FUNGAL INTERACTIONS

12 - 14 September 2023
Newcastle-upon-Tyne

PROGRAMME

British Mycological Society promoting fungal science

BRITISH MYCOLOGICAL SOCIETY ANNUAL SCIENTIFIC MEETING 2023

Why attend the Annual Scientific Meeting 2023

01 Location

Newcastle upon Tyne, great city in the NE of England.

02 Speakers

20 internationally renowned invited speakers.

03 Talks

16 offered talks, showcasing the latest research.

04 Posters

39 poster presentations.

05 Socials

3 social events, including a visit to Wylam Brewery.

06 Networking

Time to meet and talk with other mycologists.

Welcome from the Conference Chair

The theme of this year's Annual Scientific Meeting is Fungal Interactions, to coincide with the launch of our new, open access journal of the same name.

Janet Quinn,
Newcastle University, UK

Fungi are at the forefront of many world issues: food security and animal health, soil health and fertility, waste decomposition and treatment, biodeterioration, bioremediation, and biofuel production among others. Their activities directly influence ecosystem function and human wellbeing in multiple positive and negative contexts. Therefore, understanding their biology and the way they interact across natural and synthetic habitats is paramount in order to fully understand their roles and functions, and how such findings can be exploited to tackle current and future global challenges.

With thanks to the scientific advisory board:

- Janet Quinn, Newcastle University
- Elaine Bignell, University of Exeter
- Carol Munro, University of Aberdeen
- Alessandra da Silva Dantas, Newcastle University
- Mike Bromley, University of Manchester
- Neil Brown, University of Bath

The scientific advisory board has developed an exciting scientific programme covering a multitude of the important fungal interactions noted above. There are opportunities to give offered talks and poster sessions, and a lively social programme within the vibrant city of Newcastle upon Tyne. So please come to Newcastle for the Annual Scientific Meeting to support the BMS and our mission to promote fungal science!

Sunday 10 September
Student Research Conference

Are you a PhD student, arriving in Newcastle on **Sunday 10 September**?

Meet up in the afternoon/evening before and get to know everyone!

16:00 Arrival and registration

18:45 Tour of the Quayside - meet in hotel reception

Monday 11 September
Student Research Conference

09:00 **Welcome and overview of BMS member benefits and opportunities for PGR students**
Janet Quinn, Newcastle University, and BMS President

09:15 **Publishing your manuscript: what happens after submission and manuscript acceptance**
Mark Gannon, Elsevier

09:40 **Effective scientific communication and outreach**
Mark Ramsdale, University of Exeter, and Chair of FEO committee

10:05 **Multidisciplinary working**
Beth Mills, UKRI Future Leaders Fellow, University of Edinburgh

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10:30 Refreshments

Monday 11 September
Student Research Conference

11:00 **Short talks by PhD students:**

11:00 **Engineering functional fungal materials with bioactive nanoparticles; a natural interaction process for fabricating reusable heavy metal scavenger in waste-water purification**
Juwon Samuel Afolayan, Nottingham Trent University

11:10 **Fungi-on-a-Chip: Visualising Fungal-Bacterial Interactions and Fungal-Mediated Water Redistribution**
Amelia Clark, Imperial College London

11:20 **Investigating the Interactions Between Deubiquitinases and Reactive Oxygen Species in *Saccharomyces cerevisiae***
Sukhmani Kaur, Newcastle University

11:30 **Converging neighbours: Exploring interactions between *Candida* and bacterial species**
Purvi Joshi, The Maharaja Sayajirao University of Baroda

11:40 **Yeast-on-a-Chip: Development of a microfluidic device for the investigation of social interactions in synthetic yeast communities**
Seda Duman, Imperial College London

11:50 **Antagonistic Cross-kingdom Interactions - Delivery of Antifungal Toxins by the Bacterial Type VI Secretion System**
Maisie Palmer, Newcastle University

12:00 **Leveraging antagonistic fungal interactions as biocontrol for destructive forest pathogens in the genus *Armillaria***
Ed Pyne, Bangor University

12:10 **Spores-on-a-Chip: A novel microfluidic platform for investigations on arbuscular mycorrhizal fungi and their interactions**
Felix Richter, Imperial College London

12:20 **Unravelling Interactions Between Carnivorous Plants and Their Fungal Endophyte Communities: Impacts of Environment, Plant functional traits, and Host Relatedness**
Brandon Shaw, Loughborough University

Monday 11 September
Student Research Conference

12:30 **Lunch and posters**
Posters 1 - 19 will be on display during the Student Research Conference

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14:00 **Different career paths following your PhD:**

- Working in industry: *Mike Csukai, Syngenta*
- Informatics: *Evelina Basenko, FungiDB.org*
- Fellowships/academic: *Jane Usher, University of Exeter*

15:00 **Q&A session with the career development panel involving all speakers**

Are you attending the Annual Scientific Meeting,
12-14 September?

16:00 Registration begins for the Annual Scientific Meeting

19:00 Welcome buffet and networking at the Copthorne Hotel

Tuesday 12 September - Morning programme

09:00 Arrival, registration and refreshments

09:30 ***Modus operandi* of an accidental fungal pathogen of humans**
Elaine Bignell, University of Exeter, UK

10:00 **Tony Trinci Award Lecture: Filling the gaps of the fungal tree of life in a collections-based institution**
Ester Gaya, Royal Botanic Gardens Kew, UK

10:30 **The *Candida glabrata* parent strain trap**
Delma Childers, University of Aberdeen, UK

10:45 **Identification of novel host and fungal factors driving the interaction of *Aspergillus fumigatus* with the respiratory mucosa**
Margherita Bertuzzi, University of Manchester, UK

11:00 Refreshments and posters

11:30 **Black bloom in white Greenland – do fungi help?**
Nina Gunde-Cimerman, University of Ljubljana, Slovenia

12:00 **The impact of advances in genomics, chemical genetics and bioinformatics tools on the development of novel fungal & oomycete plant pathogen control agents**
Michael Csukai, Syngenta, UK

12:30 **VEuPathDB: A free bioinformatics resource that integrates omics scale data and offers tools for exploration and analysis of host and pathogen data**
Evelina Basenko, University of Liverpool, UK

12:45 **Interactions between fungi, microalgae, and bacteria, and how those modulate the fate of photosynthetic carbon in aquatic systems**
Isabell Klawonn, Leibniz Institute for Baltic Sea Research, Germany

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13:00 Lunch and posters

Tuesday 12 September - Afternoon programme

14:00 **Root-fungal interactions as drivers of ecosystem processes**
David Johnson, University of Manchester, UK

14:30 **Subversion of replicative ageing to prevent pathogenicity and drug resistance in *Candida albicans***
Alessandra da Silva Dantas, Newcastle University, UK

15:00 **Bacterial-fungal warfare – intoxication by and response to the Type VI-secreted antifungal effector Tfe2**
Katharina Trunk, Newcastle University, UK

15:15 **Interaction of fludioxonil with two-component and HOG signalling in the fungal wheat pathogen, *Zymoseptoria tritici***
Zoe Gardiner, Newcastle University, UK

15:30 Refreshments and posters

16:00 **The role of small signalling molecules and small-secreted proteins in the interaction of nematode-trapping fungi with *C. elegans***
Reinhard Fischer, Karlsruhe Institute of Technology, Germany

16:30 **The future of fungi: what to expect from fungal pathogens in the Anthropocene**
Johanna Rhodes, Radboudumc, The Netherlands

17:00 **Use of pangenome analysis to identify novel heterokaryon interaction genes influencing gene flow of azole resistance in *Aspergillus fumigatus***
Felicia Adelina Stanford, University of Nottingham, UK

17:15 **Engineering functional fungal materials with bioactive nanoparticles; a natural interaction process for fabricating reusable heavy metal scavenger in waste-water purification**
Juwon Samuel Afolayan, Nottingham Trent University, UK

17:30 Summary and end of day 1

18:00 Meet in hotel lobby to travel together to Wylam Brewery (attendees need to arrive together in time for tours of the brewery)

19:00 Visit to Wylam Brewery, including a tour of the brewery and three course dinner

Wednesday 13 September - Morning programme

09:00 Arrival, registration and refreshments

09:30 **Interactions of *Candida albicans* with bacteria and the impact on the host**
Ilse Jacobsen, Hans Knöll Institute, Germany

10:00 **Host environment sensing: drivers of fungal development and disease**
Neil Brown, University of Bath, UK

10:30 **Fungi-on-a-Chip: Visualising fungal-bacterial interactions and fungal-mediated water redistribution**
Amelia Clark, Imperial College London, UK

10:45 **Unravelling interactions between carnivorous plants and their fungal endophyte communities: Impacts of environment, plant functional traits, and host relatedness**
Brandon Shaw, Loughborough University, UK

11:00 Refreshments and posters

11:30 **Close encounters of the microbial kind**
Nancy Keller, University of Wisconsin, USA

12:00 **Microbial interactions: a world of diplomatic negotiations**
Tajalli Keshavavarz, University of Westminster, UK

12:30 **Intraspecific variation matters: Fungal traits and interactions are down to the individual, not the species**
David Hera, University of Canterbury, New Zealand

12:45 **Fungal interactions during wood decomposition**
Daniel Eastwood, Swansea University, UK

13:00 Lunch and posters

Wednesday 13 September - Afternoon programme

14:00 **Evolutionary genomics of generalist plant parasitism in *Ascomycetes***
Sylvain Raffaele, INRAE, France

14:30 **Functional genomics in *Candida glabrata*, new tools to study stress pathogenesis and drug resistance**
Jane Usher, University of Exeter, UK

15:00 **Phospholipid flippase-induced plasma membrane disorganisation in *Candida albicans* has far-reaching consequences for invasive hyphal growth, vesicular trafficking, cell wall architecture and interaction with immune receptors**
Emma Agnew, MRC Centre for Medical Mycology at the University of Exeter, UK

15:15 **Bacterial Quorum-Quenching lactonase hydrolyzes fungal mycotoxin and reduces pathogenicity of *Penicillium expansum*—suggesting a mechanism of bacterial-fungal interactions**
Livnat Afriat-Jurnou, Migal-Galilee Research Institute, Israel

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15:30 Refreshments and posters

16:00 **The fungal cell wall as a therapeutic target**
Carol Munro, University of Aberdeen, UK

16:30 **Dissecting virulence mechanisms of the fungal cereal killer, *Zymoseptoria tritici***
Jason Rudd, Rothamsted Research, UK

17:00 **President's Award Lecture: Fungi, a tale of variation**
Jan Dijksterhuis, Westerdijk Institute, The Netherlands

17:30 Short break

18:00 Poster session and drinks reception

19:30 Three course dinner at the Copthorne Hotel and BMS Auction

Thursday 14 September - Morning programme

09:00 Arrival, registration and refreshments

09:30 **Rethinking Baker's articulation of an 'ideal weed' with Death Caps: what defines the 'ideal' invasive fungus?**
Anne Pringle, University of Wisconsin, USA

10:00 **Antifungal drug resistance: An inevitable consequence of evolution**
Mike Bromley, University of Manchester, UK

10:30 **Changes as small as 2°C can alter fungal community interactions and ecological outcomes in decaying wood**
Michelle Jusino, United States Forest Service, USA

10:45 **Non-canonical interactions of anaerobic gut fungi with bacteria from the rumen microbiome**
Jolanda van Munster, Scotland's Rural College, Edinburgh, UK

11:00 Refreshments and posters

11:30 **John Webster Award Lecture: Fungal interactions in trees**
Lynne Boddy, University of Cardiff, UK

12:00 **Presentation of Howard Eggins Early Career Mycologist Awards** for best talks and best posters, summary and close

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Posters

Posters will be displayed throughout the Annual Scientific Meeting, each labelled with a number to make it easy for you to find. There is a special poster session on Wednesday 13 September at 18:00.

Posters 1-19 will also be on display during the Student Research Conference on Monday 11 September.

Poster 1:
Fungal interactions with light-activated therapeutic compounds
Chloe Barnes, Newcastle University, UK

Poster 2:
Exploring the interactions shaping the past, present and future of True Eyespot Disease of Cereals
Fareed Bhatti, Rothamsted Research, UK

Poster 3:
Chemical tools to secure a niche: *Penicillium expansum* utilizes secondary metabolites to modulate microbial community interactions
Justin Eagan, University of Wisconsin, USA

Poster 4:
Interactions between the fungus *Penicillium roqueforti* and the cheese environment - investigating the basis of bitterness
Jonathan Heale, University of Nottingham, UK

Poster 5:
Harnessing fungal sexual interactions for the control of plant disease
Lisa Humbert, Rothamsted Research, UK

Poster 6:
Differences in the bacterial and fungal composition of laboratory mice and the influence on intestinal colonisation with *Candida albicans*
Sarah Vielreicher, Hans Knöll Institute, Germany

Poster 7:
Interaction between fungal enzymes and development of outer mould-ripened cheeses
Asaph Kuria, University of Nottingham, UK

Poster 8:

Intra-species and Environmental Interactions Informing Novel Strain Development for the Mycoprotein Fungus *Fusarium venenatum*

Alex Pate, University of Nottingham, UK

Poster 9:

Identification of environmental interactions that shape human pathogenicity in fungi

Ailton Pereira da Costa Filho, Friedrich-Schiller University, Germany

Poster 10:

Development of antifungal compounds that target a core virulence determinant – the Hog1 stress-activated protein kinase

Kiymet Nur Aybuke Kilic, Newcastle University, UK

Poster 11:

Predicting the structural basis for the interaction between lysine deaceylase inhibitors and fungal specific residues in *Candida glabrata Rpd3p* enzyme

Caelainn Mcaloran, Queens University Belfast, UK

Poster 12:

The complex interaction between strain and environmental conditions in *Candida glabrata* anti-fungal tolerance

Sreyashi Acharjee, Queens University Belfast, UK

Poster 13:

Ecoevolutionary dynamics of basidiomycete biochemicals, what insights into the fungal niche can omics provide us?

