



GenomeCanada

July 22, 2021

Backgrounder

Eight Large-Scale Applied Research Projects Funded

Genome Canada announces \$24.4 million in federal support, in addition to a \$1.5M partnership between Genome Canada and Natural Resources Canada (NRCan), for eight large-scale applied research projects in Canada's natural resources and environment sectors. The projects will harness genomics research and technologies for natural resources conservation, environmental protection and sustainability. With co-funding from collaborations with provincial and other federal partners (including NRCan), universities, industry and international partners valued at \$35.4 million, this represents a total investment of nearly \$60 million.

The collective environmental impact of this investment is significant. Together, these eight projects will advance Canada's biodiversity and responsible stewardship of resources, harness biomonitoring to measure changes in living organisms to assess potential hazardous exposure, and apply bioremediation to identify and remove pollutants from water, soil and other environments. Importantly, all of these projects are designed to examine relevant aspects of genomics in society and nearly all also proactively engage Indigenous communities and incorporate Indigenous knowledge systems in their research.

Title: iTrackDNA: Non-Destructive Precision Genomics for Environmental Impact Tracking in a Global Climate Change Era

Academic Leaders: Caren Helbing (University of Victoria), Valérie Langlois (Institut national de la recherche scientifique), Jérôme Dupras (Université du Québec en Outaouais), Louis Bernatchez (Université Laval)

Genome Centres: Genome BC, Génome Québec

Total Funding: \$12,144,227

Canada is a natural resource exporting nation that values its biodiversity, clean water and distinctive ecosystems. This vast nation is at a critical juncture with competing interests between rising societal pressure for environmental sustainability and natural resources development. As a result, natural resource management decisions by Canadian communities, Indigenous peoples, industries and regulators require timely and relevant information regarding risk and impacts of human activities, especially in the context of climate change.

The analysis of environmental DNA (eDNA)—genetic material shed from organisms into their environment—is highly promising as eDNA can provide non-destructive, rapid, cost-effective and accurate biodiversity information. For example, a single scoop of water from a lake can inform the presence of at-risk, invasive, pest, and culturally & economically important animal species. However, considerable variation in data quality and poor understanding of factors affecting eDNA detection have hindered adoption in regulatory policy and natural resource management decision-making.

End-Users (e.g., governments, First Nations, NGOs and industry) are all now calling for methods standardization and accessible eDNA resources to support ecological surveys for species-at-risk monitoring; invasive species management; and granting permits and permissions for energy, mining, forestry, manufacturing and infrastructure projects. The impact is far-reaching. Better monitoring tools could help detect live pinewood nematodes and improve wood treatment efficacy testing facilitating Canadian forest products trade (worth \$33.2 billion in 2019), substantially reduce the cost of managing aquatic invasive species (e.g., \$3.6 billion annually in Ontario alone) through early detection, and protect valuable ecosystems.

The iTrackDNA project will build end-user capacity through innovative, accessible, socially responsible genomics-based analytical eDNA tools for effective decision-making by: 1) supporting the creation of a targeted eDNA detection national standard; 2) building eDNA kits to detect 100 priority invertebrates, fish, amphibians, birds, reptiles and mammals in Canadian coastal and inland ecosystems; 3) applying 10 eRNA kits for determining animal biosurveillance, biosanitation and bioremediation effectiveness; 4) generating decision support software for modeling regional biodiversity changes integrating Indigenous Ecological Knowledge; 5) developing an eDNA training, certification and inter-lab validation framework for consultants, researchers, regulators and managers; and 6) producing a guidance document on eDNA-based methods integration into management, policy and regulations.

By 2025, eDNA will undoubtedly be a mainstream assessment tool as many countries are currently investing in eDNA technology. The iTrackDNA project is poised to help Canadians reach high environmental quality standards and position Canada as an international frontrunner on eDNA standards adoption, policy development and testing.

