

The 4th Annual CanFunNet
Fungal Biology Conference
May 31 - June 2, 2023



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Thank you to our sponsors!

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About us

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Emile Glück-Thaler	Linda Horianopoulos
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Graphics	
Brent Robicheau (CFN23 logo)	Viola Halder
Conference Website	
Michael Zaigh	Conference Services at Western University

Condensed Conference Schedule

Wednesday, May 31, 2023				
11:45AM-12:00PM AST 10:45AM-11:00AM ET	Opening Remarks			
12:00PM-1:30PM AST 11:00AM-12:30PM ET	Plenary Session 1: Fungal Pathogens			
1:30PM-2:00PM AST 12:30PM-1:00PM ET	Break			
2:00PM-3:05PM AST 1:00PM-2:05PM ET	Horticultural Crop Pathology I (1A)	Fungal Disease in One Health I (2A)	Yeasts: More than a Model Organism (3A)	Fungal Genetics and Genomics I (4A)
3:05PM-3:30PM AST 2:05PM-2:30PM ET	Break			
3:30PM-4:35PM AST 2:30PM-3:35PM ET	Mycotoxins (1B)	Fungal Disease in One Health II (2B)	Medical Mycology (3B)	EvoFunPath (4B)
4:35PM-5:00PM AST 3:35PM-4:00PM ET	Break			
5:00PM-6:05PM AST 4:00PM-5:05PM ET	Horticultural Crop Pathology II (1C)	Fungal Disease in One Health III (2C)	Insights into Oomycetes (3C)	Fungal Ecology (4C)
6:30PM - 8:00PM AST 5:30PM - 7:00PM ET	Trivia & Research Roulette on Spatial Chat			

Condensed Conference Schedule

Thursday, June 1, 2023			
12:00PM-1:30PM AST 11:00AM-12:30PM ET	Plenary Session 2: Fungal Ecology & Conservation		
1:30PM-2:00PM AST 12:30PM-1:00PM ET	Break		
2:00PM-3:05PM AST 1:00PM-2:05PM ET	Lichen Biodiversity and Conservation I (5A)	Mycorrhizal Symbioses (6A)	Tribute to David Malloch (7A)
3:05PM-3:30PM AST 2:05PM-2:30PM ET	Break		
3:30PM-4:35PM AST 2:30PM-3:35PM ET	Lichen Biodiversity and Conservation II (5B)	Industrial Uses of Fungi (6B)	Fungal Pathogens of Forest Trees I (7B)
4:35PM-5:00PM AST 3:35PM-4:00PM ET	Break		
5:00PM-6:05PM AST 4:00PM-5:05PM ET	A Fungal Perspective on Conservation and Citizen Science (5C)	Endophytic Fungi (6C)	Fungal Pathogens of Forest Trees II (7C)

Condensed Conference Schedule

Friday, June 2, 2023			
12:00PM-1:30PM AST 11:00AM-12:30PM ET	Plenary Session 3: Fungi & Humans		
1:30PM-2:00PM AST 12:30PM-1:00PM ET	Break		
2:00PM-3:05PM AST 1:00PM-2:05PM ET	Canadian Fungal Collections & Collections-Based Research (8A)	Aquatic Fungi I (9A)	Fungal Genetics & Genomics II (10A)
3:05PM-3:30PM AST 2:05PM-2:30PM ET	Break		
3:30PM-4:35PM AST 2:30PM-3:35PM ET	Old Growth Forest Fungi (8B)	Aquatic Fungi II (9B)	Fungal Genetics & Genomics III (10B)
4:35PM-5:00PM AST 3:35PM-4:00PM ET	Break		
5:00PM-6:05PM AST 4:00PM-5:05PM ET	Fungal Genetics & Genomics IV (8C)	Aquatic Fungi III (9C)	Fungal Genetics & Genomics V (10C)
4:00PM-5:00PM AST 3:00PM-4:00PM ET	Workshop: Mining Mycoportal for Research		
6:30PM-7:00PM AST 5:30PM-6:00PM ET	Closing Ceremony on Spatial Chat		

Spatial Chat Schedule

Time	Event
May 31, 2023 - Wednesday 6:30PM - 8:00PM AST 5:30PM - 7:00PM ET	Trivia
	Research Roulette
June 2, 2023 5:00PM-6:00PM AST 4:00PM-5:00PM ET	Closing Ceremony
	Networking

Spatial Chat Guide

CanFunNet23 will be using Spatial Chat for our Networking events at the end of the first and last day of our conference. Please watch the following video to familiarize yourself with this social media platform: https://youtu.be/E03QN6Lr_Y0

Spatial Chat will be open for the duration of the CanFunNet23 conference.

When logging in to Spatial Chat, please use your full name. If you have any questions about the conference or about Spatial Chat, just use the spatial chat link to log in, and someone will be available in the Main Lobby to help you out.

Please use the following Code of Conduct when using Spatial Chat to ensure a safe and fun environment for all to enjoy.

Code of Conduct

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

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

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

Scavenger Hunt and Marketplace

You will be able to participate in a scavenger hunt through PheedLoop this year. Look for the mushroom logo (🍄) for the clues, then go into the scavenger hunt page to submit your answers (1 word, all caps). Each clue is worth 10, 25 or 50 points, depending on difficulty. You can also earn points (75!!) by participating in the networking events on spatial chat (Trivia and Networking).

You can claim these points in the marketplace, where you can purchase one of the following (note that inventory is limited and purchases are first come, first serve):

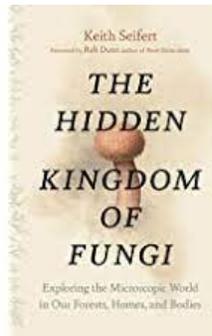
Indigo Gift Cards

\$25 or \$50

CanFunNet23 Mug



“The Hidden Kingdom of Fungi:
Exploring the Microscopic World in Our
Forests, Homes, and Bodies”
by Plenary Speaker Keith Seifert



Wednesday, May 31, 2023

Plenary Session 1: Fungal Pathogens

Moderated by: Dr. Alfredo Justo & Dr. Linda Horianopoulos

Plenary 1 - 12:00PM-1:30PM AST - Wednesday, May 31

12:00PM-12:30PM AST Plenary	James Kronstad Mechanisms for fungal sensing of the vertebrate host environment
12:30PM-1:00PM AST Plenary	Romina Gazis Tropical plant pathology: a challenging but rewarding field!
1:00PM-1:30PM AST Plenary (NR)	Christian Landry Understanding the evolution of antifungal resistance using genome editing and experimental evolution

Horticultural Crop Pathology I

Moderated by: Dr. Shawkat Ali

1A - 2:00PM-3:05PM AST - Wednesday, May 31

- | | |
|-------------------------------|--|
| 2:00PM-2:15PM AST
Standard | Shawkat Ali
Plant age and environmental conditions affect infection of lowbush blueberry by <i>Sphaerulina vaccinii</i> |
| 2:15PM-2:30PM AST
Standard | José Antonio Cervantes-Chávez
Use of Plant Growth-Promoting Bacteria as a friendly and integral alternative to improve tomato protection against damage produced by fungi |
| 2:30PM-2:45PM AST
Standard | Michael McLaughlin
The impact of plant defense elicitors and chemical fungicides on the fungal communities of Honeycrisp apples |
| 2:45PM-3:00PM AST
Standard | Asifa Munawar
Timing of ascospore release of <i>Anisogramma anomala</i> , a pathogen of eastern filbert blight in Ontario, Canada |

Fungal Disease in One Health I

Moderated by: Dr. Jennifer Geddes-McAlister

2A - 2:00PM-3:05PM AST - Wednesday, May 31

- | | |
|-------------------------------------|---|
| 2:00PM - 2:20PM AST
Mini-Keynote | Matthias Kretschmer
Mixed nutrients contribute to fungal biotrophy in <i>Ustilago maydis</i> |
| 2:20PM-2:35PM AST
Standard | Tyla Baker
Biofilms on urban aquatic plastic pollution as a reservoir for pathogenic yeasts |
| 2:35PM-2:50PM AST
Standard | Bryan Lung
Assessment of the therapeutic potential of bile acids against the fungal pathogen <i>Candida albicans</i> |
| 2:50PM-2:55PM AST
Flash | Jeff Gauthier
Complete Genome Sequences of Agricultural Azole Resistant <i>Penicillium rubens</i> encoding CYP51A and ERG11 paralogues |
| 2:55PM-3:00PM AST
Flash | Shamanth Shankarnarayan
Identifying clinically important <i>Candida</i> species using machine learning |

Yeasts: More than a Model Organism

Moderated by: Dr. Linda Horianopoulos

3A - 2:00PM-3:05PM AST - Wednesday, May 31

2:00PM-2:15PM AST Standard	Linda Horianopoulos Resistance to reactive oxygen species across diverse yeast species: Implications for industry and medicine
2:15PM-2:30PM AST Standard	K. Afrin Bari pH-dependent modulation of polyQ aggregation and toxicity in a yeast model of aging
2:30PM-2:35PM AST Flash	Rana Ahmed Using transcriptomics to provide insights into mitochondrial efflux pumps in wild-type <i>Saccharomyces cerevisiae</i> (BY4741)
2:35PM-2:40PM AST Flash	Alex Marr Evaluating diverse non-brewing yeast strains for novel new-make spirit applications
2:40PM-2:45PM AST Flash	Safia Mahabub Sauty Processivity factor PCNA has a distinct role in maintaining sub-telomeric silencing in <i>Saccharomyces cerevisiae</i>
2:45PM-2:50PM AST Flash	Édouard Unterberg-Piché Characterization of wild yeasts as potential biocontrol agents for brewing applications
2:50PM-3:05PM AST Standard (NR)	Maria-Jose Romero-Jimenez Exploring the effect of yeast species interactions and diversity on plant disease severity

Fungal Genetics and Genomics I

Moderated by: Dr. Emile Glück Thaler

4A - 2:00PM-3:05PM AST - Wednesday, May 31

2:00PM-2:15PM AST Standard	Emile Gluck-Thaler Giant Starship elements are engines of adaptive variation in fungal pathogens
2:15PM-2:30PM AST Standard	Evelina Basenko FungiDB: A free bioinformatics resource supporting research for fungal and oomycete species
2:30PM-2:45PM AST Standard	Andrew Dolson Analysis of Rif1 and Spt16 to understand their genetic interactions at the replication fork in <i>S. cerevisiae</i>
2:45PM-3:00PM AST Standard	Ashley Fisher The roles of Dbf4-dependent kinase and Chromatin Assembly Factor I in epigenetic conversion in <i>Saccharomyces cerevisiae</i>
3:00PM-3:05PM AST Flash	Nick Gervais Investigating the Role of Chromosome R in Drug Tolerance in <i>Candida albicans</i> via CRISPRa Screening

Mycotoxins

Moderated by: Dr. Mark Sumarah

1B - 3:30PM-4:35PM AST - Wednesday, May 31

3:30PM-3:50PM AST Mini-Keynote	Mark Sumarah The Deoxynivalenol Challenge
3:50PM-4:05PM AST Standard	Sheryl Tittlemier Prevalence of mycotoxins in Canadian grain
4:05PM-4:20PM AST Standard	Elizabeth Brauer Ionophore-triggered susceptibility and <i>Fusarium</i> resistance in plants

Fungal Disease in One Health II

Moderated by: Michael Woods

2B - 3:30PM-4:35PM AST - Wednesday, May 31

3:30PM-3:50PM AST Mini-Keynote	Jianping Xu Global population structure and triazole resistance in <i>Aspergillus fumigatus</i>
3:50PM-4:05PM AST Standard	Michael Woods Overcoming fluconazole resistance in <i>C. neoformans</i> by ClpX inhibition and inhibitor characterization using Proteome Integral Solubility Alteration.
4:05PM-4:20PM AST Standard	Nozethu Mjokane Activation of SARS-CoV-2 Spike protein by a fungal protease(s)
4:20PM-4:35PM AST Standard	Hendrik Steyn Evaluating the efficacy of supramolecular self-associating amphiphiles as novel antifungal substances against <i>Candida albicans</i> biofilms

Medical Mycology

Moderated by: Dr. Émilie Tremblay

3B - 3:30PM-4:35PM AST - Wednesday, May 31

3:30PM-3:45PM AST Standard	Viktoriiia Protsiuk Antifungal properties of thiazolidine derivatives
3:45PM-4:00PM AST Standard	Samuel Stack-Couture Comprehensive assessment of the contribution of the Unfolded Protein Response to <i>Candida albicans</i> antifungal resistance and pathogenicity
4:00PM-4:15PM AST Standard (NR)	Lucy Xie Pararesistance: a mutation-independent mechanism of antifungal drug resistance
4:15PM-4:20PM AST Flash (NR)	Emilie Alexander Using Deep Mutational Scanning to study how epistasis influences antifungal resistance.

EvoFunPath

Moderated by: Viola Halder

4B - 3:30PM-4:35PM AST - Wednesday, May 31

- | | |
|------------------------------------|---|
| 3:30PM-3:45PM AST
Standard | Viola Halder
Conducting genetic interaction analysis in <i>Candida albicans</i> stress response genes |
| 3:45PM-4:00PM AST
Standard | Boyan Liu
Defining remodeling of the global temporal proteome responses of <i>Fusarium</i> head blight-resistant and -susceptible wheat cultivars. |
| 4:00PM-4:05PM AST
Flash | Malaika Zarrouki
Going Against the Grain: Investigating the mechanisms of <i>Fusarium graminearum</i> pathogenesis of wheat using proximal biotinylation |
| 4:05PM-4:20PM AST
Standard (NR) | Chris Blackman
The Pan-genomic effectome of the <i>Fusarium sambucinum</i> species complex |

Horticultural Crop Pathology II

Moderated by: Dr. Shawkat Ali

1C - 5:00PM-6:05PM AST - Wednesday, May 31

- | | |
|------------------------------------|---|
| 5:00PM-5:15PM AST
Standard | Marianna Wallace
Root-inhabiting and rhizosphere mycobiomes and crop yield of corn and wheat |
| 5:15PM-5:30PM AST
Standard | Jacob Walsh
Genomic and metabolomic analysis of actinomycetes for agricultural coculturing against fungal diseases |
| 5:30PM-5:45PM AST
Standard (NR) | Rishi Burlakoti
Population diversity of <i>Botrytis</i> spp. causing fruit rot of highbush blueberry and raspberry in British Columbia |
| 5:35PM-6:00PM AST
Standard (NR) | Awais Khan
Genetic characterization of apple scab resistance: An important step to breed cultivars with durable disease resistance |

Fungal Disease in One Health III

Moderated by: Dr. Mitra Serajazari

2C - 5:00PM-6:05PM AST - Wednesday, May 31

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|--|---|
| 5:00PM-5:20PM AST
Mini-Keynote (NR) | Mitra Serajazari
Improvement of FHB resistance in wheat, a work in progress |
| 5:20PM-5:35PM AST
Standard (NR) | Daniel Charlebois
Identification and elimination of antifungal drug tolerance in <i>Candida auris</i> |
| 5:35PM-5:50PM AST
Standard | Maphori Maliehe
The potential influence of amoebal predation on <i>Cryptococcus neoformans</i> and its virulence |

Insights into Oomycetes

Moderated by: Dr. Hai Nguyen

3C - 5:00PM-6:05PM AST - Wednesday, May 31

- | | |
|------------------------------------|--|
| 5:00PM-5:15PM AST
Standard | Émilie Tremblay
Diversity of crop-associated oomycetes using metabarcoding data from aerial spore and suction traps |
| 5:15PM-5:30PM AST
Standard (NR) | Erica Goss
Investigating the genetic variation of cacao pathogen <i>Phytophthora megakarya</i> |
| 5:30PM-5:45PM AST
Standard (NR) | Emily Pfeufer
Characterization of <i>Phytophthora</i> spp. from Vietnam, the center of diversity of citrus |

Fungal Ecology

Moderated by: Jonathan Mack

4C - 5:00PM-6:05PM AST - Wednesday, May 31

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|-------------------------------|--|
| 5:00PM-5:15PM AST
Standard | Jonathan Mack
Two novel and unusual pleosporalean fungi isolated from the bark of <i>Acer saccharum</i> |
| 5:15PM-5:30PM AST
Standard | Gunjan Gupta
Microbial social profiling: studying patterns of antifungal and ecological interactions |
| 5:30PM-5:45PM AST
Standard | Sarah Gafner-Bergeron
Ectomycorrhizal colonization attributed to resistant propagules in 27-year-old clear-cuts and adjacent Engelmann spruce subalpine fir forests |

Thursday, June 1, 2023

Plenary Session 2: Fungal Ecology & Conservation

Moderated by: Dr. Gavin Kernaghan and Dr. Allison Walker

Plenary 2 - 12:00PM-1:30PM AST - Thursday, June 1

12:00PM-12:30PM AST Plenary	Yolanda Wiersma Lichen biodiversity research across scales: how looking at the small can help us to think big
12:30PM-1:00PM AST Plenary	Serita Frey Going Underground: Unearthing the role of the soil mycobiome in a warmer, fertilized world
1:00PM-1:30PM AST Plenary	Susana C. Gonçalves Challenges to advancing fungal conservation and how to overcome them

Lichen Biodiversity and Conservation I

Moderated by: Hayley Paquette

5A - 2:00PM-3:05PM AST - Thursday, June 1

- | | |
|------------------------------------|---|
| 2:00PM-2:15PM AST
Standard | David Diaz Escandón
Are all lichens the same? |
| 2:15PM-2:20PM AST
Flash | Kendra Driscoll
The lichen <i>Biatorrella heterospora</i> in Atlantic Canada: first record outside the European Alps |
| 2:20PM-2:35PM AST
Standard (NR) | Hayley Paquette
Arctic lichens gone south: the arctic-alpine lichen <i>Brodoa oroarctica</i> (Krog) Goward and its unusual disjunction in eastern North America. |

Mycorrhizal Symbioses

Moderated by: Dr. Gavin Kernaghan & Kendra Sampson

6A - 2:00PM-3:05PM AST - Thursday, June 1

- | | |
|-------------------------------|---|
| 2:00PM-2:15PM AST
Standard | Brandi Duke
Got Nifh? An exploration of ectomycorrhizal associated diazotrophs |
| 2:15PM-2:30PM AST
Standard | Joshua Frank-Webb
Complex effects of mycorrhizae on poplars under elevated temperature and CO ₂ |
| 2:30PM-2:45PM AST
Standard | Jason Pither
Improving the reliability of mycorrhizal ecology research through transparency and openness |

Tribute to David Malloch

Moderated by: Dr. Allison Walker & Dr. Greg Thorn

7A - 2:00PM-3:05PM AST - Thursday, June 1

- | | |
|------------------------------------|--|
| 2:00PM-2:15PM AST
Standard | Wendy Untereiner
“Do you want to see something neat?” - A tribute to Dave Malloch as an inspiring teacher and mycological mentor. |
| 2:15PM-2:20PM AST
Flash | Karen Vanderwolf
<i>Coprinopsis laanii</i> fruiting on mammal carcasses in an underground mine |
| 2:20PM-2:35PM AST
Standard (NR) | Scott Redhead
What could possibly go wrong? The discovery, rediscovery, discovery again, misclassification, then 9/11 history of a human pathogen – <i>Coccidioides posadasii</i> |
| 2:35PM-3:50PM AST
Standard (NR) | Richard Summerbell
Always something new in Onygenales - <i>Trichophyton indotineae</i> comes to Canada |

