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Canada

GENOMICS R&D INITIATIVE

ANNUAL PERFORMANCE REPORT 2017-2018




Through the Genomics Research and Development Initiative, federal science departments and agencies collaborate in the field of genomics research to address issues that are important to Canadians, focusing on the role of federal government research

ABOUT THE INITIATIVE

Federal science departments and agencies collaborate on genomics research projects through the Genomics R&D Initiative to address issues that matter to Canadians. This document reports on the progress of 64 research projects, including the interdepartmental Antimicrobial Resistance and Metagenomics-Based Ecosystem Biomonitoring projects

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EXECUTIVE SUMMARY

The Government of Canada's Genomics Research and Development (R&D) Initiative (GRDI) enables structured collaboration on and common approaches to genomics research across federal science departments and agencies with the overarching aim of addressing issues that matter to Canadians. The Government has funded the GRDI in three-year cycles from 1999 until 2014, when it renewed the initiative with a five-year Phase VI cycle.

The GRDI generates high-quality, genomics-based R&D solutions for use in federal laboratories to support regulatory, public policy and operational mandates in socially and economically important areas such as health care, food safety, natural resource management, agriculture and aquaculture sector sustainability and competitiveness, and environmental protection. GRDI-funded projects focus on departmental mandates and government priorities, are strategically aligned with departmental objectives, and involve strong collaboration with universities and private sectors.

About this report

The 2017–2018 GRDI Annual Performance Report follows the Performance Measurement Framework that National Research Council Canada developed in 2015. It profiles GRDI and planned results by department and draws connections to departmental objectives and program alignment architectures along with governance, coordination and accountability structures. It then reports on GRDI performance for 2017–2018 in terms of interdepartmental governance, R&D, and knowledge and networks. Appendix A presents summary statistics as well as a narrative account of R&D achievements for the period.

GRDI performance in 2017–2018

Fiscal 2017–2018 marked the fourth year of Phase VI of the GRDI. The initiative continued to support mandated research within participating departments and facilitated structured, interdepartmental collaboration. Phase VI also involves two highly coordinated interdepartmental Shared Priority Projects (SPPs): the Antimicrobial Resistance (AMR) and Metagenomics Based Ecosystem Biomonitoring (EcoBiomics) projects.

Achievements this period include:

- enhanced capacity for the timely detection and identification of microbiological food safety hazards, animal pathogens, plant pests, invasive plants, and plants with novel traits, to support government regulatory actions
- harmonized next-generation sequencing techniques at the CFIA to enable integrated, multi-purpose diagnostic activities throughout the food continuum—from protecting plant and animal health to ensuring the safety of food for Canadians
- developed and validated cutting-edge environmental DNA (eDNA) tools to support Fisheries and Oceans Canada (DFO) regulatory decisions
- used next-generation sequencing to resource profile Arctic char, Chinook salmon and Atlantic salmon
- assembled genome sequence of Stettler, a popular Canadian wheat variety, which included leveraging a web-based, open-access platform developed for the data-intensive study of diseases, pests, abiotic stresses and developmental pathways in wheat
- developed guidance for the use of genomics in regulatory toxicology, including a guidance project adopted as official guidance for Organisation for Economic Co-operation and Development (OECD) member countries
- generated a large repository of in vivo gene expression data related to in vivo toxicity of engineered nanomaterials; researchers in Europe are now using the repository to frame evidence-based research and regulatory questions
- developed a tool to help epidemiologists integrate whole-genome sequence data into outbreak investigations
- implemented a new online database and analytical platform that enables investigation of *Neisseria meningitidis* epidemiology and outbreaks at the local level
- created a national database containing the spectra of rare and under-represented bacterial pathogens, providing fast, accurate and cost-effective identification of those pathogens locally rather than through a reference centre

ADDRESSING ISSUES THAT MATTER TO CANADIANS

In 1999, the Government of Canada launched the Genomics Research and Development Initiative (GRDI) to establish and maintain core genomics research and development (R&D) capacity in federal departments and agencies. This report details the performance of the participating departments and agencies on 64 research projects under the GRDI, including the two Shared Priority Projects (SPP): the Antimicrobial Resistance (AMR) project and the Metagenomics-Based Ecosystem Biomonitoring (EcoBiomics) project.

Each year, the GRDI delivers $19.9 million in funding across:

- **Agriculture and Agri-Food Canada (AAFC)**
- **Canadian Food Inspection Agency (CFIA)**
- **Environment and Climate Change Canada (ECCC)**
- **Fisheries and Oceans Canada (DFO)**
- **Health Canada (HC)**
- **National Research Council Canada (NRC)**
- **Natural Resources Canada (NRCan)**
- **Public Health Agency of Canada (PHAC)**

GRDI-funded projects focus on departmental mandates and government priorities, are strategically aligned with departmental objectives, and involve strong collaboration with universities and private sectors. This extends to upholding regulatory, public policy and operational mandates in important areas such as health, food safety, natural resources management, environmental protection, and the sustainability and competitiveness of Canada's agriculture sector.

Phase V (2011–2014) introduced a model that mobilized resources for concerted research on issues beyond the mandates of single departments, supporting highly coordinated interdepartmental projects along shared priorities and common goals. The Government of Canada launched the AMR and EcoBiomics projects in April 2016.

The six phases of the GRDI

The federal government invested $393.3 million into the GRDI between 1999 and 2019 to fund six phases:

- $55 million for Phase I (1999–2002)
- $59.7 million each for phases II (2002–2005), III (2005–2008), IV (2008–2011) and V (2011–2014)
- $99.5 million for Phase VI (2014–2019)

Table 1: Funding allocations ($000)

DEPARTMENT/AGENCY	PHASE I 1999–2002	PHASE II 2002–2005	PHASE III 2005–2008	PHASE IV 2008–2011	PHASE V 2011–2014	PHASE VI 2014-2019
Agriculture and Agri-Food Canada	17,000	18,000	18,000	18,000	15,300	22,200
Canadian Food Inspection Agency	–	–	–	–	–	3,600
Environment and Climate Change Canada	3,000	3,000	3,000	3,000	2,550	4,000
Fisheries and Oceans Canada	2,500	2,700	2,700	2,700	2,295	3,600
Health Canada / Public Health Agency of Canada	10,000	12,000	12,000	12,000	10,200	16,000
National Research Council Canada	17,000	18,000	18,000	18,000	15,300	22,200
Natural Resources Canada	5,000	6,000	6,000	6,000	5,100	8,000
Shared Priorities	–	–	–	–	8,955	19,900
Medical Research Council[1]	500	–	–	–	–	–
Total	**55,000**	**59,700**	**59,700**	**59,700**	**59,700**	**99,500**

[1] Precursor to the Canadian Institutes of Health Research – one time allocation in fiscal year 1999-2000 to assist in the establishment and support of a Genome Canada Secretariat.

All departments have levered the GRDI funds with allocations from their A-base resources and from successful collaborations. Table 2 provides an overview of resources invested in 2017–2018 in support of GRDI projects and demonstrates that non-GRDI funds represented 1.75 times the GRDI investments. Additional in-kind investments included the sharing of technology platforms, materials and expertise with a variety of collaborators in research areas that cut across traditional departmental sectors.

Table 2: Overall investment in support of GRDI projects in 2017-2018 ($000)

DEPARTMENT/AGENCY	GRDI	NON-GRDI*	TOTAL
National Research Council Canada	4,440	8,288	12,728
Agriculture and Agri-Food Canada	4,440	9,249	13,689
Health Canada	1,600	1,692	3,292
Public Health Agency of Canada	1,600	1,779	3245
Natural Resources Canada	1,600	3,679	5,279
Environment and Climate Change Canada	800	1,777	2,577
Fisheries and Oceans Canada	720	555	1,275
Canadian Food Inspection Agency	720	3,586	4,306
SHARED PRIORITY PROJECT	**GRDI**	**NON-GRDI**	**TOTAL**
Antimicrobial Resistance	1,889	3,117	5,007
Metagenomics Based Ecosystem Biomonitoring	1,852	1,066	2,918
Coordination and Common Functions	239	47	285
Total	**19,900**	**34,835**	**54,601**

* includes estimated funds from departmental A-base and other sources

Planned results for 2017–2018

As reported in NRC's Departmental Report on Plans and Priorities Supplementary Table for the GRDI, the participating departments established a collective set of planned results for 2017–2018:

- using genomics to significantly increase Canada's share of global wheat production
- using genomics to improve the value of Canadian crops and agri-products
- using genomics for food safety, animal health and plant protection
- genomics knowledge and advice for the management of fisheries and oceans
- genomics-based tools and technologies for responsible environmental decision-making
- genomic knowledge for the Canadian health regulatory system
- commercially-relevant advances in genomics R&D related to human health
- concerted interdepartmental research along shared priorities and common goals on issues that are beyond the mandates of single departments
- genomic knowledge for forest generation and protection
- genomics knowledge to strengthen public health programs and activities related to the prevention and control of infectious disease

The participating departments and agencies developed research plans and activities to deliver on these planned results. Descriptions of these plans and activities follow.

