Program Book

The Joint CanFunNet and Great Lakes Mycology Conference

May 26-28, 2021

Schedule

WEDNESDAY, MAY 26, 2021				
8:15AM-8:30AM PT 10:15AM-10:30AM CT 11:15AM-11:30AM ET	Opening remarks and introduction			
8:30AM-10:30AM PT 10:30AM-12:30PM CT 11:30AM-1:30PM ET	Plenary session - Plant pathogens: evolution, effectors and surveillance			
10:30AM-10:50AM PT 12:30PM-12:50PM CT 1:30PM-1:50PM ET	Breakroom – on Spatial Chat			
10:50AM-11:20AM PT 12:50PM-1:20PM CT 1:50PM-2:20PM ET	Pathogen emergence and evolution (1A)		Applied ecology 1 (3A)	Hybridization (4A)
11:20AM-11:40AM PT 1:20PM-1:40PM CT 2:20PM-2:40PM ET	Breakroom – on Spatial Chat			
11:40AM-12:40PM PT 1:40PM-2:40PM CT 2:40PM-3:40PM ET	Fighting fungal infections (1B)	Yeasts in Canadian vineyards (2B)	Applied ecology 2 (3B)	Surveillance and mitigation (4B)
12:40PM-1:00PM PT 2:40PM-3:00PM CT 3:40PM-4:00PM ET	Breakroom – on Spatial Chat			
1:00PM-2:00PM PT 3:00PM-4:00PM CT 4:00PM-5:00PM ET	Fruit and vegetable pathology (1C)	Biotechnology and industrial applications (2C)	Disturbance and invasion ecology (3C)	Finding a job in Canada: institutional showcase (4C)
Starts at 5:30PM ET	Spatial Chat-Social Networking Events			

Schedule

THURSDAY, MAY 27, 2021				
8:30AM-10:00PM PT 10:30AM-12:00PM CT 11:30AM-1:00PM ET	Plenary session - Genomes to phenomes			
10:00AM-10:20AM PT 12:00PM-12:20PM CT 1:00PM-1:20PM ET	Breakroom – on Spatial Chat			
10:20AM-11:20AM PT 12:20PM-1:20PM CT 1:20PM-2:20PM ET	CPS session 1 (5A), **starts at 1:15PM ET**	Gene regulation (6A)	Fungal ecophysiology (7A)	Stress responses (8A)
11:20AM-11:40AM PT 1:20PM-1:40PM CT 2:20PM-2:40PM ET	Breakroom – on Spatial Chat			
11:45AM-12:40PM PT 1:45PM-2:40PM CT 2:40PM-3:40PM ET	CPS session 2 (5B)	Synthetic biology (6B)	Communities: from patterns to predictions (7B)	Genetics of adaptation (8B)
12:40PM-1:00PM PT 2:40PM-3:00PM CT 3:40PM-4:00PM ET	Breakroom – on Spatial Chat			
1:00PM-2:00PM PT 3:00PM-4:00PM CT 4:00PM-5:00PM ET	Fungi, old and new (5C)	Yeast as a model (6C)	Mycobiomes (7C)	New approaches for studying pathogens (8C)
Starts at 5:30PM ET	Spatial Chat-Social Networking Events			

Schedule

FRIDAY, MAY 28, 2021				
8:30AM-10:00PM PT 10:30AM-12:00PM CT 11:30AM-1:00PM ET	Plenary session - Ecology from the ground up			
10:00AM-10:20AM PT 12:00PM-12:20PM CT 1:00PM-1:20PM ET	Breakroom – on Spatial Chat			
10:20AM-11:20AM PT 12:20PM-1:20PM CT 1:20PM-2:20PM ET	CPS session 3 (9A)	Evolutionary genetics and nuclear dynamics (10A)	Biodiversity at the intersection of taxonomy & phylogeny (11A)	Surface Structures and membranes (12A)
11:20AM-11:40AM PT 1:20PM-1:40PM CT 2:20PM-2:40PM ET	Breakroom – on Spatial Chat			
11:45AM-12:40PM PT 1:45PM-2:40PM CT 2:40PM-3:40PM ET	CPS session 4 (9B)	Advances in arbuscular mycorrhizae (10B)	Endophyte ecology (11B)	Resistance (12B)
12:40PM-1:00PM PT 2:40PM-3:00PM CT 3:40PM-4:00PM ET	Breakroom – on Spatial Chat			
1:00PM-2:00PM PT 3:00PM-4:00PM CT 4:00PM-5:00PM ET	CPS session 5 (9C)	Frontiers in genomics (10C)	Fungal conservation (11C)	Molecular function (12C)
Starts at 5:30PM ET	Spatial Chat-Social Networking Events			

About Us

Organizing Committee	
Emile Gluck-Thaler – Chair	Gopal Subramaniam
Viola Halder	Greg Thorn - Local Host
Gavin Kernaghan	Émilie Tremblay
Rebecca Shapiro	Allison Walker
Heather Slinn	
Scientific Program Committee	
Emile Gluck-Thaler	Gopal Subramaniam
Brianna Ball	Émilie Tremblay
Viola Halder- Program designer	
Presentation Competition Committee	
Émilie Tremblay- Principal coordinator	Viola Halder
Outreach Committee	
Emile Gluck-Thaler	Rebecca Shapiro
Brianna Ball	Nicolette Shaw - Graphic Designer
Nicola Case	Émilie Tremblay
Viola Halder- Principal coordinator	Lauren Wensing
Conference Website and IT Management	
Michael Zaigh	Conference Services at Western University

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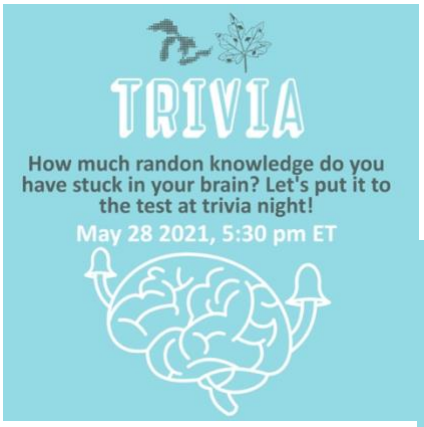

CanFunNet Concurrent Themes

Pathogen emergence and evolution
Fighting fungal infections
Yeasts in Canadian vineyards
Surveillance and mitigation
Fruit and vegetable pathology
Biotechnology and industral applications
Disturbance and invasion ecology
Finding a job in Canada: institutional showcase
Communities: from patterns to predictions
New approaches for studying pathogens
Evolutionary genetics and nuclear dynamics
Biodiversity at the intersection of taxonomy & phylogeny
Surface Structures and membranes
Advances in arbuscular mycorrhizae

Hybridization
Applied ecology
Gene regulation
Stress responses
Fungi, old and new
Fungal ecophysiology
Frontiers in genomics
Genetics of adaptation
CPS
Resistance
Mycobiomes
Yeast as a model
Synthetic biology
Molecular function
Endophyte ecology
Fungal conservation

The Joint Canadian Fungal Network and Great Lakes Mycology Conference
May 26-28th, 2021

Wednesday, May 26th

Opening remarks and introduction

11:15AM-11:30AM ET Organizing committee

Plenary session - Plant pathogens: evolution, effectors and surveillance

Moderated by: Dr. Emile Gluck-Thaler and Viola Halder
Plenary - 11:30AM-1:30PM ET

11:30AM-12:00PM ET	**Eva Stukenbrock** Interspecific hybridization in a fungal pathogen influences transposable element dynamics and shapes genome-wide variation
12:00PM-12:30PM ET	**Bart Thomma** Microbiome manipulation by a fungal plant pathogen using effector proteins
12:30PM-1:00PM ET	**Richard Hamelin** Genomic biosurveillance of forest pathogens: a story written in code
1:00PM-1:30PM ET	**Sarah Hambleton** Forays in the herbarium for rust fungi – data mining, diagnostics and systematics

Pathogen emergence and evolution

Moderated by: Dr. Jennifer Geddes-McAlister
1A - 1:50PM-2:20PM ET

Standard Talks

1:50PM-2:05PM ET	**Yue Wang** The origin of the superbug *Candida auris*
2:05PM-2:20PM ET	**Rebekah Kukurudz** In vitro evolution of posaconazole tolerance in *Candida albicans*

Wednesday, May 26th

Applied ecology 1

Moderated by: Dr. Greg Thorn
3A - 1:50PM-2:20PM ET

Standard Talks

1:50PM-2:05PM ET	**Miranda Hart** The fate of fungal biofertilizers – where do they go, and how do they get there?
2:05PM-2:20PM ET	**Cathy Fahey** Arbuscular mycorrhizal fungi inhibit pine seedling growth and nutrient uptake under different fertilization regimes

Hybridization

Moderated by: Jasmine Ono
4A - 1:50PM-2:20PM ET

Standard Talks

1:50PM-2:05PM ET	**Jasmine Ono** Hybrid Sterility in *Saccharomyces*
2:05PM-2:20PM ET	**Man You** What are the best parental pairs for *Cryptococcus* progeny?

Wednesday, May 26th

Fighting fungal infections

Moderated by: Dr. Jennifer Geddes-McAlister

1B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Jennifer Geddes-McAlister** Combatting fungal infections through the discovery and elucidation of novel anti-virulence strategies
2:55PM-3:10PM ET	**Kali Iyer** Uncovering a Novel Fatty Acid Synthesis Inhibitor with Broad-Spectrum Antifungal Activity
3:10PM-3:25PM ET	**Manjari Shrivastava** Adr1 transcription factor directs regulation of the ergosterol pathway and azole resistance in *C. albicans*

Flash Talks

3:25PM-3:30PM ET	**Emily Xiong** Identifying and characterizing genes essential for *Candida albicans* viability under diverse environmental conditions
3:30PM-3:35PM ET	**Anjali Krishna** Analyzing genetic interactions in *Candida albicans* by targeting stress response genes with uncharacterized functions

Wednesday, May 26th

Yeasts in Canadian vineyards

Moderated by: Dr. Gavin Kernaghan
2B - 2:40PM-3:40PM ET

Standard Talks

	Lihua Fan
2:40PM-2:55PM ET	Characterization of indigenous yeasts isolated from grapes and musts in Nova Scotia
	Stephanie McCann
2:55PM-3:10PM ET	Differences in non-volatile profiles produced by *S. cerevisiae* and *S. uvarum* during Pinot noir fermentation
	Adele Bunbury-Blanchette
3:10PM-3:25PM ET	Characterizing indigenous yeast communities in Nova Scotia vineyards
	Alex Marr
3:25PM-3:40PM ET	Copy Number Variation in Canadian *S. cerevisiae* Wine Yeast Genomes

Wednesday, May 26th

Applied Ecology 2

Moderated by: Dr. Greg Thorn

3B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Lauren Eldred** Phylogenetic binning of Basidiomycota, Zygomycota and Chytridiomycota using the large ribosomal subunit of the RNA gene

Flash Talks

2:55PM-3:00PM ET	**Noor Saeed Cheema** Manipulating the root mycobiome of corn (*Zea mays*) to enhance plant performance and reduce pathogen pressure
3:00PM-3:05PM ET	**Katarina Kukolj** Investigating the effects of the Blewit Mushroom Lepista nuda on the community composition of its soil environment
3:05PM-3:10PM ET	**Becky Loverock** Development of a novel assay for the detection of *Tuber melanosporum* using droplet digital polymerase chain reaction (ddPCR)

Wednesday, May 26th

Surveillance and mitigation

Moderated by: Dr. Émilie Tremblay

4B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Barsha Poudel** Genetic structure of *Macrophomina* populations associated with broadacre crops in Australia.
2:55PM-3:10PM ET	**Marwa Hassine** Evaluation of temporal distribution of airborne inoculum of *Zymoseptoria tritici* and *Puccinia triticina* in Tunisia
3:10PM-3:25PM ET	**Greg Korfanty** The population structure of *Aspergillus fumigatus* from Canadian soils
3:25PM-3:40PM ET	**Brooke Sidney** New Clade Designation and Clustering of Isolates Revealed from Whole Genome Sequencing of Clinical Canadian *Candida glabrata* Isolates

Wednesday, May 26th

Fruit and vegetable pathology

Moderated by: Dr. Leslie Holland

1C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Leslie Holland** The many faces of cranberry fruit rot: fungal complex etiology and why it matters
4:15PM-4:30PM ET	**Scott Redhead** Twinkle, twinkle, little star. How we wondered what you are? The story behind *Valdensia* (*Sclerotiniaceae*)
4:30PM-4:45PM ET	**Yaima Arocha Rosete** Passive spore trapping system and isothermal amplification to support early monitoring of potato and tomato late blight disease in Canada

Flash Talks

4:45PM-4:50PM ET	**Evgeny Ilyukhin** Fungal pathogens associated with Fruit Tree Decline in Ontario
4:50PM-4:55PM ET	**Oscar Villanueva** Pathogenicity and Virulence of a Canadian isolate of *P. capsici* on pepper

Wednesday, May 26th

Biotechnology and industrial applications

Moderated by: Dr. Isabelle Benoit Gelber

2C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Isabelle Benoit Gelber** Secondary metabolite biosynthesis in *Aspergillus niger*
4:15PM-4:30PM ET	**Barret Foster** Enhanced stress tolerance in Norwegian kveik results in increased fermentation efficiencies at extreme temperatures
4:30PM-4:45PM ET	**Saranya Chandrasekharan** Tools for gene expression in *Penicillium citrinum*

Flash Talks

4:45PM-4:50PM ET	**Tyler Watson** Growing a mushroom mat: Investigating mycelial-crop residue application to reduce early-colonizing weeds in row-crop agriculture
4:50PM-4:55PM ET	**Jordan Hofstra** The effect of various nitrogen supplementation techniques on cider fermentation – small changes cause big effects

Wednesday, May 26th

Disturbance and invasion ecology

Moderated by: Dr. Pedro Madeira Antunes
3C - 4:00PM-5:00PM ET

Standard Talks

	Pedro Madeira Antunes
4:00PM-4:15PM ET	Investigating the relationships between invasive plants and pathogens in communities – evidence and the way forward
	Liam Johnson
4:15PM-4:30PM ET	Phylogenetic prediction of the invasion potential of ectomycorrhizal fungi
	Carina Lai
4:30PM-4:45PM ET	Impacts of an invasive plant (*Vinca minor*) on native arbuscular mycorrhizal fungi
	Erica Packard
4:45PM-5:00PM ET	The impact of wildfire severity on soil fungal diversity and community composition in the Okanagan Valley

Finding a job in Canada: institutional showcase

Moderated by: Dr. Gopal Subramaniam
4C - 4:00PM-5:00PM ET

Standard Talks

	Elizabeth Foster
4:00PM-4:15PM ET	Associate Assistant Deputy Minister – Agriculture Canada – Science & Technology
	Adrian Herod
4:15PM-4:30PM ET	MITACS funded Postdoc Associate – Agriculture Canada - Policy
	Benjamin Scott
4:30PM-4:45PM ET	Business Development and partnerships – Concordia Genome Foundry

Thursday, May 27th

Plenary session - Genomes to Phenomes

Moderated by: Dr. Gopal Subramaniam and Dr. Rebecca Shapiro

Plenary - 11:30AM-1:00PM ET

11:30AM-12:00PM ET	**Jason Stajich** Evolutionary Dynamics of Fungal Genomes from *Aspergillus* to *Zygomycete*
12:00PM-12:30PM ET	**Christian Landry** Insight from the evolution of yeast hybrid populations across 700 generations in the near absence of natural selection
12:30PM-1:00PM ET	**Leah Cowen** Identifying Vulnerabilities in Fungal Pathogens Through Functional and Chemical Genomic Analyses

Plant pathogens - Omics, systematics and disease control 1

Moderated by: Dr. Miao Mindy Liu

5A - 1:15PM-2:20PM ET

1:15PM-1:20PM ET	**Barry Savile** Introduction from CPS president

Standard Talks

1:20PM-1:50PM ET	**Linda Harris (Keynote)** Gramillins: Host-specific phytotoxins produced by cereal pathogen *Fusarium graminearum*
1:50PM-2:05PM ET	**Thomas Witte** Accessory Genes and Secondary Metabolism in *Fusarium poae*
2:05PM-2:20PM ET	**Wagner Calegari Fagundes** Host specificity determines a new fungal plant pathogen population

Thursday, May 27th

Gene regulation

Moderated by: Dr. Carl de Boer

6A - 1:20PM-2:20PM ET

Standard Talks

1:20PM-1:35PM ET	**Carl de Boer** A comprehensive fitness landscape model reveals the evolutionary history and future evolvability of eukaryotic cis-regulatory DNA sequences
1:35PM-1:50PM ET	**Murat Can Kalem** Puf4 Mediates Post-transcriptional Regulation of Cell Wall Biosynthesis and Caspofungin Resistance in *Cryptococcus neoformans*
1:50PM-2:05PM ET	**Gaëlle Kouyoumdjian** Large-scale screening of activated transcription factors reveals rewiring and novel functions in *Candida albicans*

Flash Talks

2:05PM-2:10PM ET	**Manish Pareek** Conserved transcription factors cha-4 & rrg-2 orthologs are required for fruiting body development in *Coprinopsis cinerea*
2:10PM-2:15PM ET	**Rosa Eskandari** Shared components of the FRQ-less oscillator and TOR pathway maintain circadian rhythmicity in *Neurospora*
2:15PM-2:20PM ET	**Nick Gervais** Implementation of a CRISPR-based Activation System for Gene Regulation in *Candida albicans*

Thursday, May 27th

Fungal ecophysiology

Moderated by: Dr. Heather Slinn

7A - 1:20PM-2:20PM ET

Standard Talks

	Samuel Plante
1:20PM-1:35PM ET	The distinct ecological signals triggering activation of spores of closely related yeasts
	Erin Feldman
1:35PM-1:50PM ET	Differential Expression of Cell Wall Degrading Enzymes in *Oidiodendron maius* in Response to Varying Carbon Source
	Sarah Neumann
1:50PM-2:05PM ET	Investigating nitrogen transfer between *Suillus tomentosus* and *Pinus contorta* seedlings in an ectomycorrhizal network
	Sydney Gram
2:05PM-2:20PM ET	Diversity and host preferences of mycophagous insects in southern Ontario

Stress Responses

Moderated by: Linda Horianopoulos

8A - 1:20PM-2:20PM ET

Standard Talks

	Linda Horianopoulos
1:20PM-1:35PM ET	Loss of a nuclear co-chaperone sensitizes *Cryptococcus neoformans* to DNA damaging agents
	Brianna Ball
1:35PM-1:50PM ET	Global analysis of the Protein Kinase A-regulated phosphoproteome of *Cryptococcus neoformans* reveals new insight into vesicular protein trafficking
	Saif Hossain
1:50PM-2:05PM ET	Mitochondrial perturbation reduces susceptibility to xenobiotics through altered efflux in *Candida albicans*
	Malisa Fernando
2:05PM-2:20PM ET	The Unfolded Protein Response is required for antifungal drug resistance in yeast

Thursday, May 27th

Plant pathogens - Omics, systematics and disease control 2

Moderated by: Dr. Wen Chen
5B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Miao Liu** The identities and host ranges of hop and berry powdery mildews to be clarified
2:55PM-3:10PM ET	**Yaima Arocha Rosete** Multigene sequencing reveals different subgroups of '*Candidatus Phytoplasma pruni*' affecting two Canadian flowering plant species.
3:10PM-3:25PM ET	**Ryan Gourlie** Global pangenome analysis of *Pyrenophora tritici-repentis* reveals high plasticity and translocation of the ToxA gene between different chromosomes
3:25PM-3:40PM ET	**Mohamed Hafez** An updated global ToxA haplotype network with evolutionary model for this gene in necrotrophic fungal pathogens

Synthetic biology

Moderated by: Dr. Kevin Solomon
6B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Kevin Solomon** Characterization and Domestication of *Neocallimastigomycota* for Direct Biomanufacturing from Renewable Biomass
2:55PM-3:10PM ET	**Lauren Wensing** Developing a CRISPRi library to study essential gene function in antifungal-resistant *Candida albicans* isolates
3:10PM-3:25PM ET	**Mudabir Abdullah** Rapid, Scalable Combination of Genetically Engineered Loci in Yeast using CRISPR/Cas9 induced Gene Drive (CGD)
3:25PM-3:40PM ET	**Susannah Selber-Hnatiw** Secondary metabolite production in *Aspergillus niger:* methyltransferase specificity

Thursday, May 27th

Communities: from patterns to predictions

Moderated by: Himeshi Samarasinghe

7B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Himeshi Samarasinghe** Global Patterns in Culturable Soil Yeast Diversity
2:55PM-3:10PM ET	**Fantin Mesny** Genetic determinants of endophytism in the *Arabidopsis* root mycobiome
3:10PM-3:25PM ET	**Bruce Malloch** Structure and succession of salt marsh decomposer communities in the Minas Basin, Nova Scotia

Flash Talks

3:25PM-3:30PM ET	**John Hume** Ectomycorrhizal fungal communities associated with urban European hornbeam trees in British Columbia
3:30PM-3:35PM ET	**Kendra Sampson** Evaluating salt marsh rhizosphere carbon stocks and arbuscular mycorrhizal colonization in vegetation zones across a chronosequence in Nova Scotia

Thursday, May 27th

Genetics of adaptation

Moderated by: Dr. Anna Bazzicalupo
8B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Anna Bazzicalupo** Fungal heavy metal adaptation through single nucleotide polymorphisms and copy-number variation
2:55PM-3:10PM ET	**Kamaldeep Chhoker** Use of genetic screen and genome re-sequencing to understand the regulation of pigment production in the extremotolerant fungus *Exophiala dermatitidis*
3:10PM-3:25PM ET	**Carla Bautista** Interspecific hybrids show a reduced adaptive potential under DNA damaging conditions
3:25PM-3:40PM ET	**YuYing Fan** Genome-wide association analysis for triazole resistance in *Aspergillus fumigatus*

Fungi, old and new

Moderated by: Dr. Ludovic Le Renard
5C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Ludovic Le Renard** Comparative anatomy and phylogeny of fossil Callimothallus and their living relatives
4:15PM-4:30PM ET	**Jonathan Mack** Three unusual and novel synnematous hyphomycetes
4:30PM-4:45PM ET	**Alicia Banwell** A new albino mutant mushroom: Phylogenetic, genetic, and chemical analyses separating white and golden chanterelles
4:45PM-5:00PM ET	**Victoria Kennedy** Investigating the identity of a potential new *Wawelia* species

Thursday, May 27th

Yeast as a model

Moderated by: Dr. Patrick Lajoie
6C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Safia Mahabub Sauty** The role of PCNA in coordinating the functions of CAF1 and Rrm3p at paused replication forks in *S. cerevisiae*
4:15PM-4:30PM ET	**Kholoud Shaban** Investigation of key factors that regulate epigenetic conversions in *S. cerevisiae* during replication fork pausing
4:30PM-4:45PM ET	**Devina Singh** A Toolkit for automated high-throughput cloning and manipulation of DNA in budding and fission yeast
4:45PM-5:00PM ET	**Farhat Zafar** Humanized Yeast as a Platform to Measure the Functional Impact of Human Genetic Variation