Title: The Canadian BioGenome Project

Academic Leaders: Steven Jones (BC Cancer Agency), Maribeth Murray (University of Calgary)

Genome Centres: Genome BC, Genome Alberta

Total Funding: \$6,458,996

A genome contains the genetic blueprint of life. Each species possesses its own characteristic genome, shaped by millions of years of evolution allowing each organism to be specifically adapted to its environment. Through the study of these genomes, we can explore the diversity of life, how species interact, and how they create ecosystems. This project represents Canadian participation in the Earth BioGenome Project.

This is an international initiative with the goal of sequencing the genetic material for all complex life on Earth. Canada possesses significant biodiversity having approximately 80,000 plant and animal species, in environments ranging from desert to the arctic. Many of these species are under threat due to rapid changes in climate and other human-led impacts on our environment. In collaboration with scientists, Indigenous peoples and conservation groups, this project will embark on the task of determining the genetic diversity of Canada's plants and animals through genomic sequencing.

Working with our partners we will identify approximately 400 species, where a genome will aid in their conservation and increase our understanding of their underlying biology and

populations. The species we sequence are—or will be—selected based on existing and established priorities of Indigenous peoples, federal and provincial organizations and other conservation and wildlife groups. These groups and organizations have a history of (or a strong interest in) using genomic information to develop tools and solutions for the maintenance of biodiversity, monitoring, conservation, restoration and environmental management. They will immediately make use of the data we provide to develop tools such as genome-wide markers for DNA profiling, breeding, population monitoring, genetic diversity and pathogens. Through a case study approach, we will also work with partners to establish priorities for genomics tool development, policy recommendations for the use of genomics to maintain biodiversity and support conservation and management, and a user-friendly geospatial platform of genomics data and information from the project. The data generated will also be freely available to scientists in Canada and worldwide.

Title: TRIA-FoR: Transformative Risk Assessment and Forest Resilience Using Genomic Tools for the Mountain Pine Beetle Outbreak

Academic Leaders: Janice Cooke (University of Alberta), Catherine Cullingham (Carleton University)

Genome Centres: Genome Alberta, Ontario Genomics

Total Funding: \$6,598,094

The current mountain pine beetle (MPB) epidemic has killed approximately 20 million hectares of mainly lodgepole pine forests in British Columbia and Alberta. Climate change and forest management practices have contributed to unprecedented range expansion of MPB. From its historic range in central British Columbia, MPB has spread through novel habitats in Alberta, establishing in a new host, the jack pine. Jack pine is a boreal forest species with a range that extends to the Atlantic Ocean, raising the spectre of continued eastward spread of MPB. Given the importance of lodgepole and jack pine to the forest industry, their central role in providing ecosystem services and their cultural importance, there is an urgent need to enhance resiliency of forests replacing MPB-killed stands, and to quantify eastward spread risk potential of MPB.

In TRIA-FoR, we will adopt a state-of-the-art multidisciplinary and integrative approach to develop genomics-informed knowledge, tools and application frameworks that mitigate risk for the present MPB epidemic and improve resiliency in future epidemics. Risk and resiliency will be investigated in the context of MPB-pine-climate interactions that affect MPB population dynamics, human dimensions in forest resource management, and impacts on diverse communities connected to forests at risk.

TRIA-FoR research encompasses three overarching goals. (1) Enhance lodgepole pine genetic resiliency to MPB. We will identify gene-based markers that predict MPB resiliency in lodgepole pine and identify traits that contribute to MPB resiliency. To understand how genetic resiliency translates into forest resiliency, we will model the impact of planting MPB-resilient lodgepole pine on outbreaking MPB populations. (2) Improve risk assessment efficacy for MPB northern and eastern spread into the boreal forest by examining MPB – pine host – climate interactions. We will test whether jack pine forests east of Alberta can support MPB populations, or whether expanding populations require immigration from the lodgepole x jack pine hybrid zone. In tandem, we will determine how overwintering temperatures and pine host characteristics in these marginal habitats affect MPB success. (3) Develop a social sciences framework of risk management planning and resilience

building that can facilitate adoption of genomics-informed practices or technologies. We will investigate geographic, sociological, economic and policy aspects of risk related to the MPB epidemic, identifying factors that influence stakeholder willingness to adopt genomics-informed applications. This collaborative cross-scale research will enable a genomics-informed total risk and resilience management approach that can enhance forest health in the face of present and future MPB epidemics.