Lichen Biodiversity and Conservation II

Moderated by: Jonathan Cazabonne

5B - 3:30PM-4:35PM AST - Thursday, June 1

- | | |
|------------------------------------|---|
| 3:30PM-3:45PM AST
Standard | Katherine Drotos
Genomes of lichen-forming fungi are smaller than most non-lichens in both phylogenetic and symbiotic comparisons |
| 3:45PM-4:00PM AST
Standard (NR) | Christina Rinas
Experimental analysis of the altitudinal distribution limit of the Ghost Antler Lichen at Parc national du Mont-Mégantic in Québec, Canada |
| 4:00PM-4:15PM AST
Standard (NR) | Sean Rapai
Terrestrial lichen caribou forage transplant success: year 5 and 6 results |

Industrial Uses of Fungi

Moderated by: Adèle Bunbury-Blanchette

6B - 3:30PM-4:35PM AST - Thursday, June 1

3:30PM-3:45PM AST Standard	Jackson Moore Whole genome sequencing of British Columbian and Californian <i>Saccharomyces cerevisiae</i> strains reveals a novel Pacific West Coast Wine clade
3:45PM-4:00PM AST Standard	Zixuan Rosa Ren Strain Improvement of Filamentous Fungi <i>Mortierella alpina</i> for Efficient Production of Arachidonic Acid
4:00PM-4:15PM AST Standard	David Stuart Harnessing the Basidiomycete <i>Moesziomyces antarctica</i> as a sustainable biosurfactant factory
4:15PM-4:20PM AST Flash	Adèle Bunbury-Blanchette Yeast communities on grapes differ according to organic vs conventional vineyard management
4:20PM-4:25PM AST Flash	Luana Teixeira Nunes Porto Identification of a peroxidase-derived chemoattractant: a contributor to <i>Fusarium graminearum</i> pathogenicity through Ste2/3 activation

Fungal Pathogens of Forest Trees I

Moderated by: Berni van der Meer

7B - 3:30PM-4:35PM AST - Thursday, June 1

3:30PM-3:45PM AST Standard	Berni van der Meer Butternut canker phenotype binning to project diversity decline in <i>Juglans cinerea</i> L.
3:45PM-4:00PM AST Standard	Hailey Graham Identification of Douglas-fir endophytes and their metabolites that inhibit the disease Swiss needle cast

A Fungal Perspective on Conservation and Citizen Science

Moderated by: Jonathan Cazabonne

5C - 5:00PM-6:05PM AST - Thursday, June 1

- | | |
|-------------------------------|--|
| 5:00PM-5:15PM AST
Standard | Alfredo Justo
What can 1,000 barcode sequences tell us about regional fungal diversity and conservation targets? |
| 5:15PM-5:30PM AST
Standard | Latina Penkova
Differences in epigeous ectomycorrhizal fungal community composition between cut-blocks and unharvested forests persist 27-years following harvesting in a high-elevation forest |
| 5:30PM-5:45PM AST
Standard | Alisha Quandt
Examination of four biological knowledge shortfalls in the poorly studied Laboulbeniomycetes |
| 5:45PM-5:50PM AST
Flash | Allison Walker
Macrofungal conservation in Canada and target species for assessment: a starting point |

Endophytic Fungi

Moderated by: Maria Roy

6C - 5:00PM-6:05PM AST - Thursday, June 1

- | | |
|--|---|
| 5:00PM - 5:20PM AST
Mini-Keynote (NR) | Jana U'Ren
Evolution of secondary metabolite gene clusters: what is the role of fungal interactions in driving metabolic diversification? |
| 5:20PM-5:35PM AST
Standard | Paul de la Bastide
Fungal endophytes and insect herbivores affecting the health and recovery of Long's and Fernald's Braya, endangered endemic species of Newfoundland |
| 5:35PM-5:50PM AST
Standard | Aziz Ullah
Fungal endophytes of white spruce modulate tree defenses |
| 5:50PM-5:55PM AST
Flash | Maria Roy
Fungal endophytes as biocontrol agents for Apple Replant Disease |

Fungal Pathogens of Forest Trees II

Moderated by: Berni van der Meer

7C - 5:00PM-6:05PM AST - Thursday, June 1

- | | |
|------------------------------------|--|
| 5:00PM-5:15PM AST
Standard | Joey Tanney
The drought knockout: emergence of sooty bark disease (<i>Cryptostroma corticale</i>) in B.C. |
| 5:15PM-5:30PM AST
Standard (NR) | Rebecca Harkness
The emergence of native pathogens in disturbed forests: hidden complexity and diversity revealed in the genus <i>Caliciopsis</i> |
| 5:30PM-5:45PM AST
Standard (NR) | Eric Morrison
Population structure and genomic signatures of climate adaptation in <i>Neonectria faginata</i> , causative agent of beech bark disease |

Friday, June 2, 2023

Plenary Session 3: Fungi & Humans

Moderated by: Dr. Brent Robicheau and Dr. Émilie Tremblay

Plenary 3 - 12:00PM-1:30PM AST - Friday, June 2

12:00pm-12:30PM AST Plenary (NR)	Keith Seifert The Secret House: Fungal biology and diversity in the built environment
12:30PM-1:00PM AST Plenary	Melanie Jones The corruption of the wood-wide web? Evaluating the evidence supporting the structure and function of common mycorrhizal networks in forests
1:00PM-1:30PM AST Plenary	Neriman Yilmaz Mycotoxins in South Africa: old enemies new faces

Canadian Fungal Collections & Collections-Based Research

Moderated by: Tara Rintoul

8A - 2:00PM-3:05PM AST - Friday, June 2

2:00PM-2:15PM AST Standard	Tara Rintoul Fungal Symbionts: Canada's National Mycological Collections
2:15PM-2:30PM AST Standard	Spencer Goyette University of British Columbia Herbarium (UBC) fungi and lichen collections: leveraging the past to address future challenges
2:30PM-2:45PM AST Standard	James Scott UAMH Centre for Global Microfungal Biodiversity
2:45PM-3:00PM AST Flash	Olivia Crooks Eastern hemlock-associated macrofungal diversity at Kejimikujik National Park and National Historic Site
3:00PM-3:05PM AST Flash	Emma Harrower Mycologist in Residence at the UBC Herbarium

Aquatic Fungi I

Moderated by: Dr. Allison Walker

9A - 2:00PM-3:05PM AST - Friday, June 2

2:00PM-2:15PM AST Standard	Michael Cunliffe A 17-year time-series of fungal environmental DNA from a coastal marine ecosystem reveals long-term seasonal-scale and inter-annual diversity patterns
2:15PM-2:30PM AST Standard	Birch Lazo-Murphy Nitrous oxide production and isotopomer composition by fungi isolated from salt marsh sediments
2:30PM-2:45PM AST Standard	Xuefeng (Nick) Peng Fungal contribution to nitrogen and carbon cycling in the eastern tropical North Pacific oxygen minimum zone

Fungal Genetics & Genomics II

Moderated by: Viola Halder

10A - 2:00PM-3:05PM AST - Friday, June 2

2:00PM-2:15PM AST Standard	Dylan Lane Genomic Analysis of the Marine Fungi <i>Rhodotorula sphaerocarpa</i> ETNP2018 reveals adaptation to the open ocean
2:15PM-2:30PM AST Standard	Jessie MacAlpine DYRK-Family Kinases Regulate <i>Candida albicans</i> Morphogenesis and Virulence through the cAMP/PKA Pathway
2:30PM-2:45PM AST Standard	Guillaume Nguyen Complete genome sequences of fungal exotic strains isolated from High Canadian Arctic
2:45PM-2:50PM AST Flash	Gabriela Nunes Marsiglio Librais Differential regulation of the antifungal response by Tra1 across yeast species
2:50PM-3:05PM AST Standard (NR)	Sima Mohammadi Isolation and complete Genome Sequences of endophytic morphinan alkaloids production from <i>Papaver bracteatum</i>

Old Growth Forest Fungi

Moderated by: Rebecca Mader

8B - 3:30PM-4:35PM AST - Friday, June 2

3:30PM-3:45PM AST Standard	Philip Bell-Doyon Calicioid fungi and lichens from an unprotected intact forest ecosystem in Québec
3:45PM-4:00PM AST Standard	Joseph Birch Large-diameter trees and deadwood correspond with belowground ectomycorrhizal fungal richness
4:00PM-4:15PM AST Standard	Alejandro Huereca Delgado Pollen-trapping fungi: undetected and widespread hyphomycetes in western North America
4:15PM-4:20PM AST Flash	Rebecca Mader Macrofungal diversity in old-growth Eastern Hemlock stands of Kejimikujik National Park and National Historic Site, Nova Scotia, Canada

Aquatic Fungi II

Moderated by: Dr. Allison Walker

9B - 3:30PM-4:35PM AST - Friday, June 2

3:30PM-3:45PM AST Standard	Madeleine Thompson Diversity and ecology of fungi and prokaryotes in the sediments and water column of brackish and salt marshes
3:45PM-4:00PM AST Standard	Patricia Velez Deep-sea fungal diversity in Mexico: diversity and potential utilization
4:00PM-4:15PM AST Standard	Teppo Rämä Arctic driftwoodstock: new fungi and bioactive compounds

Fungal Genetics & Genomics III

Moderated by: Dr. Brent Robicheau

10B - 3:30PM-4:35PM AST - Friday, June 2

3:30PM-3:45PM AST Standard	Jordana Oliveira Transposable elements identification and expression in arbuscular mycorrhizal symbiont <i>Rhizophagus irregularis</i> during different colonization stages
3:45PM-4:00PM AST Standard	Christof Rampitsch Finding rust peptides encoded on short open reading frames

Fungal Genetics & Genomics IV

Moderated by: Bruce Malloch

8C - 5:00PM-6:05PM AST - Friday, June 2

- | | |
|-------------------------------|--|
| 5:00PM-5:15PM AST
Standard | Seyed Hananeh Ghafelehbash
The role of transcription factor, Ofi1 in the regulation of white-opaque switching and filamentation in <i>Candida albicans</i> |
| 5:15PM-5:30PM AST
Standard | Anne Hatmaker
Evolution of human pathogenesis in <i>Aspergillus flavus</i> |
| 5:30PM-5:45PM AST
Standard | Nmerichukwu Iwuchukwu
Fluorescent microscopy to identify the location of Ppp1 a novel protein in <i>Candida albicans</i> |
| 5:45PM-6:00PM AST
Standard | Sang Hu Kim
Genetic and mating-type diversity among Canadian, US and other wheat leaf rust fungal isolates using whole genome and RNA-derived sequences |
| 6:00PM-6:05PM AST
Flash | Julien Koga
Resolving the systematics of <i>Hericium</i> spp. in North America with multigene phylogenetic analysis and its implications for mushroom cultivation programs. |

Aquatic Fungi III

Moderated by: Dr. Huzefa Raja

9C - 5:00PM-6:05PM AST - Friday, June 2

- | | |
|------------------------------------|---|
| 5:00PM-5:15PM AST
Standard | Huzefa Raja
Chemical compounds from a freshwater fungus inhibit bacterial quorum sensing |
| 5:15PM-5:30PM AST
Standard | Phillip Pham
Aquatic fungi as environmental indicators for agriculturally dominated watersheds |
| 5:30PM-5:45PM AST
Standard (NR) | Jennifer Anderson
<i>Tetracladium</i> was also found -- the 'mysterious' terrestrial lives of some aquatic fungi |

Fungal Genetics & Genomics V

Moderated by: Dr. Brent Robicheau

10C - 5:00PM-6:05PM AST - Friday, June 2

5:00PM-5:15PM AST Standard	Essam Sorwar Exploring the metagenome of <i>Geosiphon pyriformis</i> - the only known fungus with a photosynthetic endosymbiont
5:15PM-5:30PM AST Standard	Jacob Steenwyk Evolutionary origin and phenotypic impact of hybridization in a cryptic fungal pathogen
5:30PM-5:45PM AST Standard	Gokalp Yildirim Resolving the haplotypes of arbuscular mycorrhizal fungi highlights the role of two nuclear populations in host interactions
5:45PM-5:50PM AST Flash	Maryam Fayyazi The metabolic regulation of the TOR pathway in <i>Neurospora crassa</i>
5:50PM-6:05PM AST Standard (NR)	Haider Alsafar Culture-independent genomics – a solution to reconstruct missing branches on the fungal tree of life

Abstracts

Using Transcriptomics to Provide Insights into Mitochondrial Efflux Pumps in Wild-type *Saccharomyces cerevisiae* (BY4741)

Ahmed, Rana*.Court, Deborah.

University of Manitoba

The concentration of antibiotics required to inhibit wild-type *Saccharomyces cerevisiae* (BY4741) growth is high compared to the amounts normally found to inhibit bacterial growth. Some studies proposed that the resistance could be linked to mitochondrial efflux pumps. However, there is currently limited evidence that *S. cerevisiae* has mitochondrial drug efflux pumps. Therefore, we are searching for candidates for drug efflux pumps in the fungal mitochondria by elucidating the changes to the transcriptional profile of *S. cerevisiae* in response to sub-lethal doses of chloramphenicol. Total RNA sequencing will be conducted to perform a comparative transcriptomic study to screen and compare uniquely differentially expressed genes between chloramphenicol-treated cell populations and control cells. Genes that will show expression differences between untreated and treated cells will be selected for further validation analysis. The transcriptomic data could provide insights into the basis for the functional characterization of genes with potential roles of resistance in fungi.

Using Deep Mutational Scanning to study how epistasis influences antifungal resistance.

Alexander, Emilie M*. M. Després, Philippe C., Dubé, Alexandre K., Landry, Christian R. Université Laval

In the field of antifungal resistance, understanding the dynamics between epistasis and evolutionary trajectories is of importance to be able to predict how pathogens evolve to resist antifungals.

In this project, we want to understand how epistasis at the protein level influences which mutations in the FCY1 gene lead to resistance to the antifungal 5-fluorocytosine (5FC). We used Deep Mutational Scanning to systematically generate all possible codon variants at certain positions in the FCY1 gene of four fungi. This library of mutants was screened against 5FC to identify which mutations lead to its resistance or maintained sensitivity.

By comparing the phenotype related to each mutation in each FCY1 ortholog, we were able to identify epistatic mutations : mutations that have different effects between orthologs. In general, a low percentage of mutations created were epistatic mutations. Furthermore, the more two orthologs diverge evolutionary, the more epistatic mutations there are.

Plant age and environmental conditions affect infection of lowbush blueberry by
Sphaerulina vaccinii

Shawkat Ali, Pervaiz, A. Abbasi, Paul D. Hilderbrand, Debra L. Moreau and Willy E.
Renderos

Agriculture and Agri-Food Canada

Septoria leaf spot and stem canker is an important disease of lowbush blueberry. Based on multi genes sequence analysis the pathogen aligns closely with *Sphaerulina amelanchier*, but was sufficiently distinct and we give it a new species designation *Sphaerulina vaccinii*. The pathogen causes premature defoliation in plants resulting in reduced growth and yields. The impact of different abiotic conditions such as free water, relative humidity (RH), temperature, light and plant age on leaf infection under controlled conditions was investigated. The hyphal penetration into stomata on abaxial leaf surfaces was tropic and the germ tubes grew in close proximity to a stomate, a penetration hypha formed at about 90° angles to the germ tube and took the closest path to the stomate. When inoculated plants were exposed to high RH (>95%) infection occurred after 1 day, 3 days or 4 days depending on the temperatures. Disease severity also increased with duration of the humid period. Younger leaves were 2.7 times more susceptible than older leaves.

Culture-independent genomics – a solution to reconstruct missing branches on the
fungal tree of life

Alsafar, Haider*; Wang, Yan

University of Toronto

Phylogenomic reconstruction of the Fungal Tree of Life has been hindered by the difficulty of obtaining genomic information of unculturable fungi, particularly for symbiotic organisms such as insect gut-dwelling species. Our current knowledge about these cryptic microbial fungi is mostly from countable cultures representing less than 10% of all known species, leaving the majority untouched impeding a comprehensive understanding of their evolutionary history and phylogenetic relationships. Here we present a culture-independent approach combining single-cell genomics and metagenomics to obtain a draft genome assembly of *Ejectosporus chimaera*, an unculturable species isolated from the hindgut of a mayfly nymph. This is the first attempt to sequence an unculturable Harpellales, pioneering our ongoing efforts to reconstruct a phylogenomic tree of insect gut symbiotic fungi. We were able to recover hundreds of Harpellales core genes from this reference-free assembly for a robust phylogeny, which placed *E. chimaera* as the earliest diverged lineage within Harpellales.

Tetracladium was also found -- the 'mysterious' terrestrial lives of some aquatic fungi
Anderson, Jennifer*
Swedish University of Agricultural Sciences

Tetracladium are quintessential aquatic hyphomycetes, known since 1970 to also occur in plant roots. Today, we still know little about the terrestrial biology of *Tetracladium* beyond reports that '*Tetracladium* was also found'. This is problematic gap in our understanding of the total biology of *Tetracladium* also impedes our capacity to understand the increasing reports of *Tetracladium* in global terrestrial metabarcoding studies. I am working to understand the total biology of *Tetracladium*. I find that most species are likely multi-niche, among which most are ACE, Aquatic hyphomycete and Endophytic. Their genomes contain signatures of biotrophy but are most enriched for saprotrophy-associated CAZymes. Species described from soil and classical aquatic hyphomycetes diverged ~70 mya and share a common soil-dwelling dimorphic yeast ancestor (100 mya). Metabarcoding data reveal interspecific differences in terrestrial distributions, including a geographically restricted species. Studies of how *Tetracladium* differentially regulate their genomes during saprotrophy and biotrophy are ongoing.

Biofilms on urban aquatic plastic pollution as a reservoir for pathogenic yeasts
Baker, Tyla, Bester, Armand, Albertyn, Jacobus, Pohl, Carolina
University of the Free State

Plastic pollution of the aquatic environment is a serious concern and poses a health risk to aquatic and terrestrial life. In addition, it can act as surfaces to which microorganisms adhere, forming a community known as the plastisphere, which includes both pathogenic and non-pathogenic microorganisms. Considering the presence of pathogenic yeast in water, plastics may act as a vector that aids in dispersal of pathogenic yeast to the surrounding environments as well as to individuals who come into contact with it. In this study, various plastic polymers were isolated from freshwater sources and their biofilms were analysed focusing on their fungal community using culture dependent and independent methods, including scanning electron microscopy, metagenome analyses, isolation and determination of fluconazole susceptibility. This revealed the presence of a variety of fungal species in the biofilms, including pathogenic yeast in the genera *Candida* and *Exophiala* with varying levels of fluconazole resistance.

pH-dependent modulation of polyQ aggregation and toxicity in a yeast model of aging
Khaleda Afrin Bari*, Sonja Di Gregorio, Julie Genereaux, Martin L. Duennwald and
Patrick Lajoie
Western university

Huntington's Disease (HD) is caused by aberrant expansion of polyglutamine repeats (polyQ) within the gene encoding the huntingtin (Htt) protein. With age, the expanded huntingtin misfolds and accumulates into toxic insoluble oligomers/inclusion bodies in neurons. Yeast chronological lifespan (CLS) is the amount of time non-dividing cells can survive in nutrient deprived condition. Using CLS experiments, we found that cells expressing expanded Htt fragments show reduced longevity. PolyQ expressing cells containing inclusion bodies live longer compared to the ones with diffused oligomers. This supports a protective role for the polyQ inclusions during aging. We found that expression of expanded polyQ increased sensitivity to acetic acid and buffering the growth media to pH 6 significantly alleviates polyQ toxicity and extended lifespan. Chronologically aged cells in buffered media displayed increased polyQ aggregation and amplified activation of the heat shock response. Thus, we identified new mechanisms that mediate age-dependent polyQ toxicity in yeast.

