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Project Directory

Project #19101

Optimizing Carbon Footprint of Poultry Farms via Smart Antimicrobial Use

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Keywords for Proposed Investigation

Research	Methods & Technologies
Reduction of attrition and flock condemnations, Improving feed conversion, Regulatory approval of novel antimicrobials, Novel poultry antimicrobials	Antimicrobial production via fermentation, Antimicrobial susceptibility testing, Induction of antimicrobial resistance, Pen trials

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Impact of antimicrobials on carbon footprint of poultry production, Regulatory categorization of natural antimicrobials as prophylactic drugs, Regulatory pathway of natural antimicrobials as nutritional supplements	Analysis of historical production data before and after antimicrobial restrictions in farming, Regulatory consultations, Stakeholder conferences

Project Information

Chicken meat is the number one source of animal protein in the Canadian diet; we consume one billion birds a year. Until recently, prophylactic use of antimicrobials was part of regular farm operations to keep animals, farm workers and consumers safe. However, to prevent a looming crisis due to emerging antimicrobial resistance in bacterial pathogens, antibiotics relevant for human health were gradually restricted. In Canada, as of December 2018, veterinary use of these drugs is by prescription only, and growth promotion claims are removed from drug labels. As a result of this regulatory change, attrition rates in broiler production has increased (especially in the form of first week mortality), flock condemnations have increased, and feed conversion rates have deteriorated – all having a negative impact on the carbon footprint of poultry farming. While the Canadian farmers have adapted to these regulations, they are still looking for alternatives to old antibiotics. This desired direction is in line with the overall objectives of this call to reduce the carbon footprint of Canada's food system, targeting a key sector for its economic viability and environmental sustainability. In this project, we will use genomics technologies to develop novel antimicrobials specifically designed for poultry farming.

Deliverables and Expected Benefits

The project will deliver novel antimicrobial peptide based in ovo injectable drugs for the hatching egg producers and nutritional supplements for broiler and layer farms to prevent avian pathogenic Escherichia coli (APEC) and Salmonella enterica serovar Enteritidis (SE) infections. The novel antimicrobials will reduce bird attrition rates and flock condemnations, and improve feed conversion rates and product standardisation. These will all have a positive impact on the carbon footprint of poultry operations, reducing carcass disposal (through incineration) and producing more animal protein with less feed. As we are targeting a global problem, our deliverables will also find an international audience.

Methodologies, Technologies and Data
It is important that new antimicrobials do not quickly induce resistance in their target bacteria. Thus, induction of resistance will be a baked-in component of our project. We will characterize the genomics and transcriptomics of acquired and intrinsic resistance to antimicrobial peptides from time-course experiments. We will generate electron microscopy images describing peptide-bacteria interactions to describe mechanisms of action and resistance. We will also electron microscopy to study peptide-host cell interactions to mitigate cytotoxicity. We will conduct pen trials to measure the efficacy of new antimicrobials in colder climates.

Integrated GE3LS
For new antimicrobials to be viable products, using them will have to be more profitable for the farmers and reduce the carbon footprint of poultry production. We will analyze historical production data before and after antimicrobial restrictions in farming. This will assume the cost-benefit balance of the new products are equivalent of the restricted drugs. We will also evaluate the value of the new products for consumers and growers in the North, where transportation challenges negatively impact both food security and sustainability.

Project #19102

The Social Implications of Genomic Agrifood Technologies: Ensuring Equity, Diversity and Inclusion in the Transition to Climate-Resilient Canadian Agricultural and Food Systems

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Keywords for Proposed Investigation

Research	Methods & Technologies
Equity Diversity and Inclusion, Agri Genomic technologies, resilient and climate smart food systems, GE3LS	Social science methodologies, Cellular Agriculture, gene edited crops

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Equity Diversity and Inclusion, climate justice, Responsible Research and Innovation	focus groups and interviews, consultation workshops, Systematic Literature Reviews, Policy and Content Analyses

Project Information

We propose a GE3LS-focused ICT research program on "Equity, Diversity, and Inclusion" (EDI) in agri-food systems genomics for climate action. There is widespread and growing interest among technology developers, researchers, farmers and others throughout the food system in finding ways to deliver better EDI outcomes. This applies to the development and application of genomic climate-smart agri-food technologies, thereby presenting a need for a social science and GE3LS-focused research dedicated to this topic. Our application aims to fill this need. Drawing on our academic, government, and industry networks, we will conduct a set of EDI-focused case studies on genomic technologies demonstrating climate mitigation potential in British Columbia: 1) Cellular agriculture and 2) Gene-edited crops. The main focus of the case studies will be the risks to and benefits for marginalized communities in the development and application of these technologies. We will also conduct a comprehensive review of GE3LS for agri-genomics more broadly. And, we will host a series of workshops with genomics experts, policy makers, and the members of other ICTs to discuss EDI and other GE3LS-related issues encountered across the portfolio of ICTs to develop policy recommendations and best practices resources for EDI in genomics for climate-smart food systems.

Deliverables and Expected Benefits

1) This program will deliver empirical social science studies on EDI and GE3LS for cellular agriculture, gene-edited crops and agri-genomics broadly. It will result in research and policy recommendations to effectively incorporate better EDI outcomes and processes into the development and deployment of genomic innovations for resilient and climate-smart food and agricultural systems.   2) The EDI and GE3LS recommendations will be packaged into a resource toolkit, which will be refined through a series of online workshops and expert

consultations, including sessions with other funded ICTs. The toolkit will be revised following the workshops based on participant feedback.

Methodologies, Technologies and Data
We will use two social science methodologies: 1) systematic literature reviews and meta-analyses on agri-food genomics to identify potential social, cultural, and ethical implications of emerging food production technologies for addressing climate change. This will include an assessment of possible GE3LS impacts of cellular agriculture and gene-edited crop applications for on-farm GHG mitigation.   2) community-engaged and qualitative methods, including interviews, focus groups, stakeholder and expert workshops, and document analyses, to identify opportunities and challenges around incorporating EDI in the development, adoption, and implementation of cellular agriculture and gene-edited crops for climate resilience in the BC and Canadian contexts.

Integrated GE3LS
The focus of this research is EDI in agri-food genomics for climate action. It will involve case studies in BC and across Canada and expert and ICT workshops to address these questions: How can cellular agriculture (precision fermentation and tissue engineering technologies) be developed and employed to reduce GHG emissions while ensuring progress on EDI, food security and climate justice? How can an EDI lens improve the development and application of gene-editing for on-farm GHG mitigation and food systems resilience (e.g., no-till crops, biological carbon sequestration, lower input crops, and crops adapted to local, indoor, and vertical systems)?

Project #19103

barleyGRAINS: Barley Genomic Research for Application of Innovative New Solutions

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Keywords for Proposed Investigation

Research	Methods & Technologies
Biological Nitrification Inhibition, Biopesticides, Carbon Footprint Reduction, Barley	Quantitative Genetics, Biological Nitrification Inhibition, Root Activity, Genomics, Environmental Response

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Consumer Customer Acceptance, Producer Response to External Changes Models, Environmental Consequences, Policy	Econometrics, Social Communication, Innovative Participatory Methodologies, Quantitative Modelling of Policy Issues

Project Information

The Canadian barley researchers and industry are ready to do their share towards Canada's ambitious plan to reduce emissions. The proposed project will use innovative, novel, and genomic approaches to gain the transformational change (upgrade) required for barley, the third largest (in acreage) crop of Canada supporting multi-billion-dollar malt, feed, and food industries, in light of climate change mitigation. The results will be delivered through four interdisciplinary teams of industry partners and Canadian and international researchers as follows: breeding-genetics-genomics, biological nitrification inhibition-agronomy, microbiome-biopesticide-pathology, and bioinformatics-database; who will work very closely with GE3LS1 team of the project. Solutions for GHG/C emissions reduction are anticipated to be delivered across entire barley industry from farmers (e.g. reduction of chemical fertilizers and pesticides use) to malters (e.g. quicker malting process) to meat producers (e.g. feed barleys with better digestibility). Additionally, we will use climate-crop-interaction-models to study the effect of climate change on barley production as well as C-footprint of Canadian barley varieties. As demonstrated to date Canada has the capacity and know-how to dominate the barley world production and exports and to quickly adopt proven innovation at large scale. By pursuing this project, Canada will be keeping abreast with today's climate and technological challenges.

Deliverables and Expected Benefits

Main deliverables of this project are: - A pre-breeding platform incorporating cutting-edge genetic/genomics tools that exploits pan-genome data to support accelerated development of climate-smart varieties. - High-quality germplasm leading to novel, improved, climate-smart and environment-friendly barley varieties; examples- feed barley with lower methanogenic potential, malt/food/feed barley with better N-use and nitrification inhibition activity. - Ready-to-use plant-based crop protection and microbial products for on farm and in malthouse use which will provide producers/processors with sustainable solutions and mitigation of C/GHG emissions. - Well-defined economic/environmental impacts, customer/consumer issues, and factors related to the ownership/control of new breeding technologies via integrated GE3LS1 research-derived questions and hands-on solutions.

Methodologies, Technologies and Data

The team will utilize genomics technologies/methods such as whole-genome-based comparative genomics, transcriptomics, informatics, genetic mapping/fine-mapping, gene isolation and characterization, gene-editing, breeder-friendly marker development in association with methods/protocols used to collect data from agronomic trials, environmental response & environment-crop interaction modeling, biological nitrification inhibition activity and N-use efficiency screening, biopesticide/microbial-derived products & field interaction with barley varieties, disease screening nurseries, and digestion/metabolomics assays to answer specific research questions on developing environment/climate-friendly end-products and germplasm for the barley industry. Sequence, transcriptomic, pan-genomes, resistance gene atlas data, and data on C/GHG footprints of Canadian barley will be generated and deposited in public domain.

Integrated GE3LS

The GE3LS1 research gives an opportunity to interpret the overall impact of the project in the context of social, economic, and regulatory environments. A stand-alone GE3LS1 activity and well-integrated GE3LS1 sub-activities within the research activities will address questions on consequences of genomic-applications/tools used and products delivered in the project, on society/consumers, environment, policy, and ethics. Specifically, export marketability, costumer/consumer preference of gene-edited and/or microbiome-treated and/or alien/wild-introgression carrying barley varieties will be studied. Advanced econometrics, modelling, causal inference methods will be deployed to answer GE3LS1 questions. The GE3LS1 activity will develop tools to inform and guide specific audiences and stakeholders.

Project #19104

Understanding and improving woody berry crop resilience to climate change

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Keywords for Proposed Investigation

Research	Methods & Technologies
Climate change resilience, Vaccinium, Grape Phytohormones	Metabolomics, Genomics, Biosensors, Agrivoltaics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Sustainability Renewable Energy	Community and stakeholder engagement, Surveys, Carbon modelling

Project Information
Woody berry crops such as blueberries, cranberries, and grapes are important traditional foods, sources of nutrients and drivers of the economy. In the last 2 years, these crops have experienced wildfires, floods, and extreme weather events. Our climate modelling work suggests agricultural production lands for these crops are shifting (https://doi.org/10.1139/cjb-2021-0090, Hirabayashi et al. in review). We propose to create a new program integrating genomics, metabolomics and hormonomics to enable berry crop production in agrivoltaics systems. Agrivoltaics is the dual use of agricultural land for crop and energy production. Current models integrate classic solar panel installations with shade grown crops like lettuce and carrots. New technologies are using organic polymers for light capture and electricity generation; new crops are needed to grow with these technologies. Key to the widespread adoption of agrivoltaics electricity generation is optimization of plant performance in light harvesting systems. Plant growth regulators (PGRs) are the chemicals produced by plants that perceive environmental cues and respond by redirecting metabolic resources. We recently developed a metabolomics toolkit for determination of >250 PGRs, conjugates, precursors and catabolites. Our work will identify and quantify how PGR signals in varietals of woody berries control growth, yield and productivity in Climate Smart systems.

Deliverables and Expected Benefits
The proposed program will integrate -omics and photovoltaics technologies to optimize transition of specific wavelength of light for berry growth and productivity in agrivoltaic systems for field, greenhouse, and controlled environment production. Specific deliverables include:
1. Determination of the specific wavelengths of light transmission through agrivoltaic solar films (ASF) for optimized plant growth regulator performance in berries

2. Determination of the effects of growth systems utilizing ASF on fruit quality, ripening time and harvest
3. Plant growth regulator biomarkers of climate resilience
4. Development of agrivoltaic technologies as alternative income streams for growers and sustainable energy solutions for agriculture.

Methodologies, Technologies and Data
1. Create a model agrivoltaic system for study of woody berry crops in greenhouse and field conditions
2. Apply hormonomics tools to understand the mechanisms of PGR responses in agrivoltaic energy systems
3. Apply comparative transcriptomics and de novo sequencing to identify genomic markers in high-performing berries from agrivoltaic experiments
4. Optimize crop selection and management systems for solar energy production concurrent with high-quality crop yields
5. Data analysis to understand mechanisms of plant growth, crop selection and energy generation for sustainable production systems
6. Develop management strategies for circular economies of agrivoltaic energy and food production systems

Integrated GE3LS
Adoption of solar technologies in agriculture requires understanding the mechanisms of plant growth regulation and the potential stakeholder challenges toward implementation putting GE3LS at the core of the program. We have extensive IDEA experience and strategic knowledge of applied solutions for accessibility and have jointly published 16 papers, co-mentored 5 students and co-developed a Metabolomics Microcredential. Through existing collaborations with Indigenous communities in BC (4+ years) we will invite integration of Indigenous ways of knowing. Data generated will be deposited in public -OMICS repositories ensuring data quality/availability. Results will enable economic development while achieving environmental targets and sustainable energy production.

Project #19105
Securing internal sources for Canadian bees

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Keywords for Proposed Investigation

Research	Methods & Technologies
importation, overwintering, cost of not pollinating, honey bees	proteomics, transcriptomics, metabolomics, apiculture

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
cost of not pollinating, agroeconomics, climate change mitigation,	modelling, survey, focus groups

Project Information
Canadian beekeepers import >60,000 "packages" of bees and nearly 300,000 honey bee queens from overseas every year. The main driver for this is that the Canadian climate does not allow them enough time to raise new bees early enough in the season. This importation has a carbon cost but the potential risk to the Canadian bee population if access to those foreign bees were to be cut off has a vastly larger carbon cost through bees' pollination activities if agricultural and its immense carbon footprint produce little to no viable products because of lack of pollination. In addition, climate change and having to depend on other countries for maintaining our own bee populations threaten our food security. The goal of this project will be to harness recently developed 'omics tools, with the collaboration of industry and tech-transfer teams, to optimize conditions for over-wintering bees at an industrial scale sufficient to supply Canada's needs. Our research will enhance Canadian Beekeepers' capacity to produce strong and healthy honeybee queens and colonies in the early spring; this is expected to result in a massive reduction in agriculture's carbon footprint, at a second of millions of tonnes of CO2.

Deliverables and Expected Benefits
The primary deliverable will be industry-ready knowledge for over-wintering honey bees, particularly queens. This will be supported by economic modelling to make the financial case for using this approach. By working with industry through the whole project, the early-adopter end-users will be applying the technology immediately upon completion of the project. In addition to the food security and financial benefits, this will also result in immediate and measurable reductions in greenhouse gas emissions through reduced importations of bees, and earlier and more effective pollination.

Methodologies, Technologies and Data
Omics: This project will employ proteomics, transcriptomics, and metabolomics to guide the optimization of overwintering conditions. It will make use of previous diagnostics that our team has developed to monitor health stress in bees. Simultaneously, we will use proteomics to monitor temperature stress in bees to ensure that fertility remains optimal. Apiculture: We will work with provincial technology transfer teams to vary temperature, density, nutrition, and disease control parameters in over-wintering operations GE3LS: economic modelling, surveys and focus groups, and field observations will be used to calculate both the economic and environmental (greenhouse gas emissions) impacts.

Integrated GE3LS
What is the economic-environmental impact of a genomics-guided domestically overwintered bee population that is stronger and more adaptable, increasing carbon storage in soil/vegetation through pollination? What are the factors that drive/challenge the adoption and spread of genomic overwintering strategies? An environmental-economic model using project data will estimate the national/global impact of climate change mitigation through resilient pollinators, reduction in carbon emissions (less importation) and the increase in carbon sequestration and agricultural output from thriving, local pollinators. Industry adoption is driven by a collaborative, inquiry-based survey to ascertain the best methods for implementing large-scale uptake of genomic overwintering tools.

Project #19106
Project Title: Microalgae cell factories for sustainable aquaculture

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Keywords for Proposed Investigation

Research	Methods & Technologies
photobioreactor optimization, strain selection and carbon offsets, aquafeed and animal feed formulation, microalgae fatty acid production	multi-omic sequencing and mass spectrometry, metabolic modeling, high-throughput automation systems, bioprocess development

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
aquaculture carbon footprint offsets, unit of nutrition, food security, consumer preference and market demand	life cycle assessment, ecosystem models, quantitative reviews, interviews and discrete choice surveys

Project Information
As global warming trends lead to heat waves and aberrant weather patterns, terrestrial and marine food systems are increasingly under threat. In this light, sustainable food production and secure supply with reduced carbon footprint are key operating challenges facing humanity in the decades to come. For example, there is currently a global shortage of OMEGA-3 fatty acids used in production of feed for the salmon aquaculture industry and loss of fisheries productivity limits this supply chain further. Alternative food systems are needed that are resilient to climate change and reduce carbon flow into the atmosphere. We believe microalgae can provide a reliable carbon negative nutrient supply needed to produce feed for the aquaculture and farming industries. Here we use multi-omic approaches (DNA, RNA, protein, and metabolites) to improve production of lipids including OMEGA-3 fatty acids by microalgae. Strains will be selected using recently developed high-throughput screening infrastructure at the University of British Columbia and profiled using a combination of sequencing and mass spectrometry to identify relevant fatty acid profiles. These efforts will enable optimization of application- or region-specific photobioreactor environments, as well as cultivation of novel strains specially selected for scalable lipid production with our industrial user partners in Canada.

Deliverables and Expected Benefits
Deliverables arising from this project will include 1) microalgae strains that overproduce OMEGA-3 fatty acids optimized for growth in industrial photobioreactor environments, as wells as methods for cultivation and oil extraction needed for aquafeed production, 2) metabolic models of fatty acid production under different photobioreactor operating conditions needed to tune production for different geographic locations, 3) a novel algae-based aquafeed optimized for salmon farming operations, and 4) technoeconomic reports on the carbon footprint of the aquaculture industry and relevant offsets and economic impacts

related to the use of algae-based aquafeed including food security, consumer preferences and market demand.

Methodologies, Technologies and Data
We will harness a high-throughput lighting system integrated within a robotic incubation platform for plate-based screening of selected microalgae strains for OMEGA-3 fatty acid production. Fatty acid profiles will be determined by LC-MS/MS using an Agilent QQQ MS system connected to a high speed autosampler. Over-producing strains will be tested under different growth conditions and perturbation states and cognate genomes and transcriptomes will be generated on the Illumina NovaSeq platform. Proteomic, metabolomic and lipidomic profiles will be generated using different mass spectrometry platforms and the combined datasets will be used to construct representative genome-scale metabolic models to inform scale-up production.

Integrated GE3LS
This proposal will address environmental and socioeconomic impacts of microalgae-derived OMEGA-3 fatty acids as drop-in replacements for fish oils in production of aquaculture feed, and as potential dietary supplements for animals and humans. Hence we will measure environmental impacts of aquaculture expansion in response to microalgae-derived OMEGA-3 fatty acids aquafeed including carbon footprint offsets, unit of nutrition and impact of algal-based feeds on food security in Canada and globally using life cycle assessment, ecosystem models and quantitative reviews. Consumer and citizen perceptions and preferences of microalgae-derived OMEGA-3 fatty acids will be assessed using interviews and discrete choice surveys.

Project #19107
Mitigating soil carbon loss and building climate resilient soils

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Keywords for Proposed Investigation

Research	Methods & Technologies
Bioamendments, cover crops, agriculture	Metagenomics, metatranscriptomics, metabolomics, microfluidics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Adoption, efficacy, cost benefit, commercialization	life cycle analysis, social life cycle costing, surveys, market analysis

Project Information
Adding carbon to soils as bio-amendments (biofertilizers, stimulants and cover crops) can both increase carbon sequestration capacity and lead to more resilient cropping systems, via improved nutrient cycling and improved adaptation to drought and flooding.   The judicious use of bio-amendments may improve both soil carbon inputs and residency. They may also reduce emissions of other greenhouse gases such as nitrous oxide and methane. Taken together, the use of bio-amendments has the potential to increase soil carbon sequestration in agricultural systems while enhancing soil resiliency to a changing climate. Currently, growers lack guidelines for the use of bio-amendments. Complementarity between cover crops and biofertilizer will greatly affect the performance of these practises, so care must be taken to choose amendments compatible with conditions. There is currently a large research gap between the potential of these products in agriculture and the current practice.   To help define best practices around soil carbon sequestration, growers need tools to understand the functional capacity of their soils. We will develop tools, including soil metagenomic, metatranscriptomic, and metabolomic-based techniques to measure functional pathways in soils. This will be applied at the farm-level to better manage soils to adapt and mitigate agricultural impacts on climate change.

Deliverables and Expected Benefits
We will define a set of genomics-based indicators of soil carbon and GHG that are robust across growing systems and associated with soil carbon and nitrogen cycles. We will further deliver microfluidics-based devises that can be used to assay soil for these bioindicators. The data from these novel biosensors will provide farmers with real-time information about soil functioning, allowing them to address imbalances in microbial guilds through use of bio-amendments. Finally, these novel tools will be used to demonstrate bio-amendment combinations most useful for increasing soil carbon sequestration and decreasing GHG emissions in a wide range of cropping systems.

Methodologies, Technologies and Data
We will use genomic technologies to develop bioindicators for soil carbon and GHG activity. Using both 16S and 18S amplicon-based metagenomics, we will identify the bacterial and fungal taxa present in soils obtained from a representative sample of agroecosystems in BC and AB. We will then conduct metatranscriptomic, metabolomic, and physicochemical analysis in parallel with the amplicon-based metagenomics, to identify transcripts (and their inferred metabolic functions) correlated with soil quality. We will use this information to construct biosensors that will identify indicator transcripts and can be run on portable devices, allowing for rapid analysis in the field.