Title: Application of Genomics to Enhance Wetland Treatment Systems for Remediation of Processed Water in Northern Environments

Academic Leaders: Douglas Muench (University of Calgary), Christine Martineau (Natural Resources Canada)

Genome Centres: Genome Alberta, Génome Québec

Total Funding: \$6,485,607

Constructed wetland treatment systems (CWTS) are one of the very few scalable and cost-effective methods to clean up large volumes of wastewaters. An in-depth understanding of how these nature-based, passive systems operate to treat industrial waste is needed to enhance treatment efficacy, particularly in northern environments that are challenged by short summers and cold winters. In the Athabasca region of northern Alberta, the surface mining of oil sands, while contributing significantly to Canada's gross domestic product and economic development, produces large volumes of oil sands process-affected water (OSPW) that has accumulated on site in tailings ponds (currently exceeding one billion m³). Recent legislation has outlined a reclamation closure timeframe for oil sands operators to restore the landscape. Efficient and large-scale OSPW remediation technologies must be made available to address these challenges.

The presence of organic compounds, in particular a broad family of organic compounds called naphthenic acids (NAs), are major contributors responsible for the toxicity of OSPW. This research project targets the reduction of OSPW toxicity through biodegradation processes involving cooperative processes between naturally occurring microbial communities and wetland plants in CWTS. However, the conditions required to establish optimal wetland biological communities to degrade and detoxify OSPW contaminants are not well understood.

This project will apply genomics-based methods to enhance and inform the efficacy of CWTS for the treatment of OSPW. Using both mesocosm-scale and an in-situ pilot scale CWTS, genomics, microbiological and chemical analyses we will: (1) identify the conditions for enhanced NA biodegradation; (2) increase our understanding of the genes/mechanisms associated with the biodegradation of NAs; (3) develop new genomics-based tools and passive sampler methods to monitor concentrations and toxicity of NAs and other OSPW contaminants; (4) develop models of CWTS treatment of NAs and other OSPW contaminants to optimize the effectiveness of wetland design; and (5) integrate emerging experimental findings with sophisticated social science methods to expand social, legal, economic, and policy frontiers in the treatment and release of OSPW.

Informed by genomics approaches and leveraging the benefits of CWTS, the proposed applied research will provide insight on the mechanisms of plant-microbe interactions to facilitate the development of a robust, 'green' and cost-effective system for the remediation of OSPW. Implications of genomics in society have been integrated in each activity to guide

CWTS development and address perspectives of CWTS implementation from social, economic and legal perspectives.

Title: GENICE II: Reimagining Monitored Natural Attenuation as an Oil Spill Response Strategy in the Arctic

Academic Leaders: Gary Stern (University of Manitoba), Eric Collins (University of Manitoba)

Genome Centre: Genome Prairie

Total Funding: \$6,904,617

Tankers transiting Canadian waters must have an agreement with a certified Oil Spill Response Organization, but no such organization covers waters north of 60°N, meaning that help is usually days or weeks away, leaving natural attenuation as the presumed mechanism by which a majority of oil would be mitigated in a large Arctic spill. Natural attenuation is the removal or transformation of oil by natural processes like microbial biodegradation, which have been shown to play a major role in the cleanup of oil spills at lower latitudes. The project team will use metagenomics, metatranscriptomics, mass spectrometry, and high-sensitivity remote sensing techniques to develop a mechanistic understanding of the fate of oil in the Arctic, and social, policy, and economic research to further our knowledge of Monitored Natural Attenuation (MNA) as a rational response strategy for oil spills.