FungiDB: A free bioinformatics resource supporting research for fungal and oomycete species

Basenko, Evelina* and Jones, Andy on behalf of the entire VEuPathDB Bioinformatics Resource Center
University of Liverpool

FungiDB (<https://fungidb.org>) is a component of the Eukaryotic Pathogen, Vector and Host Informatics Resource (VEuPathDB.org) that enables browsing, querying and mining of omics-scale datasets across diverse groups of organisms including hosts, invertebrate vectors of human disease, eukaryotic microbes, and also environmental and epidemiological studies. With FungiDB, you can access transcriptomics & co-expression data, proteomics, genetic variation (polymorphisms & copy number variation), phenotypes, & other types of data. A user-friendly web interface offers an integrated search strategy system enabling data mining and comparison across species. The integrated VEuPathDB Galaxy - My Workspace platform offers custom data analysis & visualization. You can also peruse gene record pages, submit expert knowledge via user comments, examine supporting data in JBrowse and improve gene models in Apollo, a collaborative genome annotation and curation platform. Have questions, want to nominate a dataset for integration, or invite us for a demo on Zoom? - Email us to help@fungidb.org

Calicioid fungi and lichens from an unprotected intact forest ecosystem in Québec
Philip Bell-Doyon*, Steven B. Selva, and R. Troy McMullin
Université Laval

Calicioid lichens and fungi form a diverse polyphyletic group whose species richness is often associated with old-growth forests and ecological continuity. One of the last intact forest landscapes south of the 50th parallel in Québec includes the Ya'nienhondhndeh territory, which has been the focus of a protected area project directed by the Huron-Wendat First Nation for more than ten years. To contribute to the characterization of its conservation value, we report the calicioids from the area. We identified 34 species in eight genera from 187 samples collected in old-growth stands of balsam fir, black spruce and yellow birch. Our four most remarkable discoveries are *Chaenotheca nitidula* Tibell (n = 11), *Chaenothecopsis australis* Tibell (n = 1), and *C. tsugae* Rikkinen (n = 2), which are reported for the first time from the province, as well as *Sclerophora coniophaea* (Norman) Mattsson & Middelb. (n = 18), which is rare in North America and was previously reported only once in Québec. As a result of this inventory, the Ya'nienhondhndeh is now the second richest area known for calicioids in Québec, after Parc national de la Gaspésie. We conclude that it is an ancient forest ecosystem whose conservation value is high based on its unique biodiversity, and that it warrants protection.

Large-diameter trees and deadwood correspond with belowground ectomycorrhizal fungal richness

Birch, Joseph D.*; Lutz, James A.; Struckman, Soren; Miesel, Jessica R.; Karst, Justine
Michigan State University

Large-diameter trees have an outsized influence on aboveground forest dynamics, composition, and structure though their role in shaping belowground fungal communities is largely unknown. We sought to test if (i) fungal community spatial structure matched aboveground forest structure, (ii) fungal functional guilds exhibited differential associations to aboveground trees, snag, and deadwood, and (iii) that large-diameter trees and snags have a larger influence on fungal community richness than smaller-diameter trees. Tree diameter, deadwood presence, and tree species identity explained more than twice as much variation (38.7% vs. 10.4%) for ectomycorrhizal composition and diversity than for total or saprotrophic fungi. Species identity and distance to the nearest large-diameter tree (=40.2 cm) were better predictors of richness than were the identity and distance to the nearest tree. Locally rare tree species had an outsized influence on fungal community richness. Large-diameter trees are implicated as drivers of belowground fungal diversity, particularly for ectomycorrhizal fungi.

The Pan-genomic Effectome of the *Fusarium Sambucinum* Species Complex

Blackman, Chris*

Agriculture Canada / University of Toronto

The *Fusarium sambucinum* species complex (FSAMSC) comprises prominent phytopathogenic fungi with a detrimental impact on global agriculture. Understanding the interaction between host plants and fungi is crucial to delineate underlying mechanisms of plant defence to mitigate agricultural losses. Fungal pathogens use suites of secreted proteins, called effectors, to modulate the host immune response to overcome host defences and promote colonization; however, the study of the fungal effectors has only recently gained traction. We hypothesize that the diversity of effectors within the FSAMSC can be encapsulated in a pan-genomic effectome, which can be used to identify conserved effectors. The pan-genomic effectome of the FSAMSC was described using a combination of bioinformatics tools, leading to the prediction of 125,777 candidate-secreted effector proteins (CSEPs) from 195 isolates, including 235 conserved (“core”) effector families. This research will contribute to our understanding of effector diversity within the FSAMSC, as well as provide novel targets for future disease mitigation strategies.

Ionophore-triggered susceptibility and Fusarium resistance in plants

Brauer, Elizabeth*

Agriculture & Agri-Food Canada

Bacterial and fungal plant pathogens produce ionophores – molecules which destabilize plant membranes and enable ion passage across compartments – to promote virulence during host infection. While these molecules activate immune responses in plant cells, their function in pathogenesis and recognition by plants are not well understood. We recently identified a cyclic lipopeptide called gramillin which is a virulence factor of *Fusarium graminearum* in maize. Here, we demonstrate that gramillin toxicity is limited to the plant kingdom where it induces necrotic cell death independently of active cell metabolism. The level of gramillin toxicity varies between plant species and is linked due to its cation-conducting activity in plasma membranes, where it stimulates depolarization and cation conduction. Gramillin induces cellular responses including a ROS burst, a calcium burst and membrane depolarization, and this induction is dependent on its ionophore activity. A genetic screen revealed that gramillin-induced responses in plants were independent of MAMP receptors but relied on three regulators of the MAMP response. Both gramillin and the gramillin-response genes promote susceptibility and *F. graminearum* virulence factor gene expression during infection. Together, we found that ionophore recognition in plants is dependent on a subset of the inducible immune pathway and demonstrate that fungal pathogens manipulate this recognition to coordinate attack on the host.

Yeast communities on grapes differ according to organic vs conventional vineyard management

Bunbury-Blanchette, Adele*; Fan, Lihua; Kernaghan, Gavin.
Saint Mary's University

While the domestic yeast *Saccharomyces cerevisiae* generally completes wine fermentations, many indigenous vineyard yeasts are also present in freshly pressed grape juice. When they are not suppressed, these yeasts are active in fermentation and can produce complex wines with improved sensory attributes. Vineyard yeast communities have not previously been evaluated in Atlantic Canada, despite the growing wine industry and interest in spontaneous fermentations that highlight microbial terroir. Grapes were collected and pressed from five conventionally managed and three organic vineyards in Nova Scotia. Characterization by next generation sequencing revealed that yeast community composition differed between management practices. *Sporidiobolales*, notably *Rhodotorula* and *Sporobolomyces*, were associated with conventional vineyards, while *Symmetrospora* was associated with organic vineyards. Abundance of *Filobasidium* differed between management practices at the species level. Local wine makers may apply knowledge of their vineyard yeast communities to make better use of non-traditional yeasts and spontaneous fermentations to produce high-quality wines.

Population diversity of *Botrytis* spp. causing fruit rot of highbush blueberry and raspberry in British Columbia

Burlakoti Rishi R*, Novinscak Amy, Sabaratnam Siva
Agassiz RDC, Agriculture and Agri-food Canada

Botrytis spp. causes fruit rot highbush blueberry and red raspberry in Canada including British Columbia (BC). The composition of cryptic species of *Botrytis* and their genetic diversity in BC were not studied previously. We used PCR based assays and genotyping with microsatellite markers to identify the cryptic species and understand the genetic diversity of *Botrytis* population collected from commercial highbush blueberry and raspberry farms in BC. We identified that all isolates collected from blueberry and vast majority of raspberry isolates (96%) were *Botrytis cinerea*. Four percent of raspberry isolates were *B. caroliniana*. Regardless of the host, the majority of *B. cinerea* isolates were 'boty' type (~52 to 53%) followed by 'vacuma' (35 to 37%). The frequency of TEs type and mating types varied among cultivars and locations. We will also present the genetic diversity of the pathogen population using microsatellite markers.

Identification and Elimination of Antifungal Drug Tolerance in *Candida auris*
Rasouli Koochi, Samira. Shankarnarayan, Shamanth. Galon, Clare Maristela.

*Charlebois, Daniel
University of Alberta

The human fungal pathogen *Candida auris* is of concern due to multidrug resistance and outbreaks across the globe. Fluconazole failure in *C. auris* has been attributed to antifungal “tolerance”. Tolerance is a phenomenon whereby a slow growing subpopulation of tolerant cells emerges during drug treatment. We use microbroth dilution and disk diffusion assays together with image analysis to investigate antifungal tolerance in *C. auris*. We find that 1) *C. auris* is tolerant to all three classes of antifungal drugs used to treat invasive candidiasis; 2) the tolerant phenotype reverts to the susceptible phenotype in *C. auris*; and 3) combining antifungal drugs with the adjuvant chloroquine reduces or eliminates tolerance in patient-derived *C. auris* isolates. These results suggest that tolerance contributes to treatment failure in *C. auris* infections for a broad range of antifungal drugs and that antifungal adjuvants may improve treatment outcomes for patients infected with antifungal-tolerant fungal pathogens.

Eastern Hemlock-Associated Macrofungal Diversity At Kejimikujik National Park And National Historic Site

Crooks, Olivia C.* Egger, Keith N. Smith, Matthew J. and Walker, Allison K.
Acadia University

Eastern Hemlock (*Tsuga canadensis*) is a foundational species providing a unique shaded habitat for many organisms. The invasive hemlock woolly adelgid (*Adelges tsugae*; HWA) is causing severe hemlock decline in Eastern North America and has recently reached Nova Scotia. Between 2004-2007, over 1500 hectares of Eastern Hemlock was defoliated by pale winged grey moth (*Irodopsis ephyraria*; PWG) larvae. From August-November 2022, we collected 57 hemlock-associated macrofungi from our study plot; identities were confirmed using DNA barcoding and compared with E.C. Smith Herbarium specimens from the same plot (1990s). In 2022, we discovered fungi not previously documented in our plot, and we re-documented fungi present in the 1990s herbarium collections. Ectomycorrhizal fungi dominated our collections, with *Cortinarius* being the most common genus. Fungal diversity changed but did not decline with the PWG outbreak or early HWA infestation. Fungi we documented will aid research determining the effects of HWA on forest fungi.

A 17-year time-series of fungal environmental DNA from a coastal marine ecosystem reveals long-term seasonal-scale and inter-annual diversity patterns

Christmas Nathan, Allen Ro, Allen Michael, Bird Kimberley and Cunliffe Michael*
Marine Biological Association and University of Plymouth

If and how marine fungi show long-term intra- and inter-annual diversity patterns is unknown, preventing a comprehensive understanding of marine fungal ecology. We used a 17-year environmental DNA time-series from the English Channel to determine long-term marine fungal diversity patterns. We show that community structure progresses at seasonal and monthly scales. Communities restructured every 52-weeks suggesting long-term stability in diversity patterns. Some major marine fungal genera have clear inter-annual recurrence patterns, re-appearing in the annual cycle at the same period. Low relative abundance likely non-marine taxa show seasonal input to the coastal marine ecosystem suggesting land–sea exchange. Our results demonstrate long-term intra- and inter-annual marine fungal diversity patterns. We anticipate this study could form the basis for better understanding the ecology of marine fungi and how they fit in the structure and function of the wider coastal marine ecosystem.

Fungal endophytes and insect herbivores affecting the health and recovery of Long's and Fernald's Braya, endangered endemic species of Newfoundland
de la Bastide, Paul*; Finston, Terrie; Hermanutz, Luise; Hintz, Will
Dept. of Biology, University of Victoria

Long's (*Braya longii*) and Fernald's (*B. fernaldii*) Braya are endemic to Newfoundland's Great Northern Peninsula. They are endangered due to habitat loss, chronic pathogen infections and insect herbivory. While recovery plans are being implemented, their fungal microbiome remains understudied. We examined this community and the role of insect herbivory in plant health. Plant tissues from three populations were sampled over five years, yielding 326 fungal isolates. These included 36 taxa; 16 were found once, while 12 occurred across multiple sites, sampling intervals and years. Insect herbivory and fungal infections were common. Insects were sampled over three years on the same sites to assess their microbiome. Fungal isolates were similar to plant taxa, with few exceptions. Vertical transmission of fungi is under study for two sites (pristine and disturbed), while a metagenomics study is underway to capture the broader fungal community in plants, for comparisons amongst sites and hosts.

Are all lichens the same?

Diaz Escandon, David*; Tagirdzhanova, Gulnara; Resl, Philip & Spribille, Toby.
University of Alberta

The first symbiosis ever described was the lichen symbiosis consisting of a fungus and a carbon providing photosynthetic partner. Nowadays, we know lichen symbioses did not follow a single path in evolution, but many. However, the consensus regarding the nutritional nature of the symbionts' interaction remains unchanged. Focusing on the released products induced by the symbiosis, we tested a model where lichens were not exclusively dependant on the symbiotic nutrients, but instead fungal symbionts can potentially exploit external carbon sources. We analyzed 80 lichen derived fungal genomes and based on the photosynthates released by the photosynthetic partner, we compared their enzymatic arsenals against other symbiotic and non-symbiotic fungal genomes. The different photosynthates have shaped the evolution of fungal genome machineries, suggesting that symbiosis induced photosynthates are not exclusively nutritional, but instead might play additional roles on maintaining the lichen symbioses.

Analysis of Rif1 and Spt16 to understand their genetic interactions at the replication fork in *S. cerevisiae*

Dolson, Andrew*
University of Guelph

Chromatin structure plays a critical role in the regulation of gene expression in eukaryotes. The role of histone chaperones, especially FACT, and other factors, such as Rif1, in regulating the replication fork and the transfer of histone marks to nascent DNA, maintaining chromatin state post-replication. Recent evidence has shown that the Spt16 subunit of FACT physically and genetically interacts with other replication fork factors, suggesting a role in the regulation of fork stability. It is also suggested that Rif1 genetically interacts with fork-associated factors during elongation to regulate the pausing and the rescuing of forks. The goal of my study is to analyze the genetic interactions between SPT16 and RIF1 genes with other replication factor and histone chaperone genes, as well as to describe the effects these interactions have on the stability of heterochromatic loci in model organism *Saccharomyces cerevisiae*.

The lichen *Biatorrella heterospora* in Atlantic Canada: first record outside the European Alps

Driscoll, Kendra E.*; Clayden, Stephen R.
New Brunswick Museum

Biatorrella heterospora is an inconspicuous but distinctive crustose lichen named for the variable shape and size of its ascospores. It was described 40 years ago yet has only been reported from two localities, both in the Austrian portion of the European Alps, suggesting that it is a rare species. Here we report one additional record from an apparently disjunct population in the Atlantic Canadian province of New Brunswick.

Genomes of lichen-forming fungi are smaller than most non-lichens in both phylogenetic and symbiotic comparisons

Drotos, Katherine*. McMullin, R. Troy. Spribille, Toby. Smith, M. Alex. Gregory, T. Ryan.
University of Guelph

While many fungi are symbiotic, lichen-forming fungi (LFF) exhibit unique emergent properties in their symbiotic state. In addition, LFF have arisen repeatedly across fungi and are highly diverse. The evolutionary drivers of the origin and maintenance of lichenized lineages are still largely unknown. To examine differences between fundamental cytological traits of LFF and non-LFF, we developed methodology to measure genome size of hyphal LFF using Feulgen image analysis densitometry. We measured 25 LFF spanning 2 classes and 10 orders in Ascomycota. We then compared our results with data from the Fungal Genome Size Database (www.zbi.ee/fungal-genomesize/). We found that LFF genomes are typically smaller than their closest non-LFF relatives and are also smaller than most other symbiotic states. This suggests LFF genomes experience evolutionary forces to become or stay small relative to other fungi, generating further hypotheses about the evolution of LFF and the nature of the lichen symbiosis.

Got Nifh an exploration of Ectomycorrhizal associated diazotrophs
*Duke, Brandi. Kernaghan, Gavin
Saint Mary Univeristy

Nitrogen is the most common limiting resource for plant productivity. Even though the atmosphere is composed mostly of nitrogen, it is in a form that is biological unavailable to plants. Many prokaryotes, termed diazotrophs can “fix” atmospheric nitrogen into ammonia, but this is most likely to occur in environments with low oxygen and high carbon supply. A potential and understudied habitat that provides these conditions is the mantle of ectomycorrhizae. The goal of this research is to determine if ectomycorrhizae formed by different fungal species harbour different communities of culturable potential diazotrophs, by selective culturing on nitrogen limited media, and the creation of a series of Nifh gene specific primers to confirm the potential for nitrogen fixation. Potential nitrogen fixing diazotrophs are associated with ectomycorrhizae, and these diazotrophic communities vary between habitat and the species of fungi forming the ectomycorrhizae.

The metabolic regulation of the TOR pathway in *Neurospora crassa*
Fayyazi, Maryam*; Lakin-Thomas, Patricia
York University

The Target of Rapamycin (TOR) pathway is a conserved signaling pathway that regulates metabolism, cell growth and survival in eukaryotes. Despite the significant progress in understanding the mechanistic regulation of the TOR pathway in mammalian systems and *Saccharomyces cerevisiae*, the detailed characterization of this pathway in the filamentous fungus *Neurospora crassa* is still unclear. Our research in the field of circadian rhythmicity revealed that TOR pathway activity is rhythmic. My research primarily focuses on the metabolic regulation of the TOR pathway. I use a novel assay to examine the TOR pathway activity by measuring the S6 ribosomal protein phosphorylation status in response to different metabolites such as lipids and amino acids.

The roles of Dbf4-dependent kinase and Chromatin Assembly Factor I in epigenetic conversion in *Saccharomyces cerevisiae*

Fisher, Ashley.* Yankulov, Krassimir

University of Guelph

Dbf4-Dependant Kinase (DDK) is a conserved kinase with an essential role in DNA replication initiation. DDK also phosphorylates other substrates including Chromatin Assembly Factor I (CAF1), a histone chaperone that reassembles histones into nucleosomes at replication forks (RFs). This process is essential to the maintenance of chromatin structure across generations. The mutation of a putative DDK phosphorylation site on CAF1, in conjunction with a CDK target site, leads to loss of heterochromatin-mediated gene silencing at several loci. Other evidence suggests DDK and CAF1 are present at paused RFs. I hypothesize that DDK targets CAF1 and modulates its activity at paused RFs. My goal is to demonstrate that DDK phosphorylates CAF1 in vivo and establish a connection between the activities of DDK and CAF1 in *Saccharomyces cerevisiae*. This project will provide mechanistic insight into the roles of CAF1 and DDK in replication-mediated chromatin assembly and explicate details surrounding this conserved process.

Complex Effects of Mycorrhizae on Poplars Under Elevated Temperature and CO₂

Frank-Webb, Joshua*; Ramsfield, Tod; Way, Danielle

Western University

The growth of *Populus* spp. is important economically and ecologically, but it has declined due to climate change-induced drought and elevated temperatures. Symbiotic microbes, such as mycorrhizae, have the potential to enhance plant growth under these conditions by increasing access to water and nutrients. This study isolated three mycorrhizal species from *Populus tremuloides* roots in the field and investigated their effects on hybrid poplar (*Populus x canadensis*) growth under a range of future climate scenarios. The results suggest that mycorrhizae can increase tree growth under moderate warming (+4°C), enhancing resilience to future climatic stresses. However, mycorrhizal inoculation did not increase tree height or total mass under other climate scenarios, indicating the need for further research to identify effective strategies for enhancing tree growth under future climate change conditions.

