The 5th Annual CanFunNet Fungal Biology Conference
August 6 - August 8, 2025

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Sponsors

About us

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Condensed Conference Schedule

Wednesday, August 6, 2025			
11:15AM-11:30AM ET	Opening Remarks		
11:30AM-1:00PM ET	Plenary Day 1: Fungal Genomics and Applications		
1:00PM-1:15PM ET	Break		
1:20PM-2:20PM ET	Fungal Genetics and Genomics I (1A)	Big Data in Fungal Biology (2A)	
2:20PM-2:35PM ET	Break		
2:40PM-3:40PM ET	Fungal Genetics and Genomics II (1B)	Fungal and Lichen Biodiversity (2B)	
3:40PM-3:55PM ET	Break		
4:00PM-5:00PM ET	Fungal Genetics and Genomics III (1C)	Fungal Disease in One Health (2C)	

Condensed Conference Schedule

Thursday, August 7, 2025			
11:30AM-1:00PM ET	Plenary Day 2: Evolutionary Pathways of Fungal Pathogens: Genomics, Virulence, and Precision Therapeutics		
1:00PM-1:15PM ET	Break		
1:20PM-2:20PM ET	Fungal Plant Pathology I (3A)	Medical Mycology (4A)	Aquatic Fungi (5A)
2:20PM-2:35PM ET	Break		
2:40PM-3:40PM ET	Fungal Plant Pathology II (3B)	Forest Fungal Pathogens (4B)	Mycorrhizal Symbioses (5B)
3:40PM-3:55PM ET	Break		
4:00PM-5:30PM ET	Career Workshop		

Condensed Conference Schedule

Friday, August 8, 2025			
11:30AM-1:00PM ET	Plenary Day 3: Fungal Resilience in Changing Environments: Fire, Soil Health, and Symbiosis		
1:00PM-1:10PM ET	Break		
1:10PM-2:10PM ET	Fungal Genetics and Genomics IV (6A)	Fungal Ecology & Evolution I (7A)	Fungal Applications I (8A)
2:10PM-2:25PM ET	Break		
2:30PM-3:30PM ET	Fungal Genetics and Genomics V (6B)	Fungal Ecology & Evolution II (7B)	Fungal Applications II (8B)
3:30PM-3:45PM ET	Break		
3:50PM-4:50PM ET	Fungal Genetics and Genomics VI (6C)	Fungal Disease in One Health/Cell and Developmental Biology (7C)	
5:05PM-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.

Wednesday, August 6, 2025

Fungal Genomics and Applications
Plenary 1 - 11:30AM-1:00PM EST - Wednesday, August 6, 2025
Moderated by Dr. Oualid (Walid) Ellouz & Dr. Viola Halder

11:30AM-12:00PM EST	Dr. Sophien Kamoun Think. Evolutionary. Transitions.
12:00PM-12:30PM EST	Dr. Isabelle Benoit Gelber Secondary metabolites production in *Aspergillus niger*: towards automation
12:30PM-1:00PM EST	Dr. Jon Stokes How can AI help us find new anti-fungal drugs

Fungal Genetics and Genomics I
1A - 1:20PM-2:20PM EST - Wednesday, August 6, 2025
Moderated by Dr. Brent Robicheau

1:20 PM - 1:35 PM EST	Rana Ahmed Mitochondrial Dysfunction and Pleotropic Drug Resistance in *Saccharomyces cerevisiae*
1:35 PM - 1:50 PM EST	Ken Mugambi Hi-C and HiFi PacBio Sequencing Unveils Genome Compartmentalization and RNA Operon Physical Interactions in Gigaspora margarita
1:50 PM - 2:05 PM EST	Lauren Wensing Pooled CRISPRi screening in *Candida albicans* reveals core-essential genes
2:05 PM - 2:20 PM EST	Sadri ZNAIDI Functional Portrait of the *Candida auris* Kinome

Big Data in Fungal Biology
2A - 1:20PM-2:20PM EST - Wednesday, August 6, 2025
Moderated by Dr. Linda Horianopoulos

1:20 PM - 1:35 PM EST	Katarina Aranguiz Machine learning reveals genes impacting oxidative stress resistance across yeasts
1:35 PM - 1:50 PM EST	John Wolters Losses of deeply conserved genes in the Mitotic Exit Network led to multiple rewiring events in budding yeasts
1:50 PM - 2:05 PM EST	Noah Boodhoo Practical solutions to the methodological challenges posed by mycorrhizal fungal biogeography
2:05 PM - 2:20 PM EST	Wenhan Zhang Characterizing Colony Formation in the Opportunistic Fungal Pathogen *Candida albicans*

Fungal Genetics and Genomics II
1B - 2:40PM-3:40PM EST - Wednesday, August 6, 2025
Moderated by Dr. Toby Spribille

2:40 PM - 2:55 PM EST	Anthony Hendriks Elucidating novel epistatic interactions associated with *Candida albicans* echinocandin resistance
2:55 PM - 3:10 PM EST	Gabriela Nunes Marsiglio Librais Regulation of antifungal drug resistance by catalase in *Candida albicans*
3:10 PM - 3:25 PM EST	Nadith Ranasinghe New insights into ER stress regulation in *Candida albicans*
3:25 PM - 3:40 PM EST	Harold Flohr Evolution of Genetic Network-Mediated Antifungal Resistance in Fluctuating Drug Environments

Fungal and Lichen Biodiversity
2B - 2:40PM-3:40PM EST - Wednesday, August 6, 2025
Moderated by Dr. Linda Horianopoulos

2:40 PM - 2:55 PM EST	Chris Hittinger The genomic making of yeast metabolic diversity
2:55 PM - 3:10 PM EST	Marc-André Lachance Metschnikoff's Yeast
3:10 PM - 3:25 PM EST	Michael Light Ecology of northern red oak (*Quercus rubra*) tree wound communities in Maritime Canada
3:25 PM - 3:40 PM EST	Romina Silva Espejo Tropical lichens from Campeche, Mexico

Fungal Genetics and Genomics III
1C - 4:00PM-5:00PM EST - Wednesday, August 6, 2025
Moderated by Dr. Toby Spribille

4:00 PM - 4:15 PM EST	Anne Hatmaker Sequencing of global Penicillium isolates sheds light on secondary metabolism in Fleming’s fungus and related species
4:15 PM - 4:30 PM EST	Garima Singh Evolution of fungal secondary metabolism: the rich and the poor of the fungal world
4:30 PM - 4:45 PM EST	Mika Hirano Retrobiosynthesis of privileged pharmaceutical scaffolds from non-standard amino acids
4:45 PM - 4:50 PM EST	Erica Sumbler Divergent regulation of inositol synthesis pathways between Saccharomyces cerevisiae and the fungal pathogen *Candida albicans*.

Fungal Disease in One Health
2C - 4:00PM-5:00PM EST - Wednesday, August 6, 2025
Moderated by Dr. Viola Halder

4:00 PM - 4:15 PM EST	Alex Moskaluk Systemic Mycosis in a Ferret: Diagnostic Challenges and Pathogen Insights
4:15 PM - 4:30 PM EST	Tyla Baker Pilot-scale wastewater surveillance for pathogenic yeasts in Mangaung, South Africa
4:30 PM - 4:45 PM EST	Carolina Pohl Thermotolerant insects as potential environmental niche for *Candidozyma auris*
4:45 PM - 5:00 PM EST	Chadabhorn Insuk Developing and Testing the Efficacy of a Topical Probiotic on Captive Bats to Prevent White Nose Syndrome

Thursday, August 7, 2025

Evolutionary Pathways of Fungal Pathogens: Genomics, Virulence, and Precision Therapeutics
Plenary 2 - 11:30AM-1:00PM EST - Thursday, August 7, 2025
Moderated by Dr. Jianping Xu & Dr. Linda Horianopoulos

11:30AM-12:00PM EST	Dr. Joe Heitman Epimutations evoke transient antimicrobial drug resistance
12:00PM-12:30PM EST	Dr. Adnane Sellam Sensing and signaling hypoxia in fungi
12:30PM-1:00PM EST	Dr. Adriana Morrell Harnessing soil microbial communities to support grassland restoration: Greenhouse evaluation of microbial amendments and early field establishment of native grasses.

Fungal Plant Pathology I
3A - 1:20PM-2:20PM EST - Thursday, August 7, 2025
Moderated by Dr. Oualid (Walid) Ellouz

1:20 PM - 1:35 PM EST	Matthias Kretschmer Identification of chloroplast associate effectors of the biotrophic pathogen *Ustilago maydis*
1:35 PM - 1:50 PM EST	Mohamed Hafez Abdel-Fattah Molecular diagnostics of the wheat leaf spot complex using the ß-tubulin 1 gene.
1:50 PM - 2:05 PM EST	Sara Vujakovic Characterization of the role of UmAA10 CAZyme in the morphogenesis and pathogenesis of *Ustilago maydis*

Medical Mycology
4A - 1:20PM-2:20PM EST - Thursday, August 7, 2025
Moderated by Dr. Viola Halder

	Eileen Bates
1:20 PM - 1:35 PM EST	Discovery and Characterization of Novel Small-Molecule Antifungal Drugs Proposed by Machine Learning Models
	Giancarlo Farruggia
1:35 PM - 1:50 PM EST	Experimental Evolution of Resistance of *Aspergillus fumigatus* to Triazole Antifungal Drugs
	Lucy Xie
1:50 PM - 2:05 PM EST	Stress-driven emergence of heritable non-genetic drug resistance

Aquatic Fungi
5A - 1:20PM-2:20PM EST - Thursday, August 7, 2025
Moderated by Dr. Allison Walker

	Catherine Bélanger
1:20 PM - 1:35 PM EST	Exploring Marine Fungi for Neuroactive Alkaloids: A Genomic and Biochemical Approach
	Joanna Gauthier
1:35 PM - 1:50 PM EST	Fungal functional roles in Canadian lakes along a land use gradient
	Matt Drodge
1:50 PM - 2:05 PM EST	Yeast Coast Brews: Exploring the use of marine-isolated yeasts from coastal Newfoundland for beer fermentation

Fungal Plant Pathology II
3B - 2:40PM-3:40PM EST - Thursday, August 7, 2025
Moderated by Dr. Linda Horianopoulos

2:40 PM - 2:55 PM EST	Nadir Erbilgin Foliar fungal endophytes alter white spruce defense metabolites and provide direct anti-herbivore resistance against a defoliator
2:55 PM - 3:10 PM EST	Shelley Lumba One signal, two kingdoms: Decoding plant signals in fungi
3:10 PM - 3:15 PM EST	Faizan Naeem Unraveling Multitrophic Interactions: The Influence of Mycetophagous Mites on Fungal Symbionts in the Mountain Pine Beetle System

Forest Fungal Pathogens
4B - 2:40PM-3:40PM EST - Thursday, August 7, 2025
Moderated by Jonathan Cazabonne

2:40 PM - 2:55 PM EST	Berni van der Meer The clones attack: Emphasizing the adaptability of the butternut canker pathogen
2:55 PM - 3:10 PM EST	Haolin Wei Partnership with ectomycorrhizal fungi benefits lodgepole pine seedlings against a root pathogen
3:10 PM - 3:25 PM EST	Grace Sumampong Pathogenomics of *Heterobasidion occidentale*, a fungus that causes annosus root and butt rot among conifer trees in North America – Research Update
3:25 PM - 3:40 PM EST	Jonathan Cazabonne Advancing fungal conservation in Quebec through citizen science and transdisciplinarity: the example of Mycopshaera

Mycorrhizal Symbioses
5B - 2:40PM-3:40PM EST - Thursday, August 7, 2025
Moderated by Dr. Oualid (Walid) Ellouz

2:40 PM - 2:55 PM EST	Ada Jarosch Disturbance affects diversity of arbuscular mycorrhizal fungi communities in Ontario tallgrass prairies
2:55 PM - 3:10 PM EST	Katie King Identifying the symbiotic fungi of the endangered Ram's-Head Lady Slipper orchid in Nova Scotia, Canada
3:10 PM - 3:25 PM EST	Marty Kranabetter Diverging soil peroxidase activity under ectomycorrhizal versus arbuscular mycorrhizal conifers with increasing C:N and exchangeable manganese
3:25 PM - 3:40 PM EST	Robert Ferguson Soil bacterial community selection by genetically distinct strains of arbuscular mycorrhizal fungi

Career Workshop
4:00PM-5:30PM EST - Thursday, August 7, 2025
Moderated by Dr. Patrick Lajoie

	Dr. Erik Snapp Tips for applying for a faculty position at a research intensive institution
4:00PM-5:30PM ET	Dr. Monika Yazdanian Perspectives on careers in industry
	Dr. Kimberley Dej Career in teaching at the university level

Friday, August 8, 2025

Fungal Resilience in Changing Environments: Fire, Soil Health, and Symbiosis
Plenary 3 - 11:30AM-1:00PM EST - Friday, August 8, 2025
Moderated by Dr. Patrick Lajoie & Dr. Oualid (Walid) Ellouz

