

The 6th Annual CanFunNet
Fungal Biology Conference
August 5 - August 7, 2026



Fungal Biology Across Frontiers

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Sponsors



The Company of
Biologists

pyroscience 

sensor technology

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About us

Organizing Committee	
Catherine Bachewich	Noah Boodhoo
Oualid (Walid) Ellouz	David Firer
Joanna Gauthier	Viola Halder
Linda Horianopoulos	Gavin Kernaghan
Matthias Kretschmer	Patrick Lajoie
Allison Walker	
Scientific Program Committee	
Catherine Bachewich	Noah Boodhoo
David Firer	Gavin Kernaghan
Matthias Kretschmer	Patrick Lajoie
Viola Halder (Program)	
Graphics	
Maxime Guglielmetti (Logo)	Noah Boodhoo
Viola Halder	
Conference Website	
Conference Services at Western University	

Condensed Conference Schedule

Wednesday, August 5, 2026			
11:15AM-11:30AM ET	Opening Remarks		
11:30AM-1:00PM ET	Plenary Day 1 - Fungi as producers		
1:00PM-1:15PM ET	Break		
1:20PM-2:20PM ET	Fungal Genetics and Genomics I (1A)	Mycorrhizal Symbioses I (2A)	
2:20PM-2:35PM ET	Break		
2:40PM-3:40PM ET	Fungal Genetics and Genomics II (1B)	Fungal Applications I (2B)	
3:40PM-3:55PM ET	Break		
4:00PM-5:00PM ET	Fungal Genetics and Genomics III (1C)	Fungal Ecology and Evolution I (2C)	

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Condensed Conference Schedule

Thursday, August 6, 2026			
11:30AM-1:00PM ET	Plenary Day 2 - Fungal evolution and symbioses		
1:00PM-1:15PM ET	Break		
1:20PM-2:20PM ET	Fungal and Lichen Biodiversity I (3A)	Medical Mycology (4A)	Biocontrol of Fungi (5A)
2:20PM-2:35PM ET	Break		
2:40PM-3:40PM ET	Fungal Disease in One Health (3B)	Fungal Plant Pathology I (4B)	Endophytic Fungi (5B)
3:40PM-3:55PM ET	Break		
4:00PM-5:30PM ET	Career Workshop - Telling a story in science: discussions with communication experts!		

Condensed Conference Schedule

Friday, August 7, 2026			
11:30AM-1:00PM ET	Plenary Day 3 - Fungi and Plants		
1:00PM-1:15PM ET	Break		
1:20PM-2:20PM ET	Fungal Ecology and Evolution II (6A)	Fungal Plant Pathology II (7A)	
2:20PM-2:35PM ET	Break		
2:40PM-3:40PM ET	Fungal and Lichen Biodiversity II (6B)	Mycorrhizal Symbioses II (7B)	
3:40PM-3:55PM ET	Break		
4:00PM-5:00PM ET	Fungal Applications II (6C)	Fungal Genetics and Genomics IV (7C)	
5:00PM-6:00PM ET	Closing ceremony		

Code of Conduct

The organizers are committed to making this meeting productive and enjoyable for everyone, regardless of gender, sexual orientation, disability, physical appearance, body size, race, nationality or religion. We will not tolerate harassment of participants in any form. Please follow these guidelines:

- Behave professionally. Harassment and sexist, racist, or exclusionary comments or jokes are not appropriate. Harassment includes sustained disruption of talks or other events, inappropriate physical contact, sexual attention or innuendo, deliberate intimidation, stalking, and photography or recording of an individual without consent. It also includes offensive comments related to gender, sexual orientation, disability, physical appearance, body size, race or religion.
- All communication should be appropriate for a professional audience, including people of many different backgrounds. Sexual language and imagery is not appropriate.
- Be kind to others. Do not insult or put down other attendees.

Participants asked to stop any inappropriate behaviour are expected to comply immediately. Attendees violating these rules may be asked to leave the event at the sole discretion of the organizers without a refund of any charge.

Scavenger Hunt and Prizes



You will be able to participate in a scavenger hunt through PheedLoop this year. Look for the mushroom logo (left) for the clues, then go into the scavenger hunt page to submit your answers (1 word, all caps). Each clue is worth 10, 25 or 50 points, depending on difficulty.

The top scorers will be able to choose a reward from the following list:

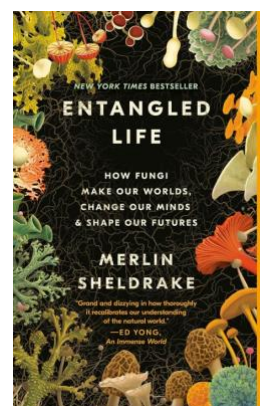
CanFunNet26 Hoodie



CanFunNet26 Mug



Entangled Life: How Fungi Make Our Worlds, Change Our Minds & Shape Our Futures



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Detailed Conference Schedule - Wednesday

Wednesday, August 5, 2026

Plenary Day 1 - Fungi as Producers

Plenary Day 1 - 11:30 AM - 1:00 PM EST - Wednesday, August 5, 2026

Moderated by: Catherine Bachewich & Linda Horianopoulos

- | | |
|---|--|
| 11:30 AM - 12:00 PM EST
(Plenary Talk) | Dr. Nancy Keller
Small Molecules, Big Mysteries: Isocyanides In Fungi |
| 12:00 PM - 12:30 PM EST
(Plenary Talk) | Dr. Steve Hallam
Zen and the art of mycofabrication |
| 12:30 PM - 1:00 PM EST
(Plenary Talk) | Dr. Michael Pyne
Mining fungal diversity for a robust acid-tolerant biomanufacturing host |

Fungal Genetics and Genomics I

1A - 1:20 PM - 2:20 PM EST - Wednesday, August 5, 2026

Moderated by: David Firer

- | | |
|--|--|
| 1:20 PM - 1:35 PM EST
(Standard Talk) | Anthony Hendriks
Elucidating novel epistatic interactions associated with <i>Candida albicans</i> echinocandin resistance |
| 1:35 PM - 1:50 PM EST
(Standard Talk) | Chris Todd Hittinger
Keystone and one-trick gene families: lessons from more than 400 million years of yeast evolution |
| 1:50 PM - 2:05 PM EST
(Standard Talk) | Ben Auxier
Diverse fungal DNA: Identification of idiomorphic regions across fungal species |
| 2:05 PM - 2:20 PM EST
(Standard Talk) | Philippe Després
Pooled CRISPRi screening reveals fungal-specific drug target candidates |

Mycorrhizal Symbioses I

2A - 1:20 PM - 2:20 PM EST - Wednesday, August 5, 2026

Moderated by: Katie King

- | | |
|--|--|
| 1:20 PM - 1:35 PM EST
(Standard Talk) | Robert Ferguson
AMF identity and plant host species interact to determine soil bacterial community structure |
| 1:35 PM - 1:50 PM EST
(Standard Talk) | Katie King
What's in a name? Describing orchid mycorrhizal fungi as an essential step in <i>Cypripedium arietinum</i> conservation in Nova Scotia |
| 1:50 PM - 2:05 PM EST
(Standard Talk) | Ruiqi Zhang
Tree–Mycorrhizal Investment Strategies Along Environmental Gradients in Nebraska Forests |
| 2:05 PM - 2:20 PM EST
(Standard Talk) | Cynthia Albracht
Field-Scale Benefits of Mycorrhizal Fungi in Agroforestry |

Fungal Genetics and Genomics II

1B - 2:40 PM - 3:40 PM EST - Wednesday, August 5, 2026

Moderated by: Patrick Lajoie

- | | |
|--|--|
| 2:40 PM - 2:55 PM EST
(Standard Talk) | Meea Fogal
A genome-scale CRISPRi approach to dissect gastrointestinal colonization in <i>Candida albicans</i> |
| 2:55 PM - 3:10 PM EST
(Standard Talk) | David Firer
A genomic view of hypermutation potential in <i>Candida auris</i> drug resistance |
| 3:10 PM - 3:25 PM EST
(Standard Talk) | Adrian Ciemniecki
Stress Resistance Genomics in Protein Powerhouse <i>Komagataella phaffii</i> ; Laboratory Evolution and Mutation Mapping for Yeast Industrial Endurance |
| 3:25 PM - 3:30 PM EST
(Flash Talk) | Laura Delage
Characterizing oxidative stress resistance in <i>Candidozyma auris</i> |
| 3:30 PM - 3:35 PM EST
(Flash Talk) | Elizabeth Mei
Mapping the genetics of parasex in <i>Candida albicans</i> |

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Fungal Applications I

2B - 2:40 PM - 3:40 PM EST - Wednesday, August 5, 2026

Moderated: Viola Halder

- | | |
|--|--|
| 2:40 PM - 2:55 PM EST
(Standard Talk) | Viola Halder
Development of an automated pipeline for fungal-based biomanufacturing |
| 2:55 PM - 3:10 PM EST
(Standard Talk) | Kaitlyn Bennett
Synthesizing Benzaldehyde from Sugar in <i>Saccharomyces cerevisiae</i> |
| 3:10 PM - 3:25 PM EST
(Standard Talk) | Michael Schulz
Fungal Firefighters: Can Fungal Inoculation Reduce the Fire Risk of Waste Wood? |
| 3:25 PM - 3:40 PM EST
(Standard Talk) | Adnan Chowdhury
Biosynthesis of novel di-phenyl Tetrahydroisoquinoline alkaloids in <i>Saccharomyces cerevisiae</i> . |

Fungal Genetics and Genomics III

1C - 4:00 PM - 5:00 PM EST - Wednesday, August 5, 2026

Moderated by: Linda Horianopoulos

- | | |
|--|---|
| 4:00 PM - 4:15 PM EST
(Standard Talk) | Linda Horianopoulos
Mechanisms of oxidative stress resistance in diverse yeast species |
| 4:15 PM - 4:30 PM EST
(Standard Talk) | Nick Gervais
Chromosome-scale CRISPR screening reveals secretory trafficking as a driver of aneuploidy-mediated antifungal tolerance |
| 4:30 PM - 4:45 PM EST
(Standard Talk) | Sara Fallah
Identification and characterization of the adamantyl diamine SQ109 as a repurposed inhibitor of squalene synthase in the fungal pathogen <i>Candida albicans</i> |
| 4:45 PM - 5:00 PM EST
(Standard Talk) | Manini Chhina
Investigating thermotolerance in <i>Nakaseomyces glabratus</i> via pooled CRISPR activation screens |

Fungal Ecology and Evolution I

2C - 4:00 PM - 5:00 PM EST - Wednesday, August 5, 2026

Moderated by: Allison Walker

4:00 PM - 4:15 PM EST (Standard Talk)	Eric Wilson Cryptic speciation in insect guts: genome-wide analyses to delimit the <i>Smittium culicis</i> complex (Kickxellomycotina, Zoopagomycota)
4:15 PM - 4:30 PM EST (Standard Talk)	Bryn Wiley A Population-Genetic Model of Nuclear Competition in Dikaryons
4:30 PM - 4:45 PM EST (Standard Talk)	Nasim Alijani Biodiversity of mould in the surface-ripened cheese environment
4:45 PM - 4:50 PM EST (Flash Talk)	Cassidy Best Prescribed fire history shapes soil fungal communities between burns

Detailed Conference Schedule - Thursday

Thursday, August 6, 2026

Plenary Day 2 - Fungal Evolution and Symbioses

Plenary Day 2 - 11:30 AM - 1:00 PM EST - Thursday, August 6, 2026

Moderated by: Noah Boodhoo & Viola Halder

- 11:30 AM - 12:00 PM EST Dr. Vasilis Kokkoris
(Plenary Talk) Cell and Network Dynamics in Arbuscular Mycorrhizal Fungi
- 12:00 PM - 12:30 PM EST Dr. Pierre-Luc Chagnon
(Plenary Talk) What are keystone soil fungi?
- 12:30 PM - 1:00 PM EST Dr. Aleeza Gerstein
(Plenary Talk) Recurrent vaginal yeast infections: epidemiology to genomic parallelism

Fungal and Lichen Biodiversity I

3A - 1:20 PM - 2:20 PM EST - Thursday, August 6, 2026

Moderated by: Noah Boodhoo

- 1:20 PM - 1:35 PM EST Jason Pither
(Standard Talk) Taking stock of biodiversity data shortfalls for ectomycorrhizal fungi in Canada
- 1:35 PM - 1:50 PM EST Philip Bell-Doyon
(Standard Talk) Microbiota and metabolome in calicioid lichens and fungi
- 1:50 PM - 2:05 PM EST Riley Henniffent
(Standard Talk) Multiscale Habitat Assessment of the Blue Felt Lichen (*Pectenium plumbeum*): Identifying Critical Habitat Characteristics across Spatial Scales in Central Newfoundland

Medical Mycology

4A - 1:20 PM - 2:20 PM EST - Thursday, August 6, 2026

Moderated: Catherine Bachewich

- | | |
|--|--|
| 1:20 PM - 1:35 PM EST
(Standard Talk) | Veronika Pavlova
Functional genomic analysis reveals genes important for <i>Candida albicans</i> fitness in response to antifungal-induced stress |
| 1:35 PM - 1:50 PM EST
(Standard Talk) | Aruni Sumanarathne
Decoupling competitive fitness and drug tolerance following <i>Candida albicans</i> adaptation to fluconazole |
| 1:50 PM - 2:05 PM EST
(Standard Talk) | Jing Lin (Lucy) Xie
Stress-driven emergence of heritable non-genetic drug resistance |
| 2:05 PM - 2:20 PM EST
(Standard Talk) | Lishita Rowjee
Antifungal susceptibility profiles of <i>Microsporum canis</i> from the United States and Ontario, Canada |

Biocontrol of Fungi

5A - 1:20 PM - 2:20 PM EST - Thursday, August 6, 2026

Moderated by: Oualid Ellouz

- | | |
|---------------------------------------|--|
| 1:20 PM - 1:25 PM EST
(Flash Talk) | Charlotte Bakker
Effect of compost tea preparation dilution and fungal community composition on suppression of grey mold (<i>Botrytis cinerea</i>) of tomato plants |
| 1:25 PM - 1:30 PM EST
(Flash Talk) | Christine Joyce Francisco
Exploring the use of exogenous double-stranded RNA for curing white pine blister rust |
| 1:30 PM - 1:35 PM EST
(Flash Talk) | Irina Popescu
Biocontrol effects of compost tea bacteria against postharvest fungal disease of tomato fruit (<i>Solanum lycopersicum</i> L.) |