Agriculture and Agri-Food Canada

AAFC will use its GRDI funding to advance Canadian Crop Genomics Initiative priorities as well as enable industry to take advantage of innovations. Activities will fall under two broad themes:

- **biodiversity, gene mining and functional analysis**—develop value-added traits (e.g., seed quality) for the highly competitive marketplace as well as make Canada's crop production more resilient against potentially catastrophic abiotic and biotic stresses to maximize sector profitability
- **improved access to biological materials and data sets**—make plant breeding more efficient, laying the scientific foundation for major advances in priority trait development and delivery for industry

Canadian Food Inspection Agency

The CFIA's genomics research will enhance the capacity and ability to regulate pests and pathogens by focusing on two thematic areas: detection and isolation, and identification and characterization. Research under these themes aligns with the agency's three business lines:

- **animal health**—support management of public health risks associated with the transmission of zoonotic diseases as well as reportable and emerging animal diseases.
- **food safety**—enhance compliance testing, source attribution and risk profiling while enabling enforcement of HC health risk assessment standards.
- **plant health**—advance early detection and rapid response capabilities, and inform regulatory decision-making regarding regulated plant pests and commodities in the agriculture and forestry sectors.

The agency will also conduct research to harmonize genomics activities across its three business lines with the aim of improving the transfer of technology and tools between them and making genomics tools more accessible to CFIA scientists.

Environment and Climate Change Canada

ECCC will continue to apply its GRDI funding under the Strategic Technology Applications of Genomics in the Environment (STAGE) program with the following priorities:

- **ecotoxicology**—establish toxicology endpoints for micro-organisms, chemicals of concern and emerging stressors, and predict the mode of action of chemicals of concern and their effects on organisms
- **wildlife conservation**—understand how genes interact within flora and fauna in response to environmental conditions, and track disease in wildlife
- **environmental monitoring**—develop indicators (e.g., gene expression profiles for key species) of ecosystem health in priority ecosystems (e.g., Great Lakes and St. Lawrence), and track pathogen sources
- **compliance and enforcement**—analyze flora and fauna to identify individual species, determine parentage and ascertain geographic origin

This work will support ECCC's obligations under the *Fisheries Act*, the *Canadian Environmental Protection Act*, and programs including the Chemicals Management Plan.

Fisheries and Oceans Canada

Genomics-enabled research within DFO will continue to align with three key themes:

- **protecting fish species and promoting sustainable harvesting**—develop and apply leading-edge genomics tools to accurately identify species, populations and stocks for fisheries management, and conserve vulnerable stocks, at-risk species and aquatic biodiversity
- **safeguarding Canadian fish and seafood products**—develop innovative genomics techniques to detect, monitor and minimize the impact of pathogens (e.g., infectious salmon anemia virus) to safeguard the health of Canada's aquatic resources and secure Canada's fish and seafood export markets
- **maintaining healthy and productive aquatic ecosystems**—develop and apply new genomics tools to monitor, mitigate and restore aquatic ecosystems

This research will support fisheries managers, who increasingly rely on innovative genomics and bioinformatics technologies to inform resource management and conservation decisions across DFO sectors and programs. Genomics can inform fisheries, biosecurity and aquaculture applications (e.g., detecting illegal product substitution at commercial vendors) where traditional fisheries science cannot. Synergistic integration with genomics approaches can also enhance traditional fisheries approaches (e.g., early detection of invasive species using environmental DNA [eDNA]).

Health Canada

Genomics research at HC will continue to focus on four priority investment areas to strengthen the department's regulatory role:

- **supporting regulatory knowledge on therapeutics and biologics**—inform and support regulatory decisions throughout the biotherapeutic product life cycle
- **supporting regulatory knowledge on food safety and nutrition**—enable detection and characterization of foodborne micro-organisms; enable characterization of health effects of food contaminants (e.g., fungal toxins, anthropogenic contaminants and seafood toxins), food allergens, nutrients, novel foods or food ingredients, and prebiotics and probiotics; and develop markers of health status and disease (e.g., cancer, diabetes, obesity, allergies and cardiovascular disease) in the context of nutrition, micro-organisms, allergens and food contaminant exposure
- **protecting human health from potential adverse effects**—protect Canadians against potential negative impacts of environmental contaminants, radiation, consumer products and pesticides

- **researching the socio-ethical impacts of genomics technologies, outputs and products**—develop approaches for the responsible integration of genomics for societal benefit, accounting for ethical, legal and socio-economic considerations

National Research Council Canada

GRDI investments will support NRC programs that require genomics-related activities to help industry and government pursue strategic national priorities with the support of mission-oriented research and technology deployments. In 2017–2018, these will be:

- **NRC's contribution to the Canadian Wheat Alliance**, which aims to improve the yield, sustainability and profitability of wheat for the benefit of Canadian farmers and the economy through improved breeding efficiency; reduced losses from drought, heat, cold and diseases; and more efficient nutrient use
- **Biologics and Biomanufacturing program**, which aims to cover all aspects of biologic development—from discovery up to pre-clinical testing—in collaboration with industry partners

NRC's Senior Executive Committee approved implementation of these programs after careful deliberation and a rigorous assessment process.

Natural Resources Canada

NRCan's Canadian Forest Service will focus on applying genomics knowledge to promote the competitiveness of Canada's forest sector, including:

- **forest generation**—develop innovative genomic applications to accelerate production of higher quality fibre to realize economic and environmental benefits for Canada
- **forest protection**—develop innovative genomic diagnostic tools to enable rapid detection and management of invasive insects and diseases that threaten the health and ecological integrity of Canadian forests, the forest sector and forest communities

Public Health Agency of Canada

GRDI research activities at PHAC apply "-omics" technologies to generate new knowledge to support public health decision-making and create tools to enhance disease prevention and control. These technologies support:

- prevention and control of priority pathogens
- response to antimicrobial resistant pathogens
- infectious disease surveillance
- public health security measures

The knowledge genomic approaches generate supports more detailed risk analyses, as well as the identification and development of new intervention points for infectious disease control and prevention.

Shared priorities

The Antimicrobial Resistance (AMR) project is a key component of the Federal Action Plan for Antimicrobial Resistance and Use in Canada. AAFC is the project coordinator, and CFIA, HC, NRC and PHAC are all involved. The project will add to understanding of the critical activities that contribute to antimicrobial resistance development. It will also shed light on critical exposure pathways through which antimicrobial bacteria reach humans, which could help validate economically sustainable technologies, practices and policies to mitigate the development of antimicrobial resistance.

AAFC also coordinates the Metagenomic-Based Ecosystem Biomonitoring (EcoBiomics) project, which involves CFIA, DFO, ECCC, NRC, NRCan and PHAC. The collaborating parties will develop advanced genomics tools to assess freshwater ecosystem biodiversity and water quality in lakes and rivers, evaluate the health of soil essential to the productivity of agricultural and forestry systems across Canada, and investigate land remediation for the oil and mining sectors. The project will support environmental responsibility, secure market access for resource products and improve social license for economic development in Canada.

How the GRDI supports government priorities

One of the GRDI's primary aims is to help participating departments and agencies make evidence-based regulatory and policy decisions called for by their respective mandates. It also seeks to support development of new policies and standards, as well as the ability to anticipate and respond to the needs of Canadians in the areas of public health, the economy, agriculture, fisheries and aquaculture, and the environment. Based on these aims, GRDI-funded projects focus on advancing departmental mandates and objectives as well as government priorities.

Going forward, the GRDI will support the goals of Canada's Innovation and Skills Plan to make Canada a world-leading centre for innovation, to help create more well-paying jobs, and to help strengthen and grow the middle class. It will also help anticipate and respond to the needs of Canadians through genomics-related innovation opportunities in health, agri-food, clean technology, digital industries and clean resources.

Department-specific details, including the strategic outcomes GRDI funding supports, follow.

Agriculture and Agri-Food Canada

Supports strategic outcome: *An Innovative and Sustainable Agriculture, Agri-Food and Agri-Based Products Sector*

AAFC uses the GRDI funding to develop and strengthen the Canadian Crop Genomics Initiative with investments into plant genomics and by forming multidisciplinary teams across Canada that focus on promoting the sustainability and competitiveness of the country's agriculture sector.

Canadian Food Inspection Agency

Supports strategic outcome: *Maintain a Safe and Accessible Food Supply and Plant and Animal Resource Base*

Genomics research outcomes support commodities and resources regulated under CFIA's program activities, including those of its food safety, animal health and zoonotic, and plant resources programs. CFIA's GRDI program targets the development and application of genomics tools for the rapid detection of food pathogens, plant pests and animal disease agents. This enables the agency to respond effectively to regulatory needs in food safety, ensure compliance, maintain consumer confidence, and minimize animal and plant disease incursions.

Environment and Climate Change Canada

Supports strategic outcomes: *1) Canada's Natural Environment is Conserved and Restored for Present and Future Generations, and 2) Threats to Canadians and their Environment from Pollution are Minimized*

The genomic research priorities under ECCC's STAGE program contribute to monitoring and understanding Canada's ecosystem, help assess risks posed by chemical pollutants to wildlife and migratory birds, and deliver practical applications that support regulatory compliance and evidence-based decision-making related to risk mitigation and conservation efforts.