Going Underground: Unearthing the Role of the Soil Mycobiome in a Warmer, Fertilized World

Frey, Serita*

University of New Hampshire

Soil fungi play key roles in carbon (C) and nutrient cycles, as decomposers of organic matter and symbionts of plants. They are also sensitive to environmental change, with shifts in the fungal community in response to global change drivers having significant consequences for soil C storage and feedbacks to climate through soil C loss. Four global change experiments at the Harvard Forest Long-term Ecological Research site (Massachusetts, USA) span 16-34 years in duration and have the same climate and similar soils, vegetation, and land-use histories, with experimental treatments including warming (+5°C above ambient), simulated N deposition (5 g m⁻² yr⁻¹), or their combination. The soil warming and N fertilization techniques used across the sites is identical, and a coordinated set of biogeochemical and microbial measurements have been made over time. This talk will focus on the biogeochemical and fungal responses to chronic soil warming, soil N enrichment, and their interactions.

Ectomycorrhizal colonization attributed to resistant propagules in 27-year-old clear-cuts and adjacent engelmann spruce ? subalpine fir forests

Gafner-Bergeron, Sarah

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Little is known about the long-term recovery of ectomycorrhizal fungi (EMF) following timber harvest despite the importance of EMF in the growth of economically important trees. This study explored the resistant propagule community of EMF in 26-year-old cut block and adjacent mature engelmann spruce?subalpine fir forests with a 6-month bioassay of spruce hybrid (*Picea engelmannii x glauca*) and subalpine fir (*Abies lasiocarpa*). The objectives were to investigate if: 1) the richness and community of resistant propagules colonizing seedlings changes between forest, edge, and clear-cut habitats, 2) the richness and community of resistant propagules colonizing spruce and fir seedlings differ, and 3) resistant propagules are important inoculum for 26-year-old and mature trees. We found no difference in richness or community by habitat, and a higher EMF richness in spruce compared to fir. *Cenococcum geophilum*, *Tylospora* sp., and *Hyaloscypha bicolor* were common on the roots of both seedlings and mature trees.

Complete Genome Sequences of Agricultural Azole Resistant *Penicillium rubens* encoding CYP51A and ERG11 paralogues

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Universite Laval

The intensive use of azoles in agriculture fueled a surge of antifungal resistance, a top-priority threat to human health. One such mechanism is the acquisition of CYP51A and ERG11 paralogues, which confer intrinsic azole resistance.

We sequenced and assembled the genome of three agricultural azole resistant *Penicillium rubens* (MT45, WM45, and BM32) on the Oxford Nanopore GridION apparatus. De novo assemblies were done with CANU v2.1 and corrected with Medaka v1.4.3. Taxonomy was assigned with Kraken v2.1.2 to *Penicillium rubens*.

Genome size was consistent with other *Penicillium* spp., i.e. 28.70 ± 0.04 Mbp with an N50 of 4.506 ± 0.002 Mbp. MT45, WM45, and BM32 had respectively 7, 8 and 10 contigs.

The presence of CYP51A and ERG11 paralogues was also confirmed and, interestingly, a large portion of the N-terminal domain did not match wild-type sequences, suggesting that this truncated portion is crucial for conferring resistance to azoles.

Tropical Plant Pathology: A Challenging but Rewarding Field!

Gazis, Romina*

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A significant portion of the world's agricultural land resides within the tropics. Most tropical areas support multiple crop cycles over the year, an essential advantage in land use. Therefore, the tropics have considerable responsibility in ensuring food security and supplies to a growing world population. Unfortunately, this nurturing environment is also extremely conducive to pest and disease establishment, growth, and spread. Limited resources available to address the numerous and continuous outbreaks of established and emerging pests and diseases is a major challenge across the region. Although at times overwhelming, the tropics also offer a myriad of opportunities for fundamental scientific discoveries, such as biodiversity surveys and ecological and evolutionary-driven studies. While my focus is solving pressing problems faced by growers, it's through my side projects that I fulfill my mycological curiosity. Join me to learn how through my tropical plant pathology program, I contribute to the advancement of mycological knowledge.

Investigating the Role of Chromosome R in Drug Tolerance in *Candida albicans* via CRISPRa Screening

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The emergence of drug-tolerant *Candida* strains is a critical threat to human health globally. One mechanism of acquiring drug tolerance that *Candida albicans* harnesses is its ability to readily undergo chromosomal rearrangements and alter ploidy to overcome stressful conditions such as antifungal drug treatment. However, the genetic pathways underpinning many aneuploidies are uncharacterized. It has recently been shown that a trisomy of chromosome R (ChrR) in *C. albicans* results in increased tolerance to certain antifungal drugs. This trisomy suggests that overexpression of one or more genes on ChrR is associated with antifungal drug response phenotypes. We recently optimized a new CRISPRa (activation) system in *C. albicans* and have employed it in single-gene perturbation studies. Here, we propose the development of a novel CRISPR-based overexpression library that will target each gene on ChrR in *C. albicans* and will allow genes and genetic mechanisms relating to antifungal drug tolerance to be discovered.

The role of transcription factor, Ofi1 in the regulation of white-opaque switching and filamentation in *Candida albicans*

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Candida albicans is a fungal pathogen that can cause infections in people with weakened immune systems. It can adapt to the host organism through different cellular shape transitions, such as filamentatous growth which plays a critical role in the fungus's virulence and white to opaque switching which play a role in mating. *C. albicans* is diploid and typically heterozygous at the central regulator locus, MTL, controlling mating type. In addition to homozygosity of MTL genotypes, white-opaque switching is necessary for mating. White and opaque cells are morphologically and genetically distinct, and the difference in gene expression is responsible for the change in their appearance. The adaptation of *C. albicans* to host niches relies on transcriptional regulatory programs that can be controlled by complex networks of transcription factors (TFs). These factors can influence the cell's phenotypic behaviour and stability by acting through DNA binding sites or through interlocking feedback loops. Zinc finger cluster transcription factors are a well-known fungal transcription factor family. A novel transcriptional regulator, Ofi1, has been identified as a candidate regulator for both white-opaque switching and filamentation in *C. albicans*. In white-opaque switching it appears to act downstream of the master regulator Wor1. A comparison of the *ofi1*^{+/ofi1}? strain, the Ofi1 activated strain and the wild type (SN148aa) strain under different carbon sources and temperatures were assessed. Activation leads to an increase in both processes, while deletion reduces the frequency of white-opaque switching. The aim of the project is to investigate the role of Ofi1 in the transcriptional programs involved in these processes.

Giant Starship elements are engines of adaptive variation in fungal pathogens
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Cramer, Robert A.

University of Neuchatel

Accessory genes are variably present among members of a species and are a reservoir of adaptive functions. In fungal pathogens, accessory genes contributing to pathogenicity represent significant fractions of genome content. However, we often lack a mechanistic understanding of how genes become accessory. Here, we demonstrate that differences in accessory gene content in many fungal pathogens is attributable to Starships, a newly described superfamily of giant mobile elements that have evolved mechanisms to transpose fungal genes as genetic cargo. By systematically annotating Starships in multiple fungal pathogens of animals and plants, we found that individual fungi harbour complex communities of elements ranging from 60-600kb in length. Active Starships represent between 1-8% of any given genome and carry diverse genes implicated in host- and environment- adaptation, including metabolic gene clusters and candidate virulence factors. Starship-associated genes typically make up around 10% of the overall accessory genome, implicating Starship activity as a direct mechanism generating variation in accessory gene content. Our results shed light on the origins of accessory variation in fungi, and reveal a novel mechanism for pathogen adaptation.

Challenges to advancing fungal conservation and how to overcome them

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It's an exciting time to be a conservation mycologist! Thanks to the continued efforts of many, recently fungal conservation has gained momentum. In 2022, we surpassed 600 fungal species assessed on the IUCN Red List of Threatened Species, allowing the first global review of the extinction risk of fungi. In addition, the new Kunming-Montreal Global Biodiversity Framework provides a unique opportunity to include fungi in national biodiversity policies, along with animals and plants. Despite these advances, we still face many challenges. Using examples from ongoing projects in the lab, I will highlight how we can overcome some of these challenges. Work underway includes combining fieldwork and computational tools to speed up the process of assessing extinction risk in fungi. We are also developing sustainable livelihoods for rural communities in Mozambique based on the wild fungi diversity of Miombo woodlands. Finally, we are working to inspire people living in our city to reconnect with nature, particularly with fungi, through citizen science and tailored community engagement activities.

Investigating the genetic variation of cacao pathogen *Phytophthora megakarya*
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Schlathoelter, Ina, Henderson, Donna, Marelli, Jean-Philippe, Brawner, Jeremy, Goss,
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Phytophthora megakarya is an aggressive and destructive pathogen that causes black pod disease of cacao in West and Central Africa. We examined genetic diversity and population structure of *P. megakarya* using genomic data from 165 isolates collected from cacao in Africa. We used genotyping by sequencing of 150 isolates and published whole genome sequences of 15 isolates to call 2,644 high quality SNPs relative to reference genome Pm1/GH34. Isolates could be assigned to one of two major clades. One clade contained isolates from Nigeria and Ghana and the other clade contained isolates collected in all regions. To examine the virulence of isolates, a diverse panel of 300 cacao clones from the International Cacao Germplasm Collection at CATIE, Costa Rica were phenotyped using excised pods shipped to the University of Florida. Genomic and phenotypic data will be used together to improve phenotypic predictions of pathogen virulence and host resistance.

Identification of Douglas-fir endophytes and their metabolites that inhibit the disease
Swiss needle cast
Graham, Hailey* McMullin, David Tanney, Joey
Carleton University

Swiss needle cast (SNC) is an endemic fungal disease impacting Douglas-fir trees in the Pacific Northwest. *Nothophaeocryptopus gaeumannii* is a fungus which physically obstructs the stomata of infected needles, causing a reduction in CO₂ uptake which leads to a decrease in growth and foliar volume in chronically infected trees. The interactions of conifer endophytes within their environments have allowed for the selection of genotypes producing ecologically functional secondary metabolites. A bioassay was developed to assess the antifungal properties of the ethyl acetate soluble culture filtrate extracts from 59 Douglas-fir endophytes against *N. gaeumannii*. Twenty-six strains that significantly inhibited the growth of *N. gaeumannii* across three distinct lineages were identified. In addition, metabolites from Douglas-fir endophytes, including *Xylaria hypoxylon*, *Rhabdocline parkeri*, and *Coleophoma* sp. were characterized. This study will direct future investigations to profile the antifungal natural products responsible for inhibiting the growth of *N. gaeumannii* from prioritized strains.

Microbial social profiling: studying patterns of antifungal and ecological interactions
Gupta Gunjan*, Labrie Steve, Filteau Marie
Univerisité Laval

Microbial interactions are crucial for ecological systems and understanding these interactions can lead to novel antifungal strategies. To this end, we present a scalable and adaptable high-throughput method for studying the growth and antifungal potential of large numbers of microorganisms, against *Kluyveromyces lactis*, *Candida boidinii*, and *Saccharomyces cerevisiae*, on M17+lactose and Synthetic allantoin media. Our results revealed that less than 5% of isolates exhibited antifungal activity against all three yeast targets, and co-culturing did not enhance antifungal production, as interaction-mediated suppression was more prevalent in our dataset. Furthermore, we found that M17+lactose is a suitable medium for screening microorganisms for antifungal activity. We also observed that consistently cooperative microorganisms did not exhibit constitutive antifungal activity, while microorganisms displaying consistent competitive behavior displayed constitutive antifungal activity. Our study represents the first report on the fundamental interactions between maple sap isolates and their antifungal abilities, creating new avenues for discovering potential antifungals.

Conducting genetic interaction analysis in *Candida albicans* stress response genes
Halder, Viola*, Shapiro, Rebecca
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Candida albicans is a commensal organism, typically found in the oral mucosa, the gut, the vaginal mucosa, and the skin of humans and other mammals. *C. albicans* is also an opportunistic fungal pathogen that may cause superficial to severe invasive and systemic infections, depending on the status of an individual's immune system.

Cells need to adapt to environmental stressors to survive, and this ability is dependent on the speed and robustness of their stress responses. For *C. albicans*, stress response factors can also modulate antifungal drug resistance, as antifungal drugs can impart different forms of stress on the fungal cell. Understanding *C. albicans* stress responses would be prudent in novel antifungal drug discovery.

We exploit a genetic approach using the CRISPR-Cas9-based genome editing platform to map out genetic interactions between fungal genes, targeting stress response genes with roles in fungal cell survival. The proposed research aims to dissect the genetic interactions underpinning *C. albicans*' response to diverse stressors. This proposed research will use cutting-edge genomic technologies to explore the genetic mechanisms by which *C. albicans* survive amidst a constantly changing environment. Leveraging this platform, we will have the ability to gain previously inaccessible biological insight into the complex genetic interaction networks in *C. albicans*, and discover fundamental processes in fungal biology, including stress tolerance.

The emergence of native pathogens in disturbed forests: hidden complexity and diversity revealed in the genus *Caliciopsis*
Harkness, Rebecca* and Sakalidis, Monique
Michigan State University

Caliciopsis pinea, causal agent of Caliciopsis canker disease (CCD) on *Pinus strobus*, was regarded as an inconsequential native pathogen since its discovery in 1920. Reports of more frequent and more severe disease have increased in the last 20 years, with tree mortality reported in some cases. Recently, ascocarps of *Caliciopsis* spp. previously unknown to the Midwest were observed on *Acer rubrum*, *Quercus velutina*, *Pinus resinosa*, *P. banksiana*, and *P. strobus* in Michigan. ITSrDNA barcoding revealed 3 putative new species of *Caliciopsis* on these hosts. Additional morphological observations, measurements, and multi-gene phylogenetic analyses were completed. Unexpectedly, group-I introns were found throughout the ribosomal genes of many of the isolates. Molecular assays used for *Caliciopsis* spp. detection will need to be reevaluated to account for group 1-introns. The discovery of these previously unknown *Caliciopsis* spp. and their genetic complexity highlights the diversity present in native forests, where microbial ecology is still understudied.

Mycologist in Residence at the UBC Herbarium
*Harrower, Emma
University of British Columbia

The biodiversity of Canada's fungi are documented in dried fungal specimens in herbaria and in genetic DNA sequences that are stored in the global GenBank Database. I present to you the story of how I came to be the first Mycologist in Residence at the UBC Herbarium. I increased the value of the collections by doing genetic analysis of the *Cortinarius* specimens that had an ITS sequence in GenBank. My analysis improved the taxonomy of the specimens, making it easier for researchers worldwide to find them and study them.

Evolution of human pathogenesis in *Aspergillus flavus*

Hatmaker, Anne*. Barber, Amelia. Drott, Milton. Alastruey, Ana. Kurzai, Oliver.
Garcia-Hermosa, Dea. Rokas, Antonis.
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The fungus *Aspergillus flavus* is responsible for devastating human disease and crop contamination. Previous research revealed distinct genetic structure within U.S. *A. flavus* populations. However, studies including clinical isolates are lacking. To define the pan-genome of *A. flavus*, we collected genomes of 250 isolates from 9 countries, including 70 newly sequenced clinical isolates. Using SNPs, we identified population clusters through a discriminant analysis of principal components (DAPC) and constructed a phylogeny. We annotated or re-annotated the genomes of all isolates and identified over 19,000 orthogroups. The core genome consisted of over 10,000 orthogroups present in at least 95% of isolates. We found that core and accessory genes exhibited differing rates of evolution. Additionally, accessory genes, including genes within biosynthetic gene clusters, were distributed unequally across the phylogeny. Although clinical isolates were present in all but one DAPC cluster, over 70% of all clinical isolates were found in a single cluster.

Resistance to reactive oxygen species across diverse yeast species: Implications for industry and medicine

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Reactive oxygen species (ROS) are encountered by yeasts during routine metabolism and through interactions with other organisms that employ ROS as defenses. Therefore, the ability of a yeast to survive in the presence of ROS has broad implications in microbial metabolism and pathogenesis. We compared the ROS resistance of over 250 yeast species in the subphylum *Saccharomycotina* to assess the distribution of ROS resistance, as well as the genetic mechanisms that underly this trait. Interestingly, we found that the most resistant species were distributed widely across the subphylum and included species in the genera *Yarrowia*, *Candida*, *Kazachstania*, and *Tetrapisispora*. We determined the presence and absence of known ROS mitigating genes and found that species with a duplicated alternative oxidase (AOX) gene had higher average ROS resistance compared to species lacking AOX or with a single copy. This suggests that modifying AOX may be useful for yeast-mediated bioproduction or antifungal strategies

Pollen-trapping fungi: undetected and widespread hyphomycetes in western North America

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University of Alberta

The degradation of pollen grains as food source is uncommon in fungi, but few groups have specialized in capturing it, mostly found in the class Orbiliomycetes. In the present contribution, we report the presence *Retiarius* species in western Canada and northwestern USA, being potentially one of the most common micro fungi in forested ecosystems. We used genus-specific PCR primers to screen various substrates, including tree bark and macrolichens, for the presence of *Retiarius*. Our screening confirmed the occurrence of multiple *Retiarius* clades in the region. We also isolated and two species are characterized two species in laboratory conditions: *R. bovicornutus* and *Retiarius* sp., both isolated from the lower surface of saxicolous lichens. To study these species, we used various microscopy techniques, and assessed its occurrence in ecosystems and ecological preferences. In addition, we profiled their carbon and nitrogen utilization using Biolog Phenotype MicroArrays.

Fluorescent microscopy to identify the location of Ppp1 a novel protein in *Candida albicans*

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Biofilms are a major source of pathogenicity in *Candida albicans* and account for about half the deaths due to systemic candidiasis. Characteristics such as the formation of extracellular matrix, hyphae, and extracellular DNA help these cells invade and adapt to host immunity and resist antifungal drugs. Biofilm formation is controlled by a transcriptional network and involves over a thousand genes including a small gene we have named PPP1 (Punctate Pattern Protein 1). This is a biofilm-upregulated gene encoding an unexamined protein found only in *C. albicans* and *dublinsiensis*. In this study, we use fluorescent microscopy to help characterize this protein by identifying its subcellular localization and links to other cellular processes. To do this, we made a fusion construct of Ppp1 with GFP using CRISPR and imaged the protein expression pattern. This was used to identify subcellular compartments with similar patterns and direct knockouts and tags of classical proteins defining these domains. Disruptions and tagging of the eisosome defining Sur7 established that Ppp1 was not a component of the eisosome. Disruptions and fusion to components of other punctate cellular elements are underway and these cells will be imaged to screen for disruption of the Ppp1 protein pattern and co-localization respectively. To authenticate the validity of our findings, image analysis will be used to quantify the colocalization of proteins, disruption of subcellular compartment localization, and the size of Ppp1 punctum. This will form the basis of future biochemical analysis for functional annotations of our protein which can be further explored for therapeutic applications.

The corruption of the wood-wide web? Evaluating the evidence supporting the structure and function of common mycorrhizal networks in forests.

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Common mycorrhizal networks (CMNs) form when hyphae physically connect roots of different plants. Although we know very little about their sizes, longevities, and roles in distributing resources in soils, these networks have caught the imagination of the public. Three messages about CMNs are prevalent in the public media: that CMNs (1) are widespread in forests; (2) move resources from large trees to seedlings, thereby increasing seedling performance; and (3) preferentially direct warning signals from trees to their offspring. We found evidence for these claims was either scanty, too variable to generalize, or non-existent. Positive citation bias and confirmation bias appear to have skewed the understanding of CMNs among scientists, while powerful storytelling has engaged the public.

What can 1,000 barcode sequences tell us about regional fungal diversity and conservation targets?