11:30AM-12:00PM EST	Dr. Matt Kasson Fungus-feeding millipedes: More fungi than legs!
12:00PM-12:30PM EST	Dr. Monika Fischer Rising from the ashes: how fungi survive and thrive after fire
12:30PM-1:00PM EST	Dr. Vanessa Dumeaux Tentative title: Phenotypic heterogeneity and non-genetic survival strategies in *Candida albicans* using single-cell transcriptomics

Fungal Genetics and Genomics IV
6A - 1:10PM-2:10PM EST - Friday, August 8, 2025
Moderated by Dr. Linda Horianopoulos

1:10 PM - 1:25 PM EST	Cameron Semper A genome-wide survey identifies a gene cluster involved in tensidol biosynthesis in *Aspergillus niger*
1:25 PM - 1:40 PM EST	Linda Horianopoulos High glycolytic rate driven by transcriptional activation in a non-conventional yeast
1:40 PM - 1:55 PM EST	Michael Pyne Screening and engineering non-conventional yeasts for production of organic acids
1:55 PM - 2:10 PM EST	Wanjun Qi *Candida albicans'* phosphate acquisition and starvation response

Fungal Ecology & Evolution I
7A - 1:10PM-2:10PM EST - Friday, August 8, 2025
Moderated by Jonathan Cazabonne

1:10 PM - 1:25 PM EST	Arseniy Belosokhov Testing Predicted Vitamin Auxotrophies in Lichen Mycobionts: Evaluating Genomic Predictions Through Physiological Assays
1:25 PM - 1:40 PM EST	Carlos Colangelo Material Properties as Fruiting Body Functional Traits: Exploring The "Why" of Morphology, Decay, and Abundance'
1:40 PM - 1:55 PM EST	Abby Spring Validation and application of a metagenomics protocol to the root-associated fungal communities of Northern wild rice (*Zizania palustris*)
1:55 PM - 2:10 PM EST	Tim Philpott Deleterious shifts in root-associated fungi after high-severity wildfire

Fungal Applications I
8A - 1:10PM-2:10PM EST - Friday, August 8, 2025
Moderated by Dr. Patrick Lajoie

1:10 PM - 1:25 PM EST	Khaleda Afrin Bari Catalase targeting to peroxisomes regulates polyQ toxicity and aggregation in yeast
1:25 PM - 1:40 PM EST	Carla Flores Leveraging the biodiversity of the St. Lawrence River for novel addiction treatment
1:40 PM - 1:55 PM EST	Natalie Tateishi Study of the antibacterial activity of Hericium and Hohenbuelia.
1:55 PM - 2:10 PM EST	Anastasia Rumpl Synthesizing Ephedrine from Sugar in *Saccharomyces cerevisae*

Fungal Genetics and Genomics V
6B - 2:30PM-3:30PM EST - Friday, August 8, 2025
Moderated by Dr. Linda Horianopoulos

2:30 PM - 2:45 PM EST	Sophia Bertolo Genomic and genetic analyses of the gourmet ectomyzorrhizal mushroom *Cantharellus enelensis* in Newfoundland
2:45 PM - 3:00 PM EST	Jezreel Dalmieda Unveiling the Global Genetic Landscape of *Candida albican*s: Diversity, Origins, and Evolutionary Insights
3:00 PM - 3:15 PM EST	Megan Hitchcock Population genomic evidence for a-a and a-a sexual reproductions in an environmental *Cryptococcus deneoformans* population
3:15 PM - 3:30 PM EST	Pengyao Jiang The discovery and effect of long-standing mild-effect mutator allele in *S. cerevisiae* populations

Fungal Ecology & Evolution II
7B - 2:30PM-3:30PM EST - Friday, August 8, 2025
Moderated by Dr. Viola Halder

2:30 PM - 2:45 PM EST	Sumhithaa Sriram Ecology and Evolutionary Genomics of Graminella pipettiformis, a Novel Trichomycete Fungus from Rouge National Urban Park, Canada
2:45 PM - 3:00 PM EST	Viola Halder Targeting polarized growth in conidial germination of fungal species: a comparative genomics approach to antifungal drug discovery
3:00 PM - 3:15 PM EST	Selina Spence Investigating anastomosis and genetic exchange between commercial and non-commercial arbuscular mycorrhizal fungi in soil
3:15 PM - 3:30 PM EST	W.G.A.S. Sumanarathne Evolutionary shifts in competitive fitness of *Candida albicans* under drug exposure

Fungal Applications II
8B - 2:30PM-3:30PM EST - Friday, August 8, 2025
Moderated by Katie King

2:30 PM - 2:45 PM EST	Hannah Cheung The use of *Aspergillus niger* in alpha-lactalbumin production
2:45 PM - 3:00 PM EST	Shilpa Jose Unraveling the potential of whole-cell fungi cultures, enzyme extracts and mediator-enhanced systems for biodeterioration of microplastics
3:00 PM - 3:15 PM EST	Ignacio Benito Labrador Identifying microplastics as a potential threat to essential fungal partners

Fungal Genetics and Genomics VI
6C - 3:50PM-4:50PM EST - Friday, August 8, 2025
Moderated by Dr. Emile Gluck-Thaler

3:50 PM - 4:05 PM EST	Emile Gluck-Thaler Starships: a new frontier for fungal biology
4:05 PM - 4:20 PM EST	Isha Jain Investigating impact of gene presence and species variation on mutation and selection across codons in eukaryotes
4:20 PM - 4:35 PM EST	Rexelle Asis Degradation and preservation: Two fates of a Starship in the tan spot genome
4:35 PM - 4:50 PM EST	Ursula Oggenfuss A multi-genome analysis of structural variants and transposable elements across *Candida albicans*

Fungal Disease in One Health/Cell and Developmental Biology
7C - 3:50PM-4:50PM EST - Friday, August 8, 2025
Moderated by Dr. Allison Walker

3:50 PM - 4:05 PM EST	Niloofar Ahmadi Proteomics for *Saccharomyces cerevisiae* efflux pumps
4:05 PM - 4:20 PM EST	Clare Maristela Galon Antifungal Tolerance and in vivo Evolutionary Dynamics of *Candida auris*
4:20 PM - 4:35 PM EST	Michel Becuwe A genetic screen identifies zinc-related genes involved in endoplasmic reticulum homeostasis
4:35 PM - 4:40 PM EST	James La Investigating Secondary Metabolism in the Human Pathogen *Talaromyces marneffei*

Abstracts

Plenary Abstracts

Think. Evolutionary. Transitions.
Sophien Kamoun
The Sainsbury Laboratory

In recent years, my lab — or perhaps it's just me — has become increasingly obsessed with evolutionary transitions: the idea that every gene has an origin and an evolutionary journey marked by gain, loss, or shifts in function. In this talk, I will explore how this perspective applies to the study of filamentous plant pathogens — fungi and oomycetes. Though phylogenetically distant, they share striking similarities in morphology and lifestyle: both are filamentous, heterotrophic, and notoriously adaptable. Their ability to evade plant immunity and shift hosts makes them ideal models for studying the evolutionary arms race between pathogens and plants. I'll also highlight how plant-pathogen coevolution has shaped — and continues to reshape —mechanisms of plant immunity.

Secondary metabolites production in Aspergillus niger: towards automation
Isabelle Benoit Gelber
Concordia University

The genus Aspergillus is an important source of bioactive secondary metabolites (SMs) such as antibiotics, cholesterol-lowering molecules and anti-cancer compounds. In fungi, genes involved in SMs biosynthesis are generally co-localized in the genome and referred to as biosynthetic gene clusters (BGCs). BGCs are often silent in laboratory conditions and economic production for biotechnological applications requires significant increases in SM production. Amongst the Aspergilli, Aspergillus niger is a well-known industrial workhorse as well as a lab organism. I will discuss the steps we are taking to genetically modify A. niger using automation for the production of secondary metabolites.

How can AI help us find new anti-fungal drugs
Jon Stokes
McMaster University

In this talk, we will explore the utility and limitations of discriminative and generative machine learning methods for anti-fungal discovery and design tasks. We will first discuss well-validated graph-based molecular property prediction algorithms, followed by contemporary molecular fragment-based anti-fungal design methods. We will then touch upon the importance of transparent user-friendly methods to efficiently design novel anti-fungal agents by biologists and chemists without computational backgrounds.

Epimutations evoke transient antimicrobial drug resistance
Joe Heitman
Duke University
Antimicrobial resistance (AMR) is a grave global public health threat.

A panoply of mechanisms underlies AMR, including mutations, tolerance, and unstable mechanisms of resistance.
Recent studies have illuminated understanding of unstable mechanisms of resistance, including aneuploidy, epimutations caused by RNAi or ectopic heterochromatin, and even prion-like elements that have been termed para-resistance.
I will discuss our recent studies: 1) revealing examples of RNAi epimutations, and ectopic heterochromatin epimutations, and 2) demonstrating that RNAi epimutants are inheritable following sexual reproduction.

Sensing and signaling hypoxia in fungi
Adnane Sellam
Université de Montréal

A critical but poorly understood aspect of eukaryotic microbes is the ability to sense and adapt to variations in the oxygen concentration in their colonized niches. Inside the human host, the opportunistic yeast Candida albicans and other pathobionts colonizes predominantly hypoxic niches such as the gastrointestinal and vaginal tracts. So far, the mechanisms that communicate oxygen status to the fungal fitness machinery in C. albicans and in many other human fungal pathogens remains mostly unexplored. In this talk, I will discuss our recent research highlighting novel mechanisms that link oxygen levels to the metabolic processes and overall fitness of fungi.

Harnessing soil microbial communities to support grassland restoration: Greenhouse evaluation of microbial amendments and early field establishment of native grasses.

Adriana Morrell
Lethbridge Polytechnic

Restoring native grasslands after industrial or agricultural disturbance presents complex challenges that demand innovative approaches beyond conventional revegetation. Soil microbial communities, particularly arbuscular mycorrhizal fungi (AMF), are increasingly recognized as key drivers of native plant establishment, soil health, and long-term ecosystem recovery. As part of a multi-year research collaboration with the Nature Conservancy of Canada and Athabasca University, our team is investigating the use of microbial amendments to support grassland restoration in Alberta.

The objective of this study is to evaluate the effectiveness of AMF inoculation in enhancing early growth and establishment of native grass species commonly used in prairie restoration.

We conducted a controlled greenhouse experiment testing the effects of three commercial AMF inoculants (Dynomyko, Mykos, and GreenGro), native topsoil from the restoration site, and a non- inoculated control on three ecologically and agriculturally important grasses: Rough Fescue, Idaho Fescue, and Bluebunch Wheatgrass. Plant performance was assessed through measurements of shoot and root biomass, plant height, leaf count, chlorophyll content, and root colonization by AMF.

Preliminary results reveal species-specific responses to AMF treatments, with certain amendments significantly improving root length, shoot and root biomass, and leaf chlorophyll content in the some of the grass species.

To bridge greenhouse results with field applications, we also report on the early transition of inoculated plugs into active restoration plots. While this phase is ongoing, initial field observations highlight the importance of site conditions in influencing transplant survival and early establishment.

These early findings contribute to a growing body of evidence supporting the integration of microbial tools into grassland restoration strategies and underscore the potential of soil biota to accelerate ecosystem recovery in disturbed prairie landscapes.

Fungus-feeding millipedes: More fungi than legs!
Matt Kasson
West Virginia University
TBD

Rising from the ashes: how fungi survive and thrive after fire
Monika Fischer
University of British Columbia

The first year following fire is a critical time of activity in the soil that lays the foundation for the rest of post-fire recovery. Several studies, including our own, have illuminated a cohort of fire-adapted fungi that uniquely respond immediately to fire, seemingly regardless of other ecosystem or environmental factors. These fungi respond in a manner that is highly dynamic, patchy, and variable between sites. We have isolated several members of this pyrophilous fungal community, sequenced their genomes, and are actively working to better understand their interactions and metabolisms in the lab. In total, we demonstrate that fire generates a dramatically altered nutrient landscape which drives the metabolism and behavior of pioneering pyrophilous fungi.

Tentative title: Phenotypic heterogeneity and non-genetic survival strategies in Candida albicans using single-cell transcriptomics
Vanessa Dumeaux
Western University
TBD

Speaker Abstracts

Molecular diagnostics of the wheat leaf spot complex using the ß-tubulin 1 gene.

Mohamed Hafez Abdel-Fattah*, Dianevys González-Peña Fundora, Ryan Gourlie, Mouldi Zid, Reem Aboukhaddour
Agriculture and Agri-Food Canada

The wheat leaf spot complex is a globally significant foliar disease caused by multiple fungal pathogens: Pyrenophora tritici-repentis (tan spot), Parastagonospora nodorum and Parastagonospora pseudonodorum (septoria nodorum blotch), Zymoseptoria tritici (septoria tritici blotch), and Bipolaris sorokiniana (spot blotch). Accurate diagnosis is challenging due to overlapping symptoms and similar morphologies. Current molecular tools often lack specificity, fail to detect all pathogens, or are not validated against other wheat-associated fungi. Notably, no assay specifically targets P. pseudonodorum, leading to underestimation of its role in leaf spot disease. To overcome these limitations, we developed a diagnostic toolkit targeting the conserved single-copy ß-tubulin 1 (tub1) gene. Species-specific primers were designed for multiplex PCR (mPCR) and TaqMan-based quantitative PCR (qPCR), enabling simultaneous, sensitive, and specific detection. The qPCR accurately quantified pathogen biomass with detection limits as low as 0.04 pg of fungal DNA. Additionally, PCR-RFLP using selected restriction enzymes allowed clear species differentiation based on unique cleavage patterns. The developed assays showed no cross-reactivity with non-targeted fungi, including barley pathogens like Pyrenophora teres, ensuring reliability in agricultural systems where host overlap occurs. This molecular toolkit offers rapid and reliable detection, quantification, and differentiation of wheat leaf spot pathogens, supporting effective disease monitoring and enhance breeding for resistance.