Hywel Evans, Swansea University, UK

Poster 14:

Yeast-on-a-Chip: Development of a microfluidic device for the investigation of social interactions in synthetic yeast communities

Seda Duman, Imperial College London, UK

Poster 15:

Converging neighbours: Exploring interactions between Candida and bacterial species

Purvi Joshi, The Maharaja Sayajirao University of Baroda, Gujarat-India

Poster 16:

Investigating the Interactions Between Deubiquitinases and Reactive Oxygen Species in *Saccharomyces cerevisiae*

Sukhmani Kaur, Newcastle University, UK

Poster 17:

Antagonistic Cross-kingdom Interactions - Delivery of Antifungal Toxins by the Bacterial Type VI Secretion System

Maisie Palmer, Newcastle University, UK

Poster 18:

Leveraging antagonistic fungal interactions as biocontrol for destructive forest pathogens in the genus *Armillaria*

Edward Pyne, Bangor University, UK

Poster 19:

Spores-on-a-Chip: A novel microfluidic platform for investigations on arbuscular mycorrhizal fungi and their interactions

Felix Richter, Imperial College London, UK

Poster 20:

Exploitation of the interaction between feedback inhibition and phenotypic heterogeneity to improve glutathione production by yeast

Mingzhi Xu, University of Nottingham, UK

Poster 21:

Harnessing bacteria, fungi, and their interactions for the biorecovery of valuable compounds in industrial and anthropogenic waste

Saskia Bindschedler, University of Neuchâtel, Switzerland

Poster 22:

The Old Pants Project: how fungi interact with textiles

Suzy Moody, Kingston University, UK

Poster 23:

A trade-off between proliferation and defense in the fungal pathogen *Cryptococcus* is controlled by the transcription factor GAT201

Edward Wallace, University of Edinburgh, UK

Poster 24:

Microfluidics for fungal-bacterial interactions: developing a platform to probe the fungal highway

Emily Masters-Clark, Imperial College London, UK

Poster 25:

ZymoSoups: A forward genetics method to understand in planta immune interactions

Graeme Kettles, University of Birmingham, UK

Poster 26:

Insights on the role of two transcription factors in *Aspergillus nidulans* suberin degradation ability

Isabel Tavares Lima Martins, ITQB-Nova, Portugal

Poster 27:

Inoculum size matters: Interaction of heteroresistance with MIC in weak-acid stress of food spoilage yeasts

Joseph Violet, University of Nottingham, UK

Poster 28:

Regulation of Phosphate Homeostasis in the Human Fungal Pathogen *Candida albicans*

Olga Ianieva, Newcastle University, UK

Poster 29:

A pilot study into how fungi interact with textiles

Rachel Harper, Kingston University, UK

Poster 30:

Love or hate – an insight into soil fungal interactions along a gradient of soil and root resources

Rodica Pena, University of Reading, UK

Poster 31:

Environmental Interactions in the networks of cord-forming wood-decay fungi

Samantha Duncan, Cardiff University, UK

Poster 32:

Investigating bioactive natural products from the fungus *Escovopsis weberi*

Claudio Greco, Swansea University, UK

Poster 33:

Small RNA profiling of the *Metarhizium brunneum – Galleria mellonella* pathosystem

Daniel Eastwood, Swansea University, UK

Poster 34:

Generating Tuneable Mycelial Networks for Directed Assembly

Dooshima Nevkaa, Nottingham Trent University, UK

Poster 35:

Investigating the effects of co-inoculation timing on interspecific interactions between *Leptosphaeria maculans* and *L. biglobosa*

Evren Bingol, University of Hertfordshire, UK

Poster 36:

One-step soft agar enrichment and isolation of human lung bacteria inhibiting the germination of *Aspergillus fumigatus* conidia

Fabio Palmieri, University of Neuchâtel, Switzerland

Poster 37:

Identification of essential components for protein secretion in the phytopathogen *Zymoseptoria tritici*

Alexander Featherstone, University of Birmingham, UK

Poster 38:

Interaction of Fungi with Hydrocarbons in Polluted Soils And Sediments

Ayodele Elizabeth Omotayo, University of Lagos, Nigeria

Poster 39:

How does Aspergillus fumigatus subvert the lung defenses during viral coinfection?

Margherita Bertuzzi, University of Manchester, UK

Elaine Bignell
University of Exeter, UK

Elaine Bignell is a Professor of Medical Mycology and a Co-Director (Research) for the MRC Centre for Medical Mycology at the University of Exeter. Her work addresses the mechanistic basis of lung diseases caused by the major mould pathogen of humans, *Aspergillus fumigatus*. Major contributions to the field have included work on the role of Aspergillus pH sensing in pathogenicity, transcriptional regulation of host adaptation, and the mechanistic basis of tissue invasion during invasive fungal lung disease.

Find out more about Elaine Bignell

Modus operandi **of an accidental fungal pathogen of humans**

Elaine Bignell, University of Exeter, UK

The air we breathe is full of fungal spores, some of which pose a deadly threat to human lung health. Globally, *Aspergillus fumigatus* is the most prevalent cause of fungal lung diseases that affect millions of people annually. However, it is currently unknown how this fungus, an important recycler of organic matter in the natural environment, evolved to survive in the mammalian lung. Both acute and chronic aspergilloses can be rapidly fatal, particularly where drug-resistant A. fumigatus isolates are involved. In light of increasing urgency to counter the threat of azole-resistant A. fumigatus, we aimed to define the regulatory landscape of A. fumigatus pathogenicity by performing a genome-scale census for transcriptional regulators driving A. fumigatus fitness during fungal lung infection. Remarkably, a robust correlation was identified for fitness behaviours of individual mutants in two mouse models of disease despite highly disparate immune status of the host. These data demonstrate the broad applicability of targeting host adaptation as an antivirulence strategy. Using fungal pH signalling as an example, a chemical genetics approach will be described that demonstrates the relevance of blocking host adaptation as an antifungal strategy.

Ester Gaya,
Royal Botanic Gardens Kew, UK

Ester Gaya discovered her passion for fungi during her undergrad 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.

Find out more about Ester Gaya

Filling the gaps of the fungal tree of life in a collections-based institution
Ester Gaya, Royal Botanic Gardens Kew, UK

The tree of life is the fundamental biological roadmap for navigating the evolution of life on Earth, and yet remains largely unknown, especially for fungi. Several initiatives have attempted to sequence fungal genomes to try to get a better reconstruction of the fungal tree of life, but only a minute fraction of fungal diversity has been covered, biassed towards species that can be grown in pure culture. An often-neglected source of fungal samples and reference material useful for the FToL reconstruction are fungal collections. Biological collections in general are crucial sources of taxonomic information but are also important to assess species distribution and richness patterns and represent the raw data for data modelling and drawing patterns of global change. As part of RBG Kew's objective of building the Plant and Fungal Trees of Life, they expanded their exploration of the more than 1.2 million specimens in Kew's fungarium to attempt to further reduce the sampling gap. Ester is also exploring ways to accelerate the discovery of the unknown fungal dimension of biodiversity and investigating the drivers of fungal diversification. She is trying to elucidate the evolution of fungal lifestyles, which have allowed the colonisation of almost all habitats on earth. Using genomic methods, she aims to get insights into the genetic determinants of these lifestyles, and is fascinated by those establishing mutualistic interactions, such as endophytic fungi and lichens, and their associated secondary metabolite diversity, and will show a couple of case studies to illustrate the type of integrative research that can be performed on non-model fungal systems.

Nina Gunde-Cimerman
University of Ljubljana, Slovenia

Research of prof. Nina Gunde-Cimerman, Chair of Molecular Genetics and Biology of Microorganisms, has been dedicated for the last 20 years to extremophilic fungi. Initially, in hypersaline environments, such as salterns around the world, later in Arctic glaciers and Ice sheets and in extreme household environments, eg dishwashers, one common denominator being low water activity. Gradually she established the world's largest strain bank of extremophilic fungi (Ex), with more than 17.000 strains.

Find out more about Nina Gunde-Cimerman

Black bloom in white Greenland - do fungi help?

Nina Gunde-Cimerman, University of Ljubljana, Slovenia

Recent studies have highlighted the extent and importance of the darkening of the Greenland Ice Sheet (GrIS). Black carbon and even more black pigmented ice-algal blooms are covering more than 30% of the GrIS surface, causing increased surface melt and reduction of albedo. Black ice algal community is competing for the scarce resources on the ice surface not only with bacteria, but also with fungi. During a three-year seasonal investigation, fungi were investigated from key GrIS surface habitats with a combination of cultivation and sequencing methods. Among the isolated fungal cultures two dominant new species were selected for a study focused on ex situ interactions of fungi with glacier ice algae. These fungi and algae surprisingly formed lichenoid assemblages, supporting algal growth. At the end of the incubation experiments and in conjunction with increased algal mortality, a substantially increased presence of non-cultivable, zoosporic *Chytridiomycota* was observed, suggesting an important role for them as decomposers or parasites of glacier ice algae.

Michael Csukai, Syngenta, UK

Mike received his BSc in Microbiology from the University of Reading before studying for a MSc in Molecular Biology and then a PhD in Genetics at the University of Leicester. He undertook his postdoctoral work in the Dept. of Molecular Pharmacology at Stanford University before moving back to the UK and into an industrial role at Zeneca and then Syngenta. Mike's work at Syngenta has primarily been focused on the discovery of fungicides and novel fungal control methods; using bioinformatic, genetics, biochemistry and cell biology tools to improve the fundamental understanding of fungal and oomycete plant pathogens.

Find out more about Michael Csukai

The impact of advances in genomics, chemical genetics and bioinformatics tools on the development of novel fungal & oomycete plant pathogen control agents

Michael Csukai, Syngenta, UK

To support the discovery and development of new active ingredients for the control of plant diseases, a wide range of chemical genetic tools are utilised and are under constant development. Historically many of these tools used the model organism *Saccharomyces cerevisiae*, but improvements in genomic information and tools make it possible to perform research directly in field-relevant plant pathogens. How this wide range of tools are used in support of novel fungicide discovery will be outlined.

David Johnson,
University of Manchester, UK

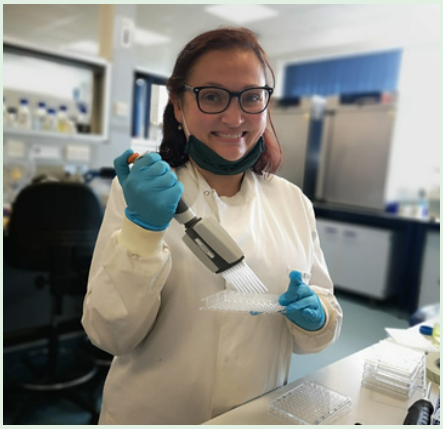
David Johnson is Chair in Soil Microbial Ecology at The University of Manchester, having moved there in 2017 after spending 12 years at Aberdeen University. He obtained his PhD and completed postdocs at the University of Sheffield. His research covers various aspects of terrestrial ecosystem ecology, but a key focus is on the biology of mycorrhizal fungi.

Find out more about David Johnson

Root-fungal interactions as drivers of ecosystem processes
David Johnson, University of Manchester, UK

Interactions between mycorrhizal plants and fungi are ubiquitous in nature and are critical for regulating numerous ecosystem processes. In this talk, David will discuss recent discoveries showcasing some of these effects, including the ability of mycorrhizal fungi to form interacting networks in soil, as conduits of energy flow into food webs, and regulators of multi-trophic interactions.

Alessandra da Silva Dantas, Newcastle University, UK



Alessandra completed her PhD in Biosciences at Newcastle University. She worked as a Postdoctoral Fellow at Newcastle University and Universidade do Estado do Rio de Janeiro, before moving to the MRC Centre for Medical Mycology first in Aberdeen and then in Exeter. She is a lecturer at Newcastle University Dental School where her lab is interested in determining how ageing heighten stress tolerance in pathogenic yeasts.

Find out more about Alessandra da Silva Dantas

Subversion of replicative ageing to prevent pathogenicity and drug resistance in *Candida albicans*

Alessandra da Silva Dantas, Newcastle University, UK

Traits related to *Candida spp*. pathogenesis and immune response have almost always been studied as the collective property of mixed populations of cells of differing ages. Yet, my lab shows that replicatively aged (RAGE) *C. albicans* cells are more tolerant to stresses found in the host environment and therefore can survive in the presence of phagocyte-imposed stresses and escape the immune system. These observations suggest that the fitness attributes associated with replicative ageing enable fungal pathogens to avoid immune surveillance and survive phagocytic killing. By understanding the fitness attributes that make RAGE cells resistant to host-imposed stresses will allow me to explore potential new diagnostic targets to identify the virulent RAGE population *in vivo* and RAGE and young-specific antifungal targets.

Reinhard Fischer, Karlsruhe Institute of Technology, Germany

Reinhard Fischer studied Biology in Marburg, Germany, followed by a postdoc at the University of Athens, Georgia, USA with Professor Bill Timberlake, from where he returned to Marburg. In 2004 he was appointed as associate professor and later as full professor at the Karlsruhe Institute of Technology (KIT). He works on secondary metabolism and light sensing in *Aspergillus nidulans* and *Alternaria alternata* and with the nematode-trapping fungus *Arthrobotrys flagrans*.

Find out more about Reinhard Fischer

The role of small signalling molecules and small-secreted proteins in the interaction of nematode-trapping fungi with *C. elegans*

Reinhard Fischer, Karlsruhe Institute of Technology, Germany

Fungal secondary metabolites and nematode-derived pheromones are crucial for prey sensing and attraction and control of trap formation. The fungal attack and nematode penetration depends on a sophisticated interplay between small-secreted proteins and lytic enzymes.

Johanna Rhodes, Radboudumc, The Netherlands

After completing her PhD in host gene regulatory networks activated in response to fungal infection at the University of Warwick, Jo moved to Imperial College London to research the pathogen itself, and focus on human infection. Her research has focused on three of the four WHO Critical Priority Group fungal pathogens: *Cryptococcus neoformans, Candida auris* and *Aspergillus fumigatus*. Now at Radboudumc in the Netherlands as a PI, Jo's research group uses a One Health approach to balance and optimise the health of humans, animals and the environment.

Find out more about Johanna Rhodes

The Future of Fungi: what to expect from fungal pathogens in the Anthropocene

Johanna Rhodes, Radboudumc, The Netherlands

After a short respite with COVID-19, our world has returned to being more interconnected than ever before. It makes sense that our human health is linked to the world around us, making significant impacts on the planet and its ecosystems. In this talk, Johanna will discuss the benefits of our continued advancements in sequencing technologies to uncover how fungi are adapting not only to us as hosts, but to the world we are shaping, to be more virulent, pathogenic, and drug resistant.

Ilse Jacobsen,
Hans Knöll Institute, Germany

Ilse studied Veterinary Medicine in Germany and South Africa before doing a PhD in Microbiology. Her lab is interested in *Candida albicans* as both a commensal and pathogen, investigating fungal-bacterial interactions, gut colonization, and systemic candidiasis.

Find out more about Ilse Jacobsen

Interactions of *Candida albicans* with bacteria and the impact on the host
Ilse Jacobsen, Hans Knöll Institute, Germany

As a commensal on mucosal surfaces, *Candida albicans* not only interacts with the host but also bacterial members of the microbiota. Ilse will present examples of enhanced bacterial virulence in the presence of the fungus and discuss the underlying mechanisms.

Neil Brown,
University of Bath, UK

Neil is a molecular fungal biologist, ex-BBSRC Fellow and Senior Lecturer at the University of Bath. He is motivated to i) discover why toxigenic fungal diseases increasingly threaten our food security and health, and ii) develop new ways to fight back. This includes understanding how fungal pathogens sense the 'taste' of their hosts and if these mechanisms can be used to 'turn off' virulence and toxins.

Find out more about Neil Brown

Host environment sensing: drivers of fungal development and disease
Neil Brown, University of Bath, UK

Fusarium Head Blight (FHB) is the number one floral disease of cereals for which there is no effective control. FHB infections increasingly contaminate our cereals with mycotoxins that threaten our health and food security . Nutrient acquisition is crucial for fungal pathogenesis. Accordingly, hosts deploy nutritional immunity, by restricting a fungal invader's access on essential micronutrients. Neil will outline how *Fusarium graminearum* responds to zinc stress by activating metal ion acquisition systems, stress-responses, and mycotoxin production. This collectively releases zinc from the host, promoting fungal survival. Therefore, zinc stress within a wheat plant acts as an environmental trigger for fungal virulence.

Nancy Keller,
University of Wisconsin, USA

Nancy P. Keller explores the roles and consequences of fungal secondary metabolism in diverse ecological settings from fungal pathogenesis of humans and plants to composition of microbial communities in food commodities. Her lab is renowned for characterizing fungal natural products and elucidating endogenous and synthetic regulation of these chemicals.

Find out more about Nancy Keller

Close encounters of the microbial kind
Nancy Keller, University of Wisconsin, USA

Bacteria and fungi reside together in diverse environmental niches ranging from soil matrices to communities within and on the host body. We find that small extracellular signalling molecules are the key coinage for inter-kingdom microbial communications that influence survival, dispersal and community composition of members of these two kingdoms.