Mycobiomes

Moderated by: Gulnara Tagirdzhanova
7C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Gulnara Tagirdzhanova** A metagenomics solution: nailing down unculturable fungi in a lichen symbiosis
4:15PM-4:30PM ET	**Sarah Adams** A Characterization of the Grape Root Microbiome Across Rootstocks and Root Depth in a Cool Climate Organic Vineyard
4:30PM-4:45PM ET	**Madison Arnold** Maternal dietary fat Intake in predicting the breast milk mycobiome
4:45PM-5:00PM ET	**Lahari Basu** A Phylogenetic Analysis Using Large Subunit Ribosomal DNA in Ascomycota

Thursday, May 27th

New approaches for studying pathogens
Moderated by: Dr. Adnane Sellam
8C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Michael Hallett** A deep learning approach to capture the essence of *Candida albicans* morphologies
4:15PM-4:30PM ET	**Philippe Després** The sequence-function landscape of an antifungal target
4:30PM-4:45PM ET	**Boyan Liu** Decoding the interaction between wheat and *Fusarium graminearum* on a systems level
4:45PM-5:00PM ET	**Alice Xue** Leveraging machine learning essentiality predictions and chemogenomic interactions to characterize a fungal-selective glutaminyl-tRNA synthetase inhibitor with potent *Candida albicans* bioactivity

Friday, May 28th

Plenary session - Ecology from the ground up

Moderated by: Dr. Greg Thorn and Dr. Alison Walker

Plenary - 11:30AM-1:00PM ET

11:30AM-12:00PM ET	**Lynne Boddy** Getting to the heart of the matter: decay of veteran trees
12:00PM-12:30PM ET	**Ian Sanders** Using mycorrhizal fungal variation to increase growth of globally important crops
12:30PM-1:00PM ET	**Justine Karst** Manipulating soil fungal communities as a tool to restore forests post-mountain pine beetle in western Canada

Plant pathogens - Omics, systematics and disease control 3

Moderated by: Dr. Wen Chen

9A - 1:20PM-2:20PM ET

Standard Talks

1:20PM-1:50PM ET	**Tyler Avis (Keynote)** Biochemical insights into the antimicrobial properties of membrane-targeting compounds produced by antagonistic microorganisms on fungal plant pathogens
1:50PM-2:05PM ET	**Michelle Thompson** Exploring the Microbes of Maize Silks
2:05PM-2:20PM ET	**Jacob Walsh** Molecular Network guided Natural Product Discovery from Ginseng Root Rot

Friday, May 28th

Evolutionary genetics and nuclear dynamics

Moderated by: Dr. Nicolas Corradi
10A - 1:20PM-2:20PM ET

Standard Talks

1:20PM-1:35PM ET	**Nicolas Corradi** The Genetics of Arbuscular Mycorrhizal Fungi
1:35PM-1:50PM ET	**Alexandra Dallaire** DNA methylation and small RNA profiling shed light on genomic organisation of the symbiotic fungus *Rhizophagus irregularis*
1:50PM-2:05PM ET	**Vikas Yadav** Sexual parasitism in Fungi: Uniparental nuclear inheritance during bisexual mating in fungi
2:05PM-2:20PM ET	**Ben Auxier** An NLR-like system delimits individuals in the basidiomycete *Coprinopsis cinerea*

Biodiversity at the intersection of taxonomy & phylogeny

Moderated by: Dr. Alfredo Justo
11A - 1:20PM-2:20PM ET

Standard Talks

1:20PM-1:35PM ET	**Alfredo Justo** Dealing with hyperdiverse lineages in Agaricales: challenges for the modern-day taxonomist
1:35PM-1:50PM ET	**Jeremy Dettman** Genome-informed selection of loci for molecular systematics: A test case with Alternaria
1:50PM-2:05PM ET	**Nourin Aman** Diversity and biogeographic relationships of Pakistan macrofungi
2:05PM-2:20PM ET	**Kendra Driscoll** Lichenicolous fungi in Atlantic Canada: documenting an overlooked component of the mycobiota

Friday, May 28th

Surface Structures and membranes

Moderated by: Nicola Case

12A - 1:20PM-2:20PM ET

Standard Talks

1:20PM-1:35PM ET	**Jessie MacAlpine** Lactobacillus-secreted Yak1 inhibitor, 1-acetyl-beta-carboline, blocks *Candida albicans* morphogenesis and biofilm formation
1:35PM-1:50PM ET	**Hanna Ostapska** Exopolysaccharides in co-operative biofilm interactions between Aspergillus fumigatus and *Pseudomonas aeruginosa*
1:50PM-2:05PM ET	**Nicole Revie** A Tetrahydro-ß-carboline Derivative Potentiates Azole Activity Against *Candida albicans* via Perturbation of Membrane Homeostasis

Flash Talks

2:05PM-2:10PM ET	**Vanessa Karina Alves da Silva** Calorie restriction reshapes cell wall in *Cryptococcus neoformans*
2:10PM-2:15PM ET	**Chris Lee** Characterizing the role of choline in *Cryptococcus neoformans* using the phospholipid N-methyltransferase Opi3
2:15PM-2:20PM ET	**Antonia Du Bois** Characterizing the Novel Bioactivity of the Compound T-042756 Against *Candida albicans*

Friday, May 28th

Plant pathogens - Omics, systematics and disease control 4

Moderated by: Dr. Miao Mindy Liu
9B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Isadora Louise Alves da Costa** Orbitides and free polyamines have similar fungicidal activity against three common pathogens of flax in vitro
2:55PM-3:10PM ET	**Sydney Forbes** Continued investigation of the *U. maydis* APSES protein encoding gene nlt1
3:10PM-3:25PM ET	**Chris Rampitsch** The ROS-targeted redox proteome of *Puccinia triticina* germlings
3:25PM-3:40PM ET	**Jun Huang** CRISPR/Cas12a induced DNA double-strand breaks are repaired by locus-dependent and error-prone pathways in a fungal pathogen

Advances in arbuscular mycorrhizae

Moderated by: Dr. Marisol Sanchez-Garcia
10B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Marisol Sanchez-Garcia** Comparative assemblomics and the use of amplified single nuclei for generating reference genomes of arbuscular mycorrhizal fungi
2:55PM-3:10PM ET	**Pierre-Luc Chagnon** Preference does not mean reliance on: plant-mycorrhizal partnerships are deterministic, yet flexible
3:10PM-3:25PM ET	**Edouard Evangelisti** Artificial intelligence enables automatic phenotyping of arbuscular mycorrhizal fungal root colonisation
3:25PM-3:40PM ET	**Shelby Law** The effect of phosphorus on arbuscular mycorrhizal mediated soil carbon storage

Friday, May 28th

Endophyte ecology

Moderated by: Dr. Heather Hager

11B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Manish Raizada** A fungal endophyte creates a hydrophobic bandage to protect its host tree from pathogen invasion
2:55PM-3:10PM ET	**Heather Slinn** Intraspecific variation in plant chemistry and land-use history in a common garden experiment, acts as an ecological filter to insect herbivory and fungal endophyte communities
3:10PM-3:25PM ET	**Jenna Dale** Foliar fungal communities in Epichloë endophyte-infected grass
3:25PM-3:40PM ET	**Lilianne Gee** Fungal endophyte discovery, characterization and function in various host grasses.

Friday, May 28th

Resistance

Moderated by: Brianna Ball

12B - 2:40PM-3:40PM ET

Standard Talks

2:40PM-2:55PM ET	**Nicola Case** The macrophage-derived protein PTMA induces filamentation of the human fungal pathogen *Candida albicans*
2:55PM-3:10PM ET	**Ola Salama** Differential Response of *C. albicans* Planktonic and Biofilm Cells to Fluconazole and Boric Acid
3:10PM-3:25PM ET	**Samuel Stack-Couture** Specific functions of the ER chaperone Kar2 regulate caspofungin resistance in *Saccharomyces cerevisiae*

Flash Talks

3:25PM-3:30PM ET	**Domenica De Luca** Genetic Determinants of Resistance in Antifungal Resistant Clinical Isolates of *Candida glabrata* in Canada
3:30PM-3:35PM ET	**Richard Summerbell** The next pandemic: *Trichophyton indotineae* in Canada

Friday, May 28th

Plant pathogens - Omics, systematics and disease control 5

Moderated by: Dr. Miao Mindy Liu

9C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Levente Kiss** A hidden friend of allergic people: *Cryptophyllachora ambrosiae*, an enigmatic fungal pathogen of common ragweed (*Ambrosia artemisiifolia*)
4:15PM-4:30PM ET	**Pooja Sridhar** Mechanisms underlying the chemotropism of *Fusarium graminearum* that enable pathogenicity

Flash Talks

4:30PM-4:35PM ET	**Tanya Sharma** Role of *Fusarium graminearum* Ste3 receptor in mediating hyphal chemotropism and pathogenesis towards cereal crops
4:35PM-4:40PM ET	**Vedha Patel** RNAi triggered systemic acquired resistance to combat emerging plant pathogens
4:40PM-4:45PM ET	**Sara Stricker** Understanding *Stemphylium vesicarium* in Ontario

Friday, May 28th

Frontiers in genomics

Moderated by: Dr. Yan Wang

10C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Yan Wang** Genome evolution and diversity of insect gut-dwelling fungi
4:15PM-4:30PM ET	**Jacob Steenwyk** A gene coevolution network maps eukaryotic cellular and genomic structure and function
4:30PM-4:45PM ET	**Eric Chen** Comparative genomics and epigenomics of Trichosporon and Cutaneotrichosporon polyploid fungi with their closest haploid relative using Nanopore long-read sequencing

Flash Talks

4:45PM-4:50PM ET	**Marc-André Lachance** *Metschnikowia* Taxogenomics
4:50PM-4:55PM ET	**Evelina Basenko** FungiDB: Tools for genomic-scale data exploration, analysis and discovery
4:55PM-5:00PM ET	**Dong Kyung Lee** *Metschnikowia* mitochondrial introns

Friday, May 28th

Fungal Conservation

Moderated by: Dr. Allison Walker and Sigrid Jakob
11C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Sigrid Jakob** Engaging Citizen Scientists To Document 10 Species Of Rare Fungi On The West Coast
4:15PM-4:30PM ET	**Alfredo Justo** Red-Listed fungal species present in Canada
4:30PM-4:45PM ET	**Lotus Lofgren** Fungal Biodiversity in the Time of Big Data: How Expanding Definitions of Conservation Can Preserve the Past and Drive the Future
4:45PM-5:00PM ET	**Michael Burzynski** Working with volunteers to survey a province's mycota

Friday, May 28th

Molecular function

Moderated by: Viola Halder

12C - 4:00PM-5:00PM ET

Standard Talks

4:00PM-4:15PM ET	**Cameron Semper** Structural and functional characterization of ARO1 from *Candida albicans*
4:15PM-4:30PM ET	**Emily Puumala** Identification of a novel lipid biosynthesis inhibitor with activity against the emerging fungal pathogen *Candida auris*
4:30PM-4:45PM ET	**Salma Rashid** Role of SAGA complex subunits in gene regulation of *Candida albicans*

Flash Talks

4:45PM-4:50PM ET	**Braydon Black** Exploring the Role of Glutathione in the AIDS-associated Fungal Pathogen *Cryptococcus neoformans*
4:50PM-4:55PM ET	**Sasi Jagadeesan** Sensitivity of Yeast to Lithium Chloride and Regulation of Translation
4:55PM-5:00PM ET	**Irsa Shoukat** Elucidating the roles of force-producing motors *in Candida albicans* mitosis: possible mechanisms for generating aneuploidy

Abstracts

Rapid, Scalable Combination of Genetically Engineered Loci in Yeast using CRISPR/Cas9 induced Gene Drive (CGD)

Abdullah, Mudabir*; Greco, Brittany M.; Vandeloo, Michelle; Laurent, Jon M.; Garge, Riddhiman K.; Akhmetov, Azat; Marcotte, Edward M.; Aashiq, H. Kachroo
Concordia University
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For decades, Baker's yeast has served as a tremendous model for biomedical research. However, with the emergence of yeast as a model eukaryote for systems/synthetic biology, there is a need for highly efficient and scalable genome engineering strategies. We have generated a library of fully characterized CRISPR-Cas9 reagents targeting many yeast loci. By combining CRISPR-Cas9 mediated DSB, yeast mating and sporulation, we demonstrate a highly efficient gene drive for precise, scar-free, and selection-less conversion of yeast to engineered loci. To quantify the efficiency of CGD, we convert the Ade2 to the knockout locus using a heterozygous diploid strain (Ade2 / ?ade2::KanMX) at ~100% efficiency. The method works with comparable efficiency on several single and multiple yeast loci. Finally, we demonstrate the feasibility of CGD to assemble multi-gene biosynthetic pathways or complexes in yeast. CGD, therefore, lays the foundation for large-scale combinatorial engineering of biological processes in a simple eukaryote.

A Characterization of the Grape Root Microbiome Across Rootstocks and Root Depth in a Cool Climate Organic Vineyard

Wright, Harrison; Ali, Shawkat; Migicovsky, Zoe; Douglas, Gavin; Yurgel, Svetlana; Bunbury-Blanchette, Adele; Franklin, Jeffery; Adams, Sarah*; Walker, Allison
Acadia University

Few horticultural crops attract more scrutiny than the wine grape (*Vitis* spp.) when it comes to taste, colour and aroma, and the relationship of these properties with site and environment. The microbiome, an influential factor affecting plant health and growth, is an understudied aspect of wine grape production. We characterized the grape (*Vitis* sp.) root microbiome (fungi and bacteria) in a cool climate vineyard while examining the roles of rootstock, root depth and soil nutrient properties in shaping microbiomes. Microbiomes were investigated in the roots of 'New York Muscat,' a popular cool climate grape hybrid cultivar, across three root types (ungrafted, '3309C' and 'Riparia Gloire') at three root depths (0–15, 15–30 and 30–50 cm), as well as in the surrounding soil and in the roots of the cover crop, a fescue grass (*Festuca* sp.). The grape root microbiome was more specialized, with fewer observed amplicon sequence variants (ASVs) for both fungi (ITS) and bacteria (16S) than in the cover crop or rhizosphere soil. Grape roots were dominated by fungal genera *Plectosphaerella* (mean relative abundance = 4.6%), *Trichosporon* (RA = 4.3%) and *Ilyonectria* (RA = 3.0%), and bacterial genera *Pseudomonas* (RA = 27.9%), *Niastella* (RA = 3.9%) and *Rhizobium* (RA = 3.3%). While no correlations were found between alpha-diversity metrics and soil parameters, *Pseudaleuria* RA was correlated with Mn, Fe and Na levels. Soil depth explained a small portion of bacterial (but not fungal) variance and taxonomic composition. Rootstock type explained a portion of both fungal and bacterial variance and taxonomic composition, confirming the role of host plant genetics in the development of the grape root microbiome.

Diversity and biogeographic relationships of Pakistan macrofungi

Aman, Nourin*; Abdul, Khalid; Jean-Marc, Moncalvo
University of Toronto, Royal Ontario Museum & University of the Punjab
Twitter: @AmanNourin

Fungal diversity in many regions of the world has been poorly explored and the geographic distribution of most species or species groups is unclear. Our study tests the hypothesis for lesser explored region, Pakistan, that climate, ecological niches and lifestyle rather than geographical proximity is a major driver to organismal distribution on Earth. Pakistan has a great deal of fungal diversity that is yet to be comprehensively documented. In this work we compile a compendium of macrofungi reported from Pakistan to date. DNA sequences data are being used to reassess the taxonomy of many species, help in the discovery of new species, and infer their biogeographic relationships. For instance, we will present a newly discovered truffle genus & species of potential economic importance, Ahmadea dalanensis. Inference of biogeographic relationships using the ITS rDNA barcode marker indicate that, generally, ectomycorrhizal taxa are more restricted geographically than saprophytic taxa.

Maternal dietary fat Intake in predicting the breast milk mycobiome

Arnold, Madison*; Quin, Candice; Durall, Daniel; Gibson, Deanna
University of British Columbia, Okanagan

Knowledge regarding the human breast milk mycobiome remains greatly limited compared with the bacteriome. While still unknown, the mycobiome could play a vital role in developing neonatal immunity and serve as the first nutritional source of fungal communities for the infant. This study aimed to describe the mycobiome in human milk, and to explore any relationships between milk fungi and maternal fat intake, as the effect of maternal diet on milk fungi has never been explored in depth. Unlike the rapidly changing bacteriome, the milk mycobiome was found to be stable over time. Though maternal diet was not a major driver in overall fungal composition, many correlations between fungal genera and various maternally consumed dietary compounds, including fatty acids, were identified. This study provides insight into potential predictors of milk fungi that could impact infant immune development, colonization resistance to pathogens, and susceptibility to chronic enteric diseases later in life.

Multigene sequencing reveals different subgroups of '*Candidatus Phytoplasma pruni*' affecting two Canadian flowering plant species

Arocha Rosete, Yaima*; Michelutti, Roberto; Scott, James
Sporometrics Inc.

Phytoplasmas are uncultivable phloem-restricted mollicutes transmitted by Hemiptera insect vectors associated with devastating economical losses in over a thousand plant species. '*Candidatus Phytoplasma pruni*' (16SrIII group) was first reported in Ontario causing peach X-disease and later in cherry, clover and grapevine. *Trillium* species (*T. grandiflorum* and *T. erectum*) and commercial potted poinsettias (*Euphorbia pulcherrima*) from Ontario were assessed for phytoplasmas by multigene sequencing targeting the 16S rRNA, elongation factor Tu (tuf) and protein translocase (SecY) genes combined with in silico restriction fragment length polymorphism (RFLP) and phylogeny. A 16SrIII-F strain was identified in *Trillium* sp., which poses a threat for these protected species, and a 16SrIII-A strain was found in poinsettia, which differs from the poinsettia branching (PoiBI) phytoplasma (16SrIII-H). Management of phytoplasma-infected trilliums and poinsettias should be cautious to prevent any potential phytosanitary risk from spread within and outside Canada, particularly for the 16SrIII-A phytoplasma, an EPPO A1quarantined pest.

Passive spore trapping system and isothermal amplification to support early monitoring of potato and tomato late blight disease in Canada

Arocha Rosete, Yaima*; To, Henry; Evans, Martin; White, Kristine; Saleh, Michael; Trueman, Cheryl; Tomecek, Joseph; Van Dyk, Dennis; Summerbell, Richard; Scott, James
Sporometrics Inc.

During the 2018, 2019 and 2020 growing seasons, passive wind-operated spore trap samplers, named Spornados were deployed in potato and tomato fields in Alberta, British Columbia, Manitoba, Prince Edward Island, and Ontario. The goal was to detect *P. infestans* through loop mediated amplification (LAMP) and lateral flow strip-based recombinase polymerase amplification (RPA-LFS) and validate against quantitative polymerase chain reaction (qPCR). Spornado-qPCR has been used for early detection of Fusarium head blight in cereal crops, sclerotinia stem rot in canola, mildews in cucurbits and grapevine, and late blight across Canada. LAMP and RPA-LFS detected *P. infestans* in 93.9% and 89.6%, respectively, of all qPCR positive samples, and amplified 10 fg of DNA in just 10 minutes. Both assays detected *P. infestans* before late blight symptoms were scouted in the field. Spornado with either LAMP or RPA-LFS proved a valuable system for early monitoring of late blight in potato and tomato.

An NLR-like system delimits individuals in the basidiomycete *Coprinopsis cinerea*

Auxier, Ben*; Debets, Fons; Aanen, Duur
Wageningen University
Twitter: @theredben

Fusion between hyphae has potential benefits, but to limit risks should be restricted to be within an individual. Fusion is allowed based on the identity of polymorphic allorecognition genes. The genes responsible for this non-self recognition are unknown in basidiomycetes. Since basidiomycetes experience an extended dikaryotic phase, non-self recognition likely functions differently from known mechanisms of ascomycetes. We present results of genetically mapping the first known basidiomycete non-self recognition locus in the model mushroom *Coprinopsis cinerea*. Genomic comparisons of additional *C. cinerea* isolates, and related species, provide evidence that non-self recognition is driven by ancient polymorphic alleles of an NLR-like system. The locus we identify appears to involve a Leucine Rich Repeat, a novel finding for fungal non-self recognition. We speculate this locus may form part of a reader-writer system, allowing the mating and cohabitation of two genomes, yet retaining the identity in all parts of the life cycle.

Biochemical insights into the antimicrobial properties of membrane-targeting compounds produced by antagonistic microorganisms on fungal plant pathogens

Avis, Tyler J.*
Carleton University

Fungal plant pathogens cause food losses, both pre- and post-harvest. Synthetic fungicides remain one of the most used control measures against these fungal plant diseases. As a consequence of resistance development as well as environmental and health risks, alternatives to synthetic fungicides are urgently needed. Biological control of fungal disease using antagonistic microorganisms has shown promise, yet results have been variable. In part, inconsistencies in efficacy relate to incomplete knowledge regarding the mechanisms of activity of the antagonists. Our research group studies antagonistic microorganisms using antibiosis as a main mode of action and focuses primarily on antimicrobials affecting the cell membranes of fungal pathogens. Our work has shown that mixtures of membrane-targeting antimicrobials have complex interactions with fungi. The susceptibility/sensitivity outcome of the interaction with the antagonist and/or its antimicrobial compounds seems partly mediated by the growth characteristics of the targeted fungus, as well as biochemical determinants withing fungal membranes.

Global analysis of the Protein Kinase A-regulated phosphoproteome of *Cryptococcus neoformans* reveals new insight into vesicular protein trafficking

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Cryptococcus neoformans is an opportunistic fungal pathogen that is an etiological agent of the dangerous disease cryptococcosis, where inadequate antifungal intervention results in life-threatening manifestations of cryptococcal meningitis. *C. neoformans* employs the cAMP/protein kinase A(PKA) signal transduction pathway via PKA-induced phosphorylation to regulate its vital virulence factors, including capsule, melanin, and laccase production. However, direct targets of Pka1 phosphorylation to initiate such regulatory events have not been completely defined. Here, Pka1-regulation was assessed with a comparative evaluation of the global *C. neoformans* phosphoproteome with a ?pka1 mutant strain using high-resolution mass-spectrometry. Our phosphoproteomics analysis revealed a novel connection to the secretory pathway, an essential component of cell wall stability and regulator of virulence factor delivery, at the host-pathogen interface. Site-directed mutagenesis of the PKA-specific phosphorylation site of a Sec7-domain-containing protein associated with vesicular protein trafficking, revealed altered secretion and virulence trait profiles using in vitro and in vivo infection models.