Integrated GE3LS
We will integrate research by a team of agricultural economists and social scientists, in partnership with stakeholders and policy makers, to ensure that the solutions we develop will be widely adopted and have the intended impact on GHG. Researchers will develop economic models of the costs and benefits of the proposed solutions, which will be used in conjunction with stakeholder surveys to identify obstacles to adoption, and solutions to these obstacles. We will also develop a plan for the commercialization of the novel, portable, field-based technology for measuring soil health.

Project #19108
How can kelp production meet Canada's net zero 2050 goals?

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Keywords for Proposed Investigation

Research	Methods & Technologies
Resiliency, Mitigation, Biodiversity, Yield	Mesocosms, Experiments, Field studies, Growth rates, Tissue quality, Ocean warming, Ocean acidificiation, eRNA, Transcriptomics, Whole genome sequencing, SNPs, eDNA, aDNA, Stable isotopes, Tracers

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Accounting, Socioeconomic, Equity, Policy	Greenhouse gas equivalents, Kelp use pathways, Carbon markets, Measurement, reporting and verification (MRV), Social, Economic, Environmental, Valuation, Ecosystem services, Procedural, Distributive, Qualitative analysis, Value-of-information, Cost-benefits

Project Information
There is a current surge in interest and investment in Canada and globally around kelp habitats as food systems, with the added benefit that they may play important 'natural' and 'low cost' roles in climate change mitigation. Growth in this sector, which includes wild harvest and aquaculture of kelp and other macroalgae, also promises to support local economies. Kelp forest habitats play a role in ocean-based carbon cycles, converting atmospheric carbon dioxide into biomass that fuels marine food webs and is harvested by humans for food and used in other land-based agricultural processes (e.g. as soil fertilizers and cattle feed). Unharvested kelp biomass may also be transported to depositional sedimentary 'carbon sinks', where kelp-derived organic carbon can potentially be sequestered. However, a rigorous accounting and verification of the net carbon flux reported for land and ocean-based 'kelp use pathways' is lacking. In response, this project will galvanize a multidisciplinary team and apply various genomic tools towards quantifying the climate mitigation potential of kelp. It will also include a full cost accounting of the benefits

and disbenefits of these pathways. This research is timely and crucial for setting evidence-based policy to guide management of kelp production and restoration in Canada.

Deliverables and Expected Benefits
The project will deliver in four key research areas that will assess how kelp use, via farming and harvesting, are accounted for and prioritized in federal and provincial net zero climate initiatives. The four areas include: 1) determining how kelp yield will respond to ocean warming and acidification; 2) measuring the greenhouse gas emissions and carbon storage associated with ocean and land-based kelp use pathways; 3) quantifying the potential positive and negative impacts of kelp use on other species, especially commercially important fish and invertebrates; and 4) understanding how kelp use affects local ecosystems, economies and human communities.

Methodologies, Technologies and Data
Diverse research methodologies will be used, including: field surveys of kelp population adaptation and connectivity (whole genome sequencing and SNPs); monitoring of ocean climate effects in kelp ecosystems (oceanographic sensors and eDNA); controlled mesocosm experiments on multiple kelp species, populations and co-cultured fish and invertebrate species (transcriptomics and eRNA); determination of kelp-associated emissions (CO_2 equivalents) in the lab, in situ and via secondary use of kelp (e.g., as cattle feed); kelp-derived sediment organic content analysis (stable isotopes, eDNA and aDNA) from hydrodynamically modeled and field-verified depositional areas; and interviews/questionnaires with representatives from coastal communities and the kelp industry.

Integrated GE3LS
Integrating information from all project activities, a multidisciplinary team will address the following questions: how do GHG emissions vary by ocean/land-based kelp use pathways; what are the direct costs of pathway implementation and their value in emerging carbon markets; what are the non-market socio-economic and ecosystem services associated with these pathways; and how is procedural equity valued by coastal and Indigenous communities in kelp industries and management? Results will be obtained via literature searches, interviews/questionnaires and models. Aggregated in a cost-benefit Value-of-Information analysis, outputs will inform decision support tools and policy for climate-resilient kelp management.

Project #19109

Using bio-based solutions to mitigate the effects of global warming on wine production and reduce its carbon footprint

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Keywords for Proposed Investigation

Research	Methods & Technologies
Climate Grape berry Physiology Disease, Heat Fire Fermentation Metabolome, Carbon footprint temperature Bio base sustainability, Wine Model Fermentation Yeast	Proteomics, metabolomics, computational modeling, viticulture transcriptomics, phenolics, genomics screening

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Sustainable Innovation Adoption, Wine region community Impact, Adaption Climate Change, Economic impact	Exploratory Focus Group, Quantitative Survey, Data elaboration, Bayesian network

Project Information

As evidenced by the 2021 growing season in BC, heat waves and forest fires are a new reality facing wine production due to climate changes. However the negative effects of global warming on grapevine disease, grape berry quality and wine fermentation are largely unexplored. We will use a bio-based solution to provide resilience to the wine industry from the impact of climate changes and to reduce greenhouse gas production during wine fermentation. We will determine how heat stress impacts grapevine diseases by assessing different rootstock-scion combinations and grape berry quality and wine sensory attributes using a metabolomic approach. In parallel, we will integrate a multi-omics approach to build a better model to map metabolic pathways associated with wine fermentation, by profiling the proteome and metabolome of diverse yeast strains during fermentation. Our new model will facilitate yeast strain screening to identify strains that can ameliorate berry physiology defects induced by climate change, such as smoke taint, during wine fermentation. As the cooling of fermentation tanks accounts for a high percentage of the carbon footprint of a winery, we will also identify yeast strains that can ferment wine at increasing temperatures to reduce greenhouse gas production.

Deliverables and Expected Benefits
This project aims to mitigate climate impacts that will affect wine production in Canada and to reduce greenhouse production associated with winemaking. The following deliverables and expected benefits are:
- Establish the effects of higher temperatures and heat-stress on grapevine diseases, the composition of grape juice and wine sensory traits;
- Identify yeast strains adapted to wine fermentation with lower carbon footprint;
- Identify yeast strains with a lower smoke taint profile and higher terpene aromatic profile in wine fermentation;
- Establish a new metabolic model of wine fermentation;
- Annotation of uncharacterized genes in genomes of wine fermentation strains

Methodologies, Technologies and Data
Transcriptomics will be used to assess impact of heat stress on grapevine and viral disease. Metabolomics will be used to profile the metabolome of grape berries and grape juice during wine fermentation. Proteomics will be used to characterize the proteome and secretome of yeast strains during fermentation. Computational modeling will be used to integrate the results from our multiple omics platform and map the produced metabolome. Bioinformatics will be used to analyze the pan-genome of wine strains. Molecular and cell biology approaches will be used to characterize potential novel genes that impact wine fermentation.

Integrated GE3LS
We have identified the following GE3LS points to integrate in our proposal:
- Determine the adaptive capacity to climate change in the Canadian wine industry using sustainable innovation
- Model the economic impact of wine production loss associated to climate changes and impact on the surrounding communities
- Survey consumer preferences for using sustainable innovations in wine production

Project #19110

Integrating genomic and ecological approaches to develop and optimally deploy climate-smart and biodiversity-friendly sunflowers

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Keywords for Proposed Investigation

Research	Methods & Technologies
Carbon deposition, insect and microbial biodiversity, inter cropping, low nutrient tolerance	Genome sequencing, genome-wide association analyse, pan genome assembly, phenotyping

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Environmental impacts, economic impacts, barriers to innovation, farmer perception	Life Cycle Assessment models, biodiversity extrapolation modeling, socio-economic assessment, farmer surveys

Project Information

The increase in agricultural productivity over the past century has been stunning, confounding Malthusian predictions, at least in the short term. However, this success has come with unsustainable environmental costs, the most concerning of which are greenhouse gas emissions and loss of biodiversity. Our project integrates genomic, ecological, economic, and social sciences approaches to develop realistic solutions to these challenges, using as a model crop rotations and inter-cropping systems in which the deep root system of sunflower complements the shallower root profiles of legumes and cereals. Building on the rich genomic and germplasm resources available for sunflower and its extremophile wild relatives, we will design sunflower genotypes that are tolerant of low-nutrient soils, have higher root:shoot ratios to increase carbon sequestration, and enhance recruitment of beneficial insects and microbes. Impacts of climate-smart and biodiversity-friendly sunflower genotypes on yield, carbon deposition, nitrous oxide emissions, herbivory, disease, and insect and microbial biodiversity will be assessed in monoculture, when intercropped with different legumes, and as a rotation crop with cereals. Lastly, our GE3LS team will estimate the social and economic costs and benefits of new cultivars and cropping strategies and identify and mitigate barriers to their use.

Deliverables and Expected Benefits

This project will provide the scientific basis for developing climate-smart and biodiversity-friendly cultivars for inter-cropping with legumes or in rotations with cereals, leading to reductions in nitrous oxide emissions, greater deposition of carbon in agricultural soils, and increased insect and microbial biodiversity. Additional deliverables include: (1) A sunflower breeding hub, providing access to resources developed by the project; (2) A decision support tool to inform farmer decision making for deploying improved varieties in different

rotational or intercropping schemes; and (3) white papers that explore barriers to deployment of recommended cropping strategies and how they might be overcome.

Methodologies, Technologies and Data
Genomic methods to be used include long-read and short-read sequencing, genome-wide association analyses, marker-assisted selection, and meta-barcoding of microbial biodiversity. High-throughput phenotyping and chemical analyses will be employed for physiological characterization, and near-isogenic lines will be developed and assessed for loci associated with traits of interest. Insect biodiversity and pollinator visitation rates will be determined using automated camera traps and AI-video tracking. Greenhouse gas emissions will be monitored using manual chambers in combination with changes in soil organic carbon content. The environmental footprint and benefits achieved from project innovations will be evaluated in a life cycle assessment framework.

Integrated GE3LS
We will quantitatively assess the environmental footprint and economic costs and benefits derived from project innovations in a life cycle assessment framework. This will be accomplished by integrating scientific data collected by the project on greenhouse gas emissions, soil carbon content, insect and microbial biodiversity, and pollinator health, with information from farmer surveys and local economic value chain analyses. We will also determine how different farmers perceive potential trade-offs between environmental, social or economic benefits and changes in agronomic practices, as well as incentives that would enhance uptake of project innovations, using interactive tutorial-based survey methods.

Project #19201
Beef on Dairy: the GENOMICS and GE3LS of it.

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Keywords for Proposed Investigation

Research	Methods & Technologies
Haplotypes, retained heterozygosity, relatedness, Molecular breeding values (MBVs)	Genome Wide Association studies, Genomtyping, Genomic best linear unbiased prediction (gBLUP), indexing

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Health, welfare, carbon footprint, consumer attitudes	bioeconomic models, producer survey, life cycle assessment, willingness to pay

Project Information
This project will use a suite of genomics tools to increase the sustainability and reduce the environmental footprint of beef-on-dairy cattle. It will employ MBVs, genomic indices and genomic heterosis to lower the carbon footprint of both the Canadian dairy and beef industries.   Molecular breeding values (MBVs) and a beef-on-beef Feeder Profit Index (FPI) have recently been developed with moderate accuracy (>40%), and each 100 points in FPI is equal to $29 in feeder net return. These genomic tools do not require pedigree information or the collection of any animal data for expensive and hard to measure traits. For feed efficiency alone, this translates through progeny equivalents into savings of ~$2000/bull. A similar genomic evaluation process is proposed for beef-on-dairy feeder production and marketing systems. The project will also apply genomics to manipulate the rumen microbiome to reduce enteric methane emissions and improve the environmental (e.g. temperature stress and infectious disease) resilience of Canadian cattle. These approaches will help improve colostrum management, early nutrition, vaccination, feeding, housing, and other issues that vary widely for beef-on-dairy calves between operations, and can result in high morbidity, mortality, and antibiotic use which contribute to inefficiencies and the overall environmental footprint of beef production.

Deliverables and Expected Benefits
Beef-on-Dairy feed efficiency and carcass tool to estimate profit Beef-on-Dairy Feeder Profit Index validated against actual data. Sire Advisory web service: On-line service to select the optimal beef bull-dairy cow mating, with the aim of minimize calving difficulty, and increasing heterosis. Rumen Microbiome- host interactions impact on enteric methane emissions: Predictive model that defines the ecology of enteric methane emissions as influenced by heterosis Life Cycle GHG Assessment of genomic improved feeders. Updated health and welfare protocols: Management practices of the dairy and beef-on-dairy

operations will be characterized to make associations between management factors and health, welfare, performance and economics.

Methodologies, Technologies and Data
GWAS and GBLUP will be conducted on the phenotypes and genotypes (GGP 100k SNPs) from ~20000 beef-on-dairy feeders sired by purebred and hybrid beef breeds (e.g., Angus, Simmental, Gelbvieh). These data will be combined with similar data from >14,000 beef-on-beef animals from Gentec's reference population. Long and short read sequencing will be used to construct hybrid assemblies of the transcriptome of the rumen microbiome – coupled to direct measurement of enteric methane emissions using Greenfeed and respiration chamber technologies. Retrospective and prospective data including management, animal and performance factors will used to conduct risk factor analyses made recommendations for BMPs.

Integrated GE3LS
Life Cycle Assessment using IPCC Tier2/3 methodology will be conducted to objectively allocate GHG emissions from the dairy cow to milk and beef production. An outcome will include a GHG reduction protocol for approval through federal and provincial governments. A bioeconomic model based on individual animal performance, carcass, cost and income data will be developed to examine factors influencing profitability and environmental outcomes. Consumer studies on "willing to pay" a premium for meat from beef-on-dairy calves with improved welfare and environmental attributes, and producer surveys to understand attitudes and challenges are proposed.

Project #19202

Enhancing Extreme Temperatures in Canola using Transcriptome and Phenomics Approaches

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Keywords for Proposed Investigation

Research	Methods & Technologies
Heat stress Cold stress Climate change RNA based biomarkers	Transcriptome analysis SNPs NGS-based RNA sequencing Chlorophyl fluorescence

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
producers experience genomic canola abiotic stress	Participatory survey engagement groups abiotic

Project Information

The Canadian agriculture and agri-food system accounts for 10% of Canada's total greenhouse gas emissions, mainly through animal production and fertilizer application. The sector has demonstrated a commitment to adopting sustainable practices that help protect Canada's air, water, and the climate. Reducing carbon footprint is one of Canada's priorities because it mitigates the effects of global climate change, improves public health, boosts the global economy, and maintains biodiversity. Developing crops that are more resilient to rapidly changing environments will be crucial for maintaining high food productivity while preserving Canada's valuable ecosystems. The overall goal of this project is to enhance extreme temperature tolerance in canola using transcriptomics and novel screening tools. Achieving this outcome will help to mitigate the carbon footprint of canola production through two primary mechanisms. First, stabilizing canola production through enhanced temperature-stress tolerance will significantly reduce the carbon footprint per unit of output, since canola production will increase with no change to inputs applied. Second, frost susceptibility of canola often leads to reseeding of fields at a significant carbon cost since the industry must produce and condition significantly more canola than is needed each year and growers must make one or more additional passes through the field.

Deliverables and Expected Benefits

Deliverables:
- New canola germplasm suitable for hybrid breeding programs.
- Protocols and models of transcriptome analysis, differential expression of gene(s) and molecular markers with potential to become industry standards.
- New intellectual property of patentable technology.
- Knowledge on the timing and effectiveness of biostimulants to enhance stress tolerance.

Benefits:
- Resilient crops to seasonal variation in extreme temperatures will guarantee stable, consistent supply for export and local industries.
- Extreme temperature tolerant canola would have the opportunity to maximize yields, improve quality and lower the risk of crop failure.
- Reduced GHG emission intensity for canola production.

Methodologies, Technologies and Data
Plant Material:
- 500 diverse genotypes (B. napus and B. juncea) including landraces and exotic germplasm, RILs and commercial varieties.
- Biostimulants will be applied as seed treatment or foliar treatments depending on the product, stress and recommended application timing. Treated and non-treated lines will be subjected to temperature acclimation and shock.
- Pollen will be collected from lines and analyzed with an Amphasys pollen analyzer.

Data:
- Survival, chlorophyll fluorescence and pollen quality parameters.
- Transcriptome analysis will include genome-wide gene expression using next-generation sequencing-based RNA Illumina sequencing technologies. This will include 2x150 bp paired-end read analysis of transcripts using a NovaSeq 6000 instrument.

Integrated GE3LS
Question: Based on producers' experience, which canola hybrids or varieties yielded the best during seasons when severe abiotic stresses were encountered?

Approach: A participatory survey will be used to engage producers in focus groups to identify canola genotypes exhibiting abiotic stress tolerance traits that will be included in the screening trials. We will plan a series of events to investigate how acceptable genomic research is to stakeholders (consumers, industry, policy makers) and producers:

Focus groups will also be asked for their perspectives on genomics-research leading to GHG emission intensity reduction vs. research leading to an absolute decrease in GHG emissions.

Project #19203
Climate change mitigation through the application of genomics to reduce pig losses in pork production

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Keywords for Proposed Investigation

Research	Methods & Technologies
Pig survival, Efficient resource utilization, Reduced environmental footprint, Pork production	Novel phenotyping, Multi-omics analysis, Machine learning and computational biology, Genomic evaluation and selection

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Producer adoption, Consumer perception, Willingness to pay, Environmental economics	Producer surveys, Consumer surveys, Economic modelling, Farm level optimization modeling

Project Information

The pork production industry is a significant contributor to the agriculture/agri-food sector and the Canadian economy. This critical production system is on the frontlines in the fight against global food insecurity, and must meet increasing food demands in a manner that is environmentally sustainable. To address this significant challenge, future production methods must concomitantly increase productivity while reducing resource utilization. An aspect of pig production that has a dramatic impact on efficiency is mortality at each phase of production. PigGen Canada has determined that 1 in 3 pigs born in commercial pig production does not survive to market weight. This is a complex multi-factorial issue that can be tackled through genomics and selection. This work will elucidate reasons for individual variation in survival to guide the development and implementation of tools and techniques that specifically address the animals at greatest risk. GE3LS research will complement the science by examining producer behaviour that could impact the rate of adoption and the social impact and trade-offs of adopting different technologies at the farm level. Overall, this research will employ genomics to curtail animal losses in pig production and reduce the environmental footprint of this important agricultural sector.

Deliverables and Expected Benefits

Expected deliverables and benefits will include: 1) new tools to increase pig survival in commercial production based on early indicators that can be integrated with other 'omics' approaches; 2) new technologies to monitor behavior, welfare and performance for early detection of at-risk pigs; and 3) new complementary analytical approaches utilizing machine

learning to integrate genomic and phenomic data to better understand factors affecting pig survival at various stages of production. The application of genomics to improve pig survival in pork production will allow this important agricultural sector to increase production efficiency and sustainability with a significantly reduced environmental footprint.

Methodologies, Technologies and Data
The research methodologies and technologies to be used will include: 1) novel phenotyping for early indicators of survival traits including animal monitoring, behavioural analysis technologies and emerging smart technologies; 2) genomics work including genotyping and genome wide association studies, transcriptomics and metagenomics; 3) generation of large data sets which will be exposed to machine learning and computational biology analyses; and 4) working with industry partners in swine breeding, where results of interests will be incorporated into genomic evaluation strategies and selection programs to reduce losses in pig production and increase efficiency of pork production.

Integrated GE3LS
GE3LS research will involve: 1) assessment of pig producer behavior change given impact of different approaches to environmental stewardship in pork production; 2) design of public policy to encourage adoption of different technology packages given public and producer attitude; 3) investigation of societal value of different combinations of technologies, outcomes and public policies; 4) ethics of different animal welfare outcomes from different pig survival and environmental enhancement combinations; and 5) role of different types of communication in changing behavior (public or producer) in technology adoption for disease resilience purposes.

Project #19204

Revealing the Dynamics of Plant-Animal-Soil Interactions to Mitigate Greenhouse Gases Emissions in Western-Canadian Rangelands

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Keywords for Proposed Investigation

Research	Methods & Technologies
Sustainable Beef Cattle Production, Animal and Soil Microbiome interactions, GHG mitigation, Rangeland Carbon Sequestration	Phenomics, Genomics, Machine Learning, Metagenomics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Market and nonmarket benefits, grassland management strategies, ecosystem goods and services	dynamic optimization model, socio-economic surveys

Project Information
Western Canada's grasslands comprise 12.7M hectares of native forages. The positive role grazing beef cattle play in supporting these plant communities by generating a variety of ecosystem benefits (e.g., biodiversity, water management and carbon sequestration), is underappreciated. New tools are needed to sustainably manage the ongoing use of native grasslands with the provision of ecosystem services, including optimization of their carbon sequestration and mitigation of their greenhouse gas emissions, thereby minimizing the footprint of beef production in the face of climate change. This will be achieved by applying multi-species 'omics tools to understand the interaction among native plants and vegetation communities, grazing animals and their dietary preferences, and the associated cattle and soil microbiomes, in a constantly changing environment (e.g., drought, extreme temperatures). Such an approach will allow us to identify cattle and grazing management strategies that optimize carbon sequestration, forage availability and utilization, beef production, and other ecosystem services from these rangelands.

Deliverables and Expected Benefits
Multi-species omics analyses will increase our understanding of complex interactions between native forages, soil and cattle microbiomes, their responses to different environmental conditions (grazing intensity/frequency, temperature, humidity, biome, etc.), and provide the basis for optimizing resource use. How plant- animal-soil interactions contribute to GHG emissions, carbon sequestration, and land-animal productivity will help deliver a portfolio of novel management strategies to lead towards resilient and sustainable beef production systems. Public benefits will include environmental protection and effective climate change actions resulting in reducing net emissions from beef production, greater

beef demand through improved social license and improved sustainability for beef producers.

Methodologies, Technologies and Data
Multiomics techniques including high-throughput phenomics, and sequencing of genomes within cattle, vegetation, diet, rumen, fecal and soil biomes, will be amassed from different grazing management scenarios conducted on-farm in collaboration with end-users; a) low-intensity, continuous grazing, b) medium-intensity grazing with rotation, and c) high-intensity, short-term rotation. Metadata collected will include environmental aspects as ambient temperatures, precipitation, etc., soil and forage genomes before/after grazing, and across seasons. The project will produce an integrated omics database tracking transformations in carbon dynamics from vegetation to soil, as mediated by microbes in rumen and hindgut, and cattle genomics, along enteric methane emissions.

