams by various fungi was analysed, and mass spectrometry data suggests that lactam conversion is mediated by a dehydrogenase. Current studies focus on the purification and identification of the respective enzyme. In conclusion, lactams efficiently inhibit fungal spore germination and biofilm formation with a potential lactam detoxification mechanism by fungal mycelium. However, understanding the mode of action of lactams and their inactivation still requires further investigation.

OFFERED TALK

Underpinning mycological research - culture collections of living fungi

Matthew J. Ryan*, Anthony Kermode, Alan Buddie

CABI, UK

The stringency and reproducibility of mycological research relies on the infrastructure that supports it. Essential to this are the culture collections of living fungi that provide services and resources to mycologists to enable them to undertake and verify their work. Egham, the location of this conference has been the home of the CABI mycological resource collection since 1992. Established in 1947 when cultures were incorporated from the UK National Type Culture Collection, the collection, aided by deposits from notable mycologists including Booth, Hawksworth, GC Ainsworth and Sutton, has grown to become one of the most relevant to global agriculture and consists of 28,000 strains representing 6,000+ species.

Successful preservation of fungi relies upon the application of optimised techniques to ensure the fungus remains stable during storage. Over the past 50 years, CABI has been at the forefront of cryopreservation research, utilising state-of-the-art methodologies, such as Stirling cycle cooling. Optimally preserved strains provide the tools for enabling broader research questions to be answered; recent research has focussed on the genus *Fusarium*, for which whole genome sequencing of historical disease isolates has allowed us to understand the evolution of the coffee wilt disease including evidence for horizontal gene transfer between different species[1]. Further, working with the Westerdijk institute, we are helping to re-evaluate the complexities of *Fusarium* phylogeny by describing new species based on the application of new molecular tools[2].

Looking to the future, collections must evolve to meet the needs of their user communities. With partners in the UK[3] and EU, we have developed methodologies for the conservation of biodiversity found in complex microbial communities within substates such as soils and seeds. Although experimental, preliminary experimental data clearly shows that unculturable fungi within the microbiome can be preserved and thus provide resources for the next generation of mycological researchers.

1. Peck LD et al. (2024) Horizontal transfers between fungal Fusarium species contributed to successive outbreaks of coffee wilt disease. PLoS Biol 22 (12): e3002480 https://doi.org/10.1371/journal.pbio.300248
2. Costa MM et al. (2024) Known from trees and the tropics: new insights into the Fusarium lateritium species complex. Studies in Mycology 109 (1): https://doi.org/10.3114/sim.2024.109.06
3. Ryan MJ et al. (2023) The UK Crop Microbiome Cryobank: a utility and model for supporting Phytobiomes research. CABI Agriculture & Bioscience 4 (53): https://doi.org/10.1186/s43170-023-00190-2

OFFERED TALK

Investigating the Role of Histone Post-translational Modifications in Antifungal Resistance

Takanori Furukawa[1, 2]*, Michael Bromley[2], Paul Bowyer[2]

[1] School of Health & Lifesciences, Teesside University, UK
[2] Manchester Fungal Infection Group (MFIG), University of Manchester, UK

Annually, more than 300 million individuals are affected by serious fungal infections, and around 3.8 million people die from fungal diseases. With the very limited arsenal of licensed antifungal drugs, emerging antifungal resistance poses a serious threat to human health on a global scale. In addition to well-characterised genetic adaptation mechanisms, emerging data are revealing that epigenetic mechanisms also play key roles in antifungal resistance. Epigenetic changes, such as post-translational modifications (PTMs) of histone proteins, can modulate gene expression profiles in response to certain stimuli, including stress imposed by antifungal compounds. Therefore, epigenetic mechanisms can influence resistance to antifungal drugs by altering the expression profiles of drug targets or genes associated with antifungal stress adaptation. However, our understanding of the role of epigenetic mechanisms in antifungal resistance is limited.

In this study, we investigated the role of histone-modifying enzymes in antifungal resistance using the major fungal pathogen of human lungs, *Aspergillus fumigatus*, as a model system. Through bioinformatic analysis of the *A. fumigatus* genome, we identified a cohort of putative genes potentially involved in histone-PTMs. Gene expression profiling revealed that *A. fumigatus* actively modulates the expression of the putative histone-PTM genes upon exposure to antifungal drugs. We generated a collection of deletion mutants for the histone-PTM genes and characterised their antifungal resistance profiles. Our analysis revealed that the loss of histone-PTM genes involved in histone H3 lysine 4 methylation (H3K4me) significantly reduces their resistance to azoles and an allylamine. Furthermore, Chromatin Immunoprecipitation sequencing (ChIP-seq) analysis targeted histone-PTMs showed that H3K4 methylation is widely present in the regulatory region of the genes associated with azole sensitivity. Overall, our results suggest that the epigenetic process involving H3K4 methylation plays an essential role in regulating gene expression programmes linked to antifungal resistance in *A. fumigatus*.

OFFERED TALK

Enhancing the conservation status of Clavariaceae (Fairy Clubs, Spindles and Corals) in ancient grassland habitats by applying molecular phylogenetics

Louise Tranter[1]*, Gareth Griffith [1], Gemma Beatty[2], Andrew Detheridge[1], Matt Wainhouse [3]

[1] Mycology, Cledwyn Bridge, Aberystwyth University, UK
[2] School of Biological Sciences, Queen's University Belfast, UK
[3] Natural England Fungi and Lichen Specialist Services & Programmes Team, UK

Despite great advances in curated genetic sequence databases such as UNITE, eDNA studies reveal many unknown taxa sequences (highlighted at IMC12 2024). For fungi, relative paucity of morphological traits contributes not just to sequence ambiguity, but also potential cryptic speciation. Species of conservation concern, the CHEGD macro-fungi assemblage (Clavariaceae, Hygrophoraceae, Entolomataceae, Geoglossaceae and *Dermoloma* spp.), are important indicator species of ancient grasslands. However, ambiguous species definitions and eDNA sequences from soil sampling that cannot be linked to species names generates difficulties for assessing the importance of sites. This is especially pertinent for Clavariaceae that often represent a high proportion of fungal biomass in ancient grasslands, though up to 50% detected via eDNA metabarcoding are unidentified or misnamed.

The research focuses on Clavariaceae genus *Clavulinopsis*. Internal transcribed spacer (ITS) DNA sequences of fruiting bodies are extracted, edited, trimmed and annotated. Fruiting body identity is verified by macro and micro morphological examination. Verified sequences are employed to build phylogenies centred around species type (or epitype) specimens. Database unidentified Clavariaceae sequences are inserted to evidence their correct naming. For the superficially distinctive species *Clavulinopsis corniculata* (Meadow Coral) phylogenetic analysis has revealed two distinct clades. This suggests speciation, though distinguishing speciation using only the ITS region is problematic. More genetic information is required. An optimised CTAB extraction for high molecular weight DNA is implemented for population sequencing. Population genetics provides greater genetic resolution and evidence of gene flow, thus enabling employment of the biological species concept, and matching this with morphological and phylogenetic species concepts. Additionally, the wide genetic variability (> 5% in the ITS locus) of these species is considered, questioning the application of speciation at the 1.5-3% threshold range.

The research aims to aid and simplify the task of field ecologists who require morphological evidence at the front line of fungal conservation.

OFFERED TALK

Rhamnolipids, antifungals for mucormycosis?

Jacob Hudson[1], Marta Farre Belmonte[1], Gary Robinson[1], Rebecca A. Hall[1]

[1]School of Biosciences, University of Kent, UK

Fungi from the order *Mucorales* are responsible for causing mucormycosis, a disease with mortality rates approaching 96% in disseminated infections. *Rhizopus* spp. are responsible for causing 70% of cases, with an incidence of 1.7 cases per million globally, but this can be 80 times higher in India due to the prevalence of uncontrolled diabetes in the country. Amphotericin B is the main treatment for mucormycosis, with some of the Triazoles displaying limited efficacy against these fungi. Therefore, new treatments to tackle this emerging infection are urgently required. In the host and environment, the fungi compete with bacteria for space and nutrients. Indeed, *Pseudomonas aeruginosa, Staphylococcus aureus*, and *Escherichia coli* have all been co-isolated from chronic cases of mucormyosis. It has been shown previously that *P. aeruginosa* siderophores inhibit *R. microsporus* spore germination via the sequestration of iron. However, saturation with iron does not entirely restore germination, suggesting that other factors may be at play. Here, we confirm that *P. aeruginosa* inhibits *R. microsporus* growth independently from siderophore mediated iron restriction. This antifungal activity is mediated by a small, secreted, heat stable molecule(s). Preliminary data using supernatant fractionation and mutants defective in rhamnolipid biosynthesis suggest that mono-rhamnolipids may be mediating the observed antifungal activity. Future work will explore the use of these molecules as potential antifungals against mucormycosis infections.

OFFERED TALK

Fungal Morphometrics: Correlating Carbon Source Variations with Mechanics and Surface Chemistry of Fungal Mycelia

Juwon S. Afolayan[1]*, Carole C. Perry[1],

[1] Biomolecular and Material Interface Research Group (BMIRG), Nottingham Trent University, UK

This study investigates the effect of different sugars and sugar concentrations on the mechanical properties and surface wettability of five fungal strains: *Aspergillus niger*, *Botrytis cinerea, Rhizopus oryzae, Trametes versicolor*, and *Schizophyllum commune*. Fungal mycelia, as a sustainable alternative to petrochemical-derived materials, offer broad applications in fields ranging from bioremediation to biomaterials. Understanding how carbon sources influence mycelial growth and properties is essential for optimizing these applications.

In the first experiment with *R. oryzae*, we tested various carbon sources, including monosaccharides (glucose, fructose, galactose, and xylose), sugar alcohol (xylitol), and disaccharides (maltose and sucrose), using minimal media (MM) and potato dextrose broth (PDB) as controls. We observed a clear preference for certain sugars, with glucose yielding mycelia exhibiting favorable mechanical properties such as thickness, strength, elongation, and stiffness. These properties were independent of whether the sugars were monomeric or polymeric.

The second experiment expanded to all five fungal strains, grown in PDB, MM, or MM supplemented with sugars at concentrations based on optimal levels from literature, which were also doubled. We examined the effects on both solid and liquid media to ensure comparable results. Increasing the sugar concentration in minimal media (from 60mM to 120mM) significantly impacted mechanical parameters and surface wettability in *A. niger*, *B. cinerea*, and *R. oryzae*, with mycelia grown in 120mM sugars exhibiting increased thickness and hydrophobicity. In contrast, higher fructose concentrations impaired growth in *T. versicolor* and *S. commune*. Notably, the study also highlighted the role of sustained nutrient availability in mycelial hydrophobicity and mechanical characteristics.

This work underscores the importance of adjusting carbon sources and concentrations to manipulate mycelial structure and properties, offering valuable insights for optimizing mycelium-based biomaterials.

