

## University of Lethbridge

### Sustainable Agriculture Showcase: Public Lecture & Conference March 31 - April 1, 2023

Oral and Poster Presentations: Speaker Information and Abstracts

#### **Keynote Speaker**

Dr. Martin Entz, Professor of Cropping Systems and Natural Agriculture,  
Department of Plant Science, University of Manitoba

#### **About Martin Entz:**

Martin Entz is a professor in the Department of Plant Science at the University of Manitoba. He received his PhD from the University of Saskatchewan in 1988 and worked as a farm manager and research agronomist before embarking on his academic career. Martin's research focusses on ecologically-integrated farming systems and empowering farmers with knowledge and other tools required to design sustainable farming systems adapted to where they live. He leads the Glenlea Long-Term Rotation Study – Canada's oldest organic vs conventional farming systems experiment, which has completed 28 years. Together with colleagues, Martin founded the U of Manitoba's Natural Systems Agriculture program, which explores cropping systems based on processes found in nature — specifically the natural grassland ecosystem of prairie Canada. Martin and his team of grad students, research associates and technicians work closely with farmers.

Since 2011, Martin has involved organic farmers directly in the development of crop varieties for organic production in partnership with Agriculture and AgriFood Canada and private grain millers. This "Participatory Plant Breeding" program now involves over 80 wheat, oat and potato farmers from across Canada. Martin works internationally, providing science support to various NGO's including the Canadian Foodgrains Bank's East Africa conservation agriculture program. Closer to home, Martin is part of Sustainable Canada Dialogues, a group of 60 Canadian scholars who propose evidence-based climate solutions and actions.

Martin teaches at the diploma, degree and graduate levels and engages farmers in teaching programs. Outside of research and teaching, Martin enjoys his family and small farm located near Libau, Manitoba.

**Title:** Nurturing Agronomy with Nature: From Theory to Practice

#### **Abstract:**

A more natural approach to agriculture is urgently needed if we are to live within planetary boundaries. The greatest urgency regards stopping biodiversity loss and climate change. I will demonstrate a system thinking model that allows students to visualize and imagine "natural" practices within agriculture that can also be applied to the larger food system. "Climate smart" agriculture can be achieved through intense use of mutualistic processes; central to these processes are biological instead of Haber-Bosch nitrogen; expanding trophic levels through, for

example, strategic use of ruminant livestock; nutrient recycling; and massively increasing landscape diversity. The Weinberg systems model also provides guidance for future education, policy and technology innovations. In an example of a post-industrial approach to crop seeding that focuses on the dual goals of less fossil fuel consumption and greater biodiversity, multiple small solar-powered autonomous seeders could allow the seeding operation to accommodate landscape features such as restored wetlands.

Traditional approaches to improving farm function involve extension, where farmers are exposed (and shown) new approaches by third party extension staff. Returning to this model will be important. And since there are no recipes to solve the myriad challenges on diverse farms and landscapes, an adaptive learning approach will be required. Working on the Canadian Prairies, Tarnoczi and Berkes concluded that “Producers were more open to new (conservation) practices when they could learn them through observation, trials, and two-way dialogue”. Therefore, farmers must be part of knowledge generation through a form of “citizen science”. The challenge now is to orient on-farm innovation to a more radically nature-based management paradigm. One place to begin is education. Canada’s colleges and universities must double down on learning and teaching “mutualistic function” in agriculture. The principles of “Ecological Economics”, where the economy is embedded in nature, not the other way around, should guide curricula. The research carried out by these institutions (together with citizens) to generate new knowledge must also emphasize nature-based solutions. This opens the opportunity for reconciliation with Canada’s indigenous communities, who hold ecological knowledge sacred and can therefore provide invaluable contributions.

### **Invited Speaker**

Harold Perry, The Perry Farm (<https://perryfarm.ca/the-perry-farm>), Taber, Alberta

**Title:** A Passion for Soil Health

### **About Harold Perry:**

Harold is a potato farmer with a lovely wife and four great kids. Harold farms 4200 irrigated acres in the Taber Alberta area with his brother Chris, father Gerald and a great crew. Potatoes are the main crop, grown for Frito Lay and McCain. Other crops grown on the farm are faba beans, flax, grains, silage corn, seed canola, mixed forage, cover crops, and green manure.

Harold has been attending soil health conferences with a network of likeminded agriculture enthusiasts he met through his Nuffield scholarship travel. Harold’s Nuffield scholarship was like a sabbatical from the day-to-day farming routine and a breath of fresh farm air. This invigorated Harold on his journey to creating resilience and health in his soils through diversity in cover-crops, green manure, crop rotation and soil amendments.

Harold Perry has held several important leadership positions including: Potato Growers of Alberta, Research Programs Chair (2002-2022); Nuffield Scholar and Director (2006-2019); Alberta Vegetable Growers, Director and Chair (2008-2017); McCain Grower Advisory Board (2017-current); McCain Farm of the Future Advisory Board (2020-current).