Integrated GE3LS
The GE3LS research will access the long-term market and non-market benefits of different grassland-management strategies. We will develop a dynamic optimization model to recognize the dynamic interactions among cattle, plants, and microorganisms. The GE3LS team will also examine how the public perceives the non-market values of the ecosystem goods and services (EGS) delivered by native grasslands. The identified values of the EGS will be incorporated into the dynamic optimization model to inform optimal grassland management decisions. We will further investigate how various policies and stochastic climatic events (e.g., drought) might affect the ecosystem and related socio-economic and environmental outcomes

Project #19205
Novel and Adaptive Rumen Microbiome targeted solutions for GHG mitigation in cattle

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Keywords for Proposed Investigation

Research	Methods & Technologies
Rumen microbial genomics solutions, Breeding and supplementation strategies, Methane emission mitigation on farm adoptions, Machine learning for predictive microbial markers	Metagenomics, Microbial genomics and rumen microbial metabolomics, Cattle genomics and functional genomics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Evaluating economic and social tradeoffs associated with omics technologies and ruminant methane emissions, Examining factors affecting adoption of new omics technologies, Assessment of current and potential regulatory approaches, Examination of consumer and producer perceptions and preferences for omics approaches to reduce methane emissions	Cost/benefit and market level modelling, Simulation modelling for decision making, Public surveys, Focus groups to establish range of attitudes and barriers to adoption

Project Information
Beef and dairy farmers are the foundation of Canada's livestock industry. The GHG footprint of Canadian beef and dairy production represent 3.4% of Canada's overall emissions (beef 2.4% and dairy 1%). Continued improvement in production efficiencies, environmental sustainability, health and welfare of Canada's cattle population is central to ensuring the sustainability and competitiveness of the cattle industry. There is growing evidence that rumen microbiomes have both beneficial and detrimental impacts on cattle productivity, methane emissions, product quality and cattle health, suggesting it as a target for the improvement of these key traits in cattle. This project will develop tools to improve feed efficiency and reduce methane emissions by 1) determining causal effects of the rumen microbiome and predictive rumen microbes based on analysis of integrated omics datasets; 2) developing novel manipulation solutions for microbial targets to reduce GHG emission from both beef and dairy sectors, and 3) implementing "Big Data" and "Analytic Solutions" for precision management of the rumen microbiome. Collectively, this will improve the sustainability and production efficiency of cattle. The target-based manipulation solutions will lead to novel breeding and dietary supplementation strategies and targeted precision management to lower methane emission from dairy/beef cattle.

Deliverables and Expected Benefits

Deliverables:

1. Microbial markers for methane emission;
2. Novel and adaptive microbial solutions to mitigate methane; and
3. Innovative management practices (3R: right genetics, right rumen microbiome for right feed/supplements) for both the beef and dairy cattle industry and rumen microbiome-driven management practices and technologies to lower CH4 emission from cattle.

Expected benefits:

1. Economical and socially effective mechanisms to implement microbiome-derived technologies for Canadian cattle producers;
2. best management practices for producers to meet carbon net-zero production by 2050; and
3. global solutions for cost-effective and sustainable ruminant production through partnerships with Holoruminant (EU) and Greencattle (USA) projects.

Methodologies, Technologies and Data

The project seeks to:

1. establish the integrated database (metagenomics, metabolomics and genotyping) of the bovine rumen microbiome related to methane and feed efficiency;
2. develop new and novel machine learning based artificial intelligence algorithms to determine causal effects of the rumen microbiome;
3. develop new and novel microbial genomics-based approaches and naturally derived microbial that can induce species-specific inhibition through microbial RNA interference for methanogens and enzyme discovery to reduce enteric methane emissions; and
4. determine interactions between host genetics and rumen microbiome in response to methane targeted feed additives, microbial solutions using genomics and metatranscriptomics and metabolomics.

Integrated GE3LS

An integrated GE3LS approach will be implemented to inform microbiome solution-driven research activities. The GE3LS component will assess the regulatory environment and state of technology use, and investigate the potential barriers to, and expected economic and social benefits of, adopting omics technologies. Methods include: cost/benefit analysis of changes in management practices, the ADOPT (Adoption and Diffusion Outcome Prediction Tool) framework to predict producers' willingness to adopt technologies, and simulation modelling to assess risks of technology adoption. Surveys and economic experiments will be conducted to examine attitudes, barriers to, and incentives required for, the adoption of methane mitigation strategies.

Project #19206

Genomics-guided pre-breeding for improved root system architecture in wheat and canola, for drought resilience, resource use efficiency and biological carbon sequestration

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Keywords for Proposed Investigation

Research	Methods & Technologies
Root system architecture, Biological carbon sequestration, Nutrient use efficiency, Drought resilience	exome capture and sequencing, promoter capture and sequencing, genome wide association studies, genomic prediction

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Impact of genetic diversity, Economics of deep root system, Estimates of soil erosion prevention, Reduction in water and nutrition use in wheat and canola	Soil C-storage, Root biomass C-storage, GHG emission reduction, Metrics related to water use and fertilizer use

Project Information
Root system architecture (RSA) determines water and nitrogen use efficiency, enhanced biological carbon sequestration and the introduction of perenniality traits in plants and influence the climate resilience of major Canadian crops e.g. wheat and canola. We propose to use genomic approaches e.g. exome capture- and promoter capture arrays of wheat to genotype a diverse panel of CIMMYT wheat accessions with 'D' genome and 'B' genome introgressions, and deep rooted Thinopyrum accessions. A set of canola accessions containing genome content from different Brassica species and other exotic germplasm will be phenotyped and genotyped for pre-breeding and screening important traits like flowering time using a canola SNP array. Near-isogenic lines (NILs) of canola for flowering time/root biomass will be evaluated using transcriptomics and metabolomics. Genotyping and phenotypic data will be used for characterizing the genomic regions governing RSA traits in wheat and canola using genome wide association study (GWAS). Genomic prediction models for selecting desired RSA traits in wheat and canola breeding populations will also be developed, since it can capture effects of hundreds of minor loci for quantitative traits. Novel genomic regions conditioning RSA traits will be identified which will be introgressed into elite breeding populations.

Deliverables and Expected Benefits
We will identify novel genomic regions governing RSA traits in wheat and canola and in addition perenniality in Thinopyrum intermedium conditioned by deep root systems. Genomic prediction models for RSA for application in pre-breeding will be developed. Elite wheat and canola pre-breeding populations with introgression of RSA regions will be available, as deep rooted grass species can store up to one ton of carbon/acre. Late-

flowering plants produce greater root biomass than early flowering and this investigation will identify gene networks. These outcomes will help to improve climate-resilience and biological carbon sequestration; and identify genes and gene-specific markers for selecting RSA.

Methodologies, Technologies and Data
Nearly 250 accessions of wheat D and B genome progenitors and T. intermedium and ~250 genetically diverse canola accessions will be phenotyped for RSA traits. Genotyping will be carried out using myBaits wheat exome- and promoter arrays and Brassica 90K SNP array. The phenotypic data will be analyzed using SAS and R. The genotypic data will be aligned to the wheat or canola assemblies for variants calling. Association genetics and genomic prediction will be performed on R. Transcriptomics and metabolomics analysis of the canola NILs developed for flowering time/root mass will be carried out to unveil the crosstalk among genes.

Integrated GE3LS
Croplands in Alberta increased from 10.22 million hectares (mha) in 2016 to 10.38 mha in 2021. Changes in land use patterns with an increase in crops and a decrease of pastures, woodlands, and wetlands has huge impact on quantity of stored carbon. Hence, what will be the impact of deep rooted cereals (wheat), oilseeds (canola) on the C-sequestration in the farm land? What will be the economic benefits arising from improved root system traits, and the environmental benefits from the carbon sequestration, reduced soil erosion, nutrient use from sub-soil? This knowledge will contribute to enhanced economic return with ecosystem services.

Project #19207
Genomic approaches to combating climate change in agriculture

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Keywords for Proposed Investigation

Research	Methods & Technologies
Tolerance, Carbon, Sequestration, Cold	whole, genome, sequencing, Nanopore

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Regenerative, Agriculture, Rural, Sustainability	Production, Systems, Approach, Genomics

Project Information

Production of annual crops can contribute to soil organic carbon (SOC) depletion and release of greenhouse gases (GHGs) through intensive cultivation and energy expenditure for field operations. In this project, we intend to promote carbon sequestration and mitigate agricultural GHG emissions by adopting practices that enhance soil organic matter through higher plant biomass inputs and by extending the crop growing season. Agronomic management strategies such as production of fall-seeded cash and cover crops can help to extend the growing season, reduce soil erosion losses during shoulder seasons and increase biomass inputs into soils thus promoting soil carbon sequestration. Fall-seeded crops can also attenuate season N2O fluxes associated with early spring thaw periods. To date, experience has shown that some crops thrive during the fall growing season while others of the same species do not. We seek to use advanced genomics approaches including whole genome sequencing to identify and characterize genes involved in cold tolerance and overwintering survival with a final goal of identifying plant varieties ideally suited for winter crop adoption in Canadian prairies. Genomics-assisted breeding can help in selecting current crops and breeding novel crop varieties for fall-seeding conditions and marginal environments depending on the specific goals.

Deliverables and Expected Benefits

This project focuses on identifying crop varieties that promote higher soil biomass input, reduce soil erosion, and reduce the carbon footprint of irrigated and dryland agroecosystems through late fall and overwintering survival. Using genomics tools to develop and identify genomic markers of crop survivability will have widespread implications and transferability to similar questions of crop sustainability in early-spring or extreme weather conditions caused by climate change. Farming Smarter's connections with the farming community and robust knowledge transfer infrastructure will be used to promote the adoption of innovative practices, achieving higher carbon sequestration and reduced GHG emissions in agricultural ecosystems.

Methodologies, Technologies and Data
Whole genome sequencing of crops with good and poor survival under extreme environmental conditions will identify potential genomic variation responsible for that survivability. This information will allow us to select suitable crop types or varieties to increase adoption of fall-seeded cash and cover crops. Information can be shared with plant breeders to inform development of climate-adapted varieties. We will take an iterative field-lab-field approach to the development of innovative practices that will include the evaluation of germplasm for desired traits under selection environments followed by testing under small-plot research conditions and conclude with integration into real-world conditions for on-farm research.

Integrated GE3LS
The consequences of climate change are far-reaching and especially impactful when resulting in growing conditions no longer ideal for long sustained crops in a region. Key multinational companies are committing publicly to regenerative agriculture and sustainability platforms. Strategies that support these initiatives must be economically viable to ensure rural communities thrive and continue to provide food security for Alberta and elsewhere. Economic considerations are likely to be key barriers to adoption of new cash and cover crop strategies. This research should accelerate selection of suitable germplasm for these new approaches.

Project #19208

PEACE (Pea Climate-Efficient): Developing climate-resilient, pea through inter-disciplinary integration of genomic technologies

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Keywords for Proposed Investigation

Research	Methods & Technologies
climate resilience, low carbon footprint, Gene regulation, Field pea diversity	Long read sequencing, genotyping by sequencing, mutagenesis, phenotyping and predictive data analytics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Economic value of advancing climate resilience in pea, modeling GHG emissions, social acceptance of genome editing, economic modeling of returns to genetic advancements in pea	Consumer preference surveys, regulatory impact analysis, National and International stakeholder engagement, expert interviews

Project Information

Canada is the largest producer and exporter of field peas in the world with most of the production occurring in the Prairie provinces. Peas are mainly cultivated to meet the global protein energy needs for the rapidly expanding human population which is expected to double the demand for plant-based protein by year 2054. In Canada alone, value of plant-based protein commodities is ~ $1.5 billion USD. Field peas generally suffer from poor yield that significantly expands its carbon footprint which is also exacerbated by unpredictable climatic conditions, particularly drought and heat. This proposal aims to integrate an inter-disciplinary approach using state-of-the-art genomic technologies to develop climate-efficient pea. Three major goals will be achieved through this PEACE project.

1. Exploit the genetic diversity through applying the genomic lens, allowing expansion of the gene pool to identify novel high-yielding, drought/heat resistant germplasms that contribute to low carbon footprint and reduced emissions
2. Engage in gene discovery-based approaches to identify regulators, manipulation of which could lead to direct reduction in emissions while simultaneously improving yield.
3. Develop novel meta-genomic technologies to uncover optimal conditions for plant-microbiome interactions to develop strategies and platforms for improved nutrient-use efficiency along with reduced GHG emissions.

Deliverables and Expected Benefits

Climate-resilient, high-yielding pea varieties with improved flavor and protein content will be delivered. Associated genomic resources will be made public for knowledge transfer. This project will directly contribute to reducing carbon footprint and GHG emissions in the large

Canadian acreage under peas. High-yielding peas will benefit Canadian agriculture industry by providing direct benefits to farmers, industries and processors. Consumers will benefit from pea with better flavour and protein content. Canadian job sector and industry will benefit from HQP developed through the project. Globally, reducing emissions and enhancing pea protein content will have major impacts in the environment and health sectors.

Methodologies, Technologies and Data
A global panel of diverse germplasm will be subjected to field phenotyping, modeling CO_2 and N_2O emissions to explore the genetic diversity to reduce carbon footprint. Cutting-edge sequencing, genotyping and regulatory genomics technologies, as well as predictive data analytics approaches will be applied to identify genomic variation underlying climate resilience. A breeder-friendly gene-editing platform will be established for rapid editing in pea for climate-resilience and for improving flavour and protein. Genetic variation will be created through mutagenesis followed by screening for drought/heat resilience. Bio-stimulants and Top-Phos applications will be evaluated and assessed for microbiome, N_2O and CO_2 emission.

Integrated GE3LS
We will create a knowledge base of international pea trade and global protein market trends, economic resilience of the crop production sector when adopting climate-smart pea varieties, and modeling greenhouse gas emissions and assessment of environmental impact of the reduction of carbon footprint. We will also evaluate Canadian and International regulatory aspects of gene editing technology and its impact on commercialization of varieties with novel traits. The know-how of consumer preferences, market trades and the effectiveness of the Canadian regulatory framework for plants with novel traits will be useful in guiding policy discourse on acceleration of genetic advancements in pea.

Project #19209

Decentralized dietary protein production using precision fermentation

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Keywords for Proposed Investigation

Research	Methods & Technologies
Precision fermentation, Fungal genomics, Genome engineering	Solid-state fermentation, Protein purification, Mass spectrometry, Strain engineering

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Environmental impact, Indigenous acceptance, Policy	Life cycle assessment, Surveys, Policy framework

Project Information
This project will seek to leverage the protein production and secretory capacity of filamentous fungi to develop a precision fermentation-based approach to producing dietary protein. The project will use genomics and transcriptomics to guide strain-engineering efforts to optimize yield and improve substrate utilization. The project will focus on the production of three main categories of proteins: animal-based dairy proteins, functional proteins from aquatic organisms, and novel proteins that can enhance the flavour profile of alternative meat products. Each of these aims will advance the nascent industry of cellular agriculture which aims to produce animal products such as meat, dairy, and cheese using cells instead of animals. Producing dietary protein using a precision fermentation approach has strong potential for reducing greenhouse gas emissions compared to production using animal systems and reduce the overall carbon footprint of these processes. Furthermore, by engineering the fungal strains for substrate utilization, this project will develop systems that can valorize waste or side-streams from existing processes, integrating this approach into a broader circular economy. This project will also work with environmental scientists to perform life cycle assessments to definitively assess the carbon footprint of the precision fermentation approaches developed within this scope of work.

Deliverables and Expected Benefits
This project will develop multiple fungal strains capable of producing high-value dietary proteins that can contribute to meat, dairy, and egg alternatives that are animal-origin free. The fungal organisms used are safe to use in existing food production. The strains produced will be the foundation of decentralized bioprocesses that allow for production of dietary protein in any location capable of housing the appropriate cultivation equipment. This will help address key issues such as food insecurity in Northern Canadian communities. The genomics-led strain engineering efforts will also help guide future usage of these organisms for other precision fermentation studies.

Methodologies, Technologies and Data
The project will adopt a "one strain, one protein" approach and leverage genomics-guided strain engineering to optimize yield and substrate utilization. These efforts have strong

potential for development of IP. We will utilize advanced genetic engineering techniques such as CRISPR-Cas9 to modify these organisms to produce proteins of interest and use low-cost substrates sourced from waste or side-streams. Proteins of interest will be secreted, allowing for lysis-free extraction and purification. The project will also explore utilizing the fungal biomass for mycoprotein production upon completion of a fermentation run, allow for further incorporation of input and output into alternative meat products.

Integrated GE3LS

1. Perform life cycle assessments on the precision fermentation processes developed to determine their land use, water use, GHG emissions, and overall carbon footprint. How does this compare to protein produced using animal-based production systems?
2. What is the perception of Northern Canadian Indigenous communities of cellular agriculture, do these communities see cellular agriculture and precision fermentation as a potential tool to improve issues of food insecurity in Northern Canadian communities?
3. Does a preliminary techno-economic assessment support the feasibility of using these precision fermentation approaches to producing dietary proteins in a decentralized manner, and specifically within Northern Canadian communities?

Project #19301
Canadian Aquaculture for a Resilient Economy (CARE)

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Keywords for Proposed Investigation

Research	Methods & Technologies
omic analysis of fish health, Inland aquaculture, Carbon dioxide remediation via algal biomass	Multitrophic aquaculture, Microalgae remediation, eDNA analysis, Transcriptome Analysis

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Economic analysis of aquaculture system design for sustainability, Benefits of aquaculture to First Nations and northern prairie communities to improve water quality and reduce reliance on traditional food harvest	Economic modelling, Water quality and environmental analyses, Socio-economic benefits surveys

Project Information

Canada's aquaculture industry is rapidly growing, however associated activities can be a detriment to their surrounding environment, for example as terrestrial operations encroach on ecologically valuable wetland areas. Equally, the industry is not optimized to take advantage of obvious benefits such as the use of algal carbon conversion which provides aquaculture nutrition via co-cultured fish feed whilst converting CO_2 emissions into biomass and other value-added products. An aquaculture system producing fish and marketable co-products in this manner without drastic water demands has the potential to improve the sustainability and economic integrity of Canadian aquaculture and to simultaneously reduce its carbon footprint. In tank integrated multi-trophic aquaculture (IMTA) is a circular economy technique where the waste products of one species are recycled and converted into feed and energy for another species. IMTA not only increases the yields of individual harvests, but also acts to ensure a sustainable food supply. This project will optimize a terrestrial in-tank IMTA on the Canadian prairies studying the impact of physiochemical factors on fish health through the correlation of physical examination and behaviour characteristics with genomic and transcriptomic analysis of fish health. Genomic selection and improvement of feed-algae for enhanced carbon capture will also be performed

Deliverables and Expected Benefits

Aquaculture in Canada today generates $3.86 billion economic activity, providing 1/3 of the total value of Canada's fisheries production. It employs 14,500 Canadians, but this success comes with environmental consequences. This project uses multiple 'omics approaches delivering (1) a model sustainable aquaculture system capable of being distributed widely across landlocked provinces (2) transcriptomic analysis of fish health and nutrition

responses and (3) experimental cultivation techniques and genomic analysis to identify physical conditions for improved accumulation of biomass and consequent reduced CO_2 emissions. This will yield a system that provides affordable nutrition to communities currently reliant on imported goods or harvests.

Methodologies, Technologies and Data
IMTA data on physiochemical factors in aquaculture such as flow rate, temperature, dissolved oxygen (dO2), pH, and concentrations of salt, NO3- , NH3, and metals to determine their cumulative effects on fish. Physical examinations of stock, studying fish skin colour, and observing of general behaviour characteristics to assess fish health correlated to transcriptome data to identify the genes differentially expressed in arctic char. Strains of algae will be isolated from local and aquatic environments with similar physiochemical conditions to those of the IMTA. Genetic material obtained directly will be used in the detection, improvement and analysis of these algae strains.

Integrated GE3LS
The aquaculture industry has grown more than 4-fold in Canada over the past 20 years, increasing access to quality food products for rural communities across Canada, albeit unevenly, while causing detrimental environmental side-effects. The GE3LS in this project uses economic analysis and community survey tools to assess the impact of proposed changes to prairie aquaculture. Specifically, the impact of the proposed IMTA systems on First Nations and remote, underserved northern prairie communities will be modelled in light of Canada's colonial legacy, extractive industries, and climate change, which have impeded their ability to rely on traditional food harvest.

Project #19302
Nutrient Cycling in Agroecosystems

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Keywords for Proposed Investigation

Research	Methods & Technologies
Agricultural Climate Solutions, Beneficial management practices, Fertilizer Reduction, Microbial Nutrient Cycling	Amplicon sequencing, Shotgun sequencing, Metatranscriptomics, Predictive Soil Mapping

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Best management practices, Agriculture climate solutions, nutrient cycling, microbiome nutrient cycling	econometrics, ethnography

Project Information
Microbiomes mediate important soil functions. Soil not only contains a diverse array of multi-trophic organisms, but also retains the functional capacity to cycle nutrients and deliver them to growing crops. Our ability to sequence and understand the diversity and function of soil microbiomes has expanded significantly with the development of genomic technologies and bioinformatics. We stand on the precipice of gaining the ability to understand how management practices and tools modify the soil microbiome to benefit agriculture. Soaring input costs have put pressure on farmers to find best management practices that support the reduction of inputs without reducing yield. The reduction of inputs not only enables increased farm profitability but can significantly reduce NO2 emissions related to fertilizer application. A better understanding of how the soil microbial community interacts with different plant communities to make soil nutrients plant available is a critical step in making beneficial management practices such as multispecies cover cropping, intercropping, relay cropping, and the use of perennials in annual cropping systems viable choice to aid in fertilizer reduction. We will use predictive soil mapping to maximize the amount of land, regions, and BMPs that can be studied to derive data useful across Canada.