Proteomics for Saccharomyces cerevisiae efflux pumps

Ahmadi*, Niloofar; Sandhu, Simran; Court, Deborah
University of Manitoba

A diverse group of efflux pumps remove toxic compounds and antimicrobials from bacteria. Our hypothesis is that, similarly, there are efflux pumps that protect Saccharomyces cerevisiae from mitochondria-targeting antibiotics like chloramphenicol. S. cerevisiae does not require mitochondrial function if it is provided fermentable carbon sources, allowing us to search for pumps in cells with limited ability to respire. We hypothesized that low levels of the drugs would activate expression of pumps. First, we determined conditions that allowed cells to grow in the presence of chloramphenicol. Preliminary LC-MS/MS experiments on isolated membranes detected several pumps known to be in mitochondria, vacuoles and the plasma membrane. Further studies comparing the proteomes of cells in the presence and absence of chloramphenicol will help us identify putative antibiotic efflux pumps.

Mitochondrial Dysfunction and Pleotropic Drug Resistance in Saccharomyces cerevisiae

Ahmed*, Rana; Court, Deborah
University of Manitoba

Multidrug resistance (MDR) presents a critical challenge in both clinical and agricultural settings, driven in part by the activity of ATP-binding cassette (ABC) transporters that mediate drug efflux. In Saccharomyces cerevisiae, the pleiotropic drug resistance (PDR) pathway, regulated by transcription factors Pdr1 and Pdr3, controls key efflux pumps such as Pdr5, Pdr10, and Pdr15. Emerging evidence suggests that mitochondrial dysfunction can activate the PDR network, though the precise mechanisms remain poorly understood. This study investigates the cellular stress responses linking mitochondrial dysfunction to PDR activation. Using chloramphenicol (CAP), a mitochondrial translation inhibitor, we induced mitochondrial stress in wild-type S. cerevisiae grown in a respiratory medium. Transcriptomic analysis across multiple time points revealed time-dependent activation of drug efflux genes, oxidative stress markers, mitochondrial chaperones, and respiration-associated genes. Notably, PDR transporter genes (including PDR5, PDR10, and PDR15) were upregulated beginning at 6 hours post-treatment, coinciding with elevated expression of SOD1, implicating oxidative stress. RT-qPCR confirmed CAP-induced upregulation of PDR1 and PDR5, while CAP sensitivity in ?pdr1 and ?pdr5 mutants demonstrated their functional roles in resistance. Functional assays supported increased efflux activity under mitochondrial stress. These findings establish a direct link between mitochondrial dysfunction and PDR activation. Ongoing studies with erythromycin and tetracycline aim to determine the generality of this response, advancing our understanding of mitochondrial-PDR crosstalk in antifungal resistance.

Machine learning reveals genes impacting oxidative stress resistance across yeasts
Katarina Aranguiz*, Linda C. Horianopoulos, Logan Elkin, Kenia Segura Abá, Drew Jordahl, Katherine A. Overmyer, Russell L. Wrobel, Joshua J. Coon, Shin-Han Shiu, Antonis Rokas & Chris Todd Hittinger
University of Wisconsin-Madison

Reactive oxygen species (ROS) are highly reactive molecules encountered by yeasts during routine metabolism and during interactions with other organisms, including host infection. Here, we characterized the variation in resistance to ROS across the yeast subphylum Saccharomycotina and used machine learning (ML) to identify gene families whose sizes were predictive of ROS resistance. The most predictive features were enriched in gene families related to cell wall organization and included two reductase gene families. We estimated the quantitative contributions of features to each species' classification to guide experimental validation and showed that overexpression of the old yellow enzyme (OYE) reductase increased ROS resistance in Kluyveromyces lactis, while Saccharomyces cerevisiae mutants lacking multiple mannosyltransferase-encoding genes were hypersensitive to ROS. Altogether, this work provides a framework for how ML can uncover genetic mechanisms underlying trait variation across diverse species and inform trait manipulation for clinical and biotechnological applications.

Degradation and preservation: Two fates of a Starship in the tan spot genome
Asis, Rexelle*, Gourlie, Ryan, Yevtushenko, Dmytro, and Aboukhaddour, Reem
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The mobility of transposable elements (TEs) enables them to shape the genomes of organisms across all domains of life. Starships are a recently discovered class of fungal TEs that are characterized by their large size (up to 500 kbp). This allows them to ferry many potentially advantageous genes, including ToxA and ToxB, which are virulence genes in the tan spot of wheat pathogen, Pyrenophora tritici-repentis (Ptr). Active Starships are mobilized by a tyrosine recombinase called a "captain," such as the one associated with Horizon, the mobilizer of ToxA. Conversely, previous evidence suggested that ToxB resides within Icarus, an inactive Starship lacking a captain. Here, we analyzed 15 long-read Ptr genomes and have confirmed these previous findings. Icarus is highly conserved among isolates and carries ToxB along with other characteristic Starship cargo genes. However, the absence of a captain indicates that Icarus is a degraded, and likely inactive, Starship.

Pilot-scale wastewater surveillance for pathogenic yeasts in Mangaung, South Africa
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Considering the emerging concern posed by invasive fungal infections, it is essential to monitor the fungal burden within communities to aid in treating affected individuals. Wastewater surveillance may be a useful tool for this endeavour. It is well-developed for bacteria and viruses, but less so for pathogenic yeast. Using culture-dependent and independent techniques, we investigated the presence of pathogenic yeasts in the wastewater influent of six different sampling points in Bloemfontein, South Africa. From these samples, Candida species were observed to be the most prominent. An optimised multiplex PCR system identified various pathogenic yeast species, which largely corresponded with the culture-dependent results. It was also observed that wastewater seems to select resistant yeast species while also supporting the growth of susceptible dose-dependent isolates which might develop acquired resistance to fluconazole in this environment. All in all, wastewater surveillance shows promise, but a few limitations must be overcome.

Catalase targeting to peroxisomes regulates polyQ toxicity and aggregation in yeast
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Oxidative stress contributes significantly to neurodegeneration, including in Huntington's Disease (HD), linked to accumulation of toxic polyglutamine (polyQ) expansions. We investigated catalase's role in mitigating age-dependent polyQ toxicity using a yeast HD model and found that deletion of the peroxisomal catalase gene (CTA1) exacerbated polyQ toxicity. Using human catalase engineered with organelle-specific targeting sequences, we discovered that targeted catalase delivery to peroxisomes substantially reduced polyQ toxicity and extended chronological lifespan in cells expressing toxic polyQ. This protection correlated with increased polyQ inclusion body (IB) formation, supporting the concept that IBs sequester toxic oligomeric species. Our findings indicate that enhanced peroxisomal catalase activity represents a promising HD therapeutic strategy by maintaining redox homeostasis and promoting protective inclusion body formation.

Discovery and Characterization of Novel Small-Molecule Antifungal Drugs Proposed by Machine Learning Models

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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 identified promising candidates from a library of approximately 12 million commercially available compounds. From these predictions, we identified 2 structurally novel molecules with potent antifungal activity against Candida albicans. These compounds have promising toxicity profiles in human embryonic kidney cells (HEK293), broad spectrum activity against diverse fungal pathogens, and retain activity against antifungal-resistant clinical isolates. This work represents a powerful new approach to antifungal drug development, which is crucial for decreasing the burden of fungal pathogens on human health.

A genetic screen identifies zinc-related genes involved in endoplasmic reticulum homeostasis

Jonathan Palmiero, Lynzie Wilkinson, Amira Aly, Arianna Forzano, Victoria Iuzzolino, Chloe LoSauro, Simrat Mangat, Nicolas McGuire, Rebecca Robinson, and Michel Becuwe*
Marist University

Endoplasmic reticulum (ER) lipid homeostasis is a tightly regulated process in which Fat-Induced Transcript 2 (FIT2) and its yeast homolog Scs3, ER-resident acyl-coenzyme diphosphatase enzymes, play a central role. Loss of FIT2 or Scs3 disrupts ER morphology and induces chronic ER stress, though the underlying mechanisms remain poorly understood. To uncover new regulators of Scs3-mediated lipid homeostasis, we performed a multicopy genetic suppressor screen in yeast and identified two zinc-related genes, IZH1 and MSC2, as genetic interactors of SCS3. Both IZH1 and MSC2 genes encode for ER resident proteins. Using UPRE-LacZ reporter assays and RT-qPCR, we found that IZH1 overexpression significantly reduces ER stress in scs3? cells under both lipotoxic and proteotoxic conditions. Additionally, IZH1 overexpression mitigates ER morphological defects caused by SCS3 deletion. MSC2 also alleviates ER stress under lipotoxic conditions, though to a much lesser extent than IZH1. These findings highlight the link between zinc metabolism and ER lipid homeostasis and suggest that modulation of zinc transport and signaling may influence Scs3 function in maintaining ER integrity.

Exploring Marine Fungi for Neuroactive Alkaloids: A Genomic and Biochemical Approach

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Biopterre

Fungi have long stood out as prolific producers of bioactive molecules with remarkable industrial and pharmaceutical value—ranging from antibiotics and antivirals to anticancer and psychoactive compounds. Marine-derived fungi, in particular, are emerging as a promising yet underexplored reservoir of neuroactive metabolites such as benzodiazepines, terpenes, and indole alkaloids. These molecules not only show efficacy against a wide spectrum of neurological disorders but also hold groundbreaking potential in the fight against opioid addiction. This project leverages an integrative approach combining functional and genetic screening with genome mining of selected fungal marine isolates. Following solid-state fermentation and a three-stage extraction protocol, alkaloids are detected using Dragendorff's reagent, enabling the identification of novel metabolites. By coupling genomic data with biochemical evidence, this work aims to uncover new molecular scaffolds with therapeutic potential—particularly for addiction treatment, an area critically lacking in effective and accessible options.

Testing Predicted Vitamin Auxotrophies in Lichen Mycobionts: Evaluating Genomic Predictions Through Physiological Assays

Arseniy Belosokhov*, Toby Spribille
University of Alberta

Recent genomic analyses suggest lichen mycobionts broadly lack biotin synthesis genes, implying vitamin auxotrophy and reframing metabolic dependencies in lichens beyond traditional carbon-nitrogen exchanges. While genomics efficiently maps metabolic potential, inferred auxotrophies rely on gene annotations extrapolated from studied organisms, leaving uncertainty about physiological manifestation. We empirically assessed biotin and thiamine dependency through factorial cultivation experiments on axenic mycobionts from diverse lichen lineages grown in vitamin-controlled conditions. This approach tested if observed growth aligns with genomic predictions or reveals potential unknown, divergent vitamin synthesis pathways undetected by genomic annotations. Our study provides direct physiological data on vitamin requirements, critically validating genome-based metabolic inferences, and underscores the necessity of empirical evidence in predictive genomic studies, thus advancing understanding of nutritional resource dynamics within lichen symbioses.

Identifying microplastics as a potential threat to essential fungal partners

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UBCO

It is in the nature of microplastics to spread, and consequently, they are being introduced as a new near-universal pollutant in every macro and microbiome. Given their size ranges from 1 micrometer to up to 5 millimeters, it is unsurprising that these plastic particulates stand to represent a new, unprecedented, and potentially catastrophic source of pollution. Herein, we hope to identify what impact the presence of these ubiquitous plastic particles can have on the plant mycobiome, more specifically, on their arbuscular mycorrhizal fungi (AMF) partners. Our steady aim is to identify the specific consequences of plastic exposure on the asymbiotic life-stage of AMF to understand if these particles represent a significant threat to the symbiosis-forming capacity of these essential fungal partners. Microplastics, due to both size and chemical structure, are uniquely positioned to damage and devastate both agricultural as well as “untouched” natural ecosystems. Their unique size and chemistry allow them to interfere with pores, thus stifling nutrient acquisition in plants, while their chemical composition offers soil microbes an unprecedented source of potential carbon; therefore, these two areas of research have received attention from the scientific community. In stark contrast, however, the impact that these minute plastics may pose on these fungal partners themselves remains largely unstudied. The system utilized in this project aims to create an environment where AMF are exposed both to a blanket presence of microplastics as well as to simulate point-sources of plastic pollutants in the hope of understanding if these, relatively new sources of pollution warrant further concern.