Tajalli Keshavarz, University of Westminster, UK

Tajalli Keshavarz is Professor Emeritus at the University of Westminster. Tajalli Kesharvaz's research interest is in microbial/cross kingdom communication (interaction), and his general interest is in philosophy and literature.

Find out more about Tajalli Keshavarz

Microbial interactions: a world of diplomatic negotiations
Tajalli Keshavarz, University of Westminster, UK

This talk will cover:

- Fungi and multi-species interactions in agricultural, clinical and food sectors
- Interactions and biofilms
- Bio-interactions: exploit or destroy?

Sylvain Raffaele, INRAE, France

Sylvain Raffaele is group leader at the INRAE laboratory for plant-microbe-environment interaction studies (LIPME) in Toulouse, France. Sylvain's research focuses on plant interactions with fungal pathogens in various environments, mostly from a molecular and genomics perspective.

Find out more about Sylvain Raffaele

Evolutionary genomics of generalist plant parasitism in *Ascomycetes*

Sylvain Raffaele, INRAE, France

The range of hosts that parasites can infect is a key determinant of the emergence and spread of disease. In fungal pathogens, host range varies from a single host genotype (specialists) to hundreds of unrelated species (generalists). In these interactions, pathogen small-secreted protein effectors play a major role in manipulating plants to facilitate disease. While molecular processes contributing to host specialization have been relatively well studied, the molecular and genetic bases of host range expansion and the evolution of generalism remain elusive. Comparative analyses in fungi from the Sclerotinia lineage revealed biased patterns of synonymous substitutions, regulatory variation and division of labor supporting the ability to colonize diverse plants. To search for candidate effectors associated with a generalist lifestyle, we analyzed the predicted structure of small-secreted proteins lacking functional annotation (orphans) across twenty *Ascomycete* genomes. We show that a majority belong to families broadly conserved at the structure level, that diversified through changes to their surface energetic landscape. The underlying mutations tend to increase the robustness of the overall effector structures while also contributing to evolvability. This mechanism could explain how conserved effector families maintained biological activity over long evolutionary timespans in different host environments.

Jane Usher,
University of Exeter, UK

Jane Usher is a BBSRC Discovery Fellow at the MRC Centre for Medical Mycology at the University of Exeter. Jane's research focuses on the human fungal pathogen *Candida glabrata* and how it can combat stress resistance from both exogenous and host sources. Using a tapestry of molecular tools Jane is identifying the critical genes invovled in stress resistance and characterising their mechanisms.

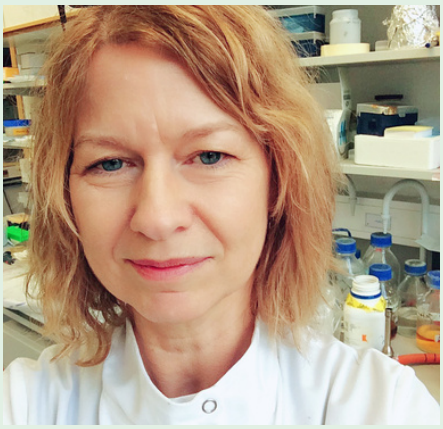
Find out more about Jane Usher

Functional genomics in *Candida glabrata*, new tools to study stress, pathogenesis and drug resistance

Jane Usher, University of Exeter, UK

The processes of life are dynamic and changes on a molecular level enable organisms to grow but to adapt and survive in different environments, such as the ability to cause disease within a human host. Jane's research focuses on the human fungal pathogen, *Candida glabrata* and how it has evolved the capabilities to withstand a challenge from the combination of environmental and imposed drug stresses.

Carol Munro, University of Aberdeen, UK



Carol Munro's research group investigates how fungal cell surface components contribute to virulence, host interactions and antifungal drug tolerance and resistance. Her group takes a number of approaches to study factors that contribute to pathogenicity and fitness such as proteomics, functional genomics, genome sequencing, high throughput phenotypic analysis and uses a range of cellular and *ex vivo* infection models. Carol, with partners at the Scottish Biologics Facility, is also developing novel biologics-based antifungal therapeutics that target the fungal cell surface.

Find out more about Carol Munro


The fungal cell wall as a therapeutic target

Carol Munro, University of Aberdeen, UK

Many fungal cell wall components are fungal specific and attractive targets for the generation of novel therapeutics and diagnostics to combat life-threatening invasive fungal infections. Carol and her group have demonstrated that fungi can modify their cell walls in response to environmental cues, including exposure to antifungal drugs, which renders them less susceptible to antifungal treatment and influences interactions with host cells. The group have developed monoclonal antibodies that target specific cell surface epitopes that are upregulated during infection and drug exposure. Carol will present proof of concept studies of their efficacy *in vivo* highlighting their potential as a new generation of biologics-based antifungals.

Jason Rudd,
Rothamsted Research, UK

Jason Rudd is a Molecular Plant Pathologist who has led research on the *Zymoseptoria tritici* vs wheat crop disease interaction for > 15 years, based at Rothamsted Research, UK. Prior to this he was employed on an EU project based in Germany studying pathogen manipulation of plant immunity. His PhD and earlier studies focussed on the regulation of plant reproduction, and was based at the University of Birmingham, UK.

Find out more about Jason Rudd

Dissecting virulence mechanisms of the fungal cereal killer, *Zymoseptoria tritici*
Jason Rudd, Rothamsted Research, UK

The ascomycete fungus *Zymoseptoria tritici* is a major threat to wheat food security, due to its rapid ability to evolve, and establish insensitivity to fungicides and disease resistant plants. Rothamsted Research's work aims to identify core weaknesses in the pathogen, through genomics approaches, which may be exploited for future improved disease control. Jason will present data from “pangenomics” and “mutagenomics” approaches which are beginning to reveal these potentially exploitable weaknesses.

Jan Dijksterhuis
Westerdijk Institute, The Netherlands

Jan Dijksterhuis encountered an above average number of different fungal species during his career. He studied yeasts, nematode-destroying fungi, biological control, Oomycetes and rust fungi before starting his work at the Westerdijk Fungal Biodiversity Institute on food - and indoor fungi. Here he worked on numerous projects together with companies and also addressed fungal resistance and resilience as well as the biology of fungal spores. Recently his interest was initiated towards towards the interaction between fungal species and bacteria.

Fungi, a tale of variation

Jan Dijksterhuis, Westerdijk Institute, The Netherlands

The Westerdijk Institute in Utrecht, NL, harbours the largest collection of fungal isolates in the world. Variation is a hallmark of evolution and I would like to address this phenomenon in the research we have done during the last decades on fungal spores. The fungal kingdom exhibit an enormous variety of traits and morphologies. The fungal spore and spore formation were an important way to identify fungi before the molecular age kicked in. A number of examples will be highlighted here. Very related species of fungi shows different traits as will be illustrated by the biology of stress-resistant ascospores. But heterogeneity does not stop at the species border as intraspecific variation can be remarkably large. The variation in heat-resistance of fungal conidia between isolates of different fungal species will be discussed. Finally, there is variation within one isolate that occurs between cells at different stages of maturation. Even the size distribution of fungal spores within a colony may play a role.

Anne Pringle, University of Wisconsin, USA

Anne Pringle is the Mary Herman Rubinstein Professor of Botany and Bacteriology at the University of Wisconsin-Madison. She was born in Kuala Lumpur, Malaysia, and grew up overseas. Having moved more or less constantly throughout her childhood, she became obsessed with dispersal and movement and now studies invasive nonpathogenic fungi.

Find out more about Anne Pringle

Rethinking Baker's articulation of an "ideal weed" with Death Caps: What defines the "ideal" invasive fungus?

Anne Pringle, University of Wisconsin, USA

As global change reshapes Earth's biodiversity attention is focused on plants and animals and the diseases killing them. Nearly ignored are the changing distributions of nonpathogenic fungi. The ectomycorrhizal Death Cap *Amanita phalloides* is native to Europe and invasive in North America. Long ago, Herbert Baker articulated his vision of an "ideal weed": using a few species as case studies, he identified the characteristics of invasive plants. But what traits define invasive mushrooms?

Mike Bromley
University of Manchester, UK

Michael Bromley is a Professor in Medical Mycology at the University of Manchester and is the Director of the Manchester Fungal Infection Group. His research focuses on drug discovery and drug resistance in fungal pathogens. While working at F2G Ltd and throughout his academic research career he has been involved in the evaluation of the antifungal drug Olorofim. He is currently leading a collaborative project to generate a genome-scale knockout mutant library in the filamentous fungal pathogen *Aspergillus fumigatus* and is developing and employing functional genomics technologies to understand genetic and environmental drivers of pathogenicity and drug resistance in fungi.

Find out more about Mike Bromley

Antifungal drug resistance: An inevitable consequence of evolution
Mike Bromley, University of Manchester, UK

Aspergillus fumigatus is a saprotrophic filamentous fungus and an opportunistic pathogen that kills in the region of 1 million people each year. The primary treatment for *Aspergillosis* is voriconazole however the use of analogous compounds for crop protection is driving a pandemic of resistance that we have been tracking since the turn of the millennium. A number of novel antifungals are close to clinical approval that promise to revolutionise treatment however the imminent deployment of new agricultural fungicides may be putting these compounds at risk by driving resistance. In this talk I will discuss the potential impact of these developments.

Lynne Boddy
University of Cardiff, UK

Lynne Boddy is a Professor of Fungal Ecology at Cardiff University and has taught and researched the ecology of fungi associated with trees and wood decomposition for over 40 years. Her current studies include the ash dieback fungus, and how climate change is affecting fungi. Lynne regularly communicates fungal science on radio and TV, and is a past president of the British Mycological Society.

Find out more about Lynne Boddy

Fungi interactions in trees

Lynne Boddy, University of Cardiff, UK

Trees are holobionts, interacting intimately with many fungi and other microbes. After touching on these, the talk will focus on interactions among and between endophytes and decomposers of woody tissues, including how initial decay communities establish, and the interactions among fungi and with the environment that drive community change.

Visit to Wylam Brewery

Founded in 2000 Wylam is a 30 barrel micro brewery based at the Palace of Arts in Exhibition Park, Newcastle upon Tyne. The brewery was founded by John Boyle and Robin Leighton, creating their first malt bills and recipes in a potting shed in the village of Wylam, Northumberland. The brews today can be found in quality pubs and bottle shops.

The Palace of Art is the last remaining building from the 1929 North East Exhibition: an ambitious project built to celebrate and encourage craft, art and industry at the start of the Great Depression.

The visit to Wylam includes a tour of the brewery, beer tasting, and a three course dinner.

The brewery is about a 40 minute walk from the Copthorne Hotel, taking in some of Newcastle's great sites en route. A mini bus will also be available. Meet in the hotel lobby from 18:15 if walking, or from 18:30 for those travelling on the mini bus.

The *Candida glabrata* parent strain trap

Jane Usher (1), Gabriela Ribeiro (2), ***Delma Childers*** *(2)*

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(2) University of Aberdeen, Institute of Medical Sciences, Aberdeen Fungal Group, United Kingdom

Reference strains are important for standardizing methodologies and providing mechanistic insights into pathogenesis. However, recent studies have shown that intraspecies phenotypic and genotypic variation affects virulence processes in major fungal pathogens. *Candida glabrata* is the second leading cause of candidiasis and undergoes extensive karyotype and phenotypic changes in response to stress. Many studies on this pathogen have been conducted on two sequenced strains, BG2 and CBS138 (ATCC 2001). Comparative data between these strains is limited, therefore we characterised metabolic, cell wall, and host-interaction attributes for BG2 and CBS138 using Omnilog, flow cytometry, microscopy, and *in vitro* and *in vivo* infection models. We found that BG2 utilized a broader range of nutrient sources than CBS138 and had reduced cell wall thickness and immunomodulatory carbohydrate exposure. Our observations may be associated with the differences we obtained in innate immune interactions and virulence between these strains. For example, both strains were phagocytosed to a similar extent, yet BG2 replicated to higher numbers in macrophages and was more virulent during *Galleria mellonella* infection than CBS138 in a dose-dependent manner. Altogether, our data identified metabolic differences between two major *C. glabrata* strains that have important implications for virulence. This work stresses the need to consider intraspecies variation when translating strain-specific data to species-level to inform robust conclusions about *C. glabrata* pathogenesis. We are also investigating how *in vitro* antifungal exposure for each strain background affects cell wall composition, subsequent innate immune interactions, and host survival in a waxworm infection model. Our preliminary data suggest that azole exposure induces distinct sub-populations of cells with altered carbohydrate exposure that may play a role in virulence. By determining the broader adaptive responses of pathogens to antifungal treatment, we will provide a better understanding of the unintended consequences of therapy which will inform strategies for adjuvant treatment approaches.

Identification of novel host and fungal factors driving the interaction of *Aspergillus fumigatus* with the respiratory mucosa

Sébastien C. Ortiz (1), Patrick J. Dancer (1), Rachael Fortune-Grant (1), Kayleigh Earle (1), Norman Van Rhijn (1), Mike Bromley (1), Sara Gago (1), ***Margherita Bertuzzi*** *(1)*

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The fungal pathogen *Aspergillus fumigatus* (Af)affects >3,000,000 individuals annually, with invasive aspergillosis having mortality rates of >50%. Airway Epithelial Cells (AECs), which cover the entire alveolar surface and comprise 24% of all cells in the human lung parenchyma, have immediate, extensive, and likely prolonged contact with *Af* conidia upon inhalation. We previously demonstrated that AECs provide a potent means of antifungal defense against *Af in vivo*, and that dysfunctional epithelial antifungal activity in at-risk patients may provide an opportunity for *Af* to exploit AECs as a safe haven to reside intracellularly. However, the fungal and host factors controlling *Af* uptake and clearance by AECs are poorly understood. To determine how healthy AECs recognise and kill *Af* and how these processes are dysregulated in disease, we exploit single-cell workflows to perform molecular, transcriptional, and cellular analyses of the *Af*-AEC interaction *in vitro* and *in vivo*. Using fluorescent auxotrophic *pyrG*- strains locked at specific morphological stages, we determined morphotype-specific interactions with AECs, whereby swollen conidia locked at 3 and 6 hours of germination are 2-fold more readily internalized than conidia locked at 0 hours. Probing with fluorescent lectins, we identified mannose as a key surface carbohydrate that show a morphotype-specific increase during germination. Supporting this, mannose and the mannose-binding lectin Concanavalin A were able to respectively reduce (by 88%) and abolish (100%) *Af* internalization. Using a combination of *Af* mutants, and AEC receptor mutants, we are systematically evaluating morphotype-specific factors on *Af* surface and characterizing key host receptors for their role in mediating fungal uptake and clearance both healthy and diseased AECs. Understanding how AECs contribute to antifungal clearance by recognizing morphotype-specific fungal factors is of mayor clinical importance as it could inform the development of much needed novel antifungal therapeutics.