Deliverables and Expected Benefits
Leveraging Living Labs sampling, and numerous plot trials that are collecting data on grazing practices, intercropping, multispecies cover cropping and relay cropping to elucidate relationships with those practices and specific plant combinations with the microbial community for the purposes of making nutrients available to the plants to reduce dependency on synthetic nutrients and related NO2 emissions. This research will contribute to on farm resilience, profitability and innovation in and validation of agricultural climate solutions.

Methodologies, Technologies and Data

Leveraging soils collected across agroecosystem biomes in Canada, we will link soil microbiomes to nutrient cycling and management practices. We use blended sequencing approaches including whole-soil whole-genome sequencing to capture the dominant microbes, metatranscriptomics to capture current activity, and amplicon sequencing to capture current and legacy diversity of the system. We bring soil metadata derived from collections in living labs including a predictive mapping sampling strategy that captures soil cores to 1 meter depth across Alberta. We combine soil genomics with a rich metadata including nutrient, soil characteristics and management histories to discover mechanisms of soil nutrient cycling.

Integrated GE3LS

Economic viability is required for the continuation of farming and ranching, especially considering diminishing returns, ascending property values and input costs. We gather management history (agronomic, economic) by engaging in open ended narrative interviews at kitchen tables for each participating farmers collecting information on beneficial management practices (BMPs) to clearly define what the practices are, why they are being implemented and how. We will look for linkages between the field practices to explore the changes in the microbial communities and function and nutrient availability from a social and economic perspective.

Project #19303

Native plant diversity to enhance ecosystem services in grazing systems

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Keywords for Proposed Investigation

Research	Methods & Technologies
Native plant diversity to enhance ecosystem services in grazing systems	Native plant diversity to enhance ecosystem services in grazing systems

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Ecosystem services, Food security	Economic modelling

Project Information
Plant diversity, both among and within species, supports greater overall biodiversity and improves ecosystem function. Grazing ecosystems are critical for the beef industry and increasing the species and genetic diversity via inclusion of native species into these systems represents a major opportunity to enhance productivity, increase carbon storage and reduce inputs, especially in response to climate-change induced stress. Many positive plant diversity effects depend on interactions between plants and other trophic levels: from soil microbiota to insect food webs. These linkages are poorly understood, especially as pertains to those that may contribute to agroecosystem sustainability. We propose using genomic and traditional tools to quantify plant, microbial, and insect biodiversity above and below ground, linking them to agroecosystem sustainability as relates to forage production, carbon storage, and nutrient retention. We will use this approach multiple systems, including native grasslands, existing experiments exploring species and genetic diversity effects on ecosystem services, and new greenhouse and field trials manipulating both the species and genetic diversity of native plants. Further, we will use drought treatments to determine how diversity effects on ecosystem services in forage systems vary with potential climate change.

Deliverables and Expected Benefits
Forages are in important element of Canadian agriculture and our research will help move this system towards a carbon-neutral, sustainable production. Our project will enhance sustainable grazing agricultural systems in western Canada by developing forage mixes that maximize multiple benefits, particularly enhanced carbon storage, improved drought tolerance, and increased biodiversity. Furthermore, our research will develop new tools to improve soil health and enhance biodiversity of ecosystem service providing insects, like pollinators.

Methodologies, Technologies and Data
In each system, we will characterize plant diversity using traditional methods. We will quantify genetic diversity in select native species using genotype by sequencing to detect genomic signals of regional adaptation and drought tolerance. Alongside these measures, we will sequence the foliar and soil microbiome, measure plant-insect (pollinators, herbivores, and predators) interactions, and quantify insect phylogenomic diversity, as

aspects of biodiversity affecting plant function. These measures will be taken across three years and combined with estimates of other ecosystem services (productivity, carbon and nutrient storage) to link enhanced plant diversity with agroecosystem sustainability in a changing and variable climate.

Integrated GE3LS
Enhancing native plant diversity has strong potential to enhance overall biodiversity and multiple ecosystem services (e.g., forage production, carbon sequestration, pollination, aesthetics, etc.). Moreover, enhanced plant diversity can better maintain these services under extreme climates, enhancing food security and stabilizing agricultural economies. While many of these services provide direct economic value others are less easily valued. We will develop economic models directly linking species and variety selection (via changes in diversity) to the economic value of grazing lands, and use both survey-based and indirect valuation approaches to estimate the increase in societal value via non-market based ecosystem services.

Project #19304

Greener Forage-Livestock Systems: Improving Perennial Legumes through Integrated Ecosystem Omics for Improved Carbon Sequestration, Climate Resilience, and Low-Emission Animal Production

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Keywords for Proposed Investigation

Research	Methods & Technologies
Physiological genomics for climate smart forage legumes, Pasture rejuvenation and microbial biodiversity for carbon sink capacity, Economic social environmental impacts of carbon neutral forage livestock systems, Genetic diversity of key perennial legumes	Reference genome, genotyping by sequencing, reduced representation sequencing, Full-length transcriptomes RNA Seq Genome Wide Association Analysis Molecular Network Models Genomic Prediction, Rumen simulation technique large scale field studies metagenomics soil microbe carbon assessment

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Barriers to implementing pasture rejuvenation, Impacts of new cultivar adoption, Receptiveness to open science, Adoption of genomic tools	Producer survey and modeling, Economic modeling and environmental impact analysis, Interviews and anonymous survey, End-user surveys

Project Information

Canadian beef and dairy industries are critical to our economy and make essential contributions to global food security. Perennial forages and pastures, foundational for livestock production and sustainability, provide opportunities to reduce Canada's carbon footprint. This project will develop and utilize genomic resources in an integrated approach across the forage-livestock ecosystem to focus on: (i) improvement of the perennial legumes, alfalfa, sainfoin, and cicer milkvetch, for climate resilience and carbon capture, (ii) pasture rejuvenation and identification of beneficial soil microbes for increasing carbon sink capacity, and (iii) improved forage nutrition and digestibility for livestock health and reduced methane emissions. Incorporating phenomics for profiling robust root systems and enhanced carbon assimilation through drought as well generating genomic resources such as a cicer milkvetch reference genome, sequence-based global diversity analyses, and full-length transcriptomes through environmental change, will support open-science databases and efficient release of new climate-smart forages. Coupled with large-scale pasture experiments, soil microbe metagenomics, and feed analyses with rumen simulations, the project will implement an integrated systems approach across the forage-livestock

ecosystem to generate modeling assessments which will promote the positive impacts to the livestock-forage industries in the quest to realize a reduced carbon economy and mitigate climate change impacts.

Deliverables and Expected Benefits
- New germplasm with high carbon sequestration potential and climate resilience
- Reduction of greenhouse emission through improved forage digestibility and productivity
- Genome sequence and Genomic breeding tools
- Improving production efficiency of pasture system using pasture rejuvenation methodologies
- Soil microbe diversity database
- Economics and adoption of new legume germplasm and its use in pasture rejuvenation
- Database development of forage crop genomics based on open-science principles and accessible to the industry and breeders

Methodologies, Technologies and Data
The integrated project will investigate perennial legume genetic diversity using Genotyping-by-sequencing and reduced-representation-sequencing and provide a foundational reference genome (long-read, Hi-C) for cicer milkvetch alongside current efforts in alfalfa and sainfoin. Novel root system phenotyping and physiological assessments of carbon traits combined with full-length transcriptomes, RNA-seq, and genome wide association studies will identify gene-network-hubs and genetic markers for greater climate resilience and carbon sequestration. A large-scale field study will rejuvenate old-grass pastures using the newest perennial legumes and measure beneficial soil-microbe-diversity using metagenomics alongside rumen simulations for methane reduction objectives. Economic-societal-environmental impact assessments will be conducted for end-user engagement.

Integrated GE3LS
The interdisciplinary, diverse collaboration is well-positioned to provide transformative science for reducing the carbon-footprint with a dedicated engagement of objective facilitating:
1. Study of the barriers to implementing pasture rejuvenation for carbon sequestration and emission reductions through producer survey and regression modeling
2. Study of new cultivar adoption impacts for sustainability and agronomics using yield models, nitrogen and carbon modeling for climate change mitigation
3. Assessing attitudes for open-science and release of genomic data through interviews, anonymous input, with website analytics upon database release
4. Assessing adoption potential of genomic tools for breeding and carbon mitigation through livestock-forage sector survey

Project #19305
ACTIVATing genomics to accelerate climate-smart crop delivery

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Keywords for Proposed Investigation

Research	Methods & Technologies
Adaptation, Stability, Breeding efficiency, Climate change	Genome sequencing, pan genomics, genotyping platforms, decision support systems

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Threats, Priorities, Carbon intensity, Economics	Survey, Economic analyses

Project Information
Climate instability is causing havoc with crop production and we can no longer rely on past climate data to predict the weather for the coming growing season. Farmers need cultivars that will perform reliably across a range of conditions i.e., environmentally stable and resilient. Furthermore, agricultural diseases and insects are predicted to become more common, adaptive, and damaging due to changing environments. Genomic technologies are a viable solution to help mitigate these challenges; however, its potential in public crop breeding programs has not been fully realized. We will ACTIVATE genomic technologies to enhance the climate resiliency and adaptive stability of grains (wheat, oat, canary seed, flax, lentil, pea, chickpea, and dry bean) with a concomitant decrease in GHG emissions. The Crop Development Centre has a successful track record of developing cultivars of these crops with wide adaptation across the Canadian prairies. Our success is the result of an integrated approach to breeding that leverages our collective expertise and our extensive network of local field-testing nurseries and strong pathology support. We will build on these strengths by fully integrating genomic-based decision support systems to ACTIVATE the latest technologies in crops that are part of a resilient, crop rotational agriculture production system.

Deliverables and Expected Benefits
Our overall deliverable will be quicker development of climate-resilient, adapted cultivars. Accelerated breeding cycles coupled with genomic selection will form the backbone. We will deploy cross-species pan-genomic resources to establish a cost-effective, sequence-based genotyping platform that incorporates functional and haplotype-tagged SNPs derived from long-read sequencing of our extensive germplasm collections. A genomic catalogue of genetic and regulatory variants that enhances decision support systems and is fully compatible with our extensive crop performance database encompassing diverse environments, disease profiles, pedigree, and low-density genotypic datasets will be

developed. These data will be integrated with an automated, user-friendly computational platform designed for genomic-assisted-selection.

Methodologies, Technologies and Data
We will identify genes or genomic regions controlling critical agronomic traits underlying stability using accelerated breeding coupled with high-throughput and precision phenotyping and sequence-based genotyping. We will apply genomic technologies to decipher common interactive pathways between grain crops and beneficial and harmful microbes that affect carbon sequestration and stressful tolerance. Identified genes will be targets for genome editing techniques to rapidly develop resilient cultivars without a loss of quality. Lastly, we will develop cross-species genotyping platforms and computational resources that integrate crop modelling with user-friendly computational decision systems to support complete integration of genomic technologies in our plant breeding programs.

Integrated GE3LS
We will focus on the breeder's equation, which formalizes the value of financial input, time, and genetic gain for breeding, and update the model to include the effects of climate change. We will engage with farmers and breeders to measure genetic gain and production value achieved towards mitigating climate change. This will determine the highest priorities in terms of targeted breeding objectives to maximize genetic gain and decrease the carbon intensity of agricultural production by reducing the amount of inputs and carbon emissions required to produce a given quantity of a crop or the dollar value of a harvest.

Project #19306
Designing Climate Adaptive Resilient Canola (DCARC)

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Keywords for Proposed Investigation

Research	Methods & Technologies
Improve carbon sequestration and photosynthetic efficiency, Develop water use efficiency for drought tolerance, Reduce Greenhouse Gas emissions with more nutrient use efficient cultivars, Gene targets for climate change adaptation	Canola TILLING population and natural diversity lines, Phenotyping and physiological screening, Genomics and proteomics, Discovery of climate adaptive traits

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Impact of climate change on canola crop performance, Agricultural practices reducing carbon footprint and soil GHG emissions, Carbon credits and their implications to producers, Economic benefits of climate adaptive canola to producers and industry	Economic and profitability frameworks, Quantifying GHG emissions, Environmental and Societal benefits, Canola Supply Chain and industry

Project Information
This project will mitigate GHG emissions and development of climate-change resilient canola with a concomitant decrease in the carbon footprint of this crop. Using "Targeted Induced Local Lesions in Genomes" (TILLING) population and natural diversity, we will identify desirable genes and gene variants to significantly improve water-use-efficiency (WUE), nutrient-use-efficiency (NUE) and photosynthetic-efficiency (PE). Improved WUE and drought tolerance will increase the resiliency of canola to withstand climate challenges. Improved NUE will reduce GHG emissions by reducing the amount of inputs, thereby reducing nitrous oxide emissions. Increased PE will both result in more climate-change resilient canola and increased CO_2 sequestration with benefits to reduce environmental carbon footprint. Development and harnessing of Brassica natural-diversity and TILLING resources will involve application of high-throughput phenotyping, physiological screening, genomics, proteomics, metabolomics, AI and machine learning. These activities will facilitate efficient gene discovery, network modeling, structural and functional characterization of targeted genes to improve WUE-drought/NUE/PE traits. Gene discoveries will be applied to improve cultivars to increase climate-change resiliency and reduce GHG emissions, for the prosperity of the Canadian canola industry. These project outcomes and proposed GE3LS activities will help improve sustainability and climate resilient traits, with positive impacts on the canola economy and agricultural environmental stewardship.

Deliverables and Expected Benefits
- Establishment of ~2500 TILLING lines as foundational resource for targeted identification of genes and traits needed to design climate-adaptive canola.
- Physiological screens and omics technologies will identify processes for efficient water and nutrient use, and CO_2 assimilation. Forward and reverse genetic screens will discover gene variants with desirable functionalities for canola breeding.
- AI-Machine learning tools to identify gene-networks and regulators associated with physiological processes
- Lines with characterized climate-resilient traits for canola breeding and cultivar development.
- Integrated GE3LS perspectives that contribute towards IP, climate adaptive canola cultivar development with positive economic impact on Canadian canola industry.

Methodologies, Technologies and Data
- Establishment of high diversity TILLING population and natural Brassica diversity lines resource. "TILLING-by-Sequencing" will identify targeted-gene-variants.
- Phenotypic/physiological diversity will be identified using these resources by analyzing key traits associated with drought/nutrient-use/photosynthetic-performance.
- Genomics/single-cell-genomics/proteomics/metabolomics/AI-Machine-learning tools will be used to identify gene variants and key regulators of essential gene networks that improve climate change resiliency and sustainability.
- Promising lines will be validated under controlled and field conditions to determine improved WUE-drought-tolerance/NUE/PE and overall performance.
- Promising traits will be assessed for potential benefits and impact on GHG and carbon footprint.
- Large transcriptomics/proteomics/single-cell-genomics/phenotypic datasets will be generated and mined.

Integrated GE3LS
In Western Canada, drought decreased canola production by 35% in 2021 and crop emissions have increased by 40% since 2005. Development of climate adaptive canola from desirable gene targets using the Brassica TILLING resource should reduce canola yield loss under drought, while improving CO_2 sequestration, fertilizer use efficiency, reducing GHG emissions. GE3LS team will investigate the economic, social and environmental benefits to stakeholders in the canola supply chain, including plant breeders/seed industry, farmers, and consumers. We will develop economic and profitability frameworks to measure economic and social benefits and use methods defined by ECCC and IPCC to quantify environmental outcomes.

Project #19307

Understanding Crop Management and Nitrous Oxide Emission Reduction Processes: A Soil Genomic Diversity and Expression Approach

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Keywords for Proposed Investigation

Research	Methods & Technologies
Nitrifiers and denitrifiers, Nitrous oxide emissions, Four R nitrogen management, Microbial community composition and function	DNA-based community profiling, qPCR of N cycling genes and transcripts, TGAS micromet, and small plot flux measurements and stable isotope probing, soil profiles and emissions`

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
DNA-based community profiling, qPCR of N cycling genes and transcripts, TGAS micromet, and small plot flux measurements and stable isotope probing, soil profiles and emissions`	Farmer perceptions, Adoption of four R practices, Barriers to understanding complex processes and innovation

Project Information

Since the announcement of the Government of Canada target to reduce N2O emissions from fertilizer by 30% of 2020 levels (by 2030), there has been pushback based on the perceived need to proportionally reduce N fertilizer application to meet this goal. Some critics argue that reducing N fertilizer use to meet the reduction target will mean lower yields and a major decline in economic and food security. Although progress has been made through better N fertilizer management (e.g., 4R management), spatial-temporal variability and the complexity of microbial ecology of N2O-producing communities have hampered our ability to reliability predict emission reductions from management practices. The relative contributions of different microbial functional guilds, including fungi, to denitrification is largely uncharacterized in Prairie soils. To complement the measurement of GHG fluxes from soil we need to know which organisms and metabolic pathways are responsible for the competing processes of N2O production and consumption to fine-tune management and avoid the "perfect storm" of conditions that drive major N2O emission events. We will deliver improved management practices by ensuring soil microbial function is manipulated to reduce N2O emissions from cropping systems. The benefit being not only reduced emissions but also improved nitrogen use efficiency.

Deliverables and Expected Benefits

We will use established genomics tools to quantify the impact of topography and N management on the abundance and activity of soil microorganisms responsible for N2O

production, consumption and net emissions. New genomics-based foundational understanding will be used to refine 4R N management tools and recommendations and to support the development and improved efficacy of new technologies, like enhanced efficiency fertilizers. We will generate data on farmer understanding and perceptions of tools to reduce soil GHG emissions and barriers to adoption of 4R practices. This new knowledge will support improved environmental and economic performance of Prairie cropping systems.

Methodologies, Technologies and Data
We will use existing field studies and infrastructure (e.g., the updated long-term TGAS facility) that measure N2O emissions under 4R N management, combined with DNA-based community profiling and quantification of N functional genes and transcripts to target and mitigate microbial N2O emission events (hot spots and hot moments). 15N stable isotope tracing will track N through the soil and to the atmosphere to understand the sources and sinks for N in cropping systems. This improved scientific understanding of "how" and "why" soil N2O fluxes occur will accelerate the refinement of 4R fertilizer management to more reliability realize emission reductions.

Integrated GE3LS
There is a high level of uncertainty for producers regarding what causes emissions of N2O and about the N2O emission reduction targets set out by the Canadian federal government. We will model the economic sustainability of 4R management practices and the contribution of N2O mitigation toward net zero emissions targets for 2050. We will evaluate farmer perceptions of their role in reducing emissions and barriers to the adoption of new technologies and practices that promote 4R nutrient stewardship.

Project #19308

Bio-inoculants for the promotion of nutrient use efficiency and crop resiliency in Canadian horticulture

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Keywords for Proposed Investigation

Research	Methods & Technologies
Nitrogen fixation, Arbuscular mycorriza fungi, Plant transcriptional networks, Plant growth promoting microbes	Metagenomics, Experimental evolution, Plant physiology, Functional genomics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Environmental impact, Economics, End user and consumer acceptance	Life cycle assessment, technoeconomic assessment, Surveys, Focus groups

Project Information

Modern agriculture's high yield is dependent upon excessive application of chemical fertilizers, namely, nitrogen, phosphorus, and potassium. However, the application of synthetic fertilizer is estimated to account for ~17.5% of the greenhouse gas emissions associated with Canadian agriculture. Microbial inoculants have the potential to significantly reduce fertilizer application and thus greenhouse gas emissions. However, the success of inoculants depends on the isolation of microbes displaying strong plant-growth promoting abilities and the ability to grow and survival in both industrial cultures and local soils. We propose a multi-pronged approach to identify novel microbial inoculants capable of maintaining current crop yields while reducing the application of chemical fertilizers. We will use genomics and metagenomics to identify novel bacterial and eukaryotic strains with potential to reduce fertilizer application and greenhouse gas emissions by improving plant nutrition, for example, through biological nitrogen fixation or phosphorus solubilization. Subsequently, the natural process of selection will be harnessed to evolve isolates with elite characteristics and to develop efficient processes for the industrial production of the inoculants. In parallel, studies of the economics and environmental impacts of inoculants will allow us to identify nutrients and crops where inoculants will have the greatest environmental impact.

Deliverables and Expected Benefits

We will deliver bacterial and eukaryotic inoculants that promote the nutrition and resiliency of major Canadian crops. Using these inoculants will significantly reduce the amount of fertilizer – and thus greenhouse gas emissions – required to support crop growth while maintaining at least the current level of crop yields. We will develop processes supporting the industrial scale-up of inoculant production to ensure that commercialization is effective, economically viable, and environmentally friendly. In addition, plant physiological and

transcriptional responses to inoculants will be quantified, the latter of which will provide targets for future breeding programs to increase plant responses to inoculation.

Methodologies, Technologies and Data
The proposed research will use shotgun metagenomic and whole genome sequencing to identify novel microbial inoculants based on the microbial community composition in the rhizospheres of crops in agricultural fields and of native plants in diverse Canadian ecosystems. Experimental evolution with genome resequencing, as well as gene editing, will be used to improve growth in industrial batch cultures, soil survival, and the plant growth promoting abilities of the novel inoculants. Physiological measurements (e.g., chlorophyl content) and transcriptomics and/or proteomics will be used to characterize the response of major Canadian crops to inoculation with the novel microbial inoculants.

Integrated GE3LS
Inoculant production is not without environmental impacts or cost. We will perform life cycle assessment (LCA) to examine the environmental impact of inoculant production and usage (including medium sterilization, maintenance of culture conditions, etc.) and techno-economic analysis (TCA) to examine the economics of inoculants versus chemical fertilizers. LCA and TCA will produce plant-specific understandings of the minimum efficacy required for inoculants to be economical and environmentally beneficial compared to fertilizers. Surveys and focus groups will produce an understanding of potential hurdles to further adoption of wildtype and evolved microbial inoculants by end-users and their acceptance by consumers.