OFFERED TALK

Assessing the Susceptibility of Mycelium-Based Composite Insulation Materials to Mould Growth

Joni Wildman[1]*, Daniel Henk[2], Pete Walker[1], Andrew Shea[1]

[1] Department of Architecture and Civil Engineering, University of Bath, UK
[2] The Milner Centre for Evolution, University of Bath, UK

The urgent need for sustainable and circular materials in the construction industry has driven increasing interest in mycelium-based composites (MBCs). MBCs are typically derived from the growth of fungal mycelium on lignocellulosic substrates. As the mycelium colonises the material it binds the substrate, forming a natural adhesive. The resulting material is dried in an oven to kill the fungi and produce an inert products that have exhibited promising thermal, acoustic, and environmental properties. However, their susceptibility to mould growth remains a concern for their widespread adoption in building applications, and research on this issue remains limited.

This study investigates the mould resistance of MBCs produced using *Ganoderma curtisii* mycelium grown on a hemp-shiv substrate. Mould susceptibility was assessed following BS EN 17886, a standardised test method for evaluating fungal growth on insulation materials. The study involved exposing MBC samples to spore suspensions of six common mould species affecting building materials: *Aspergillus niger, Trichoderma viride, Talaromyces pinophilus, Chaetomium globosum, Paecilomyces variotii*, and *Aspergillus versicolor*. Samples were subjected to controlled environmental conditions with varying temperature and humidity levels to determine critical thresholds for mould development. Qualitative and quantitative analyses were conducted to assess fungal colonisation over time.

The findings of this research establish key temperature and humidity ranges where MBCs remain resistant to mould, providing insights for their safe storage and application in construction. This work serves as a foundation for future research aimed at mitigating mould risk, including optimising substrate composition, altering MBC fabrication processes, and exploring antifungal treatments that do not detract from the sustainability of these materials.

POSTER 1

Understanding interactions of fungicides, fungi and wheat to inform the restoration of degraded agricultural land

Alice Day*, Bonnie Waring, Mathew Fisher

[1] Imperial College London, UK

Intensive agriculture relies on the repeated spraying of broad-spectrum fungicides, which harm off-target beneficial fungi and has led to a rise in antifungal resistance in crop and human pathogens. Fungicide use has created a shift in holobiont communities pushing crops and their associated microbial communities towards a state of dysbiosis.

This study aims to investigate how fungicides influence soil fungal communities and subsequently wheat yields and nutrition, with the goal of informing the restoration of degraded agricultural land using soil transplants.

24 agricultural soils, that have been exposed to agrochemicals over many years, and 24 natural soils, from unmanaged woodlands and grasslands, have been sampled from across the UK. These 48 soils were used in a paired pot experiment to grow wheat, with half receiving an application of fungicides. Fungal communities from these 48 samples have been analysed using ITS2 metabarcoding to compare the impact of land use and fungicide application on soil fungal communities and the subsequent effects on wheat yields and nutrition.

To test the potential of utilising the microbiome for restoration, the soils that produced the highest and lowest yielding wheat plants were selected as donor soils for soil transplant field trial. A thin layer of each donor soil will be applied on a conventional agricultural field, using a randomised plot design. This approach aims to shift the microbial community of the agricultural field towards that of the applied donor soil in order to increase crop yields and restore a resilient, intact microbial community that reduces the reliance on chemical fertilisers.

POSTER 2

Paradendryphiella salina – a model marine fungus for investigating the biology, ecology and biotechnology potential of macroalgae (seaweed) fungal interactions

Beth Tindall-Jones[1,2], Sophie Harley[3], Glen Wheeler[1], Mike Allen[2], Steve Michell[2], Michael Cunliffe[1,3]

1 The Marine Biological Association, UK
2 University of Exeter, UK
3 University of Plymouth, UK

Marine fungi have been known to associate with macroalgae (seaweed) for over a century, yet this relationship remains underexplored in a biological and ecological context. With the rapidly developing European seaweed industry, new biotechnological opportunities that utilise fungal-seaweed biomass could be supported with improved knowledge of fungi-seaweed interaction.

We have been developing the model marine ascomycete *Paradendryphiella salina*, an obligate marine fungus found widely on the shoreline with various marine macroalgae species. Our aims have been to better understand the relationship between *P. salina* and macroalgae through fundamental biology in an ecological context with biotechnological potential.

Comparison of *P. salina* growth with different macroalgal-produced polysaccharides (fucoidan from *Fucus serratus*, Laminarin from *Laminaria digitata*, carrageenan, ulvan and sodium alginate) were made to screen for responses to variation in chemical composition of different macroalgal species. We focused on early growth stage processes including germination and initial hyphal development. Germination rate was higher in all polysaccharides compared with no carbon controls. Variation in tip number, total hyphal length and hyphal growth unit (HGU) varied between polysaccharide exposure.

We have also explored how *P. salina* interacts with living and dead tissue using the commonly occurring macroalga Fucus serratus. We show that mycelium cover was considerably higher on dead compared to live tissue and during early stages of growth HGU was smaller on dead tissue compared to live tissue.

Paradendryphiella salina is amenable to biological and ecological studies that demonstrate versatility in response to macroalgal-produced polysaccharides and substrate status (i.e. live vs. dead) as expected for a saprotrophic fungus thriving in a complex substrate environment. These properties suggest that *P. salina* could be further developed for biotechnological applications including in valorisation strategies for seaweed biomass production.

POSTER 3

Targeting Nutrient Sensing in a Hazardous Fungal Pathogen to Turn-Off Virulence and Mycotoxins

Diah Putri[1], Louise E. Johns[1,2], Tess Dilks[2], Neil A. Brown[1]

[1] Milner Centre for Evolution, Department of Life Sciences, University of Bath, UK
[2] Rothamsted Research, UK

Fungal pathogens threaten global food security by damaging crops and contaminating food with harmful mycotoxins. Fusarium Head Blight (FHB), caused by *Fusarium graminearum*, is one of the most destructive cereal diseases, leading to significant economic losses and health risks due to mycotoxin accumulations. Current control strategies, such as fungicides and partially resistant crop varieties, have limited effectiveness at preventing mycotoxin contaminatons, highlighting the urgent need for novel and sustainable disease and mycotoxin management approaches.

Nutrient sensing plays a critical role in fungal pathogenicity, enabling fungi to adapt to host environments, regulate metabolic pathways, and coordinate virulence factor production. *F.graminearum* senses environmental changes in its host, such as polyamine plant stress signaling that promotes the pathogen to produce mycotoxins that suppress plant defenses. Targeting fungal nutrient transporters/transceptors presents a promising strategy for disease control by interfering with pathogen's ability to adapt and respond to the host environment.

This study focuses on the role of Methylammonium Permeases (MEPs), a class of fungal membrane transporters, involved in nutrient acquisition and virulence. We identified four MEP transporters in F. graminearum, which exhibit differential regulation in response to nitrogen availability and during wheat infection. Using split marker-mediated transformation, we generated MEP deletion mutants and demonstrated that FgMep4 is essential for both fungal virulence and the production of the mycotoxin deoxynivalenol (DON). The complementation of Δfgmep4 restored virulence, confirming its functional significance. RNA sequencing analyses revealed that FgMep4 influences fungal secondary metabolism and affects wheat transcriptional responses during colonization. RT-qPCR analyses suggest that FgMep4 is vital for induction of mycotoxin biosynthesis in response to polymaines. Future research will explore MEP transporter-transceptor functions in different nitrogen environments using heterologous yeast systems.

Understanding how FHB pathogens exploit host-derived nutrient signals could reveal novel antifungal targets, paving the way for innovative strategies to combat FHB and reduce mycotoxin contaminations.

POSTER 4

Dissecting the molecular mechanisms driving heightened antifungal stress resistance in aged *Candida albicans* population

Eloise Mitchell[1]*, Barry Bromilow[1], Helen Wright [2], Janet Quinn[1], Alessandra Da Silva Dantas[1]

[1] Newcastle University, UK
[2] The University of Liverpool, UK

More than 1.5 million people succumb to fungal infections each year. Worryingly, antifungal resistance (AFR) has emerged, prompting and has prompted the WHO to develop its first list of fungal priority pathogens. Two *Candida* spp. have been listed as critical priority: *Candida albicans* (one of the most common causes of bloodstream infections) and *Candida auris*, which is intrinsically resistant to most major antifungals. This surge can be attributed to advancements in medical treatments that have led to a rise in the proportion of immunocompromised patients who, which require antifungal treatment. Research has identified several key pathways within *C. albicans* that regulate antifungal resistance, however a small subset of cells in null mutants in these pathways can still survive to antifungal treatment. Our lab has previously demonstrated that replicatively aged (RAGE) C. albicans cells have displayed heightened resistance to antifungal treatment, underpinning our hypothesis that the small subset of cells that survive antifungal treatment in mutants that are highly sensitive to antifungal treatment is composed by RAGE cells and their offspring.

Using the novel 'Track and Trace' technique developed by our lab allows us to track the RAGE cell population and trace their progeny over time, providing insight into the dynamics of ageing and its impact on antifungal resistance within *C. albicans* populations. We have screened *C. albicans* cell wall mutants that are known to be sensitive to antifungals and asked whether the small subset of cells that survive antifungal treatment are RAGE cells. Using this technique, we have started identifying important cell wall regulators regulating replicative ageing in *C. albicans*. And most importantly, identifying regulators that contribute to age-dependent antifungal resistance. Identifying such mechanisms will allow for directly targeting resistant RAGE *Candida* cells as a potential antifungal strategy.

POSTER 5

Mechanisms behind virus-host interactions: how mycoviruses modulate fungal host phenotypes

Josephine L. Battersby[1,2]*, Ioly Kotta-Loizou[1,2], Robert H.A. Coutts[1], Esther Garcia-Cela[1], Ernesto Cota[2]

[1] Department of Clinical, Pharmaceutical and Biological Science, University of Hertfordshire, UK
[2] Department of Life Sciences, Imperial College London, UK

Aspergillus fumigatus, the principal etiological agent of invasive aspergillosis infections (IAIs), harbours numerous viruses, known as mycoviruses. Mycoviruses occasionally modulate fungal host phenotypes, such as alterations to secondary metabolite synthesis, virulence, and susceptibility to abiotic/biotic stresses. Aspergillus fumigatus polymycovirus 1 (AfuPmV1) is a dsRNA virus from the Polymycoviridae family, consisting of four mono-cistronic segments. Previously, AfuPmV1 was reported to cause hypovirulence of IAI in a mammalian model, suggesting a possible application of the virus as a therapeutic for the disease. As global cases of IAI's rise, amid emerging antifungal resistance, this discovery could have significant implications for fungal medicine. Despite this, the mechanisms behind these mycovirus-mediated phenotypes remain ambiguous, and the full potential of these viruses cannot be unlocked until they are further delineated.