**Invited Speaker**

Dr. Bobbi Helgason, Department of Soil Science,  
College of Agriculture and Bioresources, University of Saskatchewan

**Title:** You Are What You Eat: Soil Microorganisms as Indicators of Sustainable Soil Management

**Abstract:**

Supporting good soil stewardship is critical for food security, particularly in the face of ever-increasing demands on agroecosystems stakeholders to produce abundant, high-quality food and bioproducts. Our agricultural soils are home to vast populations of bacteria, fungi and other biota. Well-managed soils provide habitat for diverse and resilient microbial communities who toil away unseen, performing critical ecosystem services. These communities, however, are not altruistic in their behavior - there is fierce competition for resources by populations that ultimately determine the fate of agroecosystem energy and nutrients. When soil microbial communities encounter adverse nutritional or environmental conditions, the resulting imbalanced flow of resources like carbon, nitrogen and other nutrients can have negative environmental and economic consequences. Supporting the soil microbiome to sustain soil health is accomplished by managing and optimizing inputs and the soil environment, for example, through crop rotation, tillage intensity and balanced fertility. Examples of soil microbial community responses to various management practices will illustrate how the living soil is a sensitive indicator of the trajectory of sustainable soil use and guides principles of good soil stewardship.

**Invited Speaker**

Dr. Dr. Guillermo Hernandez-Ramirez, Department of Renewable Resources,  
Faculty of Agriculture, Life and Environmental Sciences, University of Alberta

**Authors:** Thilakarathna, S.K., Korschuh, M., Woods, S.A., Hernandez-Ramirez, G.

**Title:** How Nitrogen Fertilization Choices can Decrease Greenhouse Gas Emissions while Sustaining Yield in Potato

**Abstract:**

Improvements in nitrogen fertilization in croplands are needed to reduce potent nitrous oxide (N<sub>2</sub>O) emissions while sustaining high yields. We conducted a two-year study in southern Alberta to examine the effectiveness of polymer-coated urea (PCU), the nitrification inhibitor 2,4-dimethylpyrazol succinic acid (DMPSA) with granular urea and ammonium sulfate nitrate (ASN) fertilizers to reduce N<sub>2</sub>O emissions and to improve potato (*Solanum tuberosum* L.) productivity under irrigation. Sites were located in Lethbridge and Brooks, Alberta, Canada. Tuber yield, grade, specific gravity, and nitrogen uptake were quantified. Urea alone commonly exhibited the highest N<sub>2</sub>O fluxes. Admixing DMPSA with either urea or ASN lowered N<sub>2</sub>O emissions in certain cases. In one growing season at the Brooks site, DMPSA-urea reduced the N<sub>2</sub>O emissions by 57%. Likewise, in one of the four site-years in the study, 36% higher potato marketable yields were obtained when applying either ASN treated with DMPSA or PCU compared with the unfertilized controls (45 vs. 33 Mg ha<sup>-1</sup>). Results showed that under specific conditions, nitrogen application strategies using DMPSA admixed with either urea or ASN can

maintain high potato yields while reducing N<sub>2</sub>O emissions relative to soils receiving these fertilizers without this additive.

**Invited Speaker**

Dr. Kevin Floate, Insect Biocontrol, Lethbridge Research and Development Centre,  
Agriculture and Agri-Food Canada, Lethbridge, Alberta

**Title:** Cow Patty Critters: Their Season-long Suppression in Dung of Cattle Treated with a Veterinary Parasiticide

**Abstract:**

Fresh cattle dung is home to a rich community of diverse insects. Their feeding, breeding and tunnelling activities provide important ecosystem services that include the restoration of nutrients to pasture soils and increased soil permeability to water and air. By accelerating the removal of dung from the soil surface, they also eliminate breeding sites for parasites of cattle and remove the pat as a barrier to the growth of new vegetation. We recently examined how this community is affected by residues in dung of cattle treated with the parasiticide LongRange® eprinomectin. In two experiments, dung of untreated cattle supported more total insects and insect taxa than did dung of cattle treated for  $\leq 12$  weeks (Experiment 1) and  $\leq 25$  weeks (Experiment 2) previously. Suppression of individual taxa was detected in dung of cattle treated  $\leq 25$  weeks previously. Thus, cattle treated with LongRange in spring will faecally excrete residues for the entire grazing season with an associated simplification of the dung insect community. The effect of this simplification on the long-term health of dung-breeding insect populations on pastures and on dung degradation was not examined in the present study, but merits future research.

**Invited Speaker**

Dr. Jonathan Neilson, Lethbridge Research and Development Centre,  
Agriculture and Agri-Food Canada, Lethbridge, Alberta

**Title:** Impacts of Potato Production on Soil Health and Soil Health on Potato Production

**Abstract:**

It is understood that potato production, which involves land disturbance during seed bed preparation and during harvest, can have a negative impact on soil health. At the same time there are many opportunities to reduce or reverse soil health declines when growing potato. During this presentation we will explore options for adopting soil health promoting agricultural practices in potato agriculture and discuss what tools are needed to determine whether a given land management practice is having a net positive or net negative impact on both soil health and potato production.