Fisheries and Oceans Canada

Supports strategic outcomes: *1) Economically Prosperous Maritime Sectors and Fisheries, and 2) Sustainable Aquatic Ecosystems*

Genomics research is building the scientific knowledge base and expertise necessary to support priorities for fisheries and oceans management. At DFO, activities under the GRDI support genomics research for two of the three strategic outcomes of the department's program alignment architecture. The department coordinates genomics research national through its Biotechnology and Genomics Program.

Health Canada

Supports strategic outcome: *A Health System Responsive to the Needs of Canadians*

GRDI-funded research generates regulatory knowledge that contributes to the appropriate management and communication of health risks and benefits associated with food, products, substances and environmental factors. The knowledge and tools genomics research generates ultimately support departmental efforts to respond to current and emerging health issues under the aforementioned strategic outcome as well as the "Canadian Health System Policy" program activity.

National Research Council Canada

Supports strategic outcome: *Canadian Businesses Prosper from Innovative Technologies*

NRC's program alignment architecture, recently updated to reflect the department's new industry-focus, aligns with Government of Canada strategic outcomes and federal priorities as well as the NRC's business processes. NRC's performance reporting is aligned accordingly.

By contributing to research programs that focus on improving Canadian wheat and developing new biologics, the GRDI supports the NRC's:

- "Canadian Businesses Prosper from Innovative Technologies" strategic outcome
- "Technology Development and Advancement" program
- "Aquatic and Crop Resource Development" and "Human Health Therapeutics" sub programs

Natural Resources Canada

Supports strategic outcome: *Canada's Natural Resource Sectors are Globally Competitive*

The GRDI has helped NRCan's Canadian Forest Service generate important data, infrastructure and partnerships that deliver practical applications. This foundation supports NRCan's efforts to make Canada's natural resource sectors globally competitive, the program activity "Innovation for New Products and Processes," and the intended outcome "Advancing Forest Product Innovation."

Public Health Agency of Canada

Supports strategic outcome: *Strengthened public health capacity, science leadership and enhanced public health security*

PHAC uses GRDI funding to support the development of innovative tools that apply genomic and bioinformatic technologies for more effective public health interventions. The GRDI also generates leading-edge scientific knowledge to support public health decision-making and program development. It also facilitates integration of reliable and current information into public health decision-making and interventions at all levels across Canada by driving collaboration and knowledge exchange among public health professionals working at all levels of government as well as with non-governmental organizations. These functions directly support the agency's "Public Health Infrastructure" program activity.

Governance, Coordination and Accountability

Accountability can make it challenging to manage shared programs that have a collective sense of purpose because departments are vertically accountable for delivering on their mandates and spending resources. NRC established an interdepartmental governance framework for previous phases of the GRDI to ensure sound management. The same framework will be used to oversee the collective coordination for the current phase.

The GRDI governance structure includes three main elements (with support from ad-hoc advisory committees as needed):

- Assistant Deputy Minister Coordinating Committee (ADM CC)
- Interdepartmental GRDI Working Group
- a coordination function

ADM coordinating committee

Chaired by the NRC, the interdepartmental ADM CC includes ADMs from each of the GRDI-funded organizations and guest representatives from Innovation, Science and Economic Development Canada (ISED) and Genome Canada. The committee typically meets three times a year at the call of the chair—more often when the need for decision-making warrants—and is responsible for:

- determining the overall strategic direction of the GRDI
- approving investment priorities
- ensuring effective priority-setting mechanisms are established for the GRDI
- ensuring government objectives and priorities are addressed
- ensuring common management principles are implemented
- ensuring collaborations between organizations are pursued wherever relevant and possible

Interdepartmental working group

The interdepartmental working group, chaired by the NRC with membership at the director level from all participating departments and agencies and ISED, supports the work of the ADM CC. Its mandate is to support the ADM CC's strategic priority setting and overall management of the GRDI with recommendations and strategic advice. The working group meets about every two months—more often as ADM CC's needs for recommendations and advice warrant—and is responsible for:

- providing direction to GRDI activities related to operational delivery, implementation planning and investment priority setting
- supporting evaluation and reporting requirements related to the GRDI

Coordination function

Housed at NRC, the coordination function:

- provides GRDI-wide program coordination, communication, networking and outreach support (including support to the ADM CC and the GRDI working group)
- provides transparent and effective communication to departments regarding the planning cycle, process requirements, financial administration and other project management requirements
- supports SPP planning and implementation
- helps establish GRDI-wide research priorities
- facilitates interdepartmental project development and peer reviews
- ensures SPP project management plans and funding agreements are in place
- supports performance management, reporting, evaluation and communications

The GRDI coordination function is made possible by the funding set aside for shared priority activities.

GRDI's Performance Measurement Strategy Framework

GRDI Phase VI uses an updated version of the Horizontal Performance Measurement Strategy developed for Phase V. This version covers fiscal years 2014–2015 to 2018–2019 and formalizes the roles and responsibilities of the eight participating departments and agencies to promote effective monitoring and evaluation. These updates align with the Policy on Evaluation (2009) and associated Guide to Developing Performance Measurement Strategies (May 2010), as well as the policy and the associated instructions to departments for developing a management, resources and results structure (March 2013).

Appendix B includes an overview of the Performance Measurement Strategy Framework, as well as a logic model that reflects the overall objectives for the GRDI: the uptake and application of the knowledge and tools it generates for policy and regulatory decisions, key public policy priorities and private sector innovation.

HOW THE GRDI PERFORMED IN 2017–2018

NRC recorded the performance of the GRDI for 2017–2018 in three areas:

- interdepartmental governance
- research and development
- knowledge and networks

Interdepartmental governance

Coordinated management approaches

NRC provided ongoing coordination in 2017–2018, the fourth year of Phase VI, including timely secretariat support to GRDI departments and agencies and the implementation of GRDI governance, management and operating processes.

The ADM CC met three times in 2017–2018, and the GRDI working group met seven times to support collaborative decision-making.

Other activities included:

- supporting Phase VI shared priority projects and making funding available to participating departments based on the approved project management plans
- implementing the GRDI Performance Measurement Strategy following the ADM CC's finalization and approval of the Annual Performance Report for 2016–2017, and input into NRC's Departmental Results Report and Departmental Plan
- completing the GRDI evaluation under the leadership of NRC's Audit and Evaluation group and the interdepartmental GRDI evaluation working group
- implementing the Management Response and Action Plan resulting from the 2016 evaluation report

Shared priorities

Phase VI shared priority projects continued to implement their approved project management and science plans. Project leads held regular teleconferences with project participants, theme leads met bi-weekly, and all principal investigators met monthly.

Project-specific annual workshops took place in 2017 (EcoBiomics in Ottawa, March 13–15, and AMR project in London, Ontario, June 6–8) to update participants on project progress and coordinate activities for the coming year. Key end users and science advisors participated in the annual workshops and were engaged throughout the year. Project participants and collaborators took part in organized training sessions on data analysis platforms and bioinformatics software packages.

Research and development

The GRDI Performance Measurement Framework measures all activities surrounding the actual conduct of R&D, the transfer of technologies and results to stakeholders for uptake and application, and the communication of these results. All these areas are critical to ensuring GRDI-funded projects make an impact.

Annex 2 lists the direct scientific outputs for 2017–2018 and quantitative performance indicators by department/agency for:

- scientific contributions (key scientific contributions demonstrating leadership, other scientific contributions, research tools and processes)

- knowledge translation and mobilization (contributions to scientific networks)
- collaborations
- communications products
- end-user engagement and knowledge transfer activities
- research and technical personnel

Annex 3 provides highlights of the results achieved in 2017–2018 against planned results, while **Annex 4** presents a list of research tools and processes developed under the GRDI.

Several GRDI scientists received awards or prizes in recognition of the excellence of their research, as shown in Table 3.

