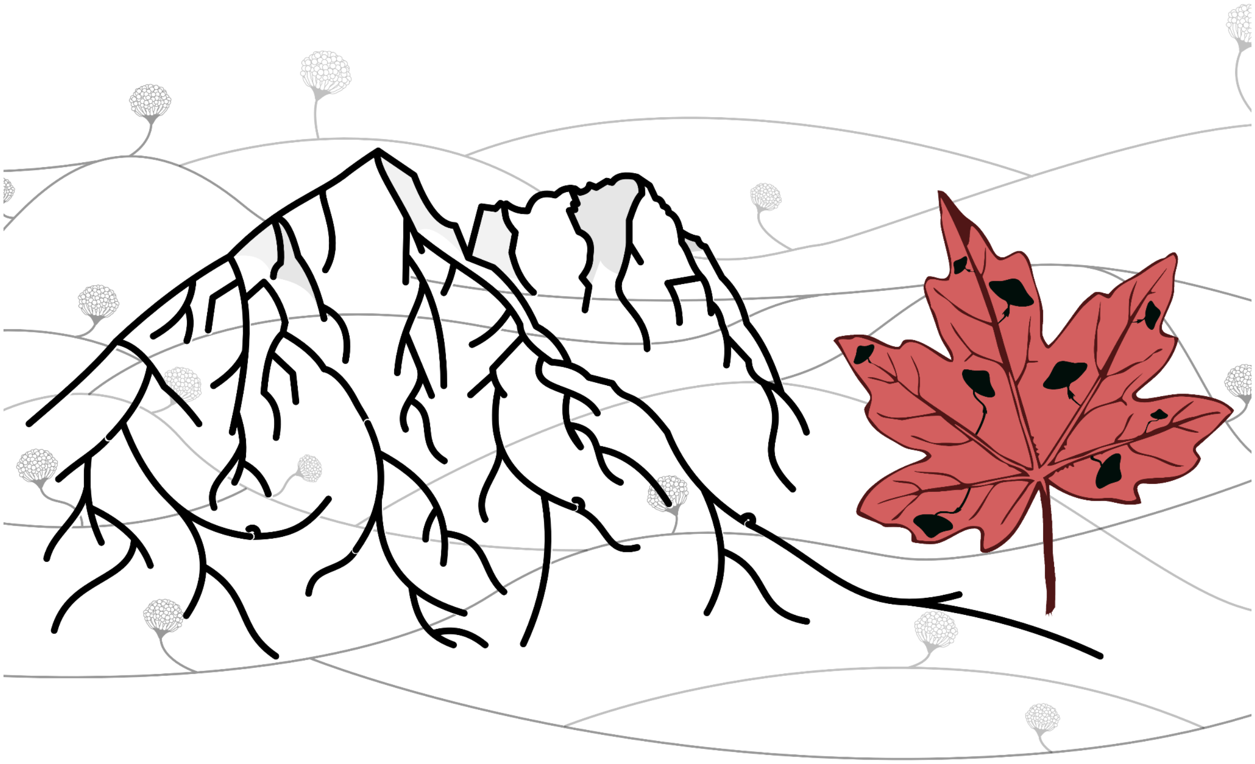
The 3rd Annual CanFunNet Fungal Biology Conference

June 1 - 3, 2022



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Conference Website	
Michael Zaigh	Conference Services at Western University

Condensed Conference Schedule

Wednesday, June 1, 2022				
8:45AM-9:00AM MT 10:45AM-11:00AM ET	Opening Remarks			
9:00AM-10:30AM MT 11:00AM-12:30PM ET	Plenary Session 1 - Fungal networks: from function to ecology and conservation			
10:30AM-11:00AM MT 12:30PM-1:00PM ET	Break			
11:00AM-12:05PM MT 1:00PM-2:05PM ET	Mycorrhizal biology, ecology and ecophysiology (1A)	The fungal component of microbiomes (2A)	Bacterial endosymbionts of fungi (3A)	Fungi in the Fossil Record (4A)
12:05PM-12:30PM MT 2:05PM-2:30PM ET	Break			
12:30PM-1:35PM MT 2:30PM-3:35PM ET	Diversity and conservation of Canadian ectomycorrhizae and macrofungi (1B)	Fungal communities in plant tissues (2B)	Pathogen stress responses and sensing (3B)	Emerging fungal pathogens (4B)
1:35PM-2:00PM MT 3:35PM-4:00PM ET	Break			
2:00PM-3:05PM MT 4:00PM-5:05PM ET		Tracking fungal communities in the environment (2C)	Symbiotic interaction between bark beetles and fungi (3C)	Pathogen 'omics and evolution (4C)
3:30PM - 5:00PM MT 5:30PM - 7:00PM ET	Trivia on Spatial Chat			

Condensed Conference Schedule

Thursday, June 2, 2022				
9:00AM-10:30AM MT 11:00AM-12:30PM ET	Plenary Session 2 - Pathogen adaptation in action			
10:30AM-11:00AM MT 12:30PM-1:00PM ET	Break			
11:00AM-12:05PM MT 1:00PM-2:05PM ET	Overcoming antifungal resistance, Part 1 (5A)	Plant disease emergence and management (6A)	Plasmodiophora brassicae biology and mitigation (7A)	The Regulatory Epigenome (8A)
12:05PM-12:30PM MT 2:05PM-2:30PM ET	Break			
12:30PM-1:35PM MT 2:30PM-3:35PM ET	Overcoming antifungal resistance, Part 2 (5B)	Detecting and monitoring fungal pathogens (6B)	Blackleg disease of canola (7B)	Molecular bases of transcription (8B)
1:35PM-2:00PM MT 3:35PM-4:00PM ET	Break			
2:00PM-3:05PM MT 4:00PM-5:05PM ET	Overcoming antifungal resistance, Part 3 (5C)	Canadian Lichen Biodiversity and Conservation (6C)	Fungal diseases of northern crops (7C)	Fungal Science Communication Workshop (8C)
3:30PM - 5:00PM MT 5:30PM - 7:00PM ET	Job Fair and Research Roulette on Spatial Chat			

Condensed Conference Schedule

Friday, June 3, 2022				
9:00AM-10:30AM MT 11:00AM-12:30PM ET	Plenary Session 3 - Evolution across genes, genomes and species			
10:30AM-11:00AM MT 12:30PM-1:00PM ET	Break			
11:00AM-12:05PM MT 1:00PM-2:05PM ET	Genetic diversity within Fungal Populations (9A)	Fungal genomes in obligate symbioses (10A)	New insights into the spread and control of fungal infections (11A)	Fungi and foods, the good, the bad and the future (12A)
12:05PM-12:30PM MT 2:05PM-2:30PM ET	Break			
12:30PM-1:35PM MT 2:30PM-3:35PM ET	Fungal genetic goods on the move (9B)	Lichen metabolism and symbiotic interactions (10B)	Candida as a model pathogen (11B)	Biotechnology and industrial applications (12B)
2:00PM-3:05PM MT 4:00PM-5:00PM ET	Closing ceremony and conference social			

Spatial Chat Schedule

Time	Event	Room
June 1, 2022 3:30PM - 5:00PM MT 5:30PM - 7:00PM ET	Trivia	Trivia - June 1
June 2, 2022 3:30PM - 4:15PM MT 5:30PM - 6:15PM ET	Research Roulette	Research Roulette - June 2
June 2, 2022 Starting at 4:00PM MT Starting at 6:00PM ET	Career Services of the University of Alberta	UA Career Services - June 2
June 2, 2022 Starting at 4:00PM MT Starting at 6:00PM ET	Free Networking/Mixer	Networking
June 3, 2022 2:00PM-3:05PM MT 4:00PM-5:00PM ET	Closing ceremony and conference social	Closing Ceremony/Networking

Career Services

Career Services of the University of Alberta is offering resume and CV reviews for CanFunNet22 participants. Bring in your CV, get some good feedback, and improve your chances to land your dream job!

The review sessions will happen June 2nd @ 4-6 pm Mountain Time (6-8 pm Eastern Time). We have 16 slots available for CanFunNet participants.

Please enter your name and email to sign up here: https://forms.gle/rJxt5zuijMXyWxTx9

Spatial Chat Guide

CanFunNet22 will be using Spatial Chat for our Networking events at the end of each day. 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 CanFunNet22 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:

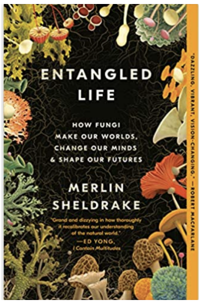
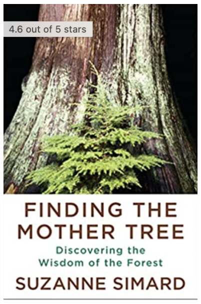
- Behave professionally. Harassment and sexist, racist, or exclusionary comments or jokes are not appropriate. Harassment includes sustained disruption of talks or other events, inappropriate physical contact, sexual attention or innuendo, deliberate intimidation, stalking, and photography or recording 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
CFN22 Mug	
“Entangled Life” by Merlin Sheldrake	
“Finding the Mothertree” by Suzanne Simard	

Plenary Session 1 - Fungal networks: from function to ecology and conservation

Moderated by: Justine Karst, Toby Spribille and Emile Gluck-Thaler
Plenary 1 - 9:00AM-10:30AM MT, June 1

9:00AM-9:30AM MT Keynote	Suzanne Simard Mother Tree Networks Help Regenerate Forests
9:30AM-10:00AM MT Keynote	Toby Kiers Quantifying trade in plant-fungal networks
10:00AM-10:30AM MT Keynote	Giuliana Furci Funga and Conservation

Mycorrhizal biology, ecology and ecophysiology

Moderated by: Melanie Jones
1A - 11:00AM-12:05PM MT, June 1

11:00AM-11:20AM MT Mini-keynote	Melanie Jones Approaches to ectomycorrhiza research: a perspective from 40 years of field- and lab-based studies
11:20AM-11:35AM MT Standard Talk	Kevin MacColl Arbuscular mycorrhizal (AM) fungal community composition in recently restored agricultural prairies differs in comparison to longer term restored and remnant prairies
11:35AM-11:50AM MT Standard Talk	Kendra Sampson Assessing arbuscular mycorrhizal colonization and rhizosphere carbon across a chronosequence of salt marshes in the Bay of Fundy, Nova Scotia
11:50AM-12:05PM MT Standard Talk	Jonathan Bennett Plant trait-based drivers of intraspecific variation in mycorrhizal responses vary with stress

The fungal component of microbiomes

Moderated by: Matthew Bakker
2A - 11:00AM-12:05PM MT, June 1

11:00AM-11:20AM MT Mini-keynote	Matthew Bakker A short guide to profiling mixed fungal communities
11:20AM-11:35AM MT Standard Talk	Etienne Yergeau The response of plant holobionts to stress: fungi as central players
11:35AM-11:50AM MT Standard Talk	Jonathan Mack The biodiversity of microfungi from the bark of the Sugar Maple (*Acer saccharum*)
11:50AM-12:05PM MT Standard Talk	Phillip Pham Metabarcoding aquatic fungi in agriculturally dominated watersheds for monitoring environmental health

Bacterial endosymbionts of fungi

Moderated by: Jessie Uehling
3A - 11:00AM-12:05PM MT, June 1

11:00AM-11:20AM MT Mini-keynote	Jessie Uehling Abundance, diversity, and functional mechanisms of bacterial endosymbiont interactions
11:20AM-11:35AM MT Standard Talk	Nicole Reynolds Mucoromycota fungal and associated bacterial communities in the rhizosphere of two different plants in the Sonoran Desert, California
11:35AM-11:50AM MT Standard Talk	Laila Partida-Martinez Fungal holobionts: hidden relationships with ecological consequences
11:50AM-12:05PM MT Standard Talk	Elizabeth Ballou A Ralstonia pickettii endosymbiont allows *Rhizopus microsporus* to evade amoeba and cause opportunistic virulence in animals

Fungi in the Fossil Record

Moderated by: Az Klymiuk
4A - 11:00AM-12:05PM MT, June 1

11:00AM-11:20AM MT Mini-keynote	Az Klymiuk Developing appropriate paradigms for assessing the plant-fungal fossil record
11:20AM-11:35AM MT Standard Talk	Ludovic LeRenard Grafting extinct branches to the Fungal Tree of Life
11:35AM-11:50AM MT Standard Talk	Leyla Seyfullah Amber as a source of fossil fungi
11:50AM-12:05PM MT Standard Talk	Tamika Nagao Cretaceous Fungal Palynomorphs of the Danek Bone Bed, Edmonton, Alberta, Canada

Diversity and conservation of Canadian ectomycorrhizae and macrofungi

Moderated by: Anna Bazzicalupo
1B - 12:30PM-1:35PM MT, June 1

12:30PM-12:50PM MT Mini-keynote	Anna Bazzicalupo Macrofungal conservation in Canada and target species for assessment: a starting point
12:50PM-1:05PM MT Standard Talk	Alfredo Justo Biodiversity of chanterelles (*Cantharellus*, *Craterellus*) and hedgehog mushrooms (*Hydnum*) in New Brunswick
1:05PM-1:10PM MT Flash Talk	Alicia Banwell At the root of it: The introduction of nursery seedlings and their fungi to conifer forests
1:10PM-1:15PM MT Flash Talk	Gavin Kernaghan Decomposition and recruitment of pine ectomycorrhizae

Fungal communities in plant tissues

Moderated by: Zamir Punja
2B - 12:30PM-1:35PM MT, June 1

12:30PM-12:50PM MT Mini-keynote	Zamir Punja The diverse and complex mycoflora present in inflorescences of cannabis (*Cannabis sativa* L., marijuana)
12:50PM-1:05PM MT Standard Talk	Alejandro Huereca Pollen-parasitic fungi: an overlooked trophic interaction?
1:05PM-1:20PM MT Standard Talk	Michelle Thompson Exploring Cultured Microbes of Pollinated Maize Silks
1:20PM-1:35PM MT Standard Talk	Bruce Malloch Temporal diversity patterns for fungi and mites associated with decaying *Sporobolus pumilus* (*Spartina patens*) in the Minas Basin, Nova Scotia

Pathogen stress responses and sensing

Moderated by: Viola Halder
3B - 12:30PM-1:35PM MT, June 1

12:30PM-12:50PM MT Mini-keynote	Kamaldeep Chhoker Carotenoid production and pigment reinitiation in *Exophiala dermatitidis* albino mutants under different media and carbon sources.
12:50PM-1:05PM MT Standard Talk	Viola Halder Genetic interaction analysis conducted in *Candida albicans* stress response genes through the use of CRISPR-Cas9-based gene drive array
1:05PM-1:20PM MT Standard Talk	Wanjun Qi Stress- and metabolic responses of *Candida albicans* require Tor1 kinase N-terminal HEAT repeats
1:20PM-1:35PM MT Standard Talk	Tanya Sharma Evidence of host-induced heterodimerization between chemotropic receptors Ste2 and Ste3 in *Fusarium graminearum*

Emerging fungal pathogens

Moderated by: Dilini Adihetty
4B - 12:30PM-1:35PM MT, June 1

12:30PM-12:50PM MT Mini-keynote	Yue Wang *Candida auris* on Apples: Diversity and Clinical Significance
12:50PM-1:05PM MT Standard Talk	Dilini Adihetty Evaluation of barley cultivars for resistance to *Cochliobolus sativus* [spot blotch] isolates from the Canadian Prairies
1:05PM-1:20PM MT Standard Talk	Helen MacDougall-Shackleton Experimental investigation of ecological niche expansion of the White-Nose Syndrome fungus *Pseudogymnoascus destructans*
1:20PM-1:35PM MT Flash Talk	Chadabhorn Insuk Efficacy of Topical Probiotics to Mitigate White Nose Syndrome in Western Canadian Bat Populations

Tracking fungal communities in the environment

Moderated by: Berni van der Meer
2C - 2:00PM-3:05PM MT, June 1

2:00PM-2:20PM MT Mini-keynote	Adele Bunbury-Blanchette Yeast communities from a Nova Scotia vineyard before and after spontaneous fermentation: a case study
2:20PM-2:35PM MT Standard Talk	Evelina Basenko FungiDB: Free online informatic tools for fungal and oomycete researchers
2:35PM-2:40PM MT Flash Talk	Devon Radford Metabarcoding mycobiota starts with evaluating specificity of primers by a new bioinformatics tool, IsPRIMER
2:40PM-2:45PM MT Flash Talk	Katarina Kukolj Investigating the effects of the Blewit Mushroom *Lepista nuda* on the community composition of its soil environment
2:45PM-2:50PM MT Flash Talk	Berni van der Meer Seasonality in Caliciopsis canker

Symbiotic interaction between bark beetles and fungi

Moderated by: Rashaduz Zaman and Dineshkumar Kandasamy
3C - 2:00PM-3:05PM MT, June 1

2:00PM-2:20PM MT Mini-keynote	Nadir Erbilgin Fungal volatiles as mediators of interspecific interactions with bark beetles
2:20PM-2:35PM MT Standard Talk	Rashaduz Zaman Ozone restricts reproduction success of ophiostomatoid fungi associated with mountain pine beetle in isolate specific manner
2:35PM-2:50PM MT Standard Talk	Dineshkumar Kandasamy Chemistry of symbiosis: Volatiles mediate interactions between conifer bark beetles and their fungal symbionts
2:50PM-3:05PM MT Standard Talk	Joey Tanney Exploring beetle-fungi-nematode interactions in spruce and mountain pine beetle

Pathogen 'omics and evolution

Moderated by: Antonia Musso
4C - 2:00PM-3:05PM MT, June 1

2:00PM-2:20PM MT Mini-keynote	Emilee Storfie Characterizing Plasmodiophora brassicae effector candidates identified in the resistance-breaking pathotype 3A infection of *Brassica napus*
2:20PM-2:35PM MT Standard Talk	Boyan Liu Proteomic profiling of novel virulence factors in the wheat fungal pathogen *Fusarium graminearum*
2:35PM-2:50PM MT Standard Talk	Sean Formby Population analysis and genome variations revealed by comparing haplophased chromosome-level genomes in isolates of the wheat leaf rust fungus, *Puccinia triticina*
2:50PM-2:55PM MT Flash Talk	Oscar Villanueva Comparative genomic analysis reveals genetic variation in the pathogenicity-related genes of Canadian *Phytophthora capsici* isolates
2:55PM-3:00PM MT Flash Talk	Laura Manerus Comparative Genomics of the *Cronartium harknessii*-Pine Pathosystem
3:00PM-3:05PM MT Flash Talk	Evgeny Ilyukhin *Cytospora* spp. associated with canker disease of spruce in Ontario, Canada.

Plenary Session 2 - Pathogen adaptation in action

Moderated by: Daniel Charlebois, Viola Halder and Stephen Strelkov
Plenary 2 - 9:00AM-10:30AM MT, June 2

9:00AM-9:30AM MT Keynote	Judith Berman Aneuploidy as a rapid mechanism of adaptation to antifungal drugs
9:30AM-10:00AM MT Keynote	Daniel Charlebois Transition from nongenetic to genetic antifungal resistance: Insights from mathematical models, genetically engineered yeasts, and pathogenic fungi
10:00AM-10:30AM MT Keynote	Gurcharn Singh Brar Pathogenomics of *Puccinia striiformis* reveals a population shift in western Canada

Overcoming antifungal resistance: part 1

Moderated by: Jennifer Geddes-McAlister
5A - 11:00AM-12:05PM MT, June 2

11:00AM-11:20AM MT Mini-keynote	Daniel Croll The threat of parallel emergence of fungicide resistance in agriculture
11:20AM-11:35AM MT Standard Talk	Michael Woods Defining the role of ClpX in reversal of antifungal resistance in *Cryptococcus neoformans*
11:35AM-11:50AM MT Standard Talk	Amrita Bharat Ten years of *Candida auris* in Canada, 2012 - 2021
11:50AM-11:55AM MT Flash Talk	Michelle Agyare-Tabbi A comprehensive analysis of the role of the DNA damage response in *Candida albicans*
11:55AM-12:00PM MT Flash Talk	Gabriela Nunes Marsiglio Librais Tra1 is a new regulator of *Candida albicans* drug resistance and pathogenicity

Plant disease emergence and management

Moderated by: Reem Aboukhaddour
6A - 11:00AM-12:05PM MT, June 2

11:00AM-11:20AM MT Mini-keynote	Reem Aboukhaddour Tan spot and its genome: a playground for scientists to explore disease emergence
11:20AM-11:35AM MT Standard Talk	Thorsten Langner Mini-chromosomes as drivers of genetic diversity and host-adaptation in the blast fungus *Magnaporthe oryzae*
11:35AM-11:50AM MT Standard Talk	Syama Chatterton Complexity of managing pea root rot caused by a complex of fungal and oomycete soilborne pathogens

Plasmodiophora brassicae biology and mitigation

Moderated by: Stephen Strelkov and Sheau-Fang Hwang
7A - 11:00AM-12:05PM MT, June 2

11:00AM-11:20AM MT Mini-keynote	Małgorzata Jędryczka Comparison of *Plasmodiophora brassicae* pathotypes in Canada and Poland
11:20AM-11:35AM MT Standard Talk	Jutta Ludwig-Müller The endophytic fungus *Acremonium alternatum* can reduce clubroot symptoms on *Brassica napus* cultivars
11:35AM-11:50AM MT Standard Talk	Hui Zhang Histopathology of the *Plasmodiophora brassicae*-Chinese Cabbage Interaction in Hosts Carrying Different Sources of Resistance
11:50AM-12:05PM MT Standard Talk	Edel Perez-Lopez Investigating clubroot resistance from a "mobile" point of view

The Regulatory Epigenome

Moderated by: Alexandra Dallaire
8A - 11:00AM-12:05PM MT, June 2

11:00AM-11:20AM MT Mini-keynote	Alexandra Dallaire Connecting epigenetics to gene and transposon territories of *Rhizophagus irregularis*
11:20AM-11:35AM MT Standard Talk	Sandra Catania Evolutionary persistence of DNA methylation for millions of years
11:35AM-11:50AM MT Standard Talk	Carlos Pérez-Arques RNAi-exclusive antifungal drug resistance is inherited after sexual reproduction in the human pathogen *Mucor circinelloides*
11:50AM-12:05PM MT Standard Talk	David Touchette Novel Antarctic yeast switches to ethanol fermentation and increases small RNA synthesis to adapt to cold.

