

BRITISH MYCOLOGICAL SOCIETY ANNUAL SCIENTIFIC MEETING

14 - 17 JULY 2025



Royal Holloway, University of London, Egham, Surrey

The British Mycological Society's 2025 Annual Scientific Meeting, including the Student Research Conference, will take place within the inspirational setting of Royal Holloway's 135 acre campus. Situated just 19 miles from London, 7 miles from Heathrow Airport, 5 miles from the historic town of Windsor with its famous castle, and, importantly for this event, just 15 miles from the Royal Botanic Gardens, Kew. Conference highlights include:

- Student Research Conference Taking place in the afternoon of Monday 14 July and morning of Tuesday 15 July, this event provides postgraduate students with the opportunity to meet fellow students and senior researchers, share their research updates, and gain some invaluable skills for life after the PhD.
- Annual Scientific Meeting 2.5 days of talks from renowned, international researchers covering an exciting and broad range of mycological topics, plus poster sessions and flash talks, starting in the afternoon of Tuesday 15 July.
- Visit to the Royal Botanic Gardens, Kew A half day visit to Kew, including exclusive smallgroup tours of the Fungarium
- Time for networking and socialising 2 evening social events, including the BMS Conference Dinner and Auction in the Founder's Dining Hall at Royal Holloway

VISIT THE FUNGARIUM

When you register for the Annual Scientific Meeting, make sure you also book onto the tour of the Fungarium at Kew Gardens. There are limited spaces and a small fee applies.

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.



MEET THE SPEAKERS

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 postdoctoral 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.

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.

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.

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.

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.

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 hostpathogen, 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.

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.

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.

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.

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.

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 sequence 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 <u>here</u>.

Fungal Community Ecology

In natural and managed systems the importance of fungi has been overlooked or understudies 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.

CALL FOR ABSTRACTS

Abstracts on any mycological research theme are welcome, and could include (but are not restricted to):

- Fungal Biodiversity and Systematics Classification and understanding the diversity of fungal species, including phylogenetic relationships.
- Fungal Ecology and Ecosystem Roles Exploring the role of fungi in decomposition, nutrient cycling, and symbiotic relationships in ecosystems.
- **Medical Mycology** Studying pathogenic fungi that impact human health, antifungal resistance, and therapeutic approaches.
- Agricultural Mycology Investigating fungi in plant pathology, soil health, and biocontrol in crop systems.
- Industrial Mycology and Biotechnology Using fungi in bioprocessing, enzyme production, and applications like bioremediation.
 Molecular Mycology and Genetics Examining fungal genetics, gene
- Molecular Mycology and Genetics Examining fungal genetics, gene expression, and molecular mechanisms governing growth and adaptation.
- Environmental Mycology Researching fungi in climate change, carbon sequestration, and their roles in natural habitats.
- **Mycotoxins and Food Safety** Studying toxic compounds produced by fungi, contamination prevention, and implications for food safety.

Presentations should showcase your latest research, and can be delivered via talk or poster. If you are a postgraduate student you can present at both the Student Research Conference and Annual Scientific Meeting, if you'd like to!



ABSTRACT DEADLINE: 28 FEBRUARY 2025

Submit your abstract: <u>britmycolsoc.org.uk</u>



REGISTRATION

Registration for the Annual Scientific Meeting includes attendance at all sessions at the 2.5 day conference, 15 - 17 July 2025, and the Tuesday evening welcome dinner. The meeting registration fee does not include the visit to Kew, Wednesday evening's dinner, or accommodation. The social events can be booked separately when registering. Bedrooms on campus can be booked directly with Royal Holloway.

Registration for the Student Research Conference includes attendance at the 1 day conference (afternoon of Monday 14 July and morning of Tuesday 15 July) plus one night's accommodation at Royal Holloway and social event on Monday evening.

Registration fees

Annual Scientific Meeting, 15 - 17 July 2025	Before 30 April 2025	From 1 May 2025
Student - BMS Member	£125	£150
Student - Non Member	£175	£200
Delegate - BMS Member	£225	£250
Delegate - Non Member	£325	£350
Visit to Kew, 15 July	£10	£10
Conference Dinner, 15 July	£20	£20
Student Research Conference, 14 - 15 July 2025		
Student - BMS Member	Free	Free
Student - Non Member	£30	£30

Registration deadline: 1 July 2025

Please note our cancellation policy: Up to and including 14 June 2025: 100% refund or you can choose to transfer the booking to someone else From 15 June 2025 onwards: No refund, but you can choose to transfer the booking to someone else up to 1 July. If you need to cancel or transfer the booking, please contact sally@britmycolsoc.info



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