Justo, Alfredo*

New Brunswick Museum

Regional studies of fungal diversity heavily rely on large-scale generation of DNA sequence data to accurately capture the diversity of macrofungi occurring in a particular area. We analyzed our current dataset of >1,000 ITS sequences, generated from voucher specimens, to see what it can tell us about mushroom diversity in New Brunswick. Hyperdiverse lineages like the Cortinariaceae harbor extensive undescribed species-level diversity (>24 taxa in NB), some of them also recorded in nearby areas (e.g. Quebec), but some only known from our regional records. We will also explore these preliminary results for groups of special interest in fungal conservation, like the waxcap mushrooms in the Hygrophoraceae. None of the sequenced NB collections of *Hygrocybe* or *Gliophorus* currently identified with a name originally described from Europe (e.g. *H. punicea*, *H. splendidissima*, *G. irrigatus*, *G. psittacinus*) actually corresponds to the European species.

Genetic characterization of apple scab resistance: An important step to breed cultivars with durable disease resistance

Khan, Awais

Cornell University

Diseases and pests are the major causes of tree loss, decreased fruit quality, yield gap and increased production costs in apples. Apple scab, caused by fungus *Venturia inaequalis*, lead to significant losses in apple production and fruit quality worldwide. We have systematically characterized apple scab resistance of 177 *Malus* accessions and identified new sources of scab resistance. We have also identified *V. inaequalis* isolates that can overcome the most frequently used apple scab resistance gene, Rvi6 (Vf), in apple breeding. We found a large number of wild *Malus* accessions and domesticated apples resistant to apple scab in the field. Several of these accessions were unrelated to sources of previously known resistance genes and are promising for apple scab genetic research and breeding. These accessions are promising for use in future genetic studies to identify novel sources of scab resistant alleles for apple breeding to develop cultivars with durable apple scab resistance.

Genetic and mating-type diversity among Canadian, US and other wheat leaf rust fungal isolates using whole genome and RNA-derived sequences

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Agriculture and Agri-Food Canada

Puccinia triticina, causing wheat leaf rust disease, is the most common rust pathogen worldwide. Variable populations exist in many wheat-growing regions including in North America where highly dynamic sub-populations evolve over time, often as a result of the introduction of wheat varieties with novel resistances. Assessing and monitoring the populations is essential for supporting resistance gene stewardship and proper disease management. Here, we compared RNA sequences from 163 Canadian isolates and DNA sequences from 51 Canadian and 7 Mexican isolates from durum wheat. We included DNA sequences from 83 previously published US isolates and additional European and Australian isolates. Mapping reads against a newly-assembled, haplophased reference genome yielded the SNPs needed for phylogenomic tree generation. The resulting analyses supported the existence of 3 major lineages in NA, with durum-infecting isolates clearly separated. Nine different homeodomain mating-type alleles were identified with various allele pairs confined to lineages, expected in clonal populations.

Resolving the systematics of *Hericium* spp. in North America with multigene phylogenetic analysis and its implications for mushroom cultivation programs.

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Hericium erinaceus is a choice edible basidiomycete that has gained popularity as a nutraceutical and dietary supplement as it produces secondary metabolites, namely erinacines and hericenones, capable of stimulating nerve growth factor (NGF) synthesis. Unfortunately, little attention has been given to the production of metabolites in other species of *Hericium* partly due to the confusion surrounding the systematics of this genus. Single gene phylogenies of *Hericium* have provided little resolution to this genus where species delimitation, monophyly, and evolutionary relationships generally are a topic of debate. The current study employed a multi-locus phylogenetic analysis to resolve evolutionary relationships within *Hericium* as it occurs in North America and evaluated the biosynthesis of erinacines by wild-collected specimens. These findings will be valuable in the attribution of medicinal value to specific *Hericium* species and strains, and ultimately for the consideration of understudied lineages in mushroom cultivation.

Mixed nutrients contribute to fungal biotrophy in *Ustilago maydis*

Kretschmer, Matthias*

Michael Smith Laboratories, The University of British Columbia

Ustilago maydis is a biotrophic plant pathogen of corn. Biotrophic plant pathogens are strictly dependent on a host to fulfill their lifecycle. The lack of information regarding nutritional requirements during biotrophy at present is limiting research progress. Here, we show that a combination of preferred and non-preferred carbon sources leads to biotrophy related phenotypes in *Ustilago maydis* in vitro. With RNAseq we identified the activation of the mating pathway and consequently the related biotrophic program including expression of secreted effectors during growth on mixed carbon sources. The biotrophy related phenotypes included accelerated growth, induction of filamentation, the production of an extracellular polysaccharide and the formation of melanin. Melanin formation in part could be linked to iron/iron-sulfur cluster and antioxidant/GSH metabolism via Grx4. Taken together, a mixture of diverse host derived nutrients supports fungal biotrophy in *U. maydis*.

Mechanisms for fungal sensing of the vertebrate host environment
Kronstad, James*
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Cryptococcus neoformans is an opportunistic fungal pathogen that causes meningoencephalitis in immunocompromised individuals such as those suffering from HIV/AIDS. The ability of the fungus to cause disease depends in large part on the elaboration of a polysaccharide capsule for protection from the host immune response. Interestingly, capsule deployment is responsive to a number of conditions relevant to the vertebrate host environment including the iron limitation resulting from nutritional immunity. We are defining the mechanisms by which *C. neoformans* acquires iron from host sources as well as the regulatory factors that sense iron and control the expression of iron uptake and virulence functions. Recent studies focus on the role of the monothiol glutaredoxin Grx4 as a key iron sensor in partnership with the transcription factors Cir1 and HapX. Importantly, we find that Grx4 is responsive to additional signals besides iron and that the protein influences a broad range of virulence-related phenotypes.

Understanding the evolution of antifungal resistance using genome editing and experimental evolution
Landry, Christian*
Université Laval

To better limit and monitor the evolution of antifungal drug resistance, we need to know the set of potential resistance mutations, the conditions that affect their likelihood of occurrence, and the fitness benefits and tradeoff they incur. We used the budding yeast and high-resolution genome editing to examine all possible mutations in one of the targets of the antifungal flucytosine. We identified the properties of resistance mutations and uncovered the existence of a very strong tradeoff between resistance and fitness. To narrow down on the most likely resistance genes, we evolved hundreds of independent resistant mutants. We identified one major resistance hub for this drug but failed to discover known resistance genes. Through further experiments, we showed that although functionally equivalent in isolation, some gene loss of function mutations failed to evolve in populations because of cooperative interactions among cells. Altogether, these projects shed new light on the conditions that will influence the routes taken by evolution during antifungal drug treatment.

Genomic Analysis of the Marine Fungi *Rhodotorula sphaerocarpa* ETNP2018 Reveals Adaptation to the Open Ocean

Lane, Dylan*; Valentine, David; Peng, Xuefeng
University of South Carolina

The genus *Rhodotorula* consists of basidiomycete yeasts that are oleaginous and carotenogenic and have been isolated from a wide range of environments. Many of these environments are oligotrophic, indicating that *Rhodotorula* yeasts can adapt their metabolic strategies to optimize survival in oligotrophic conditions. To better understand their adaptive strategies in the marine environment, *Rhodotorula sphaerocarpa* ETNP2018 was genomically compared to fourteen representative *Rhodotorula* yeasts isolated from a variety of environments. *R. sphaerocarpa* ETNP2018 was isolated from the mixed layer of the Eastern Tropical North Pacific (ETNP) oxygen minimum zone (OMZ), a region depleted in nitrates and production. It has the smallest genome of the fifteen genomes yet encodes an average number of proteins and transcription factors. Our research demonstrated that the selective pressures of the ETNP OMZ favor streamlined genomes designed to conserve nutrients, a set of core metabolisms yet reduced overall biosynthetic potential, and additional mechanisms of nutrient intake.

Nitrous oxide production and isotopomer composition by fungi isolated from salt marsh sediments

Lazo-Murphy, Birch M*; Larson, Samantha; Staines, Sydney; Bruck, Heather; McHerny, Juliane; Bourbonnais, Annie; Peng, Xuefeng
University of South Carolina

Emissions of N₂O, a potent greenhouse gas and ozone depleter, have been increasing from salt marsh environments. Denitrification is a significant source of N₂O from salt marsh sediments; it is assumed prokaryotic activity produces most N₂O, however, fungi may significantly contribute to this process. N₂O isotopologue analysis is used to estimate the contribution of different N₂O sources. The isotopologues of four isolated salt marsh sediment fungi capable of growth under sulfidic conditions were measured using isotope ratio mass spectrometry. The site preference (SP) of N₂O produced by salt marsh sediment fungi ($7.5 \pm 1.6\text{‰}$ to $33.4 \pm 1.2\text{‰}$) is lower than the SP of *Fusarium oxysporum* ($37.1 \pm 2.5\text{‰}$), which is typically used to quantify fungal N₂O. The N₂O SP values we measured should be used as endmembers in future studies attempting to quantify fungal contribution to N₂O production from salt marsh sediment.

Defining remodeling of the global temporal proteome responses of Fusarium head blight-resistant and -susceptible wheat cultivars.

Boyan Liu*, Reid Buchanan, Payton Curtis, Rebecca Shapiro, Mitra Serajazari, Jennifer Geddes-McAlister

University of Guelph

Fusarium graminearum is the primary causative agent of Fusarium head blight (FHB). This disease threatens food security by reducing crop yield and contaminating food products with mycotoxins. The destruction caused by FHB is expected to increase in severity in the coming years due to a connection with climate change. Our research uses state-of-the-art mass spectrometry-based proteomics to define the temporal and resistance-specific host-pathogen interactions between *F. graminearum* and *Triticum aestivum* (wheat). We profiled core proteome defense responses independent of cultivar but regulated across time, along with cultivar-specific responses to infection. We found that up-regulated proteins in the resistant cultivar contribute to early pathogen detection and we have identified uncharacterized fungal proteins involved in the disease progression. Our findings aim to enhance cultivar resistance's effectiveness, reduce infection severity, and develop strategies to prevent fungal disease in cereal crops.

Assessment of the therapeutic potential of bile acids against the fungal pathogen
Candida albicans

Lung, Bryan*. Lajoie, Patrick.
Western University

The incidence of fungal infections has been steadily increasing in multiple regions across the world. Consequently, identification of combination therapies should be explored to increase treatment options for vulnerable patients. It was recently suggested that bile acids may serve as potential candidates for antifungal combination therapy. However, the antifungal modulatory potential of bile acids remains poorly understood. Here, I provide a comprehensive analysis of the effects bile acids have on the toxicity of antifungal drugs in the pathogen *Candida albicans*. I found that conjugated bile acids reduced the toxicity of various classes of antifungal compounds, excluding azoles in which an increase in toxicity was observed when treating *C. albicans*. Interestingly, non-conjugated bile acids either increased or reduced the toxicity of different antifungal drugs in *C. albicans* in a treatment dependent manner. These findings may help guide the development of future antifungal strategies that target fungal infections in high-risk patients.

DYRK-Family Kinases Regulate *Candida albicans* Morphogenesis and Virulence through the cAMP/PKA Pathway

MacAlpine, Jessie*, Liu, Zhongle, Hossain, Saif, Robbins, Nicole, Cowen, Leah
University of Toronto

Candida albicans is an opportunistic human fungal pathogen that causes common mycoses in healthy populations and invasive disease in immunocompromised individuals. The fungus employs several virulence traits to cause disease, including its ability to transition from yeast to filamentous morphologies. Previous work identified that the dual-specificity tyrosine-phosphorylation regulated kinase (DYRK) Yak1 is involved in *C. albicans* hyphal morphogenesis and biofilm formation. Here, we determine that Yak1 acts downstream of Protein Kinase A (PKA) and upstream of core transcription factors to regulate filamentation. We found that hyperactivation of the cAMP-PKA pathway under physiological concentrations of CO₂ bypasses the requirement for Yak1 in the yeast-to-filament transition, mediated by a previously uncharacterized kinase, Pom1. Finally, we found that Yak1 is required for hyphal morphogenesis in a dermatitis model of *C. albicans* infection and that pharmacological inhibition of Yak1 attenuates filamentation in dermal tissue.

Two novel and unusual pleosporalean fungi isolated from the bark of *Acer saccharum* Mack, Jonathan*. Sproule, Amanda. Seifert, Keith. Smith, Myron. and Overy, David. Agriculture and Agri-Food Canada

During a survey documenting the culturable microfungi from the bark of the Sugar Maple (*Acer saccharum*), two unusual pleosporalean fungi, *Atrocalyx glutinosum* sp. nov. and *Nigrograna rubescens* sp. nov. were commonly isolated and found to be unique based on both their morphological characters and molecular phylogenetic analyses. Both species are characterized based on their pycnidial anamorph. *A. glutinosum* (*Lophiotremataceae*) excretes copious amounts of pullulan in axenic culture while *N. rubescens* (*Nigrogranaceae*) is characterized by the diffusion of dark red pigment within the culture medium. The phylogenetic placement of *A. glutinosum* was resolved using a concatenated multi-gene dataset containing the ITS, LSU and RPB2 gene loci while phylogenetic placement of *N. rubescens* was resolved using a concatenated multi-gene dataset containing the ITS, LSU, TEF1a and RPB2 gene loci.

Macrofungal diversity in old-growth Eastern Hemlock stands of Kejimikujik National Park and National Historic Site, Nova Scotia, Canada

Rebecca M. Mader*, Keith N. Egger, Matthew J. Smith, Allison K. Walker
Acadia University

Fungal communities are highly sensitive to vegetation changes and often shift during forest succession. In Kejimikujik National Park and National Historic Site (Nova Scotia, Canada), old-growth foundational Eastern Hemlock (*Tsuga canadensis*), are threatened by Hemlock Woolly Adelgid (*Adelges tsugae*) (HWA). To help predict the resistance of associated macrofungal communities to HWA hemlock disturbance, macrofungal communities before and after a 2002 – 2006 Pale-Winged Grey Moth (*Iridopsis ephyraria*) hemlock disturbance were examined. Thirty-year-old macrofungal specimens (E. C. Smith Herbarium, Acadia University) and 2020 – 2023 collections from the same hemlock stands were identified using morphology and ITS rDNA barcoding. Species richness and community composition before and after the Pale-Winged Grey Moth disturbance were compared with hemlock defoliation and environmental data to identify changes in the fungal communities. Our results expand current knowledge of how well macrofungal communities resist ecosystem disturbances and illuminate the future of macrofungi in Kejimikujik as HWA infestations intensify.

The potential influence of amoebal predation on *Cryptococcus neoformans* and its virulence

Maliehe, Maphori*, Folorunso, Sam, Ogundeji, Adepemi, Pohl, Carolina, Sebolai, Olihile
University of the Free State

Cryptococcus neoformans is an important fungal pathogen, causing life-threatening infections in susceptible hosts and has thus been placed on the WHO's fungal pathogen priority list. This organism may have acquired its virulence due to environmental pressures. Our objective was to assess if amoeba, a natural predator of cryptococcal cells, could cause sufficient pressure to enhance their resistance towards macrophage phagocytosis and virulence potential in *Galleria mellonella* larvae. Cryptococcal cells were co-cultivated with amoeba and internalised cells harvested. These cells were analysed for diameter, melanin production, resistance to macrophages and killing of larvae. Experimental cryptococcal cells were larger, produced more melanin, were less susceptible to phagocytosis by macrophages and more virulent to larvae, compared to control cells. These results suggest amoeba can prime cryptococcal cells for virulence in host organisms and highlighted important virulence factors, which may be targeted to attenuate the virulence of this important pathogen.

Evaluating diverse non-brewing yeast strains for novel new-make spirit applications.

Marr, Alex.* Measday, Vivien.

University of British Columbia

Whisky is a distilled alcoholic beverage (spirit) made from a malt liquid extract called wort, which then undergoes alcoholic fermentation commonly by *Saccharomyces cerevisiae* (SC) yeast. Most whisky distilleries utilize one of a handful of commercial distilling strains. Recently, global interest has increased for diverse non-traditional strains for spirits production, including SC and non-SC species, which offer novel organoleptic properties compared to commercial strains, and this may lead to interesting new brands of whisky. We screened 88 strains isolated from spontaneous fermentations of grapes from the Okanagan Valley (OV), representing four species, for use in whisky production. Maltose utilization, fermentation efficiency and strain lineage were criteria used to select seven strains for pilot scale wort fermentations and subsequent distillation. Fermentation and new-make spirit samples will be analyzed by high performance liquid chromatography and gas chromatography mass spectrometry respectively. This project aims to demonstrate OV yeast strain potential for industrial applications.

The Impact of Plant Defense Elicitors and Chemical Fungicides on the Fungal Communities of Honeycrisp Apples

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Agriculture and Agri-Food Canada

Epiphytic and Endophytic micro-organisms associated with plants form complex communities on or within their host plant. It has been revealed that these communities influence physiological traits, development, and host-susceptibility to abiotic and biotic stress, and it is theorized that these communities evolved alongside their hosts to form a unit of selection known as the 'Holobiont'. The microbiome is highly variable and can be influenced by abiotic factors and chemical fungicides and Plant Defense Elicitors. To date, however, the impact of Plant Defense Elicitors has not been assessed. Here, we compared the impact of Chemical Fungicides and Plant Defense Elicitors on the fungal communities of 'Honeycrisp' apples from a single orchard over two consecutive growing years. We demonstrate variation in fungal community structure and composition between tissue-types, growing season, and treatment regimes, including shifts in the abundance of key fungal genera. Furthermore, we demonstrate a loss in fungal network complexity as a result of fungicide treatment.

Activation of SARS-CoV-2 Spike protein by a fungal protease(s)

Mjokane Nozethu*, Maliehe Maphori, Folorunso Olufemi, Ogundeji Adepemi, Gcilitshana Onele, Albertyn Jacobus, Pohl Carolina, Sebolai Olihile
University of the Free State

The novel coronavirus disease of 2019 (COVID-19) caused by SARS-CoV-2 has resulted in millions of infections and deaths worldwide. To invade a cell, this virus targets cells that display ACE-2 receptors and relies on host serine protease(s). Importantly, COVID-19 may also manifest in persons with underlying microbial infections. Some of these microbes like *C. neoformans* secrete microbial protease(s) to breach the epithelial barriers for purposes of dissemination. It is in this context that microbial protease(s) may also activate the spike protein of SARS-CoV-2. A fluorogenic peptide mimetic of the S protein with a furin cleavage site was used. The biochemical efficiency of cryptococcal protease(s) to mediate cleavage of a potential furin site at the interface between the S1 and S2 subunit was compared to that of a recombinant furin. In general, this preliminary work suggests cryptococcal protease(s) have the potential to activate S protein of SARS-CoV-2 leading to host invasion.

Isolation and complete Genome Sequences of endophytic morphinan alkaloids production from *Papaver bracteatum*

Sima Mohammadi*, Jeff Gauthier , Guillaume N'guyen , Irena Kukavica-Ibrulj , Marianne Potvin , Valentine Renaud , Bahman Bahramnejad , Antony T. Vincent² , Roger C. Levesque
Laval university

Morphinan alkaloids are mainly produced by medical plants belonging to the genus *Papaver*. Fungal endophytes with the potential of producing host-like medicinal compounds constitute a main part of the unexplored fungal diversity. This study is the first to investigate isolation, identification and genomics of the endophytic fungus *Papaver bracteatum*.

A new species of *Pithoascus* was isolated from *P. bracteatum*. GC/MS and HPLC demonstrated that it could produce morphinan alkaloids. The genome of *Pithoascus* sp. was sequenced by Oxford Nanopore and an Illumina NovaSeq 6000. De novo assemblies were done in hybrid mode with MaSuRCA.

Pithoascus sp. was identified based on ITS, TUB, and EF1- α genes sequences. Genome size was consistent with other fungal in the same subclass 66.128 ± 0.05 Mbp with an N50 of 3.21 ± 0.004 Mbp. This *Pithoascus* species is introduced as a new taxon which maybe can be a model system to investigate morphinan biosynthesis.