Overcoming antifungal resistance: part 2

Moderated by: Michael Woods and Boyan Liu
5B - 12:30PM-1:35PM MT, June 2

12:30PM-12:50PM MT Mini-keynote	Jennifer Geddes-McAlister One Health of Fungal Disease
12:50PM-1:05PM MT Standard Talk	Sara Fallah Identification and characterization of molecules with novel antifungal activity against the fungal pathogen *Candida albicans*
1:05PM-1:10PM MT Flash Talk	Malisa Fernando Differential requirements for Ire1 during ER stress in *Saccharomyces cerevisiae*
1:10PM-1:15PM MT Flash Talk	Meea Fogal Creating a *Candida albicans* genome-wide CRISPR interference library for large-scale genetic analysis
1:15PM-1:20PM MT Flash Talk	Samuel Stack-Couture The regulation of endoplasmic reticulum stress in *Candida albicans*

Detecting and monitoring fungal pathogens

Moderated by: Ilakkiya Thirugnanasambandam
6B - 12:30PM-1:35PM MT, June 2

12:30PM-12:45PM MT Standard Talk	Guillaume Bilodeau International Potato Wart characterization using multiplexed microsatellite markers
12:45PM-12:50PM MT Flash Talk	Rachel Rajsp Investigating the soil microbiome of American ginseng (*Panax quinquefolius*)
12:50PM-1:05PM MT Standard Talk	Hadjer Bellah A highly multiplexed assay to monitor virulence, fungicide resistance and gene flow in the fungal wheat pathogen *Zymoseptoria tritici*
1:05PM-1:20PM MT Standard Talk	Ilakkiya Thirugnanasambandam Development of real-time immunoPCR (RT-iPCR) assays for three airborne fungal pathogens of wheat
1:20PM-1:35PM MT Standard Talk	Jacob Walsh The Chemical Ecology of *Ilyonectria mors-panacis* and Chemical Targets for Root Rot Management

Blackleg disease of canola

Moderated by: Hossein Borhan
7B - 12:30PM-1:35PM MT, June 2

12:30PM-12:50PM MT Mini-keynote	Hossein Borhan *Brassica napus* extracellular receptors and immunity against blackleg disease
12:50PM-1:05PM MT Standard Talk	Isabelle Fudal A new family of structurally conserved fungal effectors displays epistatic interactions with plant resistance proteins
1:05PM-1:20PM MT Standard Talk	Angela Van de Wouw Current fungicide use in Australia and its implications for control of blackleg disease
1:20PM-1:35PM MT Standard Talk	Jacqui Batley TBD

Molecular bases of transcription

Moderated by: Khaleda Afrin Bari
8B - 12:30PM-1:35PM MT, June 2

12:30PM-12:45PM MT Standard Talk	Khaleda Afrin Bari The SAGA complex component Tra1 regulates chronological aging in yeast
12:45PM-12:50PM MT Flash Talk	Aiman Farheen Assessing genes important for hyphal morphogenesis in the fungal pathogen *C. albicans*
12:50PM-1:05PM MT Standard Talk	Takashi Kubota SWI/SNF and the histone chaperone Rtt106 drive expression of the Pleiotropic Drug Resistance network genes
1:05PM-1:20PM MT Standard Talk	Jigeesha Mukhopadhyay Splicing Pathways in Complex Introns in Fungi: The Stacking Dolls of the Intron World
1:20PM-1:35PM MT Standard Talk	Maribel Navarro-Mendoza RNAi and heterochromatin formation act independently to control genome stability and gene expression in Mucorales

Overcoming antifungal resistance: part 3

Moderated by: Brianna Ball and Davier Gutierrez Gongora
5C - 2:00PM-3:05PM MT, June 2

2:00PM-2:20PM MT Mini-keynote	Lucy Xie Pararesistance: a mutation-independent mechanism of antifungal drug resistance
2:20PM-2:35PM MT Standard Talk	Nick Gervais Investigating the Role of Chromosome R in Drug Tolerance in *Candida albicans* via CRISPRa Pooled Screening
2:35PM-2:50PM MT Standard Talk	Courtney Geer Protein translation is compromised in the Bowen-Conradi ribosomopathy
2:50PM-3:05PM MT Standard Talk	Lauren Wensing An inducible CRISPR interference system to study the role of essential gene function during drug tolerance in antifungal resistant isolates of *Candida albicans*.

Canadian Lichen Biodiversity and Conservation

Moderated by: Troy McMullin
6C - 2:00PM-3:05PM MT, June 2

2:00PM-2:20PM MT Mini-keynote	Troy McMullin Canadian Lichen Biodiversity and Conservation
2:20PM-2:35PM MT Standard Talk	Diane Haughland Life Lessons from Lichen
2:35PM-2:50PM MT Standard Talk	Kendra Driscoll Lichenicolous fungi of Atlantic Canada: what we’ve learned, and what we still don’t know
2:50PM-3:05PM MT Standard Talk	John McCarthy Lichen Floristics in Newfoundland and Labrador – the Past and the Present, and Prospects for the Future

Fungal diseases of northern crops

Moderated by: Linda Elizabeth Jewell
7C - 2:00PM-3:05PM MT, June 2

2:00PM-2:20PM MT Mini-keynote	Linda Elizabeth Jewell Come-from-aways? New and familiar fungal phytopathogens in Newfoundland and Labrador
2:20PM-2:35PM MT Standard Talk	Pooja Sridhar Toward identification of a chemoattractant that enables Ste2-mediated directed growth of *Fusarium graminearum* on wheat
2:35PM-2:50PM MT Standard Talk	Keisha Hollman The virulence of *Plasmodiophora brassicae* on canola with ‘second-generation’ clubroot resistance
2:50PM-3:05PM MT Standard Talk	Tom Witte Evolutionary dynamics of the ergot alkaloid biosynthetic gene cluster in Canadian *Claviceps purpurea*

Fungal Science Communication Workshop

Moderated by: Matthew Kasson
8C - 2:00PM-3:05PM MT, June 2

2:00PM-3:05PM MT Workshop	Matthew Kasson Leveraging community science platforms and social media to build meaningful mycology collaborations in North America

Plenary Session 3 - Evolution across genes, genomes and species

Moderated by: Emile Gluck-Thaler, Viola Halder and Toby Spribille
Plenary 3 - 9:00AM-10:30AM MT, June 3

9:00AM-9:30AM MT Keynote	Tatiana Giraud Multiple convergent evolution events of recombination suppression in fungal mating-type chromosomes
9:30AM-10:00AM MT Keynote	Nicolas Corradi The genetics and genome biology of arbuscular mycorrhizal fungi
10:00AM-10:30AM MT Keynote	Yan Wang Unravelling cryptic evolution of insect gut-dwelling fungi using Harpellales as a model

Genetic diversity within Fungal Populations

Moderated by: Aleeza Gerstein
9A - 11:00AM-12:05PM MT, June 3

11:00AM-11:20AM MT Mini-keynote	Aleeza Gerstein *Candida* population diversity in recurrent vulvovaginal candidiasis
11:20AM-11:35AM MT Standard Talk	Anna Fijarczyk Genome size and complexity of fungal pathogens depend on their lifestyle
11:35AM-11:50AM MT Standard Talk	Abdul-Rahman Adamu Bukari *Candida albicans* clinical isolates from Manitoba reveals extensive phylogenetic diversity with limited regional clustering in a global context
11:50AM-12:05PM MT Standard Talk	Mathieu Hénault Hybridization drives mitochondrial genome instability and metabolic shift in a species with biparental mitochondrial inheritance

Fungal genomes in obligate symbioses

Moderated by: Carmen Allen
10A - 11:00AM-12:05PM MT, June 3

11:00AM-11:20AM MT Mini-keynote	Antoine Simon The strange case of alternative associations in lichenized fungi: Dr Jekyll or Mr Hyde?
11:20AM-11:35AM MT Standard Talk	Carmen Allen Tripartite fungal interactions in a natural glucuronoxylomannan matrix
11:35AM-11:50AM MT Standard Talk	Gökalp Yildirir Long reads and Hi-C sequencing illuminate the two-compartment genome of the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*
11:50AM-12:05PM MT Standard Talk	Shalini Chaudhary Selenoprotein production in insect-gut fungi

New insights into the spread and control of fungal infections

Moderated by: Tanis Dingle
11A - 11:00AM-12:05PM MT, June 3

11:00AM-11:20AM MT Mini-keynote	Tanis Dingle The changing epidemiology of *Histoplasma capsulatum* in North America
11:20AM-11:35AM MT Standard Talk	Brianna Ball Uncovering novel anti-virulence strategies to combat fungal infections
11:35AM-11:50AM MT Standard Talk	Hanna Ostapska Pre-clinical evaluation of recombinant microbial glycoside hydrolases as antibiofilm agents in experimental invasive aspergillosis and acute *Pseudomonas aeruginosa* infection
11:50AM-12:05PM MT Flash Talk	Kelly Robinson Glycosylation of deoxynivalenol by *Clonostachys Rosea*—toward identification of glycosyltransferases involved in the detoxification of DON

Fungi and foods, the good, the bad and the future

Moderated by: Marie Filteau
12A - 11:00AM-12:05PM MT, , June 3

11:00AM-11:20AM MT Mini-keynote	Sherazade Fikri Yeast *Candida krusei* and its affinity for the cranberry juice processing environment
11:20AM-11:35AM MT Standard Talk	Barret Foster Using Norwegian kveik to generate novel hybrid ale yeast with strong fermentative capabilities and stress tolerant properties
11:35AM-11:50AM MT Standard Talk	Ting Zhou Detoxification of mycotoxins through biotransformation of their chemical structures

Fungal genetic goods on the move

Moderated by: Aaron Vogan
9B - 12:30PM-1:35PM MT, June 3

12:30PM-12:45PM MT Standard Talk	Aaron Vogan Massive transposons as the crucible of evolution in fungi
12:45PM-12:50PM MT Flash Talk	Nikita Mehta Deciphering the molecular mechanisms underlying the genetic diversity in the plant pathogenic fungus *Colletotrichum gloeosporioides*
12:50PM-1:05PM MT Standard Talk	Greg Korfanty Genetic Diversity and Dispersal of *Aspergillus fumigatus* from Southeastern France
1:05PM-1:20PM MT Standard Talk	Bianca Turcu Examining nuclear transfer between homokaryotic and dikaryotic strains of *Rhizophagus irregularis*
1:20PM-1:35PM MT Standard Talk	Victoria Terry Mycorrhizal response to homokaryotic versus dikaryotic arbuscular mycorrhizal fungi.

Lichen metabolism and symbiotic interactions

Moderated by: Hadi Nazem-Bokaee
10B - 12:30PM-1:35PM MT, June 3

12:30PM-12:50PM MT Mini-keynote	Hadi Nazem-Bokaee Metabolic modelling of *Endocarpon pusillum* facilitates the study of the lichen symbiosis
12:50PM-1:05PM MT Standard Talk	Susan Egbert Identifying the Squamatic Acid Biosynthetic Gene Cluster in Lichen *Cladonia uncialis*
1:05PM-1:20PM MT Standard Talk	Duleeka Gunawardana Effect of pH and Temperature on Usnic Acid Production and Polyketide Synthase Gene (MPAS, MPAO) Expression in *Cladonia uncialis*
1:20PM-1:35PM MT Standard Talk	Gulnara Tagirdzhanova Large-scale analysis of metagenomics of lichen symbiosis

Candida as a model pathogen

Moderated by: Jessie MacAlpine
11B - 12:30PM-1:35PM MT, June 3

12:30PM-12:45PM MT Standard Talk	Jessie MacAlpine Yak1 Regulates *Candida albicans* Morphogenesis through the Ras1/PKA Pathway
12:45PM-12:50PM MT Flash Talk	Emily Xiong Identifying and characterizing genes important for *Candida albicans* fitness in diverse environmental conditions
12:50PM-1:05PM MT Standard Talk	Maikel Acosta Zaldivar Four cell surface phosphate transporters in *Candida albicans* contribute to homeostasis at distinct ambient pH and phosphate concentrations
1:05PM-1:20PM MT Standard Talk	Saif Hossain Functional genomic screens of protein kinases in *Candida albicans* reveal novel roles of orf19.3751 and IRE1 in morphogenesis
1:20PM-1:35PM MT Standard Talk	Emma Lash Characterizing the role of Ent2 in Candida albicans filamentation

Biotechnology and industrial applications

Moderated by: Linda Horianopoulos
12B - 12:30PM-1:35PM MT, June 3

12:30PM-12:50PM MT Mini-keynote	Linda Horianopoulos Identification of yeasts with high glycolytic flux for the development of novel cell factories
12:50PM-1:05PM MT Standard Talk	Susannah Selber-Hnatiw Secondary Metabolite Production in *Aspergillus niger*: methyltransferase specificity
1:05PM-1:20PM MT Standard Talk	Shane Ram Mining the *Aspergillus niger* secondary metabolome through overexpression of non-ribosomal peptide synthetases
1:20PM-1:35PM MT Standard Talk	David Stuart Engineering the kerosene fungus *Hormoconis resinae* for bioremediation of hydrocarbon contaminated soil and water

Abstracts

Tan spot and its genome: a playground for scientists to explore disease emergence

Reem Aboukhaddour, Ryan Gourlie, Mohamed Hafez, Rodrigo Ortega-Polo, Megan McDonald and Stephen Strelkov
Agriculture and Agri-Food Canada

Necrotrophic fungal pathogens cause considerable damage to crop production worldwide, and many of these pathogens in the Pleosporales have caused the sudden emergence of major epidemics on cereal crops. Tan spot of wheat (*Pyrenophora tritici-repentis*) is one example, and scientists have explored its virulence and interaction with wheat over the past 50 years. In this presentation, my aim is to provide an overview on the recent work we have done on tan spot and its pangenome, the translocation of its virulence genes on large mobile elements and the evolution of the various haplotypes of these virulence genes.

Four cell surface phosphate transporters in *Candida albicans* contribute to homeostasis at distinct ambient pH and phosphate concentrations

Acosta-Zaldívar, Maikel*. Qi, Wanjun. King, William. Vogt, Jana. Köhler, Julia R.
Boston Children's Hospital

Phosphate is an essential macronutrient. We previously found that in *Candida albicans*, the high-affinity inorganic phosphate (Pi) transporter Pho84 activates TORC1 signaling in response to Pi, and is required in oxidative- and cell wall stress. We here characterize *C. albicans*' 4 predicted cell surface Pi transporters, encoded by PHO84, PHO89, PHO87 and FGR2, using single and triple mutants in these transporters. Pho84 alone sustains cellular growth and Pi uptake over the widest range of pH and Pi concentrations. Among the studied transporters only Pho84 signals to TORC1; it is also most important for tolerance of fluconazole and amphotericin. A quadruple null mutant of these 4 transporters can use inorganic phosphate as a sole phosphate source under acidic conditions. The residual Pi uptake in these mutants seems to be provided by GPC transporters. *C. albicans* seems better adapted to Pi acquisition at low pH, a condition rarely encountered during host invasion.

Candida albicans **clinical isolates from Manitoba reveals extensive phylogenetic diversity with limited regional clustering in a global context**

Adamu Bukari, Abdul-Rahman and Gerstein, Aleeza
University of Manitoba

C. albicans is a globally distributed opportunistic human pathogen. North American isolates have been underrepresented in global phylogenetic studies. Here, we examined the phylogenetic relatedness of 43 whole-genome sequenced *C. albicans* clinical isolates from the Canadian province of Manitoba. Aneuploidies were found in three isolates and one ~115 kb duplication on Chr3 was identified in another isolate. We placed these isolates within a global phylogeny of over 250 global isolates, where Manitoba isolates clustered in 6 of the 17 previously characterized genetic clusters and two new clusters. One isolate was in a clade with isolates produced from sexual reproduction. We developed a new statistical approach to quantify observed geographic relatedness within genetic clusters for future work aimed at testing hypotheses about the factors that influence temporal stability of genetic clusters within Manitoba isolates. This work demonstrates the related yet extensive genetic diversity that exists amongst clinical isolates from Manitoba and serves as preliminary evidence of geographic co-occurrence of clonal and hybrid isolates.

Evaluation of barley cultivars for resistance to *Cochliobolus sativus* [spot blotch] isolates from the Canadian Prairies

D.D. Adihetty, K. Xi, H. Klein-Gebbinck, R. Aboukhaddour, H.R. Kutcher, J.R. Tucker, X. Wang, W. Xu, A.D. Beattie, A. Badea, T.K. Turkington, and S.E. Strelkov
University of Alberta

Spot blotch, caused by *Cochlobolus sativus* (anamorph *Bipolaris sorokiniana*), is an emerging threat to Canadian barley (*Hordeum vulgare* L.) production. Three barley cultivars, ‘AAC Synergy’, ‘CDC Fraser’, and ‘Revanche’, were screened for resistance to 11 isolates of *C. sativus* collected in 2018-2020 from the Prairie provinces of Manitoba, Saskatchewan and Alberta. Host reactions were rated for infection response (IR) on a 0 to 9 scale, 8-10 days following inoculation at the seedling stage. Four of five isolates from Manitoba were highly virulent (7.5 to 9) on all three cultivars, while the fifth was highly virulent on ‘AAC Synergy’ and ‘Revanche’, but caused an IR of 4.6 on ‘CDC Fraser’. One isolate from Saskatchewan and another from Alberta caused IRs of 4.5 and 4.8, respectively, on ‘AAC Synergy’. The results indicate that *C. sativus* populations from the Prairies may partially or completely overcome the resistance in Canadian barley cultivars.

The SAGA complex component Tra1 regulates chronological aging in yeast

Khaleda Afrin Bari[1], Matthew D. Berg[2b], Julie Genereaux[1,2], Christopher J. Brandl[2] and Patrick Lajoie1*
University of Western Ontario

Gene expression undergoes considerable changes during the aging process. The mechanisms regulating the transcriptional response to cellular aging remain poorly understood. Here, we employ the budding yeast *Saccharomyces cerevisiae* to better understand how organisms adapt their transcriptome to promote longevity. In yeast, chronological lifespan (CLS) assays are used to study the survival of non-dividing cells at stationary phase over time, providing insights into the aging process of post-mitotic cells in other organisms. Tra1 is an essential component of both the yeast SAGA/SLIK and NuA4 complexes, where it recruits these complexes to acetylate histones at targeted promoters. Importantly, Tra1 regulates the transcriptional response to multiple stresses. To evaluate the role of Tra1 in chronological aging, we took advantage of a previously characterized mutant allele that carries mutations in the TRA1 PI3K domain (tra1Q3). We found that loss of functions associated with (tra1Q3) sensitized cells to growth media acidification and shortens lifespan. Transcriptional profiling reveals that genes differentially regulated by Tra1 during the aging process are enriched for components of the response to stress; especially in Yap1 targets. Notably, expression of catalases (CTA1, CTT1) involved in hydrogen peroxide detoxification decreases in chronologically aged tra1Q3 cells. Consequently, they also display increased levels of toxic reactive oxygen species (ROS). Aged tra1Q3 cells also display reduced expression of peroxisomal genes and exhibit decreased numbers of peroxisomes as well as inability to grow on media containing oleic acid. Thus, Tra1 emerges as an important regulator of longevity in yeast via multiple mechanisms.

A comprehensive analysis of the role of the DNA damage response in *Candida albicans*

Agyare-Tabbi, Michelle*; Shapiro, Rebecca
University of Guelph

Candida albicans is a commensal fungal organism that exists naturally on human skin and mucosal surfaces. *C. albicans* is a successful pathogen due to several virulence mechanisms, and the lack of effective antifungal therapies coupled with the rising incidence of antifungal drug resistance has established this organism as a significant threat to human health. In bacteria, there is a well-established phenomenon linking treatment with antibiotics to increased rates of mutagenesis and drug resistance, mediated by error-prone polymerases. These polymerases are upregulated upon stress-induced DNA damage and facilitate rapid DNA repair while introducing mutations into the genome, ultimately driving drug resistance. This effect has yet to be characterized in pathogenic fungi such as *C. albicans*. This study aims to identify genes encoding error-prone polymerases based on known orthologs in *Saccharomyces cerevisiae* to determine their role in the DNA damage response pathway, and in mediating mutagenesis-based antifungal drug resistance.