Fungal Disease in One Health

3B - 2:40 PM - 3:40 PM EST - Thursday, August 6, 2026

Moderated by: Catherine Bachewich

- | | |
|--|---|
| 2:40 PM - 2:55 PM EST
(Standard Talk) | Erica Sumbler
Role of Inositol Metabolism in drug resistance in <i>Candida albicans</i> |
| 2:55 PM - 3:10 PM EST
(Standard Talk) | Anna Kalabina
Differential requirement for the Ire1 luminal and transmembrane domains in <i>Candida albicans</i> drug resistance and pathogenicity |
| 3:10 PM - 3:25 PM EST
(Standard Talk) | Eileen Bates
Machine Learning-Guided Discovery and Characterization of Novel Small-Molecule Antifungal Drugs |
| 3:25 PM - 3:40 PM EST
(Standard Talk) | James La
From Environmental Fungus to Human Pathogen: Unraveling Virulence in <i>Talaromyces marneffei</i> |

Fungal Plant Pathology I

4B - 2:40 PM - 3:40 PM EST - Thursday, August 6, 2026

Moderated by: Oualid Ellouz

- | | |
|--|--|
| 2:40 PM - 2:55 PM EST
(Standard Talk) | Katherine Brynjolfson
Tissue-Specific Quantification of the Wheat Leaf Spot Complex in Manitoba |
| 2:55 PM - 3:10 PM EST
(Standard Talk) | Berni van der Meer
Secondary pathogens as a comparative genomic filter for pathogenicity in the butternut canker pathosystem |
| 3:10 PM - 3:15 PM EST
(Flash Talk) | Francisco Abel Guerrero Páez
Emergence of Botryosphaeriaceae pathogens in wild olive populations in southern Spain: first report and epidemiological implications |
| 3:15 PM - 3:20 PM EST
(Flash Talk) | Beau Daigneault
Aspen Running Canker Found in Northwestern Boreal Canada |
| 3:20 PM - 3:25 PM EST
(Flash Talk) | Julia Popa
Biocontrol of postharvest fungal pathogens in pome fruit using <i>Bacillus</i> spp. |

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Endophytic Fungi

5B - 2:40 PM - 3:40 PM EST - Thursday, August 6, 2026

Moderated by: Gavin Kernaghan

Chase Pierce

2:40 PM - 2:55 PM EST (Standard Talk) Immunogold Localization of Indole-3-acetic acid (IAA) in *Metarhizium* Species During Insect Pathogenesis & Endophytic Colonization

Juliana Fanning

2:55 PM - 3:00 PM EST (Flash Talk) Fungal Endophytes for Potential Biocontrol of Hemlock Woolly Adelgid

Career Workshop - Telling a story in science: discussions with communication experts!

4:00PM-5:30PM EST - Thursday, August 6, 2026

Moderated by Joanna Gauthier & David Firer

Kenzie Arnott from *Science in the City*

Introduction on the methods and media in science communication and how it differs between audiences will be discussed. This section of the workshop will cover how to get experience and find opportunities in science communication drawn from the panelist's experience.

Marie-Andrée Fallu from the *Groupe de Recherche Interuniversitaire en Limnologie*

4:00PM-5:30PM EST The Interuniversity Research Group in Limnology (Groupe de recherche interuniversitaire en limnologie; GRIL) has been working for 20 years to promote freshwater aquatic sciences. The various ways in which it achieves this will be presented: the different methods of science communication to the general public (social media, podcasts, AquaQuiz, information booths, etc), the dissemination strategies with the help of umbrella organizations, and the science communication training program for graduate students who are members of GRIL (comics, fact sheets, etc).

Erum Razvi from *Genome Canada*

Introduction to developing scientific business cases for research and innovation will be presented. This portion of the workshop will cover how to frame ideas across the research pipeline, from discovery to innovation, with a focus on writing for funding competitions, start-up pitches, and presentations. Practical insights on communicating the problem, solution, value proposition, feasibility, and impact in a clear and compelling way will be shared.

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Detailed Conference Schedule - Friday

Friday, August 7, 2026

Plenary Day 3 - Fungi and Plants

Plenary Day 3 - 11:30 AM - 1:00 PM EST - Friday, August 7, 2026

Moderated by: Joanna Gauthier & Patrick Lajoie

- | | |
|---|--|
| 11:30 AM - 12:00 PM EST
(Plenary Talk) | Dr. Jan van Kan
You can only die once: the battle over cell death control between a fungus and its plant host |
| 12:00 PM - 12:30 PM EST
(Plenary Talk) | Dr. Xin Li
Breaking the “one nucleus, one whole genome” rule: lessons from fungi |
| 12:30 PM - 1:00 PM EST
(Plenary Talk) | Dr. Joey Tanney
From Endophytes to Epidemics: Emerging Forest Diseases in a Changing Climate |

Fungal Ecology and Evolution II

6A - 1:20 PM - 2:20 PM EST - Friday, August 7, 2026

Moderated by: Joanna Gauthier

- | | |
|--|--|
| 1:20 PM - 1:35 PM EST
(Standard Talk) | Joanna Gauthier
Fungal functional ecology across a dissolved organic carbon gradient in Canadian lakes |
| 1:35 PM - 1:50 PM EST
(Standard Talk) | Makayla Lloyd
Bioprospecting: Investigating the Toxin Droplets of <i>Pleurotus</i> |
| 1:50 PM - 2:05 PM EST
(Standard Talk) | Kevin Kosta
Analyzing the Antimicrobial Activity of Manitoban Medicinal and Culturally Important Plant Endophytes |
| 2:05 PM - 2:10 PM EST
(Flash Talk) | Gold Cummins
Nitrogen and phosphorus enrichments effects on fungal community composition in Churchill's boreal tundra ecotone |

Fungal Plant Pathology II

7A - 1:20 PM - 2:20 PM EST - Friday, August 7, 2026

Moderated by: Matthias Kretschmer

- | | |
|--|---|
| | Matthias Kretschmer |
| 1:20 PM - 1:35 PM EST
(Standard Talk) | Battleground chloroplast, a temporal and spatial meta-analysis of <i>Zea mays</i> chloroplast gene expression during biotrophic interaction with <i>Ustilago maydis</i> |
| 1:35 PM - 1:50 PM EST
(Standard Talk) | Emily Trudeau
Tracing early plant-fungus associations through plant-degrading enzyme evolution in fungi |
| 1:50 PM - 2:05 PM EST
(Standard Talk) | Annabella Lyndon
Pathogens in an endophyte world: The presence of a phytotoxin biosynthetic gene cluster reflects host-association strategy in <i>Xylaria genera</i> |
| 2:05 PM - 2:10 PM EST
(Flash Talk) | Tahiat Rahman
Molecular quantification of the wheat leaf spot complex in Alberta in 2026 |

Fungal and Lichen Biodiversity II

6B - 2:40 PM - 3:40 PM EST - Friday, August 7, 2026

Moderated by: Noah Boodhoo

- | | |
|--|--|
| 2:40 PM - 2:55 PM EST
(Standard Talk) | Romina Silva Espejo
Spatial organization of chitin in chlorolichen and <i>cyanolichen thalli</i> |
| 2:55 PM - 3:10 PM EST
(Standard Talk) | Andrew Simon
Boreal lichen photobiont networks: structure, stability, and vulnerability |
| 3:10 PM - 3:25 PM EST
(Standard Talk) | Arsenii Belosokhov
B vitamins as hidden currencies in lichen symbiosis |
| 3:25 PM - 3:40 PM EST
(Standard Talk) | Abby Spring
Determining the mycorrhizal status and root-associated fungal diversity of Northern wild rice (<i>Zizania palustris</i>) via targeted amplicon sequencing |

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Mycorrhizal Symbioses II

7B - 2:40 PM - 3:40 PM EST - Friday, August 7, 2026

Moderate by: Katie King

- | | |
|--|---|
| 2:40 PM - 2:55 PM EST
(Standard Talk) | Ken Sanderson
Do Co-occurring Coastal Dune Plants Share Their Root Fungal Partners? |
| 2:55 PM - 3:10 PM EST
(Standard Talk) | Mareike Meents
Establishment rates and species composition of AMF in <i>Plantago maritima</i> and <i>Triglochin maritima</i> in Canadian and German salt marshes |
| 3:10 PM - 3:25 PM EST
(Standard Talk) | Ada Jarosch
A Survey of Ectomycorrhizal Fungi in Carolinian Canada |
| 3:25 PM - 3:30 PM EST
(Flash Talk) | Ruthann Burke
Relationships between edaphic factors and the ericoid mycorrhizae of cranberry (<i>Vaccinium macrocarpon</i>) in Nova Scotia |

Fungal Applications II

6C - 4:00 PM - 5:00 PM EST - Friday, August 7, 2026

Moderated by: Viola Halder

- | | |
|--|--|
| 4:00 PM - 4:15 PM EST
(Standard Talk) | Ciera Wiebe
Increasing Production of Ephedrine in <i>Saccharomyces cerevisiae</i> through Adaptive Laboratory Evolution and Nonconventional Yeast Screening |
| 4:15 PM - 4:30 PM EST
(Standard Talk) | Juliana Vicente
Force-sensitive regions of fungal adhesins guide de novo inhibitor design |
| 4:30 PM - 4:45 PM EST
(Standard Talk) | Gülten Yüksesk
Engineering Immobilized Fungal Laccase Systems For Sustainable Wastewater Polishing |
| 4:45 PM - 4:50 PM EST
(Flash Talk) | Brianna House
Capturing the yeast: development of methods to isolate yeasts from complex samples |

Fungal Genetics and Genomics IV

7C - 4:00 PM - 5:00 PM EST - Friday, August 7, 2026

Moderated by: David Firer

4:00 PM - 4:15 PM EST (Standard Talk)	Allison M. Porman Swain The conserved m6A methyltransferase IME4 regulates aspects of the <i>Candida albicans</i> parasexual cycle
4:15 PM - 4:30 PM EST (Standard Talk)	Binh Tran Novel Transcriptional Profiling Approach to Study Para-Resistance in <i>C. albicans</i>
4:30 PM - 4:45 PM EST (Standard Talk)	Wanjun Qi Cascading damage to <i>Candida albicans</i> cells through thioredoxin reductase loss
4:45 PM - 5:00 PM EST (Standard Talk)	Ola Salama Comparative Analysis of <i>C. albicans</i> and <i>N. glabratus</i> in response to acute boric acid exposure

Closing Ceremony

Closing Ceremony - 5:00PM-6:00PM EST - Friday, August 7, 2026

Moderated by: Noah Boodhoo & Catherine Bachewich

Abstracts

Plenary Abstracts

Small Molecules, Big Mysteries: Isocyanides In Fungi

Nancy Keller

University of Wisconsin - Madison

TBA

Cell and Network Dynamics in Arbuscular Mycorrhizal Fungi

Vasilis Kokkoris

Vrije Universiteit (VU) Amsterdam

Arbuscular mycorrhizal (AM) fungi form vast, continuous cytoplasmic networks that connect soil with plant roots and sustain one of Earth's most widespread symbioses. Their coenocytic organization allows resources, organelles, nuclei, and signals to move through centimeter- to meter-scale mycelia without cellular boundaries, raising fundamental questions about coordination across scales. Within hyphae, AM fungi show dynamic nuclear distributions, spatially organized lipid accumulation, and sustained cytoplasmic streaming that together support rapid physiological responses. Across networks, mycelial expansion occurs through coordinated waves of tip growth and mycelial densification, linking exploratory foraging with the stabilization of long-distance transport capacity. These coupled dynamics allow AM fungi to flexibly allocate carbon and nutrients while maintaining connectivity with host roots. Yet, despite their ecological importance, the AM fungal cell remains poorly understood. Resolving how internal cellular organization integrates with network growth is essential for a mechanistic understanding of AM fungal function, efficiency, and resilience.

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What are keystone soil fungi?

Pierre-Luc Chagnon

Agriculture Canada

For decades, the concept of keystone species has fascinated ecologists. Community ecology is indeed greatly in need of parsimonious explanations for the complex interactions that occur in ecosystems. Especially in the realm of soil ecology and microbiomes, it would be useful to identify a few key species that have disproportionate effects on their environment relative to their abundance. Regardless of repeated criticisms against co-occurrence networks and the limitations of inferring ecological interactions and species roles from them, they have been used at a steady, or maybe even increasing pace, to identify keystone species in soil microbial communities. Here, I am showing multiple lines of evidence showing that the position, or "role" of a fungus in a network cannot be deemed a useful trait or proxy for its ecological importance. In fact, via simulation I am showing how simple metacommunity models completely devoid of so-called keystone species can produce networks with species of high centrality, which are often interpreted as keystone species. This suggests that the identification of keystone soil fungi based solely on network analysis may be misleading and that other ecological factors should be considered when assessing their importance in soil ecosystems. These findings highlight the need for a more nuanced understanding of the roles of soil fungi in ecosystems and caution against over-reliance on network metrics for identifying keystone species. Otherwise, we may be at risk of mischaracterizing the ecological dynamics of soil communities, overlooking the complex interactions that drive ecosystem functioning, and hallucinating patterns that do not exist in reality.

Recurrent vaginal yeast infections: epidemiology to genomic parallelism

Aleeza Gerstein

University of Manitoba

Recurrent vulvovaginal candidiasis (RVVC) is a common condition affecting people with vaginas. We enrolled 37 volunteers with a history of RVVC who visited a specialty yeast clinic and provided vaginal, rectal, oral, and skin swabs over a 1-month period. Comparing their demographics to the population at large highlighted income that points to system-level barriers to care. We also uncovered a disconnect between swab positivity and antifungal drug prescriptions. A phylogenetic analysis of short-read whole-genome sequence data from isolates of vaginal-yeast positive participants determined that vaginal, rectal, oral and skin isolates from the same participant were typically very similar, consistent with frequent migration among body sites. A comparative genomic analysis identified genomic parallelism in vaginal isolates in 40 genes. This provides evidence that vaginal yeast adapt to this unique environment, and suggests a roadmap for better understanding this chronic condition for which there is no cure.