Project #19309
Climate Change Ready Canola

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Administrative Genome Centre: Genome Prairie

Keywords for Proposed Investigation

Research	Methods & Technologies
Carbon sequestration and reduced greenhouse gas emissions, Nitrogen use efficiency, Heterosis, Optimal root architecture	Genome sequencing and genetic marker development, High-throughput root phenotyping, Epigenomics, Gene editing

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Impact of adopting climate smart canola, Benefits and risks on the farm and in the value chain	Socioeconomic analysis, Farm level and consumer survey

Project Information
The project aims to exploit the untapped variation from diploid Brassica species to improve the environmental sustainability of the polyploid canola crop in the face of a changing climate. High-throughput imaging techniques will be combined with novel computational screening tools and genomic analyses to identify valuable root phenotypes that enable the development of high-yielding canola lines grown in multiple environments. Specifically targeting the known contribution of root architecture to abiotic stress tolerance, novel variation in root system architecture will be identified in diverse Brassica diploid germplasm. The genetic structural variation underlying identified traits of interest will be uncovered using next generation sequencing technologies and markers developed to facilitate introgression into canola. Valuable variation will be captured and transferred to canola through interspecific hybridization, in addition the genome and epigenome of newly resynthesized canola lines will be studied to assess the impact of heterosis. An increased root biomass under limiting nitrogen conditions will be targeted to increase carbon sequestration while reducing greenhouse gas emissions. To quickly manipulate this phenotype, targeted gene editing will be deployed to modify known and uncovered genes involved in defining root architecture. All material will be tested in high-throughput controlled phenotyping platforms and confirmed in the field.

Deliverables and Expected Benefits
The project will identify new diversity that ensures the long-term sustainability of the canola crop; specifically, it will target traits that have been linked to generating a more climate

responsive plant, through increasing yields and enhancing carbon sequestration while reducing use of limited resources (water), and chemical inputs (fertilizer) known to contribute to the current negative climate trends. The germplasm screened and the associated information generated, including both phenotype and genomics data, will form a significant resource for breeders and academics, which will allow the continued improvement of canola and contribute to the long-term economic and environmental sustainability of canola.

Methodologies, Technologies and Data
High-throughput phenotyping using 2-D and 3-D root imaging techniques, controlled environment phenotyping using lyismeter systems, and drone imagery in the field environment will be used. They will be coupled with genomics analyses including whole genome sequencing (PacBio/ONT), optical mapping, HiC for chromatin interaction mapping, epigenome studies (methylation, ATAC, small RNA sequencing) to identify key regulatory elements. These data will be exploited through bioinformatics pipelines augmented with the latest developments in machine learning to identify complex genomic interactions and provide gene editing targets for phenotype enhancement in variety development to reduce the impact that the agriculture sector contributes to climate change.

Integrated GE3LS
Socioeconomic analysis will aim to evaluate farm-level and value chain impacts of the development of new climate smart canola. At the farm level surveys will be undertaken to generate data to assess farm-level adoption, value and risk of new canola germplasm developed using gene editing, digital phenotyping, deep learning and related technologies. We will also examine market-driven value chain incentives for the adoption of low-carbon agricultural innovations. Consumer surveys will examine consumer responses to verified low-carbon management technology to assess the mechanisms by which successful GHG mitigation and CO_2 sequestration can be verified and credibly signalled along value chains.

Project #19401
Leveraging Genomics to Achieve Dairy Net Zero

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Keywords for Proposed Investigation

Research	Methods & Technologies
Enhance methane genomic evaluations, Develop and implement impactful methane herd monitoring and benchmarking tools, Develop a roadmap for methane mitigation across ruminant species, Quantify impact of methane mitigation strategies	Genomics, Bioinformatics, Machine learning, Lice cycle analysis

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Socioeconomic assessment, Farmer preferences, Consumer willingness to pay	Economic modelling, Surveys, Focus groups

Project Information
Dairy is of great economic importance for Canada, and in 2021, it supported $7.38B in total net farm cash receipts, and contributed roughly $35B to Canada's GDP. To maintain its competitiveness, the Canadian dairy industry must seize new opportunities that demonstrates the industry's social and environmental values, ie. reducing the environmental footprint of dairy. Following similar ethically responsible pledges internationally, the Canadian dairy industry has committed to Dairy Net-Zero Pledge by 2050, with a 2030 preliminary milestone of reducing dairy GHG by 30%. This proposal will leverage genomics to achieve Dairy Net Zero in Canada and join global mitigation efforts by integrating previous and concurrent large-scale project outcomes and resources. Specific objectives include defining a multi-disciplinary GHG mitigation strategy (animal genetics/nutrition and manure management). Genetic-based mitigation strategies include improving genomic evaluations for reducing enteric methane by combining high throughput methane sniffer data from commercial farms with available milk MIR predicted methane measurements. Developing a herd monitoring and benchmarking tool that quantifies enteric methane for every herd is key to identify and understand the nutrition/management strategies used by the lowest methane-emitting farms, and to assess the impact of applying these strategies to reduce the GHG inventories of the highest methane-emitting farms.

Deliverables and Expected Benefits
The project will a) enhance the rate of genetic progress for reducing methane emissions; b) develop scientific protocols that quantify the impact and uncertainty surrounding various GHG mitigation strategies; c) identify the optimal combination of mitigation strategies, resulting in an overall roadmap for GHG management for bovines. This proposal will allow the dairy industry to drive advancements in establishing best practices for GHG mitigation,

while reaping the benefits of cumulative and permanent genetic GHG reduction. Newly developed tools to decrease GHGs will result in estimated net savings of $100M/year for the dairy industry and sizeable environmental benefits for Canada's society.

Methodologies, Technologies and Data
This project is building on the successful outcomes of previous large projects that have created the foundation for launching genomic tools and traits that enhance environmental efficiency in Canada. It will benefit from running in synergy with the objectives and current research of regional and national initiatives. An integrated genomic approach will elucidate key features of the genetic architecture of environmental efficiency traits, define variation and facilitate selection toward environmental efficiency in bovines. To ensure the optimal set of mitigation strategies while addressing industry and consumer needs, GE3LS studies will be used to integrate well-established bio-economic modelling with survey-based parameters.

Integrated GE3LS
GE3LS studies will investigate the importance of selecting for environmentally efficient bovines at all levels of the supply chain. Through survey-based approaches, consumers and farmers may be classified based on their perception of environmental traits, including the trade-off between economic gain, social responsibility, and the desired level of emission reduction. Reducing emissions is a multifactorial social challenge which must balance selection for reducing emissions to benefit greater society with maintaining a profitable, sustainable farm that supports farmer and animal well-being. By differentiating the relative importance of traits, the value of providing additional attention to emission-reducing traits may be quantified.

Project #19402

Whole Farm Microbiome and eDNA Genomics for GHG Mitigation in CEA

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Keywords for Proposed Investigation

Research	Methods & Technologies
Microbiome optimization, Pathogen and pest surveillance, Controlled environment agriculture	Life cycle analysis, Inoculants, Microbiome and eDNA analysis

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
How to best improve crop health and food security while reducing GHG footprint of vegetable production	Integrated LCA, microbiomics and metabolomics methods

Project Information

Canada has a strong tradition of greenhouse vegetable production with an annual farm gate of ca. $1.5 billion. Controlled environment agriculture (CEA) systems (e.g. hydroponic greenhouses, vertical farms) offer unprecedented opportunities to ensure food security as they are highly automated and extremely efficient, with reduced water and land uses compared to field agriculture. Importantly, the microbial constituency of these systems has not been optimized for plant health and productivity, representing an opportunity for even greater efficiency gains in food safety and sustainability accompanied by reduction in GHG emissions. We will apply microbiome analysis to water, air, plant and substratum of CEAs and metagenomics to characterizing the microbiomes that highly influence CEAs, and categorize microbial groups that may influence or be correlated with plant stress, nutrient uptake, and GHG production. We will use DNA sequencing to characterize the microbiome and life cycle analysis (LCA) to assess GHG emissions and carbon footprint. We will also attempt to engineer bioinoculant formulations of beneficial microbes to supplement the plant microbiome that promotes growth, health, and crop protection. We will use metabolomics to assess the biochemical effects of the engineered microbiome by identifying marker presence and pathway induction.

Deliverables and Expected Benefits

This project will build upon our ongoing hydroponic microbiome work by further characterizing the microbiome in water, air and substrates of CEAs that can help improve the health and yield of crop plants as well as identify beneficial metabolisms of microbial groups related to improving the carbon footprint in cultivation. For example, microbial community structure can reduce the requirement for GHG-intensive synthetic nitrogen fertilizer by fixing atmospheric nitrogen thereby enhancing crop productivity and reducing N2O emissions. We will also use our collection of beneficial bacterial strains to develop microbial inoculants for improved performance with reduced inputs.

Methodologies, Technologies and Data
We will focus on optimizing the CEA microbiome and macrofauna using genomics tools guided by LCA. We will address plant stress, nutrient uptake, biocontrol, and GHG production. The analysis will include sequencing (metagenomic and marker-based) of hydroponic and atmospheric eDNA, and plant metabolomics, to enable full characterization of the microbial and invertebrate communities associated with nutrient cycling and plant response. The microbiome functions will inform microbiome optimization through probiotic and prebiotics development along with identifying crop varieties that respond well to microbiome optimization.

Integrated GE3LS
This project addresses food safety and sustainability in CEAs. The GE3LS will be focused tightly on using LCA to determine the GHG emissions of representative forms of CEA. Guided by this knowledge, a LCA framework will be employed for determining the best opportunities for microbiome optimization, genomics-enabled pest and pathogen control, and microbiome-aware crop breeding in reducing GHG emissions in CEA production systems. It will also provide guidance on the best approaches for application of CEA to additional vegetable and fruit crops, with full consideration of market potential.

Project #19403
Advanced multi-omics to enable climate-ready horticulture

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Keywords for Proposed Investigation

Research	Methods & Technologies
Microbiome, Reduced inputs, Reduced temperature, Horticulture	Metabolomics, Genomics, Pathology, Greenhouse

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Economic viability, Consumer acceptance, Sustainability	Surveys/interviews, Life cycle analysis

Project Information
If Canada wants to reduce GHG emissions associated with our food system and provide healthier, locally produced fruits and vegetables to Canadians, we have to look towards modifying the systems used to produce the crops that consumers want. Made in Canada horticultural cropping systems will be an important tool contributing to the country's 2030 net-zero target. Our horticulture crops are not bred for our conditions, leading to reduced fruit/vegetable size, lower quality, reduced yield, and higher susceptibility to pest and disease pressures. To mitigate these issues producers turn to fertilizers, pesticides, and greenhouse heating. All of these approaches are associated with significant GHG and result in increased costs for producers.   In this project, we will investigate modifying greenhouse fruit/vegetable production systems to reduce the GHG footprint associated with fruit/vegetable farming. This will be achieved through a multi-disciplinary approach including using metabolomics and microbiome analysis to identify low-GHG producing biological agents that improve the health of crops resulting in reduced levels of fertigation and pesticide application. In addition, we will use metabolomics and genomics to identify genes associated with reduced growing temperatures and compounds produced by plants to repel insect pests, to and breed crops that require less heat and pesticides.

Deliverables and Expected Benefits
This project will create more sustainable production systems for Canadian greenhouse producers. This will include identifying microbiome agents that produce lower levels of GHG and at the same time stimulate the plant's immune systems and enable more effective nutrient uptake. This will lead to a reduced need for fertilizer and pesticides, both sources of GHG. We will also identify plant traits associated with insect resistance and temperature sensing which will be used to breed crops requiring reduced pesticides and greenhouse heating. These efforts will make production more environmentally sustainable and enable expansion of locally produced crops.

Methodologies, Technologies and Data
Mass spectrometry-based metabolomics will be used in multiple activities; 1) examination of plant nutrients and signaling molecules under various production systems, 2) determine levels of stress experienced by plants under various production systems and 3) measure

levels of biochemicals produced by plants associated with insect pest interaction. Genome sequencing and high-density genotyping will be used for determining genetic components associated with a plant's insect defense response, temperature sensing, and to characterize microbiome components and recruitment from growth substrates and within the plant. Data sets associated with mass spectrometry, genome sequence of plants and microbes, and genetic data will be created.

Integrated GE3LS
Interdisciplinary research will be conducted to understand and examine the needs and perspectives of stakeholders (e.g., growers, consumers, government) in horticulture from a socio-economic, environmental and ethical standpoint. First, an analysis of the production, consumption and trade data for Canada will be completed to identify 2-3 greenhouse crops, followed by their evaluation on parameters such as economic viability, sustainability, consumer acceptance and grower profitability. Second, using a life cycle assessment, the potential environmental impact of growing these crops in greenhouses will be assessed to provide Canadian growers with recommendations to fulfill the 2030 emissions reduction plan.

Project #19404
Climate-Smart Cultivars: Development and application of genomic tools to enable low emission crop production

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Keywords for Proposed Investigation

Research	Methods & Technologies
Plant genetics, Agronomy, Quantitative genetics	High throughput sequencing, Genomic, Mixed model analyses, Machine learning

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Risk management, Crop insurance, Public and private goods	Econometric models, Mixture models, Simulation

Project Information
Agriculture accounts for one third of anthropogenic greenhouse gas emissions. These emissions notably arise from the use of pesticides and synthetic nitrogen fertilizers. Conservation farming initiatives to cope with these emission sources include reduced pesticide and fertilizer applications. However, meaningful reductions in crop inputs can cause major production declines. Plant breeding addresses this issue by generating new cultivars that efficiently produce safe food given the same or fewer inputs. This project harnesses novel environmental and genomic data sets to develop genomic toolkits to identify crop genotypes that are greenhouse gas efficient. Specifically, the objectives of this project are: 1) to identify the allelic and pedigree compositions of both elite Ontario field crops (barley, dry bean, soybean, and wheat) and novel genotypes with favorable disease resistance and nitrogen use efficiency traits; 2) to identify the pedigrees and alleles that improve disease resistance, nitrogen use efficiency, and other key traits in specific environments, including future environments predicted by climate models; 3) to develop and apply environmental genomics predictions to select elite crop varieties that have high yields with low inputs and are stable despite climate and environmental change; and 4) to examine the economic and social consequences of utilizing climate efficient varieties.

Deliverables and Expected Benefits
This project develops new genomics-aided prediction and selection methodologies for plant improvement in environments such as those with low fertilizer and pesticide application. Mechanistic and artificial intelligence models predict elite plant genotypes and will be widely adopted if successful. The project's genetics analyses integrate with breeding programs. Thus, it will immediately contribute new cultivars, generating social and private benefits through efficient food production.   The project determines the genetic plasticity of elite breeding germplasm to climatic and management variation, thus allowing plant breeders to design climate-resilient cultivars and policy makers to accurately predict climate and management changes' impacts on plant production.

Methodologies, Technologies and Data
Plant traits such as yield, pesticide response, and disease resistance will be analyzed from 10,000s of historical and new evaluation plots across diverse environments for hundreds of

elite crop genotypes and registered varieties. The plant genotypes will be SNP-tagged or sequenced. Their trait variation will be partitioned to allelic compositions and pedigree relationships. Analyses of meteorological, topological, management, and soil information will identify genotypes and alleles adapted to specific environments. Cultivars' performances under future climate and management regimes will be estimated. Genomic tools will be developed; selections will be made from material within current breeding programs; and results field tested.

Integrated GE3LS
The nexus of changing technology, changing climate, and government policy (i.e. environmental regulations, farm support policies, public risk management programs, trade agreements) presents a highly complex, decision-making environment for farmers to navigate. This project focuses on identifying and developing climate resilient and "low emitting" crops. We will estimate the adoption of these new crops under uncertainty, a changing climate, and a publicly subsidized crop insurance program that currently disincentivizes the adoption of on-farm risk mitigating strategies. The economic and social values of these crops will be estimated, and policy changes required to optimize their adoption will be recommended.

Project #19405

Indoleamine mediated climate crisis alleviation and resilience of economically important crops in Canada

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Keywords for Proposed Investigation

Research	Methods & Technologies
Stress alleviation, Carbon sequestering, Enhanced agriculture, Indoleamines	Metabolomics, DGE via NGS, Integrated plant production system

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Omics adoption, Carbon sequestering, Culture vessel, Climate mitigations	Media communication, publications and reports, Field Demonstrations and plant distribution, IPPS tours and visits, Field demonstrations

Project Information
Climate crisis driven temperature fluctuations during flowering period continue to cause crop loss and demotivate growers who either resort to greenhouses or animal husbandry (increased energy consumption). Our research showed that indoleamines, the metabolites of tryptophan, alleviated stress induced due to such fluctuations and improved productivity in Hazelnuts. Targeted (Indoleamine pathway) DGE analyses via NGS, metabolomics of phytochemicals in deterministic phases of plant development, within the Integrated Plant Production System (IPPS) shall assist in underpinning bottlenecks of its regulation and improvement of floral resilience. This involves deep understanding of mechanisms underlying adaptive changes and implications for stress-related under-performances of hazelnuts, apples and grapes (commercially and culturally desired species for indigenous community). Increased acreage of desired plant species can be guaranteed via a streamlined, consistent, and on-demand supply chain of such resilient IPPS borne plantlets that reduce production costs while their resilience in the field assures carbon sequestering. The omics technology in conjunction with our novel plant production vessel will reduce the use of greenhouses for transplant production curtailing emissions and effluents resulting in about 100-fold reduction in operating costs along with increased acreage and enhanced mitigation of carbon footprint of Canada's food system

Deliverables and Expected Benefits
This project will provide researchers and growers with genomics driven solutions utilizing the potential of indoleamines mediated IPPS that shall ensure prompt production of desired commercial and culturally important transplants in large volumes due to which reduction of greenhouse gases and mitigation of carbon footprint of Canada's food systems shall be ensured. Inclusion of indigenous communities' interest improves the rapport and belief in accepting the genomics / metabolomics driven solutions. Enhanced Canadian economy and cultural values (indigenous community) and tremendous increase in field acreage of crops that were typically opted for greenhouses are additional benefits of this project.

Methodologies, Technologies and Data
This project involves mitigation of stress by preconditioning the IPPS generated plants with exogenous application of indoleamines for maximum survival in stressed environments and minimum field transplant shock. Elucidation of mechanisms of thermotolerance during cryobanking and field transplant will employ biochemical and molecular analyses of indoleamine pathway using DGE via NGS, transcriptomics, and UPLC-MS-MS. The role of indigenous microbiome in deploying these metabolites near the rhizosphere will also be investigated. Data generated will assist in identifying and understanding stress mitigation and the toolkits generated will be available to researchers, growers, and stakeholders.

Integrated GE3LS
Economics faculty (UoG) shall quantify the impact of indoleamine-mediated-IPPS approach upon carbon emissions by the greenhouse industry, and associated economic benefits/impacts. Knowledge sharing and translation to indigenous community will be conducted by indigenous faculty (UoG) via existing relationship with the Sixth Nations stakeholders besides addressing regulatory and environmental issues. Such information will be published and disseminated to growers via demonstrations, meetings to ease technology adoption. Periodically results from the experiments will be published in peer-reviewed journals, newsletters, interviews etc. In addition, UoG faculty shall work on GE3LS alongside personnel from social and environmental responsibility department of participating companies.

Project #19406
Omics guided technologies for scalable production of cultured meat

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Keywords for Proposed Investigation

Research	Methods & Technologies
Animal cell biology, Biomanufacturing, Stem cells, Tissue engineering	Biofabrication, Cell culture and differentiation, Proteomics and metabolomics, Bioprocess control

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Bioethics, GHG emission, Resource utilization analysis	Life cycle analysis, Ethical social and cultural (ESC) thinking

Project Information
Global meat consumption has grown by 58% in the past 20 years and is expected to further increase. Current meat production methods are wasteful and inefficient resulting in high water consumption, greenhouse gas (GHG) emission (15% of global emissions), accelerated soil erosion and pollution of waterbodies. The industry accounts for 70% of land suitable for agriculture and almost 30% of agricultural water consumption. Cultured meat, where animal tissue is grown in bioreactors, is an environmentally friendly and ethically appealing alternative as it has the potential to decrease land use (by 99%), water consumption (by 80%) and GHG emission (by 78-96%). This nascent field faces several significant challenges. These include 1) need for optimized and diverse cell sources; 2) need for low-impact (GHG) biomanufacturing to expand the cells; 3) need for appropriate additives to optimize culture and tune metabolic composition; 4) scalable, cost-effective methods for biofabrication to produce meat-like tissues; 5) Ethical, social and cultural aspects of cultured meat. In this project, we will develop solutions and technologies for these challenges by using omics (proteomic and metabolomic) analysis to guide the technology evolution integrated with life-cycle analysis to determine the impact on GHG emissions and ESC thinking to integrate user perception.

Deliverables and Expected Benefits
In this project, we will develop several resources that will benefit the ecosystem of researchers and companies in the field of cultured meat. We will develop a cell bank to host and provide diverse range of cells (primary and cell-lines) of animals of human consumption. Through omics analysis, we will develop optimal additives and growth factors that will enable low-cost and environmentally-friendly production of meat. We will also develop biomanufacturing methods that will facilitate the energy-efficient and water-recyclable production. Finally, we will develop innovative and biofabrication approaches that will mimic texture and taste of meat with minimal GHG emission characteristics.

Methodologies, Technologies and Data
Our research goals are 1) Diverse cell source development; 2) serum-free media and additives for optimized cell expansion; 3) Biomanufacturing for cell expansion and 4) Tissue engineering to produce animal meat-like tissue. These goals will be accomplished through

proteomic and metabolomic analysis of the cell and its development as it is transformed from a stem cell into a fully assembled tissue. Comparison of cultured products with natural ones will be performed at each stage to understand the biological transformations and optimized to mimic natural composition. Machine learning will be used to optimize methods for efficient production of cultured components.

Integrated GE3LS
In parallel, these technologies and materials will also undergo life cycle analysis (LCA) to understand their resource implications as well as ethical, social and cultural (ESC) analysis to understand the impact of it on the society. LCA will focus extensively on GHG emissions associated with the choices made in the science and engineering design of the technology. Land use, water consumption and energy use analysis will also be incorporated to provide a wholistic picture to optimize the choices made. This will be layered with ESC analysis to identify the optimal technology that is suitable for translation.