Tripartite fungal interactions in a natural glucuronoxylomannan matrix

Allen, Carmen*; DeLong-Duhon, Sarah; Díaz-Escandón, David; Tagirdzhanova, Gulnara; Forbes, Andrew; Spribille, Toby
University of Alberta

Tremella fuciformis is a commercially cultivated jelly mushroom valued for the medicinal and culinary properties of abundant glucuronoxylomannan (GXM) polysaccharides in the fruiting bodies. Cultivation requires a living host fungus in the genus *Annulohypoxylon* (*Xylariaceae*) that degrades woody substrates. In natural settings, *T. fuciformis* is itself host to the mycoparasite *Sporothrix epigloea* (*Ophiostomataceae*) that forms dark spine-looking perithecia on the *T. fuciformis* fruiting body. We used a combined ‘omics approach to understand the molecular mechanisms at play in this three-way symbiosis operating in a GXM-rich environment. In 2021, we sampled wild *T. fuciformis* sporocarps and associated *Annulohypoxylon* from northern red oak forests of Iowa and Missouri. We used deep metagenomic sequencing to assess the metabolic potential of the three fungal partners and the microbial community associated with senesced sporocarps. In addition, we compared the eukaryotic transcript levels in fresh sporocarps with intact GXM to senesced sporocarps with a degraded GXM matrix. Together these results provide a first-ever survey of microbial diversity in this system and provide important background for assessing the molecular nature of GXM degradation in jelly fungi.

A short guide to profiling mixed fungal communities

Matthew Bakker
University of Manitoba

‘What fungi live in this environment?’ has become a relevant question for scientists studying the decomposition of wood, the healing of skin wounds, the preservation of ancient artefacts, and a thousand other topics. This talk will walk through the process of profiling mixed communities of fungi by sequencing PCR amplicons, highlighting important decision points, best practices, and limitations of current methods. This information will prepare you to perform your own studies, or to better understand and interpret related studies in the literature.

Uncovering novel anti-virulence strategies to combat fungal infections

Ball, B*; West, H; Carruther-Lay, D; Pladwig, S; Geddes-McAlister, J
University of Guelph

Cryptococcus neoformans is an opportunistic fungal pathogen found ubiquitously within the environment and is equipped with sophisticated virulence factors that modulate the host immune system and promote fungal survival in immunocompromised individuals to cause the life-threatening disease cryptococcal meningitis. This study aims to identify and characterize novel anti-virulence strategies by deeply profiling the infection dynamics between host immune cells and *C. neoformans*. Using quantitative proteomics, we have identified novel infection-associated fungal proteins that have the potential to interact with the host, and have prioritized these candidates for characterization. A library of gene deletion strains has been constructed and characterized for phenotypic differences in the production of *C. neoformans* classical virulence factors, followed by assessment of the candidate's potential to cause infection in immune cells and murine models. This research will provide a new pipeline for alternative drug target discovery against fungal pathogens and a robust tool to control fungal diseases.

A Ralstonia pickettii endosymbiont allows *Rhizopus microsporus* to evade amoeba and cause opportunistic virulence in animals

Elizabeth Ballou
Exeter University

Opportunistic infections by environmental fungi are a growing clinical problem, driven by an increasing population of people with immunocompromising conditions. Spores of the Mucorales order are ubiquitous in the environment but can also cause acute invasive infections in humans through germination and evasion of the mammalian host immune system. How they achieve this, and the evolutionary drivers underlying the acquisition of virulence mechanisms, are poorly understood. Here we show that a clinical isolate of *Rhizopus microsporus* contains a *Ralstonia pickettii* bacterial endosymbiont required for virulence in both zebrafish and mice, and that this endosymbiosis enables secretion of factors that potently suppress growth of the soil amoeba *Dictyostelium discoideum*, as well as their ability to engulf and kill other microbes. As amoebae are natural environmental predators of both bacteria and fungi, we propose this tri-kingdom interaction contributes to establishing endosymbiosis and acquisition of anti-phagocyte activity. Importantly, we show this activity also protects fungal spores from phagocytosis and clearance by human macrophages, and endosymbiont removal renders the fungal spores avirulent in vivo. Together, these findings describe a new role for a bacterial endosymbiont in *Rhizopus microsporus* pathogenesis in animals, and suggests a mechanism of virulence acquisition through environmental interactions with amoebae.

At the root of it: The introduction of nursery seedlings and their fungi to conifer forests

Banwell, Alicia* & Thorn, Greg
Western University

Ectomycorrhizae (ECM), associations between fungi and plant roots, are important in Canada for their role in supporting boreal tree species and are of interest for their production of valuable edible mushrooms such as chanterelles (*Cantharellus*). ECMs are commonly found on woody plants in a wide range of habitats, including natural and disturbed forest stands, and seedlings reared in nurseries for reforestation efforts. Little is known about the effect that ECMs established on nursery seedlings have on forest environments once the seedlings are planted. My project will investigate whether nursery established ECMs continue to persist on seedlings once planted in forests, or if existing ECMs in forests, such as Cantharellus, replace these associations on seedlings. This knowledge can be used to improve reforestation practices by protecting existing valuable ECMs in forests, or to provide the forestry industry with the possibility of forming associations of valuable mushrooms such as *Cantharellus* on seedlings.

FungiDB: Free online informatic tools for fungal and oomycete researchers

Basenko, Evelina presenting on behalf of the entire VEuPathDB Bioinformatics Resource Center
University of Liverpool

FungiDB (https://FungiDB.org) is a free online resource enabling browsing, querying and sophisticated mining of genomic-scale datasets. FungiDB is a component of the Eukaryotic Pathogen,Vector & Host Informatics Resources (VEuPathDB.org) that integrate genomic, transcriptomic, proteomic, epigenetic, population diversity, and other types of data for eukaryotic microbes (pathogenic & nonpathogenic, free-living & parasitic), and hosts and vectors of human disease. FungiDB encompasses genomes of yeast, filamentous fungi and oomycetes. A user-friendly web interface with embedded bioinformatics tools supports in silico experiments leveraging public data and private datasets uploaded from the VEuPathDB Galaxy. With FungiDB, you can browse genomes, mine Omics-scale datasets, annotation, and the results of automated analyses (protein domains, orthology predictions, etc.), improve gene models in Apollo and capture expert knowledge via the User Comments system. Contact Us (help@fungidb.org) to nominate datasets for integration, ask a question, or schedule a lab presentation with FungiDB on Zoom!

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.
University of British Columbia

Despite the ecological importance of fungi, we still know little about their diversity in Canada. As anthropogenic impacts accelerate the speed of environmental change, it is imperative that we fill this major information gap, critical for fungal protection. To gain insight on the conservation status of Canadian macrofungi, we took advantage of the large and growing body of fungal biodiversity data from government research (Wild Species 2020), citizen science, trained independent mycologists, university, and museum biodiversity research. For mushrooms that fruit only a few days of the year and are often difficult to positively identify, there is a lot of work to overcome the uncertainty of distinguishing under-sampling from rarity. Our work stresses the importance of building a strong network of professional and amateur mycologists to develop resources, disseminate information to make educated decisions, and advance conservation actions.

A highly multiplexed assay to monitor virulence, fungicide resistance and gene flow in the fungal wheat pathogen *Zymoseptoria tritici*

Bellah Hadjer *, Gazeau Gwilherm , Marcel Thierry C. and Croll Daniel .
University of Neuchatel

Crop pathogens pose severe risks to global food production due to the rapid rise of resistance to pesticides and host resistance breakdowns. Predicting future risks requires monitoring tools to identify changes in the genetic composition of pathogen populations. Here we report the design of a microfluidics-based amplicon sequencing assay to multiplex 801 amplicons targeting virulence and fungicide resistance genes, and randomly selected genome-wide markers. We optimized primer design by integrating polymorphism data from 632 genomes. To test the performance of the assay, we genotyped 192 samples of the fungal wheat pathogen *Zymoseptoria tritici*. We found that the assay can accurately recover genotypes from pure DNA, mixed samples, low input as well as material extracted directed from infected wheat leaves. As a proof-of-concept, we show that the assay recovers the pathogen genetic structure across French wheat fields. Sustained pathogen monitoring will improve responsiveness to sustainably manage crop protection and preserve yields.

Plant trait-based drivers of intraspecific variation in mycorrhizal responses vary with stress

Bennett, Jonathan and Kuper-Psenicnik, Aisa
University of Saskatchewan

Plant mycorrhizal responses (MRs) vary from mutualism to parasitism depending on the match among the plant, fungus, and environment. This variation in MR is expected to relate to plant traits, with more positive MRs for plants with thicker roots that are less effective nutrient foragers. Plant traits also vary with the environment, however, which could obscure any relationship between plant traits and MRs or alter the MR itself. To explore intraspecific variation in MRs, we measured MRs and root traits for nine alfalfa (*Medicago sativa*) cultivars grown in low stress conditions and under drought, nutrient, and salinity stresses. Trait correlations with MRs were environment dependent: root traits were unrelated to MRs under low stress conditions, whereas thicker rooted plants exhibited positive MRs under drought and nutrient stresses but negative MRs under salinity stress. This suggests that plants traits are unlikely to consistently predict MRs.

Aneuploidy as a rapid mechanism of adaptation to antifungal drugs

Judith Berman
Tel Aviv University

While drug resistance complicates the treatment of fungal infections, the majority of problematic (persistent or recurrent) fungal infections are caused by susceptible isolates that do not respond to treatments that should inhibit them.. Tolerance and hetero-resistance are responses in which some of the cells in an isogenic population grow slowly in the presence of supra-MIC drug concentrations. These tolerant subpopulations have the potential to drive the evolution of new mechanisms for pathogen survival. Aneuploidy, a change in chromosome stoichiometry, is a frequent, rapid and transiently stable mechanism by which pathogenic yeast respond to drug stress. Aneuploidy is a common feature of many natural yeast isolates. The process by which cells become aneuploid, the fitness costs associated with aneuploidy, and the mechanisms by which they maintain the aneuploid state will be discussed.

Ten years of *Candida auris* in Canada, 2012 - 2021

Domenica G. De Luca, David C. Alexander, Tanis C. Dingle, Philippe J. Dufresne, Linda M. Hoang, Julianne V. Kus, Allison McGeer, Robyn Mitchell, Ilan S. Schwartz, and Amrita Bharat*
University of Manitob, National Microbiology Laboratory

Candida auris is associated with outbreaks in healthcare facilities and antifungal resistance. We carried out genomic characterization of all known cases of *C. auris* in Canada to monitor its emergence. Among isolates from 31 cases identified from 2012 – 2021, eighteen isolates (58%) were fluconazole resistant and contained target mutations (ERG11 F126L, Y132F, or Y143R), 12 isolates (38.7%) were amphotericin B resistant, and all were echinocandin susceptible. Nine isolates (29%) were multidrug resistant. Phylogenetic analysis based on single nucleotide variants (SNVs) showed that all Canadian isolates belonged to the four major genomic lineages, including clades I (n=14), II (n=7), III (n=5), and IV (n=5). Isolates within each clade were often clonal, however, one group of isolates from a health region cluster were much more closely related than others, differing by only 1-19 SNVs. WGS' ability to aid in identifying transmission clusters in healthcare can help to support infection prevention and control.

International Potato Wart characterization using multiplexed microsatellite markers

Bilodeau Guillaume J. *, Gagnon Marie-Claude, Shearlaw Debbie, Newton Miranda
Canadian Food Inspection Agency

Potato wart disease is caused by the quarantine soil-borne fungus *Synchytrium endobioticum*. This obligate biotrophic fungus can persist in infested fields for more than 30 years, even in absence of the host. Because of its severity and persistence, quarantine measures are enforced worldwide to avoid the spread of this disease. Usually potatoes are grown with resistant cultivars but new pathotypes constantly emerge which overcome varietal resistance. This underlines the importance of a thorough molecular characterization of potato wart outbreaks worldwide, which has previously been complicated by the availability of material and isolation from zoospores. An international panel of samples, including Canadian isolates, were tested for pathotypes and genotyped using multiplex microsatellite markers in collaboration with European countries via an Euphresco project. We genotyped 120 worldwide isolates with 21 markers split in 4 different multiplexes, compared them to mitochondrial genomic sequences, and characterized the global population structure of *S. endobioticum*.

Brassica napus extracellular receptors and immunity against blackleg disease

Hossein Borhan
Agriculture and Agri-Food Canada

Brassica napus (canola/rapeseed) race specific resistance (R) genes against blackleg disease, caused by the ascomycete fungus *Leptosphaeria maculans*, have been commonly used in canola breeding. To date five R genes against *L. maculans* (Rlm, LepR) have been cloned. LepR3 and Rlm2 are receptor like proteins (RLP) and Rlm4, RLm7 and Rlm9 are wall associated kinase like (WAKL) type class of R proteins. The corresponding effector (Avr) genes against these R genes have also been cloned. Knowledge of *B. napus* R and *L. maculans* avr genes has promoted the *B. napus-L. maculans* as an advanced pathosystem to study the molecular recognition of apoplastic fungal pathogens. We have applied point mutation and domain shuffling to better understand the function of *B. napus* WAKLs against *L. maculans*. In addition, sequence comparison of RLm4 and Rlm7 alleles has helped to define the protein motifs likely to be critical for the receptor function of WAKL type R genes. We will also present the research carried out in our lab to determine the virulent function of *L. maculans* effectors and how they are perceived by the corresponding R proteins.

Yeast communities from a Nova Scotia vineyard before and after spontaneous fermentation: a case study

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

Indigenous yeasts on wine grapes are metabolically active during fermentation and influence the flavour and aroma of wines, most evidently in wines produced by spontaneous fermentation. The vineyard yeast community composition results from complex interactions among location, natural environment, and growing practices. The composition of vineyard yeast communities in Nova Scotia is not well described, creating opportunities for characterization to inform wine production in the rapidly developing local wine industry. Next-generation sequencing and phylogenetic binning methods were used to determine yeast species present in fresh grape musts from Nova Scotia vineyards, and in corresponding products of spontaneous fermentation. Results from an organically managed vineyard are presented as a case study: several ‘core’ yeasts, notably *Aureobasidium pullulans*, *Vishniacozyma carnescens*, and *Filobasidium* spp. were common on grapes in each of two years, while the non-conventional fermentative yeast *Saccharomyces uvarum* frequently dominated post-fermentation samples instead of the expected *Saccharomyces cerevisiae*.

Evolutionary persistence of DNA methylation for millions of years

Sandra Catania*, Phillip A. Dumesic, Harold Pimentel, Ammar Nasif, Caitlin I. Stoddard, Jordan E. Burke, Jolene K. Diedrich, Sophie Cooke, Terrance Shea, Elizabeth Gienger, Robert Lintner, John R. Yates III, Petra Hajkova, Geeta J. Narlikar, Christina A. Cuomo, Jonathan K. Pritchard and Hiten D. Madhani
University of California San Francisco

Cytosine methylation of DNA is a widespread modification of DNA that plays numerous critical roles. In the yeast *Cryptococcus neoformans*, CG methylation occurs in transposon-rich repeats and requires the DNA methyltransferase Dnmt5. We show that Dnmt5 displays exquisite maintenance-type specificity in vitro and in vivo and utilizes similar in vivo cofactors as the metazoan maintenance methylase Dnmt1. Remarkably, phylogenetic and functional analysis revealed that the ancestral species lost the gene for a de novo methylase, DnmtX, between 50– 150 mya. We examined how methylation has persisted since the ancient loss of DnmtX. Experimental and comparative studies reveal efficient replication of methylation patterns in *C. neoformans*, rare stochastic methylation loss and gain events, and the action of natural selection. We propose that an epigenome has been propagated for >50 million years through a process analogous to Darwinian evolution of the genome.

Transition from nongenetic to genetic antifungal resistance: Insights from mathematical models, genetically engineered yeasts, and pathogenic fungi

Daniel Charlebois
University of Alberta

Antimicrobial resistance is an emerging healthcare crisis that poses serious socioeconomic threats across the globe. New strains of pathogenic fungi, such as *Candida auris*, are particularly concerning as they display resistance to multiple classes of antifungal drugs. Recently, novel forms antimicrobial resistance have been uncovered, including nongenetic resistance which occurs among genetically identical cells exposed to the same drug environment. However, it is unknown how nongenetic resistance affects the evolution of genetic resistance. Using a mathematical model that incorporates nongenetic and genetic forms of drug resistance, as well as resource competition between subpopulations, we find that nongenetic resistance can enhance survival while at the same time hinder the evolution of genetic resistance. We are experimentally investigating these findings using genetically engineered and pathogenic yeasts. This research aims to advance our fundamental understanding of antimicrobial resistance and identify new therapeutic approaches to improve the outcome for patients with drug-resistant infections.

Complexity of managing pea root rot caused by a complex of fungal and oomycete soilborne pathogens

Syama Chatterton, Kyle Biscaglia-Horvath, Sijan Pandit, Christine Vucurevich
Agriculture and Agri-Food Canada

Root rot of pea and lentil exploded on to the prairie agriculture landscape in 2012 – 2013 after a number of repeated wet growing seasons. The oomycete pathogen *Aphanomyces euteiches* was implicated for the first time in pea and lentil root rot in Alberta and Saskatchewan. Subsequent surveys from 2014 – 2017 revealed that this emerging pathogen was already widespread across the prairies. Fusarium species were also frequently isolated from diseased pea roots, with Fusarium avenaceum and *Fusarium redolens*, relative newcomers to the pea and lentil root microflora, the predominant fungi in most years. Greenhouse studies on the interactions between these three pathogens reveal why this complex is so difficult to manage. The pathogens interact synergistically but optimal root infection and colonization for each occurs under contrasting soil moisture conditions. The pea and lentil root rot complex is threatening sustainable pea and lentil production due to the difficulty in finding management options.

Selenoprotein production in insect-gut fungi

Shalini Chaudhary, Yibing Wu, Yan Wang
University of Toronto

Harpellales fungi (Zoopagomycota) inhabit the gut of larvae or nymphs of several aquatic insects. These fungi are globally distributed and have persisted for over 200 million years, yet the molecular basis of their symbiosis is poorly understood. Recently, selenoprotein coding genes were identified in nine fungal genomes, seven of which are Harpellales. Selenoproteins contain selenocysteine, a rare amino acid containing selenium which is incorporated by recoding the canonical UGA stop codon with additional translation machinery. The function and evolution of these proteins within the Harpellales are currently unknown. Here, I will report on our research progress using transcriptomics, phylogenetics, and protein structure prediction methods to demystify the characteristics of selenoproteins in Harpellales. I will also present our ongoing work on codon optimization diversification of the selenoprotein coding genes. Overall, this study will improve our understanding of selenoprotein evolution, and will provide insights into their involvement in this unique insect-related symbiosis.

Carotenoid production and pigment reinitiation in *Exophiala dermatitidis* albino mutants under different media and carbon sources.

Chhoker, Kamaldeep.* Harris, Steven.
University of Manitoba

Exophiala dermatitidis has been known to produce melanin via the Polyketide Synthase pathway. By using UV irradiation *E. dermatitidis* albino mutants lacking the ability to produce melanin were obtained. SNPs analysis has shown that these albino mutants have a SNV in the polyketide synthase pathway causing the loss of melanin production. Albino mutants were able to produce carotenoids (turn pink) and some were also able to reinitiate melanin production on different carbon sources. This study aims to figure out which other pathways might be responsible for melanin production in albino mutants which had SNVs in the polyketide synthase pathway and lost their ability to produce melanin. The study will also focus on carotenoid production and aim to link the SNVs responsible for carotenoids in *E. dermatitidis*.

The genetics and genome biology of arbuscular mycorrhizal fungi

Nicolas Corradi
University of Ottawa

The genetics of arbuscular mycorrhizal fungi (AMF) have been notoriously difficult to assess due to their perpetual multinucleated state, obligate plant biotrophy, and lack of observable sexual reproduction. Here, I will present recent collaborative work that combines AMF genomics, single nucleus analysis and chromatin conformation capture, and discuss how recent findings have reshaped our understanding of AMF genetics and sexual potential and uncovered intricate genetic interactions between these fungi and their plant hosts.

The threat of parallel emergence of fungicide resistance in agriculture

Daniel Croll
University of Neuchatel

In a worrisome parallel, the rise of antibiotic or antifungal resistance threatens both human health and agricultural production. The environmental homogeneity in agricultural ecosystems is thought to impose strong selection pressures to gain resistance. However, by what mechanism crop pathogens gain resistance and how geography plays a role remain largely unknown. Using a conjunction of global population genome sequencing efforts, experimental work and association mapping, we aim to understand how crop pathogens gain resistance to antifungals. We show that azole resistance in agriculture was gained repeatedly and independently across the world. We find though that fungicide resistance evolution is likely constrained by pleiotropic effects and discuss how such trade-offs could open the way to more sustainable agricultural management practices.

Connecting epigenetics to gene and transposon territories of *Rhizophagus irregularis*

Alexandra Dallaire, Bethan F. Manley, Iliana Bista, Clément Quan, Edouard Evangelisti, Charles R. Bradshaw, Navin Ramakrishna, Sebastian Schornack, Uta Paszkowski & Eric A. Miska
Royal Botanic Gardens Kew, Gurdon Institute, Sanger Tree of Life

Arbuscular mycorrhizal fungi (AMF) are soil-dwelling fungi that form obligate nutritional symbioses with most land plants. The lack of observable sexual reproduction in AMF has long called into question the mechanisms underlying their adaptation, evolution and outstanding ecological success. Here, I will discuss how DNA methylation and small RNA-mediated silencing may balance the expression of transposable elements (TEs) and their neighbouring genes, and how this may generate phenotypic plasticity and genomic heterogeneity.