Breaking the “one nucleus, one whole genome” rule: lessons from fungi

Xin Li

University of British Columbia

In eukaryotes, each nucleus typically contains at least one full set of chromosomes, a principle believed to safeguard genome integrity during reproduction. However, in two important fungal pathogens of crop plants, haploid chromosomes are unexpectedly separated into different nuclei. This surprising discovery was confirmed through various cellular and molecular methods, including chromosome counting, fluorescence in situ hybridization, flow cytometry DNA measurements, and single-nucleus PCR experiments. It raises questions about how these fungi inherit their genetic material, especially given that abnormal chromosome numbers in human nuclei are associated with aging, diseases, cancers, or developmental disorders. This discovery not only challenges existing concepts, but also opens new avenues for research in chromosome and synthetic biology.

From Endophytes to Epidemics: Emerging Forest Diseases in a Changing Climate

Joey Tanney

Pacific Forestry Centre, Canadian Forest Service, Natural Resources Canada

Climate change is reshaping forest disease dynamics by altering pathogen biology, increasing host stress, and destabilizing long-standing tree–microbiome relationships. Building on a recent framework for climate-driven emerging tree diseases, I will examine how forest pathogens emerge or intensify along a continuum between climate-pathogen diseases, where changing conditions directly favour pathogen activity, to climate-stress diseases, where heat, drought, and other stressors predispose trees to decline. Using sooty bark disease of maple and Swiss needle cast of Douglas-fir as case studies, I will highlight how Canadian Forest Service research is addressing these risks through integrated surveillance, pathology, diagnostics, genomics, microbiome research, and applied technologies. Examples include new detection tools for *Cryptostroma corticale*, studies of asymptomatic infection and disease expression in maples, endophyte-based approaches to mitigating Swiss needle cast, and AI-assisted image analysis tools for rapid disease phenotyping. Together, these efforts support earlier detection, improved risk assessment, and climate-ready forest health management.

Mining fungal diversity for a robust acid-tolerant biomanufacturing host

Michael Pyne

Western University

Engineered fungi hold great promise for displacing conventional and unsustainable routes to valuable chemicals, fuels, and pharmaceuticals. However, model hosts such as brewer's yeast (*Saccharomyces cerevisiae*) are unequipped to tolerate product concentrations required for commercial-scale production. This research summarizes our efforts to identify a robust acid-tolerant yeast for engineered production of adipic acid, a monomer used in the industrial synthesis of nylon. I will recap our screening of 122 yeast strains for tolerance to adipic acid and our subsequent domestication of *Pichia occidentalis*, a species resistant to high concentrations of adipic acid. I will also highlight our methodologies to engineer *P. occidentalis* to produce cis,cis-muconic acid, the direct precursor to adipic acid. Our work identifies new fungal hosts and enzymes for overproducing toxic metabolites and showcases the biomanufacturing advantages of tailoring microbial strains to target end products.

You can only die once: the battle over cell death control between a fungus and its plant host
Jan van Kan
Wageningen University, Laboratory of Phytopathology

TBA

Zen and the art of mycofabrication
Steven Hallam
University of British Columbia

Mycofabrication with mycelium (the three-dimensional network of filamentous fungi) has attracted tremendous attention as a method to produce functional products in a sustainable manner. Products such as mycelium-based textiles, mycelium biocomposites, and mycelium-based foods all require the production of mycelium biomass using model fungi such as reishi (*Ganoderma sichuanense*), oyster (*Pleurotus ostreatus*), and turkey tail (*Trametes versicolor*). In this nascent field, many parameters require optimization to maximize mycelium biomass production. Conventional approaches to determine optimal parameters include measuring radial growth of mycelium on agar or weighing mycelium biomass grown in liquid culture after a period of incubation. However, neither approach leverages modern high-throughput technologies for data-driven optimization. Here, we performed a response surface methodology design of experiment (RSM-DoE) study using a high-throughput microplate absorbance approach which monitored growth of reishi, oyster, and turkey tail mycelium in relation to various parameters, including temperature, malt extract concentration and yeast extract concentration. This study produced an overall recommendation of 2% w/w malt extract media supplemented by 1% w/w yeast extract at 30 °C as optimal growth parameters for these mycofabrication species. The recommendation was validated by cultivating mycelium biomass in liquid conditions under the optimized parameters, achieving +160% biomass compared to base conditions. We also demonstrated improvements to two applications under optimized conditions: multilaminated mycelium textile reached 2x thickness and mycelium biocomposites on sawdust substrate production time was cut by 50%. This work demonstrates the utility of the microplate absorbance approach as a screening tool to accelerate discovery and optimization of parameters for mycofabrication. While reishi, oyster, and turkey tail mycelium represent the most common model fungi, another ~20 species have been explored to a lesser extent by the mycofabrication community. Many promising fungal candidates remain unexplored in the context of mycofabrication. Mushrooms which are both edible and cultivable alone number in the hundreds, waiting to be optimized. The workflow described here provides a quality-driven paradigm needed to inform the next generation of mycelium-based engineered living materials.

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Speaker Abstracts

Field-Scale Benefits of Mycorrhizal Fungi in Agroforestry

Albracht, Cynthia *; Assou, Juvenal; Langhof, Maren; Werner, Stephanie
Julius Kühn Institute

Mycorrhizal fungi are known to enhance plant nutrition, growth, and health, yet most evidence has focused on arbuscular mycorrhizal associations under controlled laboratories or greenhouse conditions. In contrast, the role and practical application of fungal inoculant in field-scale agricultural systems, particularly those involving ectomycorrhizal fungi like agroforestry systems, remain insufficiently studied. In this study, commercially available inoculants containing mixtures of both ecto- and endomycorrhizal fungi were applied during the establishment of an agroforestry (alley cropping) system consisting of poplar clones (*P. nigra* x *P. maximowiczii*), red currant shrubs (*R. rubrum* cv. Jonkheer van Tets), and annual crop rotations of summer barley, faba bean and maize.

Successful establishment of mycorrhizal associations was verified through quantification of root colonization across all plant groups. We then evaluated the functional effects of fungal inoculation on crop yield, tree growth, and plant health under field conditions. Mycorrhizal fungi significantly improved both crop and wood yields beginning in the second year after planting. In crops, increased yield was primarily associated with higher thousand-grain weight rather than enhanced vegetative growth, whereas inoculated poplar trees showed greater secondary growth. Furthermore, we found inoculated trees to be less susceptible to poplar beetle infestation, exhibiting reduced feeding damage and lower mortality compared with non-inoculated controls. Our findings demonstrate that beneficial plant–fungus interactions established through commercial mycorrhizal inoculation can be successfully translated from controlled environments to agroforestry field systems. In particular, ectomycorrhizal fungi emerged as promising biostimulants for improving productivity and resilience in agricultural practice.

Biodiversity of mould in the surface-ripened cheese environment

Alijani mamaghani, Nasim;* Wilson, Tara; LaPointe, Gisele.

Postdoctoral Researcher

The microbiota of surface-ripened cheeses, consisting of bacteria, yeasts, and filamentous fungi, becomes highly diversified during aging. Opportunistic fungi such as *Scopulariopsis* spp. can cause spoilage leading to off-colour and texture defects, resulting in economic loss. The aim of this study is to evaluate the diversity of fungal isolates collected from 5 and 8-month cheeses showing black and brown colour defects. Isolates grown on PDA medium were selected randomly using the Harrison disc method and identified by Matrix-Assisted Laser Desorption/Ionized Time-Of-Flight Mass Spectrometry (MALDI-TOF MS). A total of 79 out of 160 isolates (50%) were identified as *Scopulariopsis* spp. (90% of isolates from defective cheeses, 60% of wash water isolates, 55% of floor isolates, 32% of 8-month cheese isolates and 20% of 5-month cheese isolates). The remaining 81 isolates were identified as *Aspergillus*, *Cladosporium*, and *Debaromyces*. Whole-genome sequencing will further define the genomic diversity of *Scopulariopsis* in the cheese ecosystem.

Diverse fungal DNA: Identification of idiomorphic regions across fungal species

Leng, Zhaoqi. Auxier, Ben*.

Wageningen University & Research

Particular regions of the genome are extraordinarily diverse, without recognisable sequence homology in a given chromosomal region. This is either due to ancient polymorphisms or introgression/HGT events. While some have clear biological functions (e.g. mating-type locus; het genes), most do not. To study this, we developed Idioscan, which uses genome assemblies to identify such higher divergent regions. Across 14 fungal species we found that when using more than 30 assemblies, Idioscan identification sensitivity was greater than 80%. The identified candidate genes were relatively rare, representing approximately 0.20%–6.00% of the protein-coding genes of a fungal species. On some chromosomes, idiomorphic genes had a subtelomeric distribution pattern, suggesting younger genomic regions are enriched for idiomorphs. Gene Ontology (GO) enrichment patterns were highly species-specific, with no consistent biochemical pattern of idiomorphic sequences. This work suggests that ecological niches may influence the balancing selection forces acting on these loci.

Effect of compost tea preparation dilution and fungal community composition on suppression of grey mold (*Botrytis cinerea*) of tomato plants

Bakker, Charlotte E. *, Graham, Hailey R., Smith, Myron L., Avis, Tyler J.

Carleton University

Botrytis cinerea, causing grey mold disease, is a serious pre- and post-harvest fungal phytopathogen. Conventional methods for disease control rely on chemical fungicides, which have associated health and environmental effects. A promising alternative is disease suppressive compost teas. In this study, compost teas prepared from sheep manure (SHE), bovine manure (BOV), and shrimp residue (SHR) composts at two preparation dilutions (1:5 and 1:10 compost:water) were tested for their suppressive effect against tomato grey mold. Results showed all compost teas reduced disease severity except SHE-1:5 and BOV-1:10. SHR teas, regardless of dilution, reduced disease severity and improved plant growth. SHE-1:5 impaired plant growth, by 12% compared to SHE-1:10, which had no effect on plant growth. BOV-1:10 improved plant growth by 29% relative to BOV-1:5, which had no effect on plant growth. Metagenomic analysis of the fungal component revealed that Ascomycetes, notably *Trichoderma* spp., were prominent in suppressive compost teas.

Machine Learning-Guided Discovery and Characterization of Novel Small-Molecule Antifungal Drugs

Bates, Eileen*; Arnold, Autumn; Stokes, Jonathan; Shapiro, Rebecca

University of Guelph

Effectively combatting fungal pathogens requires the development of novel antifungal drugs. Recently, machine learning has become a valuable tool for antibiotic discovery; however, the application of these models towards fungal pathogens remains extremely limited. We aim to leverage contemporary machine learning approaches to discover novel small-molecule antifungal drugs against *Candida albicans*. Using a molecular property prediction model, we conducted an in silico screen of approximately 12 million compounds. Based on these predictions, we identified 2 structurally novel compounds with potent antifungal activity against *C. albicans*, as well as other diverse fungal pathogens and antifungal-resistant clinical isolates. Currently, we are investigating the mechanism of action of these compounds using haploinsufficiency profiling and transcriptomics approaches. This work represents a powerful new approach to antifungal drug development, which is crucial for decreasing the burden of fungal pathogens on human health.

Microbiota and metabolome in calicioid lichens and fungi

Bell-Doyon, Philip*; Villarreal, Juan Carlos; Mazerolle, Marc J.; Séguin, Jean-Christophe; Quiros-Guerrero, Luis; Ferreira Queiroz, Emerson; Nothias, Louis-Félix; Wolfender, Jean-Luc; Voyer, Normand
Université Laval

Lichens are chemically unique symbiotic organisms formed by the association of a fungus with one or more photosynthetic partners and a diverse microbiota. We investigated the microbiota and metabolome in calicioid lichens and fungi, as well as putative endolichenic *Penicillium* spp. *Solirubrobacterales* (*Actinobacteria*) was the most abundant bacterial order in *Chaenotheca* samples, while *Acetobacterales* (*Proteobacteria*) dominated *Mycocalicium* and *Penicillium* samples. Bacterial alpha diversity had no effect on metabolome diversity, but fungal alpha diversity explained 35.8% of the observed variability in metabolome diversity. Fungal community composition was positively correlated with metabolome composition, while bacterial communities were not. Molecules considered exclusive to lichens such as lecanoric, protocetraric, and pulvinic acids were also biosynthesized by *Penicillium* isolates. We conclude that microbiota influences metabolome composition and diversity in lichens and non-lichenized fungi, and we argue that lichens associated with intact forest ecosystems are a promising source for the discovery of novel and bioactive molecules.

B vitamins as hidden currencies in lichen symbiosis

Belosokhov, Arseniy*; Escandón, David Díaz; Allen, Carmen; Spribille, Toby
University of Alberta

Lichens are usually described as nutritional symbioses based on photobiont-derived carbon. However, older culture studies suggested that some lichen fungi also require B vitamins, especially thiamine and biotin. We surveyed predicted biotin and thiamine metabolism in 197 lichen-forming ascomycete fungi and 118 non-lichen ascomycetes using KEGG ortholog annotations, manually curated pathway maps, and feature-association analyses. Most non-lichen fungi retained annotations consistent with synthesis of both vitamins. In contrast, most lichen fungi lacked annotations for the mappable late branch of biotin biosynthesis, while retaining genes for biotin activation and biotin-dependent enzymes. Thiamine showed a different pattern: predicted reduction was strongest in cyanolichen fungi, especially Peltigerales and Lichinales, where upstream de novo and salvage-adjacent genes were reduced but downstream activation and many TPP-dependent enzymes persisted. These results suggest that B vitamins may represent additional metabolic currencies in lichen symbiosis, alongside carbon.

Synthesizing Benzaldehyde from Sugar in *Saccharomyces cerevisiae*

Bennett, Kaitlyn. Pyne, Michael.