A new albino mutant mushroom: Phylogenetic, genetic, and chemical analyses separating white and golden chanterelles

Thorn, Greg R.; Banwell, Alicia*; Pham, Thu Huong (Nicole); Vidal, Natalia P; Manful, Charles Felix; Nadeem, Muhammad; Ivanov, Alexander G.; Szyszka Mroz, Beth; Bonneville, Michael B.; Hüner, Norman Peter Andrew; Piercey-Normore, Michele D.; Thomas, Raymond
Western University

Golden chanterelles (Cantharellus: Basidiomycota) are common edible mushrooms found worldwide. Recently, white chanterelles, lacking the orange pigments and apricot-like odour of typical golden chanterelles, have been found in Quebec (QC) and Newfoundland (NL). While a new discovery in both provinces, white chanterelles are known to exist in Europe as variants of golden species, and on the Pacific Coast of North America as an entirely white species. Phylogenetic analyses confirmed that white specimens from QC and NL were variants of Cantharellus enelensis, the common golden species found there. The analysis of two genes involved in carotenoid production revealed single base substitutions in white individuals, likely leading to loss of beta-carotene, the primary pigment in golden chanterelles, which was confirmed by chemical analyses. Additionally, fatty acids, membrane and storage lipids, phenolic acids, volatile terpenes, aldehydes and ketones were shown to be useful biomarkers in distinguishing white and golden chanterelles.

FungiDB: Tools for genomic-scale data exploration, analysis and discovery

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"FungiDB (https://fungidb.org) is a component of the Eukaryotic Pathogen & Vector Genomics Resource (VEuPathDB.org) that provides a robust, sustainable data-mining resource, expediting discovery across diverse groups of organisms including hosts (HostDB.org), invertebrate vectors of human pathogens, pathogenic and non-pathogenic species, and also examining complex environmental and epidemiological information (ClinEpiDB.org). With the VEuPathDB resource, you can:

- Browse genomes & examine gene record pages
- Create search queries to mine omics scale datasets, including genomes, functional data (e.g. transcriptomic, proteomic, variation data), annotation, & the results of in-house analyses (protein domains, orthology predictions via OrthoMCL.org, metabolic pathways, etc.)
- Analyse your own data through a private VEuPathDB Galaxy workspace & transfer your results into My Data Sets workspace to further explore the data.
- Annotate genomes via Apollo, add user comments to capture expert knowledge about phenotypes, PubMed records, etc., nominate datasets for integration & more.

Funding: NIH HHSN75N93019C00077 & Wellcome Biomedical Resources #212929/Z/18/Z"

A Phylogenetic Analysis Using Large Subunit Ribosomal DNA in Ascomycota

Basu, Lahari*; Weerasuriya, Nimalka; Thorn, Greg
Western University

In this study, naïve Bayesian classifiers and phylogenetic binning were explored as alternative methods to classify and identify the LSU-D1 sequences representing 125 Ascomycota OTUs, PCR-amplified from soil and roots and obtained by Illumina sequencing. Reference datasets used to train naïve Bayesian classifiers within QIIME2 and RDP contained misidentified sequences and suffered underrepresentation of various fungal taxa, causing classifier outputs to be inaccurate and imprecise. Phylogenetic binning, placing query sequences on a user-built reference phylogenetic tree, produced more accurate fungal identifications than those derived through naïve Bayesian classifiers. An automated binning pipeline was explored to address the temporal constraints of manual phylogenetic binning. This pipeline, although effective, was computationally demanding, did not show any significant benefit over manual phylogenetic binning, and may lead to inaccurate identifications of query fungal sequences based on a single DNA barcode region. More comprehensive and correctly identified reference databases would improve each of these methods.

Interspecific hybrids show a reduced adaptive potential under DNA damaging conditions

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Hybridization may increase the probability of adaptation to extreme stresses. This advantage could be caused by an increased genome plasticity in hybrids, which could accelerate the search for adaptive mutations. High ultraviolet (UV) radiation is a particular challenge in terms of adaptation because it affects the viability of organisms by directly damaging DNA. Here we test whether hybridization accelerates adaptive evolution in response to DNA damage, using yeast as a model. We exposed 180 populations of hybrids between species (*Saccharomyces cerevisiae* and *Saccharomyces paradoxus*) and their parental strains to UV mimetic and control conditions for approximately 100 generations. Although we found that adaptation occurs in both hybrids and parents, hybrids achieved a lower rate of adaptation, contrary to our expectations. We suggest that the lower adaptive potential of hybrids in this condition may result from the interaction between DNA damage and the inherent genetic instability of hybrids.

Fungal heavy metal adaptation through single nucleotide polymorphisms and copy-number variation

Bazzicalupo, Anna L.*; Ruytinx, Joske; Ke, Yi-Hong; Coninx, Laura; Colpaert, Jan V.; Nguyen, Nhu H.; Vilgalys, Rytas; Branco, Sara
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Human-altered environments can shape the evolution of organisms. Fungi are no exception, although little is known about how they withstand anthropogenic pollution. Here, we document adaptation in the mycorrhizal fungus Suillus luteus driven by soil heavy metal contamination. Genome scans across individuals from recently polluted and nearby unpolluted soils in Belgium revealed low divergence across isolates and no evidence of population structure based on soil type. However, we detected single nucleotide polymorphism divergence and gene copy-number variation, with different genetic combinations potentially conferring the ability to persist in contaminated soils. Variants were shared across the population but found to be under selection in isolates exposed to pollution and located across the genome, including in genes involved in metal exclusion, storage, immobilization and reactive oxygen species detoxification. Together, our results point to S. luteus undergoing the initial steps of adaptive divergence and contribute to understanding the processes underlying local adaptation under strong environmental selection.

Secondary metabolite biosynthesis in *Aspergillus niger*

Benoit Gelber, Isabelle*
Concordia University

Fungal secondary metabolites are of high interest due to their diverse bioactivities such as antibiotics, toxins, immunosuppressant and anticancer agents. The secondary metabolites profile of the industrial filamentous fungus *Aspergillus niger* has been explored bioinformatically and analytically. Some of these secondary metabolites have been characterized, however a majority is yet to be discovered and the biosynthetic gene clusters to be identified. The chemodiversity of *A. niger* secondary metabolites combined with an efficient genetic toolbox and a gold standard genome makes it an attractive host for BGC mapping and manipulations. Comparative genomics, metabolomics and phylogenetic analysis, will be presented.

Exploring the Role of Glutathione in the AIDS-associated Fungal Pathogen *Cryptococcus neoformans*

Black, Braydon*
The University of British Columbia

Cryptococcus neoformans is an encapsulated fungal pathogen that poses a significant threat to immunocompromised patients. The fungus causes cryptococcosis, a potentially fatal disease responsible for an estimated 15% of AIDS-related deaths worldwide. The Kronstad laboratory has characterized transcription factors and proteins that regulate growth and virulence functions during infection of vertebrate hosts. In particular, the monothiol glutaredoxin Grx4 is a key regulator of iron homeostasis and virulence, and grx4 mutants show impaired response to oxidative stress upon iron starvation and/or repletion. Interestingly, the growth of grx4 mutants is rescued by addition of glutathione (GSH), a key antioxidant in the fungal defense strategy. Analysis of mutants for GSH synthesis has also shown phenotypes related to iron acquisition and virulence factor elaboration. Further examination of GSH on *C. neoformans* growth and virulence will enhance our understanding of fungal pathogenesis and may provide insights for potential novel treatments for fungal diseases.

Getting to the heart of the matter: decay of veteran trees

Boddy, Lynne*; Gilmartin, Emma; Wainhouse, Matt; Wright, Rich
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As trees age the central tissues in their trunks/boles cease to be functional in the movement of water from the roots to the leaves, and these tissues are then called heartwood, and often contain polyphenols and other extractives that are inhibitory to fungi. Nonetheless, heartwood is easier for fungi to colonise than functional sapwood, and decay starts while the tree is still standing. Decay is a good thing, indeed it is essential, because it releases nutrients locked up in dead tissues, making them available again for use by trees. Moreover, this decaying wood provides habitat for thousands of species of invertebrates, birds and other mammals. This includes habitat for endangered species. I will first review heart-rot in general and then describe our recent findings with beech (Fagus sylvatica) and oak (Quercus robur) trees. Finally, I will also mention our programme for veteranising trees by inoculating with appropriate heart-rot fungi.

Characterizing indigenous yeast communities in Nova Scotia vineyards
Bunbury-Blanchette, Adele*; Fan,Lihua; Kernaghan, Gavin
Saint Mary's University

Winemaking is a growing industry in Nova Scotia (NS), but the region lacks local vineyard yeast research. While *Saccharomyces cerevisiae* is widely applied in commercial fermentations, other yeasts in pressed grape juice (must) can improve wine character. These yeasts originate from the environment (indigenous yeasts) or may be commercial yeasts persisting in the winery or vineyard. It is unclear how the environment, vineyard management practices, and commercial yeasts contribute to vineyard yeast communities and wine fermentations in NS. Grapes were collected from three organic and five conventional vineyards over two years. Illumina and PacBio sequencing were performed before and after spontaneous fermentation of musts to 1) determine yeast community compositions, and 2) assess impacts of the local environment and management practices. Saccharomycetales yeasts were highly diverse in musts from organic vineyards and all sites contained promising non-traditional yeasts. Results will inform management and fermentation practices to produce unique, high-quality wines.

Working with volunteers to survey a province's mycota
Burzynski, Michael
Foray Newfoundland and Labrador

Since 2003, Foray Newfoundland and Labrador has conducted a citizen-science survey of the fungi of the province, and almost 2,000 species of fungi and lichens have now been identified. Each species is represented by vouchers held at Grenfell Campus, MUN in Corner Brook, NL, and the Foray NL collection (now over 12,000 specimens) is available to researchers world-wide. The Foray is three-day annual event that moves from place to place within the province. Attendance is limited to 60 volunteers who collect specimens along assigned trails. The identifiers are invited mycologists and lichenologists who volunteer their time and expertise. They arrive three days early to familiarize themselves with the site. The Foray is always completely subscribed, and the original concepts still hold: the event should be enjoyable for participants of all ages and all interest levels, scientific and educational components must be integrated, and each identified specimen is carefully documented and preserved.

The macrophage-derived protein PTMA induces filamentation of the human fungal pathogen *Candida albicans*

Case, Nicola*; Duah, Kwamaa; Larsen, Brett; Wong, Cassandra; Gingras, Anne-Claude; O'Meara, Teresa; Veri, Amanda; Whitesell, Luke; Cowen, Leah.
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Evasion of killing by immune cells is crucial for fungal survival in the host. For the human fungal pathogen *Candida albicans*, internalization by macrophages induces morphogenesis from yeast to filaments, which promotes macrophage death and fungal escape. While several physical factors in the macrophage phagosome have been implicated in triggering *C. albicans* filamentation, a specific macrophage-derived factor has yet to be discovered. We explored filament-inducing stimuli within macrophages and determined that lysates prepared from macrophage-like cell lines robustly induce *C. albicans* filamentation. Enzymatic treatment of lysate implicated a phosphoprotein, and bioactivity-guided fractionation coupled to mass spectrometry identified the immunomodulatory protein prothymosin alpha (PTMA) as a candidate trigger of filamentation. Immunoneutralization of PTMA within lysate abolished its activity, strongly supporting PTMA as a filament-inducing component of macrophage lysate. Adding to the known repertoire of physical factors, this work implicates a host protein in the induction of *C. albicans* filamentation within macrophages.

Preference does not mean reliance on: plant-mycorrhizal partnerships are deterministic, yet flexible

Chagnon, PL*; Hart, MM; Klironomos ,JN; Moora, M; Öpik, M; Pither, J; Schmidt, MC; Zobel M, Fraser
Université de Montréal

Next-generation sequencing has uncovered unsuspected levels of specificity in arbuscular mycorrhizal (AM) associations. Plants and AM fungi does not appear to associate randomly in nature. This brings the possibility that plants may be a significant driver of AM fungal community assembly, and vice versa. This would have important ramifications for various fields of research such as invasion ecology, range shifts and response to climate change, etc. Yet, we have yet to demonstrate that the distribution of individual taxa is strongly tied to the distribution of their preferred partners, as it has been observed in other symbioses. Here, we present detailed data on plant and AM fungal spatial distribution across eight sites in Canada and Estonia. In all sites, we found poor evidence for "partner tracking": the spatial distribution of any given plant or AM fungus was rarely tied to the presence of a potential preferred partner. This suggests that while local mycorrhizal associations may be non-random in nature, this is unlikely to translate into strong constraint imposed on plant and fungal distribution across the landscape. The lack of a suitable/preferred partner does not appear as a plausible driver of establishment success for dispersing plants and AM fungi.

Tools for gene expression in *Penicillium citrinum*
Chandrasekharan, Saranya*; Noronha, Santosh
Indian Institute of Technology Bombay

Penicillium citrinum is a cellulase-producing filamentous fungus with potential applications in biofuel and value-added chemicals from renewable substrates. Previously, *P. citrinum* was characterized for cellulase production on various carbon sources, and its genome was sequenced. In this study, we have evaluated its ability as a recombinant protein production host. PEG-mediated protoplast method of transformation based on hygromycin resistance was established. The intracellular expression of enhanced green fluorescent protein under citrate synthase promoter of *Aspergillus niger* was demonstrated in *P. citrinum*. Further, the extracellular expression of glucose-tolerant beta-glucosidase from *Aspergillus oryzae* resulted in a 4-fold increase in beta-glucosidase activity in the three of the four transformants screened by pNPG assay. The increased activity was correlated to the presence of heterologous protein by zymogram analysis. The preliminary tools required for the gene expression in *P. citrinum* were established, paving the way for its use as a recombinant protein production host.

Comparative genomics and epigenomics of Trichosporon and Cutaneotrichosporon polyploid fungi with their closest haploid relative using Nanopore long-read sequencing
Chen, Eric*; Iwasaki, Wataru
The University of Tokyo

"Polyploidization, or duplications of the whole genome, is considered a rich source of genomic innovation. We have been able to deepen our understanding of its role in adaptation and evolution thanks to advancements in the ease and access of sequencing technology. Most of the findings, however, have been focused on artificial polyploids and ancient polyploids. Intermediate-aged polyploids, in contrast, have not been explored as extensively. Here, we present genomic analyses of three intermediate-aged polyploid-haploid fungi as a model to study polyploid evolution. This particular set of fungi includes both types of polyploidy (2x allopolyploids and 1x autopolyploid), which are known to have different gene retention patterns. Using Nanopore long-read sequencing, we report improved genome assemblies of these proposed model species and the differences in methylation patterns as a proxy for differences between the two types of polyploid."

Use of genetic screen and genome re-sequencing to understand the regulation of pigment production in the extremotolerant fungus *Exophiala dermatitidis*

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Exophiala dermatitidis is a polymorphic ascomycete black yeast with a worldwide distribution. *E. dermatitidis* can thrive in nutrient poor conditions and is also an opportunistic pathogen of humans. Presence of melanin in the cell walls of *E. dermatitidis* is thought to be the main reason this species is capable of surviving in toxic niches and nutrient poor conditions. Melanin has also been shown to play a key role in virulence of *E. dermatitidis*. In this study we performed whole genome sequencing on albino and hyper-pigmented *E. dermatitidis* mutants obtained via UV irradiation to identify mutations responsible for morphological changes and pigment loss. Preliminary results show that all albino mutants possess inactivating mutations in the PKS1 gene, whereas hyper-pigmented mutants harbour multiple mutations affecting genes implication in signaling. This study also aims to find the mutations that might be responsible for the regulation of carotenoid production and concentration in *E. dermatitidis*.

The Genetics of Arbuscular Mycorrhizal Fungi

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The genetics of arbuscular mycorrhizal fungi (AMF) have been notoriously elusive. In particular, their perpetual multinucleated state, with thousands of nuclei floating in the same cytoplasm, and their obligate biotrophy has made it difficult to perform experiments and isolate good quality DNA and single nuclei to better understand their nuclear complexity and overall biology. Here, I will present recent work based on AMF genomics and single cell/nuclei analysis, as well as new laboratory experiments, and discuss how these are now reshaping our understanding of the genetics and (para)sexual potential of arbuscular mycorrhizal fungi.

Identifying Vulnerabilities in Fungal Pathogens Through Functional and Chemical Genomic Analyses

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Microbial pathogens pose a grave threat to human health. Fungal pathogens present a particular challenge because they are eukaryotes and share many of the same biological processes as the human hosts they infect. The number of drug classes that have distinct targets in fungi is very limited and the usefulness of current antifungal drugs is compromised by dose-limiting host toxicity and the frequent emergence of high-grade resistance. New, non-cross-reactive drugs for the treatment of life-threatening fungal infections are urgently needed. Here, I discuss our recent work spanning functional and chemical genomic approaches to identify novel strategies to cripple fungal pathogens. I highlight the power of chemical genomic screens to identify novel bioactive molecules and new antifungal targets. To expand the chemical space for antifungal drug development, we explore the prospects of targeting core regulators of cellular stress response for the development of resistance-disfavoring combination regimens. Beyond targets essential for fungal proliferation and drug resistance, we define regulators of key virulence traits, such as the capacity for morphological transitions, and identify interkingdom interactions in the microbiota that modulate these traits. Together, this work identifies vulnerabilities in fungal pathogens and provides a strategy for leveraging structure-guided drug design to develop molecules that can distinguish pathogen from host and selectively cripple fungal pathogens.

Foliar fungal communities in Epichloë endophyte-infected grass

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Tall fescue (Schedonorus arundinaceus) is a cool-season grass which is widely studied due to its agricultural and economic importance as well as its symbiotic relationship with the fungal endophyte Epichloe coenophiala. This endophyte is strictly vertically transmitted and confers several benefits to its host including resistance to herbivory, drought, and some plant pathogens. Although the effects of E. coenophiala are well researched, less is known about the tall fescue microbiome as a whole and how it may be influenced by the presence of Epichloe. We used next-generation sequencing to study the foliar fungal community composition in 48 tall fescue plants grown at a field site and how these communities are correlated with Epichloe infection, concentration, and plant fitness. Sequencing revealed over 3000 amplicon sequence variants (ASVs) which differed in composition between endophyte treatments as well as between the two years measured.

DNA methylation and small RNA profiling shed light on genomic organisation of the symbiotic fungus *Rhizophagus irregularis*

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Arbuscular mycorrhizal fungi (AMF) are obligate root symbionts of a majority of land plants. They are present on all continents and in most biomes, forming a cross-kingdom relationship with plants, and even engaging in symbioses with multiple species simultaneously. AMF are known for their peculiar cellular features. Their mycelia contain hundreds of haploid nuclei that coexist within the same cytoplasm. Their apparent lack of sexual reproduction is remarkable for a eukaryotic lineage, particularly in this group of ancient organisms that have existed for over 500 million years. In the absence or rare occurrence of sex, how were these fungi able to evolve and adapt to maintain symbioses with vastly different plant hosts and to function within varied ecological niches? Three mechanisms could generate genetic variation: 1) transposable element (TE) activity, 2) horizontal gene transfer, a phenomenon that has been observed in AMF genomes, and 3) cryptic recombination, which is proposed to occur in AMF. In this work, we investigated a potential role of TEs in driving AMF genome evolution, and ways in which these asexual organisms could defend themselves against TE activity. As AMF genomes display the highest numbers of small RNA pathway genes recorded so far in any species (>30 Argonautes in *R. irregularis*), we aimed special attention at characterising small RNA pathways. In this talk, I will describe the organisation of transposable elements, DNA methylation and sRNAs at the whole genome level in the model AMF *Rhizophagus irregularis*. We bring together single-molecule DNA methylation detection, small RNA/transcriptome sequencing and proteomics data to uncover fundamental characteristics of epigenetic mechanisms in this model AMF.

A comprehensive fitness landscape model reveals the evolutionary history and future evolvability of eukaryotic cis-regulatory DNA sequences

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Mutations in non-coding cis-regulatory DNA sequences can alter gene expression, organismal phenotype, and fitness. Fitness landscapes, which map DNA sequence to organismal fitness, are a long-standing goal in biology, but have remained elusive because it is challenging to generalize accurately to the vast space of possible sequences using models built on measurements from a limited number of endogenous regulatory sequences. Here, we construct a sequence-to-expression model for such a landscape and use it to decipher principles of cis-regulatory evolution. Using tens of millions of randomly sampled promoter DNA sequences and their measured expression levels in the yeast *Sacccharomyces cerevisiae*, we construct a deep transformer neural network model that generalizes with exceptional accuracy, and enables sequence design for gene expression engineering. Using our model, we predict and experimentally validate expression divergence under random genetic drift and strong selection weak mutation regimes, show that conflicting expression objectives in different environments constrain expression adaptation, and find that stabilizing selection on gene expression leads to the moderation of regulatory complexity. We present an approach for detecting selective constraint on gene expression using our model and natural sequence variation, and validate it using observed cis-regulatory diversity across 1,011 yeast strains, cross-species RNA-seq from three different clades, and measured expression-to-fitness curves. Finally, we develop a characterization of regulatory evolvability, use it to visualize fitness landscapes in two dimensions, discover evolvability archetypes, quantify the mutational robustness of individual sequences and highlight the mutational robustness of extant natural regulatory sequence populations. Our work provides a general framework that addresses key questions in the evolution of cis-regulatory sequences.

Genetic Determinants of Resistance in Antifungal Resistant Clinical Isolates of *Candida glabrata* in Canada

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Candida glabrata can rapidly acquire resistance to azole and echinocandin antifungal drugs. We used whole genome sequencing to detect genetic markers of resistance for azole and echinocandin drugs. Sixty-nine clinical *C. glabrata* isolates resistant to at least one azole and/or echinocandin drug and 64 susceptible isolates were sequenced. Potential resistance mutations were identified in PDR1, FKS1 and FKS2. Of the 61 azole resistant isolates, 20 (33%) had known gain-of-function mutations in PDR1, with G583S (n = 4) and D876N (n = 2) being the most common. Of the 17 echinocandin resistant isolates, 13 (76%) had hotspot mutations in FKS genes. Three isolates had hotspot mutations in FKS1 while ten isolates had hotspot mutations in FKS2, with S66DAY 3 - Plenaries (n = 6) and F659L (n = 3) as the most prevalent. These results suggest that detection of genetic mechanisms of resistance may be able to predict phenotypic antifungal resistance.

The sequence-function landscape of an antifungal target

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The emergence of drug-resistant fungi is a rising threat to public health. Understanding the molecular mechanisms behind the emergence of drug resistance is crucial to inform the development of new drugs and to optimize the management of existing ones. The enzyme responsible for converting the antifungal 5-FC into the toxic nucleotide analog 5-FU, FCY1, is a widely conserved fungal-specific cytosine deaminase. We performed Deep Mutational Scanning (DMS) to test the effect of all possible amino acid substitutions on both canonical FCY1 function and 5-FC resistance in *Saccharomyces cerevisiae*. Unexpectedly, we found many mutants unfit in both conditions. We also observed important effects due to protein expression and protein-protein interaction changes. Our results provide insights into the fitness landscape of FCY1 and the mechanisms by which resistance to 5-FC can occur in yeast.

Genome-informed selection of loci for molecular systematics: A test case with Alternaria

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The sub-generic Section Alternaria, in the genus Alternaria, includes many economically important agricultural pathogens. A stable framework for systematics and species identification is essential for management and regulation purposes, however, this Section has experienced much taxonomic debate and revision. Molecular phylogenetic studies have challenged the reliability of morphological characteristics, and have also suggested that commonly used molecular markers for fungal phylogenetics may not be sufficiently informative at this taxonomic level. Here, I discuss a genome-informed method for choosing loci for molecular systematics at the population/species interface. An overview and analysis of phylogenomic resources for Section Alternaria are presented, and molecular variation and evolutionary history are assessed at a genome-wide level. Fine-scale, phylogenetic reconstruction reveals incomplete lineage sorting and the genomic distribution of gene/species tree discordance. Based on these patterns, new candidate genes can be developed into markers that are appropriately informative and diagnostic for the main lineages.