The changing epidemiology of *Histoplasma capsulatum* in North America

Tanis Dingle
Alberta Precision Laboratories - Public Health Lab

Histoplasma capsulatum is a dimorphic fungal pathogen causing systemic infections in both immunocompetent and immunocompromised human hosts. Traditionally the geographic range of Histoplasma capsulatum has been restricted to the Ohio and Mississippi river valleys extending North into Southern Ontario and Quebec. Recent evidence suggests that the geographic range of *Histoplasma capsulatum* is expanding. In this presentation, the changing epidemiology of *Histoplasma capsulatum* will be examined including presentation of genomic evidence confirming local acquisition in Alberta, Canada. Factors impacting the organism's geographic range including climate change among others will also be discussed.

Lichenicolous fungi of Atlantic Canada: what we’ve learned, and what we still don’t know

Kendra Driscoll
New Brunswick Museum

Lichenicolous fungi (LFs) are often overlooked and consequently underreported. A checklist of the species occurring in Atlantic Canada has long been in preparation, using field collections, literature review and examination of herbarium specimens to help close the knowledge gap and create an identification resource to facilitate further work on this group. Approximately 235 species have been documented so far but the ongoing discovery of species new to the region or even new to science indicates that the actual species diversity is higher than this. Further, the geographic distribution of most known LFs in the region remains poorly understood and there is insufficient data to investigate the possibility of specialized habitat or climatic requirements. These fungi are surely not immune to the pressures driving the global biodiversity crisis, but it remains difficult to assess or attempt to mitigate threats to their conservation.

Identifying the Squamatic Acid Biosynthetic Gene Cluster in Lichen *Cladonia uncialis*

Egbert, Susan* Hoffman, Jordan. Gunawardana, Duleeka. Lendemer, James. Piercey-Normore, Michele. Sorensen, John
University of Manitoba

Lichens are chemically understudied super-organisms composed of mycobionts, photobionts, and other microbial symbionts. Due to the naturally slow growth of lichens, it has been difficult to culture the mycobiont in laboratory conditions and to find host organisms for the heterologous expression of biosynthetic genes. Here we identify the BCG for squamatic acid produced in the thorn lichen, *Cladonia uncialis*. We examined the genomic data of *C. uncialis* and used annotation tools, such as antiSMASH, to identify potential squamatic acid BGCs: polyketide synthase (PKS), O-methyltransferase (OMT), and cytochrome P450(CYP450). This study proposes the final steps of squamatic acid biosynthesis including the OMT and thioesterase (TE) domain. Subsequent LC-MS/MS analysis was performed to detect and quantify squamatic acid in specimens of *C. uncialis*. This study demonstrates the proposed mechanisms for the final steps of squamatic acid biosynthesis and further elaborates on lichen secondary metabolite production and selection of heterologous hosts.

Fungal volatiles as mediators of interspecific interactions with bark beetles

Nadir Erbilgin
University of Alberta

Mountain pine beetles vector several different species of fungi. These fungi play critical roles during bark beetle host colonization including detoxifying and metabolizing toxic host terpenes, improving the host substrate quality for developing beetle larvae. We have been conducting research to shed additional light on the mutualistic fungi-bark beetle interactions and found that: (1) fungi use carbons released from the degradation process for its growth as a food source; (2) different fungal species have similar fungal volatile organic compound (FVOC) profiles; (3) FVOCs act as carbon sources and semiochemicals to mediate interspecific interactions among bark beetle-fungal symbionts; (4) fungi produce volatiles that can be attractive or inhibitive to bark beetles; (5) fungi are capable of utilizing bark beetle pheromone as nutrient source; (6) host defense metabolites affect host suitability to bark beetles through influencing their fungal symbionts and that different species of fungal symbionts respond differently to host defense metabolites.

Identification and characterization of molecules with novel antifungal activity against the fungal pathogen *Candida albicans*

Fallah, Sara*; Robbins, Nicole; Cowen, Leah
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Fungal pathogens cause life-threatening infectious diseases. Infection with *Candida albicans*, a prevalent human fungal pathogen, has a ~40% mortality rate despite treatment. Only three classes of antifungal drugs treat systemic infections - azoles, polyenes, and most recently echinocandins. Unfortunately, echinocandin efficacy against *C. albicans* is hindered by resistance development. Leveraging the Boston University Centre for Molecular Discovery's chemical library, I screened 3,936 chemically-diverse compounds, identifying 31 single-agents and 35 echinocandin-potentiating molecules that inhibited *C. albicans* growth. Future work will leverage genetic and biochemical approaches to elucidate their mode of action. Furthermore, a Broad Institute Diversity Oriented Synthesis library screen identified three compounds with broad-spectrum antifungal activity and limited human toxicity. My work suggests one compound targets ergosterol biosynthesis, one compound inhibits translation, and the mode of action of the third compound remains elusive. Overall, my research identifies compounds with novel antifungal activity that display therapeutic potential for future drug development.

Assessing genes important for hyphal morphogenesis in the fungal pathogen *C. albicans*

Farheen, Aiman*; Case, Nicola; Robbins, Nicole; Cowen, Leah
University of Toronto

Infectious fungal diseases impose a severe burden on human health. *Candida albicans* is a leading human fungal pathogen with ~40% mortality rate. A key *C. albicans* virulence trait is its capacity to transition from a yeast to filamentous form. While the circuitry governing this transition has been studied, a comprehensive understanding of genes important for this process remains elusive. My aim is to identify genes important for hyphal morphogenesis in host-relevant conditions. For this, I leveraged the GRACE collection, which consists of 3,351 heterozygous deletion mutants where the remaining allele is under the control of a doxycycline-repressible promoter. This analysis identified 368 mutants that were blocked in filamentation in RPMI supplemented with serum and incubated at 37°C with CO2. Future work will characterize the mechanism(s) by which novel morphogenetic regulators govern this virulence trait. These results will advance our understanding of the genes involved in *C. albicans* morphogenesis and virulence.

Differential requirements for Ire1 during ER stress in *Saccharomyces cerevisiae*

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Antifungal drug resistance is increasingly becoming a larger cause for mortality, especially in immunocompromised individuals. In yeast, the Unfolded Protein Response (UPR) functions to restore proteostasis of secretory proteins in the Endoplasmic Reticulum (ER) through the activation of the ER stress sensor Ire1. The Ire1 can be activated both by accumulation of misfolded proteins in the ER lumen, and ER lipid bilayer stress. This triggers the extranuclear splicing of Hac1 which leads to the UPR transcription response to restore the ER folding environment, lipid homeostasis and more. However, the mechanisms of UPR activation and genes responsible for yeast resistance from exposure to common antifungals, like azoles remains unknown. Interestingly, we found that deletion of the Ire1 gene, sensitizes cells to azole treatment, yet Hac1 splicing was absent. Using growth assays, fluorescent microscopy, and qPCR, we are seeking to characterize the importance of Ire1 in the antifungal response in *Saccharomyces cerevisiae*.

Genome size and complexity of fungal pathogens depend on their lifestyle

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Laval University

The conservation of genomic changes across fungal pathogens and the dependency of genome evolution on fungal lifestyles are only beginning to be explored. Here, we investigate genome assemblies of nearly 600 ascomycete species (class Sordariomycetes) and their genomic traits using phylogenetic and machine learning methods to understand the role of pathogenic and symbiotic lifestyles of the fungi in shaping their genome size and complexity. We find that genes, repeat content, and intergenic lengths are all strong predictors of genome size, indicating that both adaptation and drift affect genome size. While most plant pathogens expand their gene repertoire, fungal groups associated with insect species lose their genome content. Interestingly, we find that plant pathogens, which rely on insect associations for transmission between the hosts, exhibit a loss of genes related to secondary metabolism or defense mechanisms, suggesting that insect vectors take responsibility for the production of the host-entrance proteins. Fungal pathogens' genomes follow distinct evolutionary paths, and our study shows that there is no single "recipe" for becoming a successful pathogen.

Yeast *Candida krusei* and its affinity for the cranberry juice processing environment

Sherazade Fikri, Marie-Hélène Lessard, Véronique Perreault, Alain Doyen, Steve Labrie
Laval University

Canada is the second-largest producer of cranberries, which are mostly transformed in juice or in its dried form. The cranberry juice process involves clarification (ultrafiltration) and concentration (reverse-osmosis) steps using membrane processes which are known to be sensitive to biological clogging, a phenomenon that has never been studied for cranberry juice processing. The microbial profile of industrially used membranes was established leading to the isolation of several strains from the dominant microflora. Yeasts of the *Candida krusei* species were found to be dominant and were further characterized using an MLST genotyping approach. The potential impact on juice compounds was assessed through fermentation assays. The content in polyphenols, proanthocyanins, anthocyanins, organic acids, and the identification of the major compounds of the aroma profiles was performed. This project addresses the impact of biological clogging on cranberry juice quality and will help to define the actions needed to reduce its contamination.

Creating a *Candida albicans* genome-wide CRISPR interference library for large-scale genetic analysis

Fogal, Meea*; Wensing, Lauren; Gervais, Nicholas; Shapiro, Rebecca
University of Guelph

Candida albicans is an opportunistic fungal pathogen and commensal member of the human microbiota. Infections caused by *C. albicans* can be severe and life-threatening. Treating *C. albicans i*nfections is notoriously challenging due to limited availability of safe and efficacious antifungal drugs, along with the recent emergence of drug-resistant *C. albicans* strains. Thus, it is imperative that we study this pathogen to better understand the fundamental molecular mechanisms that underpin antifungal drug resistance. We propose using a transcriptional repression system, known as CRISPR interference (CRISPRi), to do this. We aim to generate a pooled CRISPRi repression library representing all ~6,100 genes in the *C. albicans* genome. We will screen this pooled genome-wide library in the presence of antifungal drugs to identify genes that, when repressed, influence antifungal drug susceptibility. This research will help to deepen our understanding of how *C. albicans* develops resistance to antifungals and fungal biology altogether.

Population analysis and genome variations revealed by comparing haplophased chromosome-level genomes in isolates of the wheat leaf rust fungus, *Puccinia triticina*

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University of British Columbia

P. triticina (Pt) is an obligate pathogen of wheat of major agricultural significance and in North-America, propagates as dikaryotic urediniospores mainly clonally along various genetic lineages, evolving virulence factors (effectors) due to ever-changing selection pressures arising from monocultures of resistant cultivars. Complete genomes are critical for pan-genome and effector compendium generation to assess allele presence and frequencies. We recently designed a haplotype-aware de novo genome assembly pipeline to generate chromosome-level genome sequences for each of the two highly dissimilar haploid nuclei in Pt isolates. We generated five more nucleus-specific genomes and improved the re-assembly of two previously published genomes, to assess structural genomic features. We find NUMTs, insertions, inversions, and deletions (some of which harbor effector genes). We can now assess over 200 isolate collections from NA, partially sequenced by Illumina. Data will be presented on gene annotations, variation in a select effector subgroup, and haplotype-specific differential gene expression.

Using Norwegian kveik to generate novel hybrid ale yeast with strong fermentative capabilities and stress tolerant properties

Barret Foster, Hollie Rowlands, Caroline Tyrawa, George van der Merwe
University of Guelph

We have recently identified and characterized a group of genetically distinct *Saccharomyces cerevisiae* ale yeast, called kveik, from Western Norway, which possess impressive fermentation characteristics and stress tolerances due to centuries of isolation and unique brewing practices. This domestication has selected for characteristics highly sought after in the fermentation industry including high flocculence, desiccation tolerance, thermotolerance, rapid sugar consumption and a resilience to high ethanol concentrations. In contrast, commonly used industrial ale yeast have a narrow range of optimal fermentation conditions and can be susceptible to various stresses like heat and osmotic pressure. We have successfully used Norwegian kveik in breeding trials to generate a variety of hybrid strains with novel fermentation applications. Preliminary fermentations and stress tolerance assays have demonstrated that these hybrids are capable of efficiently fermenting wort at a range of sugar concentrations and temperatures whilst possessing stronger stress tolerances than their industrial parents.

A new family of structurally conserved fungal effectors displays epistatic interactions with plant resistance proteins

Noureddine Lazar, Carl H. Mesarich, Yohann Petit-Houdenot, Nacera Talbi, Ines Li de la Sierra-Gallay, Emilie Zélie, Karine Blondeau, Jérome Gracy, Bénédicte Ollivier, Françoise Blaise, Thierry Rouxel, Marie-Hélène Balesdent, Alexander Idnurm, Herman van Tilbeurgh, and Isabellle Fudal*
Institut national de la recherche agronomique

Leptosphaeria maculans, causal agent of oilseed rape stem canker, is one of the few fungal pathogens where suppression of resistance-mediated recognition by an avirulence (AVR) effector has been demonstrated. Indeed, AvrLm4-7 suppresses Rlm3- and Rlm9-mediated resistance triggered by AvrLm3 and AvrLm5-9, respectively. To decipher the epistatic interaction between these L. maculans AVR effectors, we determined the crystal structure of AvrLm5-9 and obtained a 3D model of AvrLm3, based on the crystal structure of Ecp11-1, an AVR effector from Fulvia fulva. Despite a lack of sequence similarity, AvrLm5-9 and AvrLm3 are structural analogues of AvrLm4-7. Structure-informed sequence database searches identified a larger number of putative structural analogues among *L. maculans* effectors, including the avirulence effector AvrLmS-Lep2, as well as among effectors from other phytopathogenic fungi. Remarkably, transformants of *L. maculans* expressing one of these structural analogues, Ecp11-1, triggered oilseed rape immunity in several cultivars carrying Rlm3. Furthermore, this resistance could be suppressed by AvrLm4-7.

Funga and Conservation

Giuliana Furci
Fungi Foundation

Fungi have been overlooked and largely excluded from conservation strategies and environmental laws, although they provide a key to understanding our planet. Recently, thanks to the leadership of the Fungi Foundation, both Re:wild and the Species Survival Commission (SSC) of the International Union for Conservation of Nature (IUCN) announced their commitment to use “mycologically inclusive” language in their internal and public-facing communications (“fauna, flora and funga” and “animals, fungi and plants”) and to incorporate fungi in conservation strategies with rare and endangered plants and animals. The 3F initiative aims to write the Fungi kingdom of life into conservation and agricultural policy frameworks, protect it under international and domestic law, and unlock crucial funding for mycological research, surveys and educational programs.

One Health of Fungal Disease

Liu, Boyan; Ball, Brianna; Woods, Michael; Muselius, Ben; Buchanan, Reid; Woolnough, Kerry; Gutierrez Gongora, Davier; Geddes-McAlister, J.*
University of Guelph

Fungal diseases greatly impact the world around us, including our environment, food system, and health. Beginning with the food we eat, the application of fungicides to protect cereal crops from devastating fungal diseases can lead to resistance within plant pathogens. Additionally, fungicidal applications can also cause resistance within environmental pathogens, which are transmitted to humans, causing devastating disease. Our research program integrates these global challenges and leverages our diverse expertise in mass spectrometry-based proteomics and advanced bioinformatics, combined with plant biology, microbiology, immunology, biochemistry, and drug design to investigate critical interactions between the pathogen and host that drive disease progression. For example, Fusarium head blight (FHB), a globally-impactful fungal disease of cereal crops that reduces grain quality and yield through contamination with mycotoxins is often averted with the application of fungicides (e.g., azoles). However, such strategies expose environmental microbes, including the human fungal pathogen, *Cryptococcus neoformans*, to low levels of fungicide, which promotes the evolution of resistance, leading to untreatable disease. To date, we have performed extensive proteomic profiling of FHB in wheat to identify plant proteins promoting resistance to fungal infection, and fungal proteins designated as novel virulence factors and targets for inhibition. Additionally, we defined the impact of mycotoxin on the wheat host and identified host proteins associated with mycotoxin degradation for improved plant survival. For cryptococcosis, we have identified proteins critical for antifungal resistance and through small molecule inhibition studies demonstrate a reversal of resistance. Further, we have identified interactions between the host and pathogen that drive disease and suggest opportunities for inhibition and treatment. Taken together, our One Health approach bridges together environmental, animal, and human health to uncover new prevention and treatment strategies against medically- and agriculturally-relevant diseases to improve global health and food security.

Protein translation is compromised in the Bowen-Conradi ribosomopathy

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Bowen-Conradi Syndrome (BCS) is a ribosome assembly disorder, or ribosomopathy, exclusively found in the Hutterite population. BCS presents with severe developmental delay and a failure to thrive. BCS is due to a D86G variant in the Emg1 protein, required for ribosome assembly and for methylation of an 18S rRNA pseudouridine in the decoding P-site of the ribosomal small subunit. This residue is "hypermodified" and critical to translational fidelity. Here, we investigate suspected translation defects in BCS. Using a yeast BCS model system of the disorder, we probed the molecular consequences of BCS on translation using puromycin. This revealed a decrease in translational capacity and a likely change in translational preferences. Ongoing experimentation using dual luciferase translation reporters will further characterize the translational defect, which we expect includes a decrease in translational fidelity due to the location of Emg1's target residue in the decoding P-site and likely changes to the proteome.

Candida population diversity in recurrent vulvovaginal candidiasis

Aleeza Gerstein, Rebekah Kukurudz, Abdul-Rahman Adamu Bukari, Debin Habon, Beamlak Manyaz
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Vulvovaginal candidiasis (colloquially 'yeast infection') is one of the most common medical conditions affecting women of reproductive age. They usually responds well to treatment, yet a small but significant fraction of females experience recurrent yeast infections. Recurrent infection cycles could be due to two non-exclusive scenarios: (1) relapse due to incomplete vaginal eradication of yeast, or (2) vaginal eradication followed by re-infection from a reservoir elsewhere in the body. We acquired vaginal and rectal swabs from two women that suffer from recurrent infection, one with a *Candida albicans* infection and one with *Candida krusei*. We isolated a large number of colonies from each swab to examine diversity. We found considerable variation among isolates, yet no significant difference in the growth of vaginal and rectal isolates in vaginal stimulating medium or in fluconazole or boric acid resistance or tolerance. By contrast, vaginal isolates were more likely to exhibit invasive growth. Whole- genome sequencing revealed that *C. albicans* vaginal and rectal isolates are extremely closely related, suggestive of vaginal reinfection from another body site.

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

Nicholas C. Gervais, Victoria Acquaviva, Alyssa A. La Bella, Madison Best, Lauren Wensing, Meea Fogal, Alejandro Chavez, Felipe Santiago-Tirado, Ana Flores Mireles, Rebecca S. Shapiro
University of Guelph

Candida albicans is an opportunistic fungal pathogen that can lead to fatal invasive infections in immunocompromised individuals. The current treatment options for *C. albicans* infections are limited and drug-tolerant strains are becoming more prevalent. Given this, there is a pressing need to dissect the mechanisms by which *C. albicans* responds and evolves tolerance to antifungal drugs. It has been shown that a trisomy of chromosome R (CR) in *C. albicans* results in increased tolerance to certain antifungal drugs, suggesting that the overexpression of one or more genes on CR is involved. Better characterization of chromosome R through genetic manipulation will therefore promote our understanding of the molecular mechanisms mediating the acquisition of drug tolerance. Here, we propose the development of a novel CRISPR-based overexpression library that will target chromosome R in *C. albicans* and allow genes and fundamental genetic mechanisms relating to antifungal drug tolerance to be discovered.

Multiple convergent evolution events of recombination suppression in fungal mating-type chromosomes

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Convergent adaptation provides unique insights into the predictability of evolution and ultimately into processes of biological diversification. Supergenes (beneficial gene linkage) are striking examples of adaptation, but little is known about their prevalence or evolution. Basidiomycete fungi repeatedly evolved supergenes by rearrangements and recombination suppression linking two their mating-type loci. Such convergent transitions in the genomic architecture of mating-type determination indicate strong selection favoring linkage of mating-type loci into cosegregating supergenes, thus increasing the odds of gamete compatibility under selfing. Multiple ascomycetes also evolved recombination suppression around their mating-type locus. In addition, independent evolutionary strata (stepwise recombination suppression) also evolved repeatedly, with extensive rearrangements, gene losses, and transposable element accumulation. This shows that natural selection can repeatedly lead to similar genomic patterns and phenotypes, and that different evolutionary paths can lead to distinct yet equally beneficial responses to selection through different genomic changes.

Effect of pH and Temperature on Usnic Acid Production and Polyketide Synthase Gene (MPAS, MPAO) Expression in *Cladonia uncialis*

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The production of secondary metabolites in the lichen-forming fungal partner is genetically inherited but regulated to some extent by environmental variables. The objective of this study was to compare Polyketide synthase (PKS) gene expression (MPAS and MPAO) and the amount of usnic acid production in *Cladonia uncialis* lichen thallus under different temperature and pH levels. Thalli were incubated in each of two temperatures (15 °C, 22 °C), and three pH levels (4.0, 6.0, 8.0) under artificial light conditions (12 hours/day-1, 326 µmol m-2 s-1). Samples for qRT-PCR and LC-MS/MS were collected from each thallus bi-weekly for ten weeks. The results showed that MPAS and MPAO gene expression level and usnic acid production are affected by pH levels but temperature had variable effects. MPAS and MPAO expression was high in the second week in all the treatments, while usnic acid production was high in the eighth week of the experiment.