Western University

Current yeast-biosynthesis of the pharmaceutical precursor (R)-phenylacetylcarbinol [(R)-PAC] is dependent on a fossil-fuel derivative, benzaldehyde. Here, we seek to improve the sustainability of (R)-PAC by installing a metabolic pathway in *Saccharomyces cerevisiae* capable of synthesizing benzaldehyde from sugar. The benzaldehyde pathway begins with phenylpyruvate which is naturally synthesized from the shikimate and aromatic amino acid (L-Phe) pathways in yeast. Based on preliminary data, three bacterial enzymes (hydroxymandelate synthase, hydroxymandelate oxidase, and benzylformate decarboxylase) can be used together to synthesize benzaldehyde from phenylpyruvate. Benzaldehyde is immediately used for benzyl alcohol synthesis by endogenous oxidoreductases and (R)-PAC synthesis by endogenous and *Candida tropicalis* pyruvate decarboxylases. Presently, we are working on optimizing benzaldehyde production by modifying shikimate enzymes responsible for phenylpyruvate synthesis. After, we will incorporate enzymes previously tested in our lab that efficiently convert benzaldehyde to phenyl-tetrahydroisoquinoline, an important pharmaceutical scaffold, and (R)-PAC to norephedrine, a decongestant medicine and precursor to ephedrine.

Prescribed fire history shapes soil fungal communities between burns

Best, Cassidy*; Fischer, Monika

University of British Columbia

Wildfire regimes in western North America are intensifying, yet the influence of fire history on soil fungal communities remains unclear. In fire-affected ecosystems, fire history may shape belowground communities long after fire has passed, but the extent to which burn frequency and time since fire structure fungal communities remains unknown. This research examines how fire history influences soil fungal community composition and the relative abundance of pyrophilous—or fire-associated—fungi within a coastal British Columbia landscape managed with repeated prescribed burns. Soil cores were collected across contrasting burn histories at Rocky Point, Vancouver Island, where prescribed fires have been conducted since 2017. Fungal communities will be characterized using RNA-based ITS2 sequencing, while soil chemical properties will be quantified to evaluate relationships among fire history, edaphic conditions, and fungal community structure. By integrating fungal community data with soil chemistry, this study will improve understanding of how repeated burning shapes belowground fungal communities and soil recovery in fire-adapted ecosystems.

Tissue-Specific Quantification of the Wheat Leaf Spot Complex in Manitoba
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Agriculture and Agri-food Canada

The wheat leaf spot fungal complex remains a critical threat to wheat production in Canada and worldwide. Because different tissues provide distinct microclimates, species composition can vary by tissue. This study determines abundance and distribution of five major leaf spot pathogens, *Pyrenophora tritici-repentis*, *Parastagonospora nodorum*, *Parastagonospora pseudonodorum*, *Bipolaris sorokiniana*, and *Zymoseptoria tritici*, across leaf, node and grain tissues of 2025 Manitoba field samples. Pathogen DNA was quantified via TaqMan probe-based qPCR assays targeting the β -tubulin 1 gene. In leaves, *P. tritici-repentis* exhibited highest mean DNA concentration at 33.4 pg/ng (96% prevalence), then *P. nodorum* (7.33 pg/ng, 38% prevalence) and *P. pseudonodorum* (2.84 pg/ng, 98% prevalence), with *B. sorokiniana* and *Z. tritici* detected at significantly lower concentrations and frequencies. Preliminary results for node and grain indicate tissue-specific patterns, with *P. nodorum* predominant in nodes and *P. pseudonodorum* predominant in grain. These findings underscore the need for tissue-specific disease monitoring.

Relationships between edaphic factors and the ericoid mycorrhizae of cranberry (*Vaccinium macrocarpon*) in Nova Scotia
Burke, Ruthann* and Kernaghan, Gavin
Mount Saint Vincent University

Cranberries (*Vaccinium macrocarpon*) are an economically important crop in Canada, valued for their high antioxidant content and associated health benefits. In the wild, cranberries grow in nutrient poor peat bogs (sphagnum) and sandy soils, while commercial cranberry beds are sanded to improve growth. In all cases, associations with ericoid mycorrhizal (ErM) fungi allow them access to organic nutrient sources. As there has been no research on cranberry ErM in Nova Scotia specifically, this project investigated the effects of edaphic factors, such as substrate texture and pH, on ErM abundance and diversity in *V. macrocarpon* hair roots. Imaging of cleared and stained hair roots revealed that ErM colonization was lowest in peat bog habitats, and highest in cultivated farms. ErM community diversity was assessed by next-generation sequencing of fungal ITS. *V. macrocarpon* hair roots were predominantly colonized by basidiomycetous ErM fungi from the families *Clavariaceae*, *Sebacinaceae*, and *Serendipitaceae*.

Investigating thermotolerance in *Nakaseomyces glabratus* via pooled CRISPR activation screens
Chhina, Manini*, Gervais, Nicholas C., Shapiro, Rebecca S.
University of Guelph

Thermotolerant traits, favoured by climate change and rising temperatures, may exacerbate the threat fungal pathogens pose to human health. Uncovering stress tolerance mechanisms in fungi is crucial, as thermotolerance can confer cross-tolerance to stressors, including antifungal drugs. *Candida* species are the fourth most common cause of bloodstream infections, with the second most frequently isolated species being *Nakaseomyces glabratus* (*Candida glabrata*). Preliminary experimental evolution of *N. glabratus* in heat stress showed each of the 18 heat-adapted populations acquired resistance to all three major classes of antifungal drugs. Further, two populations had chromosome A (ChrA) aneuploidies, suggesting that overexpressing ChrA genes may confer thermotolerance. Paired with RNA-Seq, a pooled ChrA-targeted CRISPR activation (CRISPRa) library was constructed to investigate the influence of ChrA aneuploidy on thermotolerance and drug resistance. This work represents the first CRISPR screen in *N. glabratus* and demonstrates a powerful, high-throughput approach for functional genomics and the study of stress adaptations.

Biosynthesis of novel di-phenyl Tetrahydroisoquinoline alkaloids in *Saccharomyces cerevisiae*.
Chowdhury, Adnan* Michael Pyne
University of Western Ontario

Many modern pharmaceuticals come from natural products and their derivatives. However, their structural complexity has made synthesis inefficient and environmentally taxing. New methods of drug production must be explored to overcome these challenges. The endogenous yeast Ehrlich pathway converts non-natural amino acids into reactive fusel aldehydes. Research has shown that these products undergo a Pictet-Spengler condensation with dopamine, catalyzed by plant-derived norcoclaurine synthase (NCS). This generates "new-to-nature" di-phenyl-substituted tetrahydroisoquinoline (THIQ) scaffolds which are essential precursors for many pharmaceuticals. Here, we propose to use an engineered baker's yeast (*Saccharomyces cerevisiae*) to enable large-scale production of novel THIQ alkaloids. We demonstrate that successful deletion of native oxidoreductases (ARI1, GCY1, HFD1) increases reaction flux towards di-phenyl THIQ precursors. Further, we integrate a diverse NCS gene library and identify novel high-performing NCS variants from *Aquilegia coerulea* and *Coptis japonica*. Overall, this project will lead to the development of sustainable biomanufacturing pipelines for essential medications.

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Stress Resistance Genomics in Protein Powerhouse *Komagataella phaffii*; Laboratory Evolution and Mutation Mapping for Yeast Industrial Endurance

Ciemniecki, Adrian*; Lapolla, Sarah; Delage, Laura; Horianopoulos, Linda C.

University of Guelph

The bioproduktive capabilities of yeasts have been employed since ancient applications in alcoholic fermentations. Recent advancements have elucidated numerous species as promising microbial cell factories, especially those for recombinant protein production at which the methylotrophic yeast *Komagataella phaffii* excels. To characterize its resistance-acquiring mechanisms to common industrial stressors, *K. phaffii* was subjected to adaptive laboratory evolution (ALE) in 2 different carbon sources to generate 7 independently evolved strains expressing diverse fitness levels in phenotyping trials. Several of these oxidative-stress-evolved mutants also displayed improved growth over the parent strain in other stress conditions, suggesting overlap of adaptation pathways. Evolved isolates are being subjected to whole genome sequencing, which will allow for the identification of convergent mutations in independently evolved lineages. This research will extend our understanding of the genomic-phenomic map of *K. phaffii*, catalyzing its further genetic optimization for cell growth and survival in industrial-scale systems.

Nitrogen and phosphorus enrichments effects on fungal community composition in Churchill's boreal tundra ecotone

Cummins, Gold*. Markham, John. Az, Klymiuk.

University of Manitoba

Climate change and increasing annual temperatures are poised to affect major aspects of the nitrogen and phosphorus cycles across the globe, causing a potential increase in bioavailable nitrogen and phosphorus. For environments such as the boreal region an increase in bioavailable nitrogen may alter soil microbial community composition, but it is unclear how an increase in nitrogen and phosphorus will affect fungal diversity in the boreal tundra ecotone. To understand how additional soil nutrients will affect fungal community composition, we sampled 40 plots in Churchill's boreal tundra ecotone that were fertilized with a gradient of nitrogen and phosphorus. We then sequenced the ITS fungal DNA from each plot to help answer two primary questions 1) Does increasing soil nitrogen and phosphorous change fungal diversity in the boreal tundra ecotone? 2) Is there a difference in fungal community composition in the boreal forest and boreal tundra as soil nutrients increase?

Aspen Running Canker Found in Northwestern Boreal Canada

*Daigneault, Beau. Mihorean, Mackenzie. Bonner, Colin. Johnstone, Jill. Baltzer, Jennifer. Thorn, Greg
University of Western Ontario

First described in Alaska (USA), *Neodothiora populina* is the fungal pathogen responsible for Aspen Running Canker (ARC) which infects trembling aspen (*Populus tremuloides*). ARC can kill mature aspen trees in as little as a single growing season from symptom onset. By developing PCR primers specific to *N. populina*'s internal transcribed spacer region of nuclear ribosomal DNA (nrITS), we were able to detect the pathogen in diseased and healthy bark samples, confirming the presence of *N. populina* in the Yukon and Northwest Territories (Canada). Additionally, via a phylogeographic haplotype-based analysis of nrITS2 sequence data we have found evidence to suggest a pathogenic haplotype with a circumpolar (Holarctic) distribution, with insights into the potential origin of this disease. These findings highlight the need for increased surveillance of the disease but also raise questions about the potential for asymptomatic infections and what environmental factors could influence these disease outcomes.

Characterizing oxidative stress resistance in *Candidozyma auris*

Delage, Laura*, Bates, Eileen, Horianopoulos, Linda C., Shapiro, Rebecca
University of Guelph

During infection, pathogenic yeasts are routinely exposed to reactive oxygen species (ROS) generated by macrophages, metabolic processes, or antifungal drugs. Consequently, examining ROS resistance has clinical relevance and the potential to elucidate new antifungal drug targets. High-throughput screening revealed ROS sensitivity in *Candidozyma auris* under laboratory conditions, while a machine learning model conversely predicted ROS resistance based on gene families. As a follow-up to these analyses, we aim to further investigate this discrepancy. Hypothesizing that host cues can induce an acquired stress response, we will expose *C. auris* to stressors including increased temperature and nutrient limitations to determine whether these induce a ROS-resistant phenotype. We will then perform transcriptomic analyses to identify differentially expressed genes required for ROS resistance. This work aims to further our understanding of ROS resistance in *C. auris* with the potential to inform antifungal development, which is of critical importance for this emerging multidrug-resistant pathogen.

Pooled CRISPRi screening reveals fungal-specific drug target candidates

Després, Philippe C*, Wensing, Lauren F, Francis, Desiree, Fogal, Meea, Hendriks, Anthony, Gervais, Nicholas C, Fikry, Clara, Adamu Bukari, Abdul-Rahman, Gerstein, Aleeza C, Cuomo, Christina A, Shapiro, Rebecca S

Broad Institute, Brown University and University of Guelph

The rising rate of drug-resistant fungal infections and the emergence of intrinsically resistant pathogens pose growing clinical challenges. Because fungi are closely related to mammals, developing antifungals without toxic off-target effects is difficult. Targeted gene repression can model drug-mediated inhibition and reveal gene dosage sensitivity, but traditional approaches in the fungal pathogen *Candida albicans* are labour intensive and low throughput. Here we adapt pooled CRISPR interference (CRISPRi) screening in *C. albicans* to enable large-scale functional genomic analysis. We assess repression sensitivity of 130 essential genes conserved in fungi without close homologues in humans and identify highly dosage-sensitive genes across multiple pathways. Screening across ten environmental conditions reveals environment-dependent effects on gene sensitivity. Extending these experiments to two drug-resistant clinical isolates shows that many fitness defects are conserved across genetic backgrounds. Thus, CRISPRi pooled screening enables rapid, large-scale functional genomics across diverse genetic backgrounds in *C. albicans*.

Identification and characterization of the adamantyl diamine SQ109 as a repurposed inhibitor of squalene synthase in the fungal pathogen *Candida albicans*

Sara Fallah*, Xuefei Chen, Sunna Nabeela, Zhongle Liu, Robert Zarnowski, Luke Whitesell, Priya Uppuluri, David R Andes, Gerard D. Wright, Peter J. Stogios, Nicole Robbins, & Leah E. Cowen

University of Toronto

Candida albicans is a leading cause of fatal fungal infections, particularly in immunocompromised patients. Alarming, the current antifungal arsenal is increasingly limited by resistance. To identify novel therapeutics, we screened a Medicines for Malaria Venture compound library and discovered that the antitubercular drug SQ109 exhibits broad spectrum antifungal activity. Mechanistic analyses indicated SQ109 targets *C. albicans* squalene synthase Erg9, decreasing squalene, lanosterol, and ergosterol while increasing the precursor farnesyl pyrophosphate. Co crystallography revealed that SQ109 binds within the Erg9 substrate pocket, highlighting key residues mediating inhibition. In mouse macrophage co culture, sub inhibitory levels of SQ109 restored host cell viability by blocking intraphagosomal *C. albicans* filamentation. Finally, we highlight that SQ109 showed significant therapeutic efficacy in a mouse model of Trichophyton mentagrophytes dermatomycosis and *C. albicans* biofilm rat catheter model. Overall, SQ109 emerges as a promising repurposed drug with broad antifungal activity and anti virulence properties.