Genomic and genetic analyses of the gourmet ectomyzorrhizal mushroom Cantharellus enelensis in Newfoundland
Bertolo, Sophia*; Xu, Jianping; Guo, Xia
McMaster University

Cantharellus enelensis is a wild edible mushroom distributed in eastern North America. Its dependence on host trees makes C. enelensis highly vulnerable. The Burnt Hill population of C. enelensis near the Gros Morne National Park represents an opportunity for studying the vegetative growth of its mycelia and the dispersal of its sexual spores. Burnt Hill had a fire in 1898 that destroyed all vegetation. Interestingly, the chanterelle mushroom started to appear soon after and has been fruiting abundantly since then, while the surrounding unburnt forests had few mushrooms. We collected 124 fruiting bodies across Burnt Hill. The whole-genome sequence of the largest fruiting body is being annotated, compared with genomes from related species, and used to develop microsatellite markers. The obtained data will be used to infer the size distributions of genetic individuals, the role of vegetative growth, and the contributions of sexual spores to genetic variation.

Practical solutions to the methodological challenges posed by mycorrhizal fungal biogeography
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Mycorrhizal fungal biogeography is at a crossroads where data is being collected and published at a higher rate than ever before. This presents a great opportunity to assess the generalizability of prior knowledge through the integration of multiple sets of data for large-scale meta-analyses. We have surveyed the scientific literature for published studies having made use of next-generation sequencing technologies to characterize mycorrhizal fungal communities in natural ecosystems as well as controlled laboratory or field conditions. Our query has resulted in the identification of nearly one thousand published studies. We have identified that (1) lack of uniformity in the global distribution of sampling locations, (2) incongruences in the structure that data is reported in, and (3) inconsistent taxonomic assignment strategies are factors that hinder our ability to pool data from different sources for large-scale meta-analyses. Here, we propose practical solutions to the methodological challenges posed by mycorrhizal fungal biogeography.

Advancing fungal conservation in Quebec through citizen science and transdisciplinarity: the example of Mycopshaera

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Fungal conservation is gaining momentum worldwide. Many initiatives have emerged to ensure that fungi are included on equal footing with animals and plants in biodiversity conservation strategies. Despite more than 3,500 species of macrofungi documented in Quebec – and 474 considered threatened – the province's fungal diversity remains largely unknown, and fungi are still absent from the legal frameworks protecting threatened and vulnerable species. At the same time, citizen science is gradually establishing itself as a promising approach to improve our knowledge of fungal diversity and advance conservation efforts, especially in regions where professional mycologists are few or altogether absent. However, dialogue between amateur mycologists, the public, scientists, and socio-economic and political stakeholders remains limited. In response, several initiatives are emerging in Quebec to bridge this gap. In particular, the Mycosphaera collective, a non-profit organization, was recently created with the main aim of documenting Quebec's funga and advancing fungal conservation at the provincial and federal levels. In this talk, we will provide an overview of global fungal conservation efforts and present concrete examples of projects currently led by Mycosphaera. We will discuss the key challenges and potential solutions to advance fungal conservation in Quebec and explore the role that citizen science can play in this process. We will also highlight the importance of addressing our knowledge gaps about forest fungi, fostering dialogue across disciplines and actors within Quebec's mycology community, and making fungal conservation a real priority.

The use of Aspergillus niger in alpha-lactalbumin production
Cheung, Hannah* and Semper, Cameron
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Aspergillus niger is an industrial workhorse used to produce a variety of enzymes applicable to food production. The availability of a well-defined genetic toolkit, long history of use in biomanufacturing, and favourable regulatory status makes it an ideal cell factory for cellular agriculture and precision fermentation. This project will utilize A. niger in the production of alpha-lactalbumin, a whey constituent of mammalian milk. Genes encoding alpha-lactalbumin will be codon-optimized and integrated into the A. niger genome using Cas9-mediated homology directed repair. Fungal expression and secretion of the protein will be confirmed via SDS-PAGE and Western blot followed by chromatography purification. The fungal-derived alpha-lactalbumin will undergo biochemical and biophysical characterization to assess functional equivalence. Food safety risks will also be assessed to determine potential biological hazards and allergens. This work aims to support the development of alternative protein sources while contributing to the growing use of filamentous fungi in sustainable biomanufacturing.

'Material Properties as Fruiting Body Functional Traits: Exploring The "Why" of Morphology, Decay, and Abundance'
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McMaster University

Fungal fruiting bodies (FBs) are diverse in their morphological and physical traits; the functions of these features remain largely unknown. I plan to record and explore these traits among FBs at designated sites in the McMaster Forest Nature Preserve over time to understand what filters and subsequent competitive-stress tolerance-ruderal strategies may have brought on the observed traits.

Continuous FB traits such as hardness, mass, surface area : volume, stipe : cap, and hymenophore : trama ratio will be explored in relation to ecological site characteristics with principal component analysis. The effect of categorical FB traits on continuous FB traits will be assessed with linear mixed models. Collected data will be plotted with mitic system of all described agaricomycetes on MycoBank to understand the evolution of skeletal hyphae and functional traits.

A mechanistic understanding of fruiting body morphology in an evolutionary framework serves to elucidate what conditions drive changes in material properties, pointing to putative material property genes and downstream fungineering.

Unveiling the Global Genetic Landscape of Candida albicans: Diversity, Origins, and Evolutionary Insights
Dalmieda, Jezreel*. Xu, Jianping
McMaster University

Candida albicans is a globally distributed pathogenic yeast and a major contributor to fungal diseases. Its broad ecological and geographical range drive the genetic diversity observed across global populations, influencing virulence and antifungal resistance. In 2022, the WHO classified C. albicans as a “Critical Priority” fungal pathogen. While local and regional studies exist, large-scale global patterns remain understudied. Here, we analyzed multilocus sequence data (~5,000 isolates) from PubMLST.org, phasing haplotypes across seven loci. We assessed global genetic diversity through population differentiation, haplotype networks, and clustering analyses. AMOVA showed low but significant genetic differentiation among geographic populations. Many haplotypes were shared across regions and more broadly distributed haplotypes tended to be genetically similar. These findings suggest limited geographic structuring and highlight the potential role of global dispersal in shaping C. albicans diversity. We discuss the evolutionary implications for the origin and adaptation of this important fungal pathogen.

Yeast Coast Brews: Exploring the use of marine-isolated yeasts from coastal Newfoundland for beer fermentation
Drodge, Matthew*. McIlroy, Duncan. Bignell, Dawn.
Memorial University of Newfoundland

Beer is a popular fermented drink. Two main types of yeast are usually used for brewing most beers, Saccharomyces cerevisiae and Saccharomyces pastorianus. Brewing beers with novel yeasts may provide new flavours and properties to beers. Marine environments are underexplored for isolating yeasts. The goal of this study is to isolate yeasts from marine environments in coastal Newfoundland and assess them for potential use in beer fermentation. To our knowledge this is the first assessment of marine yeast biodiversity in Newfoundland. 165 yeast strains were isolated from sediment, seawater, and seaweed samples from multiple coastal locations across Newfoundland. Strains were identified to their most closely related species by sequencing common DNA barcoding regions. 18 species were selected and assessed for ideal brewing attributes: growth temperature, ethanol tolerance, flocculation ability, and sugar utilization. Strains showing promising characteristics will be assessed for their ability to ferment beer wort to produce ethanol.

Foliar fungal endophytes alter white spruce defense metabolites and provide direct anti-herbivore resistance against a defoliator

Erbilgin, Nadir *, Ullah, Aziz
University of Alberta

Endophytic fungi can influence plant resistance to herbivores, but their role in conifer defence against insect pests is not well understood. We examined how foliar endophytic fungi in white spruce (Picea glauca) affect resistance to the eastern spruce budworm (Choristoneura fumiferana). We analyzed 30 white spruce genotypes across two Alberta sites, assessing monoterpene and sesquiterpene profiles alongside fungal community composition. Ten fungal morphotypes were isolated and screened for metabolite production, revealing 11 secondary metabolites and 13 volatile organic compounds (FVOCs). Bioassays tested the effects of fungal mycelium and FVOCs on budworm performance and attraction. Most fungi negatively affected the budworm, with outcomes depending on fungal species and dosage. Greenhouse trials showed that modifying foliar fungal communities altered terpene defences in white spruce seedlings. These findings suggest that endophytic fungi contribute to spruce defence by directly harming budworms or emitting deterrent volatiles, enhancing the diversity and effectiveness of host chemical defences.

Experimental Evolution of Resistance of Aspergillus fumigatus to Triazole Antifungal Drugs

Farruggia, Giancarlo*. Xu, Jianping. Dalmieda, Jezreel
McMaster University

Aspergillus fumigatus is a ubiquitous and saprophytic mold but can cause significant morbidity and mortality. Antifungal resistance and climate change have increased concerns regarding pathogens such as A. fumigatus. This study aims to assess the patterns and mechanisms of resistance evolution to two first-line drugs, itraconazole and voriconazole, in A. fumigatus. Four geographically and phenotypically diverse strains of A. fumigatus were exposed to concentrations of itraconazole or voriconazole starting at half the minimum inhibitory concentration (MIC) followed by stepwise increases up to 16μg/mL. Further MIC testing was conducted to confirm resistance. Hazard ratio analyses revealed strain-dependent and drug-dependent differences in resistance development. Among the 108 evolved samples, 77% displayed itraconazole resistance and 74% showed resistance to voriconazole. Furthermore, the evolved samples had a 96% cross-resistance rate between the two drugs. Whole-genome sequence analyses are underway to help identify the mutations associated with the evolved resistance.

Soil bacterial community selection by genetically distinct strains of arbuscular mycorrhizal fungi

Ferguson, Robert*; Whitehead, Dean; Mugambi, Ken; Lapen, David; Corradi, Nicolas
University of Ottawa

Arbuscular mycorrhizal fungi (AMF) are obligate symbionts of most plants that improve plant growth by transferring nutrients into plant roots through networks of soil hyphae. Studies have found AMF species-dependent shifts in soil microbial communities via to the enrichment of specific microbial taxa, yet none have investigated this phenomenon at the level of fungal strain. This study will seek to characterize the effect of conspecific AMF strains on the presence and relative abundance of bacteria in soil grown with two different host plants. DNA will be extracted from soil samples for full-length 16S rRNA amplicon sequencing to generate bacterial community profiles of each AMF strain treatment. PERMANOVA will be performed on beta diversity data along with other explanatory variables to test for significant community differences between treatments. This project will provide a close examination of AMF strain identity as a driver of soil bacterial community structure.

Evolution of Genetic Network-Mediated Antifungal Resistance in Fluctuating Drug Environments

Flohr, Harold* , Aurin, Sanjina , Charlebois, Daniel
University of Alberta

Antimicrobial resistance (AMR) in fungi is a growing concern, with multidrug-resistant pathogenic yeasts, such as Candida auris, posing serious treatment challenges. While previous research has focused on constant drug conditions, real-world drug exposure is often variable. We investigate the evolution of antifungal resistance in fluctuating drug environments using a genetically engineered budding yeast (Saccharomyces cerevisiae) harbouring an AMR-associated gene network motif. Compared to constant drug conditions, our computational models and evolution experiments reveal that fluctuating environments lead to more pronounced growth rate drops and distinct gene expression profiles. We also observe a decrease in non-genetic variability in gene expression and an increase in genetic variability. Together, these findings suggest that fluctuating drug selection uniquely shapes the fitness landscape and tunes the balance of non-genetic and genetic adaptations.

Leveraging the biodiversity of the St. Lawrence River for novel addiction treatment

Carla Flores*, Catherine Bélanger, Félix-Antoine Bérubé-Simard, Gabriel D. Bossé
Université Laval

The opioid crisis, causing over 100,000 deaths annually in North America, current therapies (e.g., methadone, buprenorphine) have limited long-term efficiencies, which further highlights the urgent need for a novel treatment candidate. The goal of this project is to investigate the therapeutic potential of marine fungi isolated from the St. Lawrence River for opioid abuse. In collaboration with BiopTerre, we performed extracts from X fungi to test their biological effect on zebrafish.

My project focuses on 1) identifying neuroactive extracts using a large-scale behavioural assay in zebrafish larvae and 2) determining the effect of selected extracts on opioid self-administration using a novel assay created in our group.

Together, these approaches will identify which extracts have the best potential to isolate novel treatment candidates for opioid abuse. This model enables ethical, high-throughput testing and establishes Canada’s first fungal-based zebrafish platform for opioid addiction research.

Antifungal Tolerance and in vivo Evolutionary Dynamics of Candida auris

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UNIVERSITY OF ALBERTA

The pathogenic budding yeast Candida auris poses a global health threat in part due to its ability to survive antifungal treatments through both resistance and tolerance mechanisms. Unlike resistance, antifungal tolerance is a reversible, possibly non-genetic phenomenon, in which subpopulations grow slowly during drug exposure and can revert to a drug-susceptible phenotype.

Previously, we discovered antifungal tolerance in clinical C. auris isolates across all major antifungal drug classes (azoles, polyenes, and echinocandins; PMID: 36979876). We also investigated whether chloroquine, an antimalarial drug, could act as an antifungal adjuvant. In in vitro assays, chloroquine-antifungal drug combinations reduced or eliminated tolerance and resistance in several clinical isolates. More recently we found that chloroquine-antifungal drug combinations were ineffective in wax moth (Galleria mellonella) larvae infected with C. auris (unpublished data).