The project is organized as three inter-linked Activities: Activity 1 will conduct focused experimental incubations at the Ocean Sea Ice Mesocosm (OSIM) facility to observe geophysical, petrochemical, and microbial genomic responses to oil spills. Activity 2 will co-develop with four Kivalliq communities, a sustainable genomics-informed Community Based Monitoring (CBM) program that combines social and natural sciences with *Inuit Qaujimaqatuqangit*, while building a baseline understanding of seasonal cycling in Arctic marine microbial communities and serving as a sentinel in the case of an actual spill. Activity 3 will ensure policy uptake of our research findings by translating the results using a regionally specific economic model (the Oil Spill Decision Support System (OSDSS)); and implementable policy recommendations based on genomics-informed MNA.

End-of-project Deliverables: At the completion of this project, the team will deliver a comprehensive program containing the necessary ingredients for a sustainable genomics-informed MNA strategy, including: Highly Qualified Personnel (HQP) trained in advanced genomics, petroleomics, and remote sensing technologies; increased HQP capacity to conduct respectful research with Inuit communities; community-based HQP trained in natural science monitoring techniques; partnerships developed with communities, industry and academia; a sustainable CBM program co-developed for the Kivalliq region; a set of genomic biomarkers for use in CBM and MNA; protocols for the use of portable DNA sequencing devices for real-time on-site MNA; modeling software for the detection of oil in sea ice using electromagnetic scattering data; mapping resources provided of MNA seascapes and icescapes; the OSDSS application; an informed and effective policy and governance regime for Arctic marine spill prevention, preparation and response; and enhanced local and regional capacity for participating in, and leading spill-related governance.

Title: BIOSCAN–Canada

Academic Leader: Paul Hebert (University of Guelph)

Genome Centre: Ontario Genomics
Total Funding: \$7,164,054

The Global Risks Report 2020 from the World Economic Forum ranked biodiversity loss as one of the top five threats confronting humanity. Stemming this loss requires understanding how species interact and respond to changes in their environment, but this is impossible to accomplish with traditional morphological methods. DNA barcoding first emerged 15 years ago as a rapid, accurate way to discriminate species based on the sequence characterization of short segments of DNA. The International Barcode of Life Consortium, led by the Centre for Biodiversity Genomics at Guelph, involves research organizations in 40 nations which share the goal of cataloging all species and establishing a global biosurveillance system before mid-century.

Its current research program, BIOSCAN, is harnessing new technologies to make DNA barcoding faster and less expensive, advances that will broaden its application. Importantly, the technologies normally used to sequence whole genomes can be employed to gather DNA barcodes from thousands of specimens at a time. BIOSCAN-Canada is a core component of this global effort; its work will increase the cost effectiveness of DNA-based identification systems while also providing new biodiversity data with direct relevance to Canadians. For example, new species will be revealed from under-explored regions such as the Arctic and the ocean floor off British Columbia. DNA barcoding will also be used to illuminate interactions among species, such as which flowers a bee visited, and to track the shifting distributions of species in response to environmental change at previously impossible scales. Through community engagement, BIOSCAN-Canada will incorporate Indigenous ways of knowing into an accounting method for “natural capital” that extends beyond conventional economic metrics like the GDP.

By combining genomics-based biodiversity data with this accounting system, it will enable effective, timely environmental impact assessments and policymaking for the forestry, mining, and agricultural sectors as well as for conservation planning. Through such action, BIOSCAN-Canada will slow biodiversity loss, improve Indigenous relations through consultation, increase the sustainability of our agricultural and forestry sectors, and strengthen Canada’s leadership in global conservation efforts.

Title: Optimizing a Microbial Platform to Break Down and Valorize Waste Plastic
Academic Leaders: Laurence Yang, David Zechel, George diCenzo, and P. James McLellan (all at Queen’s University)
Genome Centre: Ontario Genomics
Total Funding: \$7,840,309

In Canada, 29,000 tonnes of plastic leak into the environment and oceans every year, creating severe environmental problems. Waste plastic kills 100,000 marine mammals annually, including whales, dolphins, seals, and sea lions, either through ingestion of plastic debris or entanglement in fishing gear. Another 2.8 million tonnes of plastic are sent to Canadian landfills, which creates a latent problem for future generations. Only 9% of plastic is recycled.

