BACKGROUNDER

Genomic Applications Partnership Program
Funded Projects – Round 10

The Genomic Applications Partnership Program (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. The following four projects have been selected for funding in Round 10 of GAPP, for a total investment of $13.8 million ($4.8 million from Genome Canada and $9 million from co-funding partners including provincial governments, private sector and not-for-profit organizations).

Assessing Freshwater Health Through Community Based Environmental DNA Metabarcoding
Project leaders: Elizabeth Hendriks World Wildlife Fund Canada (WWF-Canada); Laura Maclean, Environment and Climate Change Canada; Mehrdad Hajibabaei, University of Guelph
Genome Centre: Ontario Genomics
Total funding: $2.6 million

With a growing economy, increasing population, and climate change, Canada faces increased pressures on its precious resource: freshwater (20% of the world's freshwater). Current methods for monitoring the health of our watersheds remain slow, laborious, expensive and imprecise. Canada's geographic diversity and low population density makes monitoring networks a challenge to maintain. We need more efficient, comprehensive monitoring tools to inform governments, communities and industries about the true consequences of economic development on freshwater quality, to support rapid and effective protection of vulnerable ecosystems.

The WWF- Canada and Environment and Climate Change Canada (ECCC) are working with Dr. Mehrdad Hajibabaei of the University of Guelph to validate and implement a new technique called environmental DNA metabarcoding, which uses bulk environmental samples for identification of species through species specific genomic sequences (DNA 'barcodes') using high-throughput sequencing technologies. The project will generate biodiversity data for freshwater benthic macroinvertebrates, the small animals that live at the bottom of streams, rivers. The technique will be used to analyze bulk samples collected by community-based monitoring efforts across a wide range of Canadian watersheds. Sampling by community groups will be coordinated by WWF-Canada and its partner organizations such as Living Lakes Canada.

Implementation at this scale will be a world first, supporting the wider adoption of these technologies within existing environmental monitoring and assessment applications, including ECCC's Canadian Aquatic Biomonitoring Network (CABIN) which engages over 1,400 users, including federal, provincial

and territorial government agencies, First Nations, academia, industry, NGOs and environmental consulting firms.

Many of these organizations already use biomonitoring to understand and manage the impacts of resource projects such as mines, hydro dams and energy projects. By providing access to this new genomics-based technique, and by demonstrating its reliability in assessing river health, we can broaden the reach and impact of existing community-based monitoring programs, ultimately leading to better informed decisions.

Translating High Immune Response (HIR™) Genomics to Improve Beef Cattle Health and Welfare

Project leaders: Michael Lohuis, The Semex Alliance and Bonnie Mallard, University of Guelph
Lead Genome Centre: Ontario Genomics
Total funding: $1.6 million
Mitacs partnership

High Immune Response (HIR™) is a patented test developed by Dr. Bonnie Mallard and colleagues of the University of Guelph that identifies animals with naturally superior immunity. First used successfully in dairy cattle, the test is now being adapted to fight Bovine Respiratory Disease (BRD), the costliest disease of beef cattle raised on feedlots. BRD results in the death of some 53,000 beef cattle in Canada each year, an economic loss of more than $100 million. In North America as a whole, the estimated annual cost of BRD as high as $1 billion dollars/year.

Dr. Mallard is working with the Semex Alliance and through them, the Canadian Angus Association (CAA) and the American Angus Association (AAA), to develop an HIR™ genomics test for beef cattle. The application of the test could result in a significant (20-50 per cent) reduction in deaths among calves from birth to weaning age and reduce the need for antibiotics throughout the lifetime of beef cattle. All Angus bulls marketed in Canada and the United States will have access to the HIR™-genomic test, allowing beef producers to select bulls for breeding purposes better equipped to improve animal health and welfare.

The new test will demonstrate the leadership provided by Semex, the CAA and the AAA in beef cattle genomics. Integration of the HIR™ technology and selective breeding for enhanced immunity in the North American Angus population is expected to cumulatively increase BRD resistance of beef cattle over multiple generations, which if fully applied, could ultimately reduce the costs of BRD in North America by $500 million per year, $65 million of which will be in Canada. Reduced use of antibiotics will provide further benefits to consumers and retailers.

Devices for Detection and Identification of Surface Microbial Contamination in High-Risk Facilities

Project leaders: Mark McInnes, Charlotte Products Ltd., and Shana Kelley, University of Toronto
Genome Centre: Ontario Genomics
Total funding: $4.5 million

Healthcare-associated infections (HAIs) are the 4th leading cause of death in Canada, predicted to move up to second place by 2050. Attention to cleanliness and disinfection of surfaces plays a large role in reducing HAIs. However, historically it has been difficult to measure cleaning effectiveness and

meaningfully improve practices. There is a clear need for a system that can identify disease-causing bacteria and viruses on surfaces.

Charlotte Products Ltd. (CPL), a family-owned Canadian company, has developed an environmental monitoring system and optical sensor technology, called Optisolve Pathfinder®™, to complement its innovative, award-winning cleaning products. Dr. Shana Kelley is working with the company to further enhance the OptiSolve offering to allow for recognition and identification of specific pathogen species.

Dr. Kelley and her team will combine novel nanomaterials with a genomics-based approach to allow for precise identification of pathogens that cause HAIs. The resulting technology, Optisolve *Insight*, will allow hospitals long-term care facilities, and more to rapidly detect and identify infectious agents, such as MRSA, *C. difficile,* and influenza, with the resultant benefits of proactive prevention and quick interventions.

The service and technology will significantly reduce HAIs while enabling environmental services and IPAC managers and to avoid taking a "worst-case scenario" approach to infection outbreaks, which can include bed closures and cancellation of procedures. The result will be improved health of patients, residents, staff, and visitors as well as healthcare savings. This first-to-market technology will contribute to economic growth and employment for highly qualified personnel.

Development of Comprehensive Cytogenomics and Molecular Genetics Testing Using an Exome and Low-Pass Whole Genome Sequencing Combined Approach
Project leaders: Harry Gao, Fulgent Genetics, Régen Drouin, Laval University;
Genome Centre: Génome Québec
Total funding: $5.1 million

Copy number variants (CNVs – repetitive regions within the genome that vary from individual to individual) are implicated in a range of diseases and disabilities in humans, including cancer, intellectual disabilities and congenital abnormalities. Current methods for the detection of CNVs are costly and time-consuming, with limited accuracy and clinical utility, reducing the likelihood of appropriate treatment and placing an unnecessary burden on the healthcare system and on patients' health and wellbeing.

Fulgent Genetics, which has a Canadian presence in Quebec City, is working with Laval University's Dr. Régen Drouin to develop a more efficient and cost-effective test for CNVs. Their technology, NOVA[CNV+], will replace three existing cytogenetic testing methods with a next generation sequencing-based technology. The result will be improved testing resolution, accuracy, cost-effectiveness and further integration into genomic medicine.

The research team estimates that 50,000 NOVA[CNV+] tests could replace approximately 100,000 tests required each year with the current methods, saving the Canadian healthcare system at least $12.5 million per year. The development, clinical validation and implementation of this test will provide an attractive, long-term return on investment for Canada's economy and for the health of Canadians. The establishment of a clinical and commercial genomic diagnostic industry in Canada will also help put the country at the forefront of personalized genomic medicine.