## University of Lethbridge Student and Postdoctoral Fellow Presentations

**Authors:** Dhital, S., Kanschuh, M., Yevtushenko, D., Neilson, J., Flanagan, L.B.

**Title:** Screening Variation among Potato (*Solanum tuberosum* L.) Cultivars for Leaf Photosynthetic Characteristics and Water-use Efficiency: Stable Isotope Analyses

**Abstract:**

In arid southern Alberta, making efficient use of limited water resources is essential for increasing the sustainable production of potato crops. Our objective was to determine if significant variation occurred in leaf photosynthetic characteristics and water-use efficiency (WUE, ratio of carbon gained to water lost) among six cultivars of potato that are regularly grown in southern Alberta. Measurements of the stable carbon ( $\delta^{13}\text{C}$ ) and oxygen ( $\delta^{18}\text{O}$ ) isotope composition of leaf tissue were analyzed after potato plants were grown in an irrigated field experiment. There were significant differences among the six cultivars for leaf  $\delta^{13}\text{C}$ , due to associated variation in stomatal conductance. The reduced stomatal conductance could potentially increase WUE, if leaf temperature and the leaf-air vapor pressure gradient remained constant, but it could also result in lower photosynthetic carbon uptake. We did find a significant negative correlation between  $\delta^{13}\text{C}$  and aboveground biomass production and potato yield, indicating that lower stomatal conductance was limiting plant productivity. Lower stomatal conductance also resulted in reduced evaporative cooling and higher leaf temperatures, as indicated by leaf  $\delta^{18}\text{O}$  values. The increase in leaf temperature and higher leaf-vapor pressure gradient offset any increases in WUE due to lower stomatal conductance. As a result of these trade-offs, there were no significant differences among the cultivars for WUE. Potato plants with reduced stomatal conductance had lower leaf water loss but with significant consequences of higher leaf temperatures, lower potato yield, and negative impacts on WUE.

**Authors:** Rankoth, P.R.G.K.T., Flanagan, L.B.

**Title:** Using Stable Isotopes to Trace the Flow of Nitrogen and the Role of Denitrification in a Restored Prairie Wetland Complex Receiving Agro-industrial Wastewater Effluent

**Abstract:**

Municipal and agro-industrial wastewater effluent adds elevated concentrations of nitrogen into natural watersheds. These high amounts of nitrogen in aquatic ecosystems are often associated with severe environmental issues such as eutrophication, human health problems and alterations in overall ecosystem structure and function. Wetlands can provide an important ecosystem service by removing excess nitrogen levels in the effluent before it is discharged into the downstream public waterways. This study aims to measure the concentration of inorganic nitrogen from treated agro-industrial wastewater effluent input into the Frank Lake wetland complex in southern Alberta, document its uptake by the wetland, and trace its subsequent movement through the Little Bow River to the Twin Valley Reservoir using the stable isotope composition of nitrogen ( $^{15}\text{N}/^{14}\text{N}$ ) in water, sediment and tissue samples of two wetland plant species: *Typha latifolia* (cattail) and *Schoenoplectus acutus* (hard stem bulrush/ great bulrush). In addition, the study will analyze the magnitude of denitrification processes that remove nitrogen

as water moves through the wetland using both the  $^{15}\text{N}/^{14}\text{N}$  and  $^{18}\text{O}/^{16}\text{O}$  isotopic compositions of the  $\text{NO}_3^-$  molecules in the water. The study will address some critical aspects of a wetland's nitrogen cycle, using novel techniques, and providing important insights into valuable ecosystem services provided by the wetland.

**Authors:** Garcia-Rodriguez V., VandeStroet, L., Bumunang E.W., Silva-Castro V., Zaheer R., McAllister T. A., Stanford K.

**Title:** Food Waste Silage, an Option to Enhance Feedstock Sustainability

**Abstract:**

In Canada, about 11.2 million metric tons is avoidable food waste. This huge amount represents a major environmental and socio-economic problem. An alternative to reduce this impact could be using part of non-animal food waste for animal feed. This study aimed to develop a high-quality feed for farm animals based on the use of food waste. For this, we performed a silage technique using discarded fruits, vegetables, and bakery products from grocery stores (FW) to preserve their nutrients and contribute to sustainable animal feed production.

FW silage treatments were evaluated: Control, Sundried, and Passive dried during 60 ensiling days. Presented a crude protein content ( $15.25\% \pm 0.65$ - $15.70\% \pm 0.45$ ), similar to the regular grass hay ensiling (13.6%), treatments also showed a high result in crude fat ( $5.59\% \pm 2.02$ - $5.95\% \pm 2.32$ ) and a low Neutral Detergent Fiber ( $7.2\% \pm 0.57$ - $5.7\% \pm 0.14$ ). In addition, fermentation parameters showed that lactic acid content (34.38 mM) was higher than acetic acid ( $12.33 \pm 0.15$  mM), and pH decreased reasonably from  $5.24 \pm 0.1$  to  $3.91 \pm 0.08$ .

In respect of microbiology quality, there was no development of molds or yeasts during the time analyzed, also *lactobacillus spp.* counts decreased by 2  $\log_{10}$  CFU/ml at the end of ensiling. In addition, the mycotoxin content of ensiled FW product was within acceptable parameters. Silage showed aerobic stability after 20 days of aerobic exposure (pH  $3.86 \pm 0.027$ ).

Findings from this study indicate that FW silage could be a viable way of converting low-value materials into good-quality feed for farm animals. Future research in nutritional adjustments along with digestibility testing will be needed for a scaling-up process.