Lichenicolous fungi in Atlantic Canada: documenting an overlooked component of the mycobiota

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Lichenicolous fungi are a diverse group of Ascomycota and Basidiomycota that grow directly on lichens. Their lifestyles range from weakly parasitic to strongly pathogenic. These organisms have been largely overlooked in Atlantic Canada, but ongoing research led by the New Brunswick Museum is focused on remedying the situation. Data from biodiversity field surveys and studies of existing herbarium collections show that the actual species diversity is three times what has been reported so far. These efforts continue to reveal new species and significant range extensions to known species. Work is underway to publish a checklist of over 200 species of lichenicolous fungi found in Atlantic Canada, including a host index and identification keys to facilitate future work.

Characterizing the Novel Bioactivity of the Compound T-042756 Against *Candida albicans*

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Fungal pathogens impose a serious threat to human health, infecting billions and resulting in an annual death toll of over 1.5 million worldwide annually. The azoles are the most widely deployed class of antifungal, and function by targeting the ergosterol biosynthetic enzyme Erg11. However, their frequent deployment has led to widespread resistance to this antifungal class. T-042756 was identified from previous high-throughput screen as having potent activity against the human fungal pathogen *Candida albicans*. Preliminary genetic evidence suggested this compound inhibits Erg11, despite possessing a distinct chemical structure that lacks the five-membered nitrogen-containing azole ring. Future work will investigate if treatment with T-042756 results in the depletion of ergosterol and the build-up of ergosterol intermediates. Furthermore, mammalian cytotoxicity and fungal selectivity are being explored through co-culture models. Overall, this project aims to characterize the bioactivity, mechanism-of-action, and selectivity of T-042756 against *C. albicans* in order to expand the antifungal repertoire.

Phylogenetic binning of Basidiomycota, Zygomycota and Chytridiomycota using the large ribosomal subunit of the RNA gene

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An environmental metabarcoding dataset of partial LSU sequences of Basidiomycota and basal fungi were identified using four methods: simple-matching using the latest SILVA and RDP reference sets, and manual and automated phylogenetic binning. The SILVA and RDP reference sets suffered from misidentifications due to incorrect reference sequence naming and an underrepresentation of certain groups of fungi, with over half of the misidentifications being as a result of the latter. Phylogenetic binning identifications proved to be more accurate than simple-matching as it used a curated reference set and provided phylogenetic information. Automated phylogenetic binning was found to be time-inefficient because it was heavily dependent on computing power and the time to develop the reference set. More comprehensive reference sets with fewer misidentified sequences will increase the accuracy of simple-matching identifications but phylogenetic binning may remain a better choice since it is more accurate, and also provides evolutionary information about query sequences.

Shared components of the FRQ-less oscillator and TOR pathway maintain circadian rhythmicity in *Neurospora*

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Transcription/translation feedback loops regulate the expression of clock genes (including FRQ) in *Neurospora crassa*, but certain rhythms continue even when clock genes are not expressed. We previously identified a mutation (vta) that abolishes FRQ-less rhythmicity of the conidiation rhythm and affects rhythmicity when FRQ is functional. We identified VTA as a component of the TOR pathway (Target of Rapamycin). We now report that co-immunoprecipitation found TOR pathway components, including GTR2, as binding partners of VTA. A gtr2ko strain was deficient in growth responses to glucose and amino acids. Entrainment of a FRQ-less strain to cycles of heat pulses demonstrated that gtr2ko is defective in entrainment and is similar to vtako. Expression of GTR2 protein was found to be rhythmic, and VTA was required for GTR2 rhythmicity. FRQ protein exhibited the expected rhythms in the presence of GTR2, but the rhythmicity of FRQ dampened in the absence of GTR2.

Artificial intelligence enables automatic phenotyping of arbuscular mycorrhizal fungal root colonisation

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Artificial intelligence algorithms underly breakthrough advances in diverse technological and biological domains, from self-driving cars to plant pathology. These algorithms can also benefit the study of arbuscular mycorrhizal (AM) fungal symbiosis. We developed the AMFinder tool suite for in silico analysis of AM fungal colonisation and recognition of intraradical hyphal structures using convolutional neural networks. AMFinder adapts to a wide array of experimental conditions and delivers high-confidence predictions on image datasets of colonised roots of Medicago truncatula, Lotus japonicus, Oryza sativa and Nicotiana benthamiana obtained via flatbed scanning or digital microscopy. A streamlined protocol for sample preparation and imaging enables quantifying dynamic increases in colonisation in whole root systems over time. Our work provides a framework for reproducible automated phenotyping of AM fungal colonisation of plant roots and supports better documentation of AM fungal colonisation analyses.

Host specificity determines a new fungal plant pathogen population
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Host specialization is considered the strongest driver of pathogen evolution. Implementing population and comparative genomics approaches, we aim to identify evolutionary and genomic patterns of host specialization in fungal plant pathogens using the fungal pathogen *Zymoseptoria tritici* as a model of study. Unique collections of *Z. tritici* were isolated from wild (*Aegilops* spp.) and domesticated (*Triticum aestivum*) host grasses, and whole-genome sequencing was performed in a subset of isolates from each collection. We observed distinct population structure between the two host-diverging collections and particular genomic features in the *Aegilops*-infecting isolates. Phylogenetic analyses also indicated that the *Aegilops*-infecting population forms a separate *Z. tritici* cluster, leading to the hypothesis of a possible new *Z. tritici* lineage. Together with other aspects, our findings highlight the interplay between agricultural and wild hosts on the evolution of fungal plant pathogens and illustrate a possible route of crop disease emergence.

Arbuscular mycorrhizal fungi inhibit pine seedling growth and nutrient uptake under different fertilization regimes
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Mycorrhizae is a symbiotic association in which plants exchange photosynthetically derived carbon with fungi for increased access to soil nutrients. White pine (Pinus strobus) is primarily associated with ectomycorrhizal fungi (EMF), but can also be colonized by arbuscular mycorrhizal fungi (AMF), and the interactions between these mycorrhizal types under different conditions are unknown. We inoculated pines with live or sterilized EMF and AMF and grew them under a factorial combination of low, medium, or high nitrogen and phosphorus fertilization. Seedlings inoculated with AMF had lower biomass, diameter, and root:shoot ratio than seedlings without AMF. Ectomycorrhizal inoculation became less beneficial with higher phosphorus. AMF inoculation interacted with fertilization treatments to affect tissue phosphorus content and pines inoculated with AMF had lower manganese content especially in low nitrogen fertilization. Therefore, AMF negatively affect pine seedling growth partially by limiting nutrient uptake which could have implications in forest ecology and forestry.

Characterization of indigenous yeasts isolated from grapes and musts in Nova Scotia

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The natural microflora of the grape of the viticulture region significantly contributes to the unique quality characteristics of wine. Indigenous yeasts are active at early fermentation stage and can influence alcohol content, pH, viscosity, colour, the concentrations of sulfur compounds, phenolic compounds and volatile metabolites contributing to the flavor and aroma of the final products. The objectives of this study were to characterize indigenous yeasts isolated from Nova Scotia's vineyards and select yeast strains for wine fermentation and chemical analysis.
Identified yeasts were screened for oenological characteristics. Yeasts' tolerance to sulphur dioxide and ethanol concentration, ß-glucosidase activity and hydrogen sulphide production were determined. Yeast strains were selected based on the criteria of ethanol tolerance >6%, free SO2 tolerance >20 mg/L, ß-glucosidase activity positive and low hydrogen sulfide production. Characterization of yeasts revealed a wide biodiversity within each genus (species). The research results will provide useful information for the grape-wine industry.

Genome-wide association analysis for triazole resistance in *Aspergillus fumigatus*

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Aspergillus fumigatus is a common airborne fungal pathogen found in a variety of environments and substrates. The fungus is associated with life-threatening invasive infections in the immunocompromised and the main causative agent of pulmonary invasive aspergillosis. In recent years, incidence of triazole resistance in *A. fumigatus* has been increasing in numerous countries worldwide. A wide variety of mutations related to the triazole target cyp51 A - Pathogen emergence and evolution had been the main cause but occurrences of unidentified mutations conferring resistance is becoming more prevalent. In this study, a total of 196 *A. fumigatus* whole genome sequences from 12 countries were used in a genome-wide association study (GWAS) to identify genetic determinants for itraconazole and voriconazole resistance. Our analyses identified over 30 SNPs significantly associated with resistance. Together, these SNPs represent promising candidates for further functional validation testing and the investigation of putative molecular mechanisms for triazole resistance.

Differential Expression of Cell Wall Degrading Enzymes in *Oidiodendron maius* in Response to Varying Carbon Source

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The ericoid mycorrhizal (ErM) symbiosis represents an important adaptation to acidic and nutrient poor soils that species in the monophyletic plant family Ericaceae typically inhabit, including tundra, boreal forests, heathlands and peatlands – environments whose carbon sequestration capabilities are particularly sensitive to changing climate. As the most recently diverged mycorrhizal lineage, ErM fungi have retained many of their saprotrophic enzymes. RNA sequencing and droplet digital PCR were utilized to examine differential expression of cell wall degrading enzymes (CWDEs) across substrates of different carbon complexity by the ErM fungus *Oidiodendron maius*. This examination of the CWDE transcriptome of *O. maius* contributes fundamental knowledge regarding its saprotrophic nature and adds to the growing body of knowledge surrounding the mechanisms that soil fungi employ to degrade soil organic matter to effectively attain resources in this highly competitive environment, and, thereby, a deeper understanding of carbon cycling within the vulnerable ecosystems they inhabit.

The Unfolded Protein Response is required for antifungal drug resistance in yeast

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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 cope with accumulation of misfolded proteins in the Endoplasmic Reticulum (ER) through the activation of the ER stress sensor Ire1. Ire1 can be activated both by accumulation of misfolded proteins in the ER lumen, and ER lipid bilayer stress. This triggers a transcription response to restore the ER folding environment and lipid homeostasis. However, the mechanisms of UPR activation and genes responsible for yeast resistance from exposure to common antifungals, like caspofungin remains unknown. Interestingly, we found deletion of the Ire1 luminal domain, which senses misfolded protein accumulation sensitizes cells to caspofungin treatment. Using genetic screens and genome-wide transcriptome analysis, we are now seeking to identify UPR target genes required for the antifungal response in both *Saccharomyces cerevisiae* and the pathogen *Candida albicans*.

Continued investigation of the *U. maydis* APSES protein encoding gene nlt1

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Ustilago maydis is a biotrophic basidiomycete plant pathogen that infects *Zea mays* causing common smut of corn. Transcriptome and mutational analyses by others revealed that UMAG_04778 (no-leaf tumour 1, nlt1) had a controlling role in tumour development and effector gene expression. Previously the Saville lab identified nlt1 as an APSES domain containing gene in a cDNA subtraction library and assessed the impact of its deletion and overexpression on pathogenic development. This presented work describes the complementation of an SG200?nlt1 strain by ectopic expression of nlt1 from a constitutive promoter (OTEF) as well as the analysis of the filamentous growth and pathogenesis phenotypes of the complementation strain. Complementing SG200?nlt1 with constitutive expression resulted in phenotypes distinct from complementation with the native promoter. The data presented is consistent with Nlt1 having a controlling role in pathogenic development that is influenced by its level of expression.

Enhanced stress tolerance in Norwegian kveik results in increased fermentation efficiencies at extreme temperatures

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Recent research in our lab has identified a group of *Saccharomyces cerevisiae* ale yeast from Western Norway, where unique brewing techniques and centuries of isolation have resulted in a genetically distinct group of yeast, termed kveik, that differ from standard industrial brewing yeast. While kveik strains are known to be strong fermenters with increased thermotolerance, the fermentative capacity of these yeasts at a range of temperatures is poorly characterized. A number of wort fermentations were performed at temperatures ranging from 12°C to 42°C to elucidate fermentation profiles, carbon metabolism, and flavour compound production. These fermentations demonstrated that Norwegian kveik are capable of fermenting more efficiently than industrial control strains at a wider range of temperatures, effectively metabolize wort sugars at extreme temperatures and tend to produce higher concentrations of ester compounds which contribute to a fruitier beer. These results suggest that Norwegian kveik possess enhanced stress response mechanisms to survive and ferment under extreme conditions.

Associate Assistant Deputy Minister – Agriculture Canada – Science & Technology

Foster, Elizabeth
Science and Technology Branch at Agriculture and Agri-Food Canada

Dr. Liz Foster is Associate Assistant Deputy Minister of Science and Technology Branch at Agriculture and Agri-Food Canada, co-responsible for the largest provider of agricultural research in Canada, that takes place across a national network of 20 Research and Development Centres with 30 satellite research locations, working with industry, academia, provincial and territorial governments, international organizations, and others to support the growth and development of Canada's agricultural sector, and to create better opportunities for farmers and Canadians through agricultural research and innovation. Dr. Foster is also the Assistant Deputy Minister Host and Co-Chair of the Interdepartmental Indigenous Science, Technology, Engineering and Mathematics (I-STEM) Cluster. The I-STEM Cluster operates as an interdepartmental team conducting collaborative work across 11 federal departments and agencies to inform and enhance federal policies, programs, activities and recruitment related to Indigenous participation in STEM disciplines and Indigenous aspirations and innovation in land-based research and environmental stewardship

Combatting fungal infections through the discovery and elucidation of novel anti-virulence strategies

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Fungal pathogens are critically important threats to global health with over 300 million people affected by serious fungal diseases worldwide. In Canada, pathogenic fungi are a growing public health concern with the evolution of drug-resistant strains and the emergence of new pathogens. Fungal pathogens are a leading cause of human mortality, particularly among the ever-increasing population of immunocompromised individuals. The treatment of fungal infections is challenging given the similarities of potential targets in the human host, the requirement for prolonged treatment regimens, and a limited selection of clinically effective, nontoxic antifungal therapeutic options. Our research program aims to define how a fungal pathogen interacts with the host and understand why the host is unable to clear infection. Focusing on *Cryptococcus neoformans*, a highly-prevalent fungal pathogen among immunocompromised individuals, we exploit our extensive quantitative proteomics datasets of the interaction between host and pathogen at the protein level to assess options for reducing fungal virulence and combatting infection. We will provide new insights into how fungi cause disease and the mechanisms used to evade the immune response. We also aim to identify new strategies to perturb the interaction between pathogen and host to reduce our reliance on current antifungals for treatment options. This information will support the reduction of selective pressure against antifungal-resistant strains and provide new tools against emerging resistant pathogens.

Fungal endophyte discovery, characterization and function in various host grasses

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Co-evolution between the soil microbial community and plants, has led to some micro-organisms becoming incorporated within plant tissues - endophytes. Seed-borne endophytes are unique, as this point of the life-cycle represents the beginning of a life-long relationship between symbiotic partners. We investigate whether fungal endophytes belonging to one host species can be transferred for the benefit of another host species in the same family. More than 400 fungal endophyte strains were isolated from seeds that were harvested from 24 Andropogon gerardii (big bluestem) plants grown in a low-input system. 111 morphotypes were screened for beneficial properties to select candidates for further characterization and greenhouse growth experiments. Biomass, proteomics, and metabolomics measurements will determine the individual endophyte's interaction with the plant. By discovering potential plant-growth-enhancing endophyte(s) on multiple hosts, we hope to further the understanding of endophytic symbioses towards novel ecological and agronomic applications.

Implementation of a CRISPR-based Activation System for Gene Regulation in *Candida albicans*

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Candida albicans is an opportunistic fungal pathogen that is found in the microbiota of the majority of healthy adults, but can also result in invasive infections that are life-threatening in immunocompromised individuals. Traditional therapeutic options for these infections are limited, and *C. albicans* mechanisms of drug-resistance must be better understood if potential targets for new drugs are to be discovered. New genetic tools may facilitate a better understanding of this pathogen at the genetic level. Here, we report an improved CRISPRa (activation) system for targeted overexpression of genes of interest in *C. albicans*. A dCas9-VPR activator complex was constructed in a single plasmid to allow for rapid strain construction. Further, we positionally optimized this CRISPRa system based on targeting different regions upstream of the CDR1 drug transporter gene. This technology may allow strains with overexpressed genetic material to be contrasted with wild-type *C. albicans* to infer genetic function.

Global pangenome analysis of *Pyrenophora tritici-repentis* reveals high plasticity and translocation of the ToxA gene between different chromosomes

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P*yrenophora tritici-repentis* (Ptr) is a fungal pathogen that causes tan spot, a destructive foliar disease of wheat. Ptr secretes effectors (ToxA, ToxB, and ToxC), which induce necrosis or chlorosis in susceptible genotypes. A pangenome analysis of forty isolates representing different races and global origins was performed. Additionally, the chromosome organization of two isolates, races 3 and 8, was examined after long-read sequencing. Tesults show that Ptrs genome is highly plastic with a genome size of 34.8 ± 2.1 Mb, with 43% of its predicted genes present in the core while 57% are accessories. Phylogenetics show that isolates cluster based on location and their ability to secrete Ptr effectors. Long-read assemblies confirmed the translocation of ToxA between chromosomes and revealed considerable large-scale re-arrangements between races. Transposable element content varied between 7 and 17.5% of the total genome size, and these elements likely play an essential role in driving Ptr genome plasticity.

Diversity and host preferences of mycophagous insects in southern Ontario

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A speciose but often cryptic guild of insects complete their larval development inside the fruiting bodies of macrofungi. Previous studies of the diversity and interactions of fungus-associated insects have been conducted primarily in Europe, and all have been limited by the difficulty of rearing and identifying mycophagous insects in the egg/larval stages. This study is the first in North America to use DNA barcoding to identify insects of all life stages collected from macrofungi. In 2019, we collected >1,000 fruiting bodies from the Greater Toronto Area, encompassing diverse taxonomic groups and various stages of growth/decay. 500 insects, mostly eggs and larvae, were sampled from the fungi. DNA barcoding revealed 81 fly and 42 beetle OTUs. While the majority of beetles were fully identified with DNA barcoding, less than one third of flies matched to species-level database entries. Insect host preferences were more related to fruitbodies hyphal systems than taxonomic groups.

An updated global ToxA haplotype network with evolutionary model for this gene in necrotrophic fungal pathogens

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ToxA is the first proteinaceous necrotrophic effector to be identified in fungal plant pathogens. ToxA was originally identified in *Pyrenophora tritici-repentis* (Ptr) in 1989, and subsequently detected in other necrotic fungal pathogens. Here we have identified a novel ToxA haplotype in *P. nodorum* and analysed ToxA sequences previously published to provide an updated global ToxA haplotype network. Interestingly, hypothetical ToxA-like proteins were also identified in the fungal genome databases in species from Dothideomycetes and Sordariomycetes. The distribution of ToxA and ToxA-like necrotic effectors in the filamentous fungal plant pathogens seems to be more complex than we thought. The discovery of ToxA-like genes in large number of ascomycetes raises the hypothesis that an unknown fungal (or non-fungal) ancestor might be the ToxA donor to *P. nodorum* and other pathogens. We have used these information to propose an evolutionary model for ToxA in necrotrophic fungal pathogens.

A deep learning approach to capture the essence of *Candida albicans* morphologies

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This effort develops deep learning approaches for two interrelated *C. albicans* image recognition challenges. First, we develop a system that automatically detects *C. albicans* cells from microscopy images and labels each detected cell with its morphology. The model is developed across a large compendium of both calcofluor white and DIC images with cells in nine different morphological states. Our software (Candescence) exploits a fully convolutional one-stage object detector (FCOS) and a novel curriculum-based learning strategy that stratifies our images by difficulty. Second, we develop a generative adversarial network (GAN) approach to capture the essence of each *C. albicans* morphology. The models can be interrogated to identify artificial neurons from the latent space that control technical variables such as saturation but also biologically-relevant events such as the white to opaque switch. The GAN can automatically identify subtle changes from wild-type morphologies when given images from genetically perturbed *C. albicans* populations.

Forays in the herbarium for rust fungi – data mining, diagnostics and systematics
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Fungal collections preserved in the Canadian National Mycological Herbarium (DAOM), acquired over the previous 120 years, represent a valuable and accessible source of DNA for systematic studies of the obligate plant pathogens known as rusts. Specimen holdings comprise a broad diversity of plant hosts and geographic provenance, and were typically identified by experts. Since 2006, 2000 DAOM specimens, supplemented by 800 from other herbaria, were sampled to generate ITS barcodes, as a first step to evaluate the efficacy of this marker for identification purposes. Analyses of the large data set revealed three main outcomes. 1. ITS diagnostic at the species level. 2. Multiple distinct ITS barcodes for a species complex, monophyletic or polyphyletic. 3. Multiple distinct species with similar ITS barcodes. Outcomes two and three require additional data and study to resolve. The use of provisional taxon labels can aid downstream analyses pending formal revisions and clarifications of nomenclatural conflicts.

Genomic biosurveillance of forest pathogens: a story written in code
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The world's forests face unprecedented threats from invasive insects and pathogens that can cause large irreversible damage to the ecosystems. The key to reduce this threat is via vigilant biosurveillance to achieve early detection and enable better decision-making. Genomics can provide powerful new solutions to biosurveillance. The process of invasion is a story written in four chapters: transport, introduction, establishment and spread. The series of processes that lead to a successful invasion leave behind a DNA signature that tells the story of the invasion. The BioSAFE (BioSurveillance of Forest Alien Enemies) project is developing a pipeline to generate genomic tools that provide accurate identification of pathogens, assign samples to putative sources to identify pathways of spread and assess risk based on traits that impact the outbreak outcome. These next generation biosurveillance tools promise to increase our capacity to prevent and contain future forest disease outbreaks.

Gramillins: Host-specific phytotoxins produced by cereal pathogen *Fusarium graminearum*

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Fusarium graminearum is a broad host pathogen causing head blight and ear/stalk rot in cereal crops. The genome of this pathogen contains a significant number of secondary metabolite biosynthetic genes and gene clusters. A fraction of these genes have known products which include siderophores, pigments, and toxins that help the fungus overcome plant defenses. Investigating host-preferential gene expression, we identified a secondary metabolite gene cluster in *F. graminearum* responsible for the biosynthesis of novel cyclic lipopeptides, named gramillins. Gramillins are phytotoxins, causing cell death following leaf infiltration in an extensive range of plants, including maize and Arabidopsis, but not wheat. *F. graminearum* mutants unable to produce gramillins are less able to colonize maize silks but are just as virulent as wildtype *F. graminearum* on wheat spikes. Gramillins act as ionophores, promoting ion and water loss from plant cells to enhance virulence.

The fate of fungal biofertilizers – where do they go, and how do they get there?

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The use of fungal biofertilizers is common place, yet there is little data surrounding the spread of biofertilizers into the natural environment. Commercial inoculants may pose a threat to local fungal communities, which may not be resistant to alien introductions. Unfortunately, long term data on the fate and effects of commercial fungal inoculant use are lacking. Given the ubiquity of commercial inoculant use, and its ability to establish and spread from point of introduction, the use of fungal inoculants should be carefully evaluated. I will discuss gaps in our knowledge about inoculum spread and discuss steps needed to work towards best practices.

