

BACKGROUNDER

Nine Genomic Applications Partnership Program Projects Funded

Genome Canada is proud to announce the launch of nine new projects within its [Genomic Applications Partnership Program](#) (GAPP). GAPP funds translational research and development projects that address real-world challenges and opportunities as identified by industry, government, not-for-profits, and other receptors of genomics knowledge and technology.

Genomics research collaborations help Canada harness the power and potential of bio-innovation to create healthier, more sustainable and prosperous communities. Targeted investments in these partnerships support the strategic alignment of our research, postsecondary and business sectors to generate made-in-Canada solutions to complex challenges and new opportunities facing the country.

Together, the nine GAPP projects represent a total investment of \$33.5 million in research funding, of which \$11 million is from Genome Canada and \$22.5 million is from co-funding partners including provincial governments, private sector and not-for-profit organizations.

The projects in this backgrounder are listed by order of the GAPP round (17, 18, and 18a) to which they belong, then by province (West to East) through which they are funded within each round.

GAPP ROUND 17

Title: Application of Genomics-based Tools to Select for Pig Disease Resilience

Academic Leader: Michael Dyck (University of Alberta)

Receptor Leader: Bob Kemp (PigGenCanada)

Genome Centre: Genome Alberta

Total Funding: \$1,026,200

Disease is an economically important trait in Canadian pork production and is one of the most difficult challenges to manage. It also contributes to poor public perception of food animal production in terms of animal welfare, food safety, and antimicrobial resistance. Disease resilience is a quantitative trait defined as an animal's ability to maintain performance when exposed to pathogen(s). The goal of this project is to validate biological and genomic indicators of disease resilience in commercial pork production that can be measured and implemented in genetic improvement programs. This will involve validating promising disease resilience indicator traits and genomic tests in pigs that are exposed to pathogens in a controlled environment. This is expected to increase the rate of genetic improvement in pig health by 30%, increase the production of high value pork products, and improve the competitiveness in export markets.

Title: Caribou Genomics: A National Non-Invasive Monitoring Approach for an Iconic Model Species-At-Risk

Academic Leaders: Paul Wilson (Trent University) and Micheline Manseau (Environment and Climate Change Canada and Trent University)

Receptor Leader: Roxanne Comeau (Environment and Climate Change Canada)

Genome Centre: Ontario Genomics

Total Funding: \$4,072,887

Caribou has been identified as a priority species for recovery by Environment and Climate Change Canada (ECCC) in consultation with provinces, territories, and Indigenous groups. Significant efforts are being made by all levels of government to gain a better understanding of the factors affecting this iconic species, including climate change, and identify the best options for monitoring the effectiveness of recovery options. The goal of this project is to build upon their established caribou genetics research program to implement a genomics platform that will enable i) long-term, non-invasive genomic monitoring of boreal caribou, ii) allow for compatibility among different data generators and, iii) house data in an open access repository that supports analytical toolkits for use by partners. Investing in the implementation of such a genomic platform will allow comparisons through space and time to monitor the recovery of caribou populations and inform conservation efforts.

Title: Stopping Enteric Illnesses Early (Sentinel)

Academic Leaders: Lawrence Goodridge (University of Guelph) and Roger Levesque (Université Laval)

Receptor Leader: Chrystal Landgraaf (Public Health Agency of Canada)