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Fungal Endophytes for Potential Biocontrol of Hemlock Woolly Adelgid
Fanning, Juliana and Kernaghan, Gavin
Mount Saint Vincent University

Eastern hemlock (*Tsuga canadensis*) is a foundational conifer species with a critical ecological role in North American forests. However, there has been recent widespread population decline due to the invasive hemlock woolly adelgid (HWA; *Adelges tsugae*), a sap-feeding insect that causes needle loss, reduced growth and tree mortality. Current management strategies including pesticides and natural predators have limitations, including negative environmental impacts and lack of testing in cold climates. Fungal endophytes isolated from white spruce trees have exhibited toxigenic properties against eastern spruce budworm (*Choristoneura fumiferana*), demonstrating that endophytes can serve as viable biological control agents for insects. In the current study, endophytes isolated from Nova Scotia hemlock were tested for anti-insect properties using a *Drosophila melanogaster* bioassay to demonstrate repellent effects of methanolic extracts of endophyte cultures. The results support the potential of hemlock endophytes as environmentally safe biocontrol agents for long-term mitigation of HWA damage in Nova Scotia.

AMF identity and plant host species interact to determine soil bacterial community structure
Ferguson, Robert*; Zhang, Rui; Whitehead, Dean; Mugambi, Ken; Poulain, Alexandre; Lapen, David; Corradi, Nicolas
University of Ottawa

Different species of arbuscular mycorrhizal fungi (AMF) possess distinct hyphae-associated bacterial communities. We hypothesized that the effect of AMF genetic identity on the soil bacterial community is driven by fungal phenotype and is independent of plant host species. Two plant species (medic and sudan grass) were inoculated with eight strains of *Rhizophagus irregularis*. In medic, AMF strain was a significant driver of soil bacterial community structure, and different AMF strains enriched or depleted distinct bacteria at a broad taxonomic level. In sudan grass, AMF strain was not a significant driver of soil bacterial community structure, and enriched or depleted bacteria were consistent across AMF strains at a narrow taxonomic level. Our results show for the first time that even at the level of fungal strain, AMF can significantly alter the surrounding soil bacterial community, though the nature of this effect is dependent on plant host species.

A genomic view of hypermutation potential in *Candida auris* drug resistance
Firer, David*. Cauldron, Nicholas. Rhodes, Johanna. Cuomo, Christina.
Brown University

Candida auris is a globally emerging pathogen with unusually high rates of multidrug resistance. One potential driver of drug resistance evolution is hypermutation, wherein isolates mutate at elevated rates due to dysfunctional DNA repair mechanisms, such as mismatch repair (MMR). This elevated rate may lead to the accumulation of resistance-conferring mutations. As such, global characterization of *C. auris* hypermutation is essential to understanding the rapid emergence of multidrug resistance. We therefore identified mutational and phylogenetic signatures of hypermutation in 800 clinical isolates with published antifungal resistance data across all *C. auris* clades, revealing 179 candidate hypermutants harbouring frameshift or nonsynonymous MMR gene mutations. Mapping drug resistance profiles to candidates in clinically severe clades revealed associations of hypermutation with increased amphotericin B and multidrug resistance. Ultimately, this study offers novel insights into the global prevalence of hypermutation and begins to reveal its relationship to drug resistance evolution in *C. auris*.

A genome-scale CRISPRi approach to dissect gastrointestinal colonization in *Candida albicans*
Fogal, Meea. Hendriks, Anthony. Wensing, Lauren. Despres, Philippe. Gervais, Nicholas.
Hammer, Merle. Jacobsen, Ilse. Shapiro, Rebecca
University of Guelph

Candida albicans is a commensal member of the human microbiome that colonizes the gastrointestinal tract but can also serve as a source of severe systemic infection in susceptible individuals. Despite extensive research on its virulence and pathogenesis, the genetic basis of gastrointestinal colonization and commensalism remains poorly understood. To address this, we developed the first genome-scale pooled CRISPR interference (CRISPRi) library in *C. albicans*, comprising approximately 13,000 unique strains targeting ~90% of annotated genes. By tracking changes in strain abundance under selective pressures, this platform enables systematic analysis of gene-specific fitness contributions. We validated the library through in vitro functional genomic screens across nutrient-rich and physiologically relevant carbon sources, identifying context-dependent fitness requirements. We also applied the library in a murine gastrointestinal colonization model to identify genes required for colonization and persistence, establishing a versatile resource for functional genomics in *C. albicans*.

Exploring the use of exogenous double-stranded RNA for curing white pine blister rust
Francisco, Christine Joyce* and Hamelin, Richard
University of British Columbia

Cronartium ribicola is an obligate biotrophic rust fungus that causes white pine blister rust (WPBR), a disease responsible for severe declines in ecologically important five-needle pine populations across North America. Its complex heteroecious life cycle alternates between five-needle pines and alternate hosts (e.g., *Ribes* spp.), complicating disease management. RNA interference (RNAi), induced by exogenous double-stranded RNA (dsRNA), has emerged as a promising strategy for controlling fungal pathogens through targeted gene silencing. dsRNA treatments have successfully suppressed infection in other rust, and related species possessed conserved RNAi machinery. We hypothesize that *C. ribicola* has a functional RNAi pathway and can internalize exogenous dsRNA, enabling silencing of genes required for growth and pathogenicity. This project will (1) identify RNAi-associated genes in *C. ribicola*, (2) confirm uptake of exogenous dsRNA in vitro, and (3) assess dsRNA-mediated gene silencing during infection in planta. Findings will support development of sustainable RNAi-based management strategies for WPBR.

Fungal functional ecology across a dissolved organic carbon gradient in Canadian lakes
Gauthier, Joanna*; Chen Wen, Soria-Píriz, Sara; Shahabinia, Amir Reza; Valadez Cano, Cecilio; Garner, Rebecca; Pick, Frances R; del Giorgio, Paul; Grossart, Hans-Peter; Walsh, David; Xenopoulos, Marguerite A
Trent University

Aquatic fungi play critical roles in organic matter (OM) decomposition, yet their ecological functions remain understudied in lakes. To determine how fungal functional gene diversity relates to dissolved organic matter (DOM) and environmental gradients, we applied shotgun metagenomics and measured OM chemical composition in pelagic surface water of 241 lakes sampled as part of the NSERC Canadian LakePulse Network. DOM composition varied from terrestrially-derived, aromatic, and humic compounds to more autochthonous and agriculturally-influenced signatures. Our findings reveal strong spatial and environmental structuring of fungal gene profiles. Highly oxygen-unsaturated DOM was negatively associated with gene richness and significantly correlated with gene composition. Gene richness also declined in higher lake trophic states, based on total phosphorus. Lake physicochemistry and DOM explained more variation in gene composition than land use or watershed characteristics. Our study provides a valuable opportunity to examine fungal functions across environmental gradients in lakes.

Chromosome-scale CRISPR screening reveals secretory trafficking as a driver of aneuploidy-mediated antifungal tolerance

Gervais, Nicholas C*. Wensing, Lauren F. Chhina, Manini. Fogal, Meea. Després, Philippe C. Gerstein, Aleeza C. Shapiro, Rebecca S.

University of Guelph

The gain or loss of chromosomes in eukaryotes often drives beneficial phenotypes by altering the expression levels of hundreds of genes. However, the genetic basis of most aneuploidy-mediated phenotypes remains poorly understood. The leading cause of human fungal infections, *Candida albicans*, frequently acquires extra copies of chromosome R (ChrR) following exposure to azole antifungals, resulting in heightened antifungal tolerance. Here, we combine RNA-seq with parallel CRISPR activation and CRISPR interference screens to systematically identify the ChrR genes contributing to azole tolerance. Using multiplexed CRISPR-dCas12a tools, we further demonstrate that the secretory pathway regulators SEC4 and YPT31 are both necessary and sufficient for ChrR-mediated azole tolerance. By leveraging the first CRISPRa screen in a fungal pathogen, our work functionally dissects one of the most common aneuploidies observed in *C. albicans*, and provides mechanistic insight into the molecular basis of antifungal tolerance, establishing a framework for studying aneuploidy-mediated phenotypes across eukaryotes.

Emergence of Botryosphaeriaceae pathogens in wild olive populations in southern Spain: first report and epidemiological implications

Guerrero-Páez Francisco Abel*, Campos-Figueras Rafael , Márquez-Pérez María I., Montes-Osuna Nuria, Moral Juan

University of Córdoba, Department of Agronomy

Wild olive (*Olea europaea* subsp. *europaea* var. *sylvestris*) populations are key reservoirs of genetic diversity in Mediterranean ecosystems. In November 2024, branch canker and dieback symptoms were observed in a natural stand in southern Spain (Cádiz), with 5% incidence and severe canopy decline (30–45%). Fungal isolates obtained from symptomatic tissues were identified as *Neofusicoccum parvum* and *Diplodia olivarum* based on morphology and multilocus sequencing (ITS, β -tubulin and EF1-a), showing 100% identity with reference strains. Phylogenetic analyses confirmed their taxonomic placement. Pathogenicity assays on wild olive and the susceptible cultivar ‘Gordal Sevillana’ induced cankers within one month, fulfilling Koch’s postulates. This study represents the first report of these pathogens on wild olive in Spain and highlights their potential epidemiological role as a bridge between wild and cultivated hosts, with implications for disease management and breeding programs.

Development of an automated pipeline for fungal-based biomanufacturing
Halder, Viola*, Kargar, Pegah, Quach, Angela, Melgar, Mindy Gold, Nicholas, & Benoit-Gelber, Isabelle
Concordia University

Aspergillus niger is an important filamentous fungus used in industrial production of enzymes, organic acids, and bioactive secondary metabolites encoded by biosynthetic gene clusters (BGCs). Despite its biotechnological significance, genetic manipulation and functional screening of *A. niger* production strains remain labor-intensive and inefficient. Here, we describe the development of an automation workflow that integrates *A. niger* transformation, colony selection, and downstream phenotyping into a unified pipeline. Using CRISPR–Cas9-mediated gene editing and PEG-mediated protoplast transformation, we optimized liquid-handling–assisted protocols to enable automated and high-throughput processing of multiple strains. Automated DNA assembly, transformation setup, and selective recovery coupled with colony screening and phenotype-based assays. This workflow reduces hands-on time, improves reproducibility, and enables direct linkage of genotype to phenotype under defined conditions. Together, these results demonstrate a scalable platform for engineering and screening *A. niger* pathways, thereby accelerating the discovery and optimization of fungal products, including proteins and secondary metabolites.

Elucidating novel epistatic interactions associated with *Candida albicans* echinocandin resistance
Hendriks Anthony*, Fogal Meea, Shapiro Rebecca.
University of Guelph

Antifungal resistance remains a major challenge in the treatment of *Candida albicans* infections. This holds true for the echinocandins, where resistance arises from single-point mutations in the FKS1 gene, impairing drug binding and reshaping cellular fitness and regulatory pathways. To investigate the genetic basis of echinocandin resistance, we combined an echinocandin-resistant *C. albicans* mutant isogenic to a standard laboratory strain with the Shapiro lab’s regulatable CRISPR interference (CRISPRi) system. Validation of known calcineurin-dependent interactions demonstrated the utility of this approach, while characterization of candidate genes revealed strain-specific interaction profiles consistent with regulatory network reorganization in the resistant context. These findings support a model whereby development of resistance is accompanied by substantial rewiring of cellular regulatory networks. Finally, ongoing genome-wide CRISPRi screening is expanding this interaction landscape, uncovering novel determinants of the resistant phenotype. These findings highlight the complex regulatory restructuring in echinocandin-resistant *C. albicans* and provide a foundation for uncovering genetic vulnerabilities in drug-resistant strains.

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Multiscale Habitat Assessment of the Blue Felt Lichen (*Pectenia plumbea*): Identifying Critical Habitat Characteristics across Spatial Scales in Central Newfoundland

Riley Henniffent*, Justin Hodge, Dean Gillingham, Barry Francis, Francis Skeard, Ben Feltham, R. Troy McMullin and Yolanda F. Wiersma

Memorial University of Newfoundland and Labrador

Pectenia plumbea (blue felt lichen) is an epiphytic cyanolichen. In North America, it is mostly restricted to the Canadian Atlantic provinces, where it is federally listed as Special Concern. The broad environmental conditions defining its habitat are high atmospheric humidity, available liquid water, and availability of mature deciduous trees with bark pH > 5. The ecological factors and multi-scalar interactions influencing these conditions, and thus the distribution of *P. plumbea*, remain poorly understood. We assessed relationships between *P. plumbea* and environmental predictors across two spatial scales by modeling presence/absence, size, and abundance using sets of competing models. This research is in collaboration with members of Qalipu First Nation and is part of a larger effort to establish an Indigenous Protected and Conserved Area in central Newfoundland. Our findings help further delineate the distribution of *P. plumbea* and contribute to species-at-risk objectives to identify critical habitat for this species.

Keystone and one-trick gene families: lessons from more than 400 million years of yeast evolution

Hittinger, Chris Todd*

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Over the course of more than 400 million years, the ancient yeast subphylum *Saccharomycotina* has radiated into over 1,000 known species. The Y1000+ Project (<http://y1000plus.org>) recently published the genomes, quantitative phenotypic data, and a genotype-phenotype map for essentially every known species. Here, we will highlight recent discoveries related to two different kinds of gene families: one-trick gene families that control a single carbon utilization trait and keystone gene families that affect multiple carbon utilization traits. The most impactful keystone gene family encodes alpha-glucoside transporters, which controls MALtose consumption and a dozen other traits. We will also highlight the Leloir GALactose catabolic pathway, which is as a one-trick gene family that has been lost frequently and regained a few times by lateral gene transfer. Even for galactose metabolism, complexities remain because some yeasts have an alternative altGAL pathway that uses oxidoreductive reactions to consume galactose.

Mechanisms of oxidative stress resistance in diverse yeast species

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Yeasts encounter oxidative stress externally through their interactions with other organisms or internally from their own mitochondrial metabolism. Therefore, we expect that yeasts have evolved stress resistance mechanisms according to their niches. We measured the growth of diverse yeast species in the reactive oxygen species (ROS) inducing compound, tert-butyl hydroperoxide, and found that the most resistant species were widely distributed across the phylogeny. A random forest algorithm identified gene family expansions that were predictive of ROS resistance. The most predictive features were experimentally validated through overexpression or deletion strategies. This provided an overview of the convergent genetic mechanisms driving natural diversity of ROS resistance across yeasts. We are now moving into more detailed studies in specific species by evolving novel ROS resistance or understanding the environmental cues which influence resistance. Altogether, this is providing new insights into the genetic mechanisms of ROS resistance across the yeast subphylum.