Here, these molecular mechanisms will be elucidated by examining the biochemistry of each AfuPmV1 protein, mapping their interactions with fungal host components and uncovering host pathways involved. To achieve this, vectors for expression of affinity tagged AfuPmV1 proteins from (i) the *A. fumigatus* genome using CRISPR-Cas9 genome engineering, and (ii) using the *Pichia pastoris* expression system have been constructed. Following protein expression via both avenues, downstream *in vivo* and *in vitro* protein-protein interaction assays will be conducted to reveal interacting fungal host proteins or nucleic acids. Phenotypic assays will then be carried out on the *A. fumigatus* strains overexpressing individual AfuPmV1 viral proteins, to examine changes to virulence, antifungal drug resistance, and toxin production. In turn, fluorescent tagging of the viral proteins will be conducted to facilitate protein subcellular localisation by fluorescence microscopy. The findings of this investigation will provide valuable insight into the mechanisms by which mycoviruses interact with their fungal host to modify its physiology, potentially laying the foundation for manipulation of viral genomes to induce user-defined host phenotypes in the future.

POSTER 6

Investigating Fungal Spore Dispersal in UK Arable Crop Systems Under Current and Future Environmental Conditions

Patrick McClean[1], Jon West1, Kevin King[1], Yongju Huang[2]

[1] Rothamsted Research, UK
[2] University of Hertfordshire, UK

This project aims to enhance the understanding of fungal pathogen spore dispersal within UK arable crop systems and examine its potential changes under evolving climate conditions. With the goal being improve disease management strategies. The research encompasses three interconnected work streams.

Fungal Metagenomic Analysis of Spore Dispersal: Samples from plants and air will be collected throughout the growing season from wheat and oilseed rape plots at Rothamsted Farm. Air samples will be captured using spore samplers positioned above the plots and roof-based traps. Over three field seasons, environmental DNA from these samples is extracted and analysed using MinION third-generation sequencing. The fungal communities are profiled and statistically compared to explore spore dispersal dynamics and community shifts across crop rotations.

Regional Spore Dispersal in Air: The focus will be on wheat's Fusarium Head Blight (*Fusarium graminearum*) and three OSR diseases: Phoma (*Plenodomus* spp.), Sclerotinia (*Sclerotinia sclerotiorum*), and light leaf spot (*Pyrenopeziza brassicae*). Airborne spores will be sampled daily using a 7-day Burkard spore trap at Rothamsted Research. DNA from these samples will be analysed via quantitative PCR to monitor spore release patterns over multiple seasons. This data will be combined with archived records to assess temporal changes.

Impact of Changing Environmental Conditions: Study is conducted into the effects of extreme weather events, such as drought and flooding, on fungal spore release. Soil containers with OSR debris and infected wheat grain are exposed to natural and simulated weather conditions (flooding & drought). Fruiting body development is observed to help determine the impact of environmental stresses on spore release.

This study hypothesises that crop rotations and climate change will influence spore release timing and pathogen abundance, with metagenomics offering insights into spore dynamics under various management practices and climatic conditions. The outcomes will contribute to a deeper understanding of disease outbreaks UK agriculture.

POSTER 7

Fungi of Future Forests: do elevated CO_2 levels affect soil fungal community composition in oak woodland?

Rachel Calder[1,2]*, Mark A. Anthony[3], Johanna Pihlblad[2,4,5], Robert Grzesik[2,4], James Gore[2,4], Sami Ullah[2,4], Megan C. McDonald[1,2]

[1] School of Biosciences, University of Birmingham, UK
[2] Birmingham Institute of Forest Research, University of Birmingham, UK
[3] Centre for Microbiology and Environmental Systems Science, University of Vienna, Austria
[4] School of Geography, Earth and Environmental Sciences, University of Birmingham, UK
[5] Lancaster Environment Centre, Lancaster University, UK

Soil fungal communities are crucial determinants of tree health and nutrient cycling in woodlands, yet their susceptibility to global change impacts is poorly understood. The Birmingham Institute of Forest Research Free Air Carbon dioxide Enrichment facility (BIFoR FACE), a long-term experiment exposing sections of a mature oak woodland in Staffordshire (UK) to elevated CO_2 levels, offers a unique opportunity to explore soil fungal responses to anticipated rises in atmospheric [CO_2]. Soil DNA samples from treatment plots (+150 ppm CO_2) and control plots (ambient [CO_2]) at BIFoR FACE were subjected to ITS1 metabarcoding to characterise the soil fungal communities at three different time-points representing up to seven years of CO_2 enrichment. For two of these (February 2021, March 2023) O horizon samples only were available; for the final timepoint (October 2023) O and A horizons were sequenced. Significant seasonal and inter-annual variability was apparent in fungal community composition, dwarfing any treatment effects. Contrary to hypotheses, there was no evidence of increased ectomycorrhizal abundance under elevated [CO_2]; in conjunction with other work from BIFoR FACE this may suggest that trees at the site are investing more in exudates than in mycorrhizae to meet the higher nutrient demands imposed by photosynthetic enhancement under elevated [CO_2]. For the October 2023 timepoint, CO_2 enrichment significantly modified the effects of soil horizon on fungal richness ($p=0.04$) and Shannon diversity ($p=0.03$) such that differences between O and A horizons were less pronounced under elevated than ambient [CO_2]. Inferences from this finding are tentative as it was based on a small number of samples ($n=36$) from a single timepoint. Determining whether this interaction effect also exists at other timepoints, what might be driving it, and what its implications could be in terms of biodiversity-ecosystem function relationships, will be a priority for future research.

POSTER 8

Beware the air?: Exploring indoor airborne fungal communities and urban chemical pollutants

Sam Hemmings[1]*, Shane Fitzgerald[1], Dana Varaden[1], Leon Barron[1], Frank Kelly[1], Mat Fisher[1]

[1] Imperial College London, UK

In modern western societies, individuals spend up to 90% of their time indoors, yet while outdoor air quality has been extensively studied, the quality of indoor air—particularly the pollutants we inhale at home—has received less attention. Monitoring indoor air quality is essential, especially regarding exposure to mould, volatile organic compounds (VOCs), and particulate matter, all of which are linked to respiratory issues and infectious diseases. As part of the WellHome project, this study analysed airborne fungal communities in 118 homes in West London through passive air sampling conducted between 2022 and 2024, with comparisons to outdoor environments. Amplicon sequencing revealed a significant prevalence of fungal genera such as *Penicillium* and *Aspergillus* for indoor environments, alongside seasonal variations in fungal community profiles. Quantification of fungal burden using qPCR identified homes with elevated levels of specific fungal pathogens, which were linked to case studies of respiratory issues in occupants. Furthermore, significant correlations were observed between fungal community compositions and VOCs, suggesting potential interactions between biological and chemical pollutants. These findings highlight the need for comprehensive monitoring of indoor environments to better understand the combined effects of biological and chemical pollutants on air quality and public health.

POSTER 9

Genome editing to induce genome rearrangements in a human fungal pathogen

Matthew Shaw*, Alessia Buscaino

[1] University of Kent, UK

Candida albicans a member of the healthy human microbiome and an opportunistic pathogen, causing infections ranging from superficial to systemic. During systemic infection, *C. albicans* can rapidly adapt to any niche in the body and can acquire drug resistance. These traits are partially attributed to its genomic instability, which generates diversity and allows selection of fitter genotypes. This is apparent from the diversity of karyotypes seen in clinical isolates which often have breakpoints around repetitive elements. Such elements include the Major Repeat Sequence (MRS), a repeat array occurring throughout the *C. albicans* genome. We hypothesise that repetitive elements including the MRS serve as instability hotspots to facilitate genomic rearrangements and rapid evolution.

This project aims to establish a cause-and-effect relationship between repeat-associated chromosomal rearrangements and generation of fitter genotypes. To this end, we have used CRISPR-Cas9 to generate double strand breaks within repetitive elements, inducing chromosome rearrangements. These unstable strains have then been phenotyped, and evolved in clinically relevant stresses, including antifungal drugs.

Long-read, short read and RNA sequencing have then been used to characterise the novel genotypes and transcriptomes. This has shown that CRISPR-Cas9 can be used to generate different classes of chromosomal rearrangement in *C. albicans*. Strains bearing rearrangements have morphological and fitness changes, as well as reduced pathogenicity during in vivo infection models. This indicates that rearrangements at repeat loci are sufficient to generate phenotypic diversity. Preliminary experiments demonstrate that rearranged strains are also less stable and undergo more frequent karyotype changes during evolution experiments. Further work will look at the effect of this instability on their ability to adapt to stress.

POSTER 10

Harnessing the Microbiome to Combat the Threat of Fungal Mycotoxins

Oly Grey Ascione[1], Daniel Henk[1], Neil A. Brown[1],

[1] Milner Center for Evolution, Department of Life Sciences, University of Bath, UK

Fusarium mycotoxins such as deoxynivalenol (DON) are present throughout our cereals, where their detection above safe levels increasingly results in contaminated crops being downgraded to animal feed, costing Europe €100 million each year. Therefore, *Fusarium* mycotoxin contaminations of feed cereals present a growing threat to the economic viability and health of farmed animals. In turn, new ways to protect and decontaminate animal feed are urgently required. Microbes isolated from plant and soil microbiomes can have the ability to impede *Fusarium* contaminations and possess microbial enzymes with abilities to detoxify *Fusarium* mycotoxins. These microbes and their detoxifying enzymes therefore have value as feed additives.

Our objective is to identify the mechanisms that microbes of interest use to inhibit *Fusarium* growth and/or detoxify infected cereals. To start, 80 environmental *Metschnikowia* isolates were screened against the Fusarium Head Blight pathogen, *Fusarium graminarium*. Multiple *Metschnikowia* isolates showed considerable inhibitory effects against fungal germination and hyphal growth, showing their potenital to inhibit continued fungal growth and mycotoxins in contaminated feed cereals. Subsequently, we are using adaptive laboratory evolution of *Metschnikowa* in response to DON, to enhance DON tolerance and detoxification. Further genomic, mass spectrometry and genetic analysis will be used to explore mechanisms of *Fusarium* inhibition and mycotoxin degredation.

Collectively, this work will enhance our understanding and capacity to develop microbes, or the biofungicides and detoxifying enzymes they produce, as additives to mitigate the impact of increasing mycotoxin contaminations in animal feed, protecting animal health and enhancing our food security.

POSTER 11

Old Products, New Consumers: A Mycotoxin Exposure Concern

Silvia Alamo[1], Alessandra Marcon-Gasperini[1], Pablo Barcelo[1], Esther Garcia-Cela[1]*

[1]University of Hertfordshire, UK

Tempeh, a fermented soy product, has traditionally served as a nutritious, protein-rich staple in Southeast Asian cuisine. In recent years, these products have transcended their traditional boundaries, becoming popular choices among vegetarians, vegans, and health-conscious consumers worldwide, gaining global recognition as sustainable protein alternatives. Despite their nutritional benefits, the potential for mycotoxin contamination in these products remains underexplored, and current regulatory frameworks do not mandate their monitoring. The present study aims to develop a method for mycotoxins quantification using easy and cheap procedures such as the Crosstox column. Therefore, a comprehensive analysis of mycotoxin levels is essential to accurately assess consumer exposure risks and inform future safety regulations.