Evaluation of temporal distribution of airborne inoculum of *Zymoseptoria tritici* and *Puccinia triticina* in Tunisia

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Septoria tritici blotch (STB) (*Zymoseptoria tritic*i) and stripe rust (*Puccinia striiformis*) are devastating foliar diseases affecting durum wheat in regions of Tunisia. The development of severe epidemics caused by these pathogens has been reported in many wheat-growing regions worldwide including Europe, Australia, Middle East, and North America. The quantification of airborne inoculum is a good technique to predict and understand the epidemiology of *Z. tritici* and *P. striiformi*. During the 2016-2017 growing season, volumetric Burkard 7-day spore traps and quantitative PCR (qPCR) were used to continuously quantify the airborne inoculum temporal distribution at one of the disease emerging hotspot areas of northwestern Tunisia. The qPCR monitoring of *Z. tritici* revealed a number of significant peaks during different periods of the growing season, such as mid-November (384.3 spores), March (264.7 spores), mid-April until the first week of May (a daily detection mean of 75.3 spores), and a higher intensity at the end of the season on June after exceptional precipitations (600 spores). However, *P. striiformis* was detected from the start of the survey during the sowing period in November to May with peaks during March and once again in April and May. Significant quantities (527.2 spores) and detection frequencies (± 10 % of days) of *P. striiformis* were observed mainly in March and once again in April and May with 553.4 and 397.32 spores respectively. The trapped inoculum of airborne *Z. tritici* and *P. striiformis* were positively and significantly correlated with STB and stripe rust disease severity in the field. Moreover, weather conditions such as temperature, humidity and precipitation are main contributors to the production and the quantity of airborne inoculum. Our results showed that the quantification of airborne inoculum could be an indicator for early detection of *Z. tritici* and *P. striiformis* incursion and spread before symptoms become evident and thereby become a useful tool to anticipate needs for management and optimization for timing of disease control products.

MITACS funded Postdoc Associate – Agriculture Canada - Policy

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Dr. Herod holds a PhD in Microbiology and Immunology from Dalhousie University with a specialization in bacterial genetics and molecular biology. His work led to numerous research opportunities including training at Institut Pasteur in Paris, collaborating with several universities and government agencies through the Genome Canada Salmonella Syst-OMICS project, and completing a student placement at the Canada Food Inspection Agency. In 2021, Adrian joined AAFC as a Science Policy Analyst through the Mitacs Canadian Science Policy Fellowship where he is working on policy related to plant health and variety development.

The effect of various nitrogen supplementation techniques on cider fermentation – small changes cause big effects

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The anaerobic fermentation of apples (Malus Domestica Borkh.) by *Saccharomyces* yeast is an ancient process. Unlike ancient practices, modern cider producers have a variety of tools at their disposal to increase the quality and consistency of their apple-based alcoholic beverages. One such tool is through the addition of nitrogenous compounds, an essential macronutrient for *Saccharomyces* sp. The aim of this study is to explore how both native and industrial *Saccharomyces* yeasts respond to the addition of mineral nitrogen and primary amino nitrogen in the form of diammonium phosphate and a-amino acids. Additionally, the effect of supplementing with both nitrogen species at the start of cider fermentation and during stationary phase, were also compared. Key aspects of fermentation metabolism were impacted, including carbon consumption, metabolite generation, and aromatic volatile production. These results suggest cider producers can alter the composition of a beverage by simply altering their nitrogen supplementation regime.

The many faces of cranberry fruit rot: fungal complex etiology and why it matters

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Cranberry fruit rot is a fungal disease complex affecting cranberry fruit quality and yields, to varying levels, everywhere cranberry is grown. It is a disease as old as cranberry production, and at least 15 fungal species have been identified with this disease complex. In Wisconsin, cranberry fruit rot disease pressure is low to moderate most years. Previous research indicates that disease incidence may remain low season after season, but persistence of fungal pathogens changes. Isolations from rotted berries (n=972) in 2020 from 70 Wisconsin marshes revealed that 20% of fungal isolates were identified as *Colletotrichum* spp., 14% were identified as *Coleophoma* sp., and 10% were identified as *Physalospora* sp. Additional fungi were isolated and identified as representing species in the Diaporthales and Xylariales. Understanding the fungal diversity present in cranberry marshes will contribute to our enhanced understanding of the epidemiology and management of fruit rot.

Loss of a nuclear co-chaperone sensitizes *Cryptococcus neoformans* to DNA damaging agents

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Faithful replication of DNA and its repair upon damage are crucial processes for all organisms including opportunistic fungal pathogens which may incur DNA damage as a result of the host immune response. We identified a nuclear J domain co-chaperone, Dnj4, which interacts with histones 3 and 4 and is required for robust growth of *Cryptococcus neoformans* upon exposure to the DNA damaging agents including hydroxyurea, 4-nitroquinoline 1-oxide, and methyl methanesulfonate. The transcriptional response to hydroxyurea was characterized and a mutant lacking Dnj4 had impaired upregulation of several genes related to DNA damage and iron homeostasis functions when compared to the wild type strain in response to short term hydroxyurea treatment. Furthermore, we found that iron overload rescued the growth defect of the dnj4? mutant in response to hydroxyurea treatment. Altogether, this work demonstrates the importance of Dnj4 for iron acquisition and the response to DNA damaging agents in *C. neoformans*.

Mitochondrial perturbation reduces susceptibility to xenobiotics through altered efflux in *Candida albicans*

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Candida albicans is a leading human fungal pathogen, which can cause life-threatening disease in immunocompromised individuals. The ability to transition between yeast and filaments is a major virulence trait, and a key regulator of this morphogenetic transition is the molecular chaperone Hsp90. To explore the mechanisms governing *C. albicans* morphogenesis in response to Hsp90 inhibition, we performed a functional genomic screen to identify genes required for filamentation in response to the Hsp90 inhibitor, geldanamycin. Genes involved in mitochondrial function were enriched as being required for filamentation. Further exploration revealed mitochondrial dysfunction reduced susceptibility to two Hsp90 inhibitors, geldanamycin and radicicol, such that increasing compound concentration restored filamentation. Furthermore, deletion of mitochondrial genes, MSU1 and SHY1, enhanced cellular efflux. Finally, we identified Yor1 and Cdr1 as the key efflux mediators of geldanamycin and radicicol, respectively. Overall, our findings suggest mitochondrial dysregulation enhances efflux and reduces susceptibility to xenobiotics in *C. albicans*.

CRISPR/Cas12a induced DNA double-strand breaks are repaired by locus-dependent and error-prone pathways in a fungal pathogen

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CRISPR/Cas mediated genome engineering has revolutionized functional genomics. However, basic questions remain regarding the mechanisms of DNA repair following Cas-mediated DNA cleavage. We developed CRISPR/Cas12 A - Surface structure ribonucleoprotein genome editing in Magnaporthe oryzae, and found that donor DNA does not require homology for locus specific integration. Unexpectedly, genotyping from hundreds of transformants, generated by targeting different loci, suggested that frequent non-canonical DNA repair outcomes (i.e., not non-homologous end joining (NHEJ) or homologous recombination) predominate. Detailed analysis using PCR, sanger and long-read sequencing revealed i) frequent donor DNA insertion, up to 17kb, mediated by microhomology; ii) large deletions (up to 21kb) between repeat sequences; and iii) infrequent INDELs. Deleting a key component of NHEJ did not abolish the observed DNA repair outcomes. Our results suggest that underappreciated DNA repair pathways, including alternative end-joining and single-strand annealing, mediate the majority of DNA repair events in a locus-dependent and error-prone manner.

Ectomycorrhizal fungal communities associated with urban European hornbeam trees in British Columbia

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Urban trees are of growing importance in an urbanizing world, and they convey many benefits and services within cities. Ectomycorrhizal fungi are crucial for the health and resilience of their plant hosts; however, urban trees are faced with diminished communities of fungal partners along with other difficulties unique to urban spaces. Studies of diversity in mycorrhizal fungal communities often overlook broad ecological theories used to explain diversity in plant and animal communities. In this study, we utilize Illumina next-generation sequencing to characterize ectomycorrhizal fungal communities associated with a common urban tree species, *Carpinus betulus*, in three British Columbian cities, including Vancouver, Victoria, and Kelowna. Species diversity was compared across the three cities and related to ecological theory to investigate broad drivers of diversity. Furthermore, soil physical and chemical properties were analyzed at each site to identify specific soil characteristics associated with changes in community structure.

Fungal pathogens associated with Fruit Tree Decline in Ontario

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Fruit Tree Decline (FTD) affecting stone fruit trees has been observed in Ontario, Canada, orchards over the last three years. Common symptoms include branch die off, cankers, necrosis, leaf discoloration, and increased suckering leading mainly to rapid tree decline. Emergence and development of the disease can be triggered by stress caused by both abiotic and biotic factors. Identifying factors that lead to FTD symptoms are important since they will provide information that may help detect the early onset of the disorder and thereby prevent eventual crop losses. The main objective of this study was to identify fungal pathogens associated with FTD in Ontario, employing both morphological and molecular techniques. Single spore fungal cultures were isolated from wood samples collected from symptomatic trees in stone fruit orchards in Ontario. The fungal isolates were identified by morphological characteristics and phylogenetic analysis of three gene sequence data (internal transcribed spacer (ITS), translation elongation factor 1-alpha (tef1-a), and beta-tubulin (tub2)). The following fungal pathogens were identified in association with FTD symptoms: *Cytospora cf. plurivora*, *Diplodia seriata*, *Nectria cinnabarina*, and *Phomopsis velata (Diaporthe eres)*. Pathogenicity tests were conducted by inoculating mycelial plugs of each fungi into excised nectarine and apricot shoots under laboratory conditions for a 12-day period. According to necrosis length, *Diplodia seriata* was the most pathogenic in nectarines (5.2 cm) while *Cytospora cf. plurivora* appeared to be most virulent in apricots (2.2 cm) when compared to a control inoculated plug containing no mycelium. Inoculated fungal cultures were re-isolated to fulfil Koch's postulate. Future experiments will be conducted using whole genome analysis and digital droplet PCR to develop molecular-based diagnostic tools for an efficient early detection of fungal pathogens identified as either primary causes or key components of the FTD disease complexes.

Orbitides and free polyamines have similar fungicidal activity against three common pathogens of flax in vitro

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The fungi *Fusarium oxysporum* f.sp. lini and Septoria linicola are causes of fusarium wilt and pasmo in flax (*Linum usitatissimum*. Members of a third fungal genus, *Alternaria* spp., have also been found in fiber and linseed varieties of flax, and are a source of post-harvest spoilage and mycotoxins in a wide range of crops. We compared the potency of orbitides (cyclolinopeptides, CLPs) in the control of three plant pathogenic fungi of agricultural importance (*F. oxysporum*, *S. linicola* and *Alternaria* spp), with two polyamines (spermidine and spermine), and the broad-spectrum fungicide carbendazim. We chose these PAs to represent low-molecular weight, endogenous compounds that have previously been shown to inhibit fungal growth. We performed a microdilution assay to test the compounds activities against the selected fungi. The results presented

here showed that PAs and CLPs possess antifungal activities against several fungi, with spermidines being the most effective naturally occurring compound tested.

Uncovering a Novel Fatty Acid Synthesis Inhibitor with Broad-Spectrum Antifungal Activity

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The rise in drug resistance amongst pathogenic fungi, paired with the limited arsenal of antifungals available is an imminent threat to our medical system. To address this, we screened the ~20,000 molecules in the RIKEN Natural Product Depository, to identify compounds displaying antifungal activity against four major human fungal pathogens: *Candida albicans*, *Candida glabrata*, *C. auris*, and *Cryptococcus neoformans*. Through a prioritization pipeline, one compound, NPD6433, emerged as having broad-spectrum antifungal activity and minimal mammalian cytotoxicity. Chemical-genetic and biochemical assays determined that NPD6433 inhibits the enoyl reductase activity of essential fungal enzyme fatty acid synthase 1. Treatment with NPD6433 inhibited various virulence traits in these pathogens and rescued mammalian cell growth in a co-culture model with *C. auris*. Overall, this screen has enabled the identification of a novel inhibitor of fungal Fas, which provides a chemical scaffold for the development of lead molecules that inhibit this promising antifungal target.

Sensitivity of Yeast to Lithium Chloride and Regulation of Translation

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Lithium chloride (LiCl) is a widely used and heavily studied medication used for the treatment of individuals diagnosed with bipolar disorder (BD). LiCl is known to affect cell signaling and signaling transduction pathways through protein kinase C and glycogen synthase kinase-3, which are important aspects in regulating gene expression at the translational level. Additional downstream effects caused by LiCl require further investigation. In yeast, LiCl is reported to reduce the activity and alters the expression of PGM2, a gene that encodes a phosphoglucomutase involved in sugar metabolism. Reduced activity of phosphoglucomutase in the presence of galactose causes an accumulation of intermediate metabolites of galactose metabolism leading to cell toxicity. In this study, we identified genes, DAN1, DAN2 and DAN3 which increase yeast LiCl sensitivity when deleted. We further demonstrate that DAN1, DAN2 and DAN3 influence translation and exert their activity through the 5'-Untranslated region (5'-UTR) of PGM2 mRNA in yeast.

Engaging Citizen Scientists To Document 10 Species Of Rare Fungi On The West Coast

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Fungal Diversity Survey (FunDiS)

Lack of observations is a key obstacle for fungal conservation - we can't protect what we don't know. For many species there is not enough data to assess their distribution and relative rarity. Conversely, thousands of amateurs enjoy documenting fungi on citizen science platforms like iNaturalist, but few are aware of the importance of fungal conservation and the need for data. In Fall of 2020 the Fungal Diversity Survey, a small North American non-profit launched a five month pilot project to encourage amateurs to look for 10 selected rare and threatened fungi on the West Coast. The use of outreach to clubs and organizations as well as the use of social media created awareness and engagement, resulting in a significant number of observations, some of which were sequenced and vouchered. The project is considered a success and will be rolled out to other areas later this year.

Phylogenetic prediction of the invasion potential of ectomycorrhizal fungi

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While not usually thought of as invasive species, many ectomycorrhizal fungi (EMF) have been introduced to novel habitats around the world. EMF are obligate plant symbionts, and require the presence of compatible hosts in order to become established. Consequently, many of the introduced EMF identified to date occur only alongside co-introduced hosts from their native ranges. However, some EMF, including the death cap *Amanita phalloides*, have been able to form novel host associations that facilitate their naturalisation in new environments. Using information on known EMF-host pairings in conjunction with host phylogenies, I propose a method to identify likely novel hosts, and in turn the potential invasion ranges of introduced EMF. While I focus on *A. phalliodes* as a test case, this method has potential for application in any host-symbiont system, including predicting the potential spread of plant pathogens in agriculture and forestry.

Dealing with hyperdiverse lineages in Agaricales: challenges for the modern-day taxonomist

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Agaricales (Agaricomycetes, Basidiomycota) is the largest order of mushrooms, with c. 13,000 known species, which is about 10% of the roughly 135,000 species of fungi that have been described so far, out of an estimated 1.5 to 5 million extant fungal species. Certain lineages within the order are hyperdiverse, in terms of total number of species described and/or estimated to exist. We will take a closer look at the challenges posed by two hyperdiverse lineages in the families Agaricaceae and Pluteaceae. These two groups have been the focus of much taxonomic work in the past decade, integrating data from taxonomy, morphology, biogeography, and phylogenetics. We will analyze how to build modern monographic studies to document species-level biodiversity in Agaricales. These studies are essential resources for ecologists and biodiversity resource managers, especially in our current scenario of global climate change and biodiversity loss.

Red-Listed fungal species present in Canada

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The IUCN Red List is the most comprehensive information source for the conservation status of the world's biodiversity. It is widely used by governmental agencies and non-governmental organizations to make decisions on conservation priorities and strategies. While the list offers very comprehensive information for many groups of animals and vascular plants, Fungi have been traditionally underrepresented, mostly due to the peculiarities of their biology, which makes them more challenging for assessment. The Global Fungal Red List Initiative has worked intensively over the las decade to remedy this situation, and currently 436 fungal species are include in the IUCN Red List, 145 of which are present in North America. We will give an overview of the state of knowledge about these 145 taxa in Canada, focusing on voucher collections available, molecular data generated from Canadian specimens and future focus on these taxa, within the Canadian fungal conservation context.

Puf4 Mediates Post-transcriptional Regulation of Cell Wall Biosynthesis and Caspofungin Resistance in *Cryptococcus neoformans*

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Cryptococcus neoformans is resistant to caspofungin, which targets the ß-1,3-glucan synthase -Fks1. Analysis of a puf4? mutant, lacking the pumilio/FBF RNA-binding protein (RBP) family member Puf4, revealed exacerbated resistance. Puf4 binds the FKS1 mRNA 5' leader. The FKS1 mRNA was destabilized in the puf4? mutant, suggesting that Puf4 is a positive regulator of FKS1 mRNA stability. FKS1 translation was enhanced in puf4? despite destabilization of FKS1. The abundance and stability of additional cell wall biosynthesis genes were also regulated by Puf4. Analysis of cell wall components revealed that puf4? had increased chitin. We concluded that Puf4 is an important RBP that regulates mRNAs encoding fungal specific cellular structures. We analyzed the arginine methylation of Puf4 to investigate the post-translational regulation. We identified monomethyl- and dimethyl-arginine methylation sites. Our findings suggest a mechanism by which caspofungin resistance, and cell wall biogenesis, are regulated post-transcriptionally by Puf4 and its arginine methylation.

Manipulating soil fungal communities as a tool to restore forests post-mountain pine beetle in western Canada

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Mountain pine beetle has killed large areas of lodgepole pine forests in western Canada. In some stands of beetle-killed trees, lodgepole pine regeneration is limited, possibly as a consequence of the loss and change in community composition of ectomycorrhizal fungi. In this landscape-level field experiment, we tested whether we could improve pine seedling establishment in these stands by manipulating the communities of ectomycorrhizal fungi with which seedlings interact. Specifically, we tested whether we could restore ectomycorrhizal fungi in stands of beetle-killed trees by first inoculating seedlings with soil from intact pine forests and then transplanting them to field sites. Two years after planting, fungal community composition on roots of pine seedlings differed by inoculation treatment. Inoculation, however, did not affect survival, height, or biomass of seedlings. Our results demonstrate soil inoculation was not an effective practice to increase pine seedling establishment in west-central Alberta forests post-mountain pine beetle.

Investigating the identity of a potential new *Wawelia* species
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In the summer of 2019, samples of an unidentified fungus were collected from porcupine dung in New Brunswick Canada. The structure of the perithecia suggested a species of *Wawelia*, a genus in the family *Xylariaceae* originally collected in the gardens of the Wawel Castle in Poland in the early 20th century. Five species of *Wawelia* have been recognized, but sequence data are available only for the type species *Wawelia regia*. To characterize this fungus we have studied its macro- and micromorphology, as well as obtaining sequence data for the Small and Large Ribosomal Subunits and the Internal Transcribed Spacer, B-tubulin and RNA Polymerase II genes. These sequences will be aligned with those of related Xylariaceae and other ascomycetes, then phylogenetic trees constructed using Maximum Likelihood and Bayesian methods. The combined data suggest this fungus is congeneric with *Wawelia regia*.

A hidden friend of allergic people: *Cryptophyllachora ambrosiae*, an enigmatic fungal pathogen of common ragweed (*Ambrosia artemisiifolia*)
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Common ragweed is a well-known, invasive agricultural weed and producer of highly allergenic pollen. In some years, its inflorescences are destroyed in large areas by a little known, obligate biotrophic ascomycete, *Cryptophyllachora ambrosiae*. However, most of the time the fungus remains undetectable in ragweed populations. Light and transmission electron microscopy, phylogenetic analyses, artificial inoculations, and examination of old herbarium specimens and recent field samples from Hungary, Korea, Ukraine and USA deciphered its origin and pathogenesis. The North American and the Eurasian specimens represented two distinct, although closely related lineages that were only distantly related to other ascomycete lineages. Two hypotheses were developed to explain the interaction between *C. ambrosiae* and *A. artemisiifolia*: (i) as yet undetected seed-borne transmissions and latent, systemic infections; or (ii) alternative hosts. Read more here: https://rdcu.be/cgor3

The population structure of *Aspergillus fumigatus* from Canadian soils

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Aspergillus fumigatus is a saprophytic mould and opportunistic human fungal pathogen. *A. fumigatus* is the most common causative agent of a range of pulmonary infections termed aspergillosis. However, antifungal resistant strains have become a growing burden. To aid in the surveillance of resistant genotypes, we are interested in expanding our knowledge on *A. fumigatus* populations dynamics and gene flow from environmental soils. Within current literature, environmental population data in Canada is limited to Hamilton Ontario. We obtained soils collected from six locations across Canada that include New Brunswick, Northern Ontario, Western Alberta, Vancouver British Columbia, and Northwest Territories. To date, we have obtained 488 isolates from three populations. Using nine polymorphic microsatellite loci to genotype each strain, we will characterize the genetic diversity present within these populations and compare our data to previously obtained data from other countries. Our results will aid in the surveillance and prevention of aspergillosis outbreaks.

Large-scale screening of activated transcription factors reveals rewiring and novel functions in *Candida albicans*

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Transcription factors (Tfs) are responsible for critical cellular functions and behaviors in organisms, and, in *Candida albicans*, there are approximately 4% of genes that code for transcription factors. We are interested in studying the Tfs, specifically whose functions are unknown to us and can be rewired for various functions. In this study, we performed large-scale screening of 30 different activated Tfs strains of *C. albicans* against 10 phenotypic behaviors including drug resistance, heavy metal tolerance, carbon source utilization, genotoxicity, environmental factors like temperature and pH, morphological changes and adhesion, osmotic and cell wall stress. Interestingly, we found 5 transcription factors affecting morphology, 8 affecting pH tolerance and 5 temperature tolerance, 4 affecting genotoxicity, 11 affecting adhesion, and 1 resulting in multidrug resistance. The large-scale screening results not only reveal multiple rewired genes compared to a well-known species, *S. cerevisiae* but also predicted novel functions of unknown Tfs in *C. albicans*.

Analyzing genetic interactions in *Candida albicans* by targeting stress response genes with uncharacterized functions

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Candida albicans is an opportunistic fungal pathogen causing invasive infections in immunocompromised individuals. With the increase in antifungal resistance, stress response genes are excellent candidates to research as novel drug targets. To study the function of stress response factors, we are constructing a library of single and double gene mutant diploids focussing on stress response genes, including uncharacterized genes with putative functions. Analysis on combinations of mutants enables the observation of genetic interactions between these factors, and can help identify uncharacterized genes. The successful single and double mutants were exposed to antifungal drugs and other stressors to measure growth in stress conditions to monitor possible genetic interactions. These mutants were tested using concentrations optimized to wild-type *C. albicans* resistance. Our work demonstrates that these combinations of fungal genetic manipulations can help uncover interactions and functions of stress response genes which may serve as novel targets for antifungal therapeutics.