Based on our modelling predictions (PMID: 35998624), we are presently investigating the hypothesis that non-genetic resistance/tolerance enhances survival but slows the evolution of genetic resistance. We are testing this hypothesis in in vivo experiments on G. mellonella, a host with an innate immune system, infected with C. auris. By analyzing survival, population dynamics, and genetic mutations, we aim to uncover the evolutionary dynamics of C. auris during drug exposure inside the host.

Overall, this research aims to provide insights into the in vivo evolution of pathogenic yeasts, inform novel antifungal treatments, and advance our understanding of antimicrobial resistance.

Fungal functional roles in Canadian lakes along a land use gradient
Joanna Gauthier*, Marguerite Xenopoulos, Wen Chen, Rebecca Garner, Frances Pick, Hans-Peter Grossart and David Walsh
Trent University

Aquatic fungi play crucial roles in organic matter decomposition and nutrient cycling in freshwater systems. Recent advancements in genomic approaches enable the study of the functions of aquatic fungi in lakes. Using a metagenomic datasets from 350 Canadian lakes as part of the NSERC Lake Pulse Network, we examined the fungal gene composition of samples collected at the surface of the lakes and related their functions with land use and land cover in the lake's catchments as categorized using cluster analyses. Principal coordinate analysis and permutational multivariate analysis of variance were applied to test for differences in the fungal functions between land use categories. The fungal gene composition was further linked to dissolved organic carbon, color, nutrients and chlorophyll concentrations. This study will be the first to examine fungal genes in lakes on a large spatial scale and contribute to understand the role of aquatic fungi in lake biogeochemical cycles.

Starships: a new frontier for fungal biology
Gluck-Thaler, Emile*
University of Wisconsin-Madison

Fungal adaptation poses a serious threat to plant and human health because it is through this process that fungi overcome disease management efforts. Understanding the mechanisms of fungal adaptation is therefore an economic and public health priority. We recently discovered a previously hidden feature of fungal genomes: giant transposons we have named Starships. These transposons are highly unusual because they often carry dozens of genes impacting adaptive fungal phenotypes. Here, we present two case studies supporting the hypothesis that Starships are a mechanism of fungal adaptation. First, we show that Starship activity generates widespread heterogeneity within species. Second, we show that Starships mediate adaptive horizontal gene transfer both within and between species. Drawing on data across multiple model systems, we build on existing models of fungal adaptation by conceptualizing Starships as distinct genetic entities whose dynamics profoundly shape fungal biology and evolution.

Targeting polarized growth in conidial germination of fungal species: a comparative genomics approach to antifungal drug discovery

Halder, Viola*, Wang, Zheng, Trail, Frances, Yarden, Oded, & Townsend, Jeffrey P.
Yale University

Conidia germination is essential for fungal propagation, environmental colonization, and host infection. Conidia germination toward the first branch of the hyphae is a process absent in mammalian hosts and involves the polarized growth mechanism. Therefore, understanding this mechanism is crucial in advancing our knowledge of fungal biology, from initial response to the environment to the development of pathogenicity. We hypothesize that identifying genes associated with fungal conidia germination, specifically polarized growth, and their functional divergences across fungal species will provide insights into asexual spore germination and reveal potential targets for novel antifungal drugs. We performed a comparative genomic analysis to identify conserved and species-specific mechanisms regulating polar growth in filamentous fungi.

We examined gene expression during conidial germination, spanning isotropic to polarized growth and the formation of the first hyphal branch, in several fungal species grown in a common medium that represents both saprobic and pathogenic lifestyles. Disrupting polar growth mechanisms can hinder fungal virulence, presenting novel therapeutic opportunities. High-throughput screenings of small-molecule or targeted protein-degrader libraries against fungal mutants defective in genes involved in polar growth provide a systematic approach to antifungal discovery. By integrating comparative genomics, functional genetics, and high-throughput screening, we can enhance our understanding of fungal development and inform strategies for developing antifungal drugs.

Sequencing of global Penicillium isolates sheds light on secondary metabolism in Fleming's fungus and related species
Hatmaker, Anne*; Amir Rawa, Mira; Wolfe, Benjamin; Gostincar, Cene; Gunde-Cimerman, Nina; Keller, Nancy; Drott, Milton
USDA-ARS and University of Minnesota

Penicillin-producing fungi Penicillium chrysogenum and Penicillum rubens were considered the same species until P. rubens was defined in the early 2010s. We do not yet understand species relationships within the complex. To explore the evolution of P. chrysogenum and P. rubens and their secondary metabolism, we collected isolates from an array of ecological niches including natural and built environments. We sequenced the genomes of >80 isolates and downloaded available data for 25 additional isolates. We explored population structure within P. chrysogenum and P. rubens, discovering three clusters/clades possibly representing cryptic species. We also identified population-specific biosynthetic gene clusters and identified recombination in P. chrysogenum. We saw differences in metabolite production among strains of the same species, with substantial overlap between P. rubens and P. chrysogenum. Although further phenotyping is needed to characterize variation among P. chrysogenum and related species, our work sheds light on the complexities within the Penicillium genus.

Elucidating novel epistatic interactions associated with Candida albicans echinocandin resistance
Hendriks A*, Wensing L, Després PC, Fogal M, Shapiro RS
University of Guelph

Antifungal resistance remains a persistent obstacle in treating Candida albicans infections. This holds true for the echinocandins, where resistance is driven by single-point mutations in the FKS1 gene, affecting drug binding and altering cellular fitness and regulatory pathways. To explore the genetic basis of echinocandin resistance, we utilized an echinocandin-resistant C. albicans mutant isogenic with a standard laboratory strain alongside the Shapiro lab's inducible CRISPR interference (CRISPRi) system. This platform enabled systematic mapping of epistatic interactions with echinocandin resistant mutations. We validated known interactions with calcineurin signaling and assessed candidate genes identified in pooled CRISPRi screens, revealing strain-specific genetic interactions that support the reorganization of regulatory networks in the resistant context. Ongoing genome-wide CRISPRi screening continues to reveal novel genetic interactions that contribute to the resistant phenotype. These findings highlight the complex regulatory rewiring in echinocandin resistant C. albicans and provide a foundation for uncovering genetic vulnerabilities in drug-resistant C. albicans.

Retrobiosynthesis of privileged pharmaceutical scaffolds from non-standard amino acids
Hirano, Mika* Kowalski, Devin, Pyne, Michael
The University of Western Ontario

Brewer's yeast (Saccharomyces cerevisiae) produces low-molecular-weight flavor compounds via the Ehrlich pathway, which catabolizes amino acids into fusel byproducts. Recently, the yeast Ehrlich pathway has been rewired to produce opioid analgesics and over 2,000 plant benzylisoquinoline alkaloids (BIAs) derived from L-tyrosine. Engineered yeast BIA strains were observed to generate a variety of new-to-nature tetrahydroisoquinoline (THIQ) scaffolds through Ehrlich pathway catabolism of endogenous amino acids. However, it remains unclear whether non-standard amino acids can serve as nitrogen sources for THIQ biosynthesis. Here, I present an Ehrlich-inspired retrobiosynthesis of several THIQ scaffolds used in the synthesis of alkaloid drugs starting from non-standard amino acids and provide an update on our ongoing efforts to convert a THIQ scaffold (1-phenethylisoquinoline) towards a natural product pharmaceutical (colchicine). Collectively, our work unveils new metabolic routes to untapped classes of plant natural products and enables the targeted overproduction of pharmaceuticals traditionally produced using plant extraction and chemical synthesis.

Population genomic evidence for a-a and a-a sexual reproductions in an environmental Cryptococcus deneoformans population
Hitchcock, Megan*. Thorn, Veronica. Samarasinghe, Himeshi. Sun, Sheng. Heitman, Joesph and Xu, Jianping.
McMaster University

The Cryptococcus neoformans species complex (CNSC) is a critical priority fungal pathogen capable of both a-a and a-a sexual reproduction in laboratory settings. However, its mode of reproduction in natural populations remains largely unknown. Here we analyzed the whole-genome sequences of 24 environmental strains of C. deneoformans from Saudi Arabia. Single nucleotide polymorphisms (SNPs) were identified for both the nuclear and mitochondrial genomes and the four-gametes test was used to test for signatures of recombination. The nuclear genome SNP pairs located further apart on the same chromosome showed greater phylogenetic incompatibility consistent with patterns of recombination. In addition, signatures of recombination were identified within the MAT locus among the MATa isolates, suggestive of a- a mating. Together, these results provide evidence consistent with both a-a and a-a sexual reproduction within an environmental population of C. deneoformans.

The genomic making of yeast metabolic diversity
Chris Todd Hittinger*
University of Wisconsin - Madison

Yeasts of the ancient fungal subphylum Saccharomycotina have evolved to occupy every continent and biome across more than 400 million years. Much is known about genetic model systems, such as Saccharomyces cerevisiae and Candida albicans, but little is known about how their diverse metabolisms have evolved and are encoded in their genomes. Better understanding how they manage their carbon and energy budgets promises to help build a sustainable bioeconomy. Here, I will present results from the Y1000+ Project (http://y1000plus.org), which has sequenced the genome of nearly every known yeast species. I will focus on global topics, future directions, and those not being presented by lab members.

High glycolytic rate driven by transcriptional activation in a non-conventional yeast
Horianopoulos, Linda*, Rokas, Antonis, Hittinger, Chris Todd
University of Wisconsin-Madison

The model yeast Saccharomyces cerevisiae is famous for its rapid fermentation. However, this trait is not conserved across yeasts. To better understand the range of fermentative capacity across yeasts and the mechanisms underlying this variation, we assessed the glycolytic rates of diverse yeast species by measuring glucose dependent extracellular acidification rates (ECAR). Through this approach, we identified several poorly characterized species within the genus Saturnispora with rapid-ECAR, high glycolytic rates, and ethanol production even under aerobic conditions. Through comparative transcriptomics, we found that many glycolytic genes had higher expression in rapid-ECAR species. We interrogated their putative promoters and found that rapid-ECAR species had more GAL4 binding sites. Through targeted genetic manipulations, we functionally confirmed the Gal4 transcription factor is required for the high glycolytic rate phenotype. Taken together, these results show an independently evolved mechanism to increase glycolytic flux through transcriptional activation in a novel group of yeasts.

Developing and Testing the Efficacy of a Topical Probiotic on Captive Bats to Prevent White Nose Syndrome

Insuk, Chadabhorn*; Forsythe, Adrian; Fontaine, Nick; Tobin, Abigail; Lawrence, Sara; Yoell, Heather; Abraham, Celeste; Lausen, Cori; Cheeptham, Naowarat; Xu, Jianping#
McMaster University

Without proper intervention, wildlife diseases can have drastic consequences for species. White-nose syndrome (WNS) has devastated populations of several North American bat species. Four synergistic bacterial isolates with high anti-Pseudogymnoascus destructans (Pd) activities were sourced from skin microbiomes of naïve bats in British Columbia. We applied a mixture of these four Pseudomonas bacteria to bat roosts, and examined the survival and growth of these bacteria on wings of roosting bats in summer and during hibernation. We confirmed long-term adherence and successful transfer of these microbes to the wings of bats within the local population. Probiotics showed no adverse health effects on bat wing tissues. The probiotic genomes exhibited putative genes involved in the syntheses of antifungal compounds and siderophores. Probiotic cells on roosts and wings showed negative correlation with Pd cells in Washington State field trial. Our probiotics mixture represents a promising biocontrol agent against WNS in the Pacific Northwest.

Investigating impact of gene presence and species variation on mutation and selection across codons in eukaryotes

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Why are synonymous codons that code for the same amino acids used at unequal frequencies across the genome? One reason is that synonymous codons influence cellular translational and transcriptional dynamics. Therefore, we know that codon usage is shaped by both neutral and selective forces and that the balance between these two forces varies between species. We are investigating the factors shaping this balance. Leveraging the Ribosomal Overhead Cost version of the Stochastic Evolutionary Model of Protein Production Rates (ROC-SEMPPR) to disentangle the effects of natural selection from mutation biases on a comprehensive dataset of 1,154 sequenced yeast genomes, we hypothesize that species-specific genomic features and gene presence significantly shape the mutation-selection equilibrium. We are testing whether the presence or absence of genes and variations in species characteristics (genotype, phenotype, environment) correlate with codon-specific mutation and selection rates. Through data visualization and statistical modeling, this work aims to analyze the extensive metadata associated with these genomes. This approach will reveal how genomic and biological features drive codon shifts, enhancing our understanding of codon evolution in eukaryotes. The findings will refine the application of codon usage metrics in evolutionary studies and optimize heterologous gene expression by accounting for species-specific and gene-specific variations in translational selection. This research addresses fundamental questions about the dynamics of codon evolution and its impact on gene expression, contributing to a deeper understanding of translational dynamics across diverse eukaryotic lineages.