Despite the waste and environmental impact, plastic production is increasing in Canada, with an additional 4.8 million tonnes produced per year. Demand for plastic continues to grow because it is cheap to produce and has many important benefits. However, with a growing

awareness of the environmental impacts of plastic, governments and manufacturers are working towards a zero-plastic waste future. Under this paradigm, plastics will be made with recycled or biodegradable components. For this change in paradigm to succeed, government, the public, and industry will all need to play a role.

In this project a Canadian-led team consisting of multiple universities, municipal governments, and industries will drive a shift to a zero-plastic waste future by harnessing genomics technologies to create a circular economy for plastics. Our goal is to identify and engineer bacteria and enzymes that can break down plastics into recyclable components or into valuable fine chemicals more effectively than chemical conversion-based technologies. On a second front our team will conduct a holistic investigation into the impact of these new plastic biotechnologies on society, the economy, and the environment. Preliminary estimates indicate that if 90% of plastic is diverted to recycling instead of landfill, Canada could avoid \$500 million per year in costs, and create 42,000 jobs in new industries. The market for recovered waste plastic in the textiles sector alone is up to \$600 million per year. We could also save 1.8 million tonnes of CO₂ equivalents per year in greenhouse gas emissions. Globally, stopping plastics from leaking into the environment would avoid up to \$13 billion per year in damage to marine ecosystems. Ultimately, we envision a future where plastics continue to contribute to the economy in a positive way, but without the concomitant negative impact on the environment.

This project is affiliated with the Contaminants of Emerging Concern Research Excellence Network (CEC-REN) at Queen's University, which is an interdisciplinary research and innovation initiative. CEC-REN is focused on the detection and treatment of emerging contaminants in the natural and built environment that pose environmental and human health risks.

Title: Conservation Genomics of the Endangered North Atlantic Right Whale

Academic Leaders: Timothy R. Frasier (Saint Mary's University), Philip K. Hamilton (New England Aquarium)

Genome Centre: Genome Atlantic

Total Funding: \$6,185,340

The North Atlantic right whale is the world's most endangered large whale with fewer than 400 individuals remaining. This species has not recovered from whaling in the same way as other exploited species and has been in decline for the past 10 years. This lack of recovery has been attributed to two main factors: (1) a high rate of anthropogenic mortality from ship strikes and entanglement in fishing gear, and (2) a reproductive rate that is three times lower than their known potential.

To fulfil their mandate of conserving North Atlantic right whales, governing bodies such as the Fisheries and Oceans Canada (DFO) and the National Marine Fisheries Service (NMFS) in the U.S. require information on what factors are limiting recovery and what the implications are for policy and conservation planning.

Although some limiting factors have been identified, others have not—such as what factors are compromising reproduction. Even for limiting factors that have been identified, gaps remain in our understanding of the degree, and means by which, they are limiting species viability. This lack of knowledge limits the ability of DFO and NMFS to set appropriate

recovery expectations and goals, and to develop effective conservation strategies. Additionally, conservation actions taken by either country also require, and/or have implications for, other industries and groups, including the shipping and fishing industries and Indigenous communities. Therefore, effective conservation, that allows for the sustainable coexistence of whales and humans, requires collaboration with all of these parties.

We will use genomic and GE³LS (genomics and its ethical, environmental, economic, legal and social aspects) data to address these issues and improve the effectiveness and efficiency of conservation strategies in both Canada and the U.S. Our objectives are to: (1) quantify the impact of inbreeding on reproductive performance and species recovery; (2) quantify the impact of sublethal entanglements and ship strikes on health and reproduction; (3) conduct network analyses of entities involved in and/or impacted by right whale research and conservation to identify gaps so that such relationships can be developed or strengthened; and (4) conduct ethnographic research into these entities to facilitate effective communications and collaborations.

These objectives will be integrated to produce two deliverables: (1) communications with governing bodies (DFO and NMFS) regarding how conservation priorities and policy should be revised based on the genomic data; and (2) communications with industries and the other entities involved to promote changes in perceptions and behaviour. This work will result in more effective and efficient conservation of this endangered species.