Genetic interaction analysis conducted in *Candida albicans* stress response genes through the use of CRISPR-Cas9-based gene drive array

Viola Halder*, Brianna McDonnell, Anjali Krishna, Brooke Rathie and Dr. Rebecca Shapiro
University of Guelph

Candida albicans are an opportunistic fungal pathogen found in the oral mucosa, the gut, the vaginal mucosa, and humans' skin. *C. albicans* may cause superficial to severe invasive and systemic infections, depending on the status of an individual's immune system. Understanding the survival mechanisms and pathogenesis of *C. albicans* is critical for novel antifungal drug discovery. A genetic approach using the CRISPR-Cas9-based genome editing platform will target *C. albicans* stress response genes for the purposes of genetic interaction analysis. The ultimate goal is to create a deletion library of single and double stress response gene mutants to study their role in pathogen survival. This library was screened under diverse stress conditions to assess their relative fitness in terms of growth. Genetic interaction analysis was conducted to map out epistatic interactions between fungal genes involved in growth, survival, and pathogenesis based on negative or synthetic lethal genetic interactions.

Life Lessons from Lichen

Diane Haughland
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In 2005, lichens made the list - they were chosen as one of the six broad suites of species monitored by the Alberta Biodiversity Monitoring Institute. Seventeen years, 1,025 sites, and >250,000 specimens later – what are we doing with all those lichens? While understanding the distribution, relative abundance and sensitivity of our lichen flora are amongst our primary goals, we're moving far beyond maps – we are learning from those collections, and not all of the lessons are easy. From making hay when the sun shines, to learning you can't please everyone all the time, I will share our top life lessons from lichen. Along the way, I will highlight the trait-based analyses, urban monitoring, art collaborations, DNA barcoding, new species discovery, genotype-by-sequencing, contaminants deposition studies, and ecological collaborations that are hopefully helping us learn from and honor this unique, priceless collection.

Hybridization drives mitochondrial genome instability and metabolic shift in a species with biparental mitochondrial inheritance

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While mitochondrial DNA (mtDNA) is transmitted in a uniparental manner in most species, biparental mtDNA inheritance and heteroplasmy are increasingly reported. MtDNA instability and heteroplasmy have important implications for mitochondrial genetic disorders, genome evolution and speciation. However, the factors driving mtDNA instability and heteroplasmy resolution remain largely unknown. Here, we investigate these questions using the wild yeast *Saccharomyces paradoxus*, a fungal species with constitutive biparental mtDNA inheritance. We previously performed a large-scale neutral evolution experiment on 11 different hybrid crosses among natural lineages of *S. paradoxus* and its sister species *Saccharomyces cerevisiae*. Whole-genome sequencing revealed that mtDNA recombination rates were not predicted by parental divergence and were genotype-specific. However, we found a strong positive relationship between parental divergence and the rate of large-scale mtDNA deletions, which lead to the loss of respiratory metabolism. Our results show that evolutionary divergence in hybrids can predict major aspects of neutral mtDNA evolution.

The virulence of *Plasmodiophora brassicae* on canola with 'second-generation' clubroot resistance

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Clubroot, caused by *Plasmodiophora brassicae,* is a damaging soil-borne disease of canola (*Brassica napus*) in Canada. Clubroot-resistant (CR) cultivars carrying 'first-generation' resistance were introduced in 2009-10. New pathotypes of *P. brassicae* have emerged that can overcome first-generation resistance, requiring the development of new cultivars with 'second-generation' resistance. The nature of this resistance is not in the public domain and may differ among cultivars. Isolations of the pathogen were made from symptomatic second-generation CR canola crops identified in the field and tested for their virulence on a suite of seven commercial canola cultivars carrying second-generation resistance. These cultivars were also tested with selected P. brassicae pathotypes that break first-generation resistance. Preliminary results indicate about half of these cultivars developed moderate to severe levels of clubroot when challenged with pathotypes that can overcome first-generation resistance. This suggests that resistance-breaking isolates of *P. brassicae* may be difficult to control solely with resistant hosts.

Identification of yeasts with high glycolytic flux for the development of novel cell factories

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Yeasts exhibit diverse metabolic strategies, which provide conditional fitness advantages over competitors through rapid uptake of limited resources or production of antimicrobial compounds. Humankind has harnessed this by using yeasts for bioproduction of ethanol, lipids, and recombinant proteins. To identify novel yeast species with the potential to be used as bioproduction platforms, we developed a colorimetric assay to measure the glucose-induced extracellular acidification rates (ECAR) as an indication of glycolytic flux. ECAR was determined for over 300 budding yeast species using Saccharomyces cerevisiae as a high ECAR control. We identified poorly characterized species with high ECAR outside of the Saccharomycetaceae including several species of the genus *Saturnispora*. These species were subsequently confirmed to consume glucose rapidly and produce both ethanol and lipid droplets under Standard Talk growth conditions. Since they have a natural propensity to make these products of industrial interest, they are strong candidates to develop as microbial cell factories.

Functional genomic screens of protein kinases in *Candida albicans* reveal novel roles of orf19.3751 and IRE1 in morphogenesis

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The capacity to transition between yeast and filaments is a major virulence trait in the human fungal pathogen, *Candida albicans*. We have performed a comprehensive analysis of the *C. albicans* kinome to identify genes for which overexpression or depletion alters cellular morphology. We identified a novel role for the putative serine/threonine kinase orf19.3751, as a negative regulator of filamentation. Deletion of orf19.3751 resulted in aberrant nuclear content suggesting orf19.3751 is involved in cell cycle regulation. We also uncovered a novel role for the kinase Ire1, whereby overexpression of IRE1 inhibits wrinkly colony morphology on solid Spider medium while depletion of IRE1 impairs morphogenesis in liquid filamentation medium. Follow-up investigations uncovered IRE1 levels modulate *C. albicans* morphology through Hac1-dependent and -independent pathways. Overall, this work will advance our understanding of protein kinases in regulating a key virulence trait in *C. albicans*.

Pollen-parasitic fungi: an overlooked trophic interaction?

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Pollen parasitism has been documented in a few fungal groups but they have been little studied, with the exception of a few studies from Africa and Europe. In the present contribution, we report the presence of a fungus of the class Orbiliomycetes, putatively related to the genus Retiarius, commonly associated with pollen deposits on the undersurface of lichens in North America. To study this phenomenon, we used different microscopy techniques and developed molecular screening to assess the frequency of its occurrence. However, its phylogenetic identity remains to be clarified, as well as any possible role it may play in nutrient cycling.

Cytospora spp. associated with canker disease of spruce in Ontario, Canada.

Ilyukhin, Evgeny*

The spruce canker is a widespread disease in North America. Common symptoms include browning of needles, branch dieback, cankers. The disease emergence and development are often caused by abiotic factors (e.g. drought). *Valsa (Cytospora) kunzei* was found to be a causative agent of the disease. However, the species identification was performed using morphological characteristics only. Besides, pathogenicity tests were not conducted for this species on corresponding tree hosts. The main objective of this study was to properly identify fungal species causing the disease. Another goal was to evaluate pathogenicity of the species using pathogenicity assays and comparative genomics approach. *Cytospora pinastri* and *Cytospora parapiceae* sp. nov. were isolated from affected trees. The species identification was confirmed based on morphology and phylogenetic analysis. Both species caused necrotic lesions on Picea spp. Comparative genomics analysis revealed their necrotrophic lifestyle and capability to be pathogenic to related tree hosts.

Efficacy of Topical Probiotics to Mitigate White Nose Syndrome in Western Canadian Bat Populations

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McMaster University

The fungus *Pseudogymnoascus destructans* (Pd) is the causative agent of white-nose syndrome that has caused the death of millions of bats across North America. Our research team has developed a topical probiotic cocktail composed of four Pd-antagonistic Pseudomonads. Here we report the distributions of these probiotics after their applications to bat roosts. Probiotics can be detected from roost swabs after 6 months of inoculation by qPCR, consistent with their persistence in roosts. Interestingly, we were able to detect probiotics on bat wings over hibernation period. Metagenome analyses of the bat wing microbiomes revealed slight decreases in microbial diversity after probiotic application, but the evenness remain unchanged. The 16S rRNA amplicon dataset are mostly dominated by three bacterial families: Rhodobacteraceae, Pseudomonadaceae, and Enterobacteriaceae. We are now developing the technique to detect probiotic viability by using propidium monoazide (PMA) combined with real time detecting system. Moreover, we hope to gain a better understanding of how microbiomes differ in a colony throughout the year as bats move to different roosts, and different colonies.

Comparison of *Plasmodiophora brassicae* pathotypes in Canada and Poland

Noor Ramzi, Joanna Kaczmarek, Małgorzata Jędryczka*
Polish Academy of Sciences

Plasmodiophora brassicae is the cause of clubroot, a damaging disease of Brassicaceae crops worldwide. The spores of the pathogen are very persistent and hard to eradicate from soils. One of the most efficient methods to combat the pathogen is to grow resistant cultivars. The resistance is pathotype specific. The cultivars resistant to the current population of the pathogen should be grown. The pathotyping of 10 isolates from different locations in Poland was done using 4 well known pathotyping systems, including the most recent one elaborated in Canada. Eight out of 10 isolates were new to the Canadian system. The comparison of the Polish and Canadian populations of *P. brassicae* showed substantial differences what indicates that breeding for resistance done in Europe and Canada shall be carefully designed and take into consideration the number, type and spread of pathotypes across fields used for local and regional oilseed rape cultivation.

Come-from-aways? New and familiar fungal phytopathogens in Newfoundland and Labrador

Linda Elizabeth Jewell, Karen Compton, Dena Wiseman
St John's Research and Development Center, NF, AAFC

Newfoundland and Labrador (NL) has long agricultural traditions, but has been understudied by plant pathologists despite its interesting microbial community that has been uniquely influenced by European colonizers and the soil they brought to Canada as ballast on fishing vessels. From small fruits to potatoes, plants with cultural and economic significance face both common and uncommon fungal pathogens in Canada's most easterly province. Recently, we identified a genetically distinct population of Exobasidium sp. as the putative cause of a highly distinctive leaf spot on V*accinium angustifolium* (lowbush blueberry). I will discuss the results of this recent study, as well as the notorious *Synchytrium endobioticum*, causal agent of potato wart and endemic in NL. These very different fungal plant pathogens stand as examples of the under-appreciated importance of the plant-associated fungal community in NL.

Approaches to ectomycorrhiza research: a perspective from 40 years of field- and lab-based studies

Melanie Jones
University of British Columbia

An understanding of a biological system, and the best way to study it, accumulates gradually. In this presentation, I will highlight some insights into the approaches used to study the physiology and ecology of ectomycorrhizal (ECM) associations that have developed over several decades of research. I will discuss experiments with ECM fungi in pure culture, intra- and inter-specific differences in physiology, assembly of ECM fungal communities, and greenhouse versus field experiments. These may be of value to students or others who are in the early stages of studying ectomycorrhizal or other multi-trophic systems.

Biodiversity of chanterelles (***Cantharellus***, ***Craterellus***) and hedgehog mushrooms (***Hydnum***) in New Brunswick

Justo, Alfredo* & Hood, Alexander
New Brunswick Museum

Despite their popularity as edible wild mushrooms, the actual diversity of chanterelles (species of the genera *Cantharellus* and *Craterellus*) and hedgehog mushrooms (*Hydnum*) in New Brunswick is understudied. We lack data about which species occur in the province or what are their distributions, ecology and population trends. The absence of baseline knowledge about fungal diversity is a common problem across North America in general, and mostly stems from (i) the generalized used of European species names for similarly-looking species occurring in North America; and (ii) the need to study fungal diversity by a combination of traditional (morphological, ecological) and molecular (DNA sequencing) approaches. During the 2021 field season 281 collections of the target genera (85 *Cantharellus*, 27 *Craterellus*, 169 *Hydnum*) were made in NB. We will present a preliminary catalog of these genera in the province, based on morphological, ecological and molecular (nrITS, TEF1) data.

Chemistry of symbiosis: Volatiles mediate interactions between conifer bark beetles and their fungal symbionts

Dineshkumar Kandasamy
Lund University

Many insects exhibit symbioses with microbes through signaling compounds, which drive the evolutionary maintenance of mutualistic associations. Bark beetles are associated with a diverse species of symbiotic fungi that are vital for the successful colonization and development in their host trees. We investigated if volatile organic compounds emitted from different fungal symbionts could act as recognition cues for bark beetles. Using the Eurasian spruce bark beetle, Ips typographus and its fungal symbionts, we showed that bark beetles were attracted to beneficial fungi in olfactometer assays but not to commensals and pathogens. Testing fungal compounds on beetle antennae using single sensillum recording revealed that beetles detect many fungal volatiles using specialized olfactory sensory neurons. Finally, we showed that synthetic blend of fungal volatiles attracted bark beetles in olfactometer assays. These findings indicate that fungal volatiles may act as recognition cues for bark beetles to maintain specific interaction with microbial communities.

Leveraging community science platforms and social media to build meaningful mycology collaborations in North America

Matthew Kasson
West Virginia University

In the era of INaturalist and social media, countless people are posting observations and creating content on diverse topics including fungi. Research mycologists have begun to realise the power of these platforms to locate and sample contemporary specimens and build meaningful ties with amateur naturalists and mycophiles. Come learn and discuss new strategies for engaging amateur mycologists with research and forming meaningful collaborations.

Decomposition and recruitment of pine ectomycorrhizae

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Mount Saint Vincent University

Ectomycorrhizae (ECM) and their hyphae may account for up to one-third of forest primary productivity, but their decomposition and recruitment rates are unknown. Sections of humus were excised from pine-forest floors, severing all roots in the spring. Humus sections were replaced immediately and then randomly sampled over time as roots decomposed. Decomposing ECM and ECM regenerating on roots growing into the humus segments were identified by ITS sequencing. Clavulina cinerea ECM decomposed first, and mantles of most other types were degraded by the fall, except for some Cenococcum ECM that remained until the next spring. New ECM were formed by several fungal species in the first fall and second spring, but no new Cenococcum ECM formed during the 10-month experiment. We found that ECM formed by different fungi decompose at different rates and that Cenococcum is slow to decompose and also to recruit, resulting in a very low turnover rate.

Quantifying trade in plant-fungal networks

Toby Kiers
VU Amsterdam

Underground, mycorrhizal fungi form complex networks of filamentous hyphae that connect plant roots. The fungus mobilizes phosphorus and nitrogen, and trades these for host carbon in a market-like exchange. While the ubiquity and importance of underground networks is established, we have no mechanistic understanding of how a fungus evaluates its trade environment. Fungi must integrate a complex array of chemical, physical, and environmental stimuli. It is unknown how this is achieved. By integrating high-throughput imaging and video, nanoprobe-tracking, high-resolution neural network mapping, and ecological manipulations, our lab aims to develop a quantitative and predictive understanding of mycorrhizal trade – a globally ubiquitous partnership fundamental to agricultural and natural ecosystems.

Developing appropriate paradigms for assessing the plant-fungal fossil record

Az Klymiuk
University of Manitoba

The majority of the fossil record of plant-microbial interactions is heavily tilted to permineralized plant assemblages, comparatively rare paleobotanical lagerstätten where plant remains are fossilized in three dimensions at a cellular level of detail. That all permineralized assemblages are in fact wetland assemblages is a critical and as-yet neglected facet in paleoecologial investigation of plant-fungal interactions. Wetland (hydric) soils are biogeochemically hostile environments primarily controlled by microbially-mediated reduction-oxidation (redox) dynamism, affecting bioavailability of key plant nutrients. Redox dynamism is unparalleled in subaerial systems where major ecological hypotheses for plant-fungal interactions have been developed. Despite being biased towards plants living in/near hydric soils, the fossil record of plant-microbe interactions has been consistently interpreted in accordance with models of plant-microbe interaction developed in subaerially-exposed soil systems. Such paleoecological inferences can be better contextualized by studying biogeochemically-appropriate modern analogues for fossil wetland assemblages; these investigations can simultaneously establish frameworks for ecological investigations of contemporary wetlands.

Genetic Diversity and Dispersal of *Aspergillus fumigatus* from Southeastern France

Greg Korfanty, Arshia Kazerouni, Jianping Xu
McMaster University

Aspergillus fumigatus is a globally distributed saprophytic mould and known opportunistic pathogen of humans, affecting over 8,000,000 individuals worldwide. Thus, to better understand the global population structure of *A. fumigatus*, we focused on strains obtained from natural soils within southeastern France. We obtained 69 A. fumigatus isolates from Nice and Hyères and genotyped each at nine microsatellite (STR) loci. Low but significant genetic differentiation was observed between our southern French population and those from other French populations, as well as most populations around the world. Additionally, *A. fumigatus* populations from southeastern France shared many alleles with those among France collected from across Europe, Asia, and the Americas but maintained a unique population structure. Compared to the other French populations, no antifungal resistant strains were obtained. Together, our results suggest that the southeastern France soil population is significantly influenced by *A. fumigatus* populations from both national and global levels.

SWI/SNF and the histone chaperone Rtt106 drive expression of the Pleiotropic Drug Resistance network genes

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University of Aberdeen

The Pleiotropic Drug Resistance (PDR) network is central to the drug response in fungi, and its overactivation is associated with drug resistance. However, gene regulation of the PDR network is not well understood. Here, we show that the histone chaperone Rtt106 and the chromatin remodeller SWI/SNF control expression of the PDR network genes and confer drug resistance. In Saccharomyces cerevisiae, Rtt106 specifically localises to the PDR network gene promoters dependent on transcription factor Pdr3, but not Pdr1, and is essential for Pdr3-mediated basal expression of the PDR network genes, while SWI/SNF is essential both for basal and drug-induced expression. Also in the pathogenic fungus *Candida glabrata*, Rtt106 and SWI/SNF regulate drug-induced PDR gene expression. Consistently, loss of Rtt106 or SWI/SNF sensitises drug-resistant S. cerevisiae mutants and *C. glabrata* to antifungal drugs. Since they cooperatively drive PDR network gene expression, Rtt106 and SWI/SNF represent potential therapeutic targets to combat antifungal resistance.

Investigating the effects of the Blewit Mushroom *Lepista nuda* on the community composition of its soil environment

Kukolj, Katarina.* Thorn, Greg
Western University

This study aims to investigate the effects of the edible Blewit mushroom (*Lepista nuda)* on the community composition of its soil environment in coastal regions of Newfoundland, Canada. Previous studies on Blewits have discovered their antimicrobial properties in the lab, but there have been no field studies to observe how soil and the organisms in it could be changed by growth of Blewit mycelium in the natural environment. Therefore, this study includes sampling soil at various time points from known natural Blewit patches and nearby treatment plots inoculated with Blewit mycelium, in comparison to plots without Blewits. Arthropod, nematode, bacterial and fungal members of the soil community will be identified and their relative abundance determined by DNA extraction and metabarcoding analyses. These results will tell us if potential crop pests and plant pathogens are significantly reduced by growth of Blewit mycelium, essential for understanding their potential in the agricultural industry.

Mini-chromosomes as drivers of genetic diversity and host-adaptation in the blast fungus *Magnaporthe oryzae*

Thorsten Langner, Angus Malmgren, Cristina Barragan, Adeline Harant, Joe Win and Sophien Kamoun
The Sainsbury Lab

Cereal blast is a devastating plant disease and impacts the most common cereal crops, including rice, wheat, and barley. Despite a prevalent lack of sexual recombination in most natural populations, the blast fungus continuously adapts to its host plants which leads to host-jumps and recurrent pandemics. One driver of host-adaptation is rapid genomic changes that lead to gains and losses of effectors. However, the molecular details that enable these genomic changes are not well understood. We established a novel approach to analyse structural variations including mini-chromosomes and associated genes that likely contribute to virulence of the blast fungus. Mini-chromosomes contribute to the genomic diversity by horizontal mini-chromosome transfer and inter-chromosomal recombination leading to isolate-specific genome structures that involve effectors, ultimately enabling rapid adaptation to varying host conditions. We leverage this knowledge to identify novel virulence genes and to identify potential sources of resistance against the blast disease.

Characterizing the role of Ent2 in Candida albicans filamentation

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University of Toronto

To establish infection in humans, fungi must be able to grow at mammalian body temperature, and this requirement is only met by a small subset of species within the fungal kingdom. One such species is *Candida albicans*, a leading human fungal pathogen that can cause life-threatening infections in immunocompromised individuals. A key *C. albicans* virulence trait is the capacity to transition from yeast to filamentous growth states in response to temperatures exceeding 39 ºC. However, the genetic mechanisms through which elevated temperature triggers this developmental switch in *C. albicans* remain largely enigmatic. To explore this, we screened a mutant collection covering ~40% of the *C. albicans* genome and identified 40 genes required for filamentation at 39 ºC. In this work, we describe how a previously uncharacterized gene, orf19.1444, regulates filamentation by inhibiting Rga2, the GTPase activating protein of the central polarity regulator Cdc42.

Grafting extinct branches to the Fungal Tree of Life

Ludovic LeRenard
University of British Columbia

Comparing the morphology of living and fossil fungi offers the opportunity to track the evolution of fungal lineages through time by documenting extinct branches in the Fungal Tree of Life. Since morphological characters preserved in fossils are seldom studied in extant taxa, fungal characters are difficult to score and interpret. Making use of the increased resolution of molecular phylogenies for extant fungi offers new opportunities to reveal the significance of several morphological characters present in the fossil record. Using molecular phylogenies of extant leaf-inhabiting fungi with a fossil record, I summarize the necessary steps to bring together fossils and extant taxa in a phylogeny. Following this approach, I placed fossils of fly-speck from the Cretaceous of Virginia in the phylogeny of Dothideomycetes (Ascomycota). Similarly, hundreds of fossils of fungi resemble living taxa, and their morphology awaits to be scored before they can contribute to our understanding of fungal evolution.