Disturbance affects diversity of arbuscular mycorrhizal fungi communities in Ontario tallgrass prairies

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University of Western Ontario

This study investigated the differences in community composition of arbuscular mycorrhizal fungi (AMF) between disturbed and undisturbed tallgrass prairies at five locations across southwestern Ontario. Genomic DNAs were extracted from soil samples and a portion of the V4 variable region of the small ribosomal subunit was amplified and used to identify AMF present, found to represent ten genera of Glomeromycota. There was a significant difference in the community composition of the undisturbed TGP remnants and the restored TGP, with lower species diversity in the disturbed than the undisturbed sites. Diversispora and unidentified species of Entrophospora and Septoglomus were found to be potential indicators of disturbed TGPs, whereas Ambispora fennica, Diversispora, and an unidentified Glomus were found to be potential indicator taxa of undisturbed TGPs. Indicators of undisturbed sites are likely sensitive to mechanical disturbance such as tillage. These findings have implications for TGP restoration and the conservation of AMF diversity.

The discovery and effect of long-standing mild-effect mutator allele in S. cerevisiae populations

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Mutations are the source of genetic variation and a prerequisite for evolution. Despite their fundamental importance, their rarity makes them expensive to detect and difficult to study. To address this limitation, we leverage natural polymorphisms, which are historical mutations that passed the sieve of evolution, as a tool for detecting the change of mutational process in evolutionary history. We performed PCA analysis on the mutation spectra from natural polymorphisms on a few species of Saccharomyces yeasts, chosen for extensive prior population genomic and ecological knowledge and amenability for controlled lab studies. Intriguingly, strains from S. cerevisiae African beer population exhibited a conspicuous pattern in mutation spectrum, in the opposite direction from other strains, even surpassing some between-species mutation spectrum variations. Notably, a subset of French dairy strains displayed intermediate mutation spectra, and further in silico analysis is consistent with the presence of mutator alleles for A>C mutations introgressed from African beer strains. To test this hypothesis, we integrated a reporter into the genomes of several African beer and French dairy strains to be able to perform the modified fluctuation assays. Our de novo mutation spectra in these strains are in support of this hypothesis, with a very mild mutator effect. De novo mutations also surprisingly exhibited greater variation in mutation types beyond A>C, suggesting that mild mutators are more likely to preserve during evolution than strong ones. In summary, our study reveals patterns and processes of mutation rate and spectrum evolution in natural populations of budding yeast.

Unraveling the potential of whole-cell fungi cultures, enzyme extracts and mediator-enhanced systems for biodeterioration of microplastics

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Microplastics are persistent growing contaminant that requires significant attention. The ability of white-rot fungi to adapt in diverse environments make them promising candidate for the mitigation of microplastics. Microbial attachment, as well as extracellular and intracellular enzymatic action on its surface, are the primary mechanisms of microplastic biodegradation. One of the objectives of this study is to investigate at these underlying processes and compare the efficacy of whole-cell fungal systems of white rot fungi, Trametes hirsuta, against crude enzyme extract and mediator-enhanced system in achieving microplastic transformation. Microscopic analysis indicated considerable cellular proliferation around microplastics. There was an increase of about 4.9% in Mw value of microplastics after 90 days of incubation with whole-cell culture. However, the inhibition of intracellular enzyme CYP450, also achieved similar Mw change. In contrast to whole-cell culture, crude enzyme extract showed no Mw changes. However, the mediator-enhanced systems (ABTS, guaiacol) displayed indications of microplastic biodeterioration.

Identifying the symbiotic fungi of the endangered Ram's-Head Lady Slipper orchid in Nova Scotia, Canada

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Acadia University

Cypripedium arietinum is an endangered orchid found in Eastern North America. We are identifying the symbiotic fungi this plant requires for seed germination and nutrient transfer. Roots were collected in the Summer of 2024 from all known C. arietinum sites in Nova Scotia.

Roots were examined for fungal peloton structures and dissected to isolate fungi onto selective media. DNA was extracted from 114 of the resulting isolates and 73 identified through ITS rDNA barcoding. Fungal DNA isolated directly from root tissue revealed 115 genera using

PacBio amplicon sequencing. Seeds were collected in the late Summer of 2024 for ex situ seed baiting germination trials, to target fungi specifically involved in seed germination. Multiple known orchid symbionts have been identified thus far, most notably from the genus Tulasnella; however, none of the samples that we have identified to this genus have been formally described. Taxonomic placement and sequencing of additional loci are underway to formally describe these Tulasnella species. The results of the seed baiting trials are still pending, but will undergo similar microscopy, molecular, and data analysis procedures if orchid seed germination is successful. We aim to fill this crucial knowledge gap regarding C. arietinum and identify fungi that play essential roles in the germination and growth of this endangered plant, which has relevance for propagation and conservation.

Diverging soil peroxidase activity under ectomycorrhizal versus arbuscular mycorrhizal conifers with increasing C:N and exchangeable manganese

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BC Ministry of Forests

Ectomycorrhizal fungi (EMF) are purportedly involved in the enzymatic decay of soil organic matter (SOM), in contrast to arbuscular mycorrhiza (AMF). We tested this distinction in a 30-year-old mixedwood conifer trial by comparing peroxidase activity (including manganese-peroxidase [MnP]), fungal communities and mass of the humus layer between Pseudotsuga menziesii (EMF), Thuja plicata (AMF), and a 50:50 mixture across a natural productivity gradient. We found total peroxidase diverged between hosts as humus C:N ratio increased, culminating in 3- to 4-fold greater enzyme activity for EMF on low fertility soils. This soil effect also correlated significantly with exchangeable Mn, highlighting a possible further restriction on SOM turnover by EMF. Peroxidase activity was well aligned with Piloderma olivaceum and Piloderma sphaerosporum. This research highlights the adaptive enzymatic capacity of EMF communities, and underscores how soil properties (low N or high Mn) may enhance peroxidase production and SOM turnover in EMF forests

Identification of chloroplast associate effectors of the biotrophic pathogen Ustilago maydis

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UBC

Ustilago maydis a biotrophic plant pathogenic fungus which colonizes meristematic plant tissue and forms chlorotic tumors in the infected plant organs. Chloroplastic functions including photosynthesis are known to be down-regulated in gene expression in the infected tumor forming tissues. Chloroplasts are important for primary plant metabolism such as photosynthesis, secondary metabolism precursor formation or plant immunity via plant defense hormone biosynthesis. Thus, chloroplasts are a prime target for disruption of its function by pathogen effectors. We employed proteomics of isolated chloroplasts of leaves of infected Zea mays seedlings at 3, 5 and 7 dpi to identify putative Ustilago effectors of the chloroplast. The identified putative chloroplastic effectors were bioinformatically analyzed for chloroplast transit peptides and the best hit, Pce3 was further characterized. Protein pulldowns with Pce3 in the non-host Arabidopsis thaliana identified a chloroplast localized DEAD box RNA helicase RH3 as effector target. High expression of Pce3 in Arabidopsis led to similar phenotypes as known for RH3 deficient Arabidopsis lines, ranging from changes in plant morphology, chloroplast assembly, photosynthesis, and resistance to biotic and abiotic stresses. Overall, this work sheds light on the chloroplast as a target of biotrophic fungal pathogens and identifies RH3 as a mechanism by which pathogens manipulate the function of this host organelle.

Investigating Secondary Metabolism in the Human Pathogen Talaromyces marneffei
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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 ~58 biosynthetic gene clusters (BGCs) linked to secondary metabolism, nearly doubling previous estimates. Co-culturing experiments between T. marneffei and ESKAPE pathogens were conducted to promote production of bioactive small molecules. Together, these experiments advance our understanding of secondary metabolism in an important human pathogen and highlight its potential as a source of natural products.

Metschnikoff's Yeast
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In 1884, Metschnikoff published groundbreaking observations of yeast ascospores stabbing the guts of water fleas and being attacked by phagocytes, earning him the 1908 Nobel prize. He named the yeast Monospora bicuspidata, which taxonomists later reassigned to Metschnikowia, Monosporella, and Metschnikowiella, only to be declared a nomen dubium in 1961. While its taxonomy has remained obscure, the yeast has been adopted by several laboratories as part of a model system for host-pathogen interactions, under the name Metschnikowia bicuspidata. Sequence-based studies have now shown that although Metschnikowia bicuspidata is indeed a pathogen, it is not Metschnikoff’s yeast. I have examined fresh specimens of the Daphnia pathogen and explored its genome to clarify its systematics. I shall present a new genus and species assignment as well as evidence that the organism has lost the ability to reproduce sexually while retaining ascospore formation as an infection mechanism.

Ecology of northern red oak (Quercus rubra) tree wound communities in Maritime Canada

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Tree wounds represent important and understudied ephemeral habitats where diverse biological communities can form complex interactions. Wounds on living trees are unique from other ephemeral habitats where insect and fungal community ecology is better understood (e.g., phytotelma and coarse woody debris). This is because living trees respond to wounding by closing off affected tissues and this could alter community trajectories within a short timeframe.

Arthropods and fungi that can colonize living tree wounds represent an important component of forest ecosystems as they can contribute to habitat heterogeneity and can be important from a forest pest or pathogen perspective (e.g., oak wilt disease; Bretziella fagacearum [deBeer]).

This study examined tree wounds deliberately created on red oak trees (Quercus rubra L.) in an Acadian old growth forest located in New Brunswick, Canada over three consecutive years to identify arthropod and fungal species that recruit to these environments and characterize community changes at different time scales.

One signal, two kingdoms: Decoding plant signals in fungi
Ly, George. Bradley, James. Montague, Freddie R. Byun, Eric. Bunsick, Michael. McCourt, Peter. Bonetta, Dario. *Lumba, Shelley.
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Plants use hormones to regulate growth and development, but also as important environmental communication signals for plants and fungi in the rhizosphere. Although plant-fungal interactions are essential in ecosystems and agriculture, we have a limited understanding of how plants and fungi use small molecules to communicate. In my presentation, I will discuss the molecular mechanisms by which fungi respond to two critical plant hormones, strigolactones (SLs) and auxin. Using the fungal model system, Saccharomyces cerevisiae (baker's yeast), we demonstrate that SL and auxin hijack primary metabolic pathways in a variety of fungi. SL depletes phosphate (Pi) in fungi by binding a secondary site in a high-affinity Pi transporter, causing it to internalize (Bradley et al., 2024). SL-regulated Pi responses are conserved in a plant endophytic fungus called Serendipita indica and the pathogen, Fusarium graminearum. Secondly, we uncover an effect of auxin on nitrogen metabolism in fungi. Our discoveries have led to the identification of novel classes of small molecules that target critical metabolic pathways in fungi, opening up new classes of potential antifungals and druggable targets. Our results also address longstanding evolutionary questions about the molecular dialogue between plants and fungi.

Systemic Mycosis in a Ferret: Diagnostic Challenges and Pathogen Insights
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Fungal infections are common in animals, but systemic mycoses are rarely documented in small exotic species like ferrets. We present a case of a disseminated fungal infection in an immunosuppressed ferret undergoing treatment for lymphoma at the Ontario Veterinary College. During therapy, the ferret developed progressive neurological signs and was subsequently euthanized due to clinical decline. Histology revealed fungal hyphae within the cerebral cortex and lungs, consistent with a filamentous fungus. Fungal DNA sequencing from affected tissues identified the pathogen as Aspergillus spp. This case highlights the importance of recognizing fungal infections in non-traditional species, which can serve as sentinels for environmental exposure and contribute to our broader understanding of fungal disease dynamics within a One Health framework.

Hi-C and HiFi PacBio Sequencing Unveils Genome Compartmentalization and RNA Operon Physical Interactions in Gigaspora margarita

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Ottawa University

Arbuscular mycorrhizal fungi (AMF) are widespread root symbionts that improve nutrient acquisition for most plants. Recent advances in long-read sequencing and chromatin conformation capture (Hi-C) technologies have enabled chromosome-level assemblies and 3D-genome analysis in the model species Rhizophagus irregularis. However, whether the findings such as A/B compartments, associated with active and repressed chromatin, respectively, are conserved across AMF species is unclear. There also exists an open question on whether the chromosome 3D-genome conformation of these fungi changes depending on surrounding conditions. We aim to combine HiFi PacBio sequencing with Hi-C to produce a chromosome-scale assembly of Gigaspora margarita. The complete assembly reveals 43 chromosome-level scaffolds with 20 divergent rDNA copies distributed across six chromosomes. Hi-C analysis confirms the presence of A/B compartments in G. margarita, indicating that this genome organization is universal among AMF. Remarkably, these compartments are dynamic, switching in response to the endosymbiotic bacterium Candidatus Glomeribacter gigasporarum (CaGg), and we present evidence for the physical interaction of rDNA copies in AMF, presumably within the nucleolus. Overall, our findings provide a deeper understanding of the AMF nuclear genome biology, highlighting the plasticity and molecular function of their 3D genome.

Unraveling Multitrophic Interactions: The Influence of Mycetophagous Mites on Fungal Symbionts in the Mountain Pine Beetle System
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University of Alberta

The mountain pine beetle (Dendroctonus ponderosae) plays a major role in conifer forest decline across western North America. Its success is partly driven by symbiotic fungi, notably Grosmannia clavigera, Leptographium longiclavatum, and Ophiostoma montium, which aid in nutrient acquisition and tree colonization. However, the role of associated mycetophagous mites remains understudied. This research examines the impact of Histiogaster arborsignis feeding on fungal symbionts. In vitro assays revealed that mite exposure significantly reduced ergosterol content in G. clavigera and L. longiclavatum, suggesting negative effects from grazing. Preference tests showed mites favored O. montium at 4 and 24 hours but suffered high mortality after 48 hours. Interestingly, O. montium appeared to utilize dead mites as a food source, indicating a shift toward opportunistic nutrient recycling. These findings reveal complex multitrophic interactions and highlight the potential for mites to influence fungal dynamics central to MPB ecology and forest health.