**Authors:** Fisher, B.S., Burg, T.M., Floate, K.D., Wilches, D.M.

**Title:** Gut Microbiome Variance in Ground Beetles (Coleoptera: Carabidae): Effects of Host Species and Location

**Abstract:**

The various microbes, also known as the microbiome, within the gut of an animal host can be essential to its survival. For instance, many animals rely on gut microbes to synthesize vitamins they need while others offer protection from pathogens. Although other microbes may be present, the main constituent of nearly all gut microbiomes is bacteria and most studies focus on that component. Next Generation Sequencing has recently become more affordable as a method to identify nearly all the bacteria in a sample and quantify their relative abundances. Insects are ideal study animals because they are abundant, ecologically important, and can be model systems

for difficult to study animals. Gut bacteria are either acquired from the environment or inherited from a parent. This makes ground beetles, or carabids, (Coleoptera: Carabidae) a top gut microbiome study choice because of the diverse species, genera, and feeding guilds that can be found within a relatively small area where limited dispersal rates can link them to habitats. Carabids are generally considered beneficial to ecosystems, especially agroecosystems in northern temperate regions. This research aims to characterize gut microbiomes of the Carabidae family in cropland, wildland, and urbanized settings in Alberta and Montana. We will look at how gut microbiomes vary by host phylogenetic relationships and external variables (e.g., habitat or season). Many studies have delved far into carabid biology, but this is the first to study their gut microbiomes at a large scale with adequate sample sizes per species.

**Authors:** Pawluk, A., Cárcamo, H., Laird, R.

**Title:** The Impact of Spatial and Temporal Crop Diversification on Beneficial Predatory Insects

**Abstract:**

In the face of the ongoing climate crisis, there is an increasing need to solve agriculturally-driven problems in an sustainable. Beneficial predatory insects, also known as natural enemies, are an effective form of pest control that reduce the need for pesticides, thereby providing both economic and environmental benefits. Crop diversification can also promote pest-control by providing functional biodiversity and ecosystem services. However, the effects of crop diversification on natural enemies is not well understood. We intend to investigate how spatial and temporal crop diversification (achieved through shelterbelts and crop rotation schemes, respectively) affect the biodiversity and abundance of beneficial predatory insects, with a particular focus on parasitoid wasps. This study is intended to provide evidence for economically viable, sustainable agriculture targeted at local crop producers. Furthermore, it will provide one of the first hymenopteran biodiversity studies in southern Alberta, providing novel information on our valuable yet understudied native fauna.

**Authors:** Hand, N., Gerber, T., Puchbauer, M., DuMontier, L., Golsteyn, R., Kernéis S.

**Title:** *Staphylococcus aureus* Dispersal is Limited after Treatment with Alberta Plant Extracts, that Could Act as an Antibiotic Alternative

**Abstract:**

Use of antibiotics has led to an increase in antibiotic resistant strains of bacteria. This has been identified as a global health concern by the World Health Organization. To combat the emergence of antibiotic resistant bacteria, it is necessary to discover alternative strategies to antibiotic usage. Certain Alberta plant extracts cause bacteria to aggregate into “clumps.” There is little research of this phenotype, but it could serve as an alternative to antibiotic use, by limiting bacterial dispersal and infection. This study’s purpose is to characterize the plant extract-induced clump phenotype on *Staphylococcus aureus*. *S. aureus* is a bacterium of concern, with 70-80% of strains being antibiotic resistant. The rate and efficiency of clump formation is dependent on the bacterial and plant extract concentrations. This has been confirmed using a

staining technique which employs the use of crystal violet to compare clumping between samples. Clump-inducing extracts were found to maintain their clumping abilities after being heated to 90°C, giving some indication of the structural properties of clumping factors. Clump-inducing plant extracts could be used to trap bacteria found in water systems, for example, bacteria found in agricultural wastewater (many of which display antibiotic resistance). Using clump-inducing plant extracts to trap, and remove bacteria from wastewater, will reduce the dispersal of these bacteria and thereby limit the chances of human infection, and reduce the need for antibiotic usage.

**Authors:** Telfer, M., Yevtushenko, D.P., Gorzelak, M.

**Title:** Exploring Arbuscular Mycorrhizal Fungi as a Potential Disease Suppression Mechanism for Ascochyta Blight of Chickpea

**Abstract:**

Ascochyta blight is a devastating foliar fungal disease of chickpea crops worldwide. The causal agent, *Ascochyta rabiei*, has evolved resistance to QoI fungicides and there is no fully resistant variety of chickpea. In field trials at SERF, there is evidence that Ascochyta blight incidence and severity is significantly decreased when chickpea and flax are intercropped in mixed rows. Although barrier and dilution effects may play a role, it is also possible that there is a soil microbial mechanism at work. I will discuss my planned research to explore the potential of arbuscular mycorrhizal fungi (AMF) to suppress Ascochyta blight disease. Using a greenhouse-based system, I will inoculate both chickpeas and flax with AMF in a connected H-pot design. To eliminate intercropping effects, H-pot pairings will be chickpea-chickpea, chickpea-flax, and flax-flax. Size exclusion mesh will be used to (a) allow full root and AMF contact; (b) prevent only root contact; and (c) prevent root and AMF contact. *A. rabiei* will be applied at chickpea flowering and disease ratings conducted after three weeks. There will be 15 replicates of each treatment combination. Results will be statistically analyzed using R. It is important to conduct research on this system to identify a potential mechanism of Ascochyta blight resistance so that this information can be shared with chickpea producers to make decisions for sustainable agricultural practices. As a result, a potential reduction in fungicide application combined with the ability for producers to plant chickpea crops consecutively can increase chickpea acreage and yields in Canada.