VEuPathDB: A free bioinformatics resource that integrates omics scale data and offers tools for exploration and analysis of host and pathogen data

Evelina Basenko *(1) and Andy Jones (1)*

(1) Institute of Systems, Molecular and Integrative Biology, University of Liverpool, UK

VEuPathDB.org is the Eukaryotic Pathogen, Vector and Host Informatics Resource that enables browsing, querying and mining of omics-scale datasets across diverse groups of organisms (e.g., hosts (HostDB.org), invertebrate vectors of human disease (VectroBase.org), eukaryotic microbes), and also environmental and epidemiological studies (ClinEpiDB.org). FungiDB (https://fungidb.org) and HostDB (https://hostdb.org) are VEuPathDB component databases supporting fungal and oomycete and host research, respectively. FungiDB and HostDB integrate a wide range of omics scale datasets, including transcriptomics and co-expression data, proteomics, genetic variation (polymorphisms & copy number variation), phenotypes, and other types of data. VEuPathDB contains hundreds of annotated genomes including *Aspergillus, Cryptococcus, Mucor, Homo sapiens, Mus musculus*, and other species. Host, pathogen, or host-pathogen interaction datasets can be accessed and explored via a user-friendly web interface and an integrated search strategy system that enables data mining, enrichment, and comparison across species. The VEuPathDB Galaxy - My Workspace platform offers private data analysis and ability to explore the analysed data further via the VEuPathDB infrastructure and embedded tools. Gene-centric information is contained within encyclopaedia-like gene record pages that collect community expert knowledge via the user comments system. The genome browse JBrowse provides enhanced view of the supporting data as a collection of tracks (e.g., RNA-Seq coverage plots, mapped SNPs, synteny & orthology, reference sequence, predicted introns and more). Structural and functional gene annotation can be improved in Apollo, a collaborative genome annotation and curation platform. New or updated gene models become visible in VEuPathDB and, when appropriate, become synced with NCBI records. The VEuPathDB project offers a plethora of informational and learning resources. Have questions about how to get started, want to nominate a dataset for integration, or invite us for a demo on Zoom? - Email us to help@fungidb.org

Interactions between fungi, microalgae, and bacteria, and how those modulate the fate of photosynthetic carbon in aquatic systems

Klawonn Isabell *(1) (2) (3) , Dekas Anne E. (2), Parada Alma E. (2), Arandia-Gorostidi Nestor (2), Whitehouse Martin (4), Iversen Morten H. (5) (6), Walles Tim J.W. (3), Flintrop Clara M. (5) (6), Cisternas-Novoa Carolina (7), Nejstgaard Jens C. (3), Kagami Maiko (8) (9), Grossart Hans-Peter (3) (10), Van den Wyngaert Silke (3) (11)*

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Fungi are present, abundant, and active in aquatic systems, and yet they are one of the most understudied microbial groups in those systems. Combining biogeochemical, microbiological, and molecular tools, we studied the cryptic links between parasitic fungi (*Chytridiomycota*) and microalgae–bacteria associations, using two model pathosystems. We found that the parasitic fungi profoundly modified the relationship between the microalgal hosts (photosynthetic diatoms) and co-associated bacteria through several mechanisms. For instance, bacterial abundances were several times higher on individual fungal-infected diatoms compared to healthy diatoms, particularly involving the bacterial taxon Burkholderiales. The fungal parasite, including host-associated sporangia and free-swimming zoospores, derived 100% of their carbon content from the diatom host. By comparison, transfer efficiencies of photosynthetic carbon were lower to diatom-associated bacteria (67−98%) and even lower to free-living bacteria (32%).

In a natural lacustrine system, where infection prevalence reached about 50%, we calculated that 20% of the diatom-derived photosynthetic carbon was shunted to the parasitic fungi, thereby accelerating carbon transfer to higher trophic levels and bypassing the conventional microbial loop. Fungal infections further reduced the formation of sinking diatom aggregates—which are crucial for the export of carbon from surface waters to depth—and additionally promoted carbon respiration but diminished settling velocities for fungal-infected vs. non-infected aggregates. Our data imply that fungal parasites can effectively modify the fate of photosynthetic carbon and the nature of phytoplankton−bacteria interactions, with implications for microbial food webs and carbon cycling in freshwater and coastal environments.

Bacterial-fungal warfare – intoxication by and response to the Type VI-secreted antifungal effector Tfe2

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Fungi predominantly exist in polymicrobial communities which are defined by complex synergistic and antagonistic interactions. To persist within a mixed bacterial and fungal neighbourhood gram-negative bacteria employ diverse strategies including the deployment of the Type VI Secretion System (T6SS). The T6SS is a contractile nano-syringe that delivers toxic effector proteins directly into host and microbial competitor cells. Whilst a primary role attributed to the T6SS is to deliver antibacterial effector proteins into rival bacterial cells, recently it was found that this 'anti-bacterial' T6SS is also a potent anti-fungal weapon able to kill model and pathogenic fungi by delivering dedicated anti-fungal effectors. One of the first fungal-specific effectors identified is Tfe2 in Serratia marcescens, which has been shown to disrupt nutrient uptake and induce autophagy in a variety of fungal species. To further analyse the molecular mechanism of Tfe2 anti-fungal activity we deployed proteomic and lipidomic analyses, which revealed changes in the fungal membrane composition via the phospholipid, sphingolipid and ergosterol biosynthetic pathways. We hypothesize that these changes lead to rearrangements in the mitochondrial membrane composition, causing the observed reduction in energy production via the oxidative phosphorylation pathway, near complete shut-down of nascent protein synthesis and decrease in metabolic activity. We suggest that an indepth understanding of bacterial T6SS-mediated antifungal targeting mechanisms can guide the modelling of novel antifungal drug strategies.

Interaction of fludioxonil with two-component and HOG signalling in the fungal wheat pathogen, Zymoseptoria tritici

***Zoe Gardiner**, Callum Fraser and Simon Whitehall*
Biosciences Institute, Newcastle University, Newcastle upon Tyne, NE2 4HH

Zymoseptoria tritici is a fungal phytopathogen and the causative agent of Septoria Tritici blotch (STB), one of the most economically and agriculturally significant foliar diseases of wheat (1). Infection causes the formation of necrotic lesions on leaf tissue, leading to a decrease in tissue available for photosynthesis and significantly reducing crop yield (2). Fludioxonil is a phenylpyrrole fungicide which is known to target the HOG pathway, a key MAP kinase signalling pathway which regulates cellular responses to a wide range of environmental stresses in eukaryotes. Whilst the ZtHog1 MAP kinase has been shown to be essential for virulence (3), very little is known about the upstream regulators and downstream effectors of the Z. *tritici* HOG pathway.

We have identified several upstream constituents of two-component signalling, a His-Asp phosphorelay system, which regulates HOG activation and sensitivity to fludioxonil. We found that, the hybrid histidine kinase, ZtNik1, and the response regulator, ZtSsk1, are essential for the response of Z. *tritici* to fludioxonil. Deletion of either of these proteins, or deletion of ZtHog1, leads to full resistance to the fungicide. Furthermore, deletion of ZtAft1, a bZIP transcription factor and putative target of ZtHog1, also confers partial fludioxonil resistance. We have also identified other environmental stresses which are signalled through these pathways, with evidence to show ZtNik1 is a master regulator for osmotic stress in Z. *tritici*.

References:
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Use of pangenome analysis to identify novel heterokaryon interaction genes influencing gene flow of azole resistance in *Aspergillus fumigatus*

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Aspergillus fumigatus is a major cause of opportunistic aspergillosis disease. There have been increasing reports of azole resistance worldwide, posing a threat to the use of azole antifungals in the management of diseases. Therefore, it is critically important to understand the rate at which mutations leading to azole resistance can spread through populations of *A. fumigatus*. The first steps involve elucidating the mechanisms driving isolate interactions and gene flow. Within populations of *A. fumigatus*, gene flow may occur during the sexual cycle and/or the formation of heterokaryons leading to subsequent parasexual recombination. Our present study focuses on the possible interactions and gene flow due to heterokaryon formation and parasexual recombination. Such interactions are restricted by heterokaryon incompatibility (*het*) genes which are widespread in fungi. These *het* genes regulate the initiation/recognition events involving hyphal anastomoses and heterokaryon formation. This evolutionary 'guard-point' may prevent the spread of genetic infections, but conversely, it may facilitate the exchange of evolutionarily advantageous genes, e.g., azole resistance (AR*Af*) mutations. Classical genetic studies have been used to identify *het* genes in *Aspergillus* species. However, little is known about their molecular interactions.

Here, we describe the use of recent advances in sexual crossing, whole genome sequencing and the development of bioinformatics pipelines to identify novel candidate *het* genes that may be involved in heterokaryon incompatibility in *A. fumigatus*. Using the pangenome analysis, we have identified at least seven potential candidate genes that may be involved in *het* recognition. We are currently using heterokaryon complementation of auxotrophic nitrate assimilation mutants and CRISPR/Cas9 gene editing in various strains of *A. fumigatus* to experimentally validate these novel *het* gene candidates.

Engineering functional fungal materials with bioactive nanoparticles; a natural interaction process for fabricating reusable heavy metal scavenger in waste-water purification

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In this study, we developed a rapid (yet simple) method for the direct functionalization of Aspergillus niger mycelium with differentially capped (four categories) gold nanoparticles (AuNPs) without the use of intrusive chemicals. The study involved different modification phases coupled with extensive physicochemical and structural characterizations of the functionalized mycelia. The final product is being studied as a reusable scavenger in heavy metal purification from wastewater. ATR-IR revealed the unique band vibrations of the NPs on the mycelia, SEM/EDX for morphological and chemical elucidation, NPs concentration by ICP-MS, and TEM for mapping out nature of interaction after mycelia slicing. Our results showed that there are distinct patterns on the impact of concentrations and pH on the fungi response to the NPs especially when spores are transferred from spent cultures. We also identified the nature of AuNPs capping agent, and how their antifungal ability could interfere with functionalized mycelia yield. A. niger is a rapidly growing melanin producing fungus which is distinct for its filament structure and broad substrate preference. The use of fungal mycelia offers green and sustainable alternatives to petrochemical, and animal products which have general concerns with acceptability (climate change, vegan/vegetarian selection etc.). This study offers a paradigm in sustainability research and wastewater treatment, and it could be easily deployed in every economy either underdeveloped or developed.

Fungi-on-a-Chip: Visualising Fungal-Bacterial Interactions and Fungal-Mediated Water Redistribution

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Soil is a complex and variable environment, consisting of solid particles surrounded by water and air pores that are irregularly distributed. Filamentous fungi and other fungi-like microorganisms can cross the air-filled pockets within soil to access areas of higher water saturation and it has been demonstrated that fungi are able to redistribute soil water across their mycelial network (1). However, it is not known whether this ability is specific to certain species, nor has it been examined at the cellular level. Unlike fungi, bacteria require a continuous water film for motility, thus their movement throughout soil is more restricted. To overcome this, it is understood that bacteria may utilise fungal-mediated water redistribution as a dispersal mechanism (or "fungal highway") to cross regions of soil where there is low water saturation (2). Visualisation of water redistribution and bacterial movement across fungal hyphae is not possible *in situ* due to the opacity of soil and current agar-based techniques do not permit microscopy imaging. A microfluidic device was previously developed for the study of fungal-fungal interactions (FFI) at the level of the single cell, which confers numerous advantages over conventional methods (3). Utilising the FFI device, we have devised an appropriate method to visualise and quantify fungal-mediated water movement at cellular level and can explore the influence of fungal species on water transport and bacterial dispersal along hyphal networks.

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Unravelling Interactions Between Carnivorous Plants and Their Fungal Endophyte Communities: Impacts of Environment, Plant functional traits, and Host Relatedness

Brandon Shaw *(1), Dave Ryves (1), Helen Glanville (1), Jon Millett (1)*

Carnivorous plants attract, catch, and digest animal prey (primarily arthropods) and assimilate the resulting nutrients into their tissues to be used for growth and reproduction. Carnivorous plants have not been well studied for their fungal endophytes (only 12 out of approximately 600 species), perhaps owing to difficulties culturing from their atypical leaves. However, carnivorous plants could present an opportunity to study endophyte community assembly because of their unique functionality for prey capture and digestion, evolution of carnivory in multiple lineages, and divergent and convergent evolution of different trapping mechanisms within carnivorous lineages. This research aims to examine the influence of 1) environment 2) trapping mechanism (functional trait) 3) host plant relatedness (phylogeny) on endophyte community assembly. Hypothesising that trapping mechanism (plant functional trait) will be the greatest predictor of endophyte community assembly.

This research uses culturing methods and high-throughput sequencing to identify the fungal endophyte communities of several carnivorous plant species growing wild in the UK (5 species) and the US (5 species), selected to cover a range of convergently and divergently evolved trap types (pitfall, flypaper, and snap trap) across a variety of locations to address the above research aims.

We successfully cultured fungal endophytes from 5 plant species, which demonstrated low diversity of culturable fungal endophytes (6 species), with common endophytes found across multiple hosts. High throughput sequencing provides a fuller picture of endophyte communities, demonstrating differences and similarities in endophyte community assembly not revealed by culture dependent approaches. These results show the importance diverse methodology and provide insights into the fungal endophyte communities of carnivorous plants and provide a first step in understanding how fungal endophytes may contribute to carnivorous plant function.

Intraspecific variation matters: Fungal traits and interactions are down to the individual, not the species

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Intraspecific variation plays an important role in evolution as a driver of natural selection, as well as artificial selection for breeding and food production. Likewise, interactions of fungi with biotic and abiotic factors are governed by individuals, not by a species as a whole. However, many studies on fungi treat a single individual as representative of a species, unlike most research on animals and plants.

Edible mushrooms serve as excellent model organisms to explore this topic because mushrooms are relatively easy to cultivate and their production relies on trait variation in artificial selection, e.g. for enhanced yield or low spore load.

To investigate the magnitude of intraspecific variation in fungi and how variation differs across functional traits (any features that affect fitness of an organism), I cultivated 106 genetic individuals of five Pleurotus species from New Zealand in the same conditions in pine sawdust substrate bags and quantified within- and between-species variation in several traits.

My results indicate that vegetative growth traits (such as substrate mass loss and mycelial growth rate) are highly variable within species, but reproductive traits (such as time until fruiting) vary more between species.

I further compared trait variation patterns to a multi-locus phylogeny that I assembled from internal transcribed spacer 2 (ITS2), RNA polymerase II second largest subunit (RPB2), and translation elongation factor 1-alpha (Tef) sequences. I will discuss the correlations between the observed trait patterns and phylogenetic structure.

Overall, my results underscore the need to account for within-species variation when studying fungi and their interactions, as well as provide insights into natural and artificial selection of Pleurotus and the role of abiotic factors in shaping phenotypic variation.

Fungal interactions during wood decomposition

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Microbial communities responsible for wood decomposition shift as lignocellulose is depolymerised and the wood structure changes, the extent to which substrate change influences community composition remains unresolved. Antagonistic interactions between fungi lead to the formation of discrete spatial colony units within the substrate. Further competitive interactions occur as decomposition progresses, often resulting in species replacement and a new decay community structure. The environmental factors and metabolic adaptations that influence decay community structure and interaction outcomes are increasingly studied using high throughput technologies. Evidence suggests that earlier colonising species can influence subsequent communities, referred to as priority effects. Here I will summarise our research investigating the metabolic profiling of fungal communities in the dysfunctional wood of attached branches and laboratory-based wood block studies on the effect of earlier occupation on subsequent colonisation and fungal interactions.

Phospholipid flippase-induced plasma membrane disorganisation in *Candida albicans* has far-reaching consequences for invasive hyphal growth, vesicular trafficking, cell wall architecture and interaction with immune receptors

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A major reorganisation of plasma membrane (PM) phospholipids is necessary for the establishment and maintenance of cell polarity during the emergence and elongation of invasive hyphae *in Candida albicans*. Lipids such as PI4P and ergosterol become enriched in a tip-high gradient, controlled in part by the activity of flippases that flip phospholipids from the outer to the inner leaflet of the PM. We used a library of fluorescent lipid reporters with confocal microscopy to visualise the localisation and distribution of lipids and study the influence of the previously uncharacterised endomembrane-localised flippase, *Neo1*, on the PM. We have investigated the effect of *NEO1* deletion on the ability of *C. albicans* to maintain hyper-polarised hyphal growth, form a competent cell wall and tolerate membrane stress. The effect of flippase activity on the endoplasmic reticulum was studied using our novel reporter that permits imaging of the ER for the first time in *C. albicans* hyphae. We found that *Neo1* has a central role in PM lipid organisation during invasive growth. The *neo1Δ* mutant strain displays membrane trafficking defects and polarisation of membrane lipids is lost, leading to defects in hyphal morphology, invasion and directional growth - all of which are required for virulence. This loss of membrane asymmetry also has downstream effects on cell wall architecture, causing differential recognition by human immune receptors. We have therefore elucidated for the first time the role of the *C. albicans* homologue of the essential Saccharomyces cerevisiae protein, *Neo1*, with respect to invasive hypha formation.