Project #19407

Biological Enhancement of Rock Weathering for CO2 Sequestration in Agricultural Soils

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Keywords for Proposed Investigation

Research	Methods & Technologies
Soil health, Plant health, Nanosensors, Carbon sequestration	Hormonomics, Rock weathering, Metagenomics, Electrochemistry

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
C markets, Barriers and drivers, Public perception	Survey, Interview, Photovoice, Outreach

Project Information
The loss of soil carbon (C) in Ontario's agricultural lands constrains our ability to increase regional food security; declining soil fertility and increased greenhouse gas (GHG) emissions creates a critical need for regenerative agricultural management that promotes soil health and the sequestration of C in soils. Fast-weathering silicates applied to agricultural fields can sequester CO_2, but little is known about the microbial mechanisms contributing to potential soil C accrual during weathering processes. We will investigate biological enhancement of mineral weathering for CO_2 sequestration in a series of greenhouse and field experiments to assess the potential of the soil microbiome to improve crop productivity, increase C capture, maintain soil health, and decrease GHG emissions in Canada's agricultural soils. We will use a novel combination of metabolomics (soils and plants), shotgun metagenomics (soils) and newly developed electrochemical nano-sensors (soil and plant diagnostics) to assess how commercially available rock-based and biological soil amendments impact GHG release, soil C sequestration, plant health, and soil microbial functioning. We will characterize the role of the soil microbiome in CO_2 sequestration during silicate weathering, and we will evaluate the potential of commercially available biological amendments to enhance CO_2 sequestration via rock weathering in the soil environment.

Deliverables and Expected Benefits
We will assess the potential for biological enhancement of mineral rock weathering to increase soil C sequestration in Canada's agricultural soils. We will holistically characterize the potential benefits, trade-offs, and public perceptions of using non-traditional biological soils amendments and fast-weathering silicates to promote GHG mitigation under current and projected climate scenarios. Furthermore, electrochemical nanodetector sensors will be developed for real-time measurements of novel, targeted crop and soil health indicators (e.g., rhizosphere hormones) as practical field instruments for crop and soil health monitoring and as a means to lower participation costs in agricultural C removal markets.

Methodologies, Technologies and Data
Metabolites and growth regulatory compounds will be extracted from soils and plants and analyzed using LC-MS (QExactive Orbitrap HRMS). Soil and plant health metabolomics will be combined with real-time detection of targeted health indicators using electrochemical nanodetectors in response to climatic and management-induced stressors. Greenhouse gases (CO_2, CH_4, N_2O) will be measured via fourier transformed infrared technology. The soil microbiome will be characterized using shotgun metagenomics and carbon flows from plants to soils will be tracked via stable isotope probing. Surveys, interviews, and a photovoice approach will be used to assess end user and community perceptions of amendments.

Integrated GE3LS
We will use qualitative methods to understand the social context around rock weathering for CO_2 sequestration in agricultural soils. 1) Using interviews and photovoice, we will identify barriers to adoption of C-sequestration management practices. 2) Using a survey, we will identify multi-scalar social, cultural, and political factors affecting participation in C removal marketplaces across farm types. And 3), using focus groups, we will characterize customer perceptions of the impacts of enhanced rock weathering for CO_2 sequestration. This research will uncover current constraints to progress for on-farm CO_2 sequestration, and chart pathways towards farmer-led climate mitigation through genomic technologies.

Project #19408

Advancing climate smart food sustainability practices in Northern Ontario: Development of guidelines for implementation of genomics-based methods to monitor agricultural soil quality and crop health

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Keywords for Proposed Investigation

Research	Methods & Technologies
Soil microbiome, Crop production, Phytopathogenic and filimentous fungi, Biostimulant	Plant tissue RNA sequencing, Metagenomics, Plant transcriptomics, Next generation sequencing

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Feasibility, Relationship exploration, Guideline development, Policy Implications	Conducting feasibility studies of crop needs of existing First Nations community partners, Engagement of existing First Nations communities in determining genomic technologies benefits and understandings, Quantitative and data driven analysis of project outcomes, Multiple criteria and multiple participant informed data (both qualitative and quantitative)

Project Information
All plants, including crops, co-exist with microbial symbionts as well as pathogens, and, all together play key roles in the ecosystem stability and the plant physiology processes. In agroecology the use and role of biostimulants in the amelioration of fast evolving climate change-associated abiotic stresses on crops is an established prospect, however, less so on the environmental carbon footprint aspect. As a new land management practice, biostimulant use, presents the opportunity to sequester higher carbon fixation by plants through a healthier and more resilient photosynthesis. The accumulation of soil organic carbon through the increased biomass productivity aids Climate-Smart Agriculture and Food Systems practices and optimization of human inputs in agro-ecosystems. Efficacy can vary widely pending crop plant and the local conditions. To develop better-targeted crop production in the Northern communities, delving deeper into the interactions of the use of biostimulant with the indigenous crop-associated and soil microbiome is needed. Application of biostimulants in crop production could provide a long-term, cost-effective solution to sustainable plant productivity. Utilizing the power of next generation sequencing technologies, genomics technologies could demystify the effect that bio stimulants have on crops, soil, and water post-use and the benefits on soil biota over time.

Deliverables and Expected Benefits
Deliverables and expected benefits of this study include:
- Evaluation of plant-growth-promoting properties biostimulants impacts to the mitigation or reduction of the carbon footprint during the crop growth cycle, focusing on 8 to 10 different crops important in Northern communities;
- Method development for detecting phytopathogenic and beneficial filamentous fungi by genomics and transcriptomics;
- Establishing molecular diagnostic tool kits for tracking target microbial communities in soil and plant samples and physiology parameters to evaluate overall crop plant health status;
- Guidelines for implementation of genomics-based methods for crop and soil quality monitoring in Northern communities, reducing carbon footprint and need for food transport.

Methodologies, Technologies and Data
Approaches and methods required in this project include next generation sequencing (amplicon/metagenome/plant tissue RNA sequencing). DNA/RNA data collection and quality checks will generate an analytical architecture for the genomics associated data interpretation by computational bioinformatics technology. For higher-resolution understanding of the plant-microbe interaction, plant and microbial functional markers will be selected and in gene expression monitoring. The use of real-time PCR techniques will enable broad-range assessment of functional genes present in the microbes and assessment of molecular, biochemical, and physiological reactions of crops. Use of such real time monitoring might become a proxy to optimize the effectiveness of biostimulant inoculation.

Integrated GE3LS
This project addresses the following GE3LS research questions:
1. What crops are most in need for our First Nations partners and how can this study better address First Nations needs?
2. How can we support our First Nations partners in building a trust-filled relationship with genomics?
3. What guidelines are needed for genomics technologies for downstream users in Northern regions to best promote sustainable growth?
4. What decision-making paradigms and policies can be created from this project for future downstream and regional partners?

Project #19501

Identifying the molecular mechanisms of biofilm formation of necrotic enteritis in broiler chickens and custom designing a nano-enabled antibacterial combination therapy (NeACT)

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Administrative Genome Centre: Génome Québec

Keywords for Proposed Investigation

Research	Methods & Technologies
Sustainable poultry production, Quorum sensing, Nanoenabled antimicrobial combination therapy, Necrotic enteritis	Transcriptomics, Metagenomics, Metabolomics, Nanotechnology

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Economic evaluation, Industry adoption, Animal welfare	Feed conversion efficiency, Product safety data, Life cycle assessment, Animal health assessment

Project Information
Antibiotics have been successful at controlling outbreaks of necrotic enteritis (NE) in poultry. However, the removal of antibiotics from poultry production results in adverse effects on production efficiency (weight gain, feed conversion ratio, and mortality), which contributes to a greater carbon footprint of the industry. Necrotic enteritis, caused by C. perfringens, is associated with the formation of biofilms in the chicken intestine leading to intestinal damage due to the production of toxins such as netB and tpeL. Intestinal damage is associated with reduced production efficiency due to higher mortality and reduced nutrient absorption. This project will identify key pathways associated with the biofilm formation of C. perfringens and its association with the intestine of the host using transcriptomics, metagenomics, and metabolomics approaches. The project will also develop a nano-enabled antimicrobial combination therapy to disrupt biofilm formation of C. perfringens in chickens resulting in improved production efficacy, optimal nutrient utilization, and reduced mortality. This will improve the resilience, sustainability, and profitability of the Canadian poultry production. With the Canadian poultry industry moving towards antibiotic free production, the development of a nano-enabled antimicrobial combination therapy as an alternative to antibiotics against NE will reduce the carbon footprint of poultry production in Canada.

Deliverables and Expected Benefits
The deliverables of this project include development of nano-enabled combination therapy, control of necrotic enteritis in broiler chickens, commercial antibiotic free poultry production, and product registration and industry adoption of the technology. The project will conduct a life cycle assessment of the nano-enabled combination therapy and estimate GHG emission and nutrient excretion reduction. The Canadian poultry industry will be able to produce poultry sustainably and profitably with the use of nano-enabled combination therapy to

control necrotic enteritis. This will reduce the pressure on the environment, reducing carbon footprint of the industry.

Methodologies, Technologies and Data
Biofilm formation of C. perfringens will be studied in vitro, both as a surface-free microbial aggregates and surface attached as well as in vivo in chickens administered with C. perfringens. Transcriptomics of microbial aggregates and intestinal tissue samples as well as metagenomics will be performed using Ilumina's sequencing platforms. Metabolomics will be performed using ultraperformance liquid chromatography-tandem mass spectrometry. Based on the identified mechanisms of biofilm formation, a nano-enabled antibacterial combination therapy will be designed and encapsulated using biopolymers resistant to gut pH of the chicken. LCA, return on investment, GHG quantification will be performed for newly designed nano-enabled therapy.

Integrated GE3LS
Genomics approaches will help address one of the major animal welfare challenges in the poultry industry, which occurs due to necrotic enteritis. The social scientist will address opportunities and challenges of adoption of the technology in antibiotic-free poultry production practices. The technology developed based on the understanding of the disease progression will be evaluated for its economic feasibility, environmental sustainability, and performance using alternative assessment framework. Spearheaded by our regulatory partner, a study will be performed on the regulatory requirements and challenges of a nano-enabled combination therapy in the poultry industry.

Project #19502

Unleashing the biological superpowers of black soldier fly frass as an eco-friendly and sustainable fertilizer

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Keywords for Proposed Investigation

Research	Methods & Technologies
Organic fertilizer, Soil communities, Plant immune responses, Insect frass	Metagenomiccs, Metatranscriptomics, Metaproteomics, Metabolomics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Organic fertilizer, Soil health, Innocuity, Pest management	Life cycle analysis, Stakeholder survey, Economic projections, Efficacy trials

Project Information
Black soldier fly producers such as Entosystem exploit the superpowers of insects to help lower the environmental impact of agriculture by upcycling food waste into fats, proteins, and organic fertilizers. Because synthetic fertilizers were responsible for 12.75Mt CO2e in 2019, an ISO14064 life-cycle analysis has shown that the Entosystem facility would allow a reduction of 40 000T of CO2eq per year, an 89% decrease in GHG emissions when replacing synthetic fertilizers with frass. Furthermore, COVID19 and international events have highlighted the need for a resilient agronomic industry including locally produced organic fertilizers. BSF frass shows antifungal activity and a strong potential to boost the plant immune system, precious assets to organic farmers with limited resources to combat pests and diseases. Frass also promotes plant growth, induces plant defence genes, and promotes beneficial soil microbiological parameters, with a potential for increased carbon capture in soil. By using various OMICS technologies, understanding the mechanisms which underly agricultural response to frass, including changes in soil and plant ecosystems, and the potential immune-promoting response in plants, we wish to showcase frass as a viable economic alternative to traditional farming methods using synthetic fertilizers and pesticides.

Deliverables and Expected Benefits
The project will showcase the use of frass as a tool to reduce the carbon footprint of farming. Guidelines will be developed on the use of frass on various crops, it's phytoprotection potential and environmental and economic benefits. Growers will gain knowledge on the agronomic potential of frass, the improvement of soil health and explanations on the underlying mechanisms such as phyto-hormone production and chitin degradation. Furthermore, by validating if frass can act synergistically with conventional fertilizers to improve nutrient lability and efficacy, we will reduce the amount of synthetic fertilizers and pesticides used in agriculture.

Methodologies, Technologies and Data
The project will study the living community composition and the metabolic activities performed by the organisms of frass-amended (crude or heat treated) ecosystems (soil and plant). Shotgun metagenomics, validated with metatranscriptomics, will identify the living communities (microbes and insect species) and their activity. Genomics will be used to measure the induction of plant defence genes while proteomics will give insights on the levels of production of plant stress proteins. The metaproteomics will investigate the biological functions of these communities by measuring the production of phyto-hormones and changes in active metabolic processes associated to frass amendment.

Integrated GE3LS
Projections in 5 and 10 years of BSF frass production and organic farming lands will be generated to evaluate the potential of frass at a larger scale. A life cycle analysis will be performed to compare the use of locally produced frass with other organic fertilizers and verify the environmental benefits of such a substitution (reduction of GHG, pesticides and nutrient runoff). The sector stakeholders will be surveyed to identify the social and regulatory acceptability and limits of the use of frass in agriculture practices.

Project #19503

An AI decision-support tool based on soil metagenomics to reduce GHG

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Keywords for Proposed Investigation

Research	Methods & Technologies
Machine learning,decision support tool, GHG emissions, Soil metagenomics,	Machine learning, Metagenomic sequencing, IPCC tier 2 and 3 methods, Functional genomics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Agricultural practices, GHG reduction, Agricultural economics, New practices adoption	Econometrics model, Mathematical programming, Qualitative analyses

Project Information
Intensive agricultural practices can result in soil degradation via organic matter and nutrients losses and polluting dissemination of GHG, pesticides and exo-contaminants. The recent IPCC report and several scientific metanalysis have reported numerous regenerative agricultural management practices for several cropping systems that are efficient reducing GHG emissions and increasing soil health and C sequestration. However, the major obstacle that hinders the mass adoption of these sustainable practices lies in the lack of knowledge of the impact of the practices on the soil biological communities and their ecosystem functions essential to soil health and its resilience to climate changes, as well as the economic impact on the profitability of farms. We propose to fill this major gap by developing a numerical Web platform that will give access to innovative decision-support tools relying on machine-learning models based on a database of soil metagenomic-derived biomarkers' diversity and functionality, as well as soil health indicators and remote-sensing data to predict agri-environmental and economic impacts of agricultural practices within various cropping systems. This will help growers select practices that reduce GHG and promote C sequestration, N-use efficiency, crops yield and quality, and savings related to decreased uses of fertilisers and pesticides.

Deliverables and Expected Benefits
The project targets four deliverables: (1) Predictive machine-learning models of cropping systems and agricultural practices' impacts on GHG emissions and soil health resiliency; (2) A network of scientists, agronomists, growers and stakeholders of five provinces to conduct trials to validate the predictive models; (3) Database updates that compile agronomic and economic reference values using the network's collaborative approach; (4) A user-friendly Web platform that provides decision-support tools and training contents. These -omics-based models and tools will provide innovative knowledge to promote massive adoption of

best practices and policies to address the objectives of the Climate-Smart Agriculture and Food Systems initiative.

Methodologies, Technologies and Data
Machine-learning models (MLM) will be built at the onset of the project using an IRDA's database of soil metagenomics, agronomic, meteorological, pedological, physicochemical data from 2,500 geolocated cultivated sites. Estimated and field-measurements GHG emissions data will be added to database using IPCC tier 2 and 3 methods while economic data will be estimated with econometric models. The models will be validated using new data from trials conducted on replicated plots by a network of scientific and growers from five provinces. MLM and decision-support tools will be integrated into a user-friendly interface Web platform used by network's members and project's partners.

Integrated GE3LS
Growers/agronomists enlisted or not in the network will be surveyed to identify the benefits/obstacles to the adoption of sustainable practices that reduce GHG and promote soil health. The crops management systems will be categorized in terms of cost and benefits of production and of ease of adoption. Results of a cost-benefit analysis using data on crops yield/quality, practices management and inputs, rates of GHG and C sequestration, government policies and the carbon market will be integrated to the predictive models and decision-making tools. Network's members will be actively solicited to identify their expectations and validate the models and tools.

Project #19504

Mycorrhizal Fungi & Soil Microbiota: a sustainable biological solution for an increased soil carbon sequestration and a reduction of greenhouse gas emission in agroecosystems

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Keywords for Proposed Investigation

Research	Methods & Technologies
Carbon sequestration, Greenhouse gas emission, Life cycle assessment, Bioinoculants	OMICS technologies, Soil biochemical analyses, Field and Greenhouse trials

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Carbon footprints, Biotechnology adoption, Decision making, Public perception	Benefit transfer function, Incentive implementation model, Multi-criteria decision analysis, Life cycle analysis

Project Information

The continual use of chemical fertilizer for food production is economically and environmentally costly and unsustainable. In addition, inefficient utilization by crops is negatively impacting the environment. Lost phosphates lead to toxic algal blooms, and N-inputs are the major anthropogenic source of nitrous oxide, a potent greenhouse gas. Growers, along with key agribusinesses, are expressing an urgent need to enhance agroecosystem nutrient efficiency. As genomics has quickly led to biotechnological advances in other sectors, agribusiness stakeholders believe that it can be used to harness the power of soil microbes for crop nutrition. We aim to characterize genomics, diversity and community composition of microbes associated with potato and wheat rotation system, and through big data analysis approaches, relate microbiome structure and activity to crop success under different fertilizer scenarios. We will also develop and test new microbial inoculants and innovative ways to sustainably enhance the beneficial crop microbiome for a better carbon sequestration in the soil while reducing the carbon footprint of agriculture. Life cycle assessment will be undertaken to compare carbon footprint of with and without microbial inoculants. Potato and wheat rotation system is used as a model to our microbial-based technology which will be applied to other crops.

Deliverables and Expected Benefits

This project will improve carbon sequestration in the soil, reduce greenhouse gas emission and mitigate impact of global climate change. It will develop efficient mycorrhizal-based biofertilizers that will be applied as biological inputs and serve as major global carbon sink. Life cycle assessment will be made to compare carbon footprint with and without biofertilizer inputs. The outcomes will allow producers to reduce fertilizer use, while increasing organic matter in soil. We will also develop genomic-based toolkits that will help

bioinoculant industry to improve production and formulation processes and farmers to detect and quantify beneficial and pathogenic fungi in their soils.

Methodologies, Technologies and Data
We will use OMICS approaches and economic modeling, survey, and experimental methods, an integrated research team will: Assess the structure and function of soil and root microbiomes in potato-wheat system; Develop molecular toolkits for microbiological management in production fields; Use these kits to select agronomic practices for effective use of mycorrhizal-based microbial inoculants; Select optimal microbiomes for different major crop species; Assess the impact of mycorrhizal-based microbial inoculants and microbiome management on carbon sequestration and greenhouse gas emission, as well as the attitudes and technology uptake of farmers, agronomists, policy makers and the public with respect to these treatments.

Integrated GE3LS
These questions will be addressed:
- What is the carbon footprint of mycorrhizal-based fertilizers versus conventional fertilizers?
- What is the monetary value of improved crop resilience from biofertilizers? • What economic, environmental and social incentives will encourage farmers to apply biofertilizers to their crops?
- How do biofertilizer incentives depend on farmers' perceptions of climate change impacts on crops?

GE3LS research team will use life cycle assessment to determine the economic value and carbon footprint of biofertilizers compared to conventional fertilizer. Farmer surveys will determine willingness to adopt biofertilizers, considering farmer decision-making in the context of risk, uncertainty and climate change adaptation behaviour.

Project #19505

Accelerating Breeding Technology Delivery to Address Climate Change Impacts

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Keywords for Proposed Investigation

Research	Methods & Technologies
Accelerating Breeding Technology Delivery to Address Climate Change Impacts	Trait discovery, Genetic gain, Climate ready traits, Pulses

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Genomic selection, Phenomics, Sensor fusion, Proteomics	Climate conscious diets, Protein substitution, Emerging crop, Adoption

Project Information

Genomic Selection (GS) - Shortcut for the Breeding Cycle: Genomic selection as a breeding tool has matured and is realizing significant improvements in the efficiency of breeding in major crop species. However, bean breeding programs have yet to validate its benefits and develop strategies for transition and adoption. This proposal will conduct background work to modernize breeding programs in Eastern Canada and provide training. High-Throughput Phenomics (HTP) as Disruptive Tool in Crop Breeding: One of the major goals of plant breeders and geneticists is to strengthen the genotype-phenotype link to develop tools and strategies to improve crops. With the advent of more dynamic and reliable big data analysis tools and sensor technology hardware, this project will bring unparalleled resolution to the discovery of traits relevant to dry bean production. At McGill University, the Eastern Canadian Plant Phenotyping Platform (ECP3) has enabled the Hoyos-Villegas lab to construct a mobile field phenotyping sensor array that is unique in North America.

Deliverables and Expected Benefits

Deliverables:
1. Construct GS+HTP platform for pulses, emphasizing climate change mitigation.
2. A genomic-proteomic-phenomic data matrix
3. Study GS+HTP as drivers of agricultural output, protein substitution and aggregate impact on climate change.
4. Elucidation of recombination in pulses, induction of recombination events in genomic coldspots.

Benefits:
1. Reduced GHG Emissions: A GS+HTP platform for genetic gain acceleration in pulse crops. Varieties with enhanced yield and sustainability. A proteomics HTP platform.
2. Sustainable circular solutions: High protein varieties with optimized resource use efficiency. Seed quality research.
3. Resilient and sustainable food systems: Genomic-biophysical-economic model for estimation of climate change mitigation levels.

Methodologies, Technologies and Data
Hologenomics to exploit emerging technologies for pulse improvement. Implement Practical Haplotype Graph (PHG) databases. Genomic selection models using linear/non-linear and machine learning. Construct a phenomic correlation matrix of dissected traits:
- Proximal phenomics for dissected crop performance parameters using sensor arrays (imaging and point cloud)
- GWAS of metabolomics/proteomics: proteomics carried out by uHPLC/MS-MS and untargeted metabolomics by LC/QTOF-MS.
- Designer genomes: Crop growth models within GS models for better accuracies. Cost of production and yield data incorporated into Canadian Regional Agriculture Model (CRAM). Adoption of plant-based dietary protein in biophysical models and estimate climate change mitigation.

Integrated GE3LS
Pulse consumption improves diet quality. Dietary choices that promote health are needed, yet current mealtime recommendations for high quality protein intake may be insufficient and sustainable plant-protein produced with environmental benefits should be considered. Our GE3LS hypotheses:
- Consumption of locally grown pulses will equally favour Canada's circular economy, and cereal or oilseed crops grown in rotation after a pulse crop have similar or reduced greenhouse gas emissions.
- Newly developed pulse cultivars grown locally in Canada could help promote the adoption of new dietary habits, mainly with the replacement of animal protein with new plant-based alternatives.