**Authors:** Pandit S., Goyal R., Schultz E., Chatterton, S.

**Title:** Effect of Phytohormones on Disease Progression of *Aphanomyces euteiches* and *Fusarium avenaceum* Infection in Field Pea

**Abstract:**

The oomycete *Aphanomyces euteiches* and the fungus *Fusarium avenaceum* are the major contributors to the pea root rot complex (PRRC), the most devastating disease of the field pea (*Pisum sativum*). The PRRC complex can cause complete yield loss, and in the absence of resistant cultivars, the disease management options are limited. Currently, the role of



phytohormones in host defense mechanisms is poorly understood. This study aims to further our knowledge of phytohormone participation in plant defense and disease progression. The 14 days old seedlings of the susceptible cultivar ‘CDC Meadow’ were treated with 10, 50, and 100  $\mu\text{M}$  concentrations of salicylic acid (SA), ethephon (ET), methyl jasmonate (MeJA), and ethylene inhibitor, 1-methyl cyclopropene (1-MCP). The hormone treatment was followed by inoculation of *A. euteiches* zoospores and *F. avenaceum* conidia in separate experiments. There was reduced root discoloration due to *Aphanomyces* in 100  $\mu\text{M}$  SA treated seedlings compared to the controls after 7 and 14 days post inoculation (dpi). This was reflected in a lower disease severity rating (DSR) at 7 dpi. However, the pathogen biomass as quantified through qPCR did not differ significantly from the control. The SA treatment seems to have protected against Fusarium root rot as well. On the other hand, the treatment with 100  $\mu\text{M}$  ET increased Fusarium root rot DSR when observed at 7 dpi. The study suggests a different role for SA and ET in PRRC disease progression, which requires further investigation.

**Authors:** Reiter, J.W., Schultz, E.

**Title:** Fertility Defects and Seed Set Reduction in *Arabidopsis* Auxin Transport Mutants

**Abstract:**

Plant development is a complex process involving many structures and stages. Development of the floral reproductive structures is particularly important because it contributes to seed production and plant yield. During reproduction, the plant hormone auxin must be properly transported throughout the plant where it influences developmental gene expression. Auxin transport within a cell is controlled by a family of plant-specific PIN-FORMED (PIN) proteins. Together, PIN proteins and auxin are essential for seed development and production. Our research examines different lines of *Arabidopsis thaliana*, each with a unique gene mutation that affects PIN localization and auxin transport. These lines also produce fewer seed than normal plants and we hypothesize that this is due to improper auxin transport during reproductive development. We examined the male structures (anthers/pollen) and the female structures (carpels/ovules) of the flower for developmental defects. We also examined the fertilization process by conducting cross-pollination experiments. Our results suggest that male fertility is unaffected in these lines. However, female reproductive structures are not developing properly causing plants to produce fewer seed and have a lower yield. Future work will examine the cellular development of each female structure to determine how auxin transport defects impact seed production and plant fertility. Plant reproduction is critical to agricultural productivity and food production. Consequently, it is important to understand how auxin transport affects seed production so that this knowledge may eventually be applied to plant biotechnology and breeding programs to address compelling issues such as crop productivity amidst a growing global population.

**Author:** Denny, M., Bogard, M.

**Title:** Exploring Sulphate Cycling in a Restored Wetland Receiving Multiple Forms of Effluent

**Abstract:**

Wetlands are natural filters on the landscape that remove and retain pollutants in water before it is exported to downstream habitats. Sulphate ( $\text{SO}_4^{2-}$ ) availability plays a crucial role in wetland redox conditions, and thus the sulphur (S) cycle impacts ecosystem services including nutrient and toxin processing. Here we explore the S cycle in Frank Lake (southern Alberta), a restored wetland that treats effluent from municipal sewage and a beef slaughterhouse. We constructed a mass balance that showed the wetland was a net source of  $\text{SO}_4^{2-}$  during sequential wet years. The ratio of  $\text{SO}_4^{2-}$  output to input was 1.66 (a net source) and higher than for chloride (1.13), which we used as a conservative, non-biologically active reference ion. We will conduct further work to contrast the mass balance during wet years to that of recent drought years and will explore S processing using isotopic analyses.

**Authors:** Calder, B., Harding, M.W., Dickson, A., Chatterton, S., Yevtushenko, D.

**Title:** Assessing the Variability and Fungicide Resistance of *Sclerotinia sclerotiorum* isolates Collected from Different Host Crops across Canada

**Abstract:**

*Sclerotinia sclerotiorum* (Lib.) de Bary causes white mould in dry bean and sclerotinia stem rot in canola, both economically damaging diseases. Fungicides are routinely applied to manage the diseases, but the sensitivity of *S. sclerotiorum* isolates to these fungicides has not been evaluated in Canada. Although *S. sclerotiorum* has been extensively studied for many years, recent studies suggested that there is greater genetic variability in pathogen populations than previously thought. Therefore, the objectives of this study were to determine the variability of aggressiveness and virulence of *S. sclerotiorum* isolates on dry bean and canola, and characterize their sensitivities to fungicides, using a pan-Canadian population. Two hundred isolates were collected from field crops in Alberta, British Columbia, Saskatchewan, Manitoba, and Ontario. Mycelium compatibility grouping (MCG) was conducted to identify basic diversity among the isolates, and 18 MCGs have been identified to date, although testing is ongoing. The isolates were assessed for virulence and aggressiveness on two dry bean and two canola lines using a greenhouse pipette inoculation and detached leaf assay. There were clear differences among isolates, and statistical analyses are underway. Following DNA extraction, SSR marker sequencing will be conducted on representative isolates of the MCGs. Fungicide resistance testing against the most commonly used fungicide active ingredients is being conducted as part of a joint initiative with Syngenta Canada Inc. The knowledge generated from these studies will provide new insights into the diversity and fungicide resistance in *S. sclerotiorum* populations and is the first step in developing a genomics-enhanced biovigilance approach to disease management.