Table 3: GRDI participant awards and prizes for research excellence

RECIPIENT(S)	PRIZE/AWARD
George Fedak (AAFC)	Vernadsky Gold Medal for outstanding achievements in the field of genetics and selection of agricultural plants, presented by the Presidium of the National Academy of Sciences of Ukraine in December 2017
D. Gonzàlez-Peña Fundora et al. (AAFC)	Best Student Presentation, Joint Meeting of the Canadian Phytopathological Society and the Canadian Society of Agronomy in Winnipeg, Manitoba, June 18–22, 2017
L. J. Harris et al. (AAFC)	One of the top 10 papers on fungal biology downloaded in 2017: "Host-preferential *F. graminearum* gene expression during infection of wheat, barley, and maize" in *Fungal Biology* issue 120, pages 111–123
Nicholas A. Tinker (AAFC)	Award for Outstanding Associate Editor, the *Plant Genome*
Charly Philips (AAFC)	Second-place award for best poster at the 2017 Guelph Food Safety Symposium
Quail Das (AAFC)	Travel award from the American Society for Microbiology to participate in Microbe 2018 in Atlanta, Georgia, United States
Teresita Porter (AAFC)	Featured in the 150 days of Canadian Women in STEM Initiative, #CanWomenSTEM150 (2017)
James Delano (CFIA)	**1.** Distinguished Service Award from the International Council on Viruses and Other Graft Transmissible Diseases of Fruit Crops (ICVF)—in recognition of exceptional leadership and devoted service to ICVF as a member of the management board of the Council and the Scientific Committee of ICVF **2.** Food and Agriculture Organization of the United Nations' (FAO's) International Plant Protection Convention (IPPC) Certificates of Special Recognition for outstanding contribution and commitment as discipline lead for the diagnostic protocol for Citrus tristeza virus; referee for the diagnostic protocols for *Erwinia amylovora* and *Bursaphelenchus xylophilus*
Guillaume Bilodeau (CFIA)	2017 President's National Award, CFIA, for exceptional service delivery, BioSurveillance of Alien Forest Enemies (bioSAFE)
Ian Bradbury (DFO)	Three-year Cox Fisheries Scientist in Residence Award from Dalhousie University for 2017–2020
Catherine Soos et al. (ECCC)	Second place award for the best student poster at the Western College of Veterinary Medicine's Annual Graduate Student Poster competition
Yunli Wang and Rene Richard (NRC)	2017 NRC Research and Technology Breakthrough of the Year award for establishing quantitative trait loci (QTL) and expression quantitative trait loci (eQTL) research pipeline published in *BMC Bioinformatics* issue 17, page 531
Kishore Rajagopalan (NRC)	Poster Award at the Fifth Annual Protein Structure, Function and Malfunction meeting in Saskatoon, Saskatchewan, 2017

RECIPIENT(S)	PRIZE/AWARD
Sateesh Kagale (NRC)	2017 AAFC award for outstanding achievement in science, which recognizes contributions to the advancement and enhancement of agriculture and agri-food research in Canada
Lisa Xiao-Rui Li (NRCan)	University of Toronto's Hasenkampf Riggs award for cell and molecular biology co-op work
Michel Cusson (NRCan)	"Distinction entomologique" award from the Entomological Society of Quebec for lifetime achievements and contributions to entomological research, teaching and other activities related to entomology
Marisa Rankin, co-op student of Roger Johnson (PHAC)	Honourable mention for University of Waterloo's 2017 co-op student of the year

Knowledge and networks

Knowledge translation and mobilization activities are essential to maximizing the GRDI's value and applying the research and tools it generates to commercial and public-good ends as the initiative matures. These activities include the development of scientific networks, communications products, end-user engagement activities, science policy integration, science advice, protocol transfer, field trials, outreach activities, and more. Activities like these ensure research is relevant by creating opportunities to understand the needs of end users and share the results of GRDI projects with them.

Examples of knowledge and networks activities completed in 2017–2018 follow.

Antimicrobial Resistance project

The GRDI-AMR project secured a material transfer agreement with Les Aliments Breton Inc. to obtain swine fecal samples from diverse husbandry conditions. Researchers also used funding from Canada's National Sciences and Engineering Research Council (NSERC) to study cranberries as an alternative to antibiotics in swine.

CFIA applied results and training from the AMR project to implement AMR gene detection based on whole-genome sequencing for foodborne pathogens collected through food testing programs. This will allow the agency to contribute to AMR surveillance at no additional cost through its existing food surveillance programs. In 2018, CFIA was able to predict that a large proportion of Shiga-toxin producing *E. coli* bacteria collected from a veal surveillance program were resistant to multiple antimicrobial agents. The agency transferred these strains to the Canadian Integrated Program for Antimicrobial Resistance Surveillance for further characterization.

Canadian Food Inspection Agency

CFIA scientists have enhanced their capacity to improve management, analysis and interpretation of genomics data. This includes data gathering from public databases to design assays and to perform comparative genomics, incorporating better and faster tools for computing-intensive processes, and streamlining workflows through in-house scripts that automate time-consuming steps.

Fisheries and Oceans Canada

During the 2017–2018 GRDI funding year, DFO scientists developed innovative fisheries genomics tools including a fine-scale genetic tagging system for salmon hatcheries, remote in-field environmental DNA collection platforms, and more. DFO transferred the knowledge these tools generated through networks of international and Canadian partners including the International Council for the Exploration of the Sea as well as Canada's Nisga'a, Gwich'in and Sahtu First Nations communities, whose livelihoods depend on the fisheries.

EcoBiomics project

The EcoBiomics bioinformatics team presented the GRDI's bioinformatics platform and lessons learned from the procurement process at the Canadian Forest Service Cloud Workshop in March 2018. The team also trained participants on how to use the GRDI data analysis image on the General Purpose Science Cluster (GPSC) in the Canadian Forest Service cloud. Some of the provided bioinformatics tools served as a use case.

Environment and Climate Change Canada

ECCC research scientists participated in two international research projects through EcoBiomics in 2017–2018:

- the European Union's (EU's) COST Action project, "Developing new genetic tools for bioassessment of aquatic ecosystems in Europe" (DNAqua-Net), which explores metabarcoding approaches to inform European legislation, including the *Water Framework Directive* and the *Habitats Directive*
- the United Kingdom (UK) Natural Environment Research Council large grant project, "Impacts of global warming in sentinel systems: from genes to ecosystems," at Imperial College London
- an international workshop titled "Advancing Adverse Outcome Pathways for Integrated Toxicology and Regulatory Applications"

GRDI scientists at ECCC also contributed to the GRDI AMR network, the GRDI EcoBiomics network and the annual Organisation for Economic Co-operation and Development (OECD) extended Advisory Group on Molecular Screening and Toxicogenomics.

Health Canada

HC scientists participated in a number of knowledge translation and mobilization activities related to the GRDI in 2017–2018. A lead HC scientist chaired the expert panel of U.S. National Toxicology Programs on the proposed approach to genomics use in toxic dose-response modelling. Additionally, HC provided the adverse outcome pathways developed with GRDI support to several researchers in Europe to aid risk assessment and risk communication activities.

Several HC scientists serve as advisors to several international organizations on the use of genomics technology to assess risks associated with chemicals, including:

- OECD's Extended Advisory Group on Molecular Screening and Toxicogenomics Programme
- World Health Organization's International Programme on Chemical Safety
- European Centre for Ecotoxicology and Toxicology of Chemicals
- Sustainable Nanotechnologies Project Consortium
- International Life Sciences Institute Health and Environmental Science Institute Genetic Toxicology Technical Committee
- Swansea University (UK) International Science Advisory Board
- Environmental Mutagenesis and Genomics Society
- International Congress of Toxicology
- EU's Horizon 2020 project consortium

In the area of stem cells, a lead HC scientist is part of the International Committee for Standardization of Mesenchymal Stem Cells to promote a standardized approach to the growth and development of mesenchymal stem cell-based health products. These activities greatly impact international best practices for the use of omics tools in regulatory toxicology.

National Research Council Canada

In 2017–2018, researchers under the NRC's Canadian Wheat Improvement flagship program contributed to the:

- International Wheat Yield Partnership for research of photosynthetic efficiency in wheat
- Wheat Initiative led by the Institut national de la recherche agronomique as part of an expert working group on adaptation of wheat to abiotic stress

- FusResis Consortium to develop enhanced Fusarium resistance in wheat
- International pan-genome (10+) sequencing effort
- Wheat Initiative-sponsored meiosis and recombination collaborative research partnership

Natural Resources Canada

NRCan researchers continued to develop tools to map and monitor the spread of forest invasive alien species and transfer these to partners. That includes assay technology researchers developed under the GRDI that can detect the Asian gypsy moth. Partners asked NRCan to share the technology after researchers presented it to the North American Forest Commission's insects, diseases and invasive plants working group, which includes representation from the federal governments of Canada, the United States and Mexico. Another GRDI-funded NRCan scientist was the invited expert on environmental impacts of genetically modified organisms at the National Academies of Science, Engineering and Medicine's Committee of Forest Health and Biotechnology in the United States.

Public Health Agency of Canada

GRDI projects underway at PHAC include engagement with national and international partners. For instance, PHAC researchers are developing enhanced tools for preventing foodborne pathogens in partnership with established national surveillance networks FoodNet Canada and PulseNet Canada. Similarly, efforts to develop genomics-based tools for controlling and reducing antimicrobial resistance involves close collaboration with national antimicrobial resistance surveillance networks the Canadian Nosocomial Infection Surveillance Program and the Canadian Integrated Program for Antimicrobial Resistance Surveillance. These partnerships between genomics researchers and surveillance epidemiologists strengthen the GRDI project through sample and knowledge sharing, and by facilitating the transfer of research results into practice.

Internationally, PHAC genomics researchers collaborate with the World Health Organization and the Pan-American Health Organization to share knowledge and technological approaches for eradicating the measles virus, and for detecting and responding to drug-resistant human immunodeficiency virus. Work to enhance global surveillance of measles virus and antibiotic-resistant Gonorrhoea is also ongoing with partners from the World Health Organization.