Bacterial Quorum-Quenching lactonase hydrolyzes fungal mycotoxin and reduces pathogenicity of *Penicillium expansum*—suggesting a mechanism of Bacterial-Fungal interactions

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Penicillium expansum is a necrotrophic wound fungal pathogen that secrets virulence factors to kill host cells including cell wall degrading enzymes (CWDEs), proteases, and mycotoxins such as patulin. In recent years, there has been a rapid increase in research on the molecular mechanisms of pathogenicity in *P. expansum*; however, less is known regarding the bacteria–fungal communication in the fruit environment that may affect pathogenicity. Many bacterial species use quorum-sensing (QS), a population density-dependent regulatory mechanism, to modulate the secretion of quorum-sensing signaling molecules (QSMs) as a method to control pathogenicity. N-acyl homoserine lactones (AHLs) are Gram-negative QSMs. Therefore, QS is considered an antivirulence target, and enzymes degrading these QSMs have potential antimicrobial properties. Here, we demonstrate that a bacterial AHL lactonase can also efficiently degrade a polyketide lactone, patulin, secreted by *P. expansum*. The bacterial lactonase hydrolyzed patulin with a k*cat* value of 0.724 ± 0.077 s-1 and KM value of 116 ± 33.98 µM. The calculated specific activity (k*cat*/K*M*) showed a value of 6.21 × 103 s−1M−1. While the incubation of *P. expansum* spores with the purified lactonase did not inhibit spore germination, it inhibited colonization by the pathogen in apples. Furthermore, adding the purified enzyme to *P. expansum* culture before infecting apples resulted in reduced expression of genes involved in patulin biosynthesis and fungal cell wall biosynthesis. Furthermore, phylogenetic and structural analysis was used to identify putative lactonase in *P. expansum* and other fungi. Following recombinant expression and purification of the newly identified fungal enzyme, its activity with patulin was verified. These results indicate a possible role for patulin and lactonases in inter-kingdom communication between fungi and bacteria involved in fungal colonization and antagonism and suggest that lactonases can be used as potential antifungal post-harvest treatment.

Changes as small as 2°C can alter fungal community interactions and ecological outcomes in decaying wood

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Forests are important for carbon sequestration, with woody materials representing a significant carbon pool. Communities of wood decay fungi are key to the fate of this carbon, either returning it to the atmosphere in the form of carbon dioxide or to the soil in the form of recalcitrant residues. With warming global temperatures, decay rates may increase, potentially leading to increasing levels of atmospheric carbon dioxide. This increase in carbon release could be accelerated or offset by changes in fungal communities, given that some fungi (such as brown or soft rot species) may shuttle more carbon to slowly cycling soil pools, while other fungi (such as white rot species) may return more carbon to the atmosphere. In order to study the effects of changes in temperature on fungal communities, we used high-throughput amplicon sequencing to characterize fungal community composition in small diameter stem sections of balsam fir (*Abies balsamea*) and aspen (*Populus tremuloides*) incubated at 8 temperatures, ranging from 4°C to 34°C. Fungal community composition was assessed before and after incubation using two primer pairs and changes in decay rate and lignin content were also measured. Changes in temperature as small as 2°C were enough to significantly alter fungal community composition and interactions in both aspen and balsam and decomposition rate in aspen, while larger changes (4°C) had similar effects but also affected the amount of recalcitrant carbon produced by decay in aspen. These results can be used to inform models tracking the rate and fate of carbon turnover from woody materials.

Non-canonical interactions of anaerobic gut fungi with bacteria from the rumen microbiome

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Anaerobic gut fungi (AGF), phylum Neocallimastigomycota, are powerful degraders of feed in ruminants such as cows and sheep. Together with bacteria, archaea, and protozoa, AGF form the rumen microbiome, who's digestive fermentation activity strongly affects both animal health and production greenhouse gas methane. Manipulation of the rumen microbiome activity is thus a promising avenue to reduce environmental impact of ruminant farming. However, this requires better understanding of the microbiome function.

AGF play a key role in plant cell wall digestion in the rumen microbiome. They are known as primary degraders, who produce enzymes that cleave polysaccharides, and release di- and monosaccharides that are consumed by other microbes. Methanogenic archaea are scavengers relying on AGF metabolic by-product H2. We hypothesized other interactions may exist.

Here we describe the exciting uncovery of a non-canonical interaction of AGF with microbiome partners. Using an enrichment-based approach, we recovered a community of bacteria from bovine rumen fluid that stimulated growth of AGF in vitro. The bacteria promoted fungal growth in co-cultures with carbon sources that both fungi and bacteria could metabolise, and even supported growth on carbon sources that AGF alone could not metabolise. These interactions were observed across three AGF genera. Spent supernatant from bacterial cultures was sufficient to support fungal growth, indicating involvement of extracellular compounds. Analysis of compounds in the spent supernatant, via untargetted mass spectrometry-based metabolomics, and their depletion after fungal growth, provided initial insight in metabolites potentially mediating the interaction.

Our results indicate the existance of a novel type of interaction between rumen bacteria and anaerobic gut fungi, a potential cross-feeding interaction whereby AGF do not function as primary degrader but seem to take a role as consumer or scavenger. Uncovering this novel type of interaction demonstres the need to increase understanding of rumen microbial interactions across trophic levels.

Fungal interactions with light-activated therapeutic compounds

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Fungi are important pathogens of humans, animals, and plants. Fungal diseases are intrinsically difficult to treat as there are limited classes of licenced antifungals and the development of resistance is an increasingly serious problem (Robbins et al., 2016). As such, fungal pathogens are threats to human health and food security, meaning there is a need to develop new therapeutic strategies (Fisher et al., 2012).

LightOx has developed a portfolio of small molecule compounds with light-activated cytotoxic properties which overcome the limitation of current light-based treatments. LightOx compounds are known to undergo photoexcitation following UV irradiation, producing reactive oxygen species (ROS) (Chisholm et al., 2019). We are currently analysing the effect of LightOx compounds on a range of fungal species, to determine their antifungal potential.

Using soft agar overlay assays, two LightOx compounds were found to have light-dependent inhibitory effects on the growth of model yeasts species (*Schizosaccharomyces pombe* and *Saccharomyces cerevisiae*) and the key human pathogens *Candida albicans* and *Candida glabrata*. However, cell viability assays have that revealed LightOx compounds are not fungicidal. Fluorescence microscopy has demonstrated uptake of LightOx compounds into fungal cells, irrespective of their ability to inhibit growth. Current work is focussed on determining the effects of LightOx compounds on filamentous fungal pathogens, further characterisation of sub-cellular localisation and mode of action. We are also identifying mutants with altered sensitivity/resistance and preliminary analyses with S. pombe have revealed that loss of the Sty1 stress-activated MAP kinase (SAPK) results in hypersensitivity to LightOx compounds.

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Exploring the interactions shaping the past, present and future of True Eyespot Disease of Cereals

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Eyespot disease, a significant threat to cereal crops like wheat and barley, poses challenges to temperate parts of the world and global food security amid pollution and climate change. The causal agents, *Oculimacula yallundae* (OY) and *Oculimacula acuformis* (OA), closely related fungal pathogens, cause distinct lens-shaped lesions on stems. These lesions obstruct water and nutrient transport, resulting in lodging and yield losses of up to 30% (AHDB, 2023).

The disease remains underestimated and understudied, leading to knowledge gaps in pathogen interactions with its environment. Understanding OY/OA is vital for effective management due to differences in host range, epidemiology, and sensitivity to fungicides. Our study aims to expand knowledge and enhance disease control through three inter-related work packages:

1. The past: Exploring, using archive wheat (from mid-1800s to present), how OY/OA dynamics has changed in response to climate change, pollution, fungicide use and agricultural practices, similarly to previous work on wheat foliar pathogens [JW1] (Bearchell, et al., 2005).
2. The present: Investigating the degree to which OY/OA interacts with air and soil as sources of inoculum for eyespot outbreaks and assessing how this may change in response to environmental changes.
3. The future: generating high-quality genomes for both OA/OY while examining the potential for future evolution of fungicide resistance.

These comprehensive investigations into the pathosystem will inform the development of current and future management strategies for eyespot disease, ensuring its effective mitigation against the backdrop of pollution, climate change, and the challenges posed by fungicide use.

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Chemical tools to secure a niche: *Penicillium expansum* utilizes secondary metabolites to modulate microbial community interactions

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Penicillium expansum is a postharvest pathogen of apples that contaminates products with two toxic secondary metabolites, patulin and citrinin. Mutant strains incapable of producing patulin or citrinin are still pathogenic, which prompts us to ask what benefit these compounds have to *P. expansum*. We hypothesize that secondary metabolites provide *P. expansum* an ecological fitness advantage by inhibiting other microorganisms in its environment. To test this hypothesis, we assessed growth of 138 yeast and bacterial apple isolates from three orchards in Wisconsin against extracts from wildtype, a patulin deletion mutant, a citrinin mutant or a patulin/citrinin double mutant of *P. expansum*. Extracts containing patulin exhibit antimicrobial activity against the majority of our apple microbiota, with the majority of bacterial isolates showing higher sensitivity than yeast isolates. Citrinin does not play a significant inhibitory role. A subset of bacterial isolates are sensitive to extracts from the double mutant, suggesting other *P. expansum* secondary metabolites have antimicrobial activity. We are employing a model microbiome community called THOR to coculture with our *P. expansum* mutants to determine if fungal secondary metabolites can alter the composition of an established microbiome, as well as determine the ecological roles of less-characterized secondary metabolites.

Interactions between the fungus *Penicillium roqueforti* and the cheese environment - investigating the basis of bitterness

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The characteristic flavour and aroma profile of blue cheeses is created through the interaction between the blue cheese mould, *Penicillium roqueforti*, the cheese environment and the other microorganisms growing there. One important component of the flavour profile with regards to palatability is the bitterness of the product. The basis of this bitterness is not yet fully understood, but is at least partly due to the presence of increased levels of small, hydrophobic peptides produced as a by-product of protein degradation by the fungus. Recently, certain novel recombinant strains of *P. roqueforti*, produced after the discovery of the induction of sexual reproduction in this species, have been shown to exhibit varying levels of bitterness in the final cheese product, although it is not currently known why this is the case. It is hypothesised that this might be due to different levels of degradation of bitterness-causing molecules such as the small, hydrophobic peptides. The latter molecules are themselves degraded by exogenous exopeptidases, orthologues of which from closely-related species have been used in other food products as debittering agents. In this project, ten such exopeptidases have been identified in *P. roqueforti* (here referred to as *db1-10*) based on bioinformatic analysis. Their expression levels have then been characterised and compared between four different strains of the species, two of which were rated as more bitter and two as less bitter. Though it is yet to be conclusively demonstrated, initial expression studies indicate that a few candidate genes may indeed be responsible for the observed differences in bitterness. Future work aims to further resolve this issue and identify the specific molecules responsible for bitterness in blue cheeses.

Harnessing fungal sexual interactions for the control of plant disease

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There is ongoing need to develop new antifungal compounds for the control of plant and animal fungal diseases given the evolution of resistance in both agricultural and clinical settings. For example, there is growing resistance to fungicides in the phytopathogen *Pyrenopeziza brassicae* cause of light leaf spot, the most damaging fungal disease of oilseed rape in the UK. The disease has also been recorded on several brassica crops across Northern Europe, Oceania, Asia and North America. The pathogen has well described and understood dispersal mechanisms involving both asexual and sexual spore production. Asexual sporulation is responsible for local spread within fields during the main growing season, whereas later sexual sporulation allows spread of infection over greater distances facilitated by wind-borne ascospores. Current disease management involving the use of broad-spectrum fungicides is largely compromised as most European strains exhibit decreasing sensitivity, thus the development of novel more targeted disease control is required.

One possible source of new antifungals is the use of fungal growth hormones, which may alter and repress fungal growth and sporulation. We have identified signaling molecules produced during *P. brassicae* sexual interactions, referred to as Sex Factors (SF), which can almost totally repress asexual sporulation. This provides exciting potential for SF to be used as a novel antifungal compound(s) to control the spread of light leaf spot disease. Current work focuses on the dereplication of SF using analytical chemistry techniques (SFC-HPLC-MS, LCMS, NMR). The activity has been localized to certain lipid fractions. Structural information will allow synthetic access of the compounds in order to investigate SF effects in vitro at larger scales in plant and field trials. In parallel, morphological changes resulting from SF treatment have been assessed by cryo-SEM, providing insights into mechanisms of repression of asexual sporulation. Future work aims to investigate molecular targets of SF.

Differences in the bacterial and fungal composition of laboratory mice and the influence on intestinal colonisation with *Candida albicans*

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The gastrointestinal microbiota plays an important role in health and disease. One function is colonisation resistance, which limits the proliferation of pathobionts, such as the fungus *Candida albicans*, in the gut. Consequently, microbial dysbiosis induced by antibiotic treatment constitutes a major risk factor for candidiasis.
We investigated natural microbiota variation in laboratory mice to identify bacterial candidates mediating colonisation resistance against *C. albicans*. For this purpose, faecal samples from 20 C57BL/6 breeding colonies were used for 16S and ITS1 sequencing. Based on differences in taxonomic composition, α- and β-diversity, and quantitative microbial burden, 5 colonies were selected for colonisation experiments. After oral inoculation with *C. albicans*, faecal samples were collected at different time points to monitor fungal burden in the gut and changes of the intestinal microbiome.

Despite variations in microbiome composition, all five tested colonies displayed similar colonisation patterns. As expected, antibiotic treatment increased fungal colonisation. Surprisingly, sucrose supplementation of drinking water was sufficient to support substantial and stable *C. albicans* colonisation.

These results demonstrate that considerable microbiota variation in breeding colonies of laboratory mice does not necessarily affect colonisation resistance. Nevertheless, our faecal microbiome analysis identified changes in bacterial composition associated with *C. albicans* colonisation that will be further tested to identify bacterial candidates for colonisation resistance.

Interaction between fungal enzymes and development of outer mould-ripened cheeses

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The fungus *Penicillium camemberti* plays a critical role in the production of outer mould-ripened cheeses such as Camembert and Brie. However, despite its economic significance *P. camemberti* has not been widely studied and its mechanism of action with regards to cheese production and maturation has not been elaborated. Although it is known that the fungus produces extracellular proteases and lipases that interact with the cheese substrate and are key for flavour, as well as development of other characteristics of these cheeses, these enzymes have not yet been characterized at a molecular genetic level. The global market for fermented dairy products is projected to increase to US$11.1 billion by 2032 and there are market needs to improve certain quality traits of these foods. A particular issue with mould-ripened cheeses is that these contain live fungi from the point of production all the way to the supply chain, which can limits their shelf-life due to ongoing fungal activity and possible over-ripening and food spoilage. Measures that can help extend the shelf-life of these cheese will help in the reduction of food wastage as well as reduce economic losses from a manufacturer's point of view. Characterizing the fungal enzymes produced by *P. camemberti* would help identify potential areas for strain improvement work. This study aims to fill this knowledge gap by identifying the protease and lipase genes from *P. camemberti* and phylogenetically closely related species, which are primarily responsible for cheese maturation and flavour development. This will then guide future strain improvement work that will be geared towards the extension of the shelf-life of mould-ripened cheese. Work so far has involved bioinformatic analysis to identify a series of candidate lipase and protease genes, and gene expression studies are ongoing to assess possible interactions on dairy substrates.