Capturing the yeast: development of methods to isolate yeasts from complex samples

House, Brianna*; Rezaei, Zahra; Roth, Susan; Hameid, Abbas; Chouteau, Laurine; Kamaliddin, Claire

University of Alberta, FoPPS

Candida albicans is a commensal and pathogenic yeast that causes a broad range of infections, from superficial mild infections to severe bloodstream infections. In addition, *C. albicans* rapidly adapts to antifungal drugs, and antifungal drug susceptibility testing is crucial to tailor the therapeutic regimen. A limitation in human health is the relatively “low” yeast burden in samples (compared with human cells or bacteria), which makes agnostic sequencing methods less sensitive or culture-based enrichment more lengthy. To overcome these limitations and improve turnaround time in surveillance and diagnostics, we are developing a new sample enrichment method to selectively isolate yeast from primary complex samples. These method combine filtration approaches (size exclusion) and density gradient separation. Yeast recovery is assessed using culture, Colony-Forming Unit (CFU) counts, and quantitative PCR. To date, our results have shown that we recover viable yeast, and we are currently testing complex matrices to assess the method’s versatility.

A Survey of Ectomycorrhizal Fungi in Carolinian Canada

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University of Western Ontario

The aim is to address a knowledge gap about the composition of ectomycorrhizal (ECM) fungi communities in the Carolinian range of Southern Ontario and answer the question: What is the community composition of ECM and what factors may influence it?

Roots samples were collected from trees that are known ECM hosts at sites across Southern Ontario. Two sets of primer pairs were used to confirm the host identity and what fungi species are present in association with the host tree's roots. Soils cores and metadata were collected and compiled for analysis.

It was found that sample site and host tree significantly affected ECM community composition. It was also found that that land use history, and edaphic factors (such as calcium concentration) also had effects on alpha diversity of the ECM community. Many interesting species were identified, including *Pulchroboletus sclerotiorum*, a species not previously found in Canada.

Differential requirement for the Ire1 luminal and transmembrane domains in *Candida albicans* drug resistance and pathogenicity

Samuel Stack-Couture, Nathan Towriss, Anna Kalabina*, Iwona Skulska, Julie Genereaux, Rebecca S. Shapiro, and Patrick Lajoie
Western University

Candida albicans is the most common cause of invasive fungal disease in humans, and its ability to cause infection depends on the unfolded protein response (UPR), a stress pathway that helps cells cope when the endoplasmic reticulum becomes overwhelmed. The UPR is controlled by a single sensor, Ire1, which can be switched on in two different ways: through its luminal domain, which detects misfolded proteins, or through its transmembrane domain, which senses disturbances in the lipid membrane. Whether these two activation modes do different jobs in a fungal pathogen — where the cell membrane and cell wall are themselves the targets of front-line antifungal drugs — has not been explored.

To separate these two functions, we engineered a *C. albicans* strain expressing a version of Ire1 lacking an intact luminal domain, leaving it able to sense membrane stress but blind to misfolded proteins. This strain still grew in the presence of the azole antifungals fluconazole and miconazole, which target the membrane, but failed to grow under cell wall stress, echinocandin treatment, or elevated temperature. It was also unable to switch to its filamentous form, build biofilms, or cause full disease in a *Caenorhabditis elegans* infection model. RNA sequencing showed only modest changes to gene expression under normal conditions, indicating that the luminal domain matters most under stress.

Together, these findings show that membrane-stress adaptation can be uncoupled from the disease-causing functions of Ire1, suggesting that targeting the protein-sensing arm of the UPR could weaken *C. albicans* virulence and cell wall–drug tolerance while leaving azole responses intact.

What's in a name? Describing orchid mycorrhizal fungi as an essential step in *Cypripedium arietinum* conservation in Nova Scotia

King, Katie*; Kernaghan, Gavin; Walker, Allison
Acadia University

For the endangered Nova Scotia population of *Cypripedium arietinum* (R. Br), Ram's Head Lady's Slipper (RHLS), Orchidaceae, crucial biological information for conservation planning is lacking. Establishing an ex situ research population would fill these knowledge gaps. However, this is not possible without more research on RHLS mycorrhizal relationships. Orchids require Orchid Mycorrhizal Fungi (OMF) for seed germination and nutrient absorption. Our objective was to identify the OMF required for RHLS survival in Nova Scotia. We used both Sanger and PacBio sequencing to identify over 180 fungal species and over 20 in OMF genera, but only 4 of these were formally described species. Most notably, species in the prominent orchid symbiont genus *Tulasnella* (Basidiomycota) were found at all sites, but none had formal species descriptions. Describing new OMF species from these findings will provide additional taxonomic information for future studies and is an essential step towards protecting this unique orchid population.

Analyzing the Antimicrobial Activity of Manitoban Medicinal and Culturally Important Plant Endophytes

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University of Manitoba

This study was performed to measure the antimicrobial activity of a variety of endophytes that grow in medicinal and culturally important plant species such as *Zizania palustris*. We hypothesize that medicinal plants exhibit antimicrobial activity as a result of their associated endophytes. This goes along with Indigenous knowledge of the benefits of medicinal plants and has been shown in other species such as the chemotherapy drug paclitaxel. Samples were collected throughout Manitoba and cultured on PDA plates before being transferred onto LB agar plates inoculated with *E. coli*. Inhibition was defined as a ring of any size surrounding the fungal growth where there is no *E. coli*. Samples exhibiting inhibition were then sequenced to get their phylum. Our preliminary results suggest that 43 of the sampled endophytes exhibit antimicrobial properties. This can further be used to develop antibiotic therapeutics as more bacteria are developing resistances to existing antibiotic treatments.

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Battleground chloroplast, a temporal and spatial meta-analysis of *Zea mays* chloroplast gene expression during biotrophic interaction with *Ustilago maydis*
Kretschmer, Matthias*, Lee, Christopher, Kronstad, James
UBC

Ustilago maydis is a biotrophic fungal pathogen of corn and leads to chlorotic tumors on all plant tissues above soil level. Chloroplasts are important for primary plant metabolism as well as secondary metabolite biosynthesis and plant defense activities including plant defense hormone formation. The importance of chloroplasts for plant growth and health makes them prime targets for pathogens during plant infection. During tumor formation induced by *Ustilago maydis* at 10 days post infection of maize seedlings, chloroplast functions especially related to photosynthesis were found to be down regulated in gene expression. Since our initial analysis, community resources such as genome annotations, gene expression time courses and tissue specific gene expression for the host and the pathogen have evolved. We combined these available resources to elucidate the changes in chloroplast gene expression during chloroplast development in the light of the infection process and in different tissues such as the mesophyll and bundle sheath tissues. During infection the expression of chloroplast development genes leading to activation of photosynthesis genes are down regulated. The majority of changes appear after 4 days of infection, coinciding with the onset of tumor development. Similar gene expression pattern for chloroplast development during infection were found in mesophyll and bundle sheath tissues. In this analysis we highlight the temporal and spatial gene expression changes seen in chloroplasts during interaction with a biotrophic fungal plant pathogen.

From Environmental Fungus to Human Pathogen: Unraveling Virulence in *Talaromyces marneffei*

La, James* and Semper, Cameron
University of Calgary

Talaromyces marneffei is a thermally dimorphic pathogenic fungus endemic to regions of China and Southeast Asia, primarily known for causing talaromycosis—a life-threatening neglected tropical disease. Recent genomic analyses have identified a large arsenal of genes linked to the production of secondary metabolites; however, the majority of these genes and the metabolites they produce in *T. marneffei* remain uncharacterized. This project focuses on investigating the secondary metabolome of *T. marneffei* using a combinatorial approach consisting of computational analysis, genetics, and microbiology. Computational analysis revealed *T. marneffei* encodes ~52 biosynthetic gene clusters (BGCs) linked to secondary metabolism, four more than the previous estimate. Syntenic analysis, combined with publicly available RNA sequencing data capturing the fungus under thermal conditions reflective of its environmental and human host niches, can identify candidate BGCs involved in *T. marneffei* virulence. Together, these approaches advance our understanding of secondary metabolism in an important human pathogen and to highlight its potential as a source of natural products.

Bioprospecting: Investigating the Toxin Droplets of *Pleurotus*
Lloyd, Makayla*; Sinka, Jessica; Bernards, Mark; Thorn, Greg
University of Western Ontario

Pleurotus are predatory fungi that paralyze nematodes using microscopic toxin droplets. Although these toxin droplets were described several decades ago, to date, the regulation of toxin droplet abundance has been poorly understood and the contents of the droplets under-characterized. Using twenty strains spanning six species, we quantified toxin droplet abundance and characterized droplet chemistry with GC-MS sampling. As 3-octanone has been identified as potential molecule of interest, we conducted a targeted analysis of 3-octanone across all strains. We show that most *Pleurotus* strains respond to the presence of nematodes through an increase in toxin droplet production. For the first time, we report the presence of 3-octanone in *P. eryngii* and *P. populinus*. Along with the detection of structurally related ketones and additional classes of molecules with nematocidal potential, our GC-MS data provide evidence that *Pleurotus* uses a cocktail of secondary metabolites rather than a single toxin to paralyze nematode prey.

Pathogens in an endophyte world: The presence of a phytotoxin biosynthetic gene cluster reflects host-association strategy in *Xylaria* genera

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Michigan State University

Unlike other Sordariomycete lineages, fungi in the genus *Xylaria* (*Xylariaceae*) are prolific host-generalist endophytes rarely identified as plant pathogens, despite their exceptional biosynthetic capabilities. Although phytotoxic cytochalasins are implicated in all known pathogenic *Xylaria*, the genomic elements regulating their synthesis and evolutionary history have not been elucidated. As such, we performed long-read sequencing and de novo assembly for several pathogenic and endophytic *Xylaria* isolates, integrating them with publicly available genomes for comparative analyses. While biosynthetic gene cluster, CAZyme, and putative effector counts were similar across species and lifestyles, a single undescribed cytochalasin cluster (xylachalasin) was found to be present in nearly all pathogenic lineages. Additionally, pathogenic *Xylaria* formed distinct subclades within the genus, while endophyte-dominant lineages displayed xylachalasin loss events that coincided with non-pathogenicity and chromosomal rearrangements. This work in total provides novel insight into the evolutionary regulation of BGCs underlying the pathogen-endophyte lifestyle continuum in *Xylaria* fungi.

Establishment rates and species composition of AMF in *Plantago maritima* and *Triglochin maritima* in Canadian and German salt marshes

Meents, Mareike*; Albach, Dirk C.; Lundholm, Jeremy T.; Walker, Allison K.

Carl von Ossietzky University of Oldenburg

Salt marshes are increasingly threatened by climate change and pollution. Research into fungal communities in various salt marsh plants may benefit future efforts to restore salt marshes along the coasts of Canada and Germany. We will analyze arbuscular mycorrhizal establishment rates and species composition in the roots of *Plantago maritima* and *Triglochin maritima* on Canadian and German salt marshes. Samples will be taken from the coast of the North Sea in Lower Saxony, the Inner Bay of Fundy and the Atlantic coast of Nova Scotia. 18 specimens will be collected per species, half of which will be taken from the lower boundary of their distribution in the salt marsh. The other half will be taken from the upper boundary of their distribution. AMF establishment rates will be quantified using root staining and microscopy. Species composition will be analyzed using Illumina MiSeq. Results will inform future restoration practices.

Mapping the genetics of parasex in *Candida albicans*

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Meiotic recombination drives genetic diversity and facilitates adaptation in eukaryotes. However, meiosis is absent in *Candida albicans*; instead, *C. albicans* performs parasex, an irregular form of ploidy cycling that achieves the conventional meiotic outcomes of independent assortment and segregation. Briefly, in the parasexual cycle, two diploid cells fuse via mating to form a tetraploid. While these tetraploid intermediates can stably propagate, gametogenesis-promoting conditions trigger genetic crossovers and uncoordinated ploidy reduction through successive mitotic divisions. Surviving progeny are typically aneuploid, highly recombinant, and show greater phenotypic variability than the original diploid parents. While the functional parallels between parasex and meiosis have recently been resolved, the molecular factors required for parasex remain largely unknown. To address this gap, I will define loci that mediate parasex in *C. albicans* via genetic screens. As an orthogonal approach, I will use phylogenetic analysis to infer genes associated with different sexual programs among related fungal pathogens.

Functional genomic analysis reveals genes important for *Candida albicans* fitness in response to antifungal-induced stress

Pavlova Veronika*, Zhang Xiang, Hossain Saif, Myers Chad, Robbins Nicole, Cowen Leah

University of Toronto

Antifungal therapies against invasive fungal diseases are limited to three drug classes, and their efficacy is compromised by the development of drug resistance. Manogepix and nikkomycin Z are emerging antifungals with potential to augment our limited repertoire of antifungals. This project aims to identify and characterize *Candida albicans* genes that modulate susceptibility to established and emerging antifungals by leveraging a large-scale collection of *C. albicans* conditional-expression mutants. We identified genes that modulate susceptibility to caspofungin, fluconazole, nikkomycin Z, and manogepix. Further investigation of two genes, SNF6 and PAT1, for which transcriptional repression conferred hypersensitivity to manogepix, implicated the SWI/SNF complex as a general regulator of antifungal stress, and Pat1 as a specific regulator of manogepix-induced stress through P-body formation. Additionally, we showed that transcriptional repression of PRP8 and SMD2 impairs mRNA splicing of the core septin, resulting in septin mislocalization and altered cell wall homeostasis, increasing sensitivity to nikkomycin Z.