Regulation of antifungal drug resistance by catalase in Candida albicans
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Catalase (CAT1) plays a key antioxidant role in Candida albicans, protecting cells from oxidative stress and contributing to pathogenicity. To elucidate its function, the gene encoding catalase, CAT1, was deleted through targeted gene disruption using CRISPR/Cas9. Functional analyses revealed that CAT1 expression confers resistance to oxidative stress, particularly to H2O2. The cat1?/? mutant shows increased sensitivity to hydrogen peroxide, as well as to amphotericin B, and caspofungin. On the other hand, it exhibits increased tolerance to azoles. These findings suggest that CAT1 plays a role in responses to antifungal drugs. Future studies will assess whether antifungal treatments induce CAT1 expression or activity and if this response enhances cellular protection. We will also investigate catalase’s localization and regulation under stress, aiming to clarify its role in drug resistance and pathogenicity.

A multi-genome analysis of structural variants and transposable elements across Candida albicans

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Candida albicans represents a major challenge on global health, largely due to its rapid evolution of antifungal drug resistance. Beyond point mutations, structural variants (SVs), and in particular transposable elements (TEs), are an important but understudied source of adaptation. To comprehensively investigate SVs across clinical isolates of C. albicans, we performed long-read sequencing and genome-wide analyses of SV and TE in distantly related isolates. Our findings reveal a genome-wide distribution of SVs and TEs, with frequent TE insertions located near genes. Most SVs and TEs are uniquely to a single clinical isolate or clade, and TEs are often hemizygous or fragmented. TEs or fragments frequently co-occur with other types of SVs, indicating they may trigger subsequent chromosomal rearrangements. Despite the generally low TE content, our findings indicate the importance of TEs on genome evolution and allele-specific gene expression beyond their direct transpositional activity.

Deleterious shifts in root-associated fungi after high-severity wildfire

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BC Ministry of Forests

The response of fungal communities to wildfire across burn severities has important implications for recovery in Douglas-fir forests in British Columbia. Low-severity fires showed minimal differences from unburned stands, whereas high-severity fires caused a 91% decline in ectomycorrhizal fungi, and 5-27 fold increase in pathogenic fungi. Root systems of Douglas-fir seedlings mirrored these trends, with ectomycorrhizal decline and pathogen proliferation in high-severity stands. Despite high pathogen load, seedling biomass was greater at high-severity sites, driven by increased light availability. Notably, fungi within the orders Tremellodendropsidales and Sebacinales thrived in high-severity sites; these root-associated fungi generally have positive interactions with plants, including stress and pathogen resistance, potentially countering the rise in pathogenic fungi. These mesic study sites appear to be resilient, but it remains to be seen if high post-fire pathogen load results in deleterious effects on seedling performance under more xeric site conditions.

Thermotolerant insects as potential environmental niche for Candidozyma auris
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University of the Free State

The environmental niche and mode of transmission from the environment to humans of the emerging pathogenic yeast, Candidozyma auris is a subject of speculation, with hypotheses including avian species and marine environments. Interestingly, yeasts related to C. auris are associated with various insects. This prompted us to investigate a thermophilic insect, Locustana pardalina as possible host for C. auris. Here we report the isolation and identification of three C auris strains from the gut of L. pardalina as well as the phenotypic characterisation of one of these isolates. Interestingly, the isolate was able to survive at 50oC and grew at 15% NaCl. In addition, it was susceptible to the tested disinfectants and antifungals, except fluconazole. Genome sequencing and single-nucleotide polymorphism analyses placed the isolate in Clade III, which is common in South African hospitals. This highlights the potential role of thermotolerant insects in the evolution and dissemination of emerging pathogenic yeasts.

Screening and engineering non-conventional yeasts for production of organic acids
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Western University

Engineered yeasts hold great promise for displacing unsustainable routes to valuable chemicals, yet brewer’ yeast is unequipped to tolerate product concentrations required for commercial-scale production. This research summarizes our efforts to identify a robust acid-tolerant yeast for bioproduction of adipic acid (AA), a monomer used to synthesize nylon. I will recap our screening of 122 yeast strains for tolerance to AA and our subsequent domestication of Pichia occidentalis, a species resistant to high concentrations of AA. I will also highlight our methodologies to engineer P. occidentalis to produce 40 g/L of cis,cis-muconic acid (CCMA), the direct precursor to AA. Finally, I will provide an update on our progress to again screen non-conventional yeasts, this time for a novel enzyme capable of hydrogenating CCMA to AA. Our work identifies new prospective hosts and enzymes for overproducing toxic metabolites and showcases the benefits of tailoring microbial strains to target end products.

Candida albicans' phosphate acquisition and starvation response
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Candida albicans is the most common invasive fungal pathogen in humans. It's growth and survival in the host relies on rapid response to nutrient availability, which is regulated by Target Of Rapamycin Complex 1 (TORC1) signaling pathway.
One of the essential macronutrient monitored by TORC1 is inorganic phosphate (Pi). Out of the 4 Pi transporters identifiable in the C. albicans genome, single-, triple- and quadruple mutants were constructed. Analysis showed Pho84 is the most active Pi transporter at acidic and alkaline pH, and is the only one required for normal TORC1 signaling.
In vitro evolution was performed on 6 quadruple mutants lacking all 4 Pi transporters, by serial passage in Pi scarcity for 2 months. Stress phenotype analysis demonstrated different lineages evolved distinct stress response trajectories.
Whole genome sequencing (WGS) of 2 lineages showed during Pi starvation response, early large-scale genomic rearrangements were replaced by later small-scale mutations in specific genes, skewed towards those related to TORC1 signaling.

New insights into ER stress regulation in Candida albicans
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Eukaryotic cells rely on the Unfolded Protein Response (UPR) to maintain secretory protein homeostasis in the endoplasmic reticulum (ER) by detecting misfolded protein accumulation. The UPR activates transcriptional programs that adjust ER folding capacity and restore cellular balance. In yeast, Ire1 detects ER stress and initiates UPR signaling by cleaving HAC1 mRNA, enabling translation of Hac1 transcription factor, which activates ER quality control genes. While well-characterized in Saccharomyces cerevisiae, UPR function in fungal pathogens remains poorly understood. Candida albicans, a major threat to immunocompromised patients, exhibits increased antifungal sensitivity and reduced virulence when UPR-deficient, including impaired filamentous growth—a key pathogenic trait. However, the specific UPR target genes underlying these phenotypes are unknown. In this project, we investigate how UPR modulation impacts C. albicans drug resistance and pathogenicity, aiming to identify the molecular mechanisms responsible for these critical phenotypes.

Synthesizing Ephedrine from Sugar in Saccharomyces cerevisae
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Western University

Phenylpropylamino alkaloids are a class of pharmaceuticals that have been used for 5,000 years. Ephedrine—which prevents hypotension in surgery—is on the World Health Organization's list of essential medicines. Ephedrine is synthesized semi-synthetically; yeast convert exogenously-supplied benzaldehyde to (R)-phenylacetylcarbinol (PAC), which is chemically converted to ephedrine. However, unidentified yeast oxidoreductases reduce (R)-PAC production by converting benzaldehyde to byproducts. Further, benzaldehyde is produced from toluene, which derives from environmentally harmful petroleum refining processes. Here we describe a yeast-based platform for the de novo production of phenylpropylamino alkaloids. We propose a retrosynthetic route to PAC via Saccharomyces cerevisiae Ehrlich pathway catabolism of the non-standard amino acid ?-Phenylglycine. By knocking-out oxidoreductases, we increase PAC production and decrease formation of benzaldehyde-derived byproducts. We then extend the pathway to produce the phenylpropylamino alkaloids norephedrine, ephedrine, norpseudoephedrine, and pseudoephedrine. This framework enables the design of de novo retrosynthetic routes to other high-value bioproducts.

A genome-wide survey identifies a gene cluster involved in tensidol biosynthesis in Aspergillus niger
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The genome of Aspergillus niger contains a large repertoire of biosynthetic gene clusters (BGCs) involved in secondary metabolism. Fungal BGCs are seen as a rich source of novel secondary metabolites; however, discovery of these compounds is hampered by the cryptic nature of these BGCs under laboratory conditions. To characterize secondary metabolism in A. niger, we created a collection of strains each overexpressing a single BGC-associated transcription factor. Using a multi-omics analysis pipeline, we identified a previously uncharacterized BGC involved in the production of tensidol B, a potentiator of miconazole activity against the human pathogen Candida albicans.

Pathogenomics of Heterobasidion occidentale, a fungus that causes annosus root and butt rot among conifer trees in North America – Research Update
Grace Sumampong*, Jun-Jun Liu, Louis Bernier and Simon Shamoun
Canadian Forest Service, Pacific Forestry Centre

Heterobasidion occidentale, is a fungus that belongs to the H. annosum (Fr.) Bref sensu lato species complex that comprises five species of root rot pathogens. Heterobasidion occidentale causes annosus root and butt rot primarily in true fir (Abies spp.) and spruce (Picea spp.) species throughout western North America. In the last few years, our research has focused on constructing an annotated draft genome and characterizing transcriptomes to reveal candidate genes for virulence variations ideal for marker development as a diagnostic tool. Today we will provide a summary of our current research activities focused on the identification of Taqman-based markers able to distinguish H. occidentale from other Heterobasidion species in North America (H. irregulare) and Europe (H. annosum sensu stricto, H. parviporum and H. abietinum).

Tropical lichens from Campeche, Mexico
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In Mexico, as in many other tropical regions, lichen diversity is high. However, increased taxonomic studies are needed to expand our understanding of the lichen biota. Of the 2,722 species recorded for the country, only 4.52% are recorded in the Yucatán Peninsula, which is comprised of the states of Yucatán, Quintana Roo, and Campeche. Despite this, the Yucatán Peninsula is an area of high biodiversity, featuring species endemic to dry and humid tropical forests and mangroves. This study was carried out in Campeche, which has 17 reported lichen species. Branches of vascular plants with lichens were collected from two dry deciduous tropical forests in Campeche. Fifty species belonging to 38 genera were identified, of which 92% are crustose lichens. These results increase the state of lichen richness and underscore the importance of continuing lichen inventories to expand our knowledge of the lichen community.

Evolution of fungal secondary metabolism: the rich and the poor of the fungal world

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Metabolic innovations mark a crucial turning point in the evolutionary divergence of fungi and animals. Recent advances in omics-enabled biosynthetic exploration, combined with automated genome-mining pipelines, have revolutionized our ability to compare biosynthetic gene cluster (BGC) diversity across fungi and to uncover widespread, yet previously overlooked, pathways—such as those involved in ribosomally synthesized peptides and isocyanide synthases. These tools enable us to perform large scale genome mining and BGC comparison to understand how lifestyle influences the evolution and distribution of BGCs across different fungal lineages.

By comparing nearly 300 genomes—including those of lichen-forming fungi (LFF) and non-lichenized fungi—large-scale analyses reveal that lichens are significantly enriched in biosynthetic gene clusters (BGCs) compared to their non-lichenized counterparts. Notably, polyketide synthases (PKSs) dominate the biosynthetic landscape in LFF, followed by non-ribosomal peptide synthetases (NRPSs) and terpene synthases. Ribosomally synthesized peptides account for nearly 20% of the biosynthetic repertoire, while pathways previously considered rare—such as type III PKSs and isocyanide synthases—are found to be more widespread than anticipated. Despite this metabolic richness, BGC clustering analyses reveal a striking gap: only a small fraction of these clusters has been functionally characterized, leaving the vast majority unexplored. These uncharacterized clusters likely encode novel chemical scaffolds and hold untapped ecological and pharmaceutical potential.

These findings not only reinforce the status of lichens as reservoirs of unexplored metabolic diversity but also provide a genomic foundation for predicting metabolite function and ecological relevance. This omics-informed framework is critical for guiding future efforts in drug discovery, natural product chemistry, and evolutionary biology.

Investigating anastomosis and genetic exchange between commercial and non-commercial arbuscular mycorrhizal fungi in soil

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Arbuscular mycorrhizal fungi (AMF) are applied as bioinoculants worldwide to enhance plant growth. However, introducing fast-growing foreign bioinoculants into novel environments may cause invasion, and anastomosis—hyphal fusion—may be a mechanism to do so. AMF individuals can anastomose with counterparts, allowing genetically distinct nuclei to mix, but this has so far only been observed in vitro. To address whether anastomosis occurs in soil, a commercial and non-commercial isolate of AMF were grown together in pots. Individual spores were analyzed to determine if they contained commercial, non-commercial, or both genotypes. Although in low abundance, we detected both genotypes in several spores, indicating that anastomosis and genetic exchange occurred. This indicates that foreign AMF could anastomose and infiltrate a native mycelial network through nuclear competition. Therefore, this should be further explored to better understand the invasive potential of commercialized fungi.