Intra-species and Environmental Interactions Informing Novel Strain Development for the Mycoprotein Fungus Fusarium venenatum

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Fusarium venenatum is used by Quorn to produce mycoprotein, the main ingredient in its meat-alternative products. The current production strain (A3/5) has been in use for several decades and generates a product high in protein and fibre and low in fat. With additional environmental benefits, a growing consumer base and commercial competition, there are incentives to enhance the way in which *F. venenatum* interacts with the production conditions and to improve or replace the strain used with a superior one. However, there are barriers to alteration of the production process to make it more economical, such as the possibility of mycotoxin production on different sugar feedstocks and the accumulation of texture-distorting mutant strains over extended fermentation times. To address these issues, a collection of global strains of *F. venenatum* has been established. These strains are first being screened to determine if a better candidate strain already exists. Strains have been grown on various sugar feedstocks and the effects of media interaction on mycotoxin production measured by HPLC and a *Kluveromyces marxianus* bioassay. Secondly, a molecular diagnostic has been developed to determine the mating type (MAT) of isolates based on whole genome sequence data. Attempts are being made to identify a sexual cycle as a possible method for generating new strains by outbreeding of compatible MAT1-1 and MAT1-2 isolates. The interaction of each strain with different growth media, lighting conditions, and *MAT* compatible strains will be studied for their effect on outbreeding success. Additionally, the use of potentially more stable diploid strains, and inducing parasexuality, will be explored. As well as industrial benefits, these study areas present an opportunity to learn more about the general biology of the genus *Fusarium*, and elucidation of a sexual cycle would allow for studies into how various important traits are inherited.

Identification of environmental interactions that shape human pathogenicity in fungi

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Fungal diseases are responsible for over 1.6 million deaths each year, which is equivalent to tuberculosis and three times higher than malaria but, fungi have not received as much attention as bacterial and viral pathogens. Many human fungal pathogens have their native niche in soil, but much about the environmental life remains unknown. However, studying their ecological interactions can provide insight into their ability to infect humans, as their success as human pathogens has evolved here. This study aims to describe patterns in human pathogenic fungi from publicly available soil metabarcoding data. We retrieved Internal Transcribed Spacer (ITS) soil amplicon data from 7,525 samples available on NCBI. Less-frequent human pathogenic genera like *Fusarium* and *Exophiala* were prevalent globally at high abundance. More frequent human pathogens like *Aspergillus* section *Flavi* and *Fumigati* are prevalent globally, but were detected at higher levels in Asia. Co-abundance analysis showed that human-pathogenic fungi are highly connected in ecological networks compared to non-pathogenic fungal genera, and that each pathogen has its own distinct set of ecological interaction partners. To define the bacteria that are co-abundant with human pathogenic fungi in soil, we used data from 871 samples where both 16S rRNA and ITS amplicon data was available. Co-abundance analysis showed stronger correlations between pathogenic fungi and other non-pathogenic fungal genera compared to bacteria, suggesting that fungal pathogens co-habit with a diverse collection of bacteria rather than a defined set. These results shed light on the environmental ecology of human pathogenic fungi and provide a starting point for exploring of how these interactions contribute to human pathogenicity.

Development of antifungal compounds that target a core virulence determinant – the Hog1 stress-activated protein kinase

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Fungal infections kill 1.5 million people every year. Treatment options are limited and antifungal drug resistance is on the rise, highlighting a clear unmet clinical need for new antifungals. Stress responses are essential for pathogenic fungi to survive hostile host environments. Central to such responses are the stress-activated MAP kinases (SAPKs) which are key virulence determinants in all of major human fungal pathogens. Thus, drugs which target fungal SAPKs has the exciting potential to generate broad-acting antifungal treatments.

Drug repositioning is a powerful way to rapidly bring new medicines to the clinic. A structural and functional homologue of the Hog1 kinase is the human p38α kinase which is a drug target that has been investigated extensively for human disease. The use of structure-based drug discovery and fragment screening has produced numerous tool compounds and several clinical candidate compounds that target the human p38α kinase. Here I will present the structural, medicinal chemistry, and cell biology approaches to explore whether inhibitors of the human p38α kinase can be redeployed as inhibitors of the fungal kinase, with an overall goal to develop novel approaches to treat life-threatening fungal infections

Predicting the structural basis for the interaction between lysine deaceylase inhibitors and fungal specific residues in *Candida glabrata Rpd3p* enzyme

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The efficacy of antifungal drugs is compromised due to the global rise in resistant isolates of pathogenic fungi. One strategy to tackle this is to identify inhibitors of resistance mechanisms that render resistant strains more susceptible to antifungals. Inhibitors of the highly conserved class 1 lysine deacetylases (KDAC) can work synergistically with azole antifungals in *Candida spp*. Our work and others have shown that human KDAC inhibitors (KDACIs), reverse virulent and antifungal resistant phenotypes in *Candida spp*.

Here we focus on *C. glabrata*, the second most common *Candida spp.* causing blood stream infections in UK. We show that the *C. glabrata* strain lacking the KDAC Rpd3p (*cg_rpd3Δ*), phenocopies the effect of KDACi, as this strain is less virulent and more susceptible to Fluconazole. Probing the suitability of cgRpd3p as a novel antifungal target, we took an *in-silico* structure-function analysis of cgRpd3p by utilising the protein model building software AlphaFold to generate the atomic structure of cgRpd3p (G-score -0.18). Analysis of structural alignment between highly conserved HDAC2 homologue (PDB ID:3max) identified potential 'fungal specific' residues/domains which could be targeted by novel fungal-specific, non-toxic, KDACi. An alanine scan of these fungal specific residues resulted in phenotypes of reduced virulence, reduced biofilm viability and sensitisation to fluconazole, comparable to *cg_rpd3Δ*. Highlighting the importance of the fungal specific sites and validates our approach to target them pharmacologically.

Towards designing a fungal specific cgRpd3p inhibitor, we employed an *in-silico* drug screen to molecularly dock a library of 1,600 compounds of traditional KDACi compound derivatives with cgRpd3p and human HDAC2 homologue. We have identified several compounds from this analysis which we predict can target fungal specific structures with higher affinity to CgRpd3p vs the human HDAC2 homologue. Taken together our study highlights the potential and feasibility of cgPRD3p specific inhibitors in combating antifungal resistance in *C. glabtrata.*

The complex interaction between strain and environmental conditions in Candida glabrata anti-fungal tolerance

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Fungal infections caused by the *Candida* genus are currently on the rise and treatment options are increasingly limited due to the concomitant rise in antifungal resistance (AFR). The genetic mechanisms underlying AFR is a commonly researched phenomenon. More recent studies however have revealed the existence of a related, but distinct phenotype called anti-fungal drug tolerance (AFDT). AFDT can be defined as the slow growth or survival of a subpopulation pf cells above the Minimum inhibitory concentration (MIC) of the drug and is thought to contribute more to the poor treatment outcomes of patients with Candida infections (Rosenberg et al., 2018, Berman and Krysan, 2020).To date the mechanisms and factors that influence AFDT have been investigated primarily in *Candida albicans*, and there is a paucity of studies investigating this phenomenon in another *Candida spp*. Our work focusses on characterizing and understanding AFDT in *C. glabrata* to probe how universal this phenotype is within *Candida spp*.

Our initial experiments described here, involves quantifying AFDT in 6 clinical isolates of *C.glabrata*, as well as two “wild type” strains. Using both disk diffusion assays (DDAs) as well as supra-MIC growth we show that AFDT to azoles varies significantly between isolates and wild type, allowing us to identify strains exhibiting either high or low tolerance in our small sample size. Furthermore, we have found the extent of tolerance in each strain is dictated by the specific conditions being tested and factors such as media composition, pH, specific azole and temperature all have an impact on our results. Consistent with the findings in *C. albicans*, we see no correlation between AFDT and AFR of strains, as quantified by measuring the zone of inhibition on DDAs (Gerstein et al., 2016). These results demonstrate the multifactorial dependence of drug tolerance in the species *C.glabrata* and the need to unravel the precise mechanism underlying this effect.

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Ecoevolutionary dynamics of basidiomycete biochemicals, what insights into the fungal niche can omics provide us?

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The nutritional requirements of basidiomycete fungi are intrinsic to ecosystem function in temperate forest ecosystems, due to their roles in inter- and intraspecific interactions, ecological stoichiometry, and the creation of habitats. CAZymes, as well as the metabolomic profiles of select species are useful characteristics to study functional traits, because they are related to species fitness, and provide us with mechanistic links between fungi and the abiotic environment. I will be discussing a new evolutionary approach set in a Bayesian framework using omics, to explore trait covariation patterns within basidiomycete fungi, and how the metabolome is related to successional dynamics in wood decay fungi. Lastly, I will be discussing how novel image analysis techniques can be used to investigate the relationship between metabolomic expression and wood structural changes in the fungal decay community.

YEAST-ON-A-CHIP: Development of a microfluidic device for the investigation of social interactions in synthetic yeast communities

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In almost every ecosystem, microbial individuals not coexist alone. Instead, they interact and communicate to build complex ecological interaction networks that affect ecosystem structure and functioning in response to a range of biotic and abiotic stressors. [1-4]. Individual microorganisms within a microbial community may influence their neighbours by exchanging metabolites (e.g., amino acids). This knowledge can be utilised to build artificial microbial consortia based on metabolite exchange [5-7]. High-resolution imaging [8], sensor integration, and spatial and temporal manipulation [9] of cells are some technical needs for more effective interaction studies [10]. Microfluidic technologies are a promising platform that can overcome these needs. One important advantage of such technologies is that they allow the biological environment to be recreated in a very realistic way [11], simultaneously providing high-resolution, single-cell dynamic imaging. The fact that the conditions created can be controlled very precisely makes microfluidic devices very useful for discovering cell-cell and cell-environment interactions and conducting ecological studies [12]. We intend to observe interaction and communication between yeast strains under controllable environments to achieve qualitative and quantitative understanding of microbial interactions. A microchemostat device has been developed in which synthetic yeast consortia using auxotrophic S. cerevisiae strains can be monitored in real-time. Interactions between cells, and population dynamics, were dependent on amino acid concentrations. The developed device is suitable for mono- and co-culture of yeast strains.

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Converging neighbours: Exploring interactions between *Candida* and bacterial species

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The urinary tract is inhabited with diverse microflora which tend to colonise inserted urinary catheter leading to serious infections in immune-compromised patients. The colonisation often leads to the formation of biofilms, which provide the colonising bacteria the survival advantage. Over the past years, instances of polymicrobial colonisation on urinary catheters are increasing and they are not widely studied as compared to mono-species biofilms. Our study involves visualisation and analysis of the mixed biofilm consortium of *Candida albicans* and *Candida tropicalis* with each bacterial strains – *E. coli, K. pneumoniae* and *P. aeruginosa*. The specimens employed in this research were obtained from urinary catheters that were used in catheterisation of ICU patients. *Candida albicans* and *Candida tropicalis* were commonly extracted in conjunction with *E. coli, K. pneumoniae*, and *P. aeruginosa*. Biofilm biomass quantification by crystal violet (CV) assay showed that mixed species biofilms were stronger than mono-species biofilms. Confocal laser scanning microscopy was employed to visualise the cell population, morphological differences, and live-dead cell population from each combination. One of the interesting observations, include the interaction of *C. tropicalis* with bacteria. In combination with *K. pneumoniae* and *E. coli*, it was observed that bacterial strains were clustered in the pockets of *C. tropicalis* but when grown with *P. aeruginosa* the population of *C. tropicalis* was scarce and scattered. Further details regarding live and dead cells in the live-dead assay, showed that a dead population of *Candida* was more often in the lower plane of the biofilm.
Our observations revealed that, each *Candida* strain behaves differently in terms of biofilm architecture, cell density and thickness with each bacterial species.

Investigating the Interactions Between Deubiquitinases and Reactive Oxygen Species in *Saccharomyces cerevisiae*

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Reactive oxygen species (ROS) are produced from cellular processes such as respiration or from environmental sources. High levels of ROS are a vital defence mechanism in the immune system that is used against pathogens, however high levels of ROS can also cause oxidative stress which can damage DNA, proteins and lipids. Consequently, oxidative stress has been linked to the pathology of many age-related diseases. In contrast, low levels of ROS are utilised in signal transduction pathways that regulate processes such as the cell cycle. Therefore, understanding the regulation of cellular levels of ROS, and discovering how cells distinguish both the types and the levels of ROS to respond in an appropriate manner, are vital areas of research. Ubiquitin and ubiquitin-like (Ubl) proteins are reversible protein modifications that regulate many essential cellular processes. Many of the enzymes involved in the conjugation and deconjugation of these dynamic post translational modifications utilise catalytic cysteine residues, raising the possibility that these pathways function in ROS sensing mechanisms. Excitingly, work from our lab using Saccharomyces cerevisiae as a model organism provides evidence that specific deubiquitinases (DUBs), enzymes that remove ubiquitin from modified substrates, are regulated by the type and concentration of ROS. The dysregulation of the human homologues of these ROS-regulated S. cerevisiae DUBs have been linked with several disease states, therefore our findings may have wider implications for the development of clinical treatments for the benefit of human health.

Antagonistic Cross-kingdom Interactions - Delivery of Antifungal Toxins by the Bacterial Type VI Secretion System

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The human gut plays host to a multitude to microorganisms whom have complex interactions with each other to co-exist or outcompete. The gut commensal and opportunistic pathogen, *Candida albicans*, is often overlooked as an important component of the gut microbiome. However, overgrowth impacts on immune homeostasis and is linked to inflammatory bowel diseases. Recent studies revealed that Gram negative bacteria can use 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 the gut. Tfe1 is an antifungal effector with potent activity against *C. albicans* and is secreted by the *Serratia marcescens* T6SS. Tfe1 drives plasma membrane depolarisation and here I will present recent genetic, biochemical and cell biology approaches aimed at determining the precise mode of action of this effector. The widespread presence of T6SS throughout commensal gut bacteria combined with the co-colonisation of *C. albicans* suggests that T6SS-elicited antifungal effectors such as Tfe1 may play an important role in modulating the growth of this opportunistic fungal pathogen within the gut microbiome.

Leveraging antagonistic fungal interactions as biocontrol for destructive forest pathogens in the genus *Armillaria*

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Armillaria (Honey fungus) is a diverse genus of facultative necrotrophic and saprotrophic basidiomycete fungi. Some *Armillaria spp.* are highly virulent pathogens resulting in significant woody plant mortality. In coniferous agroforestry systems, pathogenic *Armillaria spp.* infection can result in a single rotation annual mortality rate of 1-2% and accumulatively a 30-50% loss of tree crops over a rotation. In other instances, *Armillaria spp.* are secondary pathogens playing critical contributing roles in the most devastating tree disease epidemics in Europe, including Ash Dieback, Acute and Chronic Oak Declines.

In nature, wood-inhabiting fungi compete fiercely with other fungi for space and access to nutrients within wood, making some dead wood fungi highly combative, and therefore making them ideal biocontrol agents able to displace harmful pathogenic fungi in wood. *Armillaria spp*. are known to be weak combatants during interactions with saprotrophic fungi, but the underlying mechanistic and functional processes driving these interaction outcomes remain uncharacterised, hindering efforts to deploy these saprotrophic fungi as biocontrol agents of *Armillaria spp.* in the UK.