Proteomic profiling of novel virulence factors in the wheat fungal pathogen *Fusarium graminearum*

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

Infection with the fungal pathogen, *Fusarium graminearum* (causative of Fusarium head blight [FHB]) in the global cereal crop, Triticum aestivum, poses a threat to food security by reducing crop yield and quality. Mycotoxins produced by the fungi, such as 15-acetyl deoxynivalenol, pose a threat to public health by contaminating feed and food products. FHB is a challenge and is expected to increase in severity in the coming years due to a connection with climate change, calling for new strategies in combating the disease. Our research uses state-of-the-art mass spectrometry-based proteomics to define host-pathogen interactions, which will identify novel candidate virulence factors, thus providing new insights into the disease and the fungal mechanisms for evading plant defense responses. We aim to identify new strategies to disrupt such interactions to enhance the effectiveness of current fungicides and explore the uncharacterized fungal proteins for providing new knowledge to researchers in the battle against FHB.

The endophytic fungus *Acremonium alternatum* can reduce clubroot symptoms on *Brassica napus* cultivars

Jutta Ludwig-Müller, Susann Auer, Nazanin Zamani-Noor
Technische Universität Dresden

Control mechanisms for clubroot in the field is characterized by hardly reproducible effects and are usually dependent on weather and soil conditions as well as resistant cultivars. Exhaustive usage of these resistances has led to the development of new and highly virulent isolates of *Plasmodiophora brassicae* in many countries, that can overcome the resistance in current commercial clubroot-resistant cultivars. A promising biocontrol organism was investigated for its potential to control clubroot of *Brassica napus*, since it was already shown to have some potential on *Brassica rapa* and *Arabidopsis thaliana* roots. The potential of the endophytic fungus *Acremonium alternatum* was investigated in combination with differentially virulent *P. brassicae* isolates and with *B. napus* cultivars exhibiting different grades of resistance to *P. brassicae*. A reproducible positive effect on the upper plant parts by *A. alternatum* treatment was visible, which could give the infected plants an advantage in the field to cope better with pathogens. Co-Authors: Susann Auer, Technische Universitaet Dresden, Germany. Nazanin Zamani-Noor, Julius-Kuehn Institut Braunschweig, Germany

Yak1 Regulates *Candida albicans* Morphogenesis through the Ras1/PKA Pathway

MacAlpine, Jessie*, Robbins, Nicole, Whitesell, Luke, Cowen, Leah
University of Toronto

The opportunistic fungal pathogen *Candida albicans* is a member of the human mucosal microbiota that can cause both superficial infections and life-threatening systemic disease. The fungus employs important virulence traits to infect its human host, including hyphal morphogenesis. Previous work identified a molecule secreted by Lactobacillus spp. that blocks *C. albicans* morphogenesis through the inhibition of a kinase, Yak1. Here, through epistatic analysis, we determined that Yak1 acts downstream of Protein Kinase A (PKA) and upstream of transcription factors Ume6, Tec1, and Brg1 to govern hyphal morphogenesis. Interestingly, Yak1 was shown to be dispensable for filamentation upon exposure to physiological concentrations of CO2, highlighting the importance of this kinase in mediating filamentation is environmentally contingent. Finally, we determined that Yak1 is important for disease pathology using a *C. albicans* dermatitis model of infection. Overall, this work provides mechanistic insight into how Yak1 regulates an important virulence trait in *C. albicans*.

Arbuscular mycorrhizal (AM) fungal community composition in recently restored agricultural prairies differs in comparison to longer term restored and remnant prairies

MacColl, Kevin*; Tosi, Micaela; Dunfield, Kari; Maherali, Hafiz
University of Guelph

Ecological restorations are aimed at restoring species composition to levels that resemble pre-disturbance levels. Most ecological restorations focus on plant and animal communities but relatively less research has been conducted on soil microbial communities. In this study, we compared the community composition of arbuscular mycorrhizal (AM) fungi, a widespread and ecologically important group of plant symbionts, in recently restored (<10 years) prairies on reclaimed agricultural lands to a range of longer term (>10 years) prairie restorations and remnant prairies. AM fungal community structure in recently restored prairies was significantly different from all other types of prairies, but most closely resembled longer term managed prairie restorations than remnant prairies. Consistent with studies on other trophic levels, these results suggest that human land-use leaves a legacy of ecological changes that may not be reversed in the short term following ecological restoration.

Experimental investigation of ecological niche expansion of the White-Nose Syndrome fungus *Pseudogymnoascus destructans*

MacDougall-Shackleton, Helen* and Xu, Jianping
McMaster University

Over the last two decades, White-Nose Syndrome (WNS), a cutaneous infection of the filamentous fungus *Pseudogymnoascus destructans* (Pd) affecting hibernating bats, has caused widespread mortality in bat species across North America. Although Pd is highly susceptible to environmental stressors such as UV radiation and temperatures outside of its growth range of ~4–20°C, it has spread rapidly across the U.S. and Canada. North American Pd isolates show significant phenotypic variation in the production of uncharacterized pigments, both on the fungal colony surface and in surrounding media, which may confer resistance to environmental stressors. Through a series of in vitro experiments, we studied the tolerance of four phenotypically-diverse Pd isolates to UV radiation, extreme temperatures, and oxidative and nitrosative stress. Our results may provide valuable insight into Pd's persistence and spread across a variety of ecological niche conditions in North America, which has profound implications for WNS response and mitigation efforts.

The biodiversity of microfungi from the bark of the Sugar Maple (*Acer saccharum*)

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Carleton University

The Sugar Maple (*Acer saccharum*), is a keystone species in Eastern North America. Despite this, taxonomic surveys enumerating the fungal populations of the bark of this tree species are lacking. Using traditional (direct observation and moist chambers) and high-throughput (particle filtration with dilution to extinction) culturing methods, this study examines the microfungi observed and isolated from A. saccharum bark and compares the efficiency of the different isolation methods employed. Bark collected from five different dead trees, from three distinct forests provide an insight on the feasibility of the high-throughput method in isolating microfungi from this substrate, an approach never previously experimented from *A. saccharum* bark. Commonly isolated taxa are discussed and compared to prior studies. Three novel species, which were commonly isolated, are described and compared to closely related taxa based on morphological and concatenated multi-gene phylogenetic analyses. Caveats and recommendations for future studies are discussed

Temporal diversity patterns for fungi and mites associated with decaying *Sporobolus pumilus* (*Spartina patens*) in the Minas Basin, Nova Scotia

Malloch, Bruce*. Kernaghan, Gavin. Walker, Allison
University of Western Ontario

Coastal salt marshes provide many ecosystem services, however little is known of the biology of decomposer taxa in these systems. This study employed above- and below-ground litterbags to characterize the fungal and mite communities associated with the dominant salt marsh grass, *Sporobolus pumilus*, in the Minas Basin, Nova Scotia. Decomposition rates of above-ground and below-ground tissues and environmental variables were quantified to contextualize temporal patterns in community composition. Above-ground litterbag mass loss peaked in July and decreased consistently over succeeding months, which positively correlated with fungal richness. Fungal and mite richness displayed inverse relationships over time, with mites gradually increasing in diversity before peaking in November, suggesting the presence of a complex detrital network where mites and fungi respond to different and possibly unrelated environmental cues. This study offers a first look at temporal community dynamics of two neglected groups of decomposers associated with *S. pumilus* in Canada.

Comparative Genomics of the Cronartium harknessii-Pine Pathosystem

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University of Alberta

The fungal pathogen *Cronartium harknessii* (J.P Moore) Meinecke is the causative agent of western gall rust. There are two primary hosts of *C. harknessii* in Canada, lodgepole pine, Pinus contorta Dougl. Ex Loud. var. latifolia, and jack pine, Pinus banksiana Lamb. Lodgepole pine displays higher susceptibility than jack pines to *C. harknessii*. Recent population genetic analyses show that there are two *C. harknessii* lineages: a more virulent western variant and a less virulent eastern variant. Using comparative transcriptomic analyses, the molecular response of lodgepole and jack pine to *C. harknessii* infection are being examined. In parallel, comparative genomics is being used to identify genomic regions that distinguish the western and eastern variants of *C. harknessii*. These analyses will allow us to define signatures for resistance and virulence in the host and pathogen, respectively, for this pathosystem.

Lichen Floristics in Newfoundland and Labrador – the Past and the Present, and Prospects for the Future

John McCarthy
Jesuits of Canada

I present an overview of progress towards the publication of an annotated catalogue of the lichens and allied fungi of Newfoundland and Labrador. The province has a rich history of lichen floristics dating from the first collections by Sir Joseph Banks in 1776. Despite this long history, a checklist or annotated catalogue of Newfoundland and Labrador lichens does not exist. I review our current understanding of lichen biodiversity in Newfoundland and Labrador as well as the recent description of several lichen species from the province new to science. Finally, I offer considerations for future lichen biodiversity research. Approximately 1270 taxa of lichens and allied fungi are currently known from the province. The rate of addition of species to the known biota has increased greatly in recent years.

Canadian Lichen Biodiversity and Conservation

Troy McMullin
Canadian Museum of Nature

We are in a global biodiversity crisis. In order to understand the extent of the crisis and ways to mitigate it, basic fundamental knowledge about species is required. This includes a sound understanding of what species are where, what species are rare, and which ones are declining. In this presentation, an overview of lichen biodiversity and conservation in Canada is provided, including distributions, species at risk, taxonomy, and threats throughout the country. Areas highlighted include Kejimkujik National Park and National Historic Site, Nunavut, Parc national de la Gaspésie, Ontario, and Prince and Edward Island. These studies help to show what we know and where there are knowledge gaps, which illustrates our ability to identify and monitor changes in populations and provides direction for future research.

Deciphering the molecular mechanisms underlying the genetic diversity in the plant pathogenic fungus *Colletotrichum gloeosporioides*

Mehta Nikita*, Baghela Abhishek
Agharkar Research Institute

Many phytopathogenic fungi undergo fusion of conidia through conidial anastomosis tubes (CATs), which is thought to facilitate horizontal gene transfer across the fungal species. We demonstrated the CAT fusion dynamics and conditions necessary for effective CAT fusion in *C. gloeosporioides* and *C. siamense*. A significant inter-specific CAT fusion was discovered between the *C. gloeosporioides* and *C. siamense*. Inter-specific CAT fusion appears to have a role in generation of phenotypic and genotypic diversity in these fungi. We found that the resultant conidia after inter-specific CAT fusion gave rise to heterokaryotic progenies with different colony features in comparison to their parental strains. Further, we carried out whole genome comparison of *C. gloeosporioides* and *C. siamense* parent with *C. gloeosporioides* heterokaryotic progeny to conclusively implicate role of CAT fusion in generation of genetic variations. The whole genome comparison clearly indicated that during inter-specific CAT fusion, DNA got transferred from *C. siamense* to *C. gloeosporioides*.

Splicing Pathways in Complex Introns in Fungi: The Stacking Dolls of the Intron World

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University of Manitoba

Fungal mitochondrial DNAs are highly variable in size partly due to the presence of mobile elements, such as self-splicing group I and group II introns that can invade cognate intron-less alleles due to the activity of intron-encoded proteins. Ribozyme-type twintrons composed of several intron modules where an existing/resident intron is invaded by a mobile intron, have been noted in a few organellar genomes. In Ophiostoma ips (Ascomycota, Ophiostomatales), the mitochondrial cob and cox3 genes harbor complex introns with a unique three component ‘trintron’ in the latter. In silico and RNAseq analysis support the “ratchet model” for resolving the complex intron in the cob gene. Investigation of complex introns through mitogenomics and deep RNA sequencing provides insight into novel features of self-splicing introns that impact “orderly splicing” and gene expression. Complex introns might provide opportunities for developing regulatory switches for synthetic biology.

Cretaceous Fungal Palynomorphs of the Danek Bone Bed, Edmonton, Alberta, Canada

Tamika Nagao, Eva Koppelhus
University of Alberta

The Danek Bone Bed is a Cretaceous site from the Horseshoe Canyon Formation. In this novel palynological survey, we sampled material from the matrix of the bone layer and examined it for fungal palynomorphs. Fossilized remains were isolated via acid digestion, heavy liquid separation, and oxidation. Fungal palynomorphs found ranged from 5 to 200 μm in size. The common palynomorph types found were hyphae, while conidia and resting structures were less common. From this preliminary assessment, nine genus level identifications were proposed, including cf. Gaeumannomyces, cf. Asterina, cf. Diporicellaesporites, cf. Fractisporonites, cf. Palambages, cf. Trichothyrites, cf. Glomus, cf. Corynesporopsis, and cf. Callimothalus. Further sampling and alternative fossil preparations will confirm these identifications and provide a more complete survey for the Cretaceous fungi at this site. This study highlights some benefits of studying fossil fungi, some challenges, and proposes directions for future research in this field.

RNAi and heterochromatin formation act independently to control genome stability and gene expression in Mucorales

Navarro-Mendoza, Maribel*; Pérez-Arques, Carlos; Heitman, Joseph.
Duke University School of Medicine

The early-diverging fungus Mucor has an intricate RNAi system with two interacting pathways that control transposable elements and gene expression. Several model organisms depend on the initial production of small RNAs to recruit the heterochromatin formation machinery, connecting post-transcriptional and transcriptional gene silencing. We conducted ChIP-seq experiments to explore this interaction between epigenetic regulatory pathways in Mucor. Our results identified the presence of H3K9me2 and -me3 at transposable elements genome-wide that are actively silenced by the canonical RNAi machinery. Surprisingly, heterochromatin levels were not significantly altered in mutants lacking key components of either the canonical or alternative RNAi pathways, indicating that RNAi is dispensable for heterochromatin maintenance. Also, the absence of heterochromatin marks at genes actively targeted by sRNAs indicates that RNAi does not in and of itself recruit the heterochromatin machinery. Our results suggest that RNAi and heterochromatin formation are independent genome defense and regulatory mechanisms in Mucorales.

Metabolic modelling of E*ndocarpon pusillum* facilitates the study of the lichen symbiosis

Hadi Nazem-Bokaee
The Commonwealth Scientific and Industrial Research Organisation

Lichenised fungi are capable of exchanging carbohydrates and inorganic molecules with their algal partner (among others in the community) during the lichen symbiosis. Little is known about the metabolic interactions between lichen symbionts leading to C-fixation (and sometimes N-fixation), and other metabolic functions. Here, we use a computational systems biology approach to explore some of the key metabolic interplays of a model lichen, *Endocarpon pusillum*, through combining the core metabolic networks of the primary mycobiont and that of the primary photobiont, Diplosphaera sp. Using this community modelling framework, we show how fixing atmospheric CO2 into carbohydrates by the photobiont and their provision to the mycobiont fuel the coupled metabolic pathways of the symbionts. This work provides important insights on the lichen symbiosis paving the way for its in vitro engineering.

Tra1 is a new regulator of *Candida albicans* drug resistance and pathogenicity

Nunes Marsiglio Librais, Gabriela; S. Shapiro, Rebecca; Lajoie, Patrick
Western University

Tra1 is an essential component of the SAGA and NuA4 transcriptional co-activator complexes that regulates gene expression. We previously demonstrated that mutations in TRA1 lead to increased sensitivity to caspofungin and reduced filamentation and pathogenicity in *C. albicans*. However, we recently found that loss of Tra1 function is also associated with increased resistance to azoles, indicating that Tra1 can differentially modulate the response to antifungal drugs. Furthermore, while Tra1 mutant fails to induce filamentation upon treatment with serum, it displays unaltered morphogenetic transition in response to Hsp90 inhibition. This suggests that the requirements for Tra1 in *C. albicans* morphogenesis depends on the nature of environmental cues. Tra1 therefore emerges as a new complex regulator of the *C. albicans* dug resistance and pathogenicity.

Pre-clinical evaluation of recombinant microbial glycoside hydrolases as antibiofilm agents in experimental invasive aspergillosis and acute *Pseudomonas aeruginosa* infection

Ostapska, Hanna*., Raju, Deepa., Lehoux, Melanie., Corsini, Rachel., Lacdao, Ira., Gilbert, Stephanie., Sivarajah, Piyanka., Bamford, Natalie C., Baker, Perrin., Nguyen, Thi Tuyet Mai., Zacharias, Caitlin A., Gravelat, Fabrice N., Howell, P. Lynne., Sheppard, Donald C.
McGill University

The mold *Aspergillus fumigatus* and bacterium *Pseudomonas aeruginosa* can form biofilms in the airways of patients with chronic lung disease. Biofilm formation by *A. fumigatus* and *P. aeruginosa* is supported by the production of the structurally similar cationic exopolysaccharides GAG and Pel, respectively. We previously demonstrated the potential for these organisms to use these exopolysaccharides to form co-operative biofilms. In this study, recombinant glycoside hydrolases (GH)s that degrade biofilm exopolysaccharides were evaluated as antimicrobial agents in mouse models of invasive aspergillosis or *P. aeruginosa* infection. Intratracheal GH administration was well tolerated by mice. GH prophylaxis resulted in reduced fungal burden in mice, possibly through augmenting pulmonary neutrophil recruitment. Combining GH prophylaxis with the antifungal posaconazole or the antibiotic ciprofloxacin resulted in a greater reduction in fungal or bacterial burden than with either agent alone. This study lays the foundation for further exploration of GH therapy in mixed fungal-bacterial infections.

Fungal holobionts: hidden relationships with ecological consequences

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Center for Research and Advanced Studies of the National Polytechnic Institute (CINVESTAV)- Irapuato

Rhizopus microsporus is an early-diverging fungal species that belongs to the phylum Mucoromycota. These fungi are used in the preparation of Asian and African fermented foods, can be pathogens of humans and plants, but are mostly soil dwellers and saprophytes. In this seminar, I will offer an overview of the discoveries that have set this species as one of the best models to investigate symbioses of fungi with bacteria and viruses, and how these interactions shape fungal biology, ecology and evolution.

RNAi-exclusive antifungal drug resistance is inherited after sexual reproduction in the human pathogen *Mucor circinelloides*

Carlos Perez-Arques, Maria Isabel Navarro-Mendoza, and Joseph Heitman
Duke University

Epimutations –heritable, epigenetic modifications that alter gene expression– may arise from RNAi, DNA methylation, and/or heterochromatin modifications, often resulting in gene silencing. Epimutations conferring drug resistance were discovered for the first time in two species of the early-diverging fungus Mucor and resulted in small RNA silencing of the gene fkbA encoding the FK506 target, FKBP12. This silencing results in unstable drug resistance that reverts to sensitivity after several mitotic growth cycles without FK506. We have discovered that epimutations in Mucor species are RNAi-exclusive and post-transcriptional, as demonstrated by lack of other repressive chromatin marks but presence of RNA polymerase II and complementary antisense sRNAs directed against epimutationally-silenced loci. Mucor epimutations are sufficiently stable to be transgenerationally inherited following sexual reproduction and meiosis, despite lacking heterochromatin marks frequently associated with epigenetic inheritance. Understanding how epimutations arise may enable their diagnosis and provide solutions to overcome the challenge of antimicrobial drug resistance.

Investigating clubroot resistance from a ""mobile"" point of view

Marina Silvestre Vañó and Edel Pérez-López
Laval University

Plasmodiophora brassicae is the causal agent of the clubroot disease affecting the canola industry worldwide. Clubroot-resistant (CR) canola varieties have been deployed as a key strategy to avoid the economic damage caused by this disease. Unfortunately, resistance is rapidly overcome by new *P. brassicae* pathotypes, highlighting the need to identify novel sources of clubroot resistance and fully understand the resistance mechanisms behind it. Arabidopsis, a member of the Brassicae family, have been partially studied as a source of CR. Indeed, a putative Arabidopsis CR gene (PBR1) was previously reported, although nothing was ever done to corroborate its role as a resistance gene or the mechanisms mediating the resistance. To further understand PBR1, we were able to trace several Arabidopsis ecotypes bearing PBR1 and study their response to P. brassicae single spore isolates with results that, not only contradict previous findings, but that point to an unexpected transposable element-mediated CR.

Metabarcoding aquatic fungi in agriculturally dominated watersheds for monitoring environmental health

Phillip Pham *, Devon Radford, Yichao Shi, David R. Lapen, Izhar U. H. Khan, Stéphane Aris-Brosou, Wen Chen
University of Ottawa

Aquatic fungi spend part of their life cycles in the aquatic environment, but beyond this, they re-main poorly described and more diversity is yet to be discovered. Moreover, their potential as markers for environmental risks is understudied. To address these knowledge gaps, we hypothesize that the aquatic fungal communities are sensitive responders to land use, meteorological, and oth-er environmental perturbations. We performed long-term bi-weekly water sampling in the agricul-turally dominated South Nation River watershed (Ottawa, Ontario), between 2016 and 2020 from 9 stream sites, and metabarcoded the rRNA gene's Internal Transcribed Spacer 2 region to character-ize the aquatic mycobiota. Using this approach, approximately 74k unique fungal barcodes were recovered, of which ~31k represented 20 classes (e.g., Agaricomycetes and Dothideomycetes) with known aquatic fungal species. With land use and water physicochemical data collected concurrent-ly, the risk indicators in the aquatic mycobiota that are associated with environmental drivers will be predicted.