APPENDIX A – SUPPLEMENTAL PERFORMANCE DETAILS

Annex 1: 2017–2018 GRDI projects and allocations from GRDI funds

GRDI FUNDS ($)	PROJECT TITLE
SHARED PRIORITY PROJECTS	
1,889,499	Antimicrobial resistance (AMR)
1,851,522	Metagenomics based environmental biomonitoring (EcoBiomics)
AGRICULTURE AND AGRI-FOOD CANADA	
86,500	Mining legume genomes for attributes of sustainable nutrient (nitrogen) acquisition through symbiosis
417,000	*Camelina sativa* as a 21st century clean energy crop for Canada
1,225,530	Targeting resistance and susceptibility genes and dissecting infection mechanisms through genomics for durable Fusarium and rust resistance in cereals
186,600	Gene-for-gene mediated resistance to midge in canola and wheat
1,136,250	Advanced genomics strategies to capture novel genetic diversity for oilseed crop improvement
1,126,600	Genetic and epigenetic variants of Canadian cereal crops for breeding and functional analysis
220,530	Improving soybean for Canadian agriculture: management of biotic stresses and symbiotic microbes
CANADIAN FOOD INSPECTION AGENCY	
70,000	Application of whole genome sequencing for molecular epidemiological investigations of bovine tuberculosis in Canada and for the high throughput discovery of novel diagnostic antigens for *Mycobacterium bovis* and *Brucella abortus*
130,000	Enhancing the CFIA's genomic capabilities for detection and characterization of high consequence known and unknown/unexpected animal viruses and their vectors/reservoirs
200,000	Whole genome sequencing technologies as tools for the detection, isolation, identification and characterization of pathogens in support of Canadian food inspection objectives
200,000	Detection and identification of plant pests and plants with novel traits using next generation sequencing
70,000	Development of diagnostic sequencing methods to monitor, detect and characterize RNA viruses of food, animals and plants, following viral contamination or infection
50,000	Development of infrastructure and bioinformatics tools to support genomics activities in CFIA's food, plant and animal business lines

ENVIRONMENT AND CLIMATE CHANGE CANADA	
23,972	Application of genomics to assess the impact of harvest and other mortality sources on vulnerable populations of North Atlantic murres
46,942	Development and validation of metabolomic techniques to evaluate impacts of large-scale environmental changes on stress responses in wildlife
91,149	Development of next-generation genomic tools to investigate cumulative effects of urban pollution and pathogens in two sentinel fish species
82,034	Environmental DNA - improving inference through validation studies
28,256	Population genetic structuring in a widely-distributed Pacific coast seabird
105,733	Hybrid data generation from traditional and DNA-based biomonitoring
54,689	Measuring genome health in wildlife populations
58,791	Metabolomics for predicting the mode of action of chemicals of concern in aquatic organisms
45,574	Metagenomic profiling of river water quality for watershed protection
62,893	Rapid assessment of algal community composition and harmful blooms using DNA barcoding and remote sensing
56,968	Toxicogenomic solutions for assessing exposure and effects of environmental contaminants in wildlife
50,132	Trancriptomic analysis of the ecotoxicological effects of nanomaterials on micro-organisms
52,866	Viable pathogen identification using DNA sequencing technology in microbial risk assessment
FISHERIES AND OCEANS CANADA	
188,500	Genomic analysis of spatial stock structure of Arctic char
131,800	Investigating population structure and connectivity of Atlantic cod in the western Atlantic using next generation sequencing
94,400	Detecting aquatic organisms ‘in the field’ using environmental DNA methods in the Canadian arctic
180,000	Parentage-based tagging of Chinook Salmon in British Columbia
106,600	Rapid and sensitive eDNA methods for early detection and mitigation of aquatic invasive species and monitoring of aquatic species at risk
HEALTH CANADA	
250,000	An integrated systems biology approach to investigate immunopotentiation induced by Respiratory Syncytial Virus vaccines
225,000	Development of genomics biomarker to provide mechanistic context and data in support of human relevance for chemicals inducing cellular stress responses
263,000	Identification of biomarkers for the standardization and risk assessment analysis of mesenchymal stem cell-based health products
100,000	MicroRNA profiling of serum and milk from toxicological studies of natural and anthropogenic chemicals as an endpoint for comparative assessment with apical endpoints within the Benchmark dosing framework
129,000	Safety of prebiotics in infants
203,000	Systems biology informed structure-activity-relationships to predict pulmonary pathology induced by nanomaterials
280,000	The coming revolution: next generation sequencing detection of de novo mutations in the offspring to identify germ cell hazards

NATIONAL RESEARCH COUNCIL CANADA	
888,000	Biologics and biomanufacturing program: development of support technology
3,552,000	Wheat improvement flagship (enhancing fusarium and rust tolerance; genomics-assisted breeding; abiotic stress; seed development)
NATURAL RESOURCES CANADA	
57,727	Accelerating the discovery of insect volatile attractant molecules with genomics
145,340	An early detection tool for Emerald Ash Borer and ash resource protection
371,520	Applied genomics for tree breeding and new applications
62,309	Development of metagenomic and bioinformatics tools to facilitate processing of trap captures
96,212	Developing molecular and environmental genomic approaches for microbial and invertebrate communities to assess ecosystem integrity in forest management
152,106	Developing the next generation biosurveillance tools for tracking and preventing forest pest invasions
27,000	Development of molecular methods to detect living Phytophthora spp. of phytosanitary concern in wood
82,467	Genomics-assisted tree breeding for improving remediation of disturbed forest ecosystems
186,860	Innovative land reclamation approaches following oil sand mining: Improving phytoremediation tree-soil microbes interactions
71,930	Spruce budworm eco-genomics: from population dynamics to population suppression
84,300	Tools for enhanced molecular detection of Asian Gypsy Moth and identification of their geographic origins
PUBLIC HEALTH AGENCY OF CANADA	
125,000	BioTools for the predictive genomics of priority foodborne pathogens
150,000	Closing the gaps in national surveillance of *Clostridium difficile*: epidemiologic and genomic characterisation of community-onset and recurrent *C. difficile* infections
75,000	Implementation of genome-based analyses to “One Health” surveillance of enteric disease
75,000	PulseNet Canada: model framework development for genomic technology delivery in a laboratory network
106,000	Single nucleotide variant subtyping of *Salmonella* Enteritidis and *Salmonella* Heidelberg
70,000	Translational analytic infrastructure for emerging pathogen discovery
80,000	Whole genome sequencing of *Neisseria meningitidis* and its application to surveillance and understanding invasive meningococcal disease molecular epidemiology dynamics
125,000	Mass spectrometry technology development
275,000	Improving surveillance of non-enteric bacterial pathogens by whole genome sequencing
100,000	Bridging the epidemiological gap for priority *Salmonella* servars through genomic characterisation and nomenclature development
284,606	Revolutionizing molecular viral characterisation strategies in support of enhanced outbreak investigation and surveillance in the next generation sequencing era

Annex 2: Quantitative indicators for performance measurement

Scientific contributions

Scientific contributions include scientific information and publications produced, accepted, in press, or published (including online) in 2017-2018. They include contributions from any project team member as long as they relate to the GRDI project. They also include contributions deriving from a previous phase of the project, if produced in 2017-2018. They do not include submitted papers or publications in draft form, nor contributions that were reported in previous years.

Key scientific contributions demonstrating leadership

NUMBER OF KEY SCIENTIFIC CONTRIBUTIONS											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	**Total**
Publications in refereed journals	8	32	20	19	22	22	31	16	12	12	**194**
Publications in refereed conference proceedings	19	11		1	2	10	4	4	2	0	**53**
Books (edited, written) and book chapters	0	0	0		0	2	0	1	0	0	**3**
Invited presentations	21	19	0	0	14	10	20	4	17	13	**121**
International conference presentations	25	7	3	16	9	17	17	5	19	5	**121**
Editorial posts for national and international journals (excludes peer reviewers)	0	9	1	5	2	0	3	0	4	2	**25**
New genomics related databases or libraries	0	4	0	2	3	2	3	9	2	1	**27**
Awards, prizes	4	3	1	3	0	2	2	1	2	1	**19**
Total	**77**	**85**	**26**	**2**	**52**	**65**	**80**	**40**	**58**	**34**	**563**

Other scientific contributions

NUMBER OF OTHER SCIENTIFIC CONTRIBUTIONS											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	**Total**
Technical reports	0	63	0	0	0	21	3	2	1	1	**91**
Other publications (ex. abstracts, notes, industry magazines, etc.)	0	3	0	3	0	4	3	0	0	3	**16**
Poster presentations at conferences	2	18	1	32	17	13	2	9	13	15	**122**
National conference presentations	10	2	0	2	1	10	10	5	6	5	**51**
Deposits in genomics related databases or libraries	0	9	0	2	1	117	1	201	4	1	**336**
Total	**12**	**95**	**1**	**39**	**19**	**165**	**19**	**217**	**23**	**25**	**616**

Research tools and processes

Research tools and processes include those produced in 2017-2018, deriving from previous phases of the GRDI if produced in 2017-2018, as well as produced in previous years if they have been improved since last reported on.