Here, we take a multi-disciplinary approach utilising several independent methodologies to provide the most in-depth characterisation of interactions between *Armillaria spp.* and saprotrophic fungi to-date. Using culture-based approaches, we demonstrate the rapid displacement of *Armillaria spp.* by saprotrophic fungi in oak sapwood. We couple this with dynamic headspace sampling of volatile organic compounds (VOCs) to identify key VOCs emitted during these interactions. Using RNA-seq, we characterise gene expression during antagonism between *A. mellea* and *Hypholoma fasciculare* to uncover the molecular processes driving interaction outcomes.

Finally, we use microscopy and vital staining to offer a qualitative evaluation of interactions at the hyphal level. Our data represents the critical preliminary evaluation of these interactions as the first step in designing future field trials and the eventual deployment of these saprotrophic biocontrol agents of *Armillaria spp.*

Spores-on-a-Chip: A novel microfluidic platform for investigations on arbuscular mycorrhizal fungi and their interactions

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The arbuscular mycorrhizal fungi (AMF) are well-known for their symbiosis with the majority of terrestrial plants. This beneficial interaction not only feeds both partners, it is also the foundation of all ecosystems, ensuring resilience as well as carbon sequestration. Due to their soil-borne nature, however, studying these important fungi at the cellular level is commonly hampered by soil's lack of transparency. Hence, we are exploiting microfluidic technology to overcome this issue and fill existing gaps in AMF research. This approach allows the creation of microenvironments using transparent polymers, mimicking key aspects of the AMF's natural habitat, while still allowing microscopy analyses to be performed.

Focussing on the physical aspects of hyphal interactions, we manufactured microfluidic devices from poly(dimethylsiloxane) and included different obstacles within the designs. After establishing a methodology for achieving on-chip spore germination, we monitored the space searching behaviour of the AMF *Rhizophagus irregularis* using bright field microscopy. Interestingly, we observed a highly dynamic hyphal response upon mechanical collision, involving cytoplasmic retraction, septa formation and reversal of the process, a phenomenon, so far undescribed to its full extent. To clarify these findings further, the fluorescent dyes FM4-64 and Calcofluor white were employed. Later, a variation of the device was developed to accommodate two different AMF strains at the same time, encouraging anastomosis events. Future work will include equipping the microdevices to facilitate the creation of chemical gradients, aiding our quest to decipher the soil ecology of AMF.

Exploitation of the interaction between feedback inhibition and phenotypic heterogeneity to improve glutathione production by yeast

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Phenotypic differences between individual cells within genetically uniform cell populations (phenotypic heterogeneity) is considered one of the factors that can lead to process instability and lowered production yields during biomanufacturing. Cell-to-cell variations in gene expression is linked to variation in metabolite productions, resulting in high and low producers within an isogenic population. While the presence of low-producing individuals can be a cause of suboptimal production, the high-producing individuals offer a promising opportunity for improving production. The interaction between the end product of a biosynthetic pathway and its upstream process is a critical regulatory mechanism in cells. This study aims to test the hypothesis that high-producing, nongenetic variants in yeast populations can be continuously selected to increase production, using glutathione (GSH) as an exemplar product. A high level of GSH inhibits further expression of the rate limiting enzyme gamma-glutamylcysteine synthetase (Gsh1). Based on this, we engineered a counterselection system in *Saccharomyces cerevisiae*, with GSH1 to be constitutively expressed under control of the TEF1 promoter and with a counterselectable marker *GAP1* under the GSH- regulated *GSH1* promoter (*pGSH1*). An 18% increase in cellular GSH level was achieved upon inclusion of D-histidine, which counterselects high *GAP1* expressing cells, i.e., low GSH-producing cells with the present construct. Results showed that the counterselection system improves GSH production by selecting phenotypic high producers. Our work demonstrates that, by exploiting a metabolite-promoter interaction, phenotypic heterogeneity can serve as a potential source of production improvement in yeast.

Harnessing bacteria, fungi, and their interactions for the biorecovery of valuable compounds in industrial and anthropogenic waste

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Bacterial-fungal interactions (BFI) are essential for ecosystem functioning. In soil, these interactions promote and maintain the biogeochemical cycling of numerous elements. As a result, BFIs have also consequences on the use of bacteria and fungi in biotechnology, as these interactions affect the behaviour, physiology and ecology of both partners. In this contribution, we will present two concrete examples in the fields of urban waste and biomining. Urban waste is a growing fraction of the waste produced worldwide and some fractions (e.g. e-waste, digested sewage sludge) contain valuable compounds such as precious metals and phosphorous, which are non-renewable resources. The recovery of critical raw materials in industrial waste is a timely issue that requires innovative and sustainable approaches. Industrial waste typically consists of a heterogeneous matrix of materials and thus a parallel can be drawn to other complex systems such as soils, where microbial interactions are essential for maintaining biogeochemical cycles. Therefore, in our research we propose to take advantage of bacterial and fungal biogeochemical capabilities towards metals, together with synergistic mechanisms that take place upon BFIs in order to recover metals in minute concentration from heterogeneous matrices. In particular, we focus on two distinct type of matrices, a solid and a liquid one using digested sewage sludge and geothermal fluids, respectively. By harnessing the natural interactions that exist between microbes, along with their ability to act as chemical reactors, an ecological, economical, and ethical strategy for the biorecovery and/or bioremediation of metals could be developed for the field of urban-biomining.

The Old Pants Project: how fungi interact with textiles

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Background: Textile waste comprises natural and petroleum-derived fibres and as such presents a complex recycling challenge. Currently, the main disposal methods used are landfill or incineration, both of which cause serious environmental damage so a cleaner and more sustainable alternative is required. It was envisaged that edible fungi may be able to bioremediate fabric and simultaneously produce a vegan source of protein.

Methods: An agar-free microcosm was used to assess the potential of a range of edible wood decay fungi to grow on semi-synthetic waste textiles (old pants). The fabrics were imaged regularly using SEM and dye extraction used to assess potential dye metabolism. The volatile and substrate metabolomes were captured and analysed to initiate assessment of the safety profile of fungal bioremediation.

Results: Potential fungal candidates were selected through bioinformatic analysis of relevant enzymes and their ability to grow on plant matter. The edible fungi were variable in their ability to grow and possibly metabolise the dye with *Lentinula edodes* and *Pleurotus ostreatus* showing the greatest growth and discoloration of the textile. *Pleurotus eryngii* performed surprisingly poorly, while *Agaricus bisporus* did not grow in our microcosm set up. Volatile analysis enabled a preliminary safety assessment of this process while substrate metabolomics gave some insight into biological mechanisms. None of the microcosms produced fruiting bodies.

Conclusion: The field is a tricky one as fabric is a highly heterogeneous substrate and many standard lab protocols do not work with this system. As 60% of all clothes contain some synthetic fibres, and with over 100 billion items of clothing produced every year there is an urgent need to find sustainable methods of disposal. This is an under-researched field but this study suggests fungi are worth further investigation.

A trade-off between proliferation and defense in the fungal pathogen Cryptococcus is controlled by the transcription factor GAT201

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Fungi adapt to grow in and respond to different environments. Fungal pathogens infecting a host survive and proliferate in environments varying in nutrients, temperature, pH, and host immune factors. Gene expression regulation is crucial for pathogen adaptation, and many transcription factors are essential for fungal virulence. Here, we use transcriptomics to understand the adaptation of *Cryptococcus neoformans* to host-like cell culture media, finding the transcription factor GAT201 to be strongly upregulated. GAT201 was previously shown to affect virulence in mouse models of infection, macrophage uptake, and the growth of defensive capsule. Serendipitously, we find that wild-type *C. neoformans* arrests growth and loses viability in host-like media at high pH, while gat201Δ mutants proliferate to produce buds and maintain viability. The effect of GAT201 on viability and gene expression is largely independent of serum addition to the media and so is not driven by host factors. GAT201-dependent genes in these conditions are strongly enriched for direct targets of Gat201 as previously measured by ChIP-seq. Another GAT201-regulated transcription factor, GAT204, is also required for growth arrest and loss of viability. The Gat201 pathway in *Cryptococcus* is independent of the classical Rim101/PacC alkaline responsive pathway. We are performing a genetic screen to map the network that allow *Cryptococcus* to maintain viability in cell culture media at high pH. Evolutionary analysis shows that Gat201 is homologous to transcription factors Sub-1/NsdD that regulate growth in filamentous fungi. We propose that Gat201 controls an environment-dependent trade-off between proliferation and defence. It is surprising that deletion of a single virulence-associated transcription factor allows *Cryptococcus* to proliferate in conditions where wild-type yeast lose viability. Our results emphasize the extraordinary phenotypic plasticity of fungi in that single-gene loss can allow fungi to adapt to restrictive environments.

Microfluidics for fungal-bacterial interactions: developing a platform to probe the fungal highway

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Ecosystem dynamics and connectivity are essential parts of describing a community's function and structure, particularly amongst microbial consortia. There are diverse mechanisms of interaction between fungi and bacteria; fungal-mediated transport of bacteria (the fungal highway) remains one of the least described. Bacteria are limited in their dispersal as they require a liquid film for active movement. Fungal hyphae provide a physical network through an unsaturated matrix, as they can bridge aggregates or pore regions. This provides a scaffold for bacteria to migrate further or access previously isolated spaces. The recent advent of novel in vitro or field-level study platforms is confirming the importance and pervasiveness of this topic. However, the systems in which this interaction occurs are often highly complex and heterogenous, such as soil. Thus, the fungal highway is difficult to investigate or to visualise in vivo. Microfluidic devices offer high-resolution, controlled-environment, real-time imaging such that interactions can be viewed at the single-cell level. Geometries and experimental design influence the interaction and allow different aspects to be probed; such as partner selection, directional travel, or the influence of the partnering species. Work is being carried out to design a device in which to elicit fungal highways and to begin to unveil their complex mechanisms.

ZymoSoups: A forward genetics method to understand in planta immune interactions

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The dothideomycete fungus *Zymoseptoria tritici* causes Septoria tritici blotch disease, a major threat to wheat productivity globally. *Z. tritici* has proven difficult to control due to the emergence of strains that that can overcome host genetic resistance provided by disease resistance (R) genes. How this fungus evolves to evade R gene recognition is not well understood, partly due to the unknown identity of most secreted effector proteins that are recognised by host R proteins to trigger immune responses. To date, identification of *Z. tritici* effector genes has been done through a combination of GWAS and QTL mapping. Whilst effective, this process is laborious and requires considerable resources. We therefore sought to develop a faster method for effector gene identification through UV mutagenesis and in planta forward genetic screens. Using the known gene-for-gene interaction between Stb6 and AvrStb6, we found that inoculations of mixtures (soups) of virulent and avirulent spores led to observable disease symptoms even when virulent spores were greatly outnumbered. We then developed a UV mutagenesis and in planta screening protocol that allowed us to screen >100,000 UV mutants for gain-of-virulence (GoV) on wheat containing Stb6. We recovered five mutants that gained virulence on the Stb6-containing wheat cultivar Cadenza. Following confirmation of GoV by single isolate inoculations, whole genome sequencing was used to identify SNPs and other mutations in comparison to the IPO323 parental strain. All five GoV mutants contained either SNPs in AvrStb6, or larger chromosomal deletions involving the AvrStb6 locus. These results would have allowed rapid identification of the AvrStb6 gene as the virulence determinant on Stb6-containing wheat. This method could be useful for identifying currently unknown effector genes in this pathogen.

Insights on the role of two transcription factors in *Aspergillus nidulans* suberin degradation ability

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The presence of suberin hallmark constituents in the soil, after the degradation of more amenable polymers has been described. The suberin is mainly present in the rhysosphere and in the soil top layers, where fungal have been accountable for most of the microbial activity (1). Suberin is a heteropolymer that is deposited between the plasma membrane and the cell wall, forming a hydrophobic protective barrier. In most plants, it is present in the roots and other protective organs like the bark (2). For long the anatomic and cellular distribution of suberin hindered its recovery in a near native state. This become possible by using an ionic liquid catalysed method for suberin selective extraction from a plant source in the form of large esterified polymeric strutures or by selective dissolution upon cryogenic milling of plant materials rich in suberin (3).

Aspergillus nidulans catabolism of near native suberin was analysed using proteomics and transcriptomics. The acquired data showed a boost of cutinolytic enzymes and suggested involvement of new regulatory elements (4). Additionally, it was observed that suberin impacts on fungal development and life-cycle. Follow-up studies focused on the deletion of 2 unknown transcription factors to dissect their role in fungi-suberin interaction. The functional characterisation of the mutants is under scrutiny, especially how deletion of each gene impacts utilisation of lipids and sexual development. This work contributes to enlighten the polyester-fungi interaction and enlarges our understanding on regulatory mechanisms during plant polyester degradation by saprotrophic fungi.

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Inoculum size matters: Interaction of heteroresistance with MIC in weak-acid stress of food spoilage yeasts

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A wide range of condiments and soft drinks are preserved with weak organic acids such as sorbic acid, however specialised yeasts such as *Zygosaccharomyces bailii* can grow in sorbic acid concentrations above the legal limit. While several mechanisms of resistance have been proposed, including metabolism of sorbic acid and maintenance of a more fermentative metabolism, *Z. bailii* has additionally been shown to exhibit high variation in cell-cell resistance to sorbic acid, suggesting a possible bet hedging strategy to produce hyper-resistant sub populations (heteroresistance). Examples of heteroresistance in contexts such as antibiotic resistance are numerous, but the relative contributions of heteroresistance and population-average resistance (IC50) to the observed Minimum Inhibitory Concentration (MIC) has not been assessed systematically. Across a panel of 26 diverse yeast species, both heteroresistance and particularly IC50 were positively correlated with predicted MIC of sorbic acid. A focused panel of 29 different isolates of spoilage yeast *Zygosaccharomyces bailii* and its interspecies hybrids *Z. parabailii* and *Z. pseudobailii* were then assayed. Applying a novel high-throughput assay for heteroresistance, it was found that IC50 but not heteroresistance was positively correlated with predicted MIC when considered across all isolates of this panel, but the heteroresistance-MIC interaction differed for the individual *Zygosaccharomyces* subspecies. Z. pseudobailii exhibited higher heteroresistance than *Z. parabailii* whereas the reverse was true for IC50, suggesting possible alternative strategies for achieving high MIC between subspecies. This work highlights the limitations of conventional MIC measurements due to the effect of heteroresistance in certain organisms, as the measured resistance can vary markedly with population (inoculum) size.

Regulation of Phosphate Homeostasis in the Human Fungal Pathogen *Candida albicans*

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The ability of fungal pathogens to assimilate nutrients from host microenvironments is essential for virulence. One such nutrient is phosphate, as a number of recent studies have highlighted the importance of phosphate acquisition in the pathogenicity of *Candida albicans* and *Cryptococcus neoformans*. In fungi, phosphate homeostasis is governed by the PHO pathway and the key transcription factor Pho4, which regulates both phosphate acquisition and the synthesis of the phosphate storage molecule polyphosphate. Previous work in our lab revealed that Pho4-mediated phosphate acquisition is important for both *C. albicans* virulence and resistance to host-encountered stresses.