Whole genome sequencing of British Columbian and Californian *Saccharomyces cerevisiae* strains reveals a novel Pacific West Coast Wine clade

Moore, Jackson*. Marr, R Alexander. Formby, Sean. Martiniuk, Jonathan. Montpetit, Rachel. Montpetit, Ben. Measday, Vivien.
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Saccharomyces cerevisiae (*S. cerevisiae*) carries out fermentation of grape sugars to ethanol and generates flavour and aroma compounds in wine. Wineries place a high value on identifying yeast native to their region to develop region-specific wine programs. We have isolated *S. cerevisiae* strains from spontaneous fermentations of grapes from wine regions in British Columbia and California, and strains from oak trees in California. Whole genome sequencing was conducted on 172 strains and phylogenetic analysis shows that they cluster into four clades: European/Wine (EW), Transpacific Oak, Beer 1/Mixed Origin, and a new clade we have designated as Pacific West Coast Wine (PWCW). The PWCW clade has high nucleotide diversity and shares genomic characteristics with North American oak strains but also has gene flow from the EW clade. This is the first study to sequence Canadian wine yeast and provides Pacific West Coast winemakers with a genomic account for regional wine characteristics.

Population structure and genomic signatures of climate adaptation in *Neonectria faginata*, causative agent of beech bark disease

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University of New Hampshire

Beech bark disease (BBD), a cankering disease of American beech (*Fagus grandifolia*), is widespread throughout Canada and the US resulting in significant ecological, aesthetic, and economic impacts on beech forests. The disease is caused by an invasive scale insect (*Cryptococcus fagisuga*) and two presumptively native fungal pathogens, *Neonectria faginata* and *N. ditissima*. Attack by *C. fagisuga* is believed to initiate fungal infection and has spread through the range of American beech in a relatively consistent spatiotemporal pattern. Interestingly, *N. faginata* is apparently isolated to the disease complex, suggesting it may have dispersed in a pattern consistent with the spread of BBD. This presents a unique opportunity to examine recent climate adaptation as the fungus has dispersed from cooler to warmer climates. Here we examine population structure and genomic signals of climate adaptation in *N. faginata* using whole-genome resequencing of 105 isolates across 17 sites in the US range of BBD. We found strong evidence of isolation by distance across the sampled range, but no clear population substructure. Genotype-environment association tests revealed 629 SNPs (occurring in or near 144 genes) associated with different climate metrics, including 56 SNPs (9 genes) uniquely associated with nongrowing season heat accumulation and 23 SNPs (4 genes) associated with the number of annual freeze-thaw cycles.

Timing of ascospore release of *Anisogramma anomala*, a pathogen of eastern filbert blight in Ontario, Canada

Asifa Munawar, Melanie Filotas, Katerina Jordan

University Of Guelph

Hazelnut trees are very susceptible to eastern filbert blight caused by the fungus, *Anisogramma anomala*. The fungus releases ascospores that infect actively growing stem tissue in young shoots. It is important to know when the spores are released under Ontario weather conditions for timely applications of preventative fungicides.

GRIPST-2009 spore sampler was used to track airborne spores from March–November 2022 at two sites in Norfolk County, Ontario. Weather and phenology data were also recorded. The first release at both sites was noted close to the bud break time (April 18-20, 2022). The highest release was observed towards the end of May at both sites, close to the mature leaf stage. The ascospores release was not observed during March and after early June 2022. Weather data is still being analyzed. The spore tracking work will continue in 2023 and the results will be used to provide management recommendations for growers.

Complete Genome Sequences of fungal exotic strains isolated from High Canadian Arctic

N'guyen Guillaume *, Hallett Emily, Mohammadi Sima , Gauthier Jeff, Renaud Valentine, Kukavica-Ibrulj Irena, Potvin Marianne, Comte Jérôme, Levesque Roger C.
Laval University / IBIS

The recent emergence of multidrug-resistant bacterial-fungal pathogens enhances the quest to find alternative antimicrobials for treating human infections. Natural compounds play critical competitive roles in stressed microbial ecological systems exacerbated by climate change. Phenotypic and genomic mining may yield unusual compounds of high biotechnological and therapeutic value.

Isolation chips (iCHIP) were used to increase diversity of culturable soil microbes from Bylot Island, High Canadian Arctic. Several rounds of lab training gave 6 exotic morphologically distinct fungi. Strains were grown and genomes analyzed using Oxford Nanopore long-read DNA sequencing. Initial genome assemblies gave 21 to 53 contigs and genome sizes varying from 31 to 34 Mbps. Genome polishing and hybrid assemblies were performed with Illumina short reads to improve genome assembly and taxonomic assignment.

Transcriptomic profiling and annotation will be performed to identify potential antimicrobial compounds in silico and phenotypic validation using competition assays.

Differential regulation of the antifungal response by Tra1 across yeast species
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Western University

Candida albicans infection is the leading cause of mortality from fungal infections. Tra1 is a conserved and essential component of the SAGA/NuA4 co-activator complexes that regulate gene expression and have been shown to regulate *C. albicans* antifungal response and pathogenicity. We previously demonstrated that mutations in TRA1 increase caspofungin sensitivity in *C. albicans*. Unexpectedly, we found that a lack of Tra1 function increases resistance to azoles in *C. albicans* in contrast with *S. cerevisiae*. In *C. albicans*, loss of Tra1 function is associated with increased expression of genes linked to azole resistance, such as ERG11 and CDR1, a membrane transporter associated with the efflux of chemicals, including azoles. Consequently, we found that tra1 mutant cells display increased efflux of the Cdr1 substrate rhodamine 6G and show reduced accumulation of intracellular fluconazole. Thus, *C. albicans* Tra1 differentially modulates the response to various antifungal drugs.

Transposable elements identification and expression in arbuscular mycorrhizal symbiont *Rhizophagus irregularis* during different colonization stages

Jordana Inácio Nascimento Oliveira*, Nicolas Corradi

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Transposable elements (TEs) are repetitive DNA which insertions can create genetic variability and novelties in gene expression regulation. The genome of *R. irregularis*, is composed by 50% of repetitive sequences. Nonetheless, 30% of TEs families remains unknown, making it difficult to address the functions of these elements are related. This improved annotation uncovered new families for LTRs, DIRS, LINE, SINE, TIRS, Crypton and Helitron orders. Furthermore, SINE elements were identified for the first time in this species, and we find that TIRs families comprise 31% of the overall TE content. This more complete classification allowed us to evaluate the expression of these elements with higher resolution across lifestages. We find that in *Medicago trunculata* TE expression is significantly upregulated in colonized roots and arbuscules (ARB) compared to extraradical mycelium. Specifically, a total of 344 and 374 TEs are upregulated in colonized roots and arbuscules, respectively, while only 93 are regulated extraradically. These results indicate that TEs play a functional role during plant host colonization stages.

Arctic lichens gone south: the arctic-alpine lichen *Brodoa oroarctica* (Krog) Goward and its unusual disjunction in eastern North America.

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Memorial University of Newfoundland and Labrador

Arctic-alpine biogeographic affinities are common in lichens. Typically, this affinity corresponds to a distribution restricted to the Arctic and the Rocky Mountains in western North America. However, some arctic-alpine lichens are also found disjunct in eastern North America. The lichen species *Brodoa oroarctica* (Krog) Goward, is an example of a remarkable disjunction in eastern North America. We report the first verified record of this species in the province of Newfoundland and Labrador, establish an updated account of its frequency and distribution in eastern North America, and discuss the importance of robust occurrence data for sound conservation planning.

Fungal contribution to nitrogen and carbon cycling in the eastern tropical North Pacific oxygen minimum zone

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Fungi's ecological role in terrestrial environments is well studied. In the open ocean, the diversity, function, and ecology of fungi remains elusive. A recent study of fungal communities in the eastern tropical North Pacific (ETNP) oxygen minimum zone showed that fungi can contribute up to 10% of nitrous oxide production from the water column. Early diverging lineages accounted for approximately one third of the metagenomic reads attributed to fungi throughout the water column. We performed eukaryotic metatranscriptomic sequencing using high-quality RNA extracted from seawater. We found that *Dikarya* fungi were expressing cellobiohydrolase and likely contributed to the hydrolysis of complex polysaccharides. Early diverging lineages, including Mucoromycota and Chytridiomycota, expressed genes related to flagella development and filamentous growth. The transcriptional profile of these marine fungi was distinct between the oxic and anoxic depths. Our findings highlight the unexpectedly active roles fungi play in nitrogen and carbon cycling in the ocean.

Differences in epigeous ectomycorrhizal fungal community composition between cut-blocks and unharvested forests persist 27-years following harvesting in a high-elevation forest

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Ectomycorrhizal (ECM) fungi are essential to ecological processes in soil, such as organic matter decomposition, redirection of carbon fluxes, and water/nutrient acquisition by plants. They are highly susceptible to tree harvesting because they depend on living roots to acquire carbon. This study aimed to compare the species richness and community composition of epigeous ectomycorrhizal fungi between 1 ha cut-blocks and the adjacent forest 27 years following harvest. We hypothesized that the species richness and community composition would differ between the cut block and the unharvested forest. Sporocarps were collected along a 90m transect, and DNA was extracted, amplified, and sequenced via Sanger sequencing for each sporocarp sampled. We found a difference in community composition and species richness between the clear-cut and forest. Furthermore, there was a decline in species richness along the boundary between the forest and the cut block, indicating an edge effect.

Characterization of *Phytophthium* spp. from Vietnam, the center of diversity of citrus
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USDA Agricultural Research Service Foreign Disease Weed Science Unit

Despite its formal description in 2010, there is much to learn about the oomycete genus *Phytophthium*'s diversity, host range, and aggressiveness. Pathogenicity tests using *P. helicoides* and P. D37 from Vietnam, global center of diversity for citrus, indicated equal aggressiveness to well-characterized *Phytophthora nicotianae* and *Phytophthora palmivora*, typical oomycete threats to U.S. citrus. *Phytophthium* species have not been documented in U.S. citrus production, however, potential limitations to diagnostic protocols may have imparted a narrow focus on *Phytophthora*. To evaluate risk to U.S. citrus, selected *Phytophthium* isolates were characterized in comparison to *Phytophthora* species. *Phytophthium* isolates had generally higher optimal growth temperatures and tolerated high pH and high salinity, variables that are implicated in climate change projections. Some *Phytophthium* isolates cross-reacted with *Phytophthora* immunostrip tests and were resistant to mefenoxam fungicide. These attributes, combined with *Phytophthium* species' cosmopolitan distribution, suggest surveillance for their potential impact on U.S. citrus production is warranted.

Aquatic fungi as environmental indicators for agriculturally dominated watersheds
Pham, Phillip*; Shi, Yichao; Lapen, David R.; Khan, Izhar U. H.; Aris-Brosou, Stéphane;
Chen, Wen
University of Ottawa

Freshwater aquatic fungi spend part of their life cycles in water, and their distribution may be affected by water conditions. Stream water conditions can be affected by agricultural runoff carrying agrochemicals, influencing microbiomes. While this has been well-documented for freshwater bacterial communities, aquatic fungal communities have been understudied. To address this, our study evaluated the impact of aquatic fungal communities to anthropological and environmental perturbations. We sampled fungal communities in surface waters of the South Nation River basin between 2016-2021 using internal transcribed spacer 2 metabarcoding. We recovered 6,571 Operational Taxonomic Units, assigned to 15 known fungal phyla. We found that alpha diversity was greatest in the forested site, compared to anthropogenically impacted sites. While significant variation in fungal communities across different land use classes, seasons, and years was observed, the water conditions and weather explained less than 5% of community variance, indicating a low contribution of species sorting.

Improving the reliability of mycorrhizal ecology research through transparency and openness.

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After the recent revelation of citation bias and over-interpretation in research on common mycorrhizal networks, the need to improve rigour in mycorrhizal ecology research is clear. We discuss how transparency, openness, and reproducibility are key to ensuring reliability of evidence, and assess the prevalence of these attributes in published mycorrhizal ecology studies. Using a standardized checklist with 21 criteria, we evaluated transparency and openness in a sample of 45 publications describing mycorrhizal ecology experiments, published in 2012, 2017, and 2022 and in three different journals. No study achieved a score better than 50%. Only nine (20%) of the publications provided access to data, and no publication provided access to all data and code necessary for reproducing the reported results. Details about experimental design were also commonly lacking. We provide guidelines for improving the reliability of mycorrhizal ecology research, and highlight helpful resources for researchers at all career stages.

Antifungal properties of thiazolidine derivatives

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University of Guelph

Fungal infections are a common cause of life-threatening diseases, especially for immunocompromised patients. *Candida* species are amongst the most common fungi responsible for these infections. Fungal pathogens have become more dangerous due to the rising development of anti-fungal drug resistance. Therefore, it is imperative to discover novel compounds with anti-fungal properties. Thiazolidine derivatives are chemical compounds with many biological activities.

Thiazolidine derivatives were tested against *Candida albicans* (wild type and clinical strain), *C. tropicalis*, *C. kefyr* and *C. lusitaniae* in disc diffusion assays. 4 out of 345 thiazolidine derivatives were chosen for further analysis due to their high level of antifungal activity.

Minimum inhibition concentration assays were utilized to determine the susceptibility of *Candida* strains to detect the lowest concentration required to inhibit growth. Synergy assays were then conducted to detect any synergy between fluconazole (a commonly used anti-fungal drug) and the 4 thiazolidine derivatives in inhibiting fungal growth.

Examination of four biological knowledge shortfalls in the poorly studied Laboulbeniomycetes

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The class Laboulbeniomycetes contains two orders of ectobionts of arthropods (Herpomycetales, Laboulbeniales) and one order of mycoparasitic fungi dispersed by arthropods (Pyxidiophorales). We examined four shortfalls: the Linnaean (knowledge gaps in species diversity), Wallacean (knowledge gaps in distributions), Latimerian (knowledge gaps in species persistence), and Scottian (knowledge gaps in species conservation assessments) shortfalls. The Linnaean shortfall in Laboulbeniomycetes is hard to predict due to inconsistent species description rates. Analysis of distribution patterns indicate Laboulbeniomycetes experience a high Wallacean shortfall, with many species having highly disjunctive known distributions. Latimerian shortfall analysis shows over half (50.1%) of Laboulbeniomycetes sampled have not been recorded in >50 years, while the group has a collective Scottian shortfall of 100%, with none of the 2,821 described species having received an IUCN threat assessment. We suggest continued study of natural history collections, expanded citizen science programs, and machine-learning identification approaches to reduce knowledge shortfalls in Laboulbeniomycetes.

Chemical compounds from a freshwater fungus Inhibit Bacterial Quorum Sensing

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is an antibiotic-resistant pathogen causing global health threat. Disrupting quorum sensing pathways, which are involved in fostering virulence, is an anti-infective tactic that is less likely to result in the emergence of resistance. In ongoing efforts to discover natural compounds from freshwater fungi to discover new treatment modalities for MRSA, we found an interesting freshwater ascomycete strain (G730) showing phylogenetic affiliations to the Leotiomyces, Ascomycota. Chemical analysis of the strain led to the isolation of three novel prenylated diresorcinols (1–3), which we ascribed trivial names leotiomyces A-C. Compounds 1-3 suppressed quorum sensing in a clinical isolate of MRSA with IC50 values ranging from 0.3 to 12.5 μ M. These compounds represent potential leads in the development of antivirulence therapeutics. Together, our results highlight the importance of interdisciplinary nature of this research on freshwater fungal secondary metabolites and its contribution to both basic and applied sciences.

Arctic driftwoodstock: new fungi and bioactive compounds

Rämä, Teppo*

UiT The Arctic University of Norway

Driftwood has been an important resource for humans in Arctic settlements and has also enabled colonization of the Arctic by wood-associated organisms, including marine fungi. The supply of driftwood and dispersal of species in the Arctic over several centuries has been enabled by long-distance transportation within sea-ice, whereas ongoing loss of sea-ice has caused a drastic decrease in this supply making arctic driftwood a threatened habitat for marine fungi. This talk presents ongoing efforts in improving our understanding of fungal communities in driftwood, marine fungi living associated with drifting and intertidal wood and recent bioactive compounds sourced from driftwood fungi, including species of Lulworthiales and the first ever compound reported from this strictly marine order of fungi.

Finding rust peptides encoded on short open reading frames

Christof Rampitsch*, Slavica Djuric-Ciganovic, Mei Huang, Zhen Yao, Mark Lubberts, Peter Verhaert

AAFC

Puccinia triticina (Pt) is an obligate fungal parasite that causes leaf rust on wheat. Host-pathogen communication at the protein level has been relatively well-studied, but the potential roles of peptides (smaller than 5 kDa) have not been examined at all. This research describes a new approach to finding peptides in this plant-pathogen interaction, using top-down LC-MS. Peptides were initially obtained from rusted wheat leaves by precipitation from acetone, followed by enrichment using RP- and SEC-HPLC. Peptides were left intact and then analyzed in a high-resolution Orbitrap mass spectrometer. For sequencing, we used a de novo sequencing approach which does not require any databases to identify peptides - as these are unlikely to be represented in published genomes. More recently we have used an N-terminal tryptic peptide enrichment strategy that improved our yield of endogenous peptides and we are currently devising strategies to determine where on the rust genome these peptides are encoded.

Terrestrial lichen caribou forage transplant success: year 5 and 6 results

Rapai, Sean*, McColl D, Collis, Brianna, Henry, Thomas, Coxson, Darwyn.

Chu Cho Environmental

The southernmountain caribou—a subpopulation of caribou found in British Columbia—is listed on Schedule 1 of the Federal Species at Risk Act as Threatened. Woodland caribou are diet specialists, relying on Cladonia subgenus Cladina lichen as a primary food source during winter months. Lichens are burned along with trees and other vegetation during stand-replacing wildfire events, a natural disturbance in caribou ranges. In an attempt to accelerate the return of post-fire forests to productive caribou winter terrestrial lichen habitat, this study examined the survival and cover of three species of transplanted lichens in a post-wildfire environment in north central British Columbia, Canada, both with and without forest litter amendments. Chlorophyll fluorescence was used to evaluate lichen survival by measuring potential photosynthetic activity. The results of this study demonstrate that transplanted fragments and mats of Cladonia subgenus Cladina had survived 5 and 6 years after being transplanted within a post-wildfire environment, and had significantly greater percent cover when compared to the controls. The Fv/Fm results indicated that transplanted lichens survived, regardless of species, propagule type, or whether amendments were applied.

What could possibly go wrong? The discovery, rediscovery, discovery again, misclassification, then 9/11 history of a human pathogen – *Coccidioides posadasii*
Redhead, Scott*

Ottawa Research & Development Centre, Agriculture & Agri-Food Canada

The genus *Coccidioides* was first described as a protozoan genus and redescribed again as another protozoan genus *Posadasia*, infecting humans. It is an example of the convoluted discovery process and naming history of fungal causal agents of human diseases. It is also an example of the complexity of nomenclatural and taxonomic Gordian knots that have festered for a century that can ultimately be resolved with resolve. Thinking outside of the box as encouraged by David Malloch, following rules as guided by Luella Weresub, and deep knowledge of fungal classification as instilled by Robert Bandoni, all Canadians, helped forge the way towards an international solution between medical and molecular mycologists.