POSTER 12

Seeking Candidates for Diesel and Petrol Remediation

Madiana van Kooten[1]*, Alessandra Marcon-Gasperini[1] , Esther Garcia-Cela[1]

[1] Department of Clinical, Pharmaceutical and Biological Science, University of Hertfordshire, UK

The global dependence on petrochemical products has led to widespread environmental contamination due to spills, industrial waste, and improper disposal. Petrochemical hydrocarbons are highly persistent pollutants with toxic, mutagenic, and carcinogenic properties, posing serious risks to both ecosystems and human health. Current remediation methods, such as recycling and chemical treatments, are costly, labor-intensive, and largely ineffective, as petrochemical pollutants continue to accumulate in landfills and the environment.

Mycoremediation emerges as a green technology. The aim of this project is to screen the resilience of *Mucor, Penicillium*, and *Fusarium* species for growth and degradation of Diesel and Petrol. This is achieved by assessing fungal diametrical growth in solid media, evaluating liquid degradation through colour changes in media containing DCIPP, and measuring enzyme production using the APIZym kit. Ultimately, this project will identify potential candidates for use in mycoremediation.

POSTER 13

Are Stressful Environments Driving Increasing Threats from Virulent, Toxic, Drug-Resistant *Fusaria*?

Rosie L Latham [1], Diah A Putri [1], Kostya Kanyuka[2], Matthew Fisher[3], Andy Borman[4], Neil A. Brown [1]

[1] Milner Centre for Evolution, Department of Life Sciences, University of Bath, UK
[2] NIAB, UK
[3] MRC Centre for Global Infectious Disease Analysis, School of Public Health, Imperial College London, UK
[4] Mycology Reference Laboratory, UK Health Security Agency, UK.

Fusaria cause serious infections of humans that are notoriously difficult to treat. The WHO classifies *Fusaria* as 'High Priority', acknowledging their increasing threat and drug resistance. *Fusaria* also cause numerous crop diseases that contaminate our food with harmful mycotoxins, directly impacting our health. But we don't know why *Fusaria* are a growing threat and why they are so difficult to treat?

Fusaria persist throughout agricultural and urban environments, where they are under pressure from environmental changes and pollution. This raises an important question about how these environmental changes are affecting *Fusaria*? To explore this, we are studying 1) how different environmental reservoirs of *Fusaria* have adapted to humans and antifungals; and 2) how laboratory stress adaptation influences virulence, toxicity and antifungal resistance.

We created a *Fusaria* collection including isolates from farm soils, crops, urban wastewaters, and clinical human patients, identifying variation in stress tolerance and antifungal susceptibility. Within *F.oxysporum*, a species complex identified in all environments, isolates from triazole-contaminated farm and urban wastewaters, were less susceptible to agricultural and/or clinical triazoles. We are now using genomics to investigate the mechanism underlying stress tolerance, host range, and drug resistance.

We have also shown that laboratory adaptation of *F.graminearum* to environmental stress reduces triazole susceptibility, while also increasing virulence and mycotoxins during wheat infection. Genomic studies point to the PacC pathway connecting reduced antifungal susceptibility, virulence, and toxicity with stress adaptation, a potential mechanism behind how environmental stress could drive Fusaria to be more aggressive, toxic and antifungal resistant.

This shows *Fusaria* in a One-health context, where increasingly stressful and contaminated environments can act as reservoirs of more aggressive, toxic, and antifungal-resistant pathogens. This provides valuable insights for surveying and mitigating the growing *Fusaria* threat across agricultural and clinical systems.

POSTER 14

Elucidating the status of type specimens deposited in the Royal Botanic Gardens Kew's Fungarium

Matteo Gelardi/Masoomeh Ghobad-Nejhad/Rosie Woods[1]*, Ester Gaya[1]

[1] Jodrell Laboratory Royal Botanic Gardens, Kew, UK

Royal Botanic Gardens Kew's Fungarium (K) is the largest fungal collection worldwide with more than 1.25 million specimens, covering a wide diversity of taxa and geographic distribution. From these, ca. 50,000 specimens are roughly categorized as original name-bearing material, i.e. types. Types are of crucial importance to understand the identity and magnitude of biological diversity. In the eDNA era, sequencing type specimens can help us accelerate the identification and description of the unknown dimension of fungal diversity. However, sampling type specimens is not straightforward. In many collections, including Kew's Fungarium, many fungal types may not have been revised since they were first deposited, in some case more than 100 years ago. With a fungal taxonomy constantly evolving, the status of many of those specimens may have changed over the years. In the context of the Fungarium Sequencing Project (FSP), we have attempted to perform the first large-scale, in-depth examination of Kew's fungal type collection to elucidate the status of assumed types. To this goal, we carefully reviewed thousands of specimens assigned to 'red folders', presumed to be types, mainly using protologue scrutiny aided by Index Fungorum, Mycobank, literature reviews, and expert knowledge. Over half of the processed specimens were selected for DNA extraction and genome sequencing; the remaining were not prioritised for sampling due to various issues: scanty material, tissues affected by mould or pests, ABS (Access and Benefits Sharing) restrictions, non-current names, or non-type specimens. This extensive type examination also offered the opportunity to re-discover obscure or lost types. From 4,245 specimens reviewed to date, 16% are holotypes, 10% isotypes, 0.3% lectotypes, and 23% are not types. Around 28% of non-type material represent original or authentic material (i.e., potential lectotypes for future typification studies). Additionally, 4% of the studied specimens are provisional names (ineditus or ad interim). Reviewed material was collected between 1773 and 2024, including specimens collected by Charles Darwin. Most specimens reviewed to date belong to the main phyla Ascomycota and Basidiomycota. Within Ascomycota, reviewed genera include *Peziza s.l., Mollisia s.l., Orbilia s.l., Lachnum s.l.*, and *Xylaria s.l.*, amongst other. Within Basidiomycota, most important genera reviewed so far include (all in their broad sense, s.l.): *Boletus, Agaricus, Hydnum, Corticium, Polyporus, Hymenochaete, Phellinus, Inonotus, Trametes, Cyphella, Stereum, Peniophora*, and *Thelephora*.

POSTER 15

Marine diatrypaceous fungi from mangroves in Egypt and Saudi Arabia

Ali H. A. Bahkali, Mohamed A. Abdel-Wahab, E. B. Gareth Jones

Department of Botany and Microbiology, College of Science, King Saud University, Saudi Arabia

Diatrypaceous fungi is represented in marine habitats by 17 species that belong to seven genera that were mainly described from mangroves. Two diatrypaceous taxa were previously described from mangroves in Egypt and Saudi Arabia: *Diatrypasimilis australiensis* Jian L. Zhou & Kohlm. and *Halocryptovalsa avicenniae* (Abdel-Wahab, Bahkali & E.B.G. Jones) Dayar. & K.D. Hyde. Another two undescribed *Cryptosphaeria* species were recently recorded from decaying intertidal wood of Avicennia marina that was collected from Safaga mangroves, Egypt and Farasan Island mangroves, Jizan, Saudi Arabia. The morphology and molecular phylogenetics of the new taxa placed them within Diatrypaceae in a basal clade to *Cryptosphaeria avicenniae* Devadatha & V.V. Sarma, Cr. bathurstensis (K.D. Hyde & Rappaz) Dayar. & K.D. Hyde and an unidentified species of *Diatrypella* (GenBank accession no. MT543100) that was isolated from mangrove rhizosphere sediments in Kenya. Both new species of *Cryptosphaeria* form a widespreading entostroma with protruding necks. The new species of *Cryptosphaeria* from the Egyptian mangroves has a Phomopsis asexual morph, while the one from the Saudi mangroves have no asexual morph both in natural wood and in pure culture.

POSTER 16

Fungarium Sequencing Project: Sampling Progress and Outputs

Emily Hodgson[1]*, Mikele Baugh[1], Lawton Riness[1], Alana Raihan[1], Aries Rasul[1], Charlotte David[1], Eleni Bethke[1], Elle Dwyer[1], Henry Miller[1], Jessica Trow[1], Josepha Becker[1], Jude McFarlane Bond[1], Kat Gregory[1], Katie Lewis-Jones[1], Louis Wellbelove[1], Ying Luo[1].

[1] Royal Botanic Gardens, Kew, UK

The Fungarium Sequencing Project (FSP) at the Royal Botanic Gardens (RBG), Kew has been sampling type specimens from its historic collection of preserved fungal material for whole genome sequencing (WGS) since August 2024. Type specimens are the first specimens to bear a new scientific name and are designated as a permanent reference for a new taxon. Obtaining whole genome sequences of type fungal material will facilitate the inference of robust phylogenetic trees, anchored by the types and stabilised by a backbone of genomic data. Publicly sharing these sequences will also open innumerable applications in ecology, conservation, agriculture, medicine, and biotechnology. Kew's Fungarium is estimated to contain approximately 50,000 type specimens. Careful prioritisation determines which specimens are targeted for sampling first. This includes verifying categories of types, the types of current scientific names, assessing taxonomic importance, as well as strict adherence to Access and Benefit-Sharing (ABS) policy, and consideration of the quality of specimen material for downstream molecular methods and bioinformatics and ensuring enough material remains for future research. As of 26th February 2025, FSP has sampled 4,000 specimens from Kew's collection, and is forecast to sample approximately 5,000 specimens by 1 April 2025.

POSTER 17

Cryptic Marine Fungi: Chlamydospore-Producing Taxa

E. B. Gareth Jones, Ali H. Bahkali, Mohamed A. Abdel-Wahab

Department of Botany and Microbiology, College of Science, King Saud University, Saudi Arabia

Many marine fungi complete their life cycles as chlamydospores (e.g., *Corollospora mediterranea*), yet most of these fungi remain undetected in culture dependent studies. Additionally, *Corollospora ramulosa* produces sclerotia-like propagules known as sclerocarps, which are capable of surviving extreme conditions on beaches. Several chlamydospore-producing fungi have been commonly recorded from marine habitats in England and Saudi Arabia. Combined 18S and 28S rDNA phylogenetic analyses have placed four chlamydospore-producing fungi within the family Halosphaeriaceae. One new genus was isolated from decaying driftwood collected from Southsea, Hampshire, England. The other three taxa were recorded from Yanbu Beach on the Red Sea coast of Saudi Arabia, which includes a new genus and two new species belonging to the genera *Corollosporopsis* and *Keraliethelia*. Chlamydospores appear to be an adaptation to the harsh conditions of coastal habitats. Further morphological and molecular studies are needed to assess the actual diversity of chlamydospore-producing taxa in marine environments.

POSTER 18

Improving Curation and Documentation of Fungal Types Alongside a Large-Scale Sequencing Project

Henry Miller

Royal Botanic Gardens, Kew, UK

The Fungarium Sequencing Project (FSP) aims to sequence the genomes of several thousand fungal types housed in Kew's collections. Beyond its research aims, the project presents a unique opportunity to enhance collection curation through a comprehensive reassessment of type specimen status, nomenclature, and taxonomic organisation. By bringing together fungal taxonomists, curators, and specimen samplers, the FSP facilitates a large-scale review of Kew's fungal collections. This process allows key curatorial challenges to be resolved, including requesting back long-term loans, databasing newly uncovered information, relocating misplaced specimens, and repairing historical damage. The integration of sequencing with curatorial improvements underscores the project's significance in advancing fungal taxonomy and collection management.