Project #19506

Development of high-throughput multi-omics tools for enhancement of biological nitrogen fixation

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Keywords for Proposed Investigation

Research	Methods & Technologies
Nitrogen metabolism, Biological nitrogen fixation, Plant breeding, Instrumentation	Genomics, Phenomics, Bioinformatics, Spectroscopy

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Technology transfer, Emissions, Business case analysis, Life cycle analysis	Practice change, Environmental sensing, Sensitivity analysis, Data management

Project Information

Nitrogen (N) is a major driver of primary productivity and sustainable development of land use increasingly will rely on organic N sources. Reduced dependency on inorganic N and improved use of plant-symbiont biological processes requires innovative solutions to mitigate fossil fuel-derived Nitrogen reliance. There are increasing expectations for cost effective and accurate means to track biological nitrogen fixation (BNF) to inform specialised endeavours such as plant breeding, farm and environmental management. In plant breeding, BNF is a critical determinant of the value of legume cultivars. However, no economical means to track BNF in forage legumes exist, resulting in bottlenecks for assessing N in soil-plant systems. Current methods to understand the N-fixing dynamics are destructive, costly, slow and inaccurate. Biophysical variations in the soil influence peak nodulation stages and internal N cycling within the plant causes data inaccuracy.

This project build on the progress that the research team has done in the development of a portable field-ready device using AI-based sensor-fusion of an optimised set of proximal sensing of plant canopies in the field. Our preliminary work has shown potential to identify morphological correlates of patterns in leaves with optical sensing technologies, such as Raman spectroscopy and Hyperspectral Imaging (Phenomics).

Deliverables and Expected Benefits

Deliverables
- A field ready device for high-throughput measurement of plant N status.
- A data platform linked to the device for estimation of BNF status in the crop, through the combination of genomics, bioinformatics and phenomics.

Expected benefits
- Reduced greenhouse gas emissions. Resilient and sustainable food systems: Temporal and spatial quantification of BNF will provide information for precision agriculture. BNF-improved cultivars.
- Novel nature-based solutions: Enable new research and development for sectors that otherwise have not experienced gain due to high cost and long-term nature of current BNF estimation. Create knowledge to enable more informed approaches to monitoring N status in crops.

Methodologies, Technologies and Data
This project addresses the questions:
- Can levels of BNF-derived metabolites in legume shoots be used as a surrogate to develop a sensor fusion system that measures net N fixation activity in root nodules?.
- Perform a genomics-metabolomics profile from controlled experiments to target Amides/Ureides and novel BNF-associated compounds. We will test if pattern recognition methods of artificial intelligence (AI) will enable a combined analysis of both data-spaces (hyperspectral imaging, Raman spectroscopy and machine vision) and connect these 'fingerprints' with BNF indicators Ureides/Amides and Isotope 15N. Sequencing of candidate genes associated with target metabolites for expression studies.

Integrated GE3LS
Legumes are important and the development of BNF-guided cropping systems enable sustainable N use. The benefits of enhanced N fixation would be perceived across all sectors of farming and a business case has been conducted for the device. However, an adoption and practice change from farming organizations will be conducted with the help of a social scientist (sensitivity analysis). This project will generate knowledge to drive conservation efforts with native legumes, with implications of native species enhancing productivity and sustainability of cropping systems (life cycle analysis). Data ownership and data management will also be analyzed by a social scientist.

Project #19507

Omics to close the loop: optimized amendment from local agrifood-waste for carbon footprint reduction

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Keywords for Proposed Investigation

Research	Methods & Technologies
Urban agriculture, Food waste, Organic fertilizer, Circular economy	Shotgun metagenomic, Phenotype microarray, Precision phenotyping, Environmental DNA

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Social Acceptability, Market and product development, Nature based climate solutions, Scalability of short circuit circular economy clusters	Stakeholder semi structured interviews, Life cycle analysis, Market opportunity assessment, Monetary valuation framework

Project Information

Conventional agriculture impacts the environment through synthetic fertilizers and pesticides use, methane and nitrous oxide emissions from livestock farming, uncontrolled decomposition of organic matter and fossil fuel consumption for crop production and transportation. Through a network of urban farmers relying on a circular economy to upcycle waste into value-added food and fertilizers, while reducing GHG emissions, we aim to exploit omics technologies to enhance production methods for better plants, livestock and societal health. The main objectives of this project are: Characterizing the transformation of organic inputs and the associated microbial diversity within four models of living bioreactors which rely on different biota and operational parameters (system enclosure, pH, temperature):

- Aerobic thermophilic composting with a diverse bacterial and fungal microbiota,
- Entotechnologies in which insects and their associated microbiota transform organic waste in high quality proteins; and
- Myciculture where cultivable fungi decompose organic matter and yield nutritious food.

Through a combined microbiomics (abundance, diversity, structure and persistence of bacterial and fungal communities) and phenomics approach (fertilizing and/or bio-stimulating power), characterizing the fertilizing by-products of each reactor system (a. compost, b. insect manure, c. spent mycelia) upon use in three representative farming contexts (fruits, vegetable and lignaceous biomass plant production).

Deliverables and Expected Benefits
The project meets the program's objectives to adapt farming to reduce CO2 emission and agrochemical inputs impacts. We propose to develop marketable technologies based on optimal and impactful reuse of waste generated by urban agricultural businesses. We anticipate several deliverables transferable for scaling up in rural areas:
- Development of omics-based prediction tool to enable farmer to properly direct waste to the optimal bioreactor;
- Isolation of microbial consortia of interest in waste pre-treatment and fertilizing amendments;
- Optimization of application protocols for specific needs by phenotyping at the farmers' sites for the co-development of reference guides.

Methodologies, Technologies and Data
Microbial communities will be investigated along the different transformation processes that will be compared. To appreciate the scalability of developed technologies, experiments will be conducted in a) controlled environment settings and b) pilot settings in collaboration with a large cluster of businesses already operating using the circular economy approach described. Both ITS, 16S sequencing and WGS will be performed to obtain an accurate functional picture and narrow down high value features and processes. MiSeq and NovaSeq platforms will be used to generate datasets that will be individually processed in R, and crossed with chemical, fitness and phenomics data.

Integrated GE3LS
The life cycle analysis approach can help to quantify the environmental impacts, including GHG emissions associated with the different bioreactors, as well as savings from conventional product substitution. The LCA will be complemented through internalizing the value of ecosystemic services provided by the real-life circular urban agriculture clusters (e.g. carbon capture in plants and sequestration in soil) and translating the impact and services values in economic costs. We will evaluate business feasibility, acceptability potential and return on investment of the individual nodes within the modeled circular urban farming cluster and model the impact of expanding this system across Canada.

Project #19508

AgroMicrobCan: a toolkit to identify microbial alternatives to pesticides

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Keywords for Proposed Investigation

Research	Methods & Technologies
Metagenomics, Biopesticides, Biostimulants, Functional modules	Illumina sequencing, Metabolomics, Genomics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Social acceptance, Economic impact, Climate change mitigation	Life cycle analysis, Modelling

Project Information
Since the effects of the green revolution and climate change became evident, scientists have been trying to identify how to reduce the excessive use of chemicals in agriculture. The use of microorganisms has been an alternative for the control of pathogens, insects, and fertilizers. But why don't we have more microorganism that can be used in agriculture? The challenges are many, starting from the difficulties that face an accurate identification of microorganisms with great potential as biocontrol and biostimulant agents, and ending with the economic challenges and social acceptance. The main objective of this project is to develop an omics-based toolkit to identify and functionally characterize biocontrol and biostimulant agents as alternative to the excessive use of pesticides, insecticides, fertilizers, and water in Canada, mitigating the carbon footprint of our food systems. For that our project will focus on the following objectives:
1. To identify functional and taxonomic modules characteristic of microorganisms with biocontrol/biostimulant potentialities through data mining;
2. To characterize microbial communities in the entomosphere, phyllosphere and rhizosphere across all of Canada;
3. To identify functional and taxonomic modules the microbial communities; and
4. To isolate microorganisms with biocontrol/biostimulant potentialities and to evaluate the potentialities of synthetic communities.

Deliverables and Expected Benefits
The expected deliverables from the project are:
1. Omics-based toolkit for the identification and characterization of microorganisms with high potentialities as biocontrol and/or biostimulant agents.
2. Metagenomic data of microbial communities in the entomosphere, phyllosphere and rhizosphere of canola and soybean fields across all Canada.
3. Metabolomic data of synthetic microbial communities with biocontrol and/or biostimulant potentialities.

4. Validated biocontrol and/or biostimulant agents.

The main impact of these deliverables will be the mitigation of climate change, the reduction of the carbon footprint of Canada's food systems, and the economic resilience of extensive agriculture, with special focus on canola and soybean production.

Methodologies, Technologies and Data
Genomics and metabolomics are the main technologies that will ensure the achievement of the deliverables in this project. We plan to start the identification of functional and taxonomic modules signature of biocontrol and/or biostimulant agents in microbial communities through data mining of genomic information freely available in data bases. In parallel, microbial communities in the "entomosphere", phyllosphere and rhizosphere of canola and soybean fields across all Canada will be characterized through metagenomics, identifying those microorganisms with biocontrol and/or biostimulant potentialities. Finally, combining classic microbiology and metabolomics we will be able to characterize and validate microbes or synthetic communities of interest.

Integrated GE3LS
Our GE3LS research will be key for the implementation of our omics-based toolkit. In Canada, several provinces are setting very ambitious goals regarding the reduction or even banning of several chemicals that strongly contribute to carbon footprint of Canada's food systems, reason why to find sustainable alternatives is essential. Through a life cycle analysis, we will evaluate how the use of biocontrol and biostimulant agents can mitigate climate change, while interviews and a socioeconomic characterization of the user sector, will allow us to know the probable acceptance of our toolkit and the best strategies for its commercialization and implementation.

Project #19509
OGINJI – Optimization of Genotype to Implement a New Juniper Industry

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Keywords for Proposed Investigation

Research	Methods & Technologies
Agroforestry, Microbiome, Climate adaptation, Juniper	Metabolomics, Genomics, Agricultural production, Marker-assisted selection

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Proximity agriculture, Market opportunity, Consumers demand, Willingness to pay	Surveys, Focus groups, Discrete choice modelling, Cost-benefit analysis

Project Information
Gin producers in Canada mainly rely on importation of juniper berries for production while the common juniper (Juniperus communis) is a native and widely distributed species in Canada that could be used as a local source of cones. However, this source is underused presently, and we know little about its variation in critical metabolites for gin production and other usages and whether there are regionally-adapted genotypes in Canada. This project aims to 1) describe the variation in key flavors (both in terms of quantity and quantities) for the common juniper that is pertinent for gin production across its distribution in Canada, 2) whether there is local adaptation in the common juniper and identify markers associated with local genotypes of specific climates, and 3) predict which genotypes will be better adapted for specific regions with regards to the future climatic conditions in terms of gin quality and productivity. This project will help develop a local agriculture of Juniper with unique attributes and will contribute to reducing the carbon footprint of gin production. Moreover, by identifying the best genotypes for the future climate at a local scale, we will contribute to developing a resilient and sustainable industry.

Deliverables and Expected Benefits
Identify the optimal genotypes to use across diverse geographic and climatic regions, focused on the Province of Quebec but adaptable to the rest of Canada.   Propose a production for lands that might otherwise be difficult for conventional agricultural production to maximize carbon sequestration. Juniper production uses perennial shrubs, we will also evaluate the environmental benefits in terms of soil stabilization, biodiversity, soil organic matter and overall carbon mass balance (including shorter supply chain). We expect to help implement an agroforestry industry to locally produce juniper cones that can then be used for microdistilleries producing gin and for other specialized markets.

Methodologies, Technologies and Data
Common junipers from various regions of Quebec and Canada will be harvested. Their cones will be studied for their metabolite contents using metabolomics. Plants will be genopyted (sequencing of reduced representation genome libraries) to predict their adaptability based on trait-genotype associations, which will be used to predict which genotypes are best fitted to the different regions. Genotyping will also help to predict which genotypes are likely to have the best flavour attributes for gin production or for other usages (food transformation, essential oils or nutraceuticals).

Integrated GE3LS
The GE3LS objectives will measure the socio-economic impacts of a proximity agriculture for juniper and propose some genotype selection and supply system. We will analyze the capacities and constraints for agricultural producers and distillers, the consumer demand for local products and finally, we will perform an economic analysis to evaluate the ins and outs of such an approach. The integrated GE3LS sections will be divided into four sections:

1. Assessing stakeholders' perceptions and potential barriers to local juniper production,
2. Social demand for local products,
3. Cost-benefit and cost-effectiveness analysis,
4. Implementing a genotype selection tool.

Project #19510
Mitigation of dairy milk production climate impact

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Keywords for Proposed Investigation

Research	Methods & Technologies
Footprint, Mitigation, Climate, Dairy Cow	Management, Genetic, Eipgenetic, Bioinformatics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Social acceptance, Animal welfare, Economic value, Relevance	Surveys, Expert analysis, Data analysis, Economics

Project Information
A reduction of the number of dairy cows is a key component to climate change mitigation. Climate change affect the productivity of dairy cows through a direct and a transgenerational epigenetic phenomenon associated with heat stress. Indeed, a combination of high ambient temperature/humidity experienced during late gestation can result in 1) lower performance during the subsequent lactation, 2) reduced daughter's lifespan and milk performance over at least three lactations and 2 generations. To address this problem, strategies that could mitigate heat-stress related impacts must be developed and compared. For instance, the direct reduction of the ambient temperature/humidity during late pregnancy, the identification of genomic markers associated with either the susceptibility and epigenetic markers associated with the phenotype are essentials tools to understand and mitigate the consequences of climate change on the animal productivity and longevity. This project is an essential step to reduce greenhouse gas emission by reducing the number of cows raised on-farm per year. This project will combine Canadian specific expertise in cow's heat stress and economic consequences (Ouellet), genetic (Schenkel), epigenetic (Sirard), animal welfare (Dallaire) modeling- management (Santschi/Miglior) to demonstrate the economic value of the heat stress mitigation effect on production, longevity and GHG/CH4 generation.

Deliverables and Expected Benefits
- A factual analysis of the effects of heat stress on dairy cows' productivity (production and reproduction) and longevity, to demonstrate the value of the mitigation proposed
- Genetic markers associated with heat stress susceptibility and a genomic integration plan for selection plan to increase animal resilience
- An epigenetic tool to identify the affected animals and to measure the value of mitigation measures
- A management/welfare analysis to ensure the mitigation benefits the animals
- A management plan for milk producers to reduce the consequences of heat stress

Methodologies, Technologies and Data
- Assess the prevalence and cost of heat stress in Canadian dairy farms using the unique value of Lactanet data set. Calculations will include effects of the dam and her offspring.
- Use genetic analysis related to observed phenotype to identify gene susceptibility for both production and longevity/fertility traits.
- Identify the epigenetic process at play during the heat effect on the mother and the future daughter to identify affected animals and provide management tools to reduce the overall footprint of dairy production.
- Integrate the information of prevention/detection/selection/welfare/mitigation into management of dairy farming using the DairyGen-Lactanet network already in place

Integrated GE3LS
According to OCDE, the world milk production is projected to grow at 1.6% p.a. over the projection period (to 997 Mt by 2029, faster than most other main agricultural commodities) https://www.oecd-ilibrary.org/). In this context, solutions must be found and validated to reduce the carbon footprint of the dairy operation while increasing production. To apply possible solution, it is important to demonstrate the effectiveness of them on using an economical and managerial perspective while covering animal ethics issues associated with welfare and the actual decreased longevity created by the heat stress across generations.

Genomics of potato wild relatives: expanding the gene pool for climate-smart agriculture

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Keywords for Proposed Investigation

Research	Methods & Technologies
Reduced greenhouse gas emissions, Low input of N and pesticides, Potato varieties, Potato breeding with wild relatives	Genome sequencing, High throughput-genotyping, Wild species introgression potato breeding, Omics for phenotyping low N tolerance and disease and pest resistance

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Environmental history of potato production, History and current problems of food and energy systems in North America, Environmental impact of new potato varieties	Digital humanities, GIS, Life cycle analysis of potato varieties

Project Information
Potato is the fourth largest food crop globally. Production requires regular application of nitrogen (N) fertilizer and chemicals to control pests and pathogens to reach profitable yields. However, inputs are a growing cost for growers, an environmental risk, and they contribute to carbon emissions in both synthesis and application. Additionally, N fertilizer use affects soil microbial processes leading to emission of nitrous oxide, a greenhouse gas 300 times more potent than carbon dioxide. A strategy to reduce greenhouse gas emissions for potato production needs to include breeding of improved varieties with traits that reduce reliance on chemical inputs, particularly N fertilizer. Potato is a cold climate crop and development of cultivation in Canada's North can address food security issues while mitigating greenhouse gas emissions in food transport. To meet these goals, breeding new potato varieties with suitability for Indigenous food use as well as agronomic traits is required for production in the North. Potato has a large number of intercrossing wild relatives, which are rich gene resources for breeding. The project will develop genomics tools to enhance use of wild relatives for breeding potato for traits that will reduce greenhouse gas emissions and enhance food security in Canada's North.

Deliverables and Expected Benefits
The project will deliver new genomics-based technologies that will enhance capabilities to utilize wild relatives in potato breeding. These tools will be used for selecting wild species with capacity for crossing with domesticated potato as well as traits that can reduce potato dependency on N fertilizer and increase pathogen and pest resistance. Additionally, selection strategies to enhance adoption of potato cultivation in the North will also be

developed. Benefits will be a potato production system with reduced greenhouse gas emissions and environmental footprint and development of potato-based food strategies for addressing food security in Canada's North.

Methodologies, Technologies and Data
The project will utilize the pan-genome for potato and wild relatives previously developed by the co-leads. Application of graph pan-genome approaches to genotyping multiple classes of genetic variation including SNPs, indels and structural variation will be developed. Additionally, genome-wide transposable elements (TE) analysis will be developed for genotyping. Species hybridization barriers, including endosperm and polyploidy, will also be studied using genome-wide approaches to develop improved strategies to cross pollinate wild species with potato. Whole genome, transcriptomes and methylomes of wild species and potato data sets will be generated. Data sets will also be generated on transposable elements and sequence variation.

Integrated GE3LS
A comprehensive framework to evaluate the impact of the new varieties and related practices on environmental costs and benefits, with a focus on mitigating greenhouse gas emissions throughout the potato value-chain will be developed using the life-cycle-analysis (LCA) approach. Main potato-producing provinces (PEI, NB, QC, ON, MB and AB) and Northern potato production in NWT and Yukon will be examined. Potato breeding involves long term investment of resources to address priorities for industrial food production as well as environmental sustainability and reduction of greenhouse emissions. Analysis of how priorities are established will be done through a historical perspective.

Project #19512

Eco-Shell-Fish: Eco-responsible exploitation and management of food marine resources

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Keywords for Proposed Investigation

Research	Methods & Technologies
Marine food resource, Pathogens, Carbon sequestration, Global climate change	(Epi)genomic methods, Metabarcoding, Microalgae labelling, Liquid biopsy

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Perception, Acceptance, Implementation, Knowledge transfer	Discourse analysis, Cost-benefit models, Decision trees, Communication tools

Project Information
Objective 1. Bivalves play a role in carbon sequestration through carbon incorporation in their shells. They also accumulate other nutriments, including nitrogen and phosphorus. We propose a novel and powerful approach to develop efficient tools evaluating this sequestration potential while at the same time enhancing food production and ecological services.

Objective 2. Climate changes modify the prevalence and virulence of various pathogens present in the marine environment and in food products with different impacts on both marine organisms and their consumers. To mitigate potential negative impact of imbalance between food products and marine environmental pathogens, we will take advantage of the most recent genomic tools to improve pathogens identification and our understanding of their effects on resources microbiomes. With these tools and knowledge, best management practices could be suggested to industry.

Objective 3. All life forms across the globe are experiencing drastic changes as a result of Global Climate Change. This incurs substantial economic costs and threats to exploited marine biodiversity including in the St. Lawrence system which sustain Canadian eastern fisheries. Maintain of future sustainability fisheries will depend on new genomic tools to predict and manage adequately the future of exploited species and to ensure economically resilient activities.

Deliverables and Expected Benefits
Our deliverables will notably allow 1) The selection of bivalve strains of interest for eco-responsible production; 2) Healthier bivalve production with regards to pathogens and human health; 3) The development of new evaluation tools for the ecosystem-based fisheries management; 4) A better acceptance and understanding of improvements generated through genomic approaches. Along with GE3LS initiatives, these deliverables will

target the following objectives of the initiative: 1) "Enhance carbon sequestration to improve performance, mitigate climate impacts and support healthy system" and 2) "Build resilient, sustainable food systems that reduce environmental impacts and greenhouse gas emission".

Methodologies, Technologies and Data
Combination of microalgae labelling with stable isotopes (15N, 13C 2H) and genomics (whole (epi)genome sequencing, transcriptomics) allowing the evaluation of the sequestration potential while at the same time coupling food production and ecological services. Development of novel predictive biomarkers that exploit the concept of liquid biopsy, a rapidly gaining ground in the biomedical area.   The development of state-of-the-art (epi)genomic methods and metabarcoding that will allow monitoring and predict how marine communities and in particular key marine species may cope with GCC (phenotypically plasticity or range shifts) for the best management practices of fisheries and aquaculture.

Integrated GE3LS
The industry is already facing scientific, social, and industrial model organization uncertainty related to GCC. Working with social sciences scientists, we will develop tools to evaluate perceptions/acceptance/implementation of genomic approaches and how new information these tools will provide may modify resource exploitation models to decrease environmental impacts and green house emissions.   We will consolidate our current partnerships while developing new ones with both governmental and industrial organizations, taking advantage of our long-standing history of intersectoral approaches and we will establish an integrated knowledge transfer strategy to efficiently transfer our deliverables to end users.