Strain Improvement of Filamentous Fungi *Mortierella alpina* for Efficient Production of Arachidonic Acid

Zixuan (Rosa) Ren*, Roberto E. Armenta; Marianne Su-Ling Brooks
Dalhousie University

Arachidonic acid (ARA) is an omega-6 fatty acid that is important for improving infant memory and eyesight and used to supplement infant formula. Microorganisms that accumulate large amounts of ARA, such as *Mortierella alpina* MA2-2, are an attractive source of ARA as they are an alternative to meat-related sources. However, microbial production of ARA from such fungal strains has not been extensively studied. In this work, ultra-violet (UV) classic mutagenesis coupled with high-throughput screening, including fatty-acid synthase inhibitor combined with tetrazolium dyes, developed for obtaining mutants with beneficial phenotypes. Ultimately, a few mutants retained wild-type phenotypes, but a fast and effective screening was achieved. In addition, adaptive laboratory evolution (ALE), the first study of the fungal species that undergoes mutation and recombination under high temperature, followed by natural selection in which the most beneficial phenotypes adapted. The adapted strain exhibited higher thermotolerance compared to the parental strain.

Experimental analysis of the altitudinal distribution limit of the Ghost Antler Lichen at Parc national du Mont-Mégantic in Québec, Canada
Rinas, Christina* and Vellend, Mark
Dalhousie University and Université de Sherbrooke

Understanding the mechanism underlying a species' distribution limit is important for predicting whether environmental change will affect its future distribution. Here, we conducted a transplant experiment to examine the effect of niche versus dispersal limitation on the elevational distribution limit of the Ghost Antler Lichen (*Pseudevernia cladonia*) in Southeastern Québec. We transplanted Ghost Antler Lichen individuals along an elevation gradient in Parc National du Mont-Mégantic, Québec: within the species' range, at the edge, and beyond its range. We observed that transplant survival and performance was the greatest within its distribution and decreased towards the edge and beyond its distribution. We suggest that the cooler and more humid conditions at the summit are important environmental factors that determine this lichen's elevational range limit. Our findings suggest that future climatic changes in these montane habitats may result in less suitable habitat for this species.

Fungal Symbionts: Canada's National Mycological Collections
Rintoul, Tara* and Asencio, Shannon
Agriculture and Agri-Food Canada

Agriculture and Agri-Food Canada's Canadian Collection of Fungal Cultures (DAOMC) and the Canadian National Mycological Herbarium (DAOM) represent the largest collections of their kind in Canada. A particular strength of these two collections is that some of their specimens are paired, maintaining living and preserved copies of the same material. This presents an opportunity to answer a broad range of research questions. These critical resources support: assessing pathogenicity, metabolomics studies, taxonomic studies, host-pathogen relationships, fungal diversity, and genetics across geographical ranges and time. Although global in scope, the collections have strong Canadian representation, with ca. 60% of specimens collected in Canada. An overview of the holdings of each collection will be presented alongside examples of current research projects utilizing these resources.

Exploring the effect of yeast species interactions and diversity on plant disease severity
Romero-Jiménez, Maria-José* ; Leopold, Devin ; Busby, Posy E.
Oregon State University

Understanding how host diversity relates to disease severity has been a longstanding question in ecology. However, the relationship between host-associated microbial diversity and host disease severity is poorly understood. Our aims in this study were to describe how the diversity of foliar yeasts and yeast interactions influence leaf rust disease severity in *Populus trichocarpa*. We created synthetic communities (SynComms) with varying levels of yeast richness and diversity. In a greenhouse experiment, we applied one of 20 yeast SynComms to leaves, followed by rust inoculation and disease measurements. While we did not find support for clear and robust relationships between community richness and disease protection, communities that included particular yeast species conferred greater protection than communities without them. In a second experiment, we inoculated poplar cuttings with one of 45 unique pairwise combinations of 10 yeasts to determine how species interactions impact disease severity. Data analysis is currently ongoing.

Fungal Endophytes as Biocontrol Agents for Apple Replant Disease
Roy, Maria*; Ali, Shawkat; Walker, Allison; Wright, Harrison; Fuller, Keith; Sumarah, Mark
Agriculture and Agri-food Canada, Acadia University

Apple Replant Disease (ARD) affects young apple trees, planted in soil that was previously used to cultivate apple or related plants. ARD results in root necrosis, reduction in plant growth, vigour and fruit yield. ARD is currently treated by chemical fumigation of orchard soil between plantings, but have harmful environmental impacts, creating a demand for alternative treatments for ARD. We are exploring fungal endophytes from healthy, mature apple roots as potential biocontrol agents to treat ARD. We tested five endophyte isolates of interest in vitro for antagonistic activity against four ARD-associated pathogens. In dual culture, we observed different types of interactions between endophytes and pathogens. The cell-free filtrate from endophyte liquid cultures demonstrated a range of antagonistic activity, with an endophyte identified as *Mortierella* sp. inhibiting all four pathogens to the greatest extent. The five biocontrol candidates were also tested in an initial anti-ARD greenhouse trial with micropropagated apple rootstocks.

Processivity factor PCNA has a distinct role in maintaining sub-telomeric silencing in *Saccharomyces cerevisiae*.

Sauty, Safia Mahabub*; Yankulov, Krassimir
University of Guelph

The sub-telomeres of *Saccharomyces cerevisiae* are transcriptionally silent due to heterochromatinization. Successful transmission of this chromatin structure is mediated by replication-coupled chromatin assembly, but the mechanism is not clearly understood.

The replication processivity factor PCNA provides a docking site for chromatin-associated factors at the advancing replication fork. Previous studies showed that mutations in PCNA lead to transient loss of silencing. I introduced a dual fluorescent reporter at the VIII sub-telomere of pcna mutants to capture their effect on silencing. The reporter was inserted in two orientations: one transcribing towards the telomere and one transcribing away. I conducted highly sensitive silencing assays and recaptured the established effect of pcna mutations with both fragments. However, the forward transcribing fragment failed to detect gene expression by low-sensitive techniques while the reverse fragment produced a bi-fold active/silent state. These findings indicate that faulty pcna exacerbates replication pausing at the telomere.

UAMH Centre for Global Microfungal Biodiversity
Scott, James*, Guardiola, Yordanka
University of Toronto

Biological collections are often thought of as lifeless cabinets filled with stuffed birds and pressed plants, but modern collections are much more than this. Cryogenic preservation techniques have been used for almost a century to preserve delicate living cells of microbes and animals, becoming an essential tool in biomedical and biological research. These collections allow researchers to manipulate organisms in a repeatable and traceable manner, supporting research in various fields such as biotechnology, drug discovery, evolutionary biology, metabolomics, pathobiology, and ecology. The presentation will focus on living cellular collections, with an emphasis on the biomedically important fungi collection at the UAMH Centre for Global Microfungal Biodiversity in the University of Toronto. UAMH contains over 12,500 living biospecimens, associated archival materials, and provenance, representing over 3,200 species, making it the largest and most significant repository of biomedically important fungi in the Western Hemisphere and one of only two top-level collections worldwide.

The Secret House: Fungal Biology and Diversity in the Built Environment
Seifert, Keith*
Carleton University

The built environment is often over-looked, but can be useful for modeling natural microbial ecology and proof-testing metagenomic methods. Buildings yield around 50–100 culturable species or 2000 OTUs in DNA-based surveys, without distinguishing tourists from residents. Air and dust samples pool spores and hyphae from multiple sources, including the outdoors. Buildings have several sub-environments and culturing or DNA sampling must consider this diversity. Most rooms are like deserts and host xerophilic fungi requiring little moisture. Kitchens, bathrooms and laundry rooms are more like tropical rain forests. Building materials, textiles, food, compost, houseplants, and animals each carry distinct fungi that may become residents. Many species are banal but understanding their biology is critical. Occupants may react to fungal spores, β -glucan, or VOCs. Indoor microbiomes are relevant to larger topics of island biogeography, urban evolution and invasive species. The direct impacts on human health emphasize that building ecology warrants more study.

Improvement of FHB resistance in wheat, a work in progress
Serajazari, Mitra
University of Guelph

Fusarium head blight (FHB) caused by *Fusarium* spp. is a fungal cereal crop disease that has a global impact on cereal production. In Canada, the primary causal agents of FHB are *F. graminearum* and *F. poae*. Notably, the *F. graminearum* mycotoxin deoxynivalenol (DON) and its derivatives suppress protein synthesis in plant cells leading to cell death in the infected host tissues. Fusarium-damaged kernels containing DON pose a threat to the food and feed industry worldwide. To combat FHB in cereals, developing genetic resistance is a highly effective strategy. However, the disease's quantitative nature poses a challenge when breeding for resistant varieties. The University of Guelph's wheat breeding program evaluates FHB resistance in wheat at an inoculated Fusarium nursery at Elora, Ontario, and studies the interaction between *F. graminearum* chemotypes and wheat genotypes under controlled environment conditions to identify the best approach to develop wheat varieties resistant to FHB.

Identifying clinically important *Candida* species using machine learning
Shankarnarayan, Shamanth* and Charlebois, Daniel
University of Alberta

Infections due to antifungal-resistant *Candida* species are rising. Identifying fungal infections quickly and accurately allows for the prompt initiation of antifungal treatment and outbreak control. We employed a machine learning approach to identify four major *Candida* species known to cause infection among patients: *C. albicans*, *C. auris*, *C. glabrata* and *C. haemulonii*. High-resolution bright field images (4000 images/species) were captured using an EVOS M7000 fluorescent microscopy imaging system. We trained a convolutional neural network (CNN) with these images. An unseen dataset of 200 images of each species were given to the trained CNN model to predict the correct label. The CNN model reached a training accuracy of 81.05% and a validation accuracy of 72.8%. The CNN model was able to predict *C. albicans* and *C. auris* in 94% and 100% of cases on unseen images, respectively, with corresponding percentage confidence averages of 74.83% and 72.72%. *C. haemulonii* and *C. glabrata* were accurately predicted in 54.3% of the cases.

Exploring the metagenome of *Geosiphon pyriformis* - the only known fungus with a photosynthetic endosymbiont
Essam Sorwar*, Mathu Malar C, Nicolas Corradi
University of Ottawa

Geosiphon pyriformis is an arbuscular mycorrhiza fungus (AMF; subphylum Glomeromycotina) that can form endosymbiosis with the cyanobacteria *Nostoc punctiforme*. The endosymbiont survives within a “bladder-like” structure that protrudes from the mycelium, where it can divide and undergo photosynthesis. To improve our understanding of the *G. pyriformis* metagenome, we extracted sequence information on its endosymbionts using available Illumina sequence data from this species and utilized a metagenomic approach that bins sequence reads based on their k-mer frequency. This approach produced genome assemblies for the expected *Nostoc* endosymbiont and Mollicutes/Mycoplasma-related endobacteria present in its bladder. Significant differences and similarities between these endobacteria and their close prokaryotic relatives are described.

Comprehensive assessment of the contribution of the Unfolded Protein Response to *Candida albicans* antifungal resistance and pathogenicity
Stack-Couture, Samuel*, Dumeaux, Vanessa, Shapiro, Rebecca, and Lajoie, Patrick
Western University

Candida albicans is the leading cause of yeast infections in humans. Antifungal resistance and pathogenicity in *C. albicans* depend on various cellular stress responses, including the Unfolded Protein Response (UPR). The UPR activates a transcriptional program that alleviates the toxic accumulation of misfolded proteins in the endoplasmic reticulum (ER), and it's activated by the ER sensor Ire1 which detects misfolded protein through its luminal domain. Critically, the specific UPR target genes that underlie *C. albicans* resistance and pathogenicity are unknown. Using RNA-Seq, we compared the transcriptional profiles of wild-type and UPR-deficient cells under ER stress- and filamentation-inducing conditions. We identified a unique set of genes that are common to both the ER stress- and filamentation-activated UPR. Additionally, we found that antifungal drugs differ in their requirement for a functional Ire1 luminal domain. These findings further our understanding of the role of the UPR in *C. albicans* antifungal resistance and pathogenicity.

Evolutionary origin and phenotypic impact of hybridization in a cryptic fungal pathogen
Steenwyk, Jacob*; Knowles, Sonja; Bastos, Rafael; Balamurugan, Charu; Gonçalves, Carla; Rinker, David; Mead, Matthew; Raja, Huzefa, Li, Yuanning; Lagrou, Katrien; Oberlies, Nicholas; Zhou, Xiaofan; Goldman, Gustavo; and Rokas, Antonis
University of California, Berkeley

The origin, genetic diversity, and variation in infection-relevant traits of the cryptic fungal pathogen *Aspergillus latus*—an allodiploid hybrid of two other known fungal species in section Nidulantes, *Aspergillus spinulosporus* and an unknown close relative of *Aspergillus quadrilineatus*—remains poorly understood. We studied 44 globally distributed isolates (41 clinical isolates; three type strains) from *Aspergillus* section Nidulantes; we found that 21 clinical isolates were *A. latus*, whereas the others were *A. spinulosporus* (8), *A. quadrilineatus* (1), or *A. nidulans* (11). Phylogenomic analyses showed that *A. latus* arose from either one or two hybridization events during the Miocene, approximately 15.4 to 8.8 million years ago. The 21 clinical isolates are sufficient to capture the *A. latus* pangenome, which contains substantial genetic diversity among gene families and biosynthetic gene clusters. Transcriptomics revealed that both parental genomes are actively expressed in nearly equal proportions and respond to environmental stimuli. Examination of infection-relevant traits—such as drug resistance profiles, growth in oxidative stressors, and secondary metabolite biosynthesis—suggests that the phenotypic profile of the hybrid *A. latus* is distinct from that of its parental and closely related species. These analyses elucidate the evolutionary origin, genomic outcome, and phenotypic impact of hybridization in a cryptic fungal pathogen, enriching our understanding of the processes that give rise to opportunistic human fungal pathogens.

Evaluating the efficacy of supramolecular self-associating amphiphiles as novel antifungal substances against *Candida albicans* biofilms

Steyn, Hendrik*, Hilton, Kira, Hiscock, Jennifer, Pohl, Carolina
University of the Free State

In 2022 the World Health Organisation identified *Candida albicans* as a critical-priority fungal pathogen. The development of novel antifungal compounds is critical to combat emerging drug resistance in pathogenic fungi. Novel supramolecular self-associating amphiphiles (SSAs) have antimicrobial effects against clinically relevant bacteria, providing a possible source of novel antimicrobial drugs. Our study evaluated the efficacy of SSAs against the *C. albicans* biofilm formation and eradication of mature biofilms and identified SSAs with the ability to inhibit biofilm formation and effect hyphal formation of *C. albicans*. The possible mechanism of action is via binding to fungal phospholipids and resultant membrane disruption. Although antifungal concentrations were also toxic in a *Caenorhabditis elegans* infection model, this paves the way for the synthesis of improved SSAs with greater antifungal selectivity.

Harnessing the Basidiomycete *Moesziomyces antarctica* as a sustainable biosurfactant factory

Stuart, D.T.*, Xu, Yuze.
University of Alberta

Moesziomyces antarctica is a halotolerant anamorphic yeast isolated from lake Vanda in Antarctica. The yeast can synthesize and secrete a glycolipid biosurfactant, MannosylErythritol Lipid (MEL), with abundant potential for human and industrial applications. We unambiguously demonstrate that a multi-pass transmembrane protein encoded by the MMF1 gene is the transporter required for secretion of MEL. We have further taken advantage of the halotolerance of *M. antarctica* (grows in up to 1.5M NaCl) to demonstrate that MEL can be produced in brackish and seawater. The salinity inhibits the growth of contaminating microbes allowing unsterilized fermentation and the water is rich in micronutrients reducing the need for added supplements. We further demonstrate the use of waste cooking oil as a carbon source for MEL production. This process spares the use of potable water, human food and energy required for sterilization, while significantly reducing the cost of MEL production.

The Deoxynivalenol Challenge
Sumarah, Mark
AAFC

The mycotoxin deoxynivalenol (DON) presents a number of challenges to farmers, producers, and consumers. In many countries, such as Canada, DON is the mycotoxin of principal concern because it can lead to major economic losses and stresses on food and feed security. The challenges discussed here include (1) understanding the different toxin profiles of *Fusarium graminearum* chemotypes/genotypes and the fate of these toxins upon interaction with the host crop, (2) the need for rapid analytical tests to measure DON and any masked or modified toxins in food and feed products, (3) DON exposure assessments in human populations to ensure health and safety, and (4) how contaminated food and feed products can be managed throughout the supply chain system. DON poses a very complex challenge that is being further exacerbated by climate change, evolving fungal populations, and the increased need for global food security.

Always something new in Onygenales - *Trichophyton indotineae* comes to Canada
Summerbell, Richard*, Scott, James.
University of Toronto Dalla Lana School of Public Health

Dave Malloch made a name for himself early on as a biosystematist of cleistothecial ascomycetes, though he was wary of incubating fox dung because the hair-rich substrate might yield skin-infecting dermatophytes. We had the consolation then that if anyone acquired a dermatophyte, it would be treatable. In Canada, we now have an outbreak of an imported species that is highly resistant to therapy and prefers to infect the buttocks, *Trichophyton indotineae*. Luckily, though it grows on humans, it doesn't grow on incubated fox dung.

The drought knockout: emergence of sooty bark disease (*Cryptostroma corticale*) in B.C.

Tanney, Joey*; Feau, Nico; Shamoun, Simon; Kope, Harry

Pacific Forestry Centre, Canadian Forest Service, Natural Resources Canada

Cryptostroma corticale (Graphostromataceae, Xylariales) is endemic to Eastern North America, found on stems and branches of dead sugar maple (*Acer saccharum*) and apparently not causing disease. Since *C. corticale* was first detection in the UK (1945), its spread in Europe is marked by the lethal sooty bark disease (SBD) of sycamore maple (*A. pseudoplatanus*), triggered by extreme heat waves and drought. Our discovery of symptomatic sycamore and Norway maple (*A. platanoides*) trees in summer 2022 is the first record of *C. corticale* in BC and likely a result of disease precipitated by the 2021 heat dome event. Current research efforts involve investigating the pathogenicity *C. corticale* on endemic *Acer* spp., and determining the origin of *C. corticale* in BC, WA, and Europe. Increasingly severe and frequent weather events under a changing climate may result in the emergence of both endemic and cryptic invasive forest pathogens.

Identification of a peroxidase-derived chemoattractant: a contributor to *Fusarium graminearum* pathogenicity through Ste2/3 activation

Luana L. T. N. Porto* , Pooja S. Sridhar, John S. Allingham, Janelle Sauvageau and Michele Loewen.

University of Ottawa

Fusarium graminearum (Fg) is responsible for a widespread and destructive disease in wheat known as Fusarium Head Blight (FHB). FHB has a devastating impact on worldwide wheat yields and grain quality. In Canada, wheat production contributed to Canada's economic growth, and its export market in 2017 was approximately \$21 billion.⁴ Although molecular mechanisms underlying host infection are yet to be fully characterized, previous work in our group has shown fungal hyphal chemotropism to be a contributor. In particular this chemotropic response was found to be induced by catalytically active host-secreted peroxidases. Interestingly, Fg strains in which FgSte2 and FgSte3 G-protein coupled receptors (GPCRs) were deleted, were no longer able to induce chemotropic responses toward peroxidase. These observations inspired the current study to identify and elucidate the identity of the peroxidase-derived ligand that binds to and activates the GPCRs in this system. Recently, through extensive fractionation, we isolated a metabolite derived from the treatment of *F. graminearum* conidia with peroxidase that stimulates chemotropism, with high-performance mass spectrometry suggesting a 400 Da putative carbohydrate moiety. Further analyses, using high-performance anion-exchange chromatography (HPAEC-pad) suggested the presence of glucosamine and an amino acid. Preliminary ¹H-NMR analysis indicated the presence of a cyclic ring in resonance that matches a tyrosine ring with -meta and -para positions shifted to 7.1 and 6.8 ppm. It also provides two doublet peaks at 7.5 and 5.7 ppm, where a 2D COSY spectra exhibited a correlation between these peaks. Scale up of the production and purification of the metabolite is underway to provide improved 1D and 2D NMR spectra. The elucidation of the peroxidase-derived ligand structure will provide a better understanding of the mechanism of *F. graminearum* chemotropism and pathogenesis enabling development of new ways to prevent FHB.