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Immunogold Localization of Indole-3-acetic acid (IAA) in Metarhizium Species During Insect Pathogenesis & Endophytic Colonization

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Brock University

Certain *Metarhizium* species produce indole-3-acetic acid (IAA) during insect pathogenesis and endophytic colonization. IAA has been implicated in enhanced insect virulence through increased formation of fungal infection structures, and increased lateral root formation during plant colonization. Although fungal-derived IAA is well documented, its ultrastructural localization within *Metarhizium* remains largely unexplored. Plant hosts (*Triticum aestivum*; wheatgrass) and insect hosts (*Galleria mellonella* larvae and *Locusta migratoria* nymphs) were inoculated with generalist and specialist *Metarhizium* species. Following host colonization or infection, immunogold labelling was used to reveal IAA signal around fungal cell walls. During insect cuticle pathogenesis, IAA labelling associated with penetration structures (appressoria), colonization structures (internal hyphae), and fungal outgrowth from mummified cadavers (conidia). In early-stage root colonization, IAA labelling was associated with fungal structures (conidia and hyphae) and the phytohormone was detected near adjacent root tissue. Strong labelling around intra-cuticle hyphae suggests a potential role for IAA during post-penetration insect infection.

Taking stock of biodiversity data shortfalls for ectomycorrhizal fungi in Canada

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Ectomycorrhizal (EcM) fungi underpin the diversity, maintenance, and functioning of northern forest ecosystems and play critical roles in global carbon and nutrient cycling. However, substantial data shortfalls limit our current understanding of their biodiversity. This is especially true in Canada, where rapid environmental change may impact the distribution and functioning of EcM fungi and their habitats. Here, we quantify and discuss seven biodiversity data shortfalls that constrain our knowledge of EcM fungi in Canada. We compiled a joint dataset of publicly accessible fungal sequence data, which included over 10,473 records representing 692 species hypotheses. We cross-referenced these against other data sources of abundance, functional trait, genomic, and species interactions. Broadly, we found that data on EcM fungal distributions, abundance patterns, evolutionary relationships, environmental niches, and host-interactions remains severely limited. Our assessment provides the foundation for a coordinated, pan-Canadian sampling effort that can be optimized to address multiple shortfalls simultaneously.

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Biocontrol of postharvest fungal pathogens in pome fruit using *Bacillus* spp.

Popa, Julia*; Luong, Olivia; Abu Odeh, Salma A.; Avis, Tyler, J.

Carleton University, Department of Chemistry

Postharvest fungal diseases, such as brown rot caused by *Monilinia* spp. and Sphaeropsis rot caused by *Sphaeropsis pyriputrescens*, contribute to the spoilage of stored pome fruit. Increased resistance to fungicides has highlighted a need for alternative control methods. Antagonistic bacteria have shown the potential to control fungal diseases. We investigated the effects of *Bacillus velezensis* against *M. laxa* and *S. pyriputrescens* in vitro, and in vivo using apples and pears. Additionally, we examined the antifungal effects of metabolites extracted from *B. velezensis*. We found that *B. velezensis* strains inhibited the growth of *M. laxa* and *S. pyriputrescens* in vivo and in vitro. Extracts containing *B. velezensis* metabolites inhibited fungal growth in vitro. LC/MS analysis confirmed the presence of iturin, fengycin, and surfactin lipopeptides in different *B. velezensis* strains responsible for antagonistic activity. This work highlights the potential of *Bacillus* spp. as biocontrol for postharvest fungal diseases of pome fruit.

Biocontrol effects of compost tea bacteria against postharvest fungal disease of tomato fruit (*Solanum lycopersicum* L.)

Popescu, Irina*; Bakker, Charlotte E.; Avis, Tyler J.

Carleton University

The control of fungal phytopathogens, including tomato disease-causing *Alternaria alternata*, *Alternaria solani* and *Botrytis cinerea*, relies on synthetic fungicides. A more sustainable approach, however, is presented through microbial biocontrol agents. *Bacillus velezensis* SH1 and SH2 and *Pseudomonas azotoformans* SH3, isolated from disease-suppressive compost tea, were tested for inhibition of mycelial growth and suppression of tomato disease. All bacteria inhibited growth of the tested fungi, especially *P. azotoformans* SH3. However, disease lesion suppression varied by pathogen and tomato cultivar. Cell-free culture filtrates from all bacteria inhibited *B. cinerea* mycelial growth, whereas mainly *B. velezensis* SH1 inhibited growth of *Alternaria* spp. Among bacterial precipitates, *B. velezensis* SH1 was the best treatment overall, while *P. azotoformans* SH3 precipitates were ineffective. LC-MS analysis confirmed both *Bacillus* bacteria produce fengycins, iturins and surfactins. Antifungal activity was likely imparted through the release of these antifungal metabolites, although the role of the compounds was variable.

Cascading damage to *Candida albicans* cells through thioredoxin reductase loss

Qi, Wanjun*. Roy, Udit. Cai, Chunhui. Acosta-Zaldívar, Maikel. Mascio, Jossalyn. Asara, John. Fierro, José. Andrés, María. Sun, Liang. Köhler, Julia.

Boston Children's Hospital

Candida albicans is the most common invasive human fungal pathogen. We show that *C. albicans* thioredoxin reductase, Trr1, is an attractive antifungal target: it is essential at human body temperature, and fungal and human thioredoxin reductases are structurally divergent, predicting high selectivity of fungal-targeted inhibitors. TRR1 depletion directly impairs oxidative damage repair but also triggers cascading disruption of stress signaling and metabolic adaptation. Impaired oxidative stress endurance and consequent amphotericin hypersensitivity are anticipated effects of TRR1 depletion. We unexpectedly find it also sensitizes *Candida* to cell wall stress and to a first-line echinocandin antifungal agent. TRR1-depleted cells have decreased cell wall glucan content. Driven by demand for NADPH reducing equivalents, these cells increase glucose-6-phosphate flux into the pentose phosphate pathway (PPP) as evinced by sharply elevated activity of the PPP's first, rate-limiting enzyme. Since UDP-glucose- the substrate for cell wall glucan biosynthesis - is also derived from glucose-6-phosphate, we propose that metabolic pathway competition for this shared intermediate between NADPH production and cell wall glucan biosynthesis underlies the cell wall weakness of TRR1-depleted cells. Decreased activity of a key UDP-glucose biosynthetic enzyme supports this mechanism. Trr1 loss of function further drives feed-forward damage cycles: accelerated respiration which increases reactive oxygen species, reduced gluconeogenesis which further limits glucose-6-phosphate availability and suppressed oxidative and cell wall stress signaling pathways. Our findings support Trr1 inhibition as a promising approach to improved treatment of *C. albicans* infections.

Molecular quantification of the wheat leaf spot complex in Alberta in 2025

Tahiat, Rahman*

Agriculture and Agri-Food Canada

The leaf spot complex is a major disease of wheat in Canada and worldwide, and is caused by 7ve primary fungal pathogens: *Pyrenophora tritici-repentis*, *Zymoseptoria tritici*, *Parastagonospora nodorum*, *Bipolaris sorokiniana*, and *Parastagonospora pseudonodorum*. Identifying and quantifying individual species within this complex remains challenging due to the overlapping foliar symptoms and cooccurrence of these species in the same infected tissue. In this study, the aim is to measure the prevalence and abundance of these species at the commercial farm level. A total of 62 wheat leaf samples collected from Alberta in 2025 were analyzed using TaqMan probe-based qPCR assays targeting the β -tubulin 1 (*tub1*) gene to detect and quantify these 7ve species. The results showed that *P. tritici-repentis* was highly prevalent and detected in 60% of tested samples with a mean DNA concentration of 0.28 pg/ng. Among the *Parastagonospora* species, *P. pseudonodorum* was highly prevalent in 87% of samples (mean 0.14 pg/ng) and was frequently detected in asymptomatic leaf tissues, indicating widespread prevalence. In contrast, *P. nodorum* occurred only in 17% of the samples (mean 0.29 pg/ng), while *B. sorokiniana* and *Z. tritici* were rare or below the detection limits. These findings provide essential baseline data to support disease monitoring and management for Alberta wheat growers.

Antifungal susceptibility profiles of *Microsporum canis* from the United States and Ontario, Canada

Rowjee, Lishita *

University of Guelph

Microsporum canis (*M. canis*) is a zoonotic dermatophyte responsible for approximately 90% of animal dermatophytosis (ringworm) cases and can also infect humans. Antifungal agents, including azoles (fluconazole, itraconazole, posaconazole, and voriconazole) and terbinafine, are commonly used for treatment. However, data on antifungal susceptibility in animal isolates remain limited. This study established susceptibility profiles for 85 *M. canis* isolates collected from Massachusetts, New Mexico, California, Colorado, and Ontario using broth microdilution testing and epidemiological cutoff values (UL-WT) determined by ECOFFinder. Fluconazole exhibited the highest MIC values, while voriconazole and terbinafine showed the greatest activity. Only one California isolate had an itraconazole MIC above the UL-WT, although no resistance classification could be made due to the absence of clinical breakpoints. No significant regional differences were observed for azoles, and Ontario isolates did not differ significantly from U.S. isolates. These findings provide baseline susceptibility data for monitoring emerging antifungal resistance in veterinary *M. canis* populations.

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Comparative Analysis of *C. albicans* and *N. glabratus* in response to acute boric acid exposure
Salama, Ola, Jones, Meaghan, Gerstein, Aleeza
University of Manitoba

Vaginal yeast infections affect approximately 75% of people with vaginas at least once in their lifetime and are primarily caused by *Candida albicans* and *Nakaseomyces glabratus*. While most patients respond to fluconazole treatment, some experience recurrent infections. Boric acid (BA) is commonly used as a second-line therapy for these cases. However, we still do not know its mechanism of action. *N. glabratus* is often treated clinically as a *Candida* species, prompting us to ask whether BA response is conserved between *C. albicans* and *N. glabratus*. We performed RNA-seq in both species following acute exposure to species-specific inhibitory concentrations of BA, and found that out of 2081 genes shared between the two species, only 61 overlapped, suggesting that BA response is not conserved between the two species. Our next step is to generate CRISPR mutants of the unique and overlapping top hits to determine their roles in withstanding acute BA exposure.

Do Co-occurring Coastal Dune Plants Share Their Root Fungal Partners?
Sanderson, Kenneth*;Richardson, Beth
Independent

Lechea maritima var. *maritima* (Cistaceae) is a COSEWIC Special Concern endemic restricted to coastal dune populations in New Brunswick and Prince Edward Island. The 2008 status report notes that *L. maritima* reliably co-occurs with the widespread dune shrub *Hudsonia tomentosa* (Cistaceae), but the role of root-associated fungi in shaping this habitat association is unknown. We used ITS metabarcoding of root samples from 19 paired sites in Prince Edward Island and New Brunswick to compare root fungal communities of the two hosts. *L. maritima* and *H. tomentosa* supported equally rich and largely overlapping fungal communities, sharing the ubiquitous ectomycorrhizal generalist *Cenococcum geophilum* at every site. Composition differed subtly by host (PERMANOVA, R^2 0.05, $p < 0.001$), with a *Cortinarius* (ECM) and a root-associated *Mycena citrinomarginata* consistently associated with *L. maritima*. The shared mycobiome suggests *L. maritima* is unlikely to be limited by host-specific fungal requirements.

Fungal Firefighters: Can Fungal Inoculation Reduce the Fire Risk of Waste Wood?

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Management of waste wood is a current and growing concern across Canada. The common practice of burning has become less attractive as its climate and ecological impacts become better known, and reduced snow cover makes winter burning less available. Rural communities creating fire breaks for wildfire risk mitigation face similar challenges, with large areas of mulched or chipped wood created that may take years to naturally decompose. In Alberta, the Town of Fox Creek and Portage College are investigating the use of native wood-decomposer fungi to reduce the fire risk of chipped wood, in cooperation with the Coldfire project based in Colorado. We have successfully isolated 101 strains belonging to 64 diverse wood-decay fungus species and are currently testing their abilities to break down white spruce wood chips under laboratory conditions at two moisture levels. The top-performing strains will be tested in field trials to begin in September 2026.

Spatial organization of chitin in chlorolichen and cyanolichen thalli

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Chitin is a structural polysaccharide in fungal cell walls and plays an important role in the integrity and organization of lichen thalli. Earlier studies suggested that chitin may be more prevalent in the hyphal walls of cyanolichens, while its occurrence and distribution may differ in lichens with green algal photobionts. However, the spatial organization of chitin within lichen thalli remains poorly explored using modern imaging approaches. This study compares chitin distribution in chlorolichens and cyanolichens by visualizing and quantifying chitin-associated fluorescence patterns across thallus regions. Using chitin-specific fluorescent staining and confocal laser scanning microscopy, we examined chitin localization in representative species from both photobiont types. We hypothesize that cyanolichens exhibit a more abundant and homogeneous chitin distribution than chlorolichens, potentially reflecting differences in nitrogen availability within the symbiosis. This work provides preliminary insight into fungal cell wall organization and structural diversity in lichen symbioses.

Boreal lichen photobiont networks: structure, stability, and vulnerability

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Lichens are often invoked as terrestrial analogs of coral–algal mutualisms, implying potential risks of symbiotic collapse. Unlike coral reefs, however, evidence for the vulnerability of lichen symbioses to environmental stressors remains mixed. Some studies suggest the existence of keystone algal symbionts, analogous to zooxanthellae, whose loss could destabilize entire communities; others emphasize the diversity and plasticity of these interactions, implying redundancy and resilience. To date, however, the absence of large-scale empirical datasets has precluded direct tests of these hypotheses. Using replicated high-throughput Illumina metabarcoding, we reconstruct the symbiotic network of a boreal lichen community, quantifying the specificity, stability, and modular structure of these associations. Through this analysis, we test key assumptions about how the organization of lichen photobiont guilds shapes community stability and vulnerability in the face of a changing climate.

Determining the mycorrhizal status and root-associated fungal diversity of Northern wild rice (*Zizania palustris*) via targeted amplicon sequencing

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Northern wild rice (*Zizania palustris*) is a macrophyte harvested from wild stands and cultivated paddies in central and eastern North America. Despite emerging agricultural interests, this plant's mycorrhization status and the diversity of its root-associated mycobiome remain unknown. Although the root-associated mycobiomes of macrophytes are poorly understood, arbuscular mycorrhizal fungi (AMF) are occasionally present. Since AMF are effective biofertilizers for wetland crops like white rice, the mycorrhizal status of wild rice in wild stands may be critical to its cultivation and restoration. Thus far, microscopy and sequencing of mesocosm-grown wild rice show that it can host AMF. Furthermore, wild rice collected from Manitoba wetlands contains AMF in the rhizosphere and aseptate hyphal colonization in the roots. To verify root mycorrhization and address whether the root mycobiome is a filtered subset of the rhizosphere mycobiome, we undertook targeted ITS amplicon sequencing of roots to complement rhizosphere data obtained from the same plants.