Validation and application of a metagenomics protocol to the root-associated fungal communities of Northern wild rice (Zizania palustris)

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The occurrence of root-associated fungi is not yet fully understood in wetland plants, despite recent indications that some contain diverse mycobiomes, including potential plant mutualists. Although arbuscular mycorrhizal fungi (AMF) can be neutral and even parasitic, there is emerging evidence that AMF provide benefits to many wetland plants, as in terrestrial soils. Dark septate endophytes (DSEs), occur in wetland plants at similar or greater frequencies than AMF, and may also confer benefits to host plants. Zizania palustris (Northern wild rice, manômin) is an emergent annual macrophyte found in shallow lakes and slow-moving rivers in central and eastern North America, where it is harvested from both wild stands and cultivated paddies. Despite the significance of this plant to Indigenous peoples and emerging agricultural interests, its' broader mycobiome has yet to be fully characterized. Microscopic examination of manômin roots from mesocosm studies shows DSEs are common, and some exhibit structures consistent with AMF yet fungal diversity in traditional rice lakes or wild stands is currently unknown. Here, we present an early assessment of rhizosphere diversity of wild stand Zizania using ITS and 18S targeted amplicon sequencing, and describe incidence of fungal tissue within roots of this culturally-significant wetland plant.

Ecology and Evolutionary Genomics of Graminella pipettiformis, a Novel Trichomycete Fungus from Rouge National Urban Park, Canada
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Trichomycetes are obligate gut-dwelling fungi found in aquatic insect larvae and nymphs in freshwater habitats. We report a new species, Graminella pipettiformis, isolated from the hindgut of Baetis sp. (Ephemeroptera) nymphs collected in Rouge National Urban Park, Canada. This is the fourth formally described Graminella species. G. pipettiformis is morphologically distinct from previously described Graminella species by its pipette-shaped holdfast, absence of lower branches from the basal cell, and significantly smaller trichospores. Using culture-independent methods, we generated the first genomic resource for G. pipettiformis the first whole-genome-wide dataset available for this genus. Phylogenomic analysis of 1,241 conserved Harpellales genes placed G. pipettiformis in the non-Smittium clade, closely related to Zancudomyces culisetae and Capniomyces stellatus. This work provides a genomic framework for unculturable fungal species and contributes to our understanding of fungal evolution in insect guts. It also lays the foundation for future genomic studies of trichomycetes inaccessible by traditional culturing.

Evolutionary shifts in competitive fitness of Candida albicans under drug exposure
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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. While fluconazole-driven adaptation in C. albicans is well-documented, the impact of evolving to different drug concentrations on the rate and breadth of adaptation remains unclear. We evolved C. albicans replicates through 10 serial bottlenecks to antifungal drug fluconazole under different concentrations (0.25-16 µg/ mL) and then measured the competitive fitness of all evolved replicates in all drug competitions. We used fluorescent-microscopic imaging and a machine learning algorithm to calculate competitive fitness. All evolved lines showed similar competitive fitness in lower drug concentrations. However, the lines evolved to higher fluconazole concentrations had much greater competitive fitness when assayed in higher drug concentrations. 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.

Divergent regulation of inositol synthesis pathways between Saccharomyces cerevisiae and the fungal pathogen Candida albicans.
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Candida albicans is an opportunistic yeast pathogen responsible for 1.6 million infections annually, with 200,000 cases resulting in death due to systemic dissemination. C. albicans rapidly develops resistance to antifungal treatments, many of which target lipid membranes. A key factor in this transition is membrane composition. Inositol, an essential molecule, serves as the head group for phosphatidylinositol (PI) in its simplest phospholipid form. Further modifications generate phosphoinositides for signaling and glycosylphosphatidylinositol (GPI) protein anchors critical for membrane integrity and virulence. While inositol biosynthesis is well-characterized in Saccharomyces cerevisiae, its regulation in C. albicans remains unclear. Unexpectedly, we found that C. albicans does not require canonical signaling pathways associated with inositol synthesis in budding yeast, including the unfolded protein response, suggesting alternative regulatory mechanisms. We hypothesize that C. albicans possesses a distinct genetic network controlling inositol biosynthesis, impacting drug resistance and pathogenicity. To map this network, we aim to identify key regulators through transcriptome analysis and antifungal tolerance assays. Understanding these pathways provide insights to the differential regulation of lipid biosynthesis across fungi.

Study of the antibacterial activity of Hericium and Hohenbuelia.
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The purpose of this study is to assess the antibiotic potential of Hericium and Hohenbuehelia through systematic testing against bacteria and identify potential antibiotic metabolites from them. Six?Hohenbuehelia?and eleven?Hericium?strains were grown on five agar media with differing carbon and nitrogen content. Mycelial plugs were taken 2 cm from the growing edge and placed on lawns of?five different bacteria; Escherichia coli, Staphylococcus aureus, S. lugdunensis, Pseudomonas aeruginosa, and Micrococcus luteus. After overnight incubation at 37 ?, the zone of inhibition was measured and used to assess antibacterial activity. There was significantly higher activity against Gram-positive bacteria and sporadic inhibition of Gram-negative species from both fungal genera. Hericium species showed significantly more antibiotic activity than Hohenbuehelia species. A strain of Hericium abietis demonstrated the most antibiotic activity. Isolation of metabolites from active fungi is underway where it is hypothesized pleurotin and erinacine A are the molecules responsible.

The clones attack: Emphasizing the adaptability of the butternut canker pathogen
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An aggressive forest pathogen Ophiognomonia clavigignenti-juglandacearum (Oc-j) has catalyzed the decline of the butternut tree (Juglans cinerea L.) to global endangerment. Though Oc-j varies in morphology and pathogenicity between isolates, these functional differences haven't been linked to its 3 genetically distinct clonal strains. We aimed to capture isolates across natural populations and then characterize the degree of functional variation between clonal strains. In 2023 we collected leaf and canker tissue from 260 trees across the range, producing >130 single-hyphal Oc-j isolates. Phylogenomic investigations have indicated substantial genetic diversity among isolates, though even genetically similar isolates have displayed significant growth speed differences in preliminary growth assays. This resource of a set of diverse living isolates with sequenced genomes contributes to our predictive capacity for butternut selection and to our understanding of the adaptability of different pathosystems.

Characterization of the role of UmAA10 CAZyme in the morphogenesis and pathogenesis of Ustilago maydis
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Ustilago maydis (Huitlacoche) is a culturally significant phytopathogen in Mexico but presents challenges to global agriculture due to its persistent infection of maize. Like other fungi, U. maydis undergoes extensive cell wall remodeling throughout its life cycle, facilitated by secreted carbohydrate-active enzymes. This work focuses on characterizing the role of auxiliary activity (AA) enzymes in fungal development and host interactions. Of particular interest is a single AA10 gene (UmAA10, UMAG_05439), which encodes a lytic polysaccharide monooxygenase active on both a- and ß-chitin. We hypothesize that UmAA10 contributes to cell wall remodeling and is essential for virulence. While gene deletion does not affect sensitivity to cell wall or membrane stressors, overexpression results in increased virulence and enhanced resistance to such stressors. Characterizing this enzyme will provide deeper insight into fungal cell wall dynamics and may inform broader studies across microbial species, as well as support applications in antifungal development or industrial biotechnology.

Partnership with ectomycorrhizal fungi benefits lodgepole pine seedlings against a root pathogen

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Armillaria root disease is one of the most serious forest diseases worldwide, threatening both conifers and hardwoods. These long-lived pathogens lead to root decay which inhibits water and nutrient uptake in plants. Ectomycorrhizal fungi are important symbionts of forest trees, and studies have shown that they can improve host tolerance to Armillaria infection. However, their effects vary with mycorrhizal species, and little research has focused on the effects of lodgepole pine (Pinus contorta) associated ECM fungi on Armillaria spp. In this study, we tested the effects of three lodgepole pine ectomycorrhizal fungi on two Armillaria species via three approaches: direct physical contact, volatile organic compound (VOC) assay (headspace), and cell-free supernatant (CFS) application. Our results suggested that all three ECM species can inhibit the growth of Armillaria spp. with direct contact while only Cenococcum geophlium inhibited Armillaria growth via VOC. Both Cenococcum geophilum and Coltricia perennis CFS reduced Armillaria growth but the degree of inhibition varied depending on the concentration applied. We further conducted a greenhouse experiment to validate the effects of the same ectomycorrhizal fungi on the two Armillaria spp. in lodgepole pine seedlings. We found that seedlings with ectomycorhizal fungi had higher shoot and root growth despite being infected by Armillaria spp. In addition, the co-inoculation of ectomycorrhizal fungi and Armillaria spp. on lodgepole pine seedlings increased the concentration of several major monoterpenes. These findings highlight that lodgepole pine associated ectomycorrhizal fungi can inhibit Armillaria growth via multiple mechanisms.

Pooled CRISPRi screening in Candida albicans reveals core-essential genes
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Candida albicans is becoming a challenge to treat due to rising antifungal resistance and limited therapies available. To identify fungal-specific vulnerabilities, we developed an inducible, scalable and portable CRISPR interference (CRISPRi) system for functional genomics analysis in C.albicans. We generated a pooled library of ~550 sgRNAs targeting 130 fungal-specific putative essential genes, and screened for dosage-sensitive genes under standard growth conditions using a barcode sequencing approach. To assess the portability and robustness of this approach, we performed parallel screens in two antifungal-resistant clinical isolates alongside the wildtype strain. Our pooled assays identified 68 dosage-sensitive genes, with approximately 50% of gene hits shared across all genetic backgrounds with enrichment in mitochondrial components, suggesting mitochondria as a promising, underexplored target space. Additionally, we assessed the wild-type pooled library across 11 environmental stress conditions and defined a set of core essential genes consistently sensitive across all conditions and strains.

Losses of deeply conserved genes in the Mitotic Exit Network led to multiple rewiring events in budding yeasts
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The mitotic exit network (MEN) is an ancient pathway in eukaryotes first discovered in Saccharomyces cerevisiae where it regulates an essential cell-cycle checkpoint. Despite being widespread among eukaryotes, the pathway has diverged in function and composition even within fungi. To understand how the MEN has evolved, we identified orthologs of all MEN components across over 1,000 species of Saccharomycotina yeasts and discovered that the S. cerevisiae composition is derived and that a critical component has been lost in Phaffomycetales yeasts. This loss led to rapid evolution of the downstream gene with striking functional consequences as revealed by complementation analysis.

Stress-driven emergence of heritable non-genetic drug resistance

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Drug resistance is a leading cause of treatment failure in infectious diseases. Here, we report a non-genetic mechanism of drug resistance in the human fungal pathogen Candida albicans 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. It is induced by transient exposure to subtherapeutic doses of the antifungal fluconazole and regulated in part by the histone deacetylase subunit Snt1 and the chromatin regulator Rap1. Notably, molecules that disrupt biomolecular condensation and prion-like inheritance block the induction of para-resistance, while histone deacetylase inhibitors promote it. We find that para-resistance is common among clinical isolates and, remarkably, passage through the mammalian gut triggers its acquisition, compromising the therapeutic efficacy of fluconazole in vivo. Our work defines a pervasive, prion-like epigenetic mechanism of stress adaptation and highlights potential strategies to mitigate the rapid emergence of drug resistance.

Characterizing Colony Formation in the Opportunistic Fungal Pathogen Candida albicans

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Candida albicans switches from harmless yeast to invasive pathogen by forming filaments—a process hard to quantify at scale. We assembled a large and diverse image library of colony morphologies across multiple growth conditions, paired with extensive metadata on strain background, culture parameters, clinical origins, and other relevant information.

We deployed convolutional variational autoencoders to learn compact latent representations of C. albicans microscopy images. Using these embeddings, our objectives are to (1) identify distinct colony-formation patterns across the isolate compendium and (2) correlate filamentation phenotypes with pathogenicity, disease severity, and other clinical and technical variables.

Our models produce high-fidelity reconstructions of filamentous structures and capture biologically meaningful variation. This framework enables rapid, automated profiling of C. albicans colony growth patterns, offering a scalable tool to link fungal form with function and disease potential—and to accelerate high-throughput screening of antifungal interventions.

Functional Portrait of the Candida auris Kinome

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Candida auris is an emerging multidrug-resistant and medical-care associated fungal pathogen. We constructed a barcoded conditional mutant strain library targeting 109 of 111 predicted C. auris kinases, using a tetracycline derivative-repressible promoter system (TETp-OFF) in the CBS12766 strain background. This resource enabled the systematic genetic perturbation of kinase expression, facilitating the identification of 10 potentially essential kinases and several others impacting in vitro fitness. Phenotypic profiling under cell-wall stress conditions revealed that C. auris relies on MAPK pathways to maintain cell wall integrity. Additional assays uncovered kinases regulating invasive growth, cell separation/aggregation and morphogenesis, linking them to nutrient adaptation and cell division. The signature-tagged design allows for multiplexed phenotyping in competitive growth assays. TETp-OFF-mediated gene repression was functionally validated in a murine model of systemic infection, enabling in vivo analysis of kinase function during pathogenesis. This genetic resource offers a powerful platform for dissecting signaling networks and advancing kinase-targeted antifungal strategies."