The diverse and complex mycoflora present in inflorescences of cannabis (*Cannabis sativa* L., marijuana)

Zamir Punja
Simon Fraser University

Cannabis is cultivated in greenhouses throughout Canada for medicinal and recreational use. Regulatory guidelines established by Health Canada require that microbial contamination by total yeasts and molds (TYM) do not exceed recommended thresholds. The nature of TYM occurring within developing cannabis inflorescences was investigated. Inflorescences of several genotypes were sampled at various times during flower development and after harvest. They were blended in water and dilution-plated onto potato dextrose agar containing 140 mg/l of streptomycin sulfate. Colonies of all fungi and yeasts were identified by PCR of the ITS1-5.8S-ITS2 region of rDNA. Up to 35 different species were recovered, with Penicillium represented by 10 species, Fusarium by 5 species, Aspergillus by 3 species and Mucor by 2 species. Other fungi included species of Cladosporium, Alternaria, Trichoderma and Botrytis. The yeasts included Pseudozyma, Rhodotorula and Meyerozyma species. Various factors that can enhance development of TYM in cannabis inflorescences will be described.

Stress- and metabolic responses of *Candida albicans* require Tor1 kinase N-terminal HEAT repeats

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Cells must continuously decide between investing their resources in growth or in surviving stressful conditions. Target of Rapamycin Complex 1 (TORC1) coordinates these decisions. A TORC1 inhibitor like rapamycin is a cidal antifungal against *Candida albicans*, but is also highly toxic to human cells by also targeting the highly conserved Hs.mTor kinase domain. The least conserved Tor1 region comprises 8 N-terminal HEAT repeats (N-HEAT). We examined their role using cells expressing N-terminally truncated Tor1 from repressible tetO (tetO-TOR1?HEAT), full-length Tor1 from tetO (tetO-TOR1) or wild type Tor1 from the native promoter. Specific stress responses were significantly impaired by loss of Tor1 N-HEAT, including those to oxidative-, cell wall-, and heat stress. Genome-wide expression analysis showed dysregulation of carbon metabolism and translational machinery biosynthesis in tetO-TOR1?HEAT cells. Targeting fungal-specific Tor1 N-HEAT with small molecules might therefore abrogate fungal viability, especially during infection when multiple stresses are imposed simultaneously by the host.

Metabarcoding mycobiota starts with evaluating specificity of primers by a new bioinformatics tool, IsPRIMER

Devon Radford *, Sarah Hambleton, Wen Chen,
Agriculture & Agri-Food Canada

The dispersion of fungal inocula, can be monitored by metabarcoding semi-conserved genomic marker regions like the internal transcribed spacer (ITS) of the rRNA gene. However, for some taxa like Pucciniales, specificity and efficiency from ‘universal’ primers can be disproportionally poorer than optimal. Hence, the first step is to ensure the selected primers have proper taxonomic coverage and specificity for the target taxa when using the metabarcoding approach. A new bioinformatics tool, named “isPRIMER”, was developed to evaluate a given set of primers in IUPAC code against both sense and antisense strands of reference sequences using a modified binary search tree algorithm and Perl regular expression pattern matching engines. Evaluation of nine forward and seven reverse ITS2 primers predicted marked variation in taxonomic coverage for major fungal phyla and selected phytopathogens. We will also present our pipeline for primer evaluation and species-level identification of phytopathogens from short metabarcodes.

Investigating the soil microbiome of American ginseng (*Panax quinquefolius)*

Rachel Rajsp*, Anka Colo, Paul Wan, Pankaj Singla, Mark Bernards, Vera Tai, Greg Thorn
Western University

Ginseng replant disease (GRD) is of high significance to the Ontario ginseng industry as it can cause the complete loss of ginseng crops. GRD occurs when a new ginseng crop is planted in a field where ginseng was grown previously. The prevalence of GRD has since limited the amount of land in North America that is available to grow ginseng. Several pathogens that have been discovered to cause rot include: *Neonectria*, *Ilyonectria*, *Phytophthora* and *Pythium*. This project will investigate new primers that permit identification of individual species of certain target fungi. Using new and existing primers, I will compare the fungal communities present at the time of harvest for both GRD and healthy ginseng soil. Next-generation sequencing (NGS) will be used to identify what species are present in the soil for each garden site.

Mining the *Aspergillus niger* secondary metabolome through overexpression of non-ribosomal peptide synthetases

Ram, Shane*. Semper, Cameron. Savchenko, Alexei.
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Aspergillus niger is a rich source of potentially novel secondary metabolites; however, their parental biosynthetic gene clusters (BGCs) are often recalcitrant to expression under laboratory conditions. Previous research has focused on the overexpression of co-localized transcription regulators or entire BCGs to elicit production of their secondary metabolite products. Limitations associated with these approaches have left much of the biosynthetic potential within *A. niger* underexplored. To address this, we sought to develop a highly tractable approach for mining the A. niger secondary metabolome by utilizing a Cas9-based system to allow for inducible overexpression of non-ribosomal peptide synthetases (NRPS). As a proof-of-concept, we overexpressed 10 NRPS enzymes to investigate their secondary metabolite products. Using this approach, we have successfully engineered *A. niger* to produce several putatively novel secondary metabolites, evident through phenotypic markers and via mass spectrometry analysis. These results validate our approach and identify candidate small molecules for further characterization.

Mucoromycota fungal and associated bacterial communities in the rhizosphere of two different plants in the Sonoran Desert, California

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Cornell University

The Mucoromycota comprises a diverse group of filamentous fungi including mycorrhizal symbionts (Glomeromycetes, Endogonomycetes) and rhizosphere-associated and soil saprotrophs (Mortierellomycetes, Mucoromycetes). Recent and ongoing discoveries about the endosymbiotic bacteria (EB) that many Mucoromycota species harbor have generated new questions regarding the effect of EB on host biology and ecology. Depending on the species, EB can influence host asexual and sexual reproduction and metabolic functioning, but for some species the host effects remain unknown. To investigate the potential role of EB in structuring Mucoromycota communities, we are using a combination of culture-based and metabarcoding methods to analyze soils collected in the Sonoran Desert (California, USA) using both bacterial and fungal primers. We utilized network analyses to visualize associations between fungal and bacterial amplicons to explore possibly novel fungal-bacterial interactions. Our results indicate both biotic filtering influenced by host plant and dispersal filtering based on geographic distance influence microbial community structure.

Glycosylation of deoxynivalenol by *Clonostachys Rosea*—toward identification of glycosyltransferases involved in the detoxification of DON

Kelly A. Robinson*, Antony St-Jacques, Michele C. Loewen
National Research Council of Canada

Clonostachys Rosea (ACM941) has strong potential to act as a biocontrol organism against *Fusarium graminearum*, a major contributor to the infection of grains through its mycotoxins, such as deoxynivalenol (DON). This crop contamination has been a continual problem in Canada resulting in large economic losses. We seek to identify glycosyltransferases in *C. Rosea* that may detoxify DON by glycosylation. Fourteen potential glycosyltransferase candidates were identified by homology modelling via SWISS-MODEL. CRISPR-Cas9 generated knockout strains for each candidate will be produced and subsequently characterized through plate confrontation assays to allow the assessment of their ability to glycosylate DON. Presently, four knockouts have been successfully generated. The enzymes found to be involved in DON detoxification can then be produced in high yields by recombinant expression and used to detoxify DON in contaminated crops; providing a bioconversion method that is environmentally-friendly and effective, helping to reduce the negative impacts of DON.

Assessing arbuscular mycorrhizal colonization and rhizosphere carbon across a chronosequence of salt marshes in the Bay of Fundy, Nova Scotia

Kendra Sampson*, Jeremy Lundholm, Danika van Proosdij, and Allison Walker
Saint Mary's University

Salt marshes are blue carbon ecosystems that accumulate and store large amounts of carbon. The increasing loss of these ecosystems reduces global carbon storage capacity and climate change mitigation abilities. Carbon is accumulated through suspended sediment and autochthonous sources within the salt marsh, which may be utilized by salt marsh vegetation and fungi. Beneficial arbuscular mycorrhizal fungi (AMF) form associations with salt marsh plant roots. We are investigating the role of AMF in carbon sequestration. We assessed AMF in dominant salt marsh plant species (Sporobolus, formerly Spartina), from low to upper high elevations, and examined the correlation between organic carbon and AMF colonization. Preliminary results show high AMF colonization rates (94%) and organic carbon densities (>0.045 g·C·cm-3) in Sporobolus michauxianus roots at older restoration sites. This research will fill many knowledge gaps on the role of belowground fungi in salt marshes and their contribution to carbon accumulation and storage.

Secondary Metabolite Production in *Aspergillus niger*: methyltransferase specificity

Selber-Hnatiw, Susannah*; Beigas, Marie; Di Falco, Marcos; Tsang, Adrian;
Benoit-Gelber, Isabelle
Concordia University

Secondary metabolites are compounds not directly involved in the growth or viability of an organism, but represent a source of pharmacologically or industrially relevant compounds that provide a selective advantage. Biosynthetic gene clusters (BGCs) encode the production of secondary metabolites and include genes responsible for the synthesis, chemical modification, and transport of products outside the cell. The methylation of secondary metabolites is a chemical modification resulting from methyltransferase activity. For instance, the neurokinin receptor antagonist BMS-192548 is tautomerized from the neuropeptide Y antagonist TAN-1612 through an O-methyltransferase tailoring enzyme that regulates the selective addition of C9-methyl groups. Methyltransferase specificity is important to our understanding of redesigning molecules, in which the product of altered methylation may lead to pharmacologically or industrially relevant secondary metabolites. As such, to examine late-stage functionalization using O-methyltransferases, this work examines how different methyltransferases can modify the methylation pattern of a molecule. The replacement of the native methyltransferase with a library of methyltransferase candidates, and the analysis of the resulting methylation pattern will be presented.

Amber as a source of fossil fungi

Leyla Seyfullah*, Christina Beimforde and Alexander R. Schmidt
University of Vienna

Ambers are rightly famous as a source of organisms preserved with often microscopic fidelity and frequently in life position. Traditionally, amber research has focused on other groups, particularly the invertebrates. However, the excellent preservation of fungi in amber has led to a wealth of new discoveries and increased interest in this neglected source of fossil fungi. Particular care is needed, however, to ensure that the specimens are verifiably fungal in nature. The oldest amber with confirmed fungal inclusions has been dated back to the Carnian (Late Triassic, around 230 million years ago), although most ambers with entrapped fungal remains are Cenozoic and Cretaceous in age. Here we will look at the potential of ambers to preserve fungi in the fossil record and the likely biases surrounding amber deposits. We will also explore why we should be excited about future amber inclusion research for increasing our understanding of fossil fungi.

Evidence of host-induced heterodimerization between chemotropic receptors Ste2 and Ste3 in Fusarium graminearum

Sharma, Tanya*. Jomphe, Robert. Sridhar, Pooja. Loewen, Michele
University of Ottawa

The phytopathogenic fungus F*usarium graminearum* is the causative agent of Fusarium head blight on wheat, reducing yields and depositing potent mycotoxins on cereal grains. Chemotropic signals arising from a host-derived peroxidase serve as the primary stimulus perceived by the fungal G -Protein Coupled Receptor (GPCR) Ste2 and transduced via the CWI-MAPK pathway. Ste2 and its cognate receptor Ste3, are known to work synergistically in yeast mating and conidial germination in *F. oxysporum*. Now, we have found that loss of FgSte3 also compromises peroxidase stimulated chemotropism. Further, both Fgste3? and Fgste2? strains were found to have attenuated CWI-MAPK signal transduction. Preliminary data from Bioluminescence Resonance Energy Transfer (BRET) and affinity pull-down experiments support peroxidase-induced heterodimerization between the FgSte2 and FgSte3 receptors. These preliminary findings and their potential relevance in mediating chemotropic sensing and *F. graminearum* pathogenicity are discussed. Funded by NSERC and NRC.

Mother Tree Networks Help Regenerate Forests

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University of British Columbia

Mother trees are the biggest trees in the forest and the hubs of the mycorrhizal fungal networks that link the community together. New research in the Mother Tree Project in the Douglas-fir forests of British Columbia shows that protection of Mother Trees when logging enhances natural regeneration and increases survival of seedling that have been planted, particularly those whose seeds have been migrated from warmer climates. The old trees protect regenerating seedlings from extreme weather and also provides them with parcels of water, nutrients and information that aids in their survival. The old trees also protect mosses, lichens and plants that require cover, and reduces greenhouse gas losses from disturbance. The regenerative network centered on old trees is crucial in the mitigation of global change and the recovery of forests following harvesting and other disturbances, and points to transformational forestry practices that combine mother tree retention with assisted migration.

The strange case of alternative associations in lichenized fungi: Dr Jekyll or Mr Hyde?

Antoine Simon; Bernard Goffinet; Dan Vanderpool; John P. McCutcheon, Nicolas Magain, Emmanuël Sérusiaux; Gulnara Tagirdzhanova; Toby Spribille
University of Connecticut

Lichens are frequently cited as a prime example among mutualistic symbiosis. These superorganisms are traditionally defined as the result of an association involving at least one fungal component and one photosynthetic partner. However, some lichens are notable for their ability to form photomorphs, which are dissimilar symbiotic products resulting from conspecific mycobionts associated with either a green alga or a cyanobacterium. This one-of-a-kind “one fungus – two lichens” situation represents an ideal model for tackling fundamental questions in symbiotic biology. Using a metatranscriptomic framework (RNA-seq), we investigated photomorphs within Dendriscosticta (Lobarioideae, Peltigeraceae), a flagship genus occurring in British Columbia, to understand what genetic factors may allow for different symbiotic outcomes in lichenized fungi. Our findings suggest that photomorph pairs of a single lichen-forming fungus exhibit contrasting morphogenetic processes, as well a notable difference in the transcript abundance of secondary metabolism-related genes.

Pathogenomics of *Puccinia striiformis* reveals a population shift in western Canada

Gurcharn Singh Brar
University of British Columbia

Little is known about which pathogen lineages of *Puccinia striiformis* are prevalent across different Canadian provinces, and many studies simply group the entire North American continent into a single locale. We evaluated the suitability of the published techniques for IDing Canadian field isolates, and use the breadth of our sequencing data to identify an analogous set of informative genes based on de novo identification of informative polymorphisms in the Canadian rust population. We place our field samples in global context, and identify a population shift in Canadian field isolates from 2010 to 2020, where isolates derived from Ethiopian and European populations have been outcompeted by the temperature-adapted North American strain, now present in all sampled provinces. This work demonstrates the benefits of the field pathogenomics approach for quick, easy identification of pathogen races from field samples, as well as from existing reference data, enabling scientists to make informed decisions.

Toward identification of a chemoattractant that enables Ste2-mediated directed growth of *Fusarium graminearum* on wheat

Sridhar, Pooja*. Sharma, Tanya. Vasquez, Vinicio. Monteil-Rivera, Fanny. Allingham, John. Loewen, Michele.
Queen's University

Fusarium graminearum causes Fusarium Head Blight in wheat, contaminating the grains with mycotoxins and thereby leading to food shortages and economic losses worldwide. Our laboratory has shown that the pheromone-sensing G protein-coupled receptor Ste2 of *F. graminearum* mediates directed growth (chemotropism) towards the catalytic product of a wheat-secreted peroxidase, however, the identity of this peroxidase-derived chemoattractant remains unknown. Recent findings from our laboratory suggest that the substrate(s) from which the chemoattractant is produced originates from the *F. graminearum* spores. We have enriched the substrate from *F. graminearum* spores and converted it into active chemoattractant in vitro using a commercial peroxidase. Preliminary analyses by liquid chromatography coupled with high resolution mass spectrometry (LC-HRMS) of the derived samples highlight a series of unique, related, polar compounds as promising candidates. Identification of the chemoattractant will deepen our understanding of the mechanisms of host-sensing by this important agricultural pathogen.

The regulation of endoplasmic reticulum stress in *Candida albicans*

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Western University

Candida albicans is the leading cause of yeast infections in humans. The Unfolded Protein Response (UPR), a cellular program that alleviates the toxic accumulation of misfolded proteins in the endoplasmic reticulum (ER), has been found to be involved in *C. albicans* antifungal resistance and pathogenicity. Various compounds have been shown to attenuate ER stress, including the bile acid TUDCA. However, mechanisms of ER stress regulation in *C. albicans* remain poorly understood. In agreement with previous studies, we found that repressing the UPR activator IRE1 sensitized *C. albicans* to antifungals and reduced its filamentation. Additionally, administration of TUDCA improved growth of yeast treated with the ER stressor tunicamycin and the antifungals caspofungin and amphotericin B. However, TUDCA significantly exacerbated fluconazole toxicity. Our findings support the role of IRE1 as an essential component in *C. albicans* antifungal resistance and pathogenicity and furthermore suggest that TUDCA differentially potentiates the toxicity of antifungal drugs.

Characterizing Plasmodiophora brassicae effector candidates identified in the resistance-breaking pathotype 3A infection of *Brassica napus*

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In western Canada, clubroot disease (*Plasmodiophora brassicae*) of canola (*Brassica napus*) is controlled mainly with clubroot-resistant (CR) cultivars. Recent pathotype shifts in *P. brassicae* populations have rendered current CR cultivars less effective. Transcripts of 28 putative pathogen effectors were found to be consistently increased following infection of *B. napus* by pathotype 3A, as determined by RNAseq analysis and confirmed with NanoString technology. Two upregulated putative effectors, SPQ99289.1 and SPR01261.1, predicted to encode a kinase domain protein and a serine carboxypeptidase, respectively, were selected for characterization. The function of the signal peptides was confirmed by directing the secretion of invertase, whose enzymatic activity upon secretion was detected by a colour change. Investigations are underway to assess the activity of each protein and their in planta localization. Functional analyses of these effectors will improve our understanding of the molecular interactions between *B. napus* and resistance-breaking pathotypes of *P. brassicae*.

Engineering the kerosene fungus *Hormoconis resinae* for bioremediation of hydrocarbon contaminated soil and water

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The saprotrophic fungus *Hormoconis resinae* is capable of growth in hydrocarbon contaminated environments and encodes metabolic pathways for the uptake and metabolism of n-alkanes and aromatic compounds. Soil and water contaminated with hydrocarbons, polycyclic aromatic hydrocarbons (PAH) and by products bitumen processing are a growing and costly problem to clean up. We find that *H. resinae* is lignolytic and capable of metabolizing toxic naphthenic acids, PAH and to a limited extent asphaltenes present in oil sands process water. Treatment with this fungus can also deplete PAH and n-alkanes from soil. The ability of H. resinae to metabolize PAH was improved through a process of random mutagenesis and Laboratory Adaptive Evolution that selected for an increased growth rate when PAH was provided as the sole carbon source. We also developed a transformation protocol and engineered *H. resinae* to over express and secrete a heterologous laccase to improve PAH degradation.

Large-scale analysis of metagenomics of lichen symbiosis

Tagirdzhanova, Gulnara*. Saary, Paul. Cameron, Ellen. Finn, Robert. Spribille, Toby
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About one fifth of described fungal species engage in lichen symbiosis. Together with unicellular phototrophs and bacteria, these fungi create lichen symbiotic architectures. We don’t know what role different organisms play in lichen symbiosis, and even the symbiont composition is documented only for a tiny fraction of lichen symbioses. We aimed to fill this gap using the plethora of lichen metagenomic data generated in recent years. We used both newly generated and publicly available data to create the first systematic survey of composition of lichen symbiosis. From these data, we recovered 1000 symbiont genomes, including fungal, algal, and bacterial symbionts. Our analysis showed that lichen bacterial communities are unexpectedly structured, with a majority of bacteria coming from just four bacterial families. Some of these bacteria possess the machinery for anoxygenic photosynthesis. Based on the genome annotations, we propose a model of flow of goods between the members of lichen symbiosis.

Exploring beetle-fungi-nematode interactions in spruce and mountain pine beetle

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Natural Resources Canada

Bark beetles (Dendroctonus, Scolytinae, Curculionidae) are closely associated with ophiostomatoid or blue stain fungi, which can confer nutritional benefits to developing insects, play a critical role in overcoming tree defences and even be detrimental to developing insects. However, bark beetle-fungi interactions are not limited to blue stain fungi and biased sampling typically discards yeasts and other filamentous fungi that may influence bark beetle success and survival. Another layer of potentially significant interactions includes the diverse nematodes hosted by bark beetles, comprising endoparasites, plant parasites, fungal-feeders and species of unknown ecology. Bark beetle-fungi-nematode interactions represent a poorly understood complex web of intimate interactions. We present preliminary results from an ongoing study assessing the diversity and interactions of fungi and nematodes associated with mountain pine beetle (*Dendroctonus ponderosae*) and spruce beetle (*D. rufipennis*) in western Canada.

Mycorrhizal response to homokaryotic versus dikaryotic arbuscular mycorrhizal fungi.

Terry, Victoria*; Kokkoris, Vasilis; Chapman, Kendyll; Turcu, Bianca; Villeneuve-Laroche, Matthew; Corradi, Nicolas
University of Ottawa

Arbuscular mycorrhizal fungi (AMF) are obligate plant symbionts with a unique nuclear organization in which thousands of nuclei co-exist. These nuclei are either genetically similar (homokaryotic) or derived from two distinct parents (dikaryotic). I am investigating the impact of these two genetic organizations on the AMF symbiosis by measuring the mycorrhizal response (MR) of potato cultivars with different degrees of domestication using representative homokaryotic and dikaryotic AMF strains. Genetic organization (dikaryotic vs homokaryotic) and domestication status of the host are both significant factors in the MR of host plants. Specifically, biomass is significantly greater when inoculated with homokaryotic AMF compared to dikaryotic AMF. ddPCR analyses show the nucleotype ratio of these dikaryotic spores shifts depending on host identity. Furthermore, phosphorus uptake is greater in wild cultivars than domesticated cultivars. Future analyses of fungal responses may shed light on the dynamics of the responses we observed among these two nuclear organizations.