POSTER 19

Synthesis and Biological Activity of New Antifungal Prodrugs

Vahid Barati[1], Ondřej Štěpánek[1], Ladislav Prener[2], Anna Hruzíková[2], Eliška Procházková[2], Adéla Čmoková[3], Miroslav Kolařík[3], Ulrike Binder[4], Ondřej Baszczyňski[1]

[1] Department of Organic Chemistry, Faculty of Science, Charles University, Czechia
[2] Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences, Czechia
[3] Institute of Microbiology, Czech Academy of Sciences, Czechia
[4] Medizinische Universität Innsbruck, Austria

Invasive fungal infections represent a global problem, causing more than 1.5 million deaths annually, especially among susceptible individuals. Pathogenic fungi are not limited to humans but are also a significant threat to animal health care and crop protection. However, drug-resistant fungi such as *Candida albicans* or *Aspergillus fumigatus* are challenging to treat. Moreover, the list of currently approved antifungals is limited, often demonstrating off-target toxicity, which complicates long-term therapies.

Self-immolative linkers developed previously in our lab offer an excellent opportunity to develop novel prodrugs which can potentially evade drug resistance while decreasing the toxicity of current antifungals.

In our work, we search for novel ways of targeting pathogenic fungi. It has been shown that suitable modifications of amphotericin B (AmB) carboxylate and/or mycosamine moiety can produce derivatives with retained antifungal effects and decreased toxicity. Thus, we prepared a series of AmB prodrugs to release the parent AmB either by non-specific enzymatic action (esterases, proteases) in the bloodstream, or directly on the site of infection upon pathogen-specific stimuli. AmB with C-28 carboxylate covered by simple POC promoiety served as a starting point for our investigation. Later we introduced more sophisticated phosphate-based promoieties, inspired by ProTide technology and our previous work on self-immolative phosphate linkers.

Synthesis, plasma stability, and cytotoxicity data of prepared AmB prodrugs in *G. mellonella* infection model will be discussed. We will also discuss various approaches to leading to prodrugging antifungal azoles.

Acknowledgement: This research was funded by the Czech Science Foundation project (O.B., grant number 23-05752S) and by Strategie AV21 project "VP33 MycoLife - the world of fungi" of the Czech Academy of Sciences. Microscopy was performed at the Laboratory of Confocal and Fluorescence Microscopy co-financed by the European Regional Development Fund and the state budget of the Czech Republic, CZ.1.05/4.1.00/16.0347, CZ.2.16/3.1.00/21515 and Czech-BioImaging large RI project LM2015062.

POSTER 20

Detecting fungicides in UK soils by LC-MS analysis

Rodrigo Leitao[1], Abdullah Shahid[2], Keng Tiong[2], Alexandra Richardson2, Leon Barry[2], Matthew C. Fisher[1]

[1]Medical Research Council Centre for Global Disease Analysis, Imperial College London, UK
[2]Environmental Research Group, School of Public Health, Faculty of Medicine, Imperial College London, UK

The evolution of antifungal resistance in the environment requires the co-occurrence of a microbe and its chemical stressor such as fungicides at the minimum selective concentration (MSC) that will confer a fitness advantage. As a result, species under chemical exposure can evolve resistance to fungicides. Additionally, there are shared mechanisms of action between fungicides and clinical antifungals, therefore resistance to fungicides can offer cross-resistance to antifungal therapeutics. This highlights the important role of a One Health approach to mitigate the spread of fungal antimicrobial resistance (fAMR). Currently, there is lack of understanding of the pathways that lead to and amplify fAMR in the human fungal pathogen *Aspergillus fumigatus*.

This research aims to quantify the exposure of *A. fumigatus* towards fungicides within the UK, and to understand the interaction between fungicide use and fAMR in the environment. To do this, we have developed and deployed passive sampling devices (PSD) in a range of soil substrate from households, agricultural fields and compositing sites for a period of 4 weeks. Microcavities within the PSD enable the confinement of chemicals from the environment which are then extracted and undergo liquid chromatography-mass spectrometry (LC-MS). This method has been developed to detect 22 different types of fungicides current used in the UK agricultural sector. The use of PSD's coupled with LC-MS will enable a scalable approach to quantify fungicide residues across soils, providing insights into the interaction between fungicide use and the emergence of fAMR.

POSTER 21

Gene family expansion drives the evolution of medicinal Erinacine A biosynthesis

Josepha Becker[1,2], Alana Raihan[1,3], Lorenzo Goppa[4], Simone Buratti[4], Emily Read[1], Carly Lin[1], Frances Pitsillides[1], Kavita Gadar[1], Niall Garvey[1], Richard Wright[5], Theo Llewellyn[6], Greg Thorn[7], Ester Gaya[1], Torda Varga[1]

[1] Royal Botanic Gardens, Kew, UK
[2] University College London, UK
[3] Queen Mary University of London, UK
[4] University of Pavia, Italy
[5] Cardiff University, UK
[6] Natural History Museum, UK
[7] Western University, Canada

Mushrooms with potential medicinal properties have long been used in Traditional Chinese Medicine (TCM) and are increasingly under study in Western medicine, including the *Hericium* genus. Despite their bioactive potential, our understanding of the evolution of fungal secondary metabolites remains limited, yet uncovering their evolutionary history could help us better target species for medicinal compound discovery. This study aimed to elucidate the evolutionary history and gene family expansion patterns underpinning the biosynthesis of Erinacine A—a diterpenoid known for its nootropic benefits. Erinacine A biosynthesis involves two distinct pathways—the initial mevalonate backbone followed by a derived 'Erinacine biosynthesis'. We compiled a dataset of 144 genomes from the *Agaricomycetes* class, including 35 newly sequenced specimens, with a focus on the Lion's Mane mushroom (*Hericium erinaceus*) and related species in the family *Hericiaceae* and reconstructed a phylogenomic tree. To further clarify species delimitation in the genus Hericium, we combined genomic and barcoding data in a genus-level phylogeny, including 107 specimens of worldwide distribution.

Our genus-level phylogeny clarified species relationships, suggesting vicariance in *Hericium*. After manually curating gene models focusing on the diterpenoid pathway, we inferred 22 orthogroups (gene families) across *Agaricomycetes* containing key enzymes involved in Erinacine A production. We found that the majority of observed gene duplications occurred in the derived 'Erinacine biosynthesis' pathway, whereas the mevalonate pathway showed comparatively few duplications. Specifically, significant gene duplications were observed mostly in cytochrome-related orthogroups, suggesting a metabolic adaptation. We also present new insights into the evolution of biosynthetic gene clusters and metabolomic, proteomic and transcriptomic analyses of specific strains.

This study provides a foundation for integrating genomic and functional data, broadens opportunities for innovative drug discovery and underscores the importance of genomic approaches in studying medicinal fungi.

POSTER 22

Tracking the tuneability of fungal mycelium through chemotrophic and imaging studies: New approaches to study engineered living materials

Ayesha Sadaf[1], Matthias Brock[2] and Carole C. Perry[1]*

[1] Materials and Interfaces Research Group, Interdisciplinary Biomedical Research Centre, School of Science and Technology, Nottingham Trent University, UK
[2] Fungal Genetics and Biology Group, School of Life Sciences, University of Nottingham, UK

Fungal imaging is pertinent to map morphological insights as a cue to the change in environmental conditions. The ability to analyse large and complex mycelium data remains one of the major bottlenecks in the analysis of the fungal hyphal network for the generation of mycelium-based materials. The current study was aimed to identify directional growth in both 2D and 3D systems by using AI mediated software, Imaris. For the first phase of the study, a model fungus *Aspergillus niger* was taken and chemotrophic index (CI) was calculated for a range of biomolecules. Based on the CI values a 2D model was developed to map the chemo sensing behaviour of *A. niger* when exposed to different pairs of biomolecules (C-C, C-N, N-N). In the second phase of the study, we examined the tunability of the mycelium of different fungal species through 3D mapping using Imaris when one carbon source was replaced by another during specific growth periods. Our results suggest that the varying layers of mycelium grown on different substrates play a crucial role in the development of mycelial mats with adjustable morphological, physicochemical, and mechanical properties. We believe our study will enhance the understanding of the chemo-sensing capabilities of fungal systems in a clearer way and facilitate the future development of directed growth in fungal-based material systems.

POSTER 23

Fungarium Sequencing Project: Specimens of Particular Interest Housed by RBG Kew's Fungarium

Mikele Baugh[1], Lawton Riness [1], Emily Hodgson[1], Alana Raihan[1], Aries Rasul[1], Charlotte David[1], Eleni Bethke[1], Elle Dwyer[1], Henry Miller[1], Jessica Trow[1], Josepha Becker[1], Jude McFarlane Bond[1], Kat Gregory[1], Katie Lewis-Jones[1], Louis Wellbelove[1], Ying Luo[1]

[1] Royal Botanic Gardens, Kew, UK

As the world's largest fungarium, the Fungarium collection at RBG Kew is a treasure trove of mycological history and important type specimens. With contributions from leading mycologists such as Reverend M.J. Berkeley, the collection of over 1.25 million fungal specimens includes species from every continent. An estimated 50,000 of these specimens are types (original specimen used to describe a species). The Fungarium Sequencing Project (FSP) aims to sequence genomes from as many of these specimens as possible, but to do so requires thorough examination of each type specimen. Since the start of the project in August 2024, specimens of varied significance have been "rediscovered." Here we present a first account of specimens of historical, scientific, economic, and cultural interest.

POSTER 24

Functionalizing mycelium for photosensing applications, a step closer to photoresponsive materials

Xin Zhang[1], Dilani Chathumalee Manchanayaka Arachchige Dona[1], Carole C. Perry[1]

[1] Interdisciplinary Biomedical Research Centre, School of Science and Technology, Nottingham Trent University, UK

Mycelium-based biomaterials have attracted significant attention within the research community in recent years as an innovative material in diverse fields. In this study, novel synthesized dye molecules with photoswitching ability have been incorporated into the mycelium of *Mucor rouxii* (*M.rouxii*). Two distinct biosorption methods were utilized: a staining method, involving the biosorption of dye molecules to living mycelium, and an inoculation method, involving he biosorption of dyes to inactive mycelium fragments. Three dye molecules were explored using the inoculation method. The resultant hybrid fungal mycelium-based materials were characterized using a combination of optical microscopy, UV-Vis spectroscopy, solid-state UV spectroscopy, and Raman spectroscopy. Microscopic images indicated that the inoculation method facilitates superior binding between hyphae and dye components within the mycelium network compared to the staining method. Quantification of the dye molecules adsorbed by the fungus was achieved by comparing the UV absorbance of the liquid media before and after inoculation, revealing that higher dye concentrations in the media promote adsorption. Additionally, the presence of dyes within the mycelial filamentous network was identified using Raman spectroscopy and spectrophotometric analysis. The data obtained indicate the successful binding of dye molecules with various chemical structures and colours to *M.rouxii*. These findings offer valuable insights and underscore the potential of using fungal mycelium-based materials for innovative photosensing applications in the field of photobiology.