Genome Centres: Ontario Genomics and Génome Québec

Total Funding: \$6,490,662

In Canada, consumption of contaminated food causes 4 million illnesses, 14,150 hospitalizations and 323 deaths each year, with an estimated annual economic burden of approximately \$4 billion, and a major impediment to the identification of contaminated food is that current surveillance methods rely on sick people to seek medical help. The Public Health Agency of Canada (PHAC), in partnership with the University of Guelph and Université Laval, aims to develop a novel, integrated approach to improved foodborne outbreak detection, beginning with metagenomic detection of foodborne pathogens in raw sewage within geographically localized monitoring sites (Quebec City, Guelph, Winnipeg), and monitoring of social media for keywords associated with enteric illness. The tools, methods and datasets generated through this project will be translated for downstream operational use into the network of Canadian foodborne surveillance programs through collaborations between PHAC and its federal/provincial/territorial partners. Implementation is expected to result in a reduction in the amount of illnesses and hospitalizations and economic savings due to a reduction in food recalls through faster detection of outbreaks. A key advantage of this flexible 'omics and social media surveillance approach is that it can be scaled for rapid detection of other pathogens, and will be immediately utilized to monitor levels of SARS-CoV-2 (the COVID-19 virus) in wastewater, as an early indicator of changing case numbers prior to clinical presentation.

Title: Bioprocess Development for Lactose Valorisation

Academic Leader: Vincent Martin (Concordia University)

Receptor Leader: Michel Pouliot (Agropur Cooperative)

Genome Centre: Génome Québec

Total Funding: \$1,950,000

Lactose, a by-product of dairy processing, is the weak link of the modern dairy industry. All other outputs of dairy processing – cream, skim milk, cheese and protein concentrates – sell into markets that are consistently profitable. In contrast, the lactose by-product referred to as ultrafiltration (UF) permeate, is a low value commodity and in many cases lactose streams are disposed of in lagoons or land spread. The goal of this project is to deliver yeast with an engineered pathway that produce fumaric acid through the fermentation of the lactose. This project is using genomics to develop a technology that converts a low value intermediate dairy by-product that is in surplus into a high value product used in the food industry and industrial applications. This will reduce the environmental impact of lactose disposal. Agropur, the receptor on this project, is a Canadian dairy-processing cooperative owned by 3,024 dairy farmers across Canada and is well positioned to implement the resulting technology.

Title: Implementation of Clinical Exomes in a Pre- and Peri-Natal Setting

Academic Leaders: Karen Bedard and Anthony Vandersteen (Dalhousie University)

Receptor Leaders: Jo Ann Brock and Sarah Dyack (IWK Health Centre)

Part of All For One Initiative: Yes

Genome Centre: Genome Atlantic

Total Funding: \$4,758,489

Rare genetic disorders affect approximately 500,000 children in Canada and constitute 30% of the pediatric inpatient population. These children often undergo lengthy and expensive diagnostic procedures and may be subject to uninformed care while waiting for a correct diagnosis. The introduction of genome wide sequencing as a diagnostic tool has been shown to be effective, with a diagnostic yield of 30-40% for patients with undiagnosed genetic disorders. Adoption into clinical practice has been slow, however, due to insufficient evidence surrounding cost savings, inconsistent description of patient phenotypic data, insufficient integration of clinical and laboratory systems, data sharing difficulties and concerns among patients about potentially significant incidental findings. The project aims to develop and assess the clinical utility and cost effectiveness of the implementation of genome wide sequencing for clinical exomes in order to begin to adopt this testing as standard of care for pediatric and prenatal populations in Atlantic Canada.

GAPP ROUND 18

Title: CLEAn pLAnt extractionN SEquencing Diagnostics (CLEANSED) for Clean Grapevines in Canada

Academic Leaders: Sudarsana Poojari (Brock University) and Xuekui Zhang (University of Victoria)

Receptor Leaders: Mike Rott (Canadian Food Inspection Agency) and Bill Schenck (Canadian Grape Certification Network)