Decoupling competitive fitness and drug tolerance following *Candida albicans* adaptation to fluconazole

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Candida albicans, an opportunistic fungal pathogen, poses significant clinical challenges, in part due to its ability to rapidly adapt to antifungal drugs. Environmental stress can induce genomic change in *C. albicans*, but whether those changes are neutral or beneficial is often unclear. This study examined changes in competitive fitness, tolerance, and genomic variation in *C. albicans* lines evolved through serial bottlenecks under different fluconazole (FLC) concentrations (0.25-16 µg/mL). All evolved lines consistently exhibited higher competitive fitness and tolerance than the ancestral lines, except for FLC0.25. The frequency of aneuploidy (especially in chromosome R) increased with the evolved drug concentration, and gene ontology analysis revealed that genes were associated with hyphal growth in populations evolved under FLC16; ongoing work is evaluating corresponding phenotypic changes. These findings strongly demonstrate that fluconazole imposes a strong selective pressure on *C. albicans*, facilitating rapid adaptation that enhances competitive fitness even in repeatedly bottlenecked populations.

Role of Inositol Metabolism in drug resistance in *Candida albicans*

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Candida albicans is an opportunistic fungal pathogen causing 1.6 million infections annually, with roughly 200,000 deaths from systemic dissemination. Antifungal resistance is a growing clinical threat, yet few therapeutics exist. Inositol is essential for generating critical lipids, including phosphoinositides for signaling and glycosylphosphatidylinositol (GPI) anchors required for membrane integrity and virulence. It is imported via Itr1 or, during deprivation, synthesized de novo through INO1. Although membrane lipid composition influences antifungal susceptibility, the contribution of inositol metabolism remains uncharacterized. Deleting INO1 increased susceptibility across all major antifungal classes even in inositol-rich media, indicating that de novo biosynthesis lowers intrinsic susceptibility independent of exogenous supply. The effect of inositol availability differed among drug classes, and transcriptional profiling revealed class-specific regulation of inositol metabolism genes under antifungal stress. Together, these findings establish inositol homeostasis as a determinant of intrinsic antifungal susceptibility, with potential to reveal new therapeutic targets.

The conserved m6A methyltransferase IME4 regulates aspects of the *Candida albicans* parasexual cycle

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Candida albicans is a human fungal pathogen that lives as a commensal on mucosal surfaces but can cause invasive infections in immunocompromised individuals. *C. albicans* has a unique parasexual cycle that involves a phenotypic switch in MTL homozygotes known as the white-opaque switch to enable efficient mating, as well as a “parameiosis” in mating products that involves recombination and concerted chromosome loss. Our research has identified a role for the conserved RNA m6A methyltransferase IME4 (a meiosis regulator in the model yeast *Saccharomyces cerevisiae*) in the parasexual cycle of *C. albicans*. Mutants lacking IME4 have impaired opaque-to-white switching and increased mating, suggestive of a role for m6A in mediating switching to the white state and preventing aberrant mating. Supporting this idea, m6A levels increase during the opaque-to-white switching process, and IME4 expression is specific to MTL homozygous strains. Current work seeks to unravel the mechanism of IME4 and m6A-mediated switching.

Novel Transcriptional Profiling Approach to Study Para-Resistance in *C. albicans*

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Candida albicans is an opportunistic fungal pathogen responsible for ~70% of global fungal infections, however limited antifungals and increasing resistance complicate treatment. While genetic mutations contribute to antifungal resistance, they do not fully explain treatment failure. Evidence from clinical isolates suggests resistance can be reversible and heritable, supporting non-genetic phenotypic heterogeneity. Recently, para-resistance has been described as a transient, heritable and epigenetically regulated state induced by subtherapeutic fluconazole exposure, enhancing growth at MICs. Bulk RNA-sequencing across three isolates revealed distinct transcriptional programs, reflecting multiple regulatory circuits. Here, we optimized a high-throughput plate-based single-cell RNA-seq workflow to profile *C. albicans* across six fluconazole conditions, multiple replicates, and two para-resistant isolates to define acquisition and maintenance signatures. We profiled ~13,000 cells with preliminary results showing transient fluconazole exposure induces >20 transcriptionally distinct clusters, including DBP10-associated para-resistant populations. These experiments will resolve the heritable transcriptional programs and regulatory factors driving this state.

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Tracing early plant-fungus associations through plant-degrading enzyme evolution in fungi
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Through their interactions with plants, fungi have shaped ecosystems in consequential ways. However, whether these associations existed in freshwater ecosystems prior to plant terrestrialization remains unknown from the fossil record alone. To interact with plants and take up nutrients, fungi secrete enzymes that breakdown plant cell wall polysaccharides. Notably, pectins and xyloglucan are found only in the streptophyte lineage, comprising land plants and their immediate ancestors. Therefore, fungal pectinases and xyloglucanases can be used as markers to infer potential interactions between early plants and fungi. We used a comparative phylogenetic approach to reconstruct evolutionary histories of fungal enzymes, utilizing available genomes of terrestrial and chytrid fungi. Since bioinformatic predictions in chytrids continue to rely largely on experimentally characterized sequences from terrestrial fungi, we utilized high-performance liquid chromatography, enzyme assays, and RNA-seq experiments to provide evidence for enzyme function beyond bioinformatic inferences in the poorly known chytrid fungi.

Secondary pathogens as a comparative genomic filter for pathogenicity in the butternut canker pathosystem

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A concerning case of disease-driven species decline is in butternut (*Juglans cinerea* L.), a broadleaf tree species native to eastern North America and considered the most cold-hardy *Juglans* spp. The scarcity of butternut was catalyzed by an aggressive fungal pathogen, *Ophiognomonia clavignenti-juglandacearum* (Oc-j). Its commonly co-located secondary pathogen *Juglanconis oblonga* (Jc.o) however, seems to occupy the same niche with less aggressive canker expansion. To support the discovery of traits in the Oc-j-butternut interaction that can be manipulated to favour survival in butternut, we have generated high-quality annotated genomes for four geographically disparate isolates of Oc-j and one isolate of Jc.o. Using comparative genomic approaches we highlight presence/absence contrasts between gene superfamilies Oc-j and Jc.o which could contribute to differences in their interaction with butternut. Our resources support deeper characterization of the butternut canker interaction and demonstrate a promising comparative angle for identifying gene families that are important in pathogenesis.

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Force-sensitive regions of fungal adhesins guide de novo inhibitor design
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Candida albicans forms resilient biofilms on host tissues and medical devices, making infections difficult to treat. Als (agglutinin-like sequence) adhesin proteins on its surface contain a conserved amyloid-forming region (AFR) that is key for biofilm growth. Fluid forces encountered in the body are thought to structurally alter Als proteins, revealing their otherwise hidden AFRs and triggering amyloid-mediated cell-cell aggregation. Using site-directed mutagenesis and fluid-flow-based aggregation assays in a *Saccharomyces cerevisiae* model, we identified residues that govern force-dependent AFR exposure. With this knowledge, we employed a computational RFDiffusion pipeline to design a small library of miniprotein binders targeting these force-sensitive regulatory regions and the AFR itself. One particular binder significantly reduced aggregation under high-force conditions, demonstrating that interfering with AFR exposure can suppress fungal cell-cell adhesion. These findings establish the force-responsive regions of Als adhesins as promising antibiofilm targets and provide a framework for developing protein-based therapeutics against *C. albicans* infections.

Increasing Production of Ephedrine in *Saccharomyces cerevisiae* through Adaptive Laboratory Evolution and Nonconventional Yeast Screening
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(R)-phenylacetylcarbinol [(R)-PAC] is a precursor to ephedrine, a WHO essential medication used to treat hypotension. Industrial (R)-PAC production utilizes the fossil fuel derivative benzaldehyde, rendering production unsustainable. The yeast Ehrlich pathway offers a sustainable alternative by facilitating the catabolism of L-phenylglycine to (R)-PAC in *Saccharomyces cerevisiae*.

Here, adaptive laboratory evolution (ALE) and nonconventional yeast screening were used to improve L-phenylglycine utilization and (R)-PAC production. ALE yielded evolved strains with three-fold increase in (R)-PAC production. Whole genome sequencing revealed missense mutations across an allosteric site in the threonine deaminase gene (ILV1). CRISPR-Cas9 was used to reengineer these mutations into non-evolved strains and demonstrated a single mutation that recapitulated the ALE phenotype. To further improve production, 31 nonconventional yeast species were screened for improved L-phenylglycine utilization. *Kluyveromyces dobzhanskii* demonstrated a 13-fold increase in (R)-PAC compared to *S. cerevisiae* and expressing the *K. dobzhanskii* ARO10 gene in *S. cerevisiae* increased (R)-PAC production 10-fold.

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A Population-Genetic Model of Nuclear Competition in Dikaryons

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Sexual life cycles typically alternate between haploid and diploid stages, with nuclear fusion occurring soon after cellular fusion. In dikaryotic fungi nuclear fusion is delayed, allowing two genetically distinct haploid nuclei to coexist and replicate within the same cytoplasm for extended periods. Although these nuclei often occur in equal proportions, some species exhibit stable deviations from an equal nuclear ratio. Using a population-genetic model, we investigated the evolutionary conditions favoring the evolution of balanced versus imbalanced nuclear ratios. We examined both the consequences of nuclear imbalance for dikaryon-level fitness and the transmission of nuclear ratios through asexual spores, where over-represented nuclei in the dikaryon are disproportionately transmitted. Our results show that recombination rate, dominance relationships, and the extent of asexual spore production strongly influence the evolution of nuclear ratio imbalance and intradikaryotic conflict. These findings reveal a trade-off between selection acting on individual nuclei and selection acting on the dikaryon.

Cryptic speciation in insect guts: genome-wide analyses to delimit the *Smittium culicis* complex (Kickxellomycotina, Zoopagomycota)

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Biodiversity remains vastly underexplored, particularly among microbial taxa. Fungi represent one of the most diverse kingdoms of life, yet their diversity is often obscured by cryptic speciation and unresolved species complexes. Multilocus phylogenetic approaches have been widely utilized to delimit fungal species, but they may lack sufficient resolution for closely related species, resulting in persistent species complexes. Genome-wide approaches provide new opportunities to resolve these complexes, including the globally distributed insect gut-dwelling fungi of the *Smittium culicis* species complex. Previous multilocus studies identified *S. culicis* as polyphyletic, forming a complex with *S. culicisoides*, *S. simulatum*, and *S. fecundum*. Here, we use phylogenomics and population genomic analyses to resolve relationships within this lineage. Our results recover two distinct clades exhibiting species-level differentiation. These findings demonstrate the effectiveness of genome-scale approaches for delimiting fungal species complexes while providing insights into their evolutionary history.

Stress-driven emergence of heritable non-genetic drug resistance

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Drug resistance is the chief cause of treatment failure for therapies targeting chronic and infectious diseases. Whether the emergence of resistance is accelerated by environmental exposure to low levels of therapeutics remains controversial. Here, we report a non-genetic mechanism of stress adaptation that promotes heritable resistance to the widely used antifungal drug fluconazole. In the human fungal pathogen *Candida albicans*, transient exposure to subtherapeutic fluconazole doses induces a protective response that we term para-resistance. Like conventional resistance mechanisms, para-resistance is heritable. However, it does not arise from genetic mutations and can revert spontaneously. Systematic analyses of para-resistant isolates suggest that its key regulators include the stress-activated MAP kinase Hog1, the histone deacetylase subunit Snt1, the chromatin regulator Rap1, and the Sko1 transcriptional factor. Notably, molecules that disrupt biomolecular condensation and prion propagation - crucial for the inheritance of protein assemblies - block the induction of para-resistance, whereas inhibiting histone deacetylases facilitates its induction. We find that para-resistance is common in clinical isolates and, remarkably, passage through the mammalian gut triggers its acquisition, compromising fluconazole's therapeutic efficacy. Our work defines a pervasive, prion-like epigenetic mechanism of stress adaptation and highlights potential strategies to mitigate the rapid emergence of drug resistance.

Engineering Immobilized Fungal Laccase Systems For Sustainable Wastewater Polishing
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Fungal extracellular oxidoreductases such as laccases have emerged as promising biocatalysts for sustainable micropollutant removal and advanced wastewater polishing applications. However, improving the operational stability and reusability of these enzymatic systems remains essential for large-scale implementation. This study investigates the engineering of immobilized fungal laccase systems using hollow mesoporous silica-covered plastic packing for wastewater polishing applications. Particular emphasis was placed on direct immobilization from laccase-rich fungal broth without enzyme purification as a strategy to improve process sustainability while reducing downstream processing requirements. The resulting biocatalytic systems exhibited enhanced tolerance to harsh pH and temperature conditions, prolonged storage stability, and sustained immobilized activity. These findings highlight the potential of engineered fungal enzymatic platforms as scalable tools for next-generation environmental biotechnologies and sustainable water treatment applications.

Tree–Mycorrhizal Investment Strategies Along Environmental Gradients in Nebraska Forests
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In plant-mycorrhizal symbioses, plants trade carbon for nutrients. The stress gradient hypothesis predicts greater carbon allocation to fungi where nutrient-uptake benefit is highest. However, recent evidence challenges this: mycorrhizal colonization can be higher in more productive environments where plants may have surplus carbon. We tested these alternative hypotheses using amplicon sequence data on arbuscular and ectomycorrhizal assemblages, soil fertility, environmental conditions, and plant productivity in a semi-arid woodland. Our results more strongly support the surplus carbon hypothesis, especially for arbuscular mycorrhizae, which exhibited higher ASV richness in areas with greater biomass growth and soil nitrogen and lower elevation (a proxy for aridity). More variable results were observed for ectomycorrhizae: their diversity increased with the relative dominance of ectomycorrhizal hosts, but not biomass growth nor soil fertility. These patterns more strongly support the surplus carbon over the stress gradient hypothesis for arbuscular mycorrhizae, implying carbon investment may shape mycorrhizal communities differently.

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