Development of real-time immunoPCR (RT-iPCR) assays for three airborne fungal pathogens of wheat

Thirugnanasambandam, Ilakkiya*, Vucurevich, Tara , Kav, Nat , Laroche, André , and Challis, Jonathan.
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Wheat is a staple food crop across the world. Tan spot (TS), fusarium head blight (FHB), and stripe rust (SR) are important wheat diseases caused by airborne fungal pathogens. Early detection of these diseases is needed to protect crop yield. The objective of this study is to detect and quantify these three airborne fungal pathogens. Polyclonal antibodies were validated and optimized against these three spores through indirect enzyme-linked immunosorbent assay (ELISA) and real-time immunoPCR (RT-iPCR). RT-iPCR assay showed improved sensitivity by 25-times for TS, 5-times for FHB, and 6-times for SR spores when compared to ELISA. These results suggest that RT-iPCR quantification using specific antibodies can be a very useful tool in detection of spores. Availability of these early detection measures will ensure sustainable yields and reduce crop losses. Future experiments will focus on evaluating cross-reactivity of antibodies against closely related pathogens and on quantifying these spores in air samples.

Exploring Cultured Microbes of Pollinated Maize Silks

Thompson, Michelle*, Shrestha, Anuja, Rinne, Jeffrey, Shearer, Charles, Limay-Rios, Victor, Reid, Lana, Raizada, Manish
University of Guelph

The style tissue of plants is an emerging area for microbiome research. I have found that maize silks house diverse, culturable microbes that may be beneficial to the plant – particularly in defense against a mycotoxigenic fungus that infects maize through exposed silks. *Fusarium graminearum* (Fg) causes Gibberella ear rot and produces dangerous mycotoxins in maize. I isolated over 1000 microbes from 14 genotypes of maize (56 silks samples). 236 bacteria were tested against Fg in vitro and 56 of these bacteria suppress Fg (at least 37 unique strains), suggesting silks are a rich source of anti-Fg bacteria. Many strains have undergone further testing including whole genome sequencing, and 5 low-risk microbes were tested against Fg in greenhouse trials. Endophytes may have coevolved with maize and pathogens, and show potential to protect our food from mycotoxins.

Novel Antarctic yeast switches to ethanol fermentation and increases small RNA synthesis to adapt to cold.

David Touchette
McGill Univesity

Fungi have been isolated and characterized from some of the harshest cryoenvironments on Earth, including Arctic glaciers, and Antarctica rocks and deserts. However, fungal adaptation strategies to low temperatures are still not fully understood. We investigated the cold-adaptative strategies of the novel Rhodotorula frigidialcoholis yeast, isolated from ice-cemented Antarctic permafrost via mRNA and sRNA transcriptomics, phenotypic profiling, and assessment of ethanol production at 0°C versus 23 °C. Our findings suggest that under cold, *R. frigidialcoholis* induces a metabolic switch from respiration to ethanol fermentation to overcome the Antarctic permafrost challenges. This was consistent with detection of ethanol production at 0ºC, the coldest temperature reported for its natural production. Furthermore, *R. frigidialcoholis* showed an increase in sRNAs diversity and abundance at 0ºC, which was consistent with the upregulation of Dicer, a key protein for RNAi, implying that post-transcriptional regulation and mRNA silencing may be novel fungal evolutionary adaptations in the cryosphere.

Examining nuclear transfer between homokaryotic and dikaryotic strains of *Rhizophagus irregularis*

Turcu, Bianca*. Kokkoris, Vasilis. Cornell, Calvin. Corradi, Nicolas.
University of Ottawa

Arbuscular mycorrhizal fungi (AMF) strains often coexist and interact within the soil through anastomosis. These genetically distinct strains are identified by putative MAT-loci, as either homokaryotic, or dikaryotic. In other fungi, anastomosis between compatible strains results in nuclear transfer, creating a spore progeny with a new combination of MAT-loci. To assess if homokaryon-homokaryon, homokaryon-dikaryon (Buller phenomenon), and/or dikaryon-dikaryon nuclear exchanges also occur in AMF, I examined anastomosis frequencies between 12 crosses of homokaryotic and dikaryotic strains of the model AMF species *Rhizophagus irregularis* using microscopy and droplet digital PCR (ddPCR). Although rare in comparison to self-fusions, anastomosis between different strains was present in all crosses. Spores analyzed using ddPCR showed that only a single spore displayed evidence of nuclear transfer between two strains. Future crossings between more closely related relatives may result in more successful nucleotype transfers which could further confirm the creation of new nuclear combinations.

Abundance, diversity, and functional mechanisms of bacterial endosymbiont interactions

Jessie Uehling
Oregon State University

Intrahyphal endosymbiotic bacteria related to the Burkholderiales and Mollicutes are frequently associated with Mucoromycota fungi. Fungal endosymbionts share genomic hallmarks of adaptation to the eukaryotic intracellular environment such as genome contraction reflective of host dependence. While comparative genomics of fungal physiology with and without endobacteria have enabled insights into host-endosymbiont interaction mechanisms, these studies have been undertaken in just a few model systems. Endosymbiont ubiquity and diversity are largely unknown, and the effects of fungal endosymbiont interactions on fungal population diversity remain undocumented. To fill these knowledge gaps, we are characterizing Mucoromycota isolates and their endosymbiotic bacteria from soils on varying geographical scales using genome sequencing and comparative genomics. Further, we are re-analyzing hundreds of raw fungal genomic data sets using novel computational pipelines to clarify how frequent and diverse fungal endosymbiont symbioses are. This talk will detail the molecular functioning, abundance, and diversity of Mucoromycota endosymbionts and provide insights into how these poly-microbial symbioses influence each other’s evolutionary trajectories.

Seasonality in Caliciopsis canker

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Caliciopsis pinea is an endemic,ubiquitous pathogenic fungus of eastern North America affecting eastern white pine (*Pinus strobus* L.; ewPine) trees with large cankers and yellowing foliage. In November of 2020, >70% of the multi-age ewPine in a Halifax city park were noted to be dead or dying with bleeding cankers and yellowing foliage. Under examination the afflicted trees were colonized by *C. pinea* and secondary canker pathogens: Allantophomopsis pseudotsugae and Sydowia polyspora. Contrasting winter versus summer sampling results suggest that secondary co-localized canker fungi are actively growing in the winter while *C. pinea* is not. Six sites across New Brunswick and Nova Scotia were identified and sampled for Caliciopsis fruiting bodies with associated canker to be followed by winter sampling and tagged for future monitoring. These samples will be screened for *C. pinea*, *A. pseudotsugae* and *S. polyspora* to examine the relationship of *C. pinea* with winter canker pathogens.

Current fungicide use in Australia and its implications for control of blackleg disease

Angela Van de Wouw and Steve Marcroft

The Australian canola industry has been rapidly increasing over the past 20 years with a record production of over 6M tonnes in 2021. Minimising yield loss due to the blackleg pathogen, Leptosphaeria maculans, is essential for Australian growers, however over the past 20 years, changes in farming practices have led to significant changes in disease epidemiology. Whilst genetic resistance remains the most effective tool for controlling blackleg, the pathogen rapidly adapts to overcome major gene resistance in Australia within only a few years of use. Fungicides have become an integral tool for managing blackleg, with control options including seed treatment and 4-8 leaf sprays being used to minimise crown canker and 30% bloom applications to minimise the impact of upper canopy infection. Whilst fungicides provide reliable control of the disease, predicting yield returns from these fungicide applications is proving more challenging.

Comparative genomic analysis reveals genetic variation in the pathogenicity-related genes of Canadian *Phytophthora capsici* isolates

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The oomycete plant pathogen *Phytophthora capsici* occurs worldwide on vegetable crops causing serious crop losses. The control of this pathogen is difficult due to presence of fungicide resistant isolates and different virulence levels among the *P. capsici* population. Comparative genomic analysis have been used to explain the difference in virulence by analyzing the pathogenicity genes. In this study, the whole genome of two *P. capsici* isolates from Ontario were sequenced using Next Generation Sequencing. The comparative genomic analysis revealed differences in the content of cytoplasmic effectors genes, genes encoding carbohydrate-active enzymes (CAZymes), secondary metabolite biosynthesis-related genes, as well in protease and protease inhibitors. To date, there are no reports on the genomic analysis of Canadian *P. capsici* isolates. The new genomic information provides important insight to the pathogenicity features of *P. capsici*. Understanding the genomic components of this pathogen and its interaction with the crops will lead to improved control strategies for phytophthora blight.

Massive transposons as the crucible of evolution in fungi

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Over the past decade, investigations into various fungal genomes have uncovered a number of large genomic regions that appear to have been horizontally transferred among strains or species, and which carry genes important for adaptation. I will present evidence that these apparently disparate phenomena are united by the action of a novel group of massive transposons, named Starships. These elements are widespread across Pezizomycotina, and can also be found in select basidiomycetes as a part of clear cases of recent horizontal transfer. Furthermore, a vast array of “cargo” genes can be found within the Starships. These include putative biosynthetic gene clusters and genes with predicted functions relating to, virulence, and metal resistance. We hypothesize that the Starships are analogs of the machinery that some bacteria use to exchange genetic material, making these the first known agents of active horizontal gene transfer in a eukaryote.

The Chemical Ecology of *Ilyonectria mors-panacis* and Chemical Targets for Root Rot Management

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Root rot of ginseng caused by Ilyonectria mors-panacis can greatly decrease crop yields often by 20-30% at the time of harvest. We isolated and characterized a number of resorcyclic acid lactones (RAL's) from *I. mors-panacis*, including previously unreported ones. These compounds play a role in immune response suppression through inhibition of ATPase activity. Additionally, we determined that the Ilyonectria siderophore N,N',N''-triacetylfusarinine C (TAFC) is critical for the ginseng pathogens' virulence. TAFC enables the fungus to acquire iron from its environment, this iron is typically released intercellularly via enzymatic degradation. We hypothesized that AfEstB, a well-characterized TAFC esterase produced by *A. fumigatus*, could be used for siderophore-targeted biocontrol of Ilyonectria. Application of purified recombinant AfEstB to ginseng roots inoculated with a virulent I. mors-panacis strain demonstrated a significant protective effect, which disappeared when AfEstB was no longer applied. These data supports targeting of Ilyonectria's iron acquisition mechanism though enzymatic degradation of TAFC as an effective means of controlling Ilyonectria root rot of ginseng.

Candida auris on Apples: Diversity and Clinical Significance

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In 2019, the U.S. Centers for Disease Control and Prevention classified the multidrug-resistant *Candida auris* as one of five pathogens posing the most urgent threats to public health. At present, the environment(s) that might have contributed to the development and spread of antifungal resistance in *C. auris* is unknown. Here, we tested whether fruits could be a source of multidrug-resistant *C. auris*. We identified genetically diverse *C. auris* strains with reduced sensitivity to major triazole dimethyl inhibitors fungicides on the surfaces of stored apples. The successful isolation o*f C. auris* from apples here calls for additional investigations into plants as a reservoir of *C. auris*. Our findings suggest that *C. auris* in the natural ecosystem may come in contact with agriculture fungicides and that stored fruits could be a significant niche for the selection of azole resistance in *C. auris* and other human fungal pathogens.

Unravelling cryptic evolution of insect gut-dwelling fungi using Harpellales as a model

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Harpellales is one of the most species-rich orders in Kickxellomycotina (Zoopagomycota) containing 38 genera with over 200 species. Fungi in Harpellales are known as insect gut dwellers and have been recorded worldwide since the first report in 1929. Comparative genomics has been helpful in identifying evolutionary hallmarks and cryptic biological interactions. Available Harpellales genomes have allowed us to discover several cryptic features, including a mosquito-originated polyubiquitin gene, whole-genome duplications, and the dual function of stop codons to produce Selenocysteine. However, the genomic information of Harpellales is not proportional to their biodiversity and the draft quality of genome assemblies hinders further investigation. With a few newly assembled genomes in our laboratory, I will discuss recent research progress in Harpellales. These results will provide new evidence for studies in insect-fungus symbioses and the non-canonical evolution of fungi in extreme environments (e.g., insect guts).

An inducible CRISPR interference system to study the role of essential gene function during drug tolerance in antifungal resistant isolates of *Candida albicans*.

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University of Guelph

The research presented here describes the use of a transcriptional repression approach known as CRISPR interference (CRISPRi) to target essential genes for repression in *Candida albicans* and elucidate gene function under antifungal drug exposure. A subset of 130 essential genes that were found to have homologs in three other medically relevant fungal pathogens, and lack human homologs, were chosen as candidates for this study as they represent putative broad-range antifungal drug targets. An inducible CRISPRi pooled library targeting these genes will be synthesized and transformed into wild-type and two antifungal resistant isolates of *C. albicans*, to generate three pooled fungal libraries. The *C. albicans* CRISPRi mutant libraries will then be subjected to competitive growth assays to identify which CRISPRi-strains are enriched or depleted after drug exposure. CRISPRi-strains that show increased sensitivity will be selected for follow-up phenotypic assessment to obtain a better understanding of the gene function during drug exposure.

Evolutionary dynamics of the ergot alkaloid biosynthetic gene cluster in Canadian *Claviceps purpurea*

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Agriculture and Agri-Food Canada

Research into ergot alkaloid production in major cereal cash crops is crucial for furthering our understanding of the potential toxicological impacts of *Claviceps purpurea* upon Canadian agriculture and to ensure consumer safety. An untargeted metabolomics approach profiling extracts of *C. purpurea* sclerotia from four different grain crops separated *C. purpurea* strains into two distinct metabolomic classes based on ergot alkaloid content. Variances in *C. purpurea* alkaloid profiles were correlated to genetic differences within the lpsA1/lpsA2 genes of the ergot alkaloid biosynthetic gene cluster from previously published genomes and from newly sequenced, long-read genome assemblies of Canadian strains. We hypothesize, based on our analysis of cluster composition and polymorphism, that ergot alkaloid production in *C. purpurea* sclerotia is dynamic and adaptive. The patterns of lpsA gene diversity described in this small subset of Canadian strains provides a framework for understanding accelerated evolution of ergot alkaloid production in *Claviceps purpurea*.

Defining the role of ClpX in reversal of antifungal resistance in *Cryptococcus neoformans*

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Cryptococcus neoformans is an opportunistic fungal pathogen known to cause lethal cryptococcal meningitis in immunocompromised individuals (e.g., HIV/AIDS). Treatment for this infection consists of three categories of antifungals: polyenes, pyrimidine analogs and azoles. However, the availability of these drugs is limited in certain regions, causing the prolonged use of fluconazole (azole) monotherapy which has lead to the increase in clinical cases of fluconazole-resistant strains of *C. neoformans*. Research conducted in the JGM laboratory at the University of Guelph has revealed that ClpX, a molecular chaperone involved with protein homeostasis, has an essential role in the mechanism of fluconazole-resistance in *C. neoformans*. Using quantitative proteomics, ClpX will be characterized by profiling the proteomes of resistant strains of *C. neoformans* after the deletion of clpX or inhibition of ClpX to further reveal the mechanism of resistance. The therapeutic potential of ClpX disruption will be assessed through in vitro and in vivo models.

Pararesistance: a mutation-independent mechanism of antifungal drug resistance

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Drug resistance is a major cause of treatment failure in infectious diseases. Recent studies revealed that adaptive epigenetic states can be induced in response to drug; however, the mechanisms remain poorly characterized. We discovered that in *Candida albicans* (a leading human fungal pathogen), transient exposure of a clonal population to fluconazole (a widely used antifungal) elicits a sustained protective response in a subpopulation of cells. This mode of stress-induced drug adaptation, which we term 'pararesistance', is heritable, like genetic-based resistance, and reversible, like epigenetically-encoded persistence and tolerance. RNA-sequencing indicates that pararesistance is distinct from known epigenetic states in *C. albicans*. Targeted chemical screen reveals that perturbing the proteostasis network strongly impacts the establishment of pararesistance. Together, this work presents a new paradigm for understanding non-genetic mechanisms that drive the rapid evolution of drug resistance, establishing a conceptual framework for developing novel therapeutic strategies that target evolutionary processes.

Identifying and characterizing genes important for *Candida albicans* fitness in diverse environmental conditions

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Candida albicans—a human fungal pathogen—is a threat to human health with mortality rates of ~40%. This project aims to identify and characterize genes important for fitness within host-relevant environments by characterizing the essential gene set for *C. albicans* in diverse environmental conditions. This will be accomplished by leveraging a collection of barcoded *C. albicans* conditional-expression diverse cues. Screening in minimal nutrient medium at 30°C identified a novel essential gene with no *S. cerevisiae* homolog, C1_09670C, which is predicted to encode subunit 3 of replication factor A (RFA). Further screens performed at physiological temperature, low iron, and serum-supplemented medium, generated a rich dataset of genes important for fitness under specific conditions including C3_06880W, an uncharacterized gene required for fitness in physiological temperatures with no functional predictions to date. This work will reveal novel insights into *C. albicans* biology which could help enable development of new therapeutic strategies.

The response of plant holobionts to stress: fungi as central players

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It is posited that multicellular host and their microbiota (the holobiont) form an evolutionary unit. Since the microbiota is generally much more dynamic and flexible than the host, rapid responses to environmental changes should be mediated by the microbiota. To test these ideas, we have subjected plants to stresses and measured the metatranscriptomic response of the root and rhizosphere. In the roots, the response of the plant itself was dwarfed by the response of the fungal endophytes, whereas the bacteria showed the most significant response in the rhizosphere. The responses could be due to shifts in the gene expression or shifts in community composition, but in all cases, it resulted in a significant re-arrangement in gene expression patterns. These results highlight that increasing plant resilience and resistance to environmental stresses will be most efficient if mediated by the microbiota, especially the fungi.

Long reads and Hi-C sequencing illuminate the two-compartment genome of the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*

Gökalp Yildirir
University of Ottawa

In this study, we combine Nanopore (ONT) sequencing with chromatin conformation capture sequencing (Hi-C) to reveal chromosome and epigenetic diversity in a group of obligate plant symbionts: the arbuscular mycorrhizal fungi (AMF). We find that five phylogenetically distinct strains of the model AMF *Rhizophagus irregularis* carry 33 chromosomes with substantial within-species variability in size, as well as in gene and repeat content. Strain-specific Hi-C contact maps reveal a ‘checkerboard’ pattern that underline two dominant euchromatin (A) and heterochromatin (B) compartments. Each compartment differs in the level of gene transcription, regulation of candidate effectors and methylation frequencies. The A-compartment is more gene-dense and contains most core genes, while the B compartment is more repeat-rich and has higher rates of chromosomal rearrangement. While the B-compartment is transcriptionally repressed, it has significantly more secreted proteins and in planta upregulated candidate effectors, suggesting a possible host-induced change in chromosome conformation.

Ozone restricts reproduction success of ophiostomatoid fungi associated with mountain pine beetle in isolate specific manner

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University of Alberta

Ozone concentration has increased in northern hemisphere. We investigated the potential impact of increased ozone concentration on the growth of three fungal symbionts of mountain pine beetle *Grosmannia clavigera*, *Ophiostoma montium*, and *Leptographium longiclavatum*. We subjected fungi to 100ppb/day ozone treatment for four days and estimated their growth, spore and ergosterol production. Overall, increased ozone reduced growth up to 93% across all fungal species. However, there were variations within species (isolates) in their responses to the increased ozone. For instance, one isolate of *L. longiclavatum* had the highest growth reduction (93%), but also had the highest spore production, relative to the other isolates of *L. longiclavatum*. Moreover, ergosterol production as a proxy to total fungal biomass was reduced in some but not all isolates of fungi tested. We conclude that ozone hinders the reproduction success in MPB's fungal symbionts by restricting their growth, spore and ergosterol production.

Histopathology of the *Plasmodiophora brassicae*-Chinese Cabbage Interaction in Hosts Carrying Different Sources of Resistance

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Clubroot is a serious soil-borne disease of crucifers caused by the obligate parasite *Plasmodiophora brassicae.* The histopathology of clubroot resistance in two Chinese cabbage (*Brassica rapa* ssp. pekinensis) inbred lines Bap055 (controlled by the CRa) and Bap246 (control by unknown recessive gene), challenged with pathotype 4 of P. brassicae, was evaluated. The Chinese cabbage cultivar "Juxin" served as a susceptible check. Despite their resistance, primary and secondary infection were observed to occur in Bap055 and Bap246. Infection occurred most quickly on "Juxin", and the slowest on Bap246. At 14 DPI, the percentage of cortical infection in "Juxin", Bap055 and Bap246 was 93.3, 20.0, and 11.1%, respectively. Secondary infection in both of these resistant hosts was restricted compared with "Juxin", and the vascular system remained intact. The defense mechanisms and expression of resistance appears to differ between Chinese cabbage cultivars carrying different sources of resistance.

Detoxification of mycotoxins through biotransformation of their chemical structures

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Mycotoxins produced by certain types of fungi (molds) are toxic compounds with great variations in chemical structures and can cause adverse effects on plants, animals and humans. Among the Innovative strategies and technologies are being explored and developed to mitigate mycotoxin contaminations, the biological detoxification by transforming chemical structures of the mycotoxins has showed very promising results in many studies and is attracting more and more researchers and industrial developers due to its specificity, acceptance by consumers, and possible utilization under mild processing conditions. This presentation will reveal the development of the mycotoxin biodetoxification strategy. Two mycotoxins significant to Canada, deoxynivalenol and patulin, will be used as examples to provide understanding of using different mycotoxin transformations for detoxifying mycotoxins and demonstrate various potential applications of the biodetoxification for mitigating mycotoxins in agri-food value chain.