Genome Centres: Genome British Columbia, Génome Québec, Ontario Genomics

Total Funding: \$6,353,644

Grapevine virus disease management has been identified by the grape grower and wine industries as a top priority for long-term sector sustainability. Losses of over \$23 million per year are currently incurred by grape growers due to reduced yield of infected grapes and increased fruit rejection by wineries. To replace the currently infected acreage and meet ongoing renewal of vineyards the industry needs access to 6.7 million domestically produced, virus free vines/year. There will be two separate pathways for implementation and commercialization. To accommodate these demands, the Canadian Food Inspection Agency (CFIA) Sidney Centre for Plant Health (CPH) requires a

rapid, cost effective genomic solution to replace the over 30 molecular and bioassays currently performed on , which can take up to three years to complete. By implementing a high throughput sequencing method at the CFIA the costs of analysis will be reduced and analysis time will be reduced for industry priority varieties imported into Canada as well as audit testing from certified foreign sources destined to commercial planting. Reducing the testing time to 10 days allows grape growers to rapidly improve the health of their vineyards. Domestically, the Canadian Grape Certification Network (CGCN) is commercializing high throughput sequencing through its partner Cool Climate and Oenology Viticulture Institute for the certification of propagation material in nurseries and grapevines obtained through CPH, and for monitoring of production vineyards.

Title: Fast-Track Breeding of Powdery Mildew-Resistant Cannabis

Academic Leader: Marco Todesco (University of British Columbia), Loren Rieseberg (University of British Columbia)

Receptor Leader: Greg Baute (Aurora Cannabis)

Genome Centre: Genome British Columbia

Total Funding: \$4,265,446

Cannabis is projected to become one of the largest crops in Canada over the next decade. However, current cannabis cultivars lack many desirable agronomic traits, including resistance to powdery mildew infection, and are poorly suited to the large-scale production needed to satisfy this growing market. A genomic resource will be created that will allow the project team to assess the levels of susceptibility and resistance to powdery mildew within the cannabis germplasm and begin to introduce powdery mildew resistance into Aurora's breeding program. The improved cannabis cultivars will result in reduced losses to pathogen contamination and increase product quality. The breeding pipeline itself will also be used in the future to identify other important production and higher-value traits and introduce them into cannabis cultivars with superior agronomic performance, allowing Aurora to not only grow it's revenues beyond \$1B, but also to produce a secure supply of medical cannabis for Canadians.

Title: Development and Validation of a Genomic-Based Diagnostic Tool of the Virulence Profile of *Phytophthora Sojae*, a Major Pathogen of Soybean

Academic Leader: Richard Bélanger (Université Laval)

Receptor Leader: Julien Vivancos (Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec)

Genome Centre: Génome Québec

Total Funding: \$3,256,326

Soybean production has rapidly increased over the past decade and is now the third most important crop in Canada. This rapid expansion has been accompanied by an increase in *Phytophthora* root rot, a disease caused by *Phytophthora sojae*, which causes revenue losses of over \$50 million annually in Canada. The most effective control method currently available relies on the use of soybean cultivars carrying resistance genes against specific pathotypes of *P. sojae* present in soybean fields. A diagnostic tool will be developed and offered to growers, allowing them to choose soybeans lines with the appropriate *P. sojae* resistance genes, and to breeders to deploy new soybean varieties resistant to the various pathotypes of *P. sojae* in Canadian fields. The implementation of this technology could save Canadian soybean growers over \$20 million annually through the accurate exploitation of disease resistance. It is also expected to reduce the number of fungicide applications for the management of soybean diseases.

GAPP ROUND 18a

Title: Optimizing the eDNA Approach to Monitor Biodiversity in Canada's Marine Protected Areas

Academic Leader: Jennifer Sunday (McGill University)

Receptor Leaders: Emily Rubidge and Ryan Stanley (Department of Fisheries and Oceans, Canada)

Genome Centre: Génome Québec

Total Funding: \$757,409

Canada is investing in its large Marine Protected Area (MPA) network, spanning approximately 805,000 km², to preserve marine biodiversity and promote healthy, functional, and resilient marine ecosystems. However current biodiversity sampling methods are inadequate to monitor biodiversity within a network of this size. The project team proposes to use environmental DNA (eDNA) metabarcoding to evaluate and optimize marine monitoring survey designs. The results of this project will be the first quantitative evaluation of eDNA survey design in a marine setting and will provide a foundation for decisions in monitoring investment using this technology in the Canadian MPA network.