Diversity and ecology of fungi and prokaryotes in the sediments and water column of brackish and salt marshes

Thompson, Madeleine* and Peng, Xuefeng
University of South Carolina

Fungi and prokaryotes are key drivers of biogeochemical processes in marshes. Few studies have examined fungi and prokaryotes and their potential interactions in marsh ecosystems. We performed a metabarcoding survey, targeting the small and large rRNA genes and the internal transcribed spacer region of prokaryotes and microbial eukaryotes in the sediment and water column of a salt marsh and brackish marsh in South Carolina, USA. Early diverging fungi dominated brackish marsh communities. In contrast, salt marsh communities were dominated by Dikarya fungi. Network analyses revealed nearly exclusively negative interactions between fungi and prokaryotes in the sediment, suggesting competition. Interactions among early diverging fungi were primarily positive, suggesting a shared niche. Our work reveals novel fungal diversity in estuarine sediments and water column. The identification of potential interactions enables the design of targeted experiments to elucidate the mechanism of such interactions and their impact on biogeochemical cycles.

Prevalence of mycotoxins in Canadian grain

Tittlemier, Sheryl*
Canadian Grain Commission

Grains are an important food source, as well as agricultural commodity, for Canadians. Many mycotoxins occur in Canadian cereal and pulse grains. The most relevant mycotoxins are deoxynivalenol, ochratoxin A, *zearalenone*, and ergot alkaloids, but other *Fusarium*- and *Alternaria*-related mycotoxins have also been observed in Canadian grain. Mycotoxin occurrence in grain is influenced by a number of factors, including temperature and precipitation during the growing season, storage conditions, cultivar disease resistance, and the microbiome of the growing location. Proper sampling plans, procedures, and equipment must be used to accurately analyze grain for mycotoxins since there are a number of factors that introduce variance into the overall analytical process. Temporal and geographical trends in mycotoxin occurrence can affect monitoring and surveillance, while localized fungal infection and subsequent mycotoxin production leads to a highly heterogeneous grain matrix that requires particular handling in the laboratory to minimize variance in analytical results.

Diversity of crop-associated oomycetes using metabarcoding data from aerial spore and suction traps

Tremblay, Émilie D.*; Goulet, Benoit B.; Brunet, Bryan M. T.; Lord, Étienne; Parent, Jean-Philippe

Agriculture and Agri-Food Canada

Phytopathogens are a major threat to food security impacting crops, seeds, and animal feed. Threats to plant health caused by phytopathogens, such as oomycetes, are becoming increasingly prevalent in new regions with more permissive conditions resulting from climate change. For example, the introduction and spread of phytopathogenic adventive species can lead to increasingly strict international trade regulations such as the inclusion of new pests to a regulated pest list, impacting imports and exports. In this project, we use High-Throughput Sequencing—specifically metabarcoding—to assess the biodiversity of oomycete phytopathogens and characterize their incidence from aerial spore and suction traps in agricultural fields located in Ontario and Quebec. Preliminary results from our workflow will be presented. This study will provide baseline information on crop health in relation to phytopathogenic oomycete incidence. It will also improve risk readiness and response measures through the future development of predictive models to forecast oomycete distribution.

Fungal endophytes of white spruce modulate tree defenses

Aziz Ullah, Ateeq Shah, Federico Antonioli, Shih-hsuan (Ethan) Chen, Rashaduz Zaman, Nadir Erbilgin

University of Alberta

Plant endophytic fungal communities have drawn increasing attention due to their potential roles in plant herbivory resistance. However, experimental demonstration of whether fungal endophytes can also alter plant secondary metabolites is unknown. We grow 30 different white spruce families (20 trees/family) from seeds in a growth chamber. After ten months of vegetative growth, we inoculated five fungal endophytes into the foliage's of half of the seedlings., *Cladosporium halotolerans*, *Cladosporium cladosporioides*, *Chalara* sp., *Geopyxis* sp., and *Didymella* sp.; the remaining half of the seedlings were not inoculated and set as control treatment. After two months of inoculation, we collected the foliage and weighed above ground fresh biomass from both inoculated and control seedlings. The spruce families with higher endophytic fungal abundance also had higher monoterpene and sesquiterpene concentrations and foliage biomass. All together, these results demonstrate that fungal endophytes can enrich the defense metabolites of spruce trees along with improving growth.

Characterization of wild yeasts as potential biocontrol agents for brewing applications
Unterberg-Piché, Édouard*. Filteau, Marie.
Université Laval, INAF

The ever-increasing demand for new and innovative beers has driven brewers around the world to provide products with distinct flavors and properties. However, artisanal productions and especially some beer types such as non-alcoholic beers and spontaneously fermented beers are prone to contamination. Since the addition of chemical agents to improve the preservation of beer is a very unpopular solution, a more acceptable strategy would be the use of bioprotective cultures. To this end, we sought to characterize a collection of 577 wild yeast strains. Using an automated high-throughput approach, we measured antimicrobial activity against seven fungal and four bacterial spoilage agents on universal beer agar (UBA). We found that over 15% exhibited activity against at least one target. Our next goal will be to evaluate the compatibility of the selected strains with brewing applications and to measure their bioprotective potential in model fermentations.

“Do you want to see something neat?” - A tribute to Dave Malloch as an inspiring teacher and mycological mentor.
Untereiner, Wendy.
Brandon University

Dave Malloch was a motivating instructor who trained numerous undergraduate and graduate students during his career at the University of Toronto. His success as an instructor and supervisor reflected his expertise in the taxonomy of many groups of Fungi, his boundless (and highly contagious) enthusiasm for these organisms, and the delight he took in sharing his mycological discoveries. His oft-repeated question, “Do you want to see something neat?”, was an invitation to anyone within earshot to drop whatever they were doing and look at the Fungi that had caught his attention. Dave’s approach to teaching mycology required a high level of student involvement, but it fostered his students’ curiosity, encouraged them to ask questions, and strengthened their problem-solving skills. This presentation will focus on how my experiences as one of Dave’s graduate students informed my teaching style and the ways I engage students in mycology.

Evolution of secondary metabolite gene clusters: what is the role of fungal interactions in driving metabolic diversification?

U'Ren, Jana

The University of Arizona

Species of *Xylariaceae* (Sordariomycetes) are common wood- or litter-degrading saprotrophs or woody pathogens in temperate or tropical ecosystems, as well as endophytes of phylogenetically diverse plants and lichens. Xylarialean endophytes are well-known for the production of diverse bioactive compounds and recent genomic analyses suggest that the diversification of secondary metabolite gene clusters (SMGCs) is driven by horizontal gene transfer, yet the ecological roles of these metabolites is largely unknown. We used untargeted metabolomics to assess the metabolic activity of seven xylarialean fungi when grown alone or in co-culture. Overall, we observed that most co-cultures resulted in a deadlock between isolates, indicative of the production of inhibitory secondary metabolites. Statistical analyses revealed that a total of 1,370 features were over-produced in co-culture, yet there was little metabolite overlap among pairs of isolates. Our results are consistent with fungal interactions to potentially drive the diversification of SMGCs in xylarialean fungi.

Butternut canker phenotype binning to project diversity decline in *Juglans cinerea* L. van der Meer, Berni M.*; Solomon, Jack P.; Schumacher, Emily; Hoban, Sean; Romero-Severson, Jeanne; Williams, Martin.

Natural Resources Canada

Butternut (*J. cinerea* L.) populations are annually declining under the invasive fungal pathogen *Ophiognomonia clavignenti-juglandacearum*. Individuals exhibit rapid spread of large cankers, crown dieback, and reduced seed production. Previously, 464 non-related individuals representing 6 New Brunswick populations were assessed for tree vigour on a scale of one (low vigour) to four (high vigour). Using 11 microsatellite markers we examined diversity indices for phenotype-predicted future subsets of each population (vigour 1-4, 2-4, 3-4 and 4). Average population size decreased 49% from initial (1-4) to only high vigour (4) individuals. Allelic richness declined across all populations; heterozygosity remained constant, indicating the genetic diversity of butternut populations is declining. Ongoing research re-assesses the current phenotypes, 9 years later, to approximate real-time diversity decline, while collecting isolates to examine the functional diversity of the pathogen. The extirpation of New Brunswick's disjunct butternut populations represents the loss of vital genetic resource.

Coprinopsis laanii fruiting on mammal carcasses in an underground mine
Vanderwolf, Karen, McAlpine, Donald, Justo, Alfredo
University of Waterloo

Fungi are important decomposers of organic material, including animal waste. Ammonia and postputrefaction fungi grow in soil enriched in ammonium and nitrogen from carcasses. In 2014 we observed mushrooms fruiting on the flesh of a dead muskrat (*Ondatra zibethicus*) in an abandoned underground copper mine in southeastern New Brunswick. We placed an adult beaver (*Castor canadensis*) carcass near the muskrat to facilitate fungal colonization and fruiting. The beaver carcass was colonized by a variety of molds, especially *Acaulium caviariforme*. We observed mushrooms of an unidentified copriniid on the flesh 6 years and 9 months after carcass placement. Using morphological and molecular (nrITS) data, we identified the mushrooms as *Coprinopsis laanii*, a rarely encountered species generally considered lignicolous. We discuss the role of *C. laanii*, and other post-putrefaction fungi, in cave environments.

Deep-sea fungal diversity in Mexico: diversity and potential utilization
Velez Patricia*
Instituto de Biología, UNAM

Since the first fungus documented from an oceanic sample in Mexico in 1984, the formal exploration of deep-sea biomes developed until the early XXI. These exploration efforts have reached deep-sea plains, hydrothermal vents, and oxygen minimum zones, revealing an extraordinary taxonomic and functional diversity characterized by the occurrence of abundant, widely distributed, uncultured phylotypes that remain to be described. In addition, fungal isolates obtained from deep-sea samples across the Gulf of Mexico have been proposed as valuable elements for the bioremediation of marine oil spills, as they have demonstrated the ability to metabolize aliphatic hydrocarbons and extra-heavy crude oil. In this sense, metabolomic data has revealed the chemical and antimicrobial potential of deep-sea derived isolates, highlighting that culture temperature is the primary factor modeling metabolite features. Despite incipient advances, a lot of work remains to be done to conclude on fungal diversity figures and ecological roles in deep-sea.

Macrofungal conservation in Canada and target species for assessment: a starting point
Bazzicalupo, Anna; Gonçalves, Susana C.; Hébert, Rémi; Jakob, Sigrid; Justo, Alfredo;
Kernaghan, Gavin; Lebeuf, Renée; Malloch, Bruce; Thorn, R. Greg; Walker, Allison K.*
Acadia University

Despite the ecological importance of fungi, we still know little about their diversity in Canada. A barrier to implementing fungal conservation initiatives is the lack of fungal distribution data. As anthropogenic impacts accelerate environmental change, this information gap must be filled, to protect fungi. To gain insight into the conservation status of Canadian macrofungi, we explored the growing body of fungal biodiversity data from government, citizen science, trained independent mycologist, university, and museum biodiversity research. Most macrofungi are data deficient; their geographic distribution, habitat requirements, and abundance in Canada are unknown. For mushrooms that rarely fruit and are difficult to identify, work is needed to distinguish under-sampling from rarity. We are building a strong network of professional and amateur mycologists to develop resources and disseminate information to make educated decisions and advance conservation actions. Several fungi can be prioritized; a short list is presented for consideration for formal conservation assessment.

Root-Inhabiting and Rhizosphere Mycobiomes and Crop Yield of Corn and Wheat
Wallace, Marianna*. Kandasamy, Saveetha. Saldias, Soledad. Lazarovits, George.
Thorn, R. Greg.
The University of Western Ontario

The root mycobiome plays a direct role in plant productivity, and the study of its community composition allows for identification of organisms that influence plant health. To better understand the role of fungal community composition in crop productivity, the root-associated mycobiomes of historically high and low yield sites of corn and wheat planted in rotation were characterized and analyzed along with soil physicochemical variables and yield at harvest. In each field studied, root and rhizosphere mycobiomes reflected significant differences in fungal species composition. Several soil variables were found to be predictors of differences in composition of sample types including soil texture and pH. The genera *Fusicolla*, *Epicoccum*, and *Tetracladium* were positively correlated with yield, and *Neonectria*, *Pythium*, *Corynespora*, and *Mrakia* were negatively correlated. Understanding how root-associated fungal communities may be linked to crop health could aid in the development of community management tools that maximize crop productivity.

Genomic and Metabolomic Analysis of Actinomycetes for Agricultural Coculturing Against Fungal Diseases

Walsh, Jacob*. Medina, Ricardo. Surette, Matthew. Wright, Gerard
McMaster University

As global populations continue to increase, so too does the demand for food security from which fungal borne agricultural diseases threaten. Although fungicides have traditionally been used to treat against fungal diseases, some agricultural fungicides have long environmental persistence and deleterious health effects. Coculturing, or bio-fungicides, is a growing industry in which bacteria are cocultured with agricultural products. Using a Hidden Markov Model (HMM) dataset, an in-house collection of 600 actinomycece genomes were screened for attributes which maybe beneficial for plant coculturing, such as oxidative, heat and cold stress resistance, hydrolytic enzymes, and mineral solubilization. This screen was followed by phenotypic assays to further validate the genomic screening. A mandatory criterion was to display antifungal activity, using various phytopathogenic fungi as antifungal models. The strains which passed the antifungal activity assays are screened though metabolomic analysis using a LC-MS, GNPS, and anti-smash workflow to determine a chemical profile.

Lichen biodiversity research across scales: how looking at the small can help us to think big

Wiersma, Yolanda
Memorial University of Newfoundland

As a landscape ecologist, I am interested in how spatial patterns of habitat patches influence ecological processes and in turn how ecological processes influence spatial landscape patterns. The challenge of doing landscape ecology is that most of the time, we work at large landscape extents; thus, it is difficult to do rigorous experiments, and replication is quite impossible. By scaling down my perspective to “lichen landscapes”, we have been able to do research in my group that addresses landscape ecology questions in a different way. In this talk, I will show how we can adopt “trees as landscapes” as a model system for landscape ecology. I will highlight several research projects from my lab group that link lichen ecology and landscape ecology across scales, with a focus on research in Atlantic Canada. In addition, I will show how lichen research can help inform management and conservation issues.

Overcoming fluconazole resistance in *C. neoformans* by ClpX inhibition and inhibitor characterization using Proteome Integral Solubility Alteration.

Woods, M.* Bermas, A. Ball, B. Muselius, B. Chan, N. McAlister, J. Geddes-McAlister, J. University of Guelph

Of the known invasive fungal species, *Cryptococcus neoformans*, an opportunistic mammalian fungal pathogen found ubiquitously in the environment, is the major causative agent of cryptococcosis in immunocompromised individuals (e.g., HIV/AIDS). The recent emergence of fluconazole resistant strains is a consequence of fluconazole monotherapy as the primary prescribed treatment and environmental exposure to azole fungicides used in agriculture leading to the development of the cross-resistance observed in the clinic. Recent proteomic findings in the Geddes-McAlister lab have led to the discovery of ClpX, an ATP-dependent unfoldase involved in protein homeostasis, to be essential in maintaining fluconazole resistance in *C. neoformans* in vitro and in vivo during host infection. Investigations of the global inventory of proteins influenced by ClpX disruption give insight into mechanisms driving resistance. Together, our approach proposes an innovative method to overcome fluconazole resistance in cryptococcal infections on- and off-target interactions of an effective inhibitor with putative clinical applications.

Pararesistance: a mutation-independent mechanism of antifungal drug resistance

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Drug resistance is a major cause of treatment failure. Here, we describe a mutation-independent mechanism of stress adaptation that accelerates the acquisition of drug resistance in the human fungal pathogen, *Candida albicans*. We discovered that transiently exposing a clonal population to the antifungal fluconazole elicits a sustained protective response in a subpopulation of cells. It confers cross-protection against multiple drugs, and facilitates the rapid emergence of resistance to high doses of fluconazole. We coined the term 'pararesistance' to describe a high-frequency adaptive state that is heritable and reversible. Pararesistance can manifest as multiple transcriptionally distinct states. In one such state, many pararesistance-specific genes are regulated by Sko1, an intrinsically disordered transcription factor that forms puncta in pararesistant isolates. Further, molecules that perturb protein condensation and prion-like assembly block the acquisition of pararesistance. Thus, our work presents a protein-based mechanism of stress adaptation that drives the rapid evolution of drug resistance.

Global population structure and triazole resistance in *Aspergillus fumigatus*

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Aspergillus fumigatus is a common environmental mold and an opportunistic human fungal pathogen. Each year, millions of people are infected by this fungus, causing a diversity of disease symptoms ranging from allergies to invasive aspergillosis, resulting in hundreds of thousands of deaths. Over the last three decades, antifungal resistance has been increasingly reported in both natural and clinical populations of this species. In this talk, I will describe our efforts on understanding the spatial genetic structures of *A. fumigatus*, including identifying potential hotspots for the origins of drug resistance and the patterns of spread of triazole-resistance genes and strains. The relevance of our results to One Health will be briefly discussed.

Resolving the haplotypes of arbuscular mycorrhizal fungi highlights the role of two nuclear populations in host interactions

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Arbuscular mycorrhizal fungi (AMF) are prominent root symbionts with a multinucleate cytoplasm that can carry thousands of nuclei deriving from two parental strains and varying in relative abundance in a large syncytium. Here, we set out to improve our understanding of such remarkable genetics by resolving the nuclear genomes of all publicly available AMF heterokaryons using PacBio HiFi and Hi-C sequencing. We find that all AMF heterokaryons carry two sets of homologous chromosomes, where genes associated with plant colonization reside in gene-sparse, repeat-rich compartments. The co-existing nuclear genomes are phylogenetically related but differ significantly in content and epigenetics, resulting in nucleus-specific regulatory programs during mycorrhizal interactions. AMF heterokaryons carry signatures of past genetic exchange indicative of sexual reproduction, followed by clonal haplotype evolution. This work uncovers the contribution and origin of nuclear genomes present in AMF heterokaryons and opens avenues for improvement and environmental application of these strains.

Mycotoxins in South Africa: old enemies new faces

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Experts predict that the global population will reach 10 billion by 2050, and approximately 1 in 4 people being Sub-Saharan African. Despite this population growth, hunger remains a significant problem. One major food safety concern is mycotoxins, which are common contaminants of food.

Maize is a crucial crop and a staple food in South Africa. However, fungal communities that infest maize can have a severe impact on its production. Unfortunately, in South Africa, there is insufficient information on the mycotoxin-producing species present in stored maize.

In this talk I will share the results from our survey where we tested 350 pre-stored maize seed samples for the presence of 12 mycotoxins using LC-MS/MS. Based on these results, 54 samples were selected for fungal community profiling using a culture-dependent approach. This research sheds light on the diverse fungal communities and mycotoxins presents in stored maize in South Africa.

Going Against the Grain: Investigating the Mechanisms of *Fusarium graminearum* Pathogenesis of Wheat Using Proximal Biotinylation

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The phytopathogenic fungus *Fusarium graminearum* is the causal agent of fusarium head blight in wheat . Pathogenicity stems, in part, from secreted proteins called effectors that suppress host immunity and promote disease . Understanding the mechanisms of *Fusarium* effectors that lead to infection is crucial for developing strategies to improve host resistance . This research focuses on characterizing the molecular interaction between effectors and the host using genetic (CRISPR-Cas9) and proteomics-based tools . A biotin-ligase (TurboID) based approach will identify host interaction partners for known effector proteins. The impact of this research will be an effector-host interactome network and may spur novel disease mitigation strategies.