**Authors:** Fernando, W.O.K., Flanagan, L.B.

**Title:** Carbon Sequestration Capacity of a Prairie Pothole Wetland under Warm and Dry Conditions

**Abstract:**

Wetlands have been suggested to be important “nature-based solutions” to climate change because of the ecosystem services they provide, such as sequestration of atmospheric carbon dioxide (CO<sub>2</sub>). Despite only covering 5 to 8% of the earth's land surface, wetland soils are thought to contain up to one-third of the carbon that is present in organic soils worldwide. However, in prairie pothole wetlands there can be substantial year-to-year variation in the growth and productivity of wetland plants that influence the magnitude of carbon sequestration. We used the eddy covariance technique to study net carbon sequestration during May-September 2022 in a prairie pothole wetland near High River, Alberta that was dominated by bulrush plants (*Schoenoplectus acutus*). The study was conducted during a time-period that was warmer and had precipitation inputs that were altered from the long-term normal pattern. Despite the warmer and relatively dry weather in 2022, the wetland was still a significant sink for atmospheric CO<sub>2</sub> during the study period with a net uptake of 47 g C m<sup>-2</sup> resulting from 632 g C m<sup>-2</sup> of photosynthesis and 585 g C m<sup>-2</sup> of respiration. This indicated that the significant ecosystem service of CO<sub>2</sub> sequestration can occur in a prairie pothole wetland even during warm and dry weather conditions. The next step in this research is to evaluate how much of the carbon uptake as CO<sub>2</sub> is offset by simultaneous methane emissions by the wetland.

**Authors:** Hasan, M., Schultz, E.

**Title:** Root Responses to Phosphorus Deficiency Assessed on Nutrient Media and Lightweight Expanded Clay Aggregates (LECA)

**Abstract:**

Root system architecture (RSA) involves the spatial and temporal distribution of roots in the soil and facilitates the uptake of water and nutrients. Lateral roots and root hairs are major determinants of RSA and provide the root system a high degree of developmental plasticity. For their optimum growth and development, plants require some macronutrients, among which phosphorus is of great importance. Reduced availability of phosphorus causes defects in plant growth and development. RSA is highly plastic to P deficiency and compensates this deficiency by modulating the length and density of lateral roots and root hairs. Very little is known about the involvement of auxin transport in the phosphate signaling pathways. My research aims at understanding if defects in auxin transport, caused by different gene mutations, could also affect the RSA's response to Phosphate deprivation. Researchers most often assess RSA on nutrient media solidified with agar, which allows easy observation of roots and tight control of nutrient conditions but is unnatural because of light exposure and restricted growth area. To provide a better understanding of nutrient dynamics in a more natural condition, I will also be developing a root growth system using Light Weight Expanded Clay Aggregate (LECA). LECA has a neutral pH and a high absorbency which better resembles natural soil conditions. The separate, small pellets of LECA make the roots more accessible while reducing damage during uprooting and

the volume of LECA could be easily scaled up. Thus, LECA can be an ideal medium for RSA studies, including the effects of nutrients on RSA structure.

**Authors:** Todoschuk, J.M., Laird, R.A., Hoover, S.E.R.

**Title:** Effects of *Vairimorpha* Species and Spore Load on the Western Honey Bee (*Apis mellifera*) Foraging Behaviour

**Abstract:**

*Vairimorpha* is a genus of fungal gut pathogens that infects honey bee colonies worldwide. Canadian honey bee colonies (*Apis mellifera* L.) are infected by two species of *Vairimorpha*: *V. apis* and *V. ceranae*. *Vairimorpha* infection, especially *V. ceranae*, exerts energetic stress on young honey bees, which they compensate for with accelerated physiological maturation and abnormal feeding behaviours. I hypothesize that this energetic stress influences their foraging behaviours, specifically by inducing precocious foraging and biases in foraging choices for nectar, pollen and/or water. I will compare the effects of *V. apis* and *V. ceranae* with varying infection intensity by inoculating uninfected honey bees and releasing them into experimental colonies. I will measure the age inoculated bees first start foraging by observing the entrance of each colony when the bees are 7-21 days old; any inoculated bees found foraging during this time are prematurely foraging. To assess the foraging choices made by infected bees, I will analyze the pollen on their hind legs and nectar or water in their stomachs. This project will show how individual infection leads to behavioural changes that subsequently affect colony success.