NUMBER OF RESEARCH TOOLS AND PROCESSES											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	**Total**
Research tools	20	10	18	16	12	21	15	18	18	11	**159**
Research processes	16	11	11	11	7	9	4	21	22	0	**112**
Total	**36**	**21**	**29**	**27**	**19**	**27**	**19**	**39**	**40**	**11**	**271**

Knowledge translation and mobilization

Knowledge translation and mobilization activities include the development of scientific networks, communications products, end-user engagement activities, science policy integration, science advice, transfer of protocols, field trials, outreach activities, etc. They ensure that research remains relevant to solve specific problems by maximizing opportunities to understand the needs of targeted end-users and active dissemination of GRDI results to them.

Contributions to scientific networks

NUMBER OF CONTRIBUTIONS TO SCIENTIFIC NETWORKS											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	**Total**
Participation in government meetings/seminars/advisory panels related to regulations or policy in Canada and internationally	7	9	14	13	22	0	8	3	25	7	**108**
Participations in national or international genomics-related committees	12	11	3	10	7	5	4	9	12	4	**77**
National or international genomics research peer review committees served on	3	7	2	2	4	4	2	0	1	0	**25**
Participation in national conferences	15	2	1	4	1	11	1	1	15	7	**58**
Participation in international conferences	30	7	3	1	5	16	2	2	26	4	**96**
Total	**40**	**36**	**23**	**30**	**39**	**36**	**17**	**15**	**79**	**22**	**364**

Collaborations

Collaborations by department/agency, expressed in terms of number of individual research collaborators in 2016-2017 from an organization different from that of the project's lead scientist, and who are directly involved in the delivery of the project. The GRDI involves many research collaborative relationships among government-based science organizations, universities, industry, and other research institutes, both nationally and internationally.

NUMBER OF RESEARCH COLLABORATORS											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	**Total**
Canadian universities	18	13	28	32	9	4	29	14	39	26	**212**
International universities	28	2	12	13	7	4	24	4	14	5	**113**
Other international research organizations	16	2	4	6	6	1	23	3	16	2	**79**
Other Canadian research institutions	3	0	0	3	6	2	3	0	4	0	**21**
Private sector	5	0	3	5	3	10	3	0	3	1	**33**
Other government departments	16	15	14	25	9	0	9	10	28	21	**147**
Other public sector organizations such as provinces, municipalities, and Non-Governmental Organizations	1	3	11	1	0	3	24	26	5	1	**75**
Total	**87**	**35**	**72**	**85**	**40**	**24**	**115**	**57**	**109**	**56**	**680**

Communications products

NUMBER OF COMMUNICATIONS PRODUCTS											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	**Total**
Media interviews	4	0	11	0	0	2	3	0	2	1	**23**
Press releases	0	0	6	0	0	0	0	0	7	0	**13**
Newspaper and magazine articles	1	1	3	0	0	2	1	1	7	0	**16**
Community presentations	8	5	2	1	0	0	0	0	4	2	**22**
Brochures, fact sheets, web pages	1	1	2	1	1	1	2	1	5	0	**15**
Total	**14**	**7**	**24**	**2**	**1**	**5**	**6**	**2**	**25**	**3**	**89**

End-user engagement and knowledge transfer activities

NUMBER OF OUTREACH ACTIVITIES											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	**Total**
End-user consultations	9	14	9	5	16	0	4	0	11	2	**70**
Public meetings	3	1	3	2	1	0	0	0	0	1	**11**
Science advice, including to senior management	13	3	1	3	8	0	9	1	21	4	**63**
Outward material transfer agreements	9	0	0	0	0	0	3	0	3	0	**15**
Transfer of standard operating procedures	4	27	1	0	1	0	0	1	0	0	**34**
Disclosures	2	0	0	0	0	12	0	0	1	0	**15**
Active patents, patent applications, patents issued	6	0	0	0	0	9	0	0	1	0	**16**
Licenses issued	0	0	0	0	0	0	0	0	0	0	**0**
New formal collaborative agreements / standard operating protocols	0	0	0	1	0	0	0	0	0	0	**1**
Knowledge transfer workshops with stakeholders/end-users	13	4	4	4	15	2	1	9	11	6	**69**
Requests for research results, papers, collaborations	13	6	5	8	1	not tracked	1	0	46	3	**83**
Total	**72**	**55**	**23**	**23**	**42**	**23**	**18**	**11**	**94**	**16**	**377**

Research and technical personnel

Research and technical personnel by department/agency expressed in terms of number of persons engaged in projects funded by the GRDI in 2017–2018, including but not exclusive to personnel financed through GRDI funds.

NUMBER OF RESEARCH AND TECHNICAL PERSONNEL											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	**Total**
Research scientists	53	24	18	30	17	54	21	33	31	17	**298**
Research professionals	7	17	24	10	13	10	17	33	21	12	**154**
Research technicians	76	15	18	19	17	152	19	16	19	16	**367**
Post-doctoral/visiting fellows	8	1	10	8	3	27	3	4	5	2	**71**
Graduate students	9	4	2	10	3	3	7	2	13	0	**53**
Undergraduate students	20	2	2	12	6	2	3	13	15	10	**85**
Administrative officers	0	0	1	3	0	0	0	1	0	0	**5**
Total	**173**	**63**	**75**	**92**	**59**	**238**	**70**	**102**	**104**	**57**	**1033**
Total estimated full-time equivalents	**81.82**	**19**	**26**	**36**	**20**	**47**	**38.9**	**34**	**41.95**	**44.05**	**389**

Annex 3: Highlights of results achieved in 2017–2018

Interdepartmental research along shared priorities and common goals

Participating departments/agencies: AAFC, CFIA, ECCC, DFO, NRC, NRCan, PHAC

Scientific coordination: ECCC, AAFC

Project management: AAFC

Water and soil biodiversity are paramount to sustain diverse ecosystem services and economic activities across Canada. Genomics tools are the only tools available to characterize this complex biodiversity. The EcoBiomics project enables a more comprehensive perspective of water and soil as living systems by developing advanced genomics tools to:

- assess freshwater ecosystem biodiversity and water quality in lakes and rivers
- evaluate the health of soil, which is essential to the productivity of agricultural and forestry systems across Canada
- investigate soil remediation for the oil and mining sectors

Project highlights:

- Participants are now using the bioinformatics platform hosted on the General Purpose Science Cluster (GPSC) in Dorval for metagenomics data analysis. This has enabled coordination across seven federal departments and agencies.
- The Sequence Database, which manages genomic data and metadata, has been enhanced to support standardized sequence submission to the Saskatoon NRC facility, customized to support metagenomic workflows, and upgraded to add functionality for environmental metadata capture and project-level reporting.
- Researchers completed experiments on soil, water and invertebrate sample collection and nucleic acid extraction methods. Participants implemented the results, which will soon be published as standard operating procedures (SOPs).
- Scientists collected more than 2,300 soil, water and invertebrate samples across Canada for DNA sequencing. The NRC's sequencing facility processed a total of 47 sequencing runs on the Illumina MiSeq (metabarcoding) and HiSeq (metagenomics) platforms.
- Departments provided bioinformatics training to more than 80 project participants. Training included an introduction to the GPSC, Galaxy genomic workflows and R for metagenomics, as well as the creation of a bioinformatics working group.
- Researchers continued discussions with end-user groups on protocols for implementing genomic monitoring and selecting candidate genomic observatories. These groups included ECCC's National Water Quality Monitoring Program and the Canadian Aquatic Biomonitoring Network (CABIN).
- In February 2018, AAFC jointly hosted a workshop at the Max Planck Institute for Marine Microbiology in Bremen, Germany, entitled "Enhancing interoperability and coordination of long-term omics observations." The objective was to facilitate the creation of a well-integrated, global network of omics observatories delivering coherent insight into ecosystem health and function. A new task force called the Global Omic Observatory Network (GLOMICON) will mobilize this effort further. GLOMICON will operate under the international Group on Earth Observations Biodiversity Observation Network (GEO BON).

Antimicrobial Resistance (AMR) Project

Participating departments/agencies: AAFC, CFIA, HC, PHAC and NRC
Scientific coordination: AAFC
Project management: AAFC

The project will add to understanding of the critical activities that contribute to antimicrobial resistance development. It will also shed light on critical exposure pathways through which antimicrobial bacteria reach humans, which could help validate economically sustainable technologies, practices and policies to mitigate the development of antimicrobial resistance.