POSTER 25

Fungi in Thai mangroves: Novel taxa, marine adaptations and phylogenetic insights

Carlo Chris S. Apurillo[1,2,3,4], Chayanard Phukhamsakda[3], Kevin D. Hyde[2,3], E.B. Gareth Jones[5,6]

[1]School of Science, Mae Fah Luang University, Thailand
[2]Key Laboratory of Phytochemistry and Natural Medicines, Kunming Institute of Botany, Chinese Academy of Sciences, China
[3]Center of Excellence in Fungal Research, Mae Fah Luang University, Thailand
[4] Department of Science and Technology-Center for Research in Science and Technology (CReST), Philippine Science High School-Eastern Visayas Campus, Philippines
[5]Department of Botany and Microbiology, College of Science, King Saud University, Saudi Arabia
[6]Nantgaredig, UK

Mangrove ecosystems connect terrestrial and marine environments, fostering diverse yet largely unexplored fungal communities. These habitats impose selective pressures, including fluctuating salinity, tidal submersion, and organic-rich substrates, which may drive fungal adaptation to marine conditions. In our survey of fungi from mangroves in Pranburi, Thailand, we introduced *Pseudomelanconiella* as a new genus, with *Pseudomelanconiella mangrovei* as its type species—the first *Melanconiellaceae* member reported from a marine habitat, expanding the family's ecological range. Additionally, we described two novel species, *Peroneutypa hibisci* and *Nemania hydei*, and recorded *Vaginatispora microarmatispora* and *Clonostachys viticola* from mangroves in Thailand. Although marine fungi do not belong to a single evolutionary lineage, our phylogenetic analyses revealed clustering of marine species in some genera. In *Peroneutypa*, five out of 43 known species are marine, with three (*P. hibisci, P. mangrovei*, and *P. scoparia*) forming a distinct clade. Similarly, in *Nemania*, five out of 43 species are marine, with three (*N. hydei, N. maritima*, and *N. viridis*) clustering in a well-supported lineage. Likewise, *Vaginatispora microarmatispora* groups with *V. armatispora* and *V. scabrispora*, both marine fungi, reinforcing marine specialization in this genus. In contrast, *Clonostachys viticola*, newly recorded from a marine habitat, does not cluster with *C. rosea*, the only other marine-associated species in the genus, suggesting an independent evolutionary adaptation. Our findings indicate that fungal adaptation to marine environments follows multiple trajectories, with some lineages forming marine-specialized clades while others, like *Clonostachys*, adapting independently. As marine fungi remain underexplored, further studies may reveal additional adaptive mechanisms.

POSTER 26

Study on the Antimicrobial Efficiency of Lichen Extract Combined with Metal Nanoparticles

Thanyalak Panjai[1], Pakrakphon Poonskkho[1], Theerapat Luangsuphabool[2], Anthony J.S. Whalley[3], Ek Sangvichien[4]

[1] National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand
[2]Biotechnology Research and Development office, Department of Agriculture, Thailand
[3]School of Pharmacy and Biomolecular Science, Liverpool John Moores University, UK
[4]Department of Biology, Faculty of Science, Ramkhamhaeng University, Thailand

This study aims to evaluate the effectiveness of lichen extracts combined with silver nanoparticles (Ag NPs) and zinc nanoparticles (Zn NPs) for inhibiting growth of bacteria, yeasts, and plant pathogenic fungi. The inhibition zone diameter measurement method assessed the antimicrobial properties, highlighting its potential applications in the food, agricultural, and medical industries. The increasing resistance of microorganisms to conventional antibiotics necessitates the exploration of alternative antimicrobial agents. Lichen metabolites are a natural source of bioactive compounds with antimicrobial potential, and when combined with metal nanoparticles, they enhance its microbial inhibition properties.

The preliminary results showed that lichen extract combined with metal nanoparticles exhibited significant antimicrobial activity, particularly against bacteria such as *Staphylococcus aureus*, *Bacillus subtilis*, and *Escherichia coli*, as well as plant pathogens like *Fusarium* spp. and *Bipolaris* spp. These findings indicated that their potential of lichen extracts as natural antimicrobial agents. Additionally, Zn NPs demonstrated higher effectiveness than Ag NPs in inhibiting certain plant pathogenic fungi, such as Fusarium spp., with statistical significance.

Based on this study, lichen extract combined with metal nanoparticles may serve as a safe and effective microbial control agent. However, further research on their mechanism of action, as well as safety assessments on living organisms and the environment, is necessary to ensure its industrial application is both safe and effective.

POSTER 27

Call off the dogs! Sniffing out *Hymenogaster* with distribution modelling

Alexandra Dombrowski[1,2], Jan M. A. Klink[3], A. Tobias Jansson[1], Ellen Larsson[1], R. Henrik Nilsson[1]

[1] University of Gothenburg, Sweden
[2] Royal Botanic Gardens, Kew, UK
[3] Lund University, Sweden

Hymenogaster (Agaricales, Basidiomycota) live underground and form mycorrhizal partnerships with a variety of trees. Their generalist preferences and hypogeous habit make them difficult to find. One method is to use dogs traditionally trained to find delicious ascomycete truffles. This does work, but *Hymenogaster* are less fragrant and less enticing to our four legged friends - who are much more likely to focus on digging up *Tuber* or *Elaphomyces*. Here we trial the method of using distribution modelling with abiotic parameters and biotic constraints to predict where we can find *Hymenogaster* in Sweden. If this method successfully guides us to new collections, it may be utilized to plan fieldwork trips for other elusive taxa.

POSTER 28

The UK Crop Microbiome Cryobank: a national resource for research and development

Matthew Ryan, Tim Mauchline[2], Jacob Malone[3], Susan Jones[4], Ian Clark[2], Rodrigo Taketani[2], Catriona Thompson[3], Miguel Bonin[1], Helen Stewart[1], Nicola Holden[5]

[1] CABI, UK
[2] Rothamsted Research, UK
[3] John Innes Centre, UK
[4]James Hutton Institute, UK
[5] SRUC, UK

Plant microbiomes are the communities of fungi and bacteria essential to the functioning of the phytobiome. A healthy, functional phytobiome is critical to crop health, improved yields and quality food. However, crop microbiomes are relatively under-researched, and this is associated with a fundamental need to underpin research through the provision of a supporting infrastructure. The BBSRC funded UK Crop Microbiome Cryobank (UKCMC) project has developed a unique, integrated and open-access resource to enable the development of solutions to improve soil and crop health. Six key UK crops have been targeted, including wheat, barley and oil seed rape. From this a resource collection of 36000 microbial isolates and 4,800 soil rhizoplane samples has been generated. All samples have been subjected to amplicon sequencing, associated bioinformatics workflows, and development of the project data catalogue. Short-read amplicon sequencing (16S rRNA gene for bacteria and ITS region for fungi) of all samples was implemented to describe the rhizosphere and bulk soil communities, for the multiple crop-soil combinations. Through the publicly available database www.agmicrobiomebase.org we have ensured that data related to the physical samples and isolates are not only linked to provenance and metadata but, essentially, have active links to EBI's European nucleotide archive and the MGnify platform. In describing the approaches being taken, from characterisation, cryopreservation and analysis of the crop microbiome through to potential applications, we will also show how biological questions can be asked of the dataset which is shedding light on how crops preferentially recruit microbes on the basis of function.Finally, we will focus on the methods used for cryopreservation of soil samples and the conservation and recovery of fungal and bacterial isolates. Combined, this will facilitate a mechanism to conserve biodiversity, but also as a potential facilitator of sustainable agriculture systems that mitigate against climate change.

POSTER 29

Fungarium Sequencing Project: Sampling Methods from the Royal Botanic Gardens, Kew's Fungarium

Lawton Riness[1]*, Mikele Baugh[1], Emily Hodgson[1], Alana Raihan[1], Aries Rasul[1], Charlotte David[1], Eleni Bethke[1], Elle Dwyer[1], Henry Miller[1], Jessica Trow[1], Josepha Becker[1], Jude McFarlane Bond[1], Kat Gregory[1], Katie Lewis-Jones[1], Louis Wellbelove[1], Ying Luo[1]

[1] Royal Botanic Gardens, Kew, UK

The Fungarium Sequencing Project (FSP) aims to sequence whole genomes from tissue samples collected from type specimens deposited in three UK collections-based institutions: Royal Botanic Gardens Edinburgh (RBGE), Royal Botanic Gardens, Kew (RBG, Kew), and the Natural History Museum (NHM). These sequences will provide invaluable data across science with uses in taxonomy, ecology, agriculture, medicine, and biotechnology. Of the three collections, the Fungarium at RBG, Kew is the largest and most taxonomically complete in the world, containing approximately 1.25 million specimens and an estimated 50,000 holding type status. Facilitating tissue sampling at this scale has posed many challenges. The major limiting factors are specimen size and condition, Access and Benefit Sharing (ABS) restrictions, taxonomic uncertainty, and the expert knowledge and skill sets required. Here we present a standardised procedure for specimen sampling for large-scale sequencing efforts. Workflows include sampling prioritisation decision-making, as well as review processes for curation, taxonomy, country-specific ABS policy, and sample quality checks. We provide best practices for sampling using aseptic techniques and diverse taxonomic groups and present our data management organisation and process.

POSTER 30

Inter-cladal variation in the response to environmental stress in the emerging fungal pathogen *Candida auris*

Asha Root[1], Vikram Dard[1], Grace Bryceland[1], Janet Quinn[1], Alison Day[2]

[1]Biosciences Institute, Faculty of Medical Sciences, Newcastle University, UK
[2]School of Medicine, Faculty of Medical Sciences, Newcastle University, UK

Candida auris is an emerging fungal pathogen that was first identified in 2009 and has since been shown to be responsible for several nosocomial outbreaks of candidaemia across the world. Infections caused by *C. auris* are difficult to treat as strains have been identified which are resistant to all major classes of antifungal drugs. Interestingly, it has also been demonstrated by whole genome sequencing that more than four distinct clades of *C. auris* have evolved simultaneously on three different continents with isolates belonging to different clades showing significant genetic differences.

The environmental niche inhabited by *C. auris* is different from that of the most common human fungal pathogen *C. albicans* with the former colonising the skin compared to the latter residing in the gut. Therefore, the environmental conditions encountered by these two pathogens differ significantly. An important virulence trait of fungal pathogens is their ability to respond to environmental changes encountered during the course of infection and this is regulated in *C. albicans* and *C. auris* by the stress-activated protein kinase (SAPK) Hog1. Given the genetic variation in *C. auris* isolates belonging to different clades, inter-cladal differences in the *C. auris* response to different environmental stress conditions may be predicted, however, such differences have not been elucidated.

Here we report the results of investigations into the responses of *C. auris* isolates belonging to different clades to changing environmental stress conditions. Activation of Hog1 in response to different stresses in different clades is also considered. These findings highlight differences in stress responses between *C. auris* isolates belonging to different clades but also, interestingly, show variation between isolates within the same clade. These findings highlight the variation in the response to stress within the *C. auris* species and may have implications for Hog1 regulation and virulence.