**Authors:** Schimpf, N., Yevtushenko, D.P.

**Title:** Antimicrobial, Cytotoxic, and Synergistic Activities of Five Linear Plant-derived Host Defense Peptides for Engineering Disease Resistance in Plants

**Abstract:**

Crop losses due to microbial diseases reduce global food production by one third. Limited efficiency of traditional practices to control plant pathogens hinders food production, especially in developing countries. Recent reports suggest that modes of actions of plant native host defense peptides (HDPs) can allow for long-term host resistance against a broad range of microorganisms without negative impact on the environment. This study seeks to evaluate HDPs for antimicrobial and cytotoxic activities *in vitro* and express promising candidates in potato plants for enhanced disease resistance. Fungal conidia and bacteria were incubated with various concentrations and combinations of peptides for 24 h to assess antimicrobial activity. Cytotoxicity was investigated by challenging mesophyll protoplasts and mammalian cells using colorimetric viability assays. HDP coding sequences were introduced into plants by *Agrobacterium*-mediated transformation. Singly, HDPs SM-985, Ib-AMP 1Q, shepherin 1, and P4650 were active against bacterial and/or fungal pathogens. P4650 and BnPRP1 interacted synergistically in combinations with other peptides, decreasing minimum inhibitory concentrations (MICs) by as much as 83%. P4650 was the only single peptide toxic to protoplasts, with more than 96% loss in cell viability at 100  $\mu$ M. No single HDP nor

combinations were toxic to mammalian cells. Although three three-peptide combinations inhibited all fungal spores at 20-50  $\mu\text{M}$  concentrations and bacteria at 2.5  $\mu\text{M}$ , HDP combination designated as 3D was given precedence for expression in potato plants because of a distinct lack of phytotoxicity. Transgenic plants will be challenged by pathogens in future research to assess host resistance.

**Authors:** Munawar, M., Rahman, A.U., Castillo, P., Yevtushenko, D.P.

**Title:** Identification of *Filenchus* Species from Cultivated Areas of southern Alberta, Canada

**Abstract:**

Phytonematodes are microscopic, worm-like organisms residing in plants and soil. Most of these nematodes are harmless, but some seriously threaten crop production. Soil nematodes attracted attention because they are sensitive to soil disturbances; any shifts in their population reflect changes in the soil microenvironment. Nematode diversity surveys allow researchers to identify dominant nematode species and assess their risk levels in cultivated areas. The current study aims to characterize five *Filenchus* species (*F. cylindricus*, *F. hazenensis*, *F. sheri*, *F. thornei* and *F. vulgaris*) detected in our recent soil surveys. Four of the recovered species are new records in Canada, while *F. hazenensis* is a native species previously described from high arctic areas. Morphologically the recovered species have slender bodies, four lateral lines, short delicate stylets ( $>15\mu\text{m}$ ) and filiform tails. Molecular characterization was carried out using rDNA diagnostic genes. *Filenchus* species are polyphagous, migratory nematodes, generally classified as fungal or plant root hair feeders. These nematodes are not considered pest species; their ecological significance rendered them a subject of higher interest in soil health and conservation studies. Moreover, their mycophagy has been tested against several phyto-pathogenic and saprophytic fungi. We anticipate that these species are not pathogenic to plants; they are phyto-friendly and propagate on fungal propagules in soil or rhizosphere. The data obtained during this study will facilitate accurate species identifications and likely aid in decision-making on whether these species qualify to become part of crop management programs.

**Authors:** Rahman, A.U., Munawar, M., Korschuh, M., Tenuta, M., Harding, M.W.  
Yevtushenko, D.P.

**Title:** The Complex Nature of Potato Early Dying Disease in Alberta: Insights from a Study of *Verticillium dahliae*, *V. albo-atrum*, and *Colletotrichum coccodes*

Potato Early Dying (PED) is a serious problem faced by potato growers worldwide. PED refers to the premature death of potato plants caused by a combination of soilborne fungi, including *V. dahliae*, *V. albo-atrum*, *Colletotrichum coccodes*, *Fusarium* species, and the nematode *Pratylenchus penetrans*. In Alberta, however, the causative agents of PED remained poorly understood. Hence, our study aimed to bridge this knowledge gap by identifying and quantifying the incidence and abundance of *V. dahliae* and *V. albo-atrum* in southern Alberta and investigating their association with PED disease severity and potato yield loss. Soil samples were collected from 62 potato fields during the fall of 2020 and 2021 and analyzed by qPCR for the

presence and quantity of *V. dahliae* and *V. albo-atrum*. The results showed that *V. dahliae* was prevalent, being detected in 71% and 45% of the fields in 2020 and 2021, respectively. In contrast, *V. albo-atrum* was found only in one field in 2020. In the summer of 2021 and 2022, fields selected according to the *V. dahliae* soil inoculum levels were surveyed to assess PED severity and the presence of *V. dahliae* and *C. coccodes* in plants tissues. *C. coccodes* was detected in 59% and 41% of the plant samples collected in 2021 and 2022, respectively, along with *V. dahliae*. Potato fields with high *V. dahliae* inoculum levels in the soil usually displayed more PED symptoms and, in some instances, lower yields. However, even some low inoculum fields showed PED symptoms, suggesting other factors might contribute to the PED complex.