Project highlights:

- Current methods enable scientists to measure and predict antimicrobial resistance (AMR) phenotypes well, but they are less effective at associating AMR with methods of transmission. "MOB-suite" is a new analytical tool that is freely available to GRDI-AMR and other researchers and can predict AMR phenotypes as well as the mechanisms of transmission associated with them. The software allows researchers to understand which mechanisms of transfer can be associated with specific antimicrobial resistance genes (ARGs) isolated in surveillance and outbreak investigations, and enable them to measure the frequency of transfer associated with the more commonly found mobile genetic elements (MGEs). In addition, researchers have developed a comprehensive database of closed plasmid genomes from data arising from this project as well as from public databases. Together, these tools will improve the ability of risk modellers and policy makers to assess the risk of spread of ARGs associated with certain classes of MGEs.
- Researchers are developing a large collection of bacterial sequences to gain a better understanding of the spread of AMR in the food supply. Researchers have completed more than 6,000 draft bacterial genomes and 48 shotgun metagenomes. They developed novel sequencing approaches to enable more accurate characterization of mobile elements within these genomes. More than 1,000 closed plasmid sequences are now available to support the study of mobile elements within whole-genome sequencing (WGS) data.
- Scientists completed studies using enterococci to assess the impact of beef production systems on the one-health AMR continuum. They found that enterococci associated with AMR differed clearly between humans and cattle.
- Scientists conducted research that showed that use of antimicrobials in poultry led to a clear increase in AMR bacteria in poultry litter, some of which could pose a risk to human health. They found that plant bioactives had the potential to reduce AMR in poultry.
- Researchers collected several thousand isolates throughout the production continuum of swine raised with and without antibiotics. They are now assessing these isolates to determine the impact of these vastly different production practices on AMR.
- Researchers assessed the impact of treatment of biosolids on AMR in soils and cropped produce and identified treatment methods that could reduce the AMR spread. They found that swine manure compost harboured more AMR genes that persist longer in the environment than yard or food waste compost.
- Scientists generated specific antimicrobial-resistant strains of *Salmonella* and *E. coli* to enable more detailed tracking of their movement within soil environments.
- Researchers continued to work on the Integrated Assessment Model, including finalizing the mathematical approach and input data formats. They carried out preliminary simulations to test the validity of the model based on two risk profiles. Calibration and validation will continue throughout the remainder of the project.
- Researchers completed a draft quantitative microbial risk assessment model for *Salmonella* Heidelberg in poultry.

Commercially relevant advances in areas of genomics R&D related to human health

NRC has used GRDI support over the years to advance multiple projects with the overall objective of improving cancer treatment. This multi-pronged approach is grouped into three activity thrusts:

Better cancer diagnosis and prognosis

Historical data suggest early detection is crucial for the ultimate control and prevention of cancer. There have been substantial efforts to improve cancer early detection, but relatively few approaches have proven sufficiently effective. Recent advances in genome sequencing provide tremendous potential for the development of tools to aid cancer early detection.

NRC scientists have developed a software tool, eTumorMonitor, which starts from a healthy individual's genetic makeup and is able to predict key personalized cancer-driver genes whose mutations are required for the first steps of malignant transformation (i.e., the formation of the cancer founder cells). The identity of the genes will then be used for the early detection of tumors. This approach has been validated on breast cancer data sets and is now being applied to pediatric leukemia in collaboration with clinicians and scientists at the Centre hospitalier universitaire (CHU) Sainte-Justine in the context of the new Innovation Centre in Applied Micro-Analytics for Pediatric Medicine (I-CAMP).

Developing novel, biologics-based therapeutic modalities

Target selection is a critical first step in the development of effective protein-based therapeutics that have the potential to "attack" cancer in novel ways. NRC continues to improve its target selection and prioritization by using multiple bioinformatic and experimental approaches to identify the most promising candidates. Following intensive characterization and screening in multiple assays, researchers generate antibodies or other protein traps against these targets and earmark the highest performing candidates for further development. NRC is partnering these assets with Canadian small and medium enterprises once they have completed in vivo validation.

NRC has also seen more requests from potential partners for collaborations involving target identification and antibody development for very specific indications. This development pipeline has yielded one therapeutic that has reached the human clinical trial stage (anti-Clusterin antibody, Alethia Biotherapeutics). Formation Biologics licensed a second candidate in 2017, with clinical trials targeted for summer 2018.

Optimization of NRC's proprietary biologics expression platform

Antibodies and other protein-based therapeutics are large, complex molecules that have to be reliably manufactured at scale to enable clinical testing and, ultimately, commercialization. NRC's Chinese Hamster Ovary (CHO) cell production platform has been a cornerstone of the organization's biomanufacturing strategy and is widely used for work with NRC clients and collaborators as well as for internal research and development. NRC scientists are continually seeking to improve its performance.

NRC's proprietary CHO-BRI cell line has been fully sequenced, and researchers are using this genomic information as the basis for understanding production characteristics. Researchers are also using the information in combination with metabolomic analysis as part of process improvement and cellular engineering for significant improvements in yield.

Improving Canada's health regulatory system

Assessing the safety of prebiotics for infants

Maternal milk contains a wide variety of carbohydrates that are not digested in the small intestines of infants but pass into the large intestines, where they serve as an energy source for the developing bacterial community. Some infant formulas contain easily fermentable carbohydrates to mimic this function. There is a large body of scientific literature linking these carbohydrates to gut bacteria composition, immunological function and gastrointestinal disease. For this reason, it is important to assess the short- and long-term effects of fermentable carbohydrates on the developing gut bacteria of infants.

HC researchers are studying the impact and long-term effects of dietary fermentable carbohydrates on the gut bacterial community of weaning rats. Their goal is to use genomics-based methods to assess how these carbohydrates influence the composition of gut bacteria in growing infants and whether these changes can be related to changes in the metabolism and gene expression of the cells in the large intestine. They have found that the gene expression of intestinal cells varies depending on diet, sex and age. Interestingly, it appears that changes seen in weaning rats are reversed after two months of feeding them regular food. Further analysis is needed to determine how these changes may impact later intestinal function.

This project has already increased awareness among HC regulators of the physiological outcomes that are potentially associated with consuming fermentable materials, especially as they apply to infant formula. Researchers are now developing methods for monitoring the microbiome metagenomics response. Immunological analyses are now complete, and researchers have begun work on statistical analysis/interpretation.

Measuring the health effects of fungal toxins and chemical contaminants in food with microRNA

MicroRNA (small, non-coding ribonucleic acid [RNA]) is important for regulating gene expression and translating genes into protein products. HC researchers set out to identify and characterize microRNA molecules found in rodent serum and milk that are associated with dietary exposure to fungal toxins and chemical contaminants detected in foods. The research team has so far completed an analysis of the microRNA from isolated RNA in serum and liver samples of rodents exposed to several brominated flame retardants, as well as from fungal toxin studies, to determine the potential biomarkers of liver damage.

The team has also completed benchmark dose-modelling of apical endpoints (e.g., toxicological effects involving body weight, liver lesions, organ weights, hematology endpoints and biochemistry endpoints) for specific types of flame-retardant chemicals and fungal toxins. The team has developed and published a manuscript, and has developed and submitted for publication a paper highlighting the research findings. They are currently preparing two more papers.

The work will ultimately generate important regulatory toxicology data that will enhance HC's ability to detect and respond to fungal toxins and chemical contaminants in food Canadians consume.

Predicting pulmonary pathology induced by nanomaterials

Nanomaterials are tiny materials measuring less than 100 nanometres that can induce harmful effects in experimental animals. In the first study of its kind, HC researchers are combining toxicogenomics and computational tools to identify and analyze the potential toxic effects of different classes of nanomaterials on lung cells and tissues. They repeatedly exposed mouse lungs to various nanomaterials—including multi-walled carbon nanotubes and copper oxide and titanium dioxide nanomaterials—to study the toxic effects. They found that the nanomaterials induced sustained pro-inflammatory-, pro-emphysema- and pro-fibrotic-like responses. Furthermore, in ex vivo, precision-cut lung slices were exposed to 25 individual silica nanomaterials of different sizes and surface modifications to investigate potential toxicity. Pristine silica with no surface modification induced more pro-inflammatory responses than surface-modified silica.

Researchers have shared their results with HC's regulators and presented them to the international regulatory community at international meetings and conferences. HC can use the methods developed in the study to prioritize nanomaterials for further toxicological investigation and to help with the rapid screening of potentially harmful nanomaterials.

Understanding the respiratory syncytial virus vaccine

Respiratory syncytial virus is a highly contagious virus that infects the respiratory tracts of infants and young children. It is the most common cause of bronchitis. Dozens of prototype vaccines have been under development for the last 50 years, but no vaccine has yet been approved for the prevention of this infection. The slow

pace of respiratory syncytial virus vaccine development is largely due to a lack of understanding of both the disease and the critical elements for evaluating the efficacy and safety of the vaccine.

This project aims to improve understanding of the safety and efficacy of candidate vaccines. Scientists conducting animal studies on prototype vaccines have identified toxicity associated with certain forms of candidate vaccines and shed light on some of the underlying mechanisms. The team is exploring its study-animal model for the investigation of vaccine-induced toxicity. In addition, researchers observed that some forms of vaccine could induce lung and blood disorders.

The team has communicated its data to other government researchers and academics.