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

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This study will investigate the effects of the medicinal and edible Blewit mushroom (Lepista nuda) on the community composition of its soil microbiome in coastal environments in Newfoundland, Canada. Previous studies on Blewits have discovered antimicrobial properties in the lab, but no studies have been conducted in their natural environment. Soil will be sampled from known Blewit fairy rings and nearby treatment plots inoculated with Blewit mycelium. Arthropod, nematode, bacterial and fungal members of the soil community will be identified, and their relative abundance determined by DNA metabarcoding analyses and microscopy. These results will tell us if potential crop pests and plant pathogens are significantly reduced by the growth of the Blewit mycelium, which could lead to use of Blewits as a biopesticide and co-crop. Additionally, there will be experiments to quantify the Blewit mushroom harvest in nearby barren fields amended with different fish-waste compost formulations and Blewit inoculum.

In vitro evolution of posaconazole tolerance in *Candida albicans*
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Numerous studies have examined resistance to the triazole fluconazole, the first line treatment for many *Candida* infections; however, much less is known about resistance to posaconazole, a newer triazole. We exposed replicates from eight strains of *C. albicans* to posaconazole for 50 generations with 24hr and 72hr transfers. Widespread extinction occurred in the 24hr transfer experiment, with the probability of extinction influenced by strain background. Replicates that underwent 72hr transfers rarely acquired drug resistance, yet improvement in drug tolerance was observed in replicates from 6 of 8 strain backgrounds. Cross-tolerance to fluconazole was observed; however, was not present for other drug classes. Karyotypic variation was also widely seen in evolved replicates, predominantly in chromosomes 3, 6, and R. These findings document the first occurrence of cross-tolerance between triazoles, and highlights that adaptation to drug is influenced by strain background.

***Metschnikowia* Taxogenomics**
Lachance, Marc-André*; Lee, Dong Kyung; Hsiang, Tom
University of Western Ontario

We examined correlations between three species delineation criteria using haplontic yeasts of the genus *Metschnikowia*. Average nucleotide identity (ANI), determined from draft genome sequences, is a better predictor of species boundaries defined from reproductive isolation than barcode sequence identity, However, no single criterion provides clear-cut answers, and a wholistic approach to species delineation remains desirable.

Impacts of an invasive plant (*Vinca minor*) on native arbuscular mycorrhizal fungi
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Mutualistic associations between plants and arbuscular mycorrhizal fungi (AMF) are widespread and play a vital role in plant biodiversity and ecosystem function. Plant invasions may benefit from the changes they can cause to AMF associations, but this is poorly understood. *Vinca minor* (Apocynaceae) is an invasive plant originating from Europe that is escaping into urban forests throughout North America. While data show that *V. minor* negatively impacts local diversity and is allelopathic, its effect on native AMF is unknown. We will present the results of a survey of Acer saccharum seedlings growing in both invaded and uninvaded forested areas in Northern Ontario to assess differences in AMF root colonization. Furthermore, data on plant community composition and soil nutrient levels in invaded, edge, and uninvaded plots will be discussed.

Insight from the evolution of yeast hybrid populations across 700 generations in the near absence of natural selection

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Fungal evolution has been punctuated by important events that include hybridization among closely related species. In budding yeasts, hybridization has been observed in contexts influenced by human activities such as brewing, but also in natural populations. These hybridization events are thought to have led to rapid adaptation and sometimes species formation. However, it is difficult to determine if rapid evolution was driven by hybridization or if it was only incidental. To determine if hybridization itself accelerates molecular changes without the confounding effect of natural selection, we performed a large-scale experiment in which we measured a diversity of changes that take place in hundreds of hybrid crosses. We evolved populations for more than 700 generations in the near absence of natural selection and measured traits such as fertility, movements of transposable elements, mutation rates and rates of whole-genome duplication. I will present the highlights of these experiments.

The effect of phosphorus on arbuscular mycorrhizal mediated soil carbon storage

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Arbuscular mycorrhizal (AM) fungi contribute to carbon storage by transporting carbon from plant hosts into soil through the production of hyphae and, potentially, glomalin-related soil protein. However, AM fungal-mediated carbon storage may decrease in high phosphorus environments because AM fungi are less mutualistic. To test this prediction, we grew Trifolium pratense in a common background soil inoculated with soil from 10 sites with varying histories of phosphorus deposition. We expect that plants inoculated with soil from higher phosphorous sites will have lower biomass and root colonization by AM fungi, resulting in lower glomalin-related soil protein production. Contrary to expectations, plants inoculated with AM fungi from higher phosphorus sites had a greater biomass than plants inoculated with AM fungi from lower phosphorus sites. This result suggests that AM fungal inoculum derived from soil with a high legacy of soil phosphorus remains beneficial to plants.

Comparative anatomy and phylogeny of fossil *Callimothallus* and their living relatives

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University of British Columbia

Interpreting the morphology of fossil fungi is essential to tracking fungal evolution through time. The fossil genus *Callimothallus* is represented by hundreds of specimens, the earliest at least 66 million years old. To relate *Callimothallus* to living fungi, we estimate the phylogeny of similar extant taxa using four-locus data from 65 species and a phylogenomic dataset of 101 Dothideomycetes. We then use parsimony analysis of 13 morphological characters to place *Callimothallus* fossils into the phylogeny of living fungi. *Callimothallus* appears most closely related to asexual Muyocopronales that produce conidia from radiate plates of hyphae bearing small pores. Interpreted as an ancient, asexual Muyocopronales, the fossil *Callimothallus* corralesense from the Maastrichtian of Colombia (72–66Ma) provides the earliest evidence for this lineage of leaf-inhabiting fungi. By linking the fossil age to a living clade, we contribute a rigorously analyzed calibration point towards estimates of geological age of Ascomycota.

***Metschnikowia* mitochondrial introns**

Lee, Dong*
University of Western Ontario

Upon assembling 71 mitochondrial genomes belonging to yeasts of the genus *Metschnikowia* we found that self-splicing introns are prevalent in certain mitochondrial genes and can contribute towards high diversities observed among the genomes. Intraspecies variation observed in some of the introns suggests that these visitors evolve independently from their host genomes.

Characterizing the role of choline in *Cryptococcus neoformans* using the phospholipid N-methyltransferase Opi3

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The basidiomycete fungus *Cryptococcus neoformans* serves as a useful model for investigating mechanisms of fungal pathogenesis. This pathogen is the causative agent of cryptococcal meningitis in immunocompromised patients, contributing to over a million cases a year worldwide. Several virulence factors contribute to the growth of C. neoformans in immunocompromised patients including formation of a polysaccharide capsule which impairs detection by pathogen recognition receptors to impede phagocytosis within the host. It is known that phospholipids from macrophages and amoebae supernatants trigger capsule formation thus highlighting important roles for phospholipids in capsule enlargement. In this work, I characterized the OPI3 gene in *Cryptococcus neoformans* responsible for phosphatidylcholine biosynthesis. I show Opi3 is required for growth in nutrient limited conditions and is rescuable with both choline and phosphatidylcholine. Moreover, the opi3 mutant exhibits a choline auxotrophic phenotype in vitro, but sufficient levels of choline are present during mice infections to support cryptococcal growth.

The identities and host ranges of hop and berry powdery mildews to be clarified

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Powdery mildews on hops (*Humulus, Cannabaceae*) and strawberries/blackberries (*Fragaria* and *Rubus*, *Rosaceae*) have not been recognized consistently since de Candolle described *Erysiphe humuli* on hops (1815). Wallroth (1819) considered *E. humuli* as a synonym of *Alphitomorpha macularis*, and *A. aphanis* on *Aphanes* (*Rosaceae*). Both *A. macularis* and *A. aphanis* were moved to *Sphaerotheca*, then *Podospshaera*. In North America, *P. macularis* (sensu lato) was recorded on a wide range of hosts in 15 families, including hops and berries. In Europe, *P. macularis* (sensu stricto) was circumscribed as a species restricted on hops, while *P. aphanis* was on a wide range of hosts including berries. Here, we present a phylogenetic tree of 93 rDNA ITS sequences, showing that both species have wide host ranges: *P. macularis* can occur on *Humulus* as well as *Rosaceae*, whereas *P. aphanis* occurs on hosts in *Rosaceae* and additional families.

Decoding the interaction between wheat and *Fusarium graminearum* on a systems level

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The fungal pathogen, *Fusarium graminearum* poses a threat to global economy, public health, and agriculture, signified by million of dollars in losses every year, due to poor crop yield and reduced quality. Mycotoxin, which produced by the fungal as a secondary metabolite, contaminating crops and threatening the livestock and poultry industries, consequentially affecting human health. The current methods in constraining the fungus are limited, restricted, or not applicable in field. We used state-of-the-art mass spectrometry-based proteomics to assess the interaction during infection of wheat caused by *F. graminearum.* An in-depth dynamic view of host-pathogen interaction across time points and cultivars was investigated. We aim to identify virulence factors in the pathogen, and infection-specific candidate in the host; new insight into the fungal infection and the mechanism in clearance of the pathogen can be provided. This research can further harness strategies for combating the globally important, agricultural fungal pathogen.

Fungal Biodiversity in the Time of Big Data: How Expanding Definitions of Conservation Can Preserve the Past and Drive the Future

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Although species and ecosystem conservation is necessarily the foundation of preserving Fungal biodiversity, there is value in expanding our definition of conservation to include the protection of biological collections, ecological metadata, genetic and genomic data, and the methods and code used for our analysis. The protection of diverse data can be facilitated by applying open science strategies, which have the added benefits of increasing communication, collaboration and the integration of high throughput processing. To do this, we need new tools, including an updated framework for describing and tracking species that are uncultured or unculturable, computational infrastructure for diverse data curation and streamlined accessibility, and the continued integration of functional predictions to link genetic diversity to functional diversity. Here, we examine how technology is being integrated into biodiversity and conservation frameworks, including the real and perceived challenges to implementation.

Development of a novel assay for the detection of *Tuber melanosporum* using droplet digital polymerase chain reaction (ddPCR)

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The nascent Canadian truffle industry represents an agricultural sector that is virtually unexplored. *Tuber melanosporum*, the perigord or black truffle, is one of the most highly valued of all Tuber species due to its gastronomic qualities. The prized fruiting bodies are the product of sexual reproduction between two individuals of opposing mating types, dictated by the MAT genes. The subterranean lifestyle of *T. melanosporum* coupled with the high financial investment for producers warrants research regarding the identification of *T. melanosporum* in the soil. Here, we present a novel assay for absolute quantification of *T. melanosporum* using droplet digital PCR (ddPCR). A duplex reaction was used to target both MAT gene variants. Results will highlight the effectiveness and specificity of the assay, which will be used for subsequent novel research in a Canadian truffle orchard.

Lactobacillus-secreted Yak1 inhibitor, 1-acetyl-beta-carboline, blocks *Candida albicans* morphogenesis and biofilm formation

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The fungal pathogen *Candida albicans* is a common member of the mucosal microbiota that is also the causative agent of vaginal candidiasis. Fungal overgrowth associated with these infections often develops after a decline in bacterial abundance due to antibiotic use. Current research is focused on exploiting probiotic Lactobacillus species to combat vaginal candidiasis. Here, we determined Lactobacillus secrete a factor that represses *C. albicans* morphogenesis, an important virulence trait. Bioassay-guided fractionation linked this activity to 1-acetyl-beta-carboline (1-ABC), and genetic approaches identified the target of 1-ABC as the kinase Yak1. In follow up, we selected for mutants with restored capacity to filament in the presence of 1-ABC coupled with genome sequencing, identifying amino acid substitutions in the putative phosphatase Oca6 and the transcription factor, Rob1. Finally, we found 1-ABC inhibited *C. albicans* biofilm formation in culture. Overall, these insights better define the mechanisms contributing to the virulence of this opportunistic pathogen.

Three unusual and novel synnematous hyphomycetes
Mack, Jonathan*; Overy, David; Seifert, Keith

Canadian forests boast an incredible diversity of microfungi, several of which have yet to be described. Appearing as ropey stalks bearing noticeable aggregations of spores, synnematous hyphomycetes are often observed, arising from the bark of fallen tree branches found on the forest floor. Multiple field excursions to hardwood forests have led to the repeated observance of several interesting specimens of synnematous hyphomycetes. Three species were distinct enough in terms of morphological and molecular analyses to be considered novel, two of which likely represent new genera. An informal description of these unique species will be presented. Unique morphology will be illustrated using macro and microphotographs and preliminary phylogenetic placement using their internal transcribed spacer (ITS) rDNA gene sequences will be shared. The potential ecological and taxonomic interest of these new species will also be discussed along with associated challenges in formal taxonomic description of these taxa.

Investigating the relationships between invasive plants and pathogens in communities – evidence and the way forward
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Plant community structuring depends on co-evolutionary processes leading to plant-soil biota feedbacks. However, altered plant-fungal interactions stemming from non-native plant introductions can severely change those feedbacks, thereby increasing the vulnerability to invasions. We investigated how non-native, invasive (Vincetoxicum rossicum and Alliaria petiolata) and native plants associate with potential plant pathogens; and, whether such pathogens are more likely to be detrimental to native or non-native hosts. Using metagenomic tools, we found no distinct differences in fungal pathogen community composition in coexisting non-native and native plants in an old-field, suggesting the naturalization of non-native plants. Conversely, we found evidence that invasive plants can promote pathogens potentially capable of negatively impacting native hosts. Our data indicate that plant-pathogen interactions may contribute to explaining the difference between plant invasion versus naturalization in communities. However, to what extent pathogens may eventually become detrimental to their invasive hosts is unknown and this will also be discussed.

Structure and succession of salt marsh decomposer communities in the Minas Basin, Nova Scotia

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Coastal salt marshes are declining habitats providing many ecosystem services, however little is known about decomposer taxa in northern salt marshes. We employed a litter bag experiment to characterize the fungal and mite communities associated with the dominant salt marsh grass Sporobolus pumilus (formerly Spartina patens) 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. We documented 17 fungal species and 26 mite species, the majority of which were undescribed, and provide morphological descriptions for the fungi. Fungal and mite communities exhibited negatively correlated trends in species richness through time, suggesting the presence of a complex detrital network that extends beyond decomposition of salt marsh grasses. We provide a preliminary understanding of decomposer biodiversity associated with S. pumilus in Canada.

Copy Number Variation in Canadian *S. cerevisiae* Wine Yeast Genomes

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Vineyards in wine regions around the world have proven to be reservoirs of yeast with oenological potential. *Saccharomyces cerevisiae* (*S. cerevisiae*), carries out fermentation of grape sugars to ethanol as well as generating flavour and aroma compounds in wine. We have isolated thousands of *S. cerevisiae* colonies from spontaneous fermentations of grapes from the Okanagan Valley (OKV) and genotyped them using microsatellite analyses. Wineries place a high value on identifying yeast native to their region to develop a region-specific(terroir) wine program. The genomes of 75 OKV wine strains with different microsatellite profiles were sequenced using Illumina paired end reads and compared to representative genomes from global wild and domestic strain subpopulations. Phylogenetic analysis based on biallelic SNP data for these strains show that OKV strains cluster into four clades: commercial wine (CW), Okanagan Valley wine (OV), North American oak (NAO) and sake. Recent reports on the genotype-phenotype relationship of *S. cerevisiae* attribute gene copy number variations (CNVs) to larger portions of trait variations than single nucleotide polymorphisms (SNPs). Therefore, we analyzed CNVs in OKV strains to find evidence of domestication and wine making traits. We find that gene loss is prominent in domestic strains having lost on average 493 more genes per genome than wild strains. Strains in the CW and OV wine clades have gene CNV reflective of wine making traits such as tolerance to environmental stress, carbohydrate metabolism and nutrient requirements. NAO strains demonstrate higher diversity in gene content as evidenced by elevated CNV in genes absent from CW and OV clades, and this may reflect their generalist niche in the wild. To the best of our knowledge, this is the first study to show the isolation of strains from spontaneous wine fermentations that are genetically related to a strain isolated from North American oak. To validate the suitability of these strains for wine making, future studies should emphasize phenotypic data for OKV strains.

Differences in non-volatile profiles produced by *S. cerevisiae* and *S. uvarum* during Pinot noir fermentation

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While *Saccharomyces cerevisiae* is the most commonly used yeast for fermenting wine, there has been recent interest in other species such as *Saccharomyces uvarum*, which has been shown to ferment competitively and produce unique chemical profiles. Nevertheless, there has been little work done regarding its effect on the profiles of wine in relation to *S. cerevisiae* strains. The objective of this study was to determine the effects of temperature and different yeast strains on the fermentation kinetics and non-volatile profile of Pinot noir. Small-scale fermentations of Pinot noir juice at both 15 °C and 25 °C were conducted with 11 unique yeast strains (six indigenous *S. uvarum*, one commercial S. uvarum, one indigenous *S. cerevisiae*, and three commercial *S. cerevisiae*). Topics, which may help to shape the organoleptic profile of a wine, including kinetics, residual sugars, ethanol, glycerol content, and the production of non-volatile compounds, will be discussed.

Genetic determinants of endophytism in the *Arabidopsis* root mycobiome

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Roots of *Arabidopsis thaliana* do not engage in symbiotic association with mycorrhizal fungi but host taxonomically diverse fungal communities that influence health and disease states. We sequenced the genomes of 41 isolates representative of the *A. thaliana* root mycobiota for comparative analysis with 79 other plant-associated fungi. We identified a set of 84 gene families predicting best endophytism, including families encoding plant cell-wall degrading enzymes acting on xylan (GH10) and cellulose (AA9). These genes also belong to a core transcriptional response induced by phylogenetically-distant mycobiota members in *A. thaliana* roots. Recolonization experiments with individual fungi indicated that strains with detrimental effects in mono-association with the host not only colonize roots more aggressively than those with beneficial activities but also dominate in natural root samples. We identified and validated the pectin degrading enzyme family PL1_7 as a key component linking aggressiveness of endophytic colonization to plant health.

Investigating nitrogen transfer between *Suillus tomentosus* and *Pinus contorta* seedlings in an ectomycorrhizal network

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Most conifer trees exist in symbiosis with ectomycorrhizal fungi, forming mycorrhizal networks when hyphae from the same fungal individual connect two or more root systems. Soil nutrients, including nitrogen, are taken up by hyphae and translocated to roots, but it is unclear what factors affect the fungal allocation of nitrogen to individual plant hosts within a mycorrhizal network. One such factor may be plant nutrient status. To investigate this possibility, Petri plate microcosms were constructed containing two *Pinus contorta* seedlings connected by *Suillus tomentosus* mycelium. Seedlings received 72-hour-long foliar treatments of either urea or H2O. Afterwards, 15NH4Cl or 15N-labelled glycine was supplied to hyphae. Based on a small number of successfully labelled seedlings, we found seedlings that received foliar treatments of urea had higher atom% 15N excess values than seedlings that received foliar treatments of H2O, but only when the nitrogen was supplied to hyphae as glycine.

Hybrid Sterility in *Saccharomyces*

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Reproductive isolation, and consequently speciation, builds up from a combination of isolating barriers. We investigated the potential genetic causes of intrinsic reproductive isolation between two closely related species of budding yeast, *Saccharomyces cerevisiae* and *S. paradoxus*. F1 crosses between these species are viable but infertile. Two potential causes for this sterility are chromosome mis-segregation during meiosis and genic incompatibilities. All chromosomes in *Saccharomyces* yeast are essential. Thus, a gamete missing a single chromosome is inviable. We show that chromosome mis-segregation is common in this hybrid, and that it is linked to genome-wide sequence divergence. Build-up of genic incompatibilities, where genes that work well in their parental genetic background do not work well together in a hybrid genetic background, is thought to be a common mechanism for speciation. We break the first species barrier by restoring recombination in the hybrid, allowing us to uncover evidence of genic incompatibilities in this system.

Exopolysaccharides in co-operative biofilm interactions between *Aspergillus fumigatus* and *Pseudomonas aeruginosa*

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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 related cationic exopolysaccharides GAG and Pel, respectively. We hypothesize that during co-infection, secretion of these similar polymers may support co-operative biofilm interactions. *P. aeruginosa* were observed to adhere to *A. fumigatus* hyphal GAG and to GAG-coated coverslips. Incubation of *P. aeruginosa* with GAG from *A. fumigatus* culture supernatants enhanced bacterial biofilm formation and increased resistance to the antibiotic colistin. Fluorescent microscopy demonstrated incorporation of GAG within these *P. aeruginosa* biofilms. While enhancement of *A. fumigatus* biofilm formation by Pel-containing culture supernatants could be demonstrated, inhibition of fungal growth by bacterial small molecules predominated under in vitro conditions. Collectively, these findings suggest that these organisms have the capacity to form co-operative biofilms in chronic lung disease.

The impact of wildfire severity on soil fungal diversity and community composition in the Okanagan Valley

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With climate change, more frequent and severe wildfires will create unpredictable outcomes for forest regeneration. Pyrophilous (fire-loving) fungi may play an important role early in regeneration, but there is little ecological knowledge of these fungi. To describe soil fungal communities one- and two-months following wildfire, soils were sampled on the surface and in mineral horizons from replicate microplots that had experienced five levels of fire severity. Extracted DNA was analyzed by next-generation sequencing. Fungal alpha diversity decreased with fire severity in both soil horizons. Fire severity also affected community composition, but changes between one- and two-months post-wildfire occurred only in the surface layer. Pyronema domesticum predominated in burnt communities. Dominance shifted from ectomycorrhizal to saprotrophic species with increasing severity. My results suggest that wildfire severity influences the diversity and composition of fungal communities in both surface and mineral layers, but immediate successional changes occur primarily in the surface layer.

Conserved transcription factors cha-4 & rrg-2 orthologs are required for fruiting body development in *Coprinopsis cinerea*

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Fruiting body (FB) development in mushrooms is a highly regulated and complex process. Here we are reporting the role of two conserved transcription factors in FB development in *Coprinopsis cinerea*, a model species of choice to study multicellularity and FB development. The homokaryotic fruiting *C. cinerea* AmutBmut pab1-1 strain was used to create individual deletion strains of cha-4 and rrg-2 genes using CRISPR-Cas9 genome editing based on in-vitro assembled RNP complex with DNA repair cassette. cha-4 is a metabolic transcription factor having role in oleate metabolism and nitrogen starvation, while rrg-2 is a stress regulator. Confirmed deletion strains were analysed for FB development on YMG medium under standard conditions. cha-4 knockout strain showed normal growth but complete loss of FB formation while rrg-2 knockout strain showed reduced aerial hyphae formation with complete loss of FB formation. Further, mechanism to affect the FB formation need to be analysed in more detail.

RNAi triggered systemic acquired resistance to combat emerging plant pathogens

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Continuous emergence of plant pathogens has severe consequences on crop plants and plant ecosystems. Thus, novel approaches to control plant diseases that are environmentally friendly and cost-effective are needed. RNA interference (RNAi) is a natural gene regulation and antiviral response mechanism in eukaryotes. Transgenic and non-transgenic plant-based RNAi approaches have shown great potential to target specific plant pathogens. In concert with a RNAi approach, compounds that are capable of promoting plant defense mechanisms have previously proven to trigger systemic acquired resistance in plants and can also be considered. The objective of this project is to develop and assess approaches that can be used in the short term to mitigate the effects of Tomato brown rugose fruit virus (ToBRFV), which is a serious emerging threat to greenhouse tomato production in Canada. Disease regulator products such as HEADS UP (Chlorothalonil), ACTIGUARD 50WG (Acibenzolar-S-methyl) and EZ-GRO (10% Salicylic) will be tested alone and in combination with pre market dsRNA formulations to effectively manage ToBRFV disease without compromising overall crop production and impacting its economic value.