**Authors:** Spengler, M., Russell, A.G.

**Title:** Investigation into the Biotechnological Capabilities of the Protist *Euglena gracilis*

**Abstract:**

In recent years, microalgae have received attention due to their ability to be utilized as sources of renewable resources such as fuel and food. Advantages of utilizing microalgae as a source of sustainable resources include their ability to be cultivated in a wide range of environments and growth conditions. *Euglena gracilis*, a unicellular protist organism classified as a microalga, is also capable of being exploited as a source of sustainable bioproducts. While *E. gracilis* can be easily cultivated, challenges have risen as the production of sustainable bioproducts is economically unfeasible in its current state. Efforts to improve the yield of bioproducts in *E. gracilis* include the manipulation of metabolic pathways responsible for producing the bioproducts themselves. However, this effort has been hampered due to the lack of information necessary to manipulate the pathways such as the lack of a fully sequenced genome leading to a general lack of understanding in *Euglena* biology. The goal of my research is to develop or provide information to help develop genetic tools in *E. gracilis*. This goal is being achieved by investigating if microRNAs are present in *E. gracilis*, a class of biological molecules responsible for regulating gene expression. MicroRNAs as well as any proteins they associate with, will hopefully be identified by examining and isolating an Argonaute protein homolog suspected to interact with *E. gracilis* microRNAs. Identifying a mechanism of gene regulation in *E. gracilis* may contribute to improving the yield of bioproducts and further the current understanding of *E. gracilis* biology.

**Authors:** Shafique, M.S., Korschuh, M., Foster, J., Harding M., Yevtushenko, D.P.

**Title:** Management of Powdery Scab of Potatoes in Alberta

**Abstract:**

Powdery scab is an emerging potato disease caused by the fungal-like pathogen *Spongospora subterranea* f. sp. *subterranea*. The visible symptoms include root galls and tuber blemishing on potatoes. In addition, it is the sole vector for the potato mop-top virus (PMTV) that causes spraing in tubers, thereby making them unsuitable for processing and consumption. Study of pathogen population levels in soils and its impact on potato production is necessary to manage

this disease. Currently, no effective treatments are available to control *S. subterranea* in Alberta. Our research focuses on the detection of the pathogen(s) involved in powdery scab of potatoes and evaluating a potential chemical treatment to control this disease in the province. Different fungicides were applied in-furrow at planting in the seed potato field with a known history of powdery scab, using a small-plot replicated design. Soil samples were collected from experimental plots before treatments. Disease assessment was done by taking total and marketable yield. The suspected tubers will be subjected to further morphological and molecular analyses. The results of our study will improve the diagnostics of powdery scab and will provide a possible solution to reduce the impact of this disease in potato fields of Alberta.

**Authors:** Gourlie, R., McDonald, M., Hafez, M., Yevtushenko, D., Aboukhaddour, R.

**Title:** The Effector Gene *ToxB* is Present on a Putative Starship Transposon in *Pyrenophora tritici-repentis* (tan spot of wheat)

**Abstract:**

The role of transposable elements in the evolution of virulence has been well detailed for *ToxA* (the necrosis coding gene) and its carrying wheat pathogens. Here, we provide evidence for the first time for the potential mobility of *ToxB* (the chlorosis coding gene) via a large and novel transposable element in the tan spot pathogen (*Pyrenophora tritici-repentis*). In this study, the genomes of two *P. tritici-repentis* (Ptr) isolates, one carrying *ToxB* and another carrying its non-functional homolog *tox**b*, were sequenced with PacBio RS II and assembled with Flye+Pilon. Comparison with reference isolates lacking the *ToxB/tox**b* genes showed a large 294 to 340 kb region with no co-linearity to reference chromosomes. Edge analysis revealed terminal-inverted repeats which indicated a possible transposon activity. Gene annotations within the region confirmed the presence of known “Starship” cargo genes and DDE transposases in the ‘captain’ position. DDE transposases are known to be associated with some Class II transposons (e.g. Mutator, hAT, etc.) and are known captains of bacterial ICE transposons. Searching the available fungal genomes revealed that the distribution of ToxB-like protein sequences extends beyond the genus *Pyrenophora* into other genera of the class Dothidiomycetes. Additionally, the putative ToxB protein homologs are also present in Sordariomycetes and Leotiomycetes classes. These findings together suggest that *ToxB* could have been mobile at certain evolutionary times contrary to the previous assumption of its vertical inheritance.

**Authors:** Bumunang, E.W., Garcia-Rodriguez, V., Silva-Castro, V., Zaheer, R., McAllister, T. A., Stanford, K.

**Title:** Metagenomic Analysis of Ensiled Grocery Food Waste

**Abstract:**

Metagenomics is the analysis of genetic material purified directly from environmental samples by sequencing and enables taxonomic identification of the microbial communities present. This study aimed to evaluate the silage produced with different mixtures (fruit, vegetables, bread, and

bakery products) of food waste (FW) after 60 days for microbial community and functional diversity. The FW was ground to a particle size of 1 cm<sup>2</sup> and three treatments in duplicates were obtained: control (refrigerated), sundried (outside the building) and passive-dried (inside the building). The DNA of the ensiled FW was extracted for two metagenomic sequencing approaches; specific regions sequencing including 16S rRNA (bacterial diversity), 18S rRNA (species differences in eukaryotes), internal transcribed spacer (ITS; for fungal classification) and shotgun sequencing. Specific coding region sequencing is more precise while shotgun sequencing can better identify the most abundant organisms. Therefore, we are using these two methods for comparative analysis and to enable us to capture the entire microbial community. Analysis of the metagenomic data is ongoing with the intention to characterize potential pathogenic bacteria and antimicrobial resistance genes within the ensiled FW to confirm that the ensiled FW is safe to feed to cattle. We are awaiting data for specific region sequencing. Overall, we expect to confirm if this approach is useful for silage analysis.