POSTER 31

From Fungal Chemistry to crop security: decoding sex hormones and their biosynthetic pathways

Lisa Humbert[1,2], Paul S Dyer[2], Mike Birkett[1], Matthias Brock[2], David Withall[1]

[1] Protecting Crops and the Environment, Rothamsted Research, UK
[2] School of Life Sciences, University of Nottingham, UK

The rapid evolution of resistance in both agricultural and clinical settings emphasizes the need and urgency to develop new antifungal compouds for the control of plant and animal pathogens. *Pyrenopeziza brassicae* causes light leaf spot disease of brassicas and is the most damaging fungal disease of oilseed rape in the UK. The disease is well established on various brassica crops across Nothern Europe, Oceania and Asia, and has recently spread to North America. The pathogen has well described dispersal mechanisms involving both asexual sporulation, for local spread during the main growing season, and sexual spore production allowing spread of the infection over greater distances via ascospores. Current disease management involving the use of broad-spectrum fungicides is largely compromised as most European strains exhibit increasing resistance. Thus the development of novel more targeted disease control is required.

Regarding fungal metabolites, one possible source of new antifungals is the use of fungal hormones, which may alter and repress fungal growth and sporulation. Signalling molecules produced during *P. brassicae* sexual reproduction, referred to as Sex Factors (SF), have the ability to almost totally repress asexual sporulation in laboratory cultures. We used *in-planta* experiments to demonstrate reproducible SF activity on a larger scale, indicating exciting potential for SF to be used as novel antifungal compound(s) to control light leaf spot disease. Using analytical chemistry techniques, we characterized potential molecular structures of SF. Scanning electron microscopy in combination to time-course experiments provided insights into mechanisms of repression of asexual sporulation triggered by SF. This allowed the identification of potential SF targeted receptors and related activated proteins through transcriptomic data analysis at different time points. Ongoing work aims to investigate SF biosynthetic genes and target receptors using CRISPR/Cas 9 gene editing. Results demonstrate that fungal secondary metabolites may offer more sustainable prospects for future crop protection.

POSTER 32

Developing large-scale lab methodologies for whole genome sequencing of ancient and historical fungal material

Emily Read[1], Carly Lin[1], Clementine Geeves[1], Brandon Shaw[1], Lottie Goodman[1], Niall Garvey[1], Emily Watters[1], Seth Blake[1], Kavita Gadar[1], Ruben Mole[1], Sergio Latorre[2], Ester Gaya[1]

[1] Royal Botanic Gardens, Kew, UK
[2] University College London, UK

The Fungarium Sequencing Project (FSP) is an ambitious project which aims to sequence the genomes of several thousand type specimens held in three UK collections-based institutions: Royal Botanic Gardens Edinburgh (RBGE), Royal Botanic Gardens Kew (RBG Kew), and the Natural History Museum (NHM). This is the first large-scale attempt at sequencing fungal genomes from historical collections and offers a unique opportunity to revise and optimize existing methodologies for DNA extraction and library preparation of historical and ancient DNA material. Whereas some of these methods have been successfully used with a handful of fungi, mostly plant pathogens, a comparative study across a diverse range of taxonomic groups, lifestyles and habitats is still missing. The performance of two widely used extraction methods — CTAB and PTB — was assessed. Here, we present the effect of modifications (e.g., precipitation time) introduced in various steps of both protocols and their effect in relation to various parameters, including DNA yield and purity, library quality, and sequencing success, amongst others. Two library preparation methods were additionally tested: the Santa Cruz Reaction (SCR) and Latorre protocol (Latorre et al. 2020). Both methods proved successful in creating libraries from genomic DNA input from both CTAB and PTB extraction methods, but differences were detected based on the type of material. A summary of main results and a decision-making guideline on protocols for fungal genome sequencing from archival collections is presented.

Latorre, Sergio M., et al. Isolation, library preparation, and bioinformatic analysis of historical and ancient plant DNA. Current Protocols in Plant Biology 5,4 (2020)

POSTER 33

Fungal FLC proteins that are essential for cell wall integrity and Ca^{2+} homeostasis belong to a novel transmembrane protein superfamily

Rachael Murray[1], Joanne Thompson[1], Jelena Baranovic[1], Edward Wallace[1]

[1] School of Biological Sciences, University of Edinburgh, UK

In fungi, the FLC family of transmembrane proteins are essential for cell wall integrity and Ca^{2+} homeostasis but we have little understanding of their molecular function. The family, including *Saccharomyces cerevisiae* FLC1-4, *Schizosaccharomyces pombe* PKD2, and *Neurospora crassa* Spray, were annotated as Ca^{2+} channels belonging to the transient receptor potential superfamily. However, structural and phylogenetic evidence supporting this classification is lacking, and the molecular functions underlying observed phenotypes remain unknown.

We performed the first thorough bioinformatic and phylogenetic analysis of the FLC protein family and found that they belong to a novel eukaryotic transmembrane protein superfamily distinct from known Ca^{2+} channels. This family has a unique transmembrane domain with nine transmembrane helices. Members of the family are found in diverse eukaryotic phyla, but not in vertebrates. The shared transmembrane domain is coupled to variable extracellular N-terminal domains in different organisms, reminiscent of sensory signalling proteins.

Our phylogenetic analysis suggests that a gene duplication in an ancestor of dikarya gave rise to two fungal FLC subtypes. The human fungal pathogen *Cryptococcus neoformans* encodes one FLC protein from each subtype, and we show that *C. neoformans* Flc1 is required for growth at 37°C, cell wall integrity, and Ca^{2+} homeostasis, similar to type 1 FLC proteins in other fungi. The cell wall integrity defect of flc1Δ is rescued by calcium depletion, either using EGTA or by deleting a calcium import channel *CCH1*. RNA-seq analysis revealed FLC1-dependent differential regulation of chitin synthesis genes and transporters, as well as differential induction of the calcineurin-Crz1 pathway.

Overall, our data support the hypothesis that the FLC proteins are involved in calcium regulation and cell wall integrity, through an as-yet unknown mechanism.

POSTER 34

Rezafungin for Treating a Complex *Candida* Infection

Patryk Majewski[1*], Joanna Whittaker[1], Imogen Jones[2], Darius Armstrong-James[2], Jamie Cheong[2], Annette Clarkson[3], Patrick Doyle[4], Jonathan Snape[1], Timothy Kemp[1], Anthony Cadwgan[1], Seema Desai[1]

[1] University Hospitals of North Midlands NHS Trust, UK
[2] Guy's and St Thomas' NHS Foundation Trust, UK
[3] Nottingham University Hospitals NHS Trust
[4] Frimley Health NHS Foundation Trust, UK

This case report provides a treatment overview for a patient with a chronic *Candida dubliniensis* infection of an aortic graft. Blood cultures isolated *Candida dubliniensis*, which was sensitive to Amphotericin B, Caspofungin, Fluconazole, Flucytosine, Itraconazole, Voriconazole, Anidulafungin, and Posaconazole. The patient was treated with Ambisome 5 mg/kg and Caspofungin 150 mg once daily in case of CNS involvement. Once the patient improved and stabilised, he was discharged to a rehabilitation facility where he continued to receive daily Caspofungin 150 mg and Fluconazole 400 mg

After months of antifungal treatments and multiple hospital admissions with complications from the infected graft, the patient became stable enough for outpatient treatment through OPAT (outpatient parenteral antimicrobial therapy). The treatment regimen changed from daily intravenous (IV) caspofungin infusion and oral (PO) fluconazole to weekly IV rezafungin infusion and continued PO fluconazole. This case report outlines the management of the infected aortic graft and how switching to weekly rezafungin infusion enabled the use of OPAT services in the later stages of complex fungal infection treatment.

OPAT provides greater flexibility in patient treatment options, allowing patients to be discharged from hospital while still requiring IV treatments. This can be facilitated either at patients' homes with support from community teams or through hospital clinics. This option can promote earlier discharge, freeing up hospital beds and lowering the risk of healthcare-acquired infections.

Rezafungin treatment via OPAT is a viable option for complex graft *Candida* infections requiring long-term IV antifungal therapy. This treatment offered an improvement in the patient’s quality of life and a cost-saving measure by facilitating earlier discharge.

POSTER 35

Novel-to-Nature NRPS-Like Benzoquinone Products

Nicholas R Moody[1], Matthias Brock[1]

[1]School of Life Sciences, University of Nottingham, UK

Non-reducing non-ribosomal peptide synthetases like (NRPS-like) enzymes lack the condensation domain found in NRPSs and typically condense two identical aromatic α-keto acids. This leads to the production of a (semi-)symmetric compound with an enzyme dependent substrate-interconnecting core moiety. The purple jelly disc fungus *Ascocoryne sarcoides* contains an NRPS-like enzyme called AcyN that is essential to produce the purple compound ascocorynin. In fact, AcyN produces polyporic acid from phenylpyruvate, which is subsequently functionalised by a specific monooxygenase to form ascocorynin as confirmed by heterologous expression of acyN either alone or in combination with its monooxgynease in *Aspergillus oryzae*. Here, we studied the product formation by AcyN when A. oryzae cultures were supplemented with functionalised phenylalanine which is efficiently converted into the corresponding alpha ketoacid by fungal transaminases. HPLC analyses combined with mass spectrometry revealed the production of novel metabolites that were in line with the functionalised side chain deriving from the substrate. While native NRPS-like enzymes may require further modification to use a wider range of functionalised substrates, these experiments show that a naturally highly substrate-selective NRPS-like enzyme can effectively incorporate non-natural substrates. This broadening of the substrate spectrum in combination with the co-expression of tailoring enzymes can result in a wide range of novel-to-nature metabolites.

POSTER 36

Building a scalable bioinformatics strategy for sequencing historical fungal collections

Wu Huang[1]*, Niall Garvey[1], Lia Obinu[1], Torda Varga[1], Ester Gaya[1], Samuel Stainton[1]

[1] Jodrell laboratory, Royal Botanic Gardens Kew, UK

Whole genome sequencing (WGS) of a comprehensive fungal collection offers transformative potential for resolving the fungal tree of life, uncovering novel metabolic pathways, and informing biodiversity conservation. However, sequencing historical specimens, and especially old type material, featuring degraded DNA at scale introduces unique technical and analytical challenges. The variety of biological features of the specimen, inconsistent source of contaminants, the level of contamination, and DNA degradation are all key considerations. As part of the ongoing Fungarium Sequencing Project (FSP) at Kew, we are developing and optimising a dedicated bioinformatics pipeline to process over 7,000 fungal and lichen genomes, with genomic material extracted from fungarium samples spanning decades or even hundreds of years old. Here, we present a bioinformatic roadmap towards fungarium genome assemblies

Building upon 300 fungal genomes generated in a pilot sequencing study, we identified critical decision points in the analytical workflow — from assessing pre-sequencing quality metrics to guide lab work, read preprocessing, contamination detection and removal, to developing hybrid assembly approaches to scale up the workflow to suit the needs of a large-scale genome assembly endeavor. The insights gained directly inform the computational strategy for the FSP, ensuring data quality, reproducibility, and efficient release to public repositories. This methodological roadmap will not only accelerate the delivery of the FSP but also establish best-practice guidelines for processing genome sequences from historical fungal collections globally.