The distinct ecological signals triggering activation of spores of closely related yeasts

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Spore activation is an important developmental decision in fungi as it initiates the transition from dormant and stress resistant cells to vegetative cells. Here we examine the biochemical signals triggering spore activation in a natural species complex of the budding yeast *Saccharomyces paradoxus* (lineages SpA, SpB, SpC and SpC*). While quantitatively monitor spore activation, we dissect the composition of culture media to identify the components necessary and/or sufficient to activate spores. We show that two of the North American lineages (SpC and SpC*) diverge from the other North American (SpB) and European (SpA) lineages in terms of germination signal as their spore activation requires inorganic phosphate. Our results reveal that the way budding yeast interpret environmental conditions during spore activation diverged among closely related and incipient species, which means that it may play a role in their ecological differentiation and reproductive isolation.

Genetic structure of Macrophomina populations associated with broadacre crops in Australia

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The genus Macrophomina accommodates a number of generalist plant pathogenic species that cause damping off, seedling blight and charcoal rot in >800 plant species worldwide. Despite its economic importance on a range of crops in Australia, the genetic diversity and population structure of Macrophomia remains unknown. This study aims at investigating the genetic diversity and evolution of the pathogen population(s) and sources of inoculum that contribute to charcoal rot epidemics on various crops in Australia. Genotyping-by-sequencing conducted on Macrophomina isolates collected from broadacre crops detected two distinct and genetically differentiated clusters that did not correspond to locations or plant hosts. Further multi-locus phylogenetic analyses revealed one of these clusters as a novel species. Recurrent genotypes within and between different sampling locations suggested that seedborne inoculum could be an important source of dispersal of Macrophomina in Australia. These findings have important implications for integration of effective disease management strategies.

Identification of a novel lipid biosynthesis inhibitor with activity against the emerging fungal pathogen *Candida auris*

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Candida auris has established itself as a global public health burden since its discovery in 2009. Its facile transmissibility and resistance to the three main antifungal drug classes highlight an urgent need for new strategies to combat *C. auris* infections. Here, we endeavoured to identify compounds with novel bioactivity against *C. auris*. Screening the Medicines for Malaria Venture's Pathogen Box library revealed a molecule, MMV688766, with fungicidal activity against *C. auris*. Chemogenomic profiling unveiled heterozygous deletion of the fatty acid synthetase gene, FAS1, as well as sphingolipid biosynthesis genes, AUR1 and LCB2, result in hypersensitivity to MMV688766, suggesting this compound modulates lipid homeostasis. In support of this, lipidomic profiling demonstrated that MMV688766 treatment causes reductions in fatty acids and sphingolipid intermediates. Collectively, this work highlights a molecule with efficacy against an emerging fungal pathogen and suggests targeting lipid homeostasis may be an effective strategy to combat *C. auris* infections.

A fungal endophyte creates a hydrophobic bandage to protect its host tree from pathogen invasion

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Yew trees are amongst the oldest trees in nature, yet surprisingly their bark is constantly punctured by persistent branching, making them susceptible to pathogen invasion. A remarkable fungal endophyte (Paraconiothyrium SSM001) grows towards these pathogen entry points and secretes hydrophobic beads embedded with a potent fungicide. The beads coalesce and form an internal barrier against environmental pathogens – analogous to an antibiotic bandage. Not entirely benevolent, however, the fungal endophyte also stimulates its host plant to kill competitor fungal endophytes by producing the same fungicide, to which it is resistant to. The competitor endophytes also directly stimulate Paraconiothyrium to synthesize the same fungicide. The fungicide is the billion dollar cancer drug, Taxol. These observations suggest multi-way, life-and-death ecosystem interactions within Yew trees. More generally, since plant cells are immobile, locked in by cell walls, plants may possess endophytes to act as mobile defense systems, similar to human white blood cells.

The ROS-targeted redox proteome of *Puccinia triticina* germlings
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Urediniospores of *Puccinia triticina* can germinate on distilled water to form a dense network of germlings. Germ-tube growth requires pathogen-generated ROS, and can be suppressed with inhibitors of ROS production. Signalling mediated through ROS/redox-sensing protein interactions have been demonstrated in other fungi, and NADPH oxidase(s) (Nox) mutants, which produce less ROS, are generally non-pathogenic. We have germinated *P. triticina* (wheat leaf rust) urediniospores on distilled water in the presence of DPI (diphenyleneiodonium chloride), an inhibitor of Nox, to suppress germ-tube growth. To determine which proteins are potentially targeted by Nox-generated ROS, we used iodo-TMT (tandem mass tags) to label reduced and oxidized cysteine residues differentially with isotopic-tags. Using this approach, we have identified 388 candidate proteins with a change in redox status, but without a change in overall protein abundance, compared to an untreated control. The analysis is on-going and findings will be presented.

Role of SAGA complex subunits in gene regulation of *Candida albicans*
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SAGA (Spt-Ada-Gcn5 acetyltransferase) is a highly conserved, multiprotein co-activator complex consisting of five distinct modules. It has two enzymatic functions, histone acetyltransferase (HAT) and deubiquitinase (DUB) that modulate gene expression. Earlier studies have highlighted the importance of the SAGA complex in regulating transcription initiation, elongation, and telomere maintenance. Though, more recent research has shown that SAGA is responsible in other facets of gene expression, thus performs a more extensive role in controlling over-all processes. We analysed conditional and null mutants of the SAGA complex modules; HAT module (Ngg1), Dub module (Ubp8), Recruitment module (Tra1), architecture module (Spt7) and TBP interaction unit (Spt8) to assess their role in filamentation, invasiveness and biofilm formation.

Twinkle, twinkle, little star. How we wondered what you are? The story behind *Valdensia* (*Sclerotiniaceae*)

Redhead, Scott*
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Ottawa Research & Development Centre, Agriculture & Agri-Food Canada
Valdensia is a monotypic genus parasitic on Ericaceae. It is widespread across Canada, the bordering USA, and Eurasia. The fungus, *Valdensia heterodoxa*, was 'discovered' 100 years ago and first named 2 years later in 1923 by Beniamino Peyronel, an Italian mycologists and Pier Andrea Saccardo's last student. Valdensia causes large rapidly expanding necrotic leaf spots and severe defoliation on its preferred hosts (*Vaccinium*, *Gaultheria*). Despite the highly visible symptoms the identity of the causal agent was a mystery and the fungus hid in plain sight for over a century. Peyronel unlocked the mystery by describing complex, multicellular, barely visible to the naked eye, star-shaped propagules that actively jumped off of the leaf spots leaving the surfaces bare and free of 'spores'. This is the story of discovery, multiple naming, rediscovery, and advances in study of a fungus that threatens the blueberry industry on one hand and was used in a patent for biocontrol on the other hand.

A Tetrahydro-ß-carboline Derivative Potentiates Azole Activity Against *Candida albicans* via Perturbation of Membrane Homeostasis

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Invasive fungal infections have transitioned from a rare curiosity to a major cause of human mortality. Combination drug therapy represents a promising strategy to expand antifungal target space and overcome drug resistance. To this end, we screened ~20,000 compounds from the RIKEN Natural Product Depository against *Candida albicans* in combination with the azole antifungal, fluconazole. This screen identified NPD827, a molecule that acts synergistically with fluconazole against both azole-sensitive and -resistant isolates. NPD827 directly disrupted lipid homeostasis, resulting in the accumulation of toxic sphingoid bases, and depletion of glucosylceramides. These alterations reduced mobility and function of membrane-associated proteins and inhibited key virulence traits, including filamentation and biofilm formation. Further, mutations in VPS4 and genes encoding ESCRT-III complex components implicated the multi-vesicular body pathway in NPD827 resistance. Collectively, this work identified a promising antifungal compound that potentiates azole activity against leading human fungal pathogens via disruption of membrane homeostasis.

Manipulating the root mycobiome of corn (*Zea mays*) to enhance plant performance and reduce pathogen pressure

Saeed Cheema, Noor*; Thorn, R. Greg; Kandasamy, Saveetha; Weerasuriya, Nimalka; Saldias, Soledad; Lazarovits, George
University of Western Ontario

Manipulating the root myco- and microbiome of crops could potentially increase yield by reducing pathogen pressure and improving access to soil water and nutrients. However, identifying organisms that can induce these effects remains a challenge. My objective is to investigate how selected fungal isolates affect plant performance and the root mycobiome when applied to soil in which corn seedlings are grown under growth room conditions. In previous studies, A&L Biologicals observed major productivity differences within fields of corn, soybean, and wheat rotations. Root-associated fungi from corn were identified via metabarcoding and soil fungi were isolated in culture. Comparing the fungal communities in high- versus low-yielding sites may help identify key fungal candidates to use as an inoculum to improve crop health and productivity. Corn seeds will be sown into soil from low-yielding sites that is inoculated with potentially beneficial strains, with or without a co-inoculated soilborne fungal pathogen of corn.

Differential Response of *C. albicans* Planktonic and Biofilm Cells to Fluconazole and Boric Acid

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Candida albicans is the most prevalent cause of vulvovaginal candidiasis. The majority of infections are successfully cleared with the azole drug fluconazole; though ~5% of females experience recurrence. Boric acid, a broad-spectrum antimicrobial, has been used successfully as an alternative treatment, yet its mode of action is poorly understood. We examined the phenotypic responses of different *C. albicans* clinical strains to fluconazole and boric acid. Compared to fluconazole, strains had significantly less variation for boric acid resistance and drug tolerance (the ability of a subpopulation to grow slowly in high levels of drug). Furthermore, although biofilms were insensitive to even high levels of fluconazole, boric acid inhibited *C. albicans* biofilm formation in a dose-dependent manner and reduced preformed biofilm biomass and metabolic activity. Interestingly, at high boric acid concentrations, drug tolerance correlated with biofilm activity, suggesting a mechanistic link. These differences could explain boric acid effectiveness in recurrence prevention.

Global Patterns in Culturable Soil Yeast Diversity

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Yeasts (i.e., unicellular fungi) fulfill essential roles in soil ecosystems as decomposers and nutrition sources for fellow soil-dwellers. Broad-scale investigations of soil yeasts poses a methodological challenge as metagenomics are of limited use on targeted groups of organisms. Here we characterize global soil yeast diversity using fungal DNA barcoding on yeasts cultured from 3826 soil samples collected from nine countries in six continents. We identify mean annual precipitation and international air travel as two significant predictors of soil yeast community structure and composition worldwide. Anthropogenic influences on soil yeast communities, directly via travel and indirectly via climate change, are concerning as we found common infectious yeasts frequently distributed in soil in several countries. Our discovery of 41 novel species highlights the need to revise the current estimate of 1500 recognized yeast species. Our findings demonstrate the continued need for culture-based studies to advance our knowledge on environmental yeast diversity.

Evaluating salt marsh rhizosphere carbon stocks and arbuscular mycorrhizal colonization in vegetation zones across a chronosequence in Nova Scotia

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Saint Mary's University

Salt marshes are essential ecosystems that stabilize coastlines while providing a habitat for many invertebrates, juvenile fishes, and birds. Unfortunately, due to the anthropogenic changes, salt marshes are declining worldwide. Salt marshes can accumulate and store large amounts of carbon. Carbon is trapped from the atmosphere and sediment which is utilized by salt marsh vegetation and their fungal associates. Recent studies have found that arbuscular mycorrhizal fungi (AMF) form associations with saltmarsh plants. We are investigating the role of AMF in helping salt marshes sequester carbon. We are evaluating how rhizosphere carbon stocks vary with vegetation types across a chronosequence of salt marshes in comparison with dykeland habitats fringing the Bay of Fundy, Canada. We found high AMF colonization rates in Spartina pectinata roots with varying organic carbon rates. A further understanding of carbon stocks and mycorrhizal associations will increase our knowledge of their contributions to salt marsh restoration methods.

Comparative assemblomics and the use of amplified single nuclei for generating reference genomes of arbuscular mycorrhizal fungi

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Genome sequencing of arbuscular mycorrhizal fungi has been largely hindered by the difficulty to obtain clean axenic cultures that allow the isolation of high-quality DNA. We developed a new method to sequence single nuclei from an ungerminated spore extracted directly from soil. This method showed to be very promising to generate reference genomes from only a handful of nuclei, and was used to sequence the genome of the species Claroideoglomus claroideum. However, since no reference genome of such species was available it was not possible to compare our method with traditional cultured-based methods. In this study, we sequenced single nuclei and assembled the genome of Rhizophagus irregularis DAOM197198, this strain has previously been sequenced and a reference genome of assumed high quality is available. We evaluated the performance of six genome assembly workflows for single nuclei data, and compared them to the published high-quality reference genome in order to find a method that generates the best possible genome assembly from single nuclei data.

Using mycorrhizal fungal variation to increase growth of globally important crops

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Arbuscular mycorrhizal fungi form symbioses with most terrestrial plant species, including all our major crops (wheat, rice, potato, maize and cassava). In this presentation, I will explore how intra-specific variation in the model mycorrhizal fungal species Rhizophagus irregularis contributes to variation in plant gene expression and growth and whether this can be used to actually increase the productivity of globally important crops such as cassava in regions of the world where increasing production of food will have the greatest benefit to the rapidly growing human population.

The role of PCNA in coordinating the functions of CAF1 and Rrm3p at paused replication forks in *S. cerevisiae*

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Epigenetic marks regulate chromatin structure and gene expression independent of DNA sequence. The faithful transmission of the epigenetic marks is orchestrated at the advancing replication fork by DNA clamp protein PCNA and several histone chaperones. Certain mutations in PCNA (pcna-6, pcna-8, pcna-79) reduce gene silencing at the sub-telomeric regions and the mating-type loci in *S. cerevisiae*. Previous studies in our lab indicated that helicase RRM3, which resumes elongation at replication pause sites, can promote epigenetic conversion. I have analyzed the interaction of PCNA with Rrm3p and CAF1 by yeast two-hybrid assay. All mutant pcna bound poorly to CAF1, while Rrm3p bound poorly to pcna-6, pcna-8, but quite well to pcna-79. The differential interactions indicate that several mechanisms are employed in causing loss of silencing in pcna-mutant strains. I'll perform genetic interaction assays and chromatin immunoprecipitation (ChIP) to investigate the interplay between CAF1 and Rrm3p in chromatin maintenance at paused forks.

Business Development and partnerships – Concordia Genome Foundry

Scott, Benjamin
Concordia Genome Foundry

Dr Scott recently joined the Concordia University Genome Foundry as a Business Development & Partnerships Engagement Advisor. His post-doctoral and PhD research focused on engineering cellular signaling to develop biosensors for industrially relevant compounds, and to create cell-based therapies. As a graduate student he founded SynBio Canada to strengthen the national research community, to advocate for trainee needs, and highlight their accomplishments

Secondary metabolite production in *Aspergillus niger*: methyltransferase specificity

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Fungal secondary metabolites (SM) represent an important source of pharmacologically and industrially relevant compounds. Genes involved in the synthesis, chemical modification, and secretion of SMs are often co-localized in the genome, namely biosynthetic gene clusters (BGCs) [1]. Using the genetic toolbox of *Aspergillus niger* [2], BGCs can be manipulated. The BGC producing neurokinin receptor antagonist TAN-1612/BMS-192548 involves the addition of a methyl group by an O-methyltransferase [3]. Understanding the specificity of the methyltransferases (MT) is relevant in designing compounds with improved biological activities. This project aims to replace the native MT with selected candidate MTs and analyze the resulting methylation pattern. BGC engineering and SM profiles of the mutant strains will be presented.

[1] Meyer et al. PMDI: 18201856; [2] Song et al. PMDI: 30142205; [3] Li et al. PMDI: 21866960."

Structural and functional characterization of ARO1 from *Candida albicans*

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The shikimate pathway involves conversion of phosphoenolpyruvate and erythrose-4-phosphate into chorismate, the biosynthetic precursor of aromatic amino acids. In most fungi, five of the seven reactions are mediated by the pentafunctional enzyme ARO1, which converts 3-Deoxy-D-arabinoheptulosonate 7-phosphate to 5-enolpyruvylshikimate-3-phosphate. Because the shikimate pathway is absent from mammals, it has been proposed as a target for antimicrobials. *Candida albicans* is considered an emerging threat to public health due to the rise of multidrug resistance. Consequently, the development of new antifungals is needed and ARO1 is seen as a viable target due to its essentiality; however, ARO1 in *C. albicans* remains poorly characterized. To address this, we pursued structural and functional characterization of ARO1. We generated high-resolution crystal structures encompassing the entire enzyme and, with enzymatic assays, discovered unexpected activity associated with ARO1. Our results highlight a potentially novel avenue for development of antimicrobials targeting the shikimate pathway in *C. albicans*.

Investigation of key factors that regulate epigenetic conversions in *S. cerevisiae* during replication fork pausing

Shaban, Kholoud*; Yankulov, Krassimir
University of Guelph

The active or silent state of eukaryotic genes is controlled by heterochromatin or euchromatin structures, which are faithfully transmitted through multiple cycles of DNA replication. Such epigenetic mechanisms guarantee the continuity of tissue-specific gene expression over multiple cell divisions. Epigenetic conversions play important roles in cell differentiation or adaptation and are involved in multiple health disorders. The mechanisms of epigenetic conversions will be investigated using *S. cerevisiae* as a model organism. I hypothesize that stalling of the replication forks predisposes to epigenetic conversions. I will also develop a novel assay to study the effect of different genes on epigenetic conversions in different silent loci in the yeast genome, using fluorescent microscopy and FACS analyses. A strong supporting evidence for my suggested model will lead to a major advance in our views on epigenetic inheritance. It will also appeal to the fields of fundamental epigenetics, cancer epigenetics, cell differentiation and epidemiology.

Role of *Fusarium graminearum* Ste3 receptor in mediating hyphal chemotropism and pathogenesis towards cereal crops

Sharma,Tanya*; Bonner, Chris; Sridhar, Pooja; Subramaniam, Rajagopal; Loewen, Michele
University of Ottawa

The phytopathogenic fungus *Fusarium graminearum* causes Fusarium head blight on wheat. Chemotropic signals from host plants serve as the primary stimulus for redirecting growth of fungal pathogens. Previous research has highlighted role of a G Protein Coupled Receptor (GPCR) FgSte2 in sensing a catalytic product of host peroxidase. Ste2 and Ste3 are known to work together in regulating pheromone induced mating and conidial germination in *S. cerevisiae* and *F. oxysporum* respectively, but possibility of FgSte3 mediating chemotropism towards host remains unexplored. A combination of in-vitro chemotropism plate assays and in-vivo wheat head infection assays were used to assess the effect of loss of gene function. Our investigations revealed that loss of Ste3 compromises peroxidase chemotropism and abrogates the ability of fungi to cause infection on wheat heads. Ongoing investigations include transcriptomic and proteomic approaches to understand the cellular changes induced by peroxidase.

Elucidating the roles of force-producing motors in *Candida albicans* mitosis: possible mechanisms for generating aneuploidy

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The microtubule (MT)-based mitotic spindle undergoes extensive rearrangements to attach and separate chromosomes before the cell divides. Defects in this process can lead to lethal aneuploidies. However, *Candida albicans* actively generates aneuploidy as a stress-adaptation strategy. We are interested in providing a mechanistic understanding of how aneuploidy arises in *C. albicans* through the actions of MTs and their associated motor proteins. Unique from other eukaryotes, we show that *C. albicans* relies on kinesin-14 for spindle assembly, while kinesin-5 and dynein provide spindle elongation forces. Individual motor loss results in dramatic spindle defects and aneuploidy. We hypothesize that these motors are critical parts of a stress-adaption mechanism in which *C. albicans* regulates motor activity to promote mitotic errors. In support of this, we found that kinesin-5- and kinesin-14-depleted cells have enhanced resistance to fluconazole. Our future goals will investigate how these motors are regulated to facilitate stress-induced genome instability and adaptation.

Adr1 transcription factor directs regulation of the ergosterol pathway and azole resistance in *C. albicans*

Shrivastava, Manjari*; Kirbizakis, Eftyhios; Kouyoumdjian, Gaëlle Séréna; Ruiz, Daniel; Whiteway, Malcolm
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Transcription factors play key roles in the regulation of cellular processes and therefore can be good targets to investigate the control of characteristics such as drug resistance, morphogenesis and pathogenicity in the fungal pathogen *Candida albicans*. We selected at set of poorly characterized transcription factors, activated them, and looked for identifiable phenotypes. We found that activation of the transcription factor Orf19.2752 (Adr1) conferred significant resistance against fluconazole. In *Saccharomyces cerevisiae* Adr1 is carbon source-responsive zinc-finger transcription factor required for transcription of the glucose-repressed gene ADH2 and of genes required for ethanol, glycerol, and fatty acid utilization. Motif scanning of promoter elements suggests that Adr1 may be rewired in the fungi and involved in the ergosterol synthesis pathway in *C. albicans*. Previous studies have identified the zinc-cluster transcription factor Upc2 as a regulator of the ergosterol pathway in both fungi, so we examined the relationship of Adr1 and Upc2 in sterol biosynthesis in *C. albicans*. Phenotypic profiles of both ADR1 and UPC2 mutants in *C. albicans* showed differential growth in the presence of fluconazole, a fungicide that competitively binds to Erg11. ADR1 homozygous deletion results in sensitivity to the drug while upregulation generates a fluconazole resistant strain.

New Clade Designation and Clustering of Isolates Revealed from Whole Genome Sequencing of Clinical Canadian Candida glabrata Isolates

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Candida glabrata is an increasingly common fungal species that causes mucosal and systemic infections in humans. Despite global distribution of *C. glabrata*, not much is known about the local phylogenetic structure and clade designation of Canadian isolates. There are currently no Canadian *C. glabrata* isolates on the Public databases for molecular typing and microbial genome diversity, an open-access database with population sequence data for over 100 microbial species and genera. We whole-genome sequenced 18 clinical *C. glabrata* isolates acquired in 2012-2013 from the major regional hospital in Winnipeg, Manitoba. We placed these isolates into a global phylogenetic context with 107 additional isolates from the Sequence Read Archive database. We identified 13 clades, expanding from seven clades identified in a previous study. Our isolates clustered with other Canadian isolates and were enriched in four clades. These findings indicate the need to further expand the current *C. glabrata* clade designation.

Calorie restriction reshapes cell wall in *Cryptococcus neoformans*

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Cryptococcus neoformans is a major fungal pathogen. During infection, the physiological conditions of the host are characterized by nutritional limitations. Specifically, low glucose concentrations can be found in bronchoalveolar lavage and cerebrospinal fluids. Conversely, the fungal cell wall promotes primarily interactions with the host immune response. In this study, we characterized the cell wall dynamics during restricted glucose availability. *C. neoformans* cells were grown in synthetic media supplemented with different glucose concentrations. Subsequently, the cell wall of yeast cells was analysed by transmission electron microscopy, flow cytometry and fluorescence microscopy. The thickness of the cell wall was remarkable decreased in the cells grew in the media with low glucose concentration. In accordance with this, important components of the fungal cell wall were significantly diminished, such as mannoproteins, chitin and chitooligomers. These findings suggest that the dynamic of the cell wall of *C. neoformans* can change during infection dependent on the growth conditions.