Regulation of the Pho4 transcription factor has been well characterised in the model yeast *Saccharomyces cerevisiae*. Under phosphate replete conditions the Pho80-Pho85 cyclin-CDK complex phosphorylates Pho4 which prevents its nuclear accumulation. However, in phosphate limiting environments, changes in inositol pyrophosphate levels signal to the Pho81 CDK inhibitor which subsequently blocks Pho80-Pho85 activity. The resulting unphosphorylated Pho4 accumulates in the nucleus and activates a suite of genes involved in phosphate acquisition and homeostasis. Investigation into the regulation of the Pho4 transcription factor in *C. albicans* has uncovered several differences to that documented in *S. cerevisiae*. Here I will present our findings on the different wiring of the Pho81 CDK inhibitor in C. albicans Pho4 regulation, and the importance of inositol pyrophosphates in triggering phosphate starvation responses.

A pilot study into how fungi interact with textiles

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Background: Textile waste comprises natural and petroleum-derived fibres and as such presents a complex recycling challenge. Currently, the main disposal methods used are landfill or incineration, both of which cause serious environmental damage so a cleaner and more sustainable alternative is required.

Methods: A novel agar-free microcosm was developed to assess the potential of two wood decay fungi to grow on semi-synthetic textiles. The microcosms were incubated on a range of fabrics with an increasing elastane content. The fabrics were imaged regularly, with the volatile metabolome and the percentage of dye remaining in the fabric analysed at 3, 5 and 8 month timepoints.

Results: The agar-free microcosm was developed with a view to industrial scalability and demonstrated that low tech, low maintenance microbial growth on fabric was achievable. The fungi used, one brown rot and one white rot, both grew successfully on all fabrics, showing minimal impact of the increasing synthetic content. The white rot fungus was able to bioremediate the dye (Reactive Black 5) from all fabrics, while the brown rot fungus microcosms showed minimal dye loss from the highest elastane content microcosm only. Volatile analysis enabled a preliminary safety assessment of this process, and showed that volatile release was minimal in all microcosms.

Conclusion: 60% of all clothes contain some synthetic fibres, and with over 100 billion items of clothing produced every year there is an urgent need to find sustainable methods of disposal. This is an under-researched field but this study suggests fungi are worth further investigation.

Love or hate – an insight into soil fungal interactions along a gradient of soil and root resources

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Soil fungi govern the dynamics of carbon soil sequestration. In most forest ecosystems, two major fungal groups dominate the microbial biomass and control organic matter turnover, either directly by decomposition (saprotrophic fungi) or indirectly by affecting plant nutrition and productivity (ectomycorrhizal fungi). In carbon cycling, saprotrophic and ectomycorrhizal fungi play contrasting roles. Ectomycorrhizal fungi, which live in symbiosis with trees, enhance plant productivity and channel the photosynthetic carbon to the soil, augmenting soil carbon sequestration. Saprotrophic fungi, in contrast, decompose organic matter, reducing soil carbon stores and increasing respiration. Competitive interactions between these two fungal guilds may result in the suppression of saprotrophic fungal activity and, consequently, in the deceleration of decomposition under a phenomenon known as the “Gadgil effect”. The stress gradient hypothesis (SGH) provides a conceptual frame of changes in species’ interactions with environmental stress. Still, it remains unclear if it holds for soil fungi and how it encompasses multiple negatively related stressors. Here we employed an algorithm based on generalised Lotka-Volterra equations and investigated SGH in root and soil fungal communities under a gradient of soil fertility and root carbon resources. The two gradients were negatively related. We found that under conditions of lower soil fertility or root carbon resources, fungal guilds showed rather positive than negative influences on each other, supporting SGH. Saprotrophic and ectomycorrhizal guilds showed a reciprocal negative influence under high soil fertility, confirming the premises for the Gadgil effect, but they positively influence each other, giving rise to facilitative interactions under lower soil fertility. By integrating the two gradients, we found that SGH held true for the dominant stress gradient in the system. We speculate that under lower soil fertility, the reciprocal positive interactions of soil fungal guilds may contribute to maintaining soil biodiversity and nutrient cycling.

Environmental Interactions in the networks of cord-forming wood-decay fungi

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Cord-forming wood-decay fungi play a crucial role in nutrient cycling and ecosystem dynamics. However, our understanding of their foraging tactics and the mycelial networks they create is limited, restricting our ability to understand how they acquire resources and respond to environmental change. Here, we outline how our research aims to bridge this knowledge gap by investigating the responses of wood-decay fungi and the dynamics of their mycelial networks to different environmental conditions (e.g., resource availability).

The study focuses on saprotrophic mycelial networks and their interactions with the environment. We examine the foraging strategies of two cord-forming fungi, Hypholoma fasciculare and Phanerochaete velutina, observing how they respond to different resource availability scenarios.

By applying recent technological and computational advances in image processing and network analysis to well-established soil microcosm methods, we aim to elucidate complex mycelium-environment interactions and gain insights into the mechanisms underlying fungal foraging strategies.

Findings will enhance our understanding of how wood decay fungi respond to and influence their environment, whilst also contributing to a broader understanding of mycelium-resource interactions and the ecological significance of wood decay fungi in nutrient cycling processes. Such work could provide valuable insights for the development of sustainable ecosystem management strategies and environmental conservation practices.

Investigating bioactive natural products from the fungus *Escovopsis weberi*

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New sources of bioactive molecules are required in the hunt for new chemical diversity to address the current antimicrobial resistance (AMR) crisis. Despite most antibiotics deriving from natural products, discovery efforts have focused on only a small section of the tree of life. Under-exploited sources of bioactive compounds include highly specialized fungi evolving in competitive environments: an excellent example is the ant-nest pathogen *Escovopsis weberi*. Garden ants (Acromyrmex) live in symbiosis with the garden fungus *Leucoagaricus gongylophorus* and *Pseudonocardia* bacteria that grow on the ant cuticle and produce anti-infective molecules which help protect the fungus garden from infection. This tight mutualistic relationship prevents invasion by the co-evolved pathogen *E. weberi*, which can cause ant colony collapse.1,2 Bioinformatics analysis of *E. weberi* genomes revealed 26 biosynthetic gene clusters (BGCs), most of which are unique to *E. weberi.* Heterologous expression system is being optimised for the production of compounds from these unique BGCs. Metabolomics analysis identified uncharacterised metabolites produced on rice and oats cultures, which are being purified and tested for different activities.

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Small RNA profiling of the *Metarhizium brunneum – Galleria mellonella* pathosystem

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Enotompathogenic Metarhizium species infect invertebrate hosts through a series of regulated developmental changes from germinating spores, appressorial penetration, blastospore-driven colonisation and reversion to hyphal form during emergence from the host to sporulate. Proliferation and establishment involve the interaction with host physiology and immune defences and genetic and biochemical have focused on key molecular mechanisms driving the infection process. Pathogen-derived small RNA molecules, such as microRNAs, during the infection cycle have received much less attention, despite being implicated in morphological development in other systems. MicroRNAs were isolated and sequenced from different stages of *Metarhizium brunneum* infection of *Galleria mellonella*. MicroRNAs were mapped to host and pathogen genomes to identify putative gene targets and finer scale gene expression during infection were measured by qPCR across three different hosts, *G. mellonella*, *Tenebrio molitor* and *Schistorcerca gregaria*. Host enzymatic defence measurements were also compared during the infection process. The contribution of microRNAs in *Metarhizium*-insect antibiosis are discussed.

Generating Tuneable Mycelial Networks for Directed Assembly

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In our search to understand the effects of environmental changes on the structure and Biochemistry of fungi, a range of fungal species have been cultured in liquid (Potato Dextrose Broth) and solid (Potato Dextrose Agar) media under varying and controlled environmental conditions. The growth, structure, and morphology of the fungal mycelia mat has been studied extensively. We have also studied the biochemistry of the key components (chitin, carbohydrates, and proteins). These components have been identified and characterised. In addition, we also observed effect of temperature change and an additional glucose (in the media) on the on the mycelial Physical Properties. Our hypothesis is that by understanding how the local environment affects chemical synthesis and growth patterns we will be able to tailor the structure of functional composite materials based on fungal mycelia.

Investigating the effects of co-inoculation timing on interspecific interactions between *Leptosphaeria maculans* and *L. biglobosa*

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Phoma stem canker is an economically damaging disease of oilseed rape, caused by two co-existing pathogens *Leptosphaeria maculans* and *L. biglobosa. L. maculans* produces a phytotoxin called sirodesmin PL. Our previous work showed that *L. biglobosa* has an antagonistic effect on the production of sirodesmin PL if it was simultaneously co-inoculated with *L. maculans*. Here, we investigated the effects of sequential co-inoculation on interactions between the two pathogens in terms of sirodesmin PL production. Clarified v8 broths were inoculated with *L. maculans* first, then sequentially with *L. biglobosa* at 1, 3, 5 or 7 days later, and vice versa. Controls were *L. maculans* only, *L. biglobosa* only, and *L. maculans* & *L. biglobosa* co-inoculated simultaneously. Secondary metabolites were extracted from culture filtrates at 14 days post inoculation and analysed with HPLC. Mycelia were freeze-dried, weighed, and homogenised for DNA extraction and qPCR. Results showed no significant differences in mycelial weight between treatments. Both sirodesmin PL and its precursors were not produced if *L. biglobosa* was inoculated before *L. maculans*, this was due to *L. biglobosa* inhibiting the growth of *L. maculans*, confirmed by qPCR. However, the antagonistic effects of *L. biglobosa* were lost if it was co-inoculated 5 days after *L. maculans*. There is a need to investigate the mechanisms of the antagonistic effects of *L. biglobosa* to develop new strategies for sustainable control of phoma stem canker.

One-step soft agar enrichment and isolation of human lung bacteria inhibiting the germination of *Aspergillus fumigatus* conidia

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Fungi of the genus *Aspergillus* are widespread in the environment where they produce large quantities of airborne conidia. Inhalation of *Aspergillus spp*. conidia in immunocompromised individuals can cause a wide spectrum of diseases, ranging from hypersensitivity responses to lethal invasive infections. Upon deposition in the lung epithelial surface, conidia encounter and interact with complex microbial communities that constitute the lung microbiota. The lung microbiota has been suggested to influence the establishment and growth of *Aspergillus spp*. in the human airways. However, the mechanisms underlying this interaction have not yet been sufficiently investigated. In this study, we aimed to evaluate the presence of commensal bacteria antagonistic to *Aspergillus* in the lung. To this end, we enriched and isolated bacterial strains able to inhibit the germination of conidia from bronchoalveolar lavage fluid (BALF) samples of lung transplant recipients. We used a novel enrichment method based on a soft agar overlay plate assay in which bacteria are directly in contact with conidia and for which inhibition can be readily observed during enrichment. We isolated a total of five bacterial strains, identified as *Pseudomonas aeruginosa*, and able to inhibit the germination and growth of *Aspergillus fumigatus* in a soft agar confrontation assay, as well as in a high-throughput multiplate assay. Moreover, we also showed a strong inhibition of *A. fumigatus* growth on Calu-3 cell culture monolayers. However, the isolated *P. aeruginosa* strains were shown to cause significant damage to the cell monolayers. Overall, we validated this novel one-step enrichment approach for the isolation of bacterial strains antagonistic to *A. fumigatus* from BALF samples. This opens up a new venue for targeted enrichment of antagonistic bacterial strains against specific fungal pathogens.

Identification of essential components for protein secretion in the phytopathogen *Zymoseptoria tritici*

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Septoria tritici blotch (STB), caused by the ascomycete fungus *Zymoseptoria tritici*, is one of Europe's most devastating diseases of wheat. With increased levels of resistance to fungicides now common, new fungicide targets involved in essential *Z. tritici* processes are required. Following its invasion through wheat leaf stomata, *Z. tritici* hyphae remain exclusively in the apoplastic space, secreting effector proteins for the manipulation of the host immune response. The various mechanisms of effector action emphasise the need for novel targets that address all effector proteins, such as the pathway(s) for their secretion from fungal cells. Essential components for protein secretion are well known in model yeasts, however, this information is lacking for Z. tritici and other phytopathogenic fungi.

To identify essential secretory pathway components, this project first aims to develop a reporter assay for *Z. tritici* protein secretion using the luciferase CLuc system previously employed in yeast, where protein secretion is sensitively measured as luminescence (Kanjou *et al*., 2007). To transform *Z. tritici* with the CLuc gene, a 'soft' selectable landing site will be used in which the succinate dehydrogenase locus gains a point mutation that confers carboxin resistance (Kilaru et al., 2015). This reporter system will be used in large-scale forward genetics screens by UV mutagenesis to identify mutants impaired in protein secretion. Our recent progress towards this aim will be reported.

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Interaction of Fungi with Hydrocarbons in Polluted Soils And Sediments

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One of the major environmental problems today is hydrocarbon contaminations resulting from the activities related to the petrochemical industry. This study examined the existence of indigenous fungi involved in the bioremediation of hydrocarbons in contaminated soils and sediments. The samples were collected from nine different crude oil polluted sites within selected geographical locations in Nigeria. The samples pH ranged from 4.8 to 8.5, which is a suitable pH for fungi growth in soil. Similarly, organic matter content ranged from 0.76 to 49.08% and lastly, salinity ranged from 0.336 to 3.442%. Microbiological analysis of the samples indicated the presence of indigenous fungi. The isolates were screened for hydrocarbon biodegradation potential in Mineral Salts Medium (MSM) and crude oil served as the only carbon and energy source. The screening revealed the following genera of hydrocarbon-degrading fungi: *Aspergillus, Geotricum, Fusarium, Candida* and *Schizosaccaromyces*. They had varying biodegradative potential and grew profusely on MSM. *Aspergillus niger, Candida rugosa*, and *Geotricum* spps showed highest growth on MSM over a 30 days period. The Gas Chromatography Mass Spectrometry profile of the crude oil at the end of the biodegradation revealed that *Aspergilus niger* had the lowest reduction in the polyaromatic hydrocarbon contents (2.0667 x 10-5 ppm) when compared to the control (0.1500 ppm). Under optimum environmental and nutritional conditions, the identified fungi could be crucial for bioremediation of crude oil polluted areas.

How does *Aspergillus fumigatus* subvert the lung defenses during viral coinfection?

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Aspergillus fumigatus (Af), a critical human fungal pathogen according to the WHO, annually causes more than 20 million pulmonary infections with four million having life threatening disease. Recently, it has been reported that coinfections caused by *Af* are frequent and double the mortality in patients with severe Influenza or COVID-19. Patients with viral-associated pulmonary aspergillosis do not exhibit typical risk factors for fungal disease, so it is unclear why they are susceptible to *Af* infections. Alarmingly, viral-fungal coinfections occur in a background of limited treatments and increasing resistance to antimicrobials. Therefore, we urgently need to understand how *Af* infects the lungs of patients with common viral infections. Airway epithelial cells (AEC) play a crucial role in host defence against inhaled pathogens by controlling pathogen survival and the activation of the downstream immune responses. Impaired *Af* clearance by macrophages and neutrophils has been observed in animal models of post-influenza pulmonary aspergillosis. Since AEC are the first point of contact of inhaled pathogens and the host, it is likely that dysfunctional AEC antimicrobial responses early after coinfection underpins rapid disease progression. Combining the use of *in vitro* models of *A. fumigatus* viral co-infection of AECs, bar-seq sequencing, live cell imaging, transcriptomics, and *in vivo* models of disease we have observed that respiratory viruses supress AEC responses that normally prevent *Af* colonisation, while *Af* simultaneously facilitates viral disease progression. In addition, our results indicates that some fungal proteins might have positive and negative influences in co-pathogenesis. Therefore, understanding the mechanistic basis of Af infection of AEC during viral coinfection will allow us to develop new therapies and strategies to identify those most at-risk.