POSTER 37

Physicochemical and Metagenomic Characterization of Desert Soil: Advancing Desert Truffle Cultivation in Saudi Arabia

Sakhr alhuthali[1], Suleiman K Bello[2], Ahmed M Bageel[2], Ahmed M Al-Hejin[3], Paul W Thomas[4]

[1] Chemical and Materials Engineering Department, Faculty of Engineering, King Abdulaziz University, Saudi Arabia
[2] Department of Agriculture, Faculty of Environmental Sciences, King Abdulaziz University, Saudi Arabia
[3] Department of Biological Science, Faculty of Science, King Abdulaziz University, Saudi Arabia
[4] Faculty of Natural Sciences, University of Stirling, UK

Researchers are investigating plant-based proteins to combat malnutrition and mitigate climate change, with desert truffles emerging as a promising, sustainable option. Desert truffles offer an environmentally friendly alternative to traditional protein sources. However, their cultivation is constrained by environmental factors, such as rainfall and soil conditions. This study aimed to examine the soil characteristics and microbial communities associated with desert truffles in Saudi Arabia. Truffle fields were divided into high-yield (≈50 kg/ha annually) and low-yield (≈2 kg/ha annually) categories. Soil physicochemical properties, except total nitrogen, did not significantly impact yield. Total soil nitrogen was negatively correlated with truffle yield, but low nitrogen alone did not fully explain the differences, as wild truffle fields with low nitrogen also yielded fewer truffles. In contrast, truffle yield positively correlated with calcium carbonate content. The study suggests that irrigation practices, particularly during the fruiting season, may be a key factor influencing yield differences. Microbial analysis revealed that high-yield farms had lower bacterial richness and diversity than low-yield ones. Bacteria genera like *Geodermatophilus* and *Rubrobacter* were found in both farm types, though in greater numbers in low-yield fields, while *Streptomyces* dominated high-yield farms. Fungal diversity was higher in high-yield farms, with Sordariomycetes, Dothideomycetes, Eurotiomycetes, and Glomeromycetes being the most prevalent groups. This study highlights the complex interplay of environmental and microbial factors influencing desert truffle productivity.

POSTER 38

Natural Occurrence of Fumonisins in Pre-Harvest and Post-Harvest Maize in South Africa: A South African Maize Trust Project

Oluwasola A. Adelusi[1,]; Patrick B. Njobeh[1]; Kulsum Kondiah[1]; Nnamdi Nwulu[2]; Sarah De Saeger[1,3]

[1]Department of Biotechnology and Food Technology, Faculty of Science, University of Johannesburg, South Africa
[2]Department of Electrical and Electronic Engineering Science, Faculty of Engineering, University of Johannesburg, South Africa
[3]Centre of Excellence in Mycotoxicology and Public Health, Department of Bioanalysis, Faculty of Pharmaceutical Sciences, Ghent University, Belgium

Mycotoxins, particularly fumonisins, are toxic secondary metabolites produced by toxigenic fungi that frequently contaminate crops, thus compromizing food security and safety. Fumonisins in maize have been strongly associated with high prevalence of esophageal cancer in the Transkei region in the Eastern Cape of South Africa, primarily due to the dietary reliance on maize, a staple food frequently contaminated with fumonisins, particularly fumonisin B_1 (FB_1). In this study, 80 maize samples, i.e., 40 pre-harvest (at maturity) and 40 post-harvest (2 -3 months after harvest) collected from maize farmers in Gauteng Province, South Africa were analyzed for fumonisin levels using Ultra-High-Performance Liquid Chromatography Tandem Mass Spectrometry (UHPLC-MS/MS). The results revealed contamination in 35.0, 28.8, and 13.8% of FB_1, FB_2, and FB_3, respectively. Notably, FB_1 have higher levels in post-harvest maize (<LOQ – 6446.97 µg/kg) compared to pre-harvest maize (<LOQ – 2226.1 µg/kg). Similarly, FB_2 concentrations in post-harvest maize (<LOQ – 3506.84 µg/kg) were higher than those in pre-harvest maize (<LOQ – 1734.24 µg/kg). A comparable trend was observed for FB_3, with post-harvest maize (<LOQ – 259.9 µg/kg) showing higher levels than those in pre-harvest maize (<LOQ – 76.34 µg/kg). Statistical analysis using Independent sample t-test confirmed significantly ($p \leq 0.05$) higher fumonisin levels in post-harvest maize than in pre-harvest maize. As a significant mycotoxin group, contamination levels found in this study highlights the urgent need for robust monitoring programs, enhanced agricultural practices, and targeted mitigation strategies for improved quality and safety of South African maize principally during storage and processing.

POSTER 39

The genetics of speciation in *Saccharomyces*

Jasmine Ono[1,2], G. Ozan Bozdag[3,4], David W. Rogers[4], Ellen McConnell[4], Emre Karakoc[5], Jai A. Denton[6], Neil Hunter[7], Jun-Yi Leu[8], Duncan Greig[2,4]

[1] University of Nottingham, Nottingham, UK
[2] University College London, London, UK
[3] Georgia Institute of Technology, Atlanta, GA, USA
[4] Max Planck Institute for Evolutionary Biology, Plön, Germany
[5] Wellcome Sanger Institute, Hinxton, Cambridge, UK
[6] Okinawa Institute of Science and Technology, Onna-son, Japan
[7] University of California, Davis, Davis, CA, USA
[8] Academia Sinica, Taipei, Taiwan

New species are formed when they become reproductively isolated, usually as a consequence of a combination of isolating barriers. We investigated the potential genetic causes of reproductive isolation between two closely related species of budding yeast, *Saccharomyces cerevisiae* and *S. paradoxus*. F1 crosses between these species are viable but infertile, with 99% of gametes failing to survive. We find that the primary reproductive barrier is chromosomal divergence, which results in mis-segregation of chromosomes during meiosis due to the rejection of recombination. All chromosomes in *Saccharomyces* yeast are essential, so a gamete missing a single chromosome is inviable. In this system, a lack of recombination is the cause of hybrid sterility. We then break this chromosomal species barrier by restoring recombination in the hybrid, allowing us to uncover evidence of genic incompatibilities between diverged alleles from the two parental species.

POSTER 40

A standardised fungal collection framework for the Darwin Tree of Life Project

Ben Blades[1], Clare Blencowe[1], Alexandra Dombroski[1,2], Ester Gaya[1*], Sahr Mian[1], Paul Kersey[1]

[1] Royal Botanic Gardens, Kew, UK
[2] University of Gothenburg, Sweden

The Darwin Tree of Life (DToL) project is one of several initiatives across the globe working towards the goal of sequencing all complex life on Earth, in a joint effort known as the Earth BioGenome Project. The DToL project is focussing in particular on sequencing the genomes of 70,000 species of eukaryotic organisms in Britain and Ireland, a region with one of the best known and studied biota in the world, including Fungi. The kingdom Fungi can benefit enormously from high quality genome sequences, from improving our understanding of fungal diversity, evolution and adaptation, to finding new tools in medicine and biotechnology. When densely sampled in a region, as in the DToL project, complete genomes can also aid in much needed conservation efforts. DToL samples are collected and processed with the oversight of a Genome Acquisition Laboratory (GAL) where taxonomic experts prepare collected specimens into sequencing-ready samples. RBG Kew has led the efforts of fungal sample acquisition alongside RBG Edinburgh, CABI, and the MBA. Here we present a standardised framework for specimen processing, from field collection and identification to culturing and cryopreservation. We also showcase the taxonomic diversity of the collected fungi and their geographic distribution, and provide a summary of the fungal genomes sequenced to date. Finally, we describe a partnership developed with the British Mycological Society and the wider UK field mycology community, which has been essential to secure our sampling targets and provide additional taxonomic expertise. A model to follow in biodiversity genomics research.

POSTER 41

Defining the antifungal mode of action of miltefosine to unlock its potential in targeting eukaryotic pathogens

Tanmoy Chakraborty[1], Lizzie Marriott[2], Neil Gow[3], Gustavo H. Goldman[4], Michael Barrett[5], Paul W. Denny[2], Janet Quinn[1]

[1] Biosciences Institute, Faculty of Medical Sciences, Newcastle University, UK
[2] Department of Bioscience, Durham University, UK
[3] MRC Centre for Medical Mycology, University of Exeter, UK
[4] Faculdade de Ciencias Farmaceuticas de Ribeirao Preto Universidade de São Paulo, Brazil
[5] School of infection and immunity, University of Glasgow, UK

The rise of antimicrobial resistance (AMR) is a critical global health concern. While much of the focus has been on antibiotic resistance, antifungal drug resistance is an equally pressing threat, exacerbated by the slow development of new antifungal agents. This challenge is further fuelled by the emergence of multidrug-resistant fungal pathogens such as *Candida auris*. A key obstacle in antifungal drug development is the close evolutionary relationship between fungi and humans, which limits the availability of selective drug targets. Miltefosine, an FDA- and WHO-approved drug for visceral leishmaniasis, has recently been approved and repurposed for systemic candidiasis treatment. Despite its potential, significant knowledge gaps remain regarding its precise mode of action and broad-spectrum antifungal efficacy. Recent studies suggest that miltefosine targets ergosterol and inositolphosphorylceramide (IPC)-based sphingolipids, similar to its mechanism in protozoan parasites.

Our study aims to elucidate miltefosine's antifungal mode of action in greater detail. Using fluorescent-tagged *Saccharomyces cerevisiae* reporter strains, we are holistically defining the impact of miltefosine on the plasma membrane and membrane-bound organelles. This is complimented with systematic screening of fungal deletion libraries for mutants that display altered resistance, and in-depth omics profiling to capture the fungal response to miltefosine. Microevolution experiments are also ongoing to determine whether *Candida albicans* can develop resistance to miltefosine and if such resistance confers cross-resistance to other antifungals. Keys findings will be presented showcasing insights into miltefosine’s mode of action and therapeutic potential, and its implications for antifungal resistance.

With thanks to our sponsor

As a global leader in scientific information and analytics, Elsevier helps researchers and healthcare professionals advance science and improve health outcomes for the benefit of society. We do this by facilitating insights and critical decision-making with innovative solutions based on trusted, evidence-based content and advanced AI-enabled digital technologies.

We have supported the work of our research and healthcare communities for more than 140 years. Our 9,500 employees around the world, including 2,500 technologists, are dedicated to supporting researchers, librarians, academic leaders, funders, governments, R&D-intensive companies, doctors, nurses, future healthcare professionals and educators in their critical work. Our 2,900 scientific journals and iconic reference books include the foremost titles in their fields, including Cell Press, The Lancet and Gray's Anatomy.

Together with the Elsevier Foundation, we work in partnership with the communities we serve to advance inclusion and diversity in science, research and healthcare in developing countries and around the world.

Elsevier is part of RELX, a global provider of information-based analytics and decision tools for professional and business customers. For more information on our work, digital solutions and content, visit www.elsevier.com.

SHARE YOUR EXPERIENCE #BMS2025

Please tag the British Mycological Society in your posts!

Bluesky:
@britmycolsoc.org.uk

X:
@britmycolsoc

LinkedIn:
british-mycological-society

britmycolsoc.org.uk

British Mycological Society promoting fungal science