A Toolkit for automated high-throughput cloning and manipulation of DNA in budding and fission yeast

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Budding and fission yeast continue to serve as outstanding models for biomedical research. While budding yeast is emerging as a representative eukaryote for synthetic-biology with readily available fully-characterized toolkits, fission yeast has lagged in part due to the lack of similar resources. Furthermore, the development of Genome Foundries demands compatible platforms that enable modular, multipart cloning with precision. Here, we present toolkits combining the gateway and golden gate technologies for precise, automated, high-throughput cloning and genome engineering for both yeasts.
For budding yeast, we modified a previously available toolkit into robotics-compatible vectors. For fission yeast, this platform provides a new set of vectors for modular assemblies, including a fully characterized collection of promoters and terminators. Additionally, we engineered a non-toxic, codon-optimized, genome-editing tool for efficient modifications of the fission yeast genome. Finally, we show the utility of the toolkit for precision cloning and the expression of heterologous proteins in yeasts.

Intraspecific variation in plant chemistry and land-use history in a common garden experiment, acts as an ecological filter to insect herbivory and fungal endophyte communities

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Phytochemistry is an important mediator of community assembly and species interactions and is an important factor shaping insect herbivores, their enemies and the colonization of fungi. We sought to quantify the heritability of Piper sancti-felicis chemistry, herbivory and fungal endophyte communities as well as other ecological filters of these communities. We found that land-use history had a meaningful effect on fungal endophyte community composition. In addition, parents and offspring differed greatly in their fungal endophyte communities, which was partially attributed to phytochemical diversity and herbivory. There were no compounds, or species interaction measures that were heritable across parents and their offspring, however a factor analysis showed that there were latent variables extracted from metabolomics data that were highly heritable. Lastly, we found that there were important chemical differences between parents and offspring and that this had a meaningful impact on the ability of specialist herbivores to mount an immune response.

Characterization and Domestication of Neocallimastigomycota for Direct Biomanufacturing from Renewable Biomass

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Early-diverging anaerobic fungi (phylum Neocallimastigomycota) resident in the digestive tracts of large herbivores are attractive platforms for bioenergy due to their robust ability to degrade untreated lignocellulosic feedstocks. Anaerobic fungi have undergone significant horizontal gene transfer to secrete fungal- and bacterially-derived enzymes forming the largest known fungal array of biomass-degrading enzymes. These enzymes robustly degrade diverse agricultural, food, and forestry wastes with equal efficiency, including substrates rich in syringyl lignin that are poorly hydrolyzed by other fungi. However, there are no existing tools to probe their physiology or engineer them for industrial applications. In this talk, I will describe our progress towards closing the AT-rich genomes of this phylum as well as discuss our ongoing efforts to create genetic and epigenetic tools to control cellular phenotypes.

Mechanisms underlying the chemotropism of *Fusarium graminearum* that enable pathogenicity

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Fusarium graminearum causes Fusarium Head Blight in wheat, leading to food shortages and economic losses worldwide. Despite being an extensively studied pathogen, the factors that enable *F. graminearum* to sense and mediate directed growth (chemotropism) towards the host cells it colonizes are yet to be elucidated. Our laboratory has shown that the pheromone-sensing G protein-coupled receptor Ste2 of *F. graminearum* mediates chemotropism towards the catalytic product of a wheat-secreted peroxidase. Our ongoing work focuses on identifying the substrates that are converted by peroxidase into the chemoattractant product. We are using in vitro assays to isolate the substrate and product from *F. graminearum* spores, complemented by transcriptomics analyses to identify pathways leading to their production. Our preliminary findings from these studies will be presented. Characterization of the chemoattractant and the cellular changes it induces will deepen our understanding of the mechanisms of host-sensing by this important pathogen.

Specific functions of the ER chaperone Kar2 regulate caspofungin resistance in *Saccharomyces cerevisiae*

Stack-Couture, Samuel*; Lajoie, Patrick
Western University

The echinocandin family member caspofungin is an antifungal drug that disrupts the fungal cell wall. Activation of the unfolded protein response (UPR), an endoplasmic reticulum (ER) signaling pathway that is activated to resolve the toxic accumulation of misfolded proteins, has been implicated in yeast resistance to caspofungin. Cell wall damage is known to increase ER oxidation and activate the UPR in yeast, however, how the UPR specifically regulates the antifungal resistance response remains unclear. Here, we utilized a strain carrying a mutant allele of the ER chaperone Kar2/BiP lacking its sole cysteine (Kar2-C63A), which displays increased sensitivity to ER hyperoxidation. We found that Kar2-C63A cells were hypersensitive to caspofungin. Thus, our results suggest that specific functions of the ER protein quality control machinery control resistance to caspofungin.

Evolutionary Dynamics of Fungal Genomes from *Aspergillus* to Zygomycete
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Global efforts to sequence the fungal tree of life have produced genomes for thousands of fungal isolates. Lowered costs for genomics tools and efforts to populate public databases with sequences have widened access to these resources to the researchers. We have used these data in pursuit of resolving phylogenetic relationships and trait evolution with a focus on the zygomycete and chytrid fungi. We have deployed low coverage genome sequencing on hundreds of zygomycete strains to test its utility in species identification and phylogenetics. In addition, we are using population genomics and analysis of the pan-genome to assess within species evolution in Batrachochytrium dendrobatidis and *Aspergillus fumigatus*. These studies are helping examine the dynamic nature of fungal genomes from populations to phyla.

A gene coevolution network maps eukaryotic cellular and genomic structure and function
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Gene coevolution—which refers to gene pairs whose evolutionary rates covary across speciation events—is often observed among functionally related genes. We present a comprehensive gene coevolution network inferred from the examination of nearly three million gene pairs from 332 budding yeast species spanning ~400 million years of evolution. The network captured key principles of cellular structure and function, such as genetic pleiotropy. By mapping the network onto the genome structures of *Saccharomyces cerevisiae* and the *Candida albicans*, we discovered that coevolving gene pairs are not clustered, but are most often located on different chromosomes. Examination of the phenotypic impact of network perturbation using fitness data from mutant strains suggests deletion of densely connected genes are more likely to negatively impact fitness. The gene coevolution network captures the hierarchy of cellular function, provides a roadmap for genotype-to-phenotype discovery, and portrays the genome as an extensively linked ensemble of genes.

Understanding *Stemphylium vesicarium* in Ontario
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The fungal *pathogen Stemphylium vesicarium* can infect over 500 species and causes diseases of asparagus and onion in Ontario. The yield loss on onion and asparagus caused by this pathogen are not known, and current research focuses on identifying overwintering sites, sources of primary inoculum, and patterns in spore production to provide a better understanding the pathogen's life cycle. This research confirmed that sexual reproduction occurs on onion leaf residue left in the field, and that the structures and spores produced can survive overwinter whether above-ground or buried. Also, six years of air-borne spore concentration data was modeled against weather variables. This analysis showed that days with vapour pressure deficit <0.5 kPa were strongly associated with low spore production. The presentation will describe the life cycle of *Stemphylium vesicarium* in Ontario and how this new information affects disease management in the field.

Interspecific hybridization in a fungal pathogen influences transposable element dynamics and shapes genome-wide variation
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Genome analyses have revealed a profound role of introgression in the evolution of fungi. We have analyzed signatures of introgression along the genome of the plant pathogenic fungus *Zymoseptoria tritici*. Introgressed segments are found throughout the genome, exhibit a unique haplotype pattern and overlap with more than 1000 predicted genes. We find an enrichment of transposable elements associated with introgressed segments suggesting that hybridization may contribute to the horizontal spread of TEs. Recent integration of an active LINE element via introgression was accompanied by non-functionalization of the dim2 gene responsible for DNA methylation in *Z. tritici*. We have used population genomic data to reconstruct the evolutionary history of DNA methylation loss in *Z. tritici* and we investigate the functional relevance of dim2 in TE silencing and in-activation using genetics approaches and evolution experiments. Together our findings shed light on mechanisms of rapid genome evolution in fungal pathogens

The next pandemic: *Trichophyton indotineae* in Canada
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In 2017, it was noticed that an unusually high proportion of isolates in the *Trichophyton* mentagrophytes complex of dermatophytes (ringworm fungi) were resistant to the commonly used drug terbinafine. The resistance was connected with distinctive mutations in the squalene epoxidase gene. The resistant form rapidly increased in prevalence in India and was soon recorded in other countries, apparently introduced by travellers. In 2018, Kano et al., in Japan, noted that it had distinctive laboratory characters and sequence SNPs, and described it as *Trichophyton indotineae*. We document an abrupt surge in incidence of cases of this organism in the Brampton-Mississauga-West Toronto area of Ontario.

A metagenomics solution: nailing down unculturable fungi in a lichen symbiosis
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The study of unculturable fungi as players in microbial communities is hindered by methodological constraints. Many have complex life cycles and as eukaryotes possess complex genomes that can present a challenge for metagenomics. Together, these factors make it difficult to study non-model host-microbe interactions. Lichen symbioses are a stable association between multiple fungal species and a unicellular phototroph. In many of these symbioses, basidiomycete yeasts occur as secondary fungal symbionts in addition to the “dominant” fungal partner, a hyphal ascomycete. By selectively dissolving the extracellular matrix that embeds the yeasts, we created a sample enriched in yeasts cells. We binned the metagenome produced from this sample and obtained nearly complete genomic assemblies of three fungal symbionts. Comparative analysis of the three fungal genomes provides the first evidence for the role yeasts play in a lichen symbiosis and the nature of their relationship with the dominant members of the symbioses.

Microbiome manipulation by a fungal plant pathogen using effector proteins
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During colonization of their plant hosts, fungal pathogens secrete so-called effector proteins to promote disease development. Many of these effector proteins target components of the host immune system. Increasing evidence shows that the microbiome of a host plant plays a crucial role in its health, and that hosts actively shape their microbiomes in their attempts to suppress disease. We propose that pathogens evolved in turn to manipulate the host's microbiome to their advantage, leading to promotion of disease. In our studies on the fungal plant pathogen Verticillium dahliae, causal agent of vascular wilt disease in a wide diversity of hosts, we have identified effector proteins that display antimicrobial activity and facilitate host colonization through the selective manipulation of their microbiomes. Moreover, we found that Verticillium dahliae particularly suppresses antagonistic bacteria with its effector proteins.

Exploring the Microbes of Maize Silks
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Fusarium graminearum is a pathogenic fungus causing Gibberella ear rot (GER) in maize, and produces dangerous mycotoxins which are harmful to humans and livestock. *Fusarium graminearum* (and other mycotoxigenic fungi) frequently invade maize through exposed silks, which are unusually long style tissue. Some maize genotypes are partially resistant to silk invading pathogens – Do those maize plants host certain microbes in the silk to defend the entryway to developing grain? Over 1000 microbes were isolated from 56 silk samples coming from 14 genotypes of maize, and taxonomic identification revealed that silks do indeed host a diversity of culturable bacteria and fungi! We have discovered many bacteria which suppress *F. graminearum* growth in vitro. These microbes may have coevolved with maize to protect the grain from mycotoxigenic fungi, and could potentially be used as a treatment to prevent mycotoxins from contaminating food. We are characterizing them further!

Pathogenicity and Virulence of a Canadian isolate of *P. capsici* on pepper

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Phytophthora capsici is a soil borne plant pathogen that has spread globally infecting economically important crops. In Ontario, infection of peppers, tomatoes and cucurbits by *P. capsici* has become severe problem in recent years. *P. capsici* virulence may vary depending on geographic location but little is known about the pathogenicity of Canadian isolates. The aim of this study is to determine the pathogenicity and comparative virulence of a Canadian *P. capsici* isolate and two isolates from New York state and Michigan state, USA. Pure culture of *P. capsici*, isolated from Ontario, was established and characterized using morphological and molecular techniques. The molecular identification of the Canadian isolate was conducted by sequencing the ITS region, after which the complete genome was sequenced using both Illumina and PacBio sequencing technology to obtain reliable assembly and annotation. The virulence of different isolates from Ontario, New York and Michigan was evaluated by inoculating pepper leaves with a suspension of 5 × 104 zoospores/ml. Disease progression in terms of lesion development was measured 5 days after inoculation using the software ImageJ. Preliminary results show that there is a difference in virulence between the tested isolates, the most virulent isolate came from New York followed by Michigan and lastly the isolate from Ontario. A greenhouse experiment is currently being conducted to test the pathogenicity of isolates on greenhouse-grown pepper plants. The annotated and characterized genome assembly of the Canadian *P. capsici* will be compared with other *P. capsici* to gain insights into its pathogenic lifestyle. Improved understanding of *P. capsici* interactions with host plants may enable pathologists to more effectively evaluate strategies to control phytophthora leaf blight, root and crown rot diseases.

Molecular Network guided Natural Product Discovery from Ginseng Root Rot

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Fungal crop infections are a major concern to Canadian ginseng producers. One such disease is disappearing root rot in ginseng caused by Ilyonectria mors-panacis. Twenty-two strains of Ilyonectria with varying degrees of virulence were analysed by non-targeted LC-MS/MS and the data were processed using PCA followed by MS/MS molecular networking with GNPS. The strain that produced the largest variety of secondary metabolites was then grown in a large-scale fermentation and extracted. I. mors-panasis produces an abundance of resorcylic acid lactones, a compound class that has been previously identified as having anti-fungal properties. We have also found several other biologically relevant metabolites including siderophores from this fungus, which are used for iron uptake and we are focusing on this system as a method of disease control. This research contributes to a better understanding of ginseng root rot disease, and the methods applied here can be easily used for other agricultural pathogens.

The origin of the superbug *Candida auris*

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Candida auris was first isolated from the ear discharge of a Japanese patient in 2008. Since then, this fungus has infected 4,733 patients in over 33 countries. Globally, the mortality rates attributable to invasive *C. auris* infection range from 30% to 59%. The reasons why this species began spreading widely in recent years is a mystery. So far, all isolates of this pathogen have been obtained from patients and hospital environments. However, the natural ecological niche(s) of *C. auris* remained unknown. In this presentation, I will describe our collaborative work with Indian colleagues and describe the first report and genome sequence analyses of *C. auris* strains from salt marsh wetland in Andaman Islands and fruit samples in New Dehli, both in India. Our analyses reveal unique genotypic and phenotypic properties of these environmental *C. auris* strains and significantly expand our understanding of the ecology and evolution of this multidrug-resistant superbug.

Genome evolution and diversity of insect gut-dwelling fungi

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Asellariales, Harpellales, and Orphellales are three major orders (Kickxellomycotina, Zoopagomycota) known for insect gut fungal symbionts. Recent genomic investigations on Harpellales have brought us many unexpected findings, although we still lack genomic resources for Asellariales and Orphellales due to challenging culture techniques. Harpellales genomes are featured with low GC content (26-37%). As a result of long-term associations with Diptera insects (~270 million), some Harpellales are left with detectable genomic hallmarks including a mosquito-like polyubiquitin gene potentially acquired from insect hosts, as well as potential whole-genome duplications suggested by comparative genomics using nine Harpellales genome sequences. The production of Harpellales genomes also leads to the discovery of the 21st amino acid (Selenocysteine) in Harpellales, representing a unique lineage across the fungal tree of life. The increasing efforts to produce additional genomic resources in other orders (Asellariales and Orphellales) will help improve our understanding of these enigmatic gut-dwelling fungi.

Growing a mushroom mat: Investigating mycelial-crop residue application to reduce early-colonizing weeds in row-crop agriculture

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Properties such as density, strength, and versatility have led to increasing industrial utilization of mycelium produced by a number of saprotrophic basidiomycetes. My research aims to determine if application of a fungal mycelium-crop residue slurry can function as an effective weed control in agriculture. I am currently investigating whether a mycelial-crop residue mixture can create a barrier with sufficient tensile strength, once applied to the soil surface, to demonstrate significant reduction in early-colonizing weed prevalence. Initial trials are underway in a controlled, replicable greenhouse environment. These trials will be followed by field trials in active agricultural plots. I will discuss my investigation, preliminary results and observations from fungal candidate species, as well as future direction of such an application in the agricultural sector.

Developing a CRISPRi library to study essential gene function in antifungal-resistant *Candida albicans* isolates

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Investigating essential genes in *Candida albicans* is a vital step in characterizing putative antifungal drug targets. As some of these essential genes are conserved between fungal organisms, developed therapies targeting these genes have the potential to be broad range antifungals. In order to study these genes, we used a precise transcription repression approach known as CRISPR interference (CRISPRi). CRISPRi uses an endonuclease dead Cas9 protein that can be targeted to a precise location where it binds and prevents RNA-polymerase transcription activity. Through the construction of an essential gene CRISPRi-sgRNA library, we can begin to study the function of essential genes under different conditions and identify genes that are involved in critical processes such as drug tolerance in antifungal-resistant background strains. These genes can ultimately be characterized as putative targets for novel antifungal drug development, or targeted as a means to sensitize drug-resistant strains to antifungal treatment.

Accessory Genes and Secondary Metabolism in *Fusarium poae*

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In agriculture, fungal secondary metabolites produced by plant pathogens and spoilage fungi can be mycotoxins acting as virulence factors that directly impact crop yields and market suitability. One reason for observed intra-species variations in secondary metabolism arises from the presence of lineage-specific accessory chromosomes (ACs) encoding secondary metabolite biosynthetic gene clusters. In this short talk I will describe how we are using untargeted mass spectrometry-based metabolomics and whole genome sequencing to profile Canadian *Fusarium poae* populations with a focus on strain-specific secondary metabolism and accessory chromosomes. The consensus chemical profiles produced by culturing isolates in a variety of media conditions will complement a 'pan-Canadian' genome produced though a combination of long- and short-read sequencing. This work will inform future pathogenicity trials and an understanding of how dynamic genomic compartments are evolving in this species.

Identifying and characterizing genes essential for *Candida albicans* viability under diverse environmental conditions

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Candida albicans—a human fungal pathogen—is a major threat to human health with mortality rates of ~40% despite treatment. This project aims to address a gap in knowledge about the genes that enable pathogen survival within the host by characterizing the essential gene set for *C. albicans* in diverse environmental conditions. This will be accomplished by screening a collection of *C. albicans* mutants, in which gene expression is regulated through a doxycycline-repressible promoter system, under host-relevant conditions. Preliminary investigation unveiled 199 genes that were uniquely essential in minimal medium at 30°C and 17 genes that were uniquely essential in RPMI at 37°C. This suggests investigation of genes required for growth under diverse conditions will unveil a plethora of previously unexplored essential genes. Our results will reveal comprehensive lists of *C. albicans* genes that are essential in host-relevant environmental conditions, revealing novel drug targets important for future antifungal development.

Leveraging machine learning essentiality predictions and chemogenomic interactions to characterize a fungal-selective glutaminyl-tRNA synthetase inhibitor with potent *Candida albicans* bioactivity

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Candida albicans is a leading cause of invasive fungal infections, however treatment is threatened by a dearth of antifungals and the emergence of resistance. Thus, there is an urgent need to identify novel therapeutic targets to expand the antifungal armamentarium. A promising approach is the discovery of essential genes, as most antimicrobials target essential bioprocesses. Despite characterization of gene essentiality in *Saccharomyces cerevisiae*, defining essential targets in pathogens of interest is necessary. Here, we generated essentiality predictions for all *C. albicans* genes. We leveraged these predictions with chemogenomic datasets to assign mode-of-action to a recently identified antifungal compound, T-035897, which displayed potent bioactivity against *C. albicans*. To determine mode-of-action, we performed haploinsufficiency profiling, resistant mutant selection, and a translation reporter assay, which concluded T-035897 targets the glutaminyl tRNA synthetase Gln4. Finally, T-035897 selectively abrogated fungal growth in co-culture. Thus, leveraging essentiality datasets is a powerful approach to characterize novel antifungals.

Sexual parasitism in Fungi: Uniparental nuclear inheritance during bisexual mating in fungi

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Some animal species require an opposite-sex partner for their sexual development but discard the partner’s genome before gamete formation, generating hemi-clonal progeny in a process called hybridogenesis. In this study, we discovered this mode of sexual parasitism in fungi, specifically in a basidiomycete fungus, *Cryptococcus neoformans*. *C. neoformans* has two mating types, MATa and MAT?, which produce recombinant meiotic progeny during sexual reproduction. Here, we observed exclusive uniparental inheritance of nuclear genetic material in a fraction of the F1 progeny produced during bisexual reproduction. Analysis of strains expressing fluorescent reporter proteins revealed instances where one parental nucleus was present in the terminal basidium where meiosis and sporulation occur. Whole-genome sequencing revealed the nuclear genome of the progeny was identical with one or the other parental genome, whereas the mitochondrial genome was always inherited from the MATa parent. Uniparental sporulation was also observed in natural isolate crosses where it resulted in mainly MAT? progeny, a bias also observed in *Cryptococcus* ecological distribution. The meiotic recombinase Dmc1 was found to be critical for uniparental reproduction. These findings reveal an unusual mode of eukaryotic microbial sexual reproduction that shares features with hybridogenesis in animals and has a significant ecological impact on fungi.

What are the best parental pairs for *Cryptococcus* progeny?
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Hybridization between more divergent organisms is likely to generate more novel genetic interactions and genetic variations. However, the relationship between parental genetic divergence and progeny phenotypic variation remains largely unknown. Here, we investigated the patterns of such relationship using the human pathogenic fungus *Cryptococcus*. Progeny with different genetic background were collected and genotyped by PCR-RFLP at 16 genetic markers. Also, they were phenotyped for growth ability, melanin production, and fluconazole susceptibility. We found that, as genetic distance increases between parental strains, hybrid progeny showed increased fluconazole resistance and growth at 37 ? but decreased melanin production under various stresses. However, under each tested condition, there was a diversity of phenotypic variations among progeny, including: (i) similar to one of the parents; (ii) intermediate between the parents; (iii) outside the parental phenotypic range. Together, our results indicate the enormous potentials of *Cryptococcus* hybrids in their evolution and adaptation to diverse conditions.

Humanized Yeast as a Platform to Measure the Functional Impact of Human Genetic Variation
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Thousands of human genomes are currently available, revealing several thousand variations in our genes. A grand challenge is to determine the impact of each missense mutation on human health. Functional replacement of yeast genes with their human equivalents implies that humanized-yeast can model human genetic variation. The replaceability links the fitness of the defective human protein with the fitness of the yeast, such as a slower growth. We demonstrate the approach for a rare human genetic disorder, mevalonate kinase deficiency, by conditionally replacing the yeast ScERG12 with the corresponding human gene, HsMVK. We show the yeast growth as an easily measured proxy for the proper functioning of HsMVK by testing 33 variants. Our data shows the impact of the human gene expression and yeast genetic background on distinguishing disease-causing mutations from common polymorphism. Together with previous work, this study establishes a humanized-yeast platform to understand human genetic variation at scale.