Meta-twin: A metagenomic driven digital twin for environmentally sustainable forage systems

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Keywords for Proposed Investigation

Research	Methods & Technologies
Soil health, Silage, Greenhouse gas, Metagenomic	Digital twin, Artificial intelligence, Sequencing, GHG modeling

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
User experience, Decision support tool, Legal practice, Return of investment	Survey, Literature reviews, UX evaluation, Profitability

Project Information
At least 40% of GHG emissions from milk production are the result of forage production including N2O emissions, loss of organic matter from the soil, production of CO_2 from silage spoilage and fuel consumption in harvesting. Forage production is complex to manage because it integrates multiple systems (soil, plants, harvesting, conservation and feeding the animals), lasts over long periods of time and is affected by multiple agronomic, environmental and economic factors. To improve the sustainability of forage production and significantly reduce GHG emissions from dairy production, Canadian dairy farmers need to address two challenges: 1) Integration of the entire system from the soil to the cow for holistic management and 2) Simulated decision-making process for facilitating the adoption of better management practices. Within the framework of this project, we will respond to these two challenges by 1) Developing decision support tools integrating the soil to the plant and the silage functionality derived from metagenomics that will improve simulations for the entire system and reduce uncertainty and 2) Integrating the metagenomic driven decision tool inside a digital twin allowing producers to obtain recommendations and prescriptions adapted specifically to his/her farm resulting in more resilient, profitable and environmentally sustainable agriculture.

Deliverables and Expected Benefits
Deliverables
1. Metagenomic functionality indicators derived from soil, fresh forage and silage
2. Interpretable machine learning engine which can simulate different interactions (soil to plant, plant to soil, plant to silage & silage to cow) with data collected, scalable for all of Canada.
3. Digital twin integrating those different models for optimizing forage management practices and reducing GHG emissions, profitability and herd performance and health.

Expected benefits
1. Decision support tool integrating metagenomic functionality indicators with forage management
2. Easier and better management of forage systems allowing the producer to reduce the risks of making decisions for aiming GHG reduction.

Methodologies, Technologies and Data
- The data collection on 50 dairy farms for a period of 2 years o Soil, forage and silage microbiome using 16S and ITS amplicon MiSeq, QIIME DADA2 and PICRUSt2 pipelines. Then metagenomic functional indicators will be generated.
    o Soil parameters
    o Agronomic practices
    o Forage yield and quality
    o Silage quality
    o Herd performance and health records
    o Farm costs of production
- All data will be integrated in simulations for modelling the following relationships: soil to plant, plant to soil, plant to silage & silage to cow with the following machine learning techniques (Active Learning and Causal inference approaches)

Integrated GE3LS
-Evaluation of the GHG emissions of different simulations or practices with Holos model and extra missing modules on GHG of silage dry matter loss and farm equipment use. -Evaluation of the profitability of different practices at the farm level. -Evaluation of user experience criteria required and crucial for the use of the decision support tool and genomic engine with a user experience evaluation. -Evaluation of the legality of the decision support tool to provide diagnostics and prescriptions to producers without the agronomist or veterinarian and being use byagronomists and veterinarians.

Project #19601

Land and Sea: Bras d'Or Lakes carbon sequestration impacts on food security

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Keywords for Proposed Investigation

Research	Methods & Technologies
Climate change, food security, carbon sequestration	eDNA, oyster breeding

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Wild pollinators, oysters, biodiversity, engagement	eDNA, shellfish hatchery, meetings

Project Information

This research aims to reduce greenhouse gas emissions and decrease the carbon footprint of those who live in the Bras d'Or Lake area by utilizing genomics tools to increase local food production (food security), reduce transportation emissions to acquire food, and increase carbon sequestration through plant and shellfish production in and around the Bras d'Or Lake.   Genomics tools such as eDNA will help understand the diversity of plants and animals in and around the Bras d'Or Lake as well as variants within those populations; brood stock management practices driven by genomics will provide for increased shellfish production and carbon sequestration. Along with knowledge Traditional Ecological Knowledge holders from Indigenous and non-Indigenous communities, genomics tools will help to develop a better understanding of differences in those organisms from various locations around the Bras d'Or Lake where sub-species or variants may better perform that ecosystem services thus better utilizing their capacity for increased crop and shellfish production. These two focus areas will help to create sustainable, local, food production that will reduce greenhouse gas emissions and increase the carbon sequestration capacity of the area. Developing this capacity within local communities is of paramount importance as we strengthen our partnerships for research together.

Deliverables and Expected Benefits
- Establish knowledge of organisms in and around the Bras d'Or Lake and terrestrial ecosystems to understand ways to reduce green house gas emissions from local food production/acquisition and increase food security. This could be applied to other areas of Canada
- Establish baseline data against which future monitoring can be gauged against, both TEK and genomics changes.
- Increase populations of organisms that sequester carbon

- Engage local communities, Indigenous and non-Indigenous, as active participants given their knowledge and deep cultural connection to the land and water to provide a model that could be used in other Indigenous communities

Methodologies, Technologies and Data
- Standard field sampling methodologies, microscopic analysis, statistical analysis
- Genomics tools such as PCR, eDNA, barcoding, DNA sequencing to determine species and variants among local pollinators for increased crop production
- Genomics tools for artificial selection through oyster hatchery breeding protocols for disease resistance, meat/shell production, and survivability of larvae
- Data sets created include those generated from pollinators, oysters, and additional sets as determined by community
- Datasets will be publicly available.

Integrated GE3LS
- How do changes recognized by TEK correspond to changes detected using genomics tools?
- How do Indigenous and non-Indigenous communities wish to learn/use genomics tools to decrease their carbon foot print and increase food security?
- What are effective means to better engage communities on research project of this nature?
- How can genomics tools better assist Indigenous communities on the path of self-determination?
- What role can genomics tools assist Indigenous and rural communities with rural economic development?

These questions are best addressed by focused, in-community discussions led by local partners who work with us regularly in the research arena.

Project #19602
Genomic Research for Algae-based Aquaculture Diets (GRAAD)

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Keywords for Proposed Investigation

Research	Methods & Technologies
Aquaculture, algae, circular food system, salmon	Bioprospecting, lipidomics, microbiomics, transcriptomics

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Carbon sequestration, consumer acceptance, circular aquaculture, decarbonization	Mathematical modelling, market research, consumer surveys

Project Information
Algae in the ocean has incredible potential for sequestering carbon from greenhouse gas emissions. Algae (microalgae and seaweeds) have recently taken on more relevance in aquaculture and the Canadian marketplace. Algae have huge health/nutritional benefits, as nutraceuticals for consumers, but also for livestock and aquaculture nutrition. They are an important part of a circular food system for the future. 'Blue foods' have the lowest carbon footprint compared to any other form of animal agriculture. Given that climate change will have extreme demands on our food system, blue foods have the most potential for keeping up with food security. Aquaculture is a major source of Canadian seafood production and exports, with Atlantic salmon being the largest in quantity and value. Climate change, disease, and sustainability are threats/challenges to salmon production. Nutrition is an important solution to combat health and disease issues in farmed salmon. The nutritive components in algae are a solution to these threats by improving salmon growth, immunity, and product quality. Functional genomics are urgently needed in this space to 1) understand and improve the carbon sequestration power of algae, and 2) use algae as supplements for salmon to improve sustainable production and combat stress/disease related to climate change.

Deliverables and Expected Benefits
This work will bio-prospect, grow, and test novel microalgae and seaweeds as nutritive and functional ingredients for farmed fish health and growth by using a multi-omics approach to determine their efficacy in aquaculture. The resulting microalgae and seaweeds can be commercialized and marketed as nutritive and bioactive substances that can improve salmon aquaculture sustainability, particularly under environmental stress and disease. The benefits include:
1. valuable carbon sequestration by algal products and commercial opportunity for novel algal production,
2. circular-based farmed salmon production (via use of dietary algae),
3. healthful, nutritionally fortified salmon products for Canadians.

Methodologies, Technologies and Data
The primary innovation of this proposal is to develop novel algae that have ideal characteristics for commercial production and aquaculture feeds. We will achieve this by first bioprospecting new algal species that have unique properties and characteristics that benefit commercial production and aquaculture. Genomics tools will be used as part of the bioprospecting. Second, a multi-omics approach will allow us to measure fish metabolism and the immune response to develop solutions to adapt to the challenges faced in the salmon aquaculture industry. The multi-omics data generated from the project will be published and made publicly available.

Integrated GE3LS
The GELS component will address two key areas. First, we will calculate the carbon sequestration opportunity from industry-grown algae in short- and long-term estimates and estimate decarbonization in salmon aquaculture by adopting a circular-based feed using algae. Second, we will assess consumer understanding and acceptance of 1) marketplace-ready microalgae and seaweed products, 2) circularity in aquaculture food systems, and 3) consuming salmon that were raised on feeds that include microalgae and seaweed products.

Project #19603

Multi-locational Assessment of C sequestration potential of microbiomes under different tillage and cropping systems in Canada

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Keywords for Proposed Investigation

Research	Methods & Technologies
Carbon sequestration, Agricultural tillage systems, microbiome function, cover crops	Amplicon and whole genome sequencing, soil chemical/physical/biological parameters, crop rotation, tillage

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Sustainability of crop production, cost efficient agriculture, global warming, soil biodiversity	Stockholder surveys, GHG emission, microbial diversity

Project Information

Soil is the largest sink of the atmospheric carbon taken in by plants during photosynthesis. Carbon sequestration in the agricultural system is crucial in prevention of the danger of climate change. In order to improve crop yield, farmers often incorporated tillage which distorts the soil structure promoting release of large amounts of carbon to atmosphere and therefore aggravating trend of global warming. About 110 billion metric tons of carbon have been released from the top layer of soil in the past 12,000 years due to the expansion of farmland. Microorganisms are known to play a significant role in soil nutrient chemistry, biogeochemical cycles, and overall soil health. However, little is known about the potential of microorganisms to serve as indicators for synergistic carbon sequestration in agricultural soils. In this research we will evaluate microbial communities associated with agricultural soils across Canada under maximum, minimum and zero tillage with different leguminous cover cropping systems. We will evaluate the microbiome response to agricultural practises and correlate it to soil physical/chemical parameters and carbon emission levels to identify key microbial taxa involved in carbon sequestration. We will also assess the agricultural and environmental factors influencing prevalence of these taxa in soil.

Deliverables and Expected Benefits

The project is a regenerative initiative that will provide for the first-time ecological diversity relevance of tillage and leguminous cover cropping practices generating comprehensive data on the microbiome distribution and diversity across selected Canadian agricultural farms under different agricultural practises. Furthermore, this research project will provide an insight into the best agricultural system that offers a high level of carbon sequestration with optimal retention and agronomic productivity as well as deliver the tools to employ microbiomes into efficient carbon sequestration. In general, this will lead to the adoption of a negative-emission technology in Canada and beyond, especially for cold climates.

Methodologies, Technologies and Data
The effect of cover crops such as legumes and grasses will be tested. The list of cover crops will be defined after consultations with stakeholders. Soil physico-chemical and biological parameters, such as soil C, phosphates, nitrogen and enzymes will be evaluated. The soil microbiome will be evaluated using 16S and 18S rRNA and ITS short reads (Illumina MiSeq 2x300 bp PE) and full-length (PacBio Sequel2) amplicon sequencing, as well as metagenome (whole genome) sequencing (NextSeq 2x150 bp PE) and analysed using standard bioinformatic approaches. Raw sequence data will be deposited to NCBI. There will be farmers' survey and workshop outreach.

Integrated GE3LS
This research will use of the input from stakeholders to identify agricultural systems (cover/follow crops), which are under the most need for the ecological assessments. The outcomes of this research will provide new directions to improve sustainability of crop production across Canada, resulting in decreased of green-house gas emission. The application of the results of this research could also improve crop yield and quality and provide cost efficient ways for crop production.

Project #19604

Selection of cleaner-fish broodstock that are resistant to bacterial infectious diseases, thermotolerant, have enhanced immunity following immunization, and perform well when reared on a carbon-neutral diet.

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Keywords for Proposed Investigation

Research	Methods & Technologies
Resilient and sustainable aquaculture-food systems; effective immunization of disease and thermo-tolerant broodstock to prevent diseases and mortalities; carbon-neutral food production using photosynthetic microbes	Genomics, transcriptomics, immunology, genetic engineering

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
What are the legal implications for utilization of selected fish for Atlantic Canada? What is the importance of cultivation and utilization of an endangered (listed) fish species of conservation concern? What are the most critical aspects to address regarding the carbon footprint of aquaculture?	Literature review, surveys and interviews, workshops, data analysis

Project Information
Sea-lice infestations at Atlantic Canada aquaculture sites can be controlled utilizing lumpfish (Cyclopterus lumpus) as cleaner-fish. Indeed, lumpfish production has emerged as a major priority in the aquaculture sector. The use of cleaner-fish is particularly attractive as they are very effective at delousing, and this eliminates the need for chemotherapeutants and stressful technologies. However, climate change, susceptibility to diseases, lack of effective vaccines, and mortalities due to high temperatures are major challenges facing the use of cleaner-fish. We will select lumpfish broodstocks that are resistant to pathogens and thermotolerant, and evaluate vaccines and the use of carbon-neutral diets under controlled and field conditions. To accomplish this, we will sequence the genome and profile the transcriptome of: i) vaccinated and non-vaccinated pathogen-resistant lumpfish as compared to susceptible-fish; ii) vaccinated and non-vaccinated thermotolerant lumpfish vs. intolerant-fish; iii) selected vaccinated fish fed with a microbial (cyanobacteria)-based diet vs. those fed typical diets; and iv) selected vaccinated lumpfish that survive in commercial conditions. This research will greatly enhance the effectiveness of lumpfish as cleaner-fish, improve their health/welfare, provide novel data on whether microbial-based diets can/may

reduce the carbon footprint of salmon aquaculture, and ensure this industry's resiliency and economic and environmental sustainability.

Deliverables and Expected Benefits
The proposed research will: 1) identify bacterial-resistant, vaccine-responsive and thermotolerant lumpfish broodstocks; 2) develop a polyvalent vaccine(s) that protect lumpfish from local and potentially emergent pathogens; 3) develop an aquafeed based on a cyanobacteria strain optimized for its fatty-acid profile and that sequesters CO_2. These pathogens resistant and thermotolerant lumpfish will allow the industry to prolong the use of these fish for delousing; provide the industry with fish optimized for Atlantic Canada; and provide biomass for value-added by-products. Importantly, this research will also evaluate whether a novel feed ingredient (cyanobacteria) can be used to greatly decrease this sector's carbon footprint.

Methodologies, Technologies and Data
Chromium and PacBio sequencing technologies will be used to sequence the genome of male and female lumpfish broodstocks that are pathogen-resistant and thermotolerant, as compared to susceptible lumpfish. Assembly and annotation will be conducted at Compute Canada using bioinformatic tools. SNPs also will be identified. A cyanobacteria strain used for carbon-capturing will be genetically engineered to develop a diet that enhances lumpfish health. RNA-seq will be conducted using nova-seq-Illumina on resistant-thermotolerant and susceptible fish under different treatments. Fish for genomic/transcriptomics analyses will be selected based on their physiology, genetics, and immunity. Multivariate statistical techniques will be utilized for comparative studies.

Integrated GE3LS
Here, we will explore the following questions: What are the legal aspects of using selected pathogen resistant-thermotolerant fish in Atlantic Canada? What is the importance of the cultivation and utilization of an endangered/listed fish species with regard to conservation and marine biodiversity? What are the most critical factors that must be addressed with regard to reducing the carbon footprint of salmon aquaculture? We will conduct a full/comprehensive literature review and engage with academic, government, aquaculture industry and social scientists, and NGO's, to answer these questions. Surveys, meetings and workshops will allow us to produce a white paper answering these questions.

Project #19605
Accelerating adaptation of Northern cropping systems-North4Food

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Co-lead Genome Centre(s): Genome Prairie

Keywords for Proposed Investigation

Research	Methods & Technologies
Phytobiomes, adaptive diversity, soil carbon sequestration, crop productivity	Soil and plant metagenomics, soil biogeochemistry, agricultural systems, integrated data science

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
Cropping systems resilience, economic viability, soil health/environmental health/human health, policy implications	Rapid needs assessments, design-based implementation research, good food principles: FLEdGE (Food: Locally embedded, Globally Engaged)

Project Information
Knowledge that plants' adaptive properties are supported by microbial species that live with and within plants is rapidly accumulating but focused on crops with climatic and soil conditions not necessarily transferrable to boreal regions. We address the gap in our understanding of boreal phytobiomes (i.e., microbial community associated with a plant both internally and externally) and generate tools that facilitate utilization of plant microbiomes for adaptation of crops to boreal growing conditions. We will develop a nationally consistent, locally relevant, approach to data collection and verification for understanding the composition and function of locally relevant phytobiomes. This involves an understanding of plant species and landraces, associated endophytes and the larger microbial communities with which they interact. This information will be employed to develop flexible, locally adaptable tools for crop adaptation through leveraging local, native microbiomes employing multiple discovery pathways: in-vitro, controlled conditions and in-situ. The goal is to develop genomic tools to support fast, cheap and easy to implement techniques for leveraging local microbiomes functionalities. Central to this is ensuring resilience (elasticity of targeted agro-ecosystems to buffer for unpredictable deteriorations in growth conditions) and sustainability (verify and propose biological and/or agro-ecological practices that prevent deleterious effects to the local ecosystems).

Deliverables and Expected Benefits
Co-selection and breeding of phytobiomes with the crop through leveraging locally adapted genomic diversity, including a focus on rhizosphere microbiomes, for developing robust, replicable protocols (complete microbiome toolbox) that allows leveraging of local genomic resources for crop production. This will facilitate climate-resilient and environmentally

sustainable cropping systems, including preferred rotations of cereals with legumes. Enhanced nutrient use efficiencies will both mitigate nutrients losses to the environment (i.e., mitigate N emissions) and encourage the uptake of locally adaptable and deployable climate smart practices. Technology verification across the country will support the development of locally relevant, economically viable and socially responsible solutions.

Methodologies, Technologies and Data
Soil to plant microbiome surveys across growth regions; transfer and in-planta selection of inoculated microbiomes via: co-germination, donor-litter to seed transfer, transfer to recipient calli (in-vitro during somatic embryogenesis), in-field bioaugmentation though the use of donor plant litter inocula or co-cultivation protocols (e.g., including hedgerows as donor systems). Verification of the advantages of endemic vs. cosmopolitan recipients. We will develop a database of plant microbiome stability, [plant] inter- and intra-specific, and the stability across plant species and regional specificity [i.e., microbiome biogeography and plant species specificity] across the soil-to-plant continuum.

Integrated GE3LS
A critical risk is that boreal expansion of agriculture occurs in advance of a necessary understanding and thorough assessment of knowledge ensuring that it: 1) supports climate mitigation; 2) is environmentally sustainable; 3) identifies and addresses best cropping options; 4) addresses key elements of food security; 5) considers the concerns, desires, needs, and constraints of local communities. Design-Based Implementation Research principles will guide the research: 1) a focus on persistent problems of practice from multiple stakeholders' perspectives, 2) a commitment to iterative, collaborative design, 3) refining theory and knowledge through practice and implementation and 4) capacity building to sustain change.

Project #19606

Enhancing resilient and sustainable potato production system through climate-smart agriculture practices and next generation genomic technologies

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Keywords for Proposed Investigation

Research	Methods & Technologies
sustainable potato production; carbon emission; potato wart; transcriptomics and bio-surveillance	climate modeling; precision agriculture; gene sequencing; potato wart pathotyping

Keywords for Proposed Integrated GE3LS Investigation

Research Questions	Methods
carbon emission reduction; potato wart control; climate-resilient potato varieties; sustainable potato production	Next Generation Sequencing; bioinformatics toolkit development; pathogenicity mechanisms; multiplex qPCR assays

Project Information

As the third most important food crop in the world, potatoes are facing increasing biotic and abiotic stresses from pests like potato wart to extreme heat and droughts. Current uniform management practices with inadequate attention to spatial soil and crop variations increase both production cost and GHG emissions. Developing climate-smart and sustainable potato production systems is critically important to safeguard global food security and mitigate GHG emissions. To tackle the underlying causes of these negative impacts and provide long term solutions to climate change, an interdisciplinary research team will be established to develop precision agriculture technologies and IoT (Internet of Things) platforms through the integration of genomics-based bio-surveillance technologies to promote sustainable potato production with significant mitigation potential of GHG emissions in the face of climate change. In addition to the development precision agriculture technologies to mitigate climate change, genomic and transcriptomic approaches will be employed to investigate the virulence and disease mechanisms of potato wart and the genomic architecture of potato resistance to ensure food security. By incorporating climate modeling, precision agriculture, and advanced genomic technologies, this project will facilitate the development of climate-smart best management practices to improve farm profitability and mitigate climate change by lowering GHG emissions.

Deliverables and Expected Benefits
- An enhanced bio-surveillance and IoT platform will be established to efficiently monitor potato health and production under regulatory management on potato wart and other biotic and abiotic stresses.
- Significant achievement will be made in understanding the Canadian pathotypes of potato wart and their virulence and pathogenicity mechanisms in selected varieties.
- Develop best management practices through the combination of cover crops, plowing and application pyrolyzed bio-solids applications to improve soil health and mitigate climate change by sequestering carbon.
- Propose a suite of climate smart best management practices to ensure food security and lower GHG emissions in the face of climate change.

Methodologies, Technologies and Data
The research methods and technologies to be used in this project include:
- High-resolution climate models for seasonal climate prediction and long-term climate projection
- Monitoring, quantification, and modelling of GHG emissions under various growing and climatic conditions for major potato varieties with life cycle analysis
- Develop genome-based bio-surveillance system, integrated with remote sensing to explore potato wart pathotyping, virulence, and pathogenicity mechanisms to implement control mechanisms.

The datasets to be generated include:
- High-resolution climate data
- Soil, crop, yield, and GHG emissions data for numerous potato fields.
- Genomic and transcriptomic sequencing datasets for selected potato varieties

Integrated GE3LS
The socio-economic benefits and outcomes of this project will arise from the development of climate smart agriculture technologies to mitigate climate change. It is anticipated that the proposed research will improve the current knowledge base of the potato industry, provide innovative technologies to mitigate climate change through the development and implementation of climate-smart potato production systems, increase potato marketability and supply, and improve socioeconomic conditions in Atlantic Canada. The knowledge generated and the systematic biosurveillance system established from this study will address concerns of the industry and the consumers and may increase their confidence and acceptance in potato products.