Using next-generation sequencing to detect de novo mutations to identify germ cell hazards

A *de novo* mutation is a genetic change that appears for the first time in a family member. *De novo* mutations are associated with a diverse array of genetic phenotypes or observable characteristics, and they appear to contribute to a wide range of human diseases. Evidence suggests that many environmental agents cause DNA damage, thus increasing the risk of inherited mutations and genetic disease in offspring.

HC scientists are using genomic technologies to analyze chemically induced heritable mutations in animals and humans. The research team has applied advanced genomic technologies to measure heritable large-scale genome changes in mice exposed to benzo(a)pyrene (BaP), a common environmental pollutant found in cigarette smoke. The researchers conducted and published a literature review on the effects of paternal smoking on sperm and the consequences to offspring. They sequenced nine genomes to detect mutations in children with fathers who smoked. They also conducted a power analysis to establish the best experimental design for detecting mutations in studies using human families.

WGS of six mouse families showed a doubling of mutations in the offspring of mice exposed to BaP. The completed genome sequence of the MutaMouse transgenic model served as a frame of reference for identifying new mutations in the offspring of exposed males. The team has implemented a bioinformatics pipeline to establish the mutation spectrum in the sperm of exposed mice. Future research will use this pipeline for sperm-offspring comparisons and heritability assessments.

Standardizing and assessing the risk of stem cell-based health products

Stem cells have tremendous potential to treat diseases for which there are currently no cures, but their use can be risky. HC researchers are developing diagnostic tools to thoroughly evaluate the risks and benefits associated with the therapeutic use of human mesenchymal stem cells, a type of adult stem cell. Researchers determined that stem cells from bone marrow contribute to leukemia and found potential differences between stem cells from the bone marrow of leukemia patients and from that of healthy individuals. They also found two specific biomarkers that distinguished sarcoma-forming cells from clinically effective stem cells.

The researchers also examined the limits of stem cell expansion, an operation critical to the processing of stem cells for therapeutic use. They established the maximum number of times a stem cell can be expanded without losing its therapeutic effectiveness. This finding allowed the research team to identify proteins whose secretion was directly linked to the stem cells' therapeutic function.

The successful validation of these biomarkers and findings will support the development of diagnostic tests for evaluating the safety and efficacy of stem cell-based health products.

Assessing the health effects of chemicals

Traditional toxicology tests used to evaluate the health effects of chemicals are both time consuming and expensive. HC researchers are developing and validating genomics-based toxicology methods that promise to save time and money compared to traditional tests. The new methods can predict whether a chemical will cause DNA damage or other adverse genetic effects.

The researchers applied genomics signatures (patterns of gene expression changes) to identify agents that cause various toxic effects. The team's major accomplishment was to successfully validate a signature that predicts the ability of chemicals to damage DNA in cultured cells relevant to humans. This work was submitted to the U.S. Food and Drug Administration's Biomarker Qualification Program to advance regulatory uptake of this signature. Researchers produced guidelines for the use of genomics in regulatory toxicology, one of which the OECD adopted as a project for international harmonization. The research also informed the development of the National Toxicology Program's approach to the use of genomics data in dose-response assessment.

Strengthening public health programs

Controlling and preventing foodborne illness

PHAC research addresses the critical need for scientific and technical innovation in pathogen detection and characterization to improve the identification of outbreaks, as well as accurate and timely source attribution. The surveillance programs of FoodNet Canada and the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) monitor foodborne pathogens and the use of and resistance to antibiotics in the food chain. These programs monitor various points along the "farm-to-fork" continuum: farms, surface waters, food production and public health laboratories.

Researchers are developing genomic epidemiology approaches to food safety to support these programs. These new approaches will help identify risk factors, sources of exposure, virulence factors, determinants of AMR and transmission dynamics along the food chain of *E. coli*, *Salmonella* and *Campylobacter*. GRDI researchers are working to transition the PulseNet Canada network's enteric disease surveillance from traditional molecular methods to WGS. This will enable all network members to apply WGS to foodborne disease surveillance and food safety.

Researchers have also designed a translation framework to encompass all aspects of genomics in the context of PulseNet Canada. Its implementation across Canada is proceeding on schedule.

Detecting and determining the genomic epidemiology of priority pathogens

PHAC researchers are developing and applying modern and innovative technologies (e.g., genomics and mass spectroscopy) alongside advanced scientific computing to address the strategic need to enhance Canada's public health capacity for rapid identification of infectious pathogens.

Rapid identification, close surveillance and effective outbreak response are essential to preventing and controlling viral diseases. Genomics researchers at PHAC are developing advanced bioinformatics technologies that will be implemented into federal laboratory services that respond to HIV-1; hepatitis A, B and C viruses; influenza virus; and measles virus. They are also developing a series of laboratory processes and bioinformatics tools that will revolutionize our existing molecular viral characterization strategies. These tools will enable more informative disease surveillance and timely disease outbreak investigations. This work will also provide the core infrastructure extendable to other viral pathogens, facilitating the adoption of WGS as a routine technology protecting public health.

Canadian, American and European scientists have worked together to establish a national mass spectrometry database to support diagnostic laboratories across Canada. The mass spectroscopy identification of bacteria helps Canadian public health laboratories and hospitals identify uncommon and rare bacterial pathogens. It also supports the implementation of new technology that can identify infectious disease pathogens rapidly, inexpensively and accurately. In addition, researchers are developing proteomics assays capable of identifying bacterial toxins that will provide a rapid and inexpensive method to detect and respond to highly pathogenic bacterial infections.

Invasive meningococcal disease, caused by *Neisseria meningitidis*, emerged unexpectedly in Quebec in 2003 and has remained endemic there since that time. PHAC researchers have developed a new genomic database and analysis platform that has been used to analyze the WGS data of 51 historical isolates. Their data show that a unique clone of this pathogen is circulat-

ing endemically within the province of Quebec. Notably, by characterizing the presence of vaccine targets in the endemic clone, the data also predict that an existing vaccine could be used to control the disease. In addition, the tools developed by PHAC researchers will help physicians identify strains of *Neisseria* that may be associated with increased transmission, severity of disease, higher case fatality rates or unusual clinical presentations.

Addressing antimicrobial resistance in communities and hospitals

Reducing the growing threat AMR poses is one of PHAC's highest priorities due to the risk of losing the ability to manage infectious diseases in humans and animals. To that end, GRDI-supported researchers are developing genomics-based technologies and methods to promote appropriate antibiotic usage and effective infection control procedures. They are also developing new tools and procedures that will enhance our capacity to detect and track AMR pathogens.

These activities can help reduce the risk posed by antibiotic-resistant infections while supporting the management and treatment of infectious diseases. Examples include:

- ***Clostridium difficile***—Research is underway to minimize the burden of *C. difficile* in Canadian hospitals through better understanding of transmission routes and recurrent cases in health-care and other settings. Most infection control and prevention guidelines have focused mainly on patients within hospital settings, but the emerging problem of community-onset infection and recurrent infection means new information is needed. Studies of risk factors for recurrent infection are intended to provide new clinical prediction tools to identify patients at the highest risk of recurrent infection. This would allow for more targeted preventive and therapeutic interventions for patients with *C. difficile* infection.
- ***Neisseria gonorrhoeae***—Researchers are developing a method to carry out WGS of *N. gonorrhoeae* directly from leftover urine samples collected by clinics. The expected long-term public health outcomes will include improved *N. gonorrhoeae* outbreak response, enhanced antimicrobial stewardship, and better understanding of *N. gonorrhoeae* dissemination and AMR transmission

Increasing Canada's share of global wheat production

The Canadian Wheat Improvement flagship program, funded in part by the GRDI, is the NRC's contribution to a large-scale research alliance established to improve the yield, sustainability and profitability of Canadian wheat for the benefit of Canadian farmers and the Canadian economy. The Canadian Wheat Alliance (CWA) includes major contributions by the NRC, AAFC, the University of Saskatchewan and the Government of Saskatchewan.

This program has developed strong expertise in genomics and developmental aspects relevant to performance and yield in wheat.

Improving breeding practices

Researchers are working on improving a number of necessary resources including genomic sequences and annotation, large collections of genetic markers, high-throughput genotyping and the development of new populations for wheat breeding.

Researchers are conducting pan-genome sequencing of Canadian wheat to generate an atlas of inter-varietal genomic variations underlying important agronomic traits in Canadian wheat. The atlas will help to develop strategies to maximize genetic gains and breeding efficiency, thereby increasing mean annual yield growth. Researchers have so far established a near-reference-quality genome sequence assembly of Stettler, a popular wheat variety in Canada. Researchers will sequence an additional 50 lines in the near future—including Canadian elite wheat cultivars, wild relatives, specialized genetics stocks and synthetic wheat—to define the Canadian wheat pan-genome.

The analysis of crop pan-genomes helps:

- capture the complete repertoire of genes in a species
- provide a multifaceted and accurate view of genetic diversity

- understand structural variations that exhibit enriched association with phenotypic traits
- develop precise associations of genotypes and heritable agronomic traits

Scientists have established a multiple genotyping and bioinformatics platform to support Canadian wheat researchers and breeders with a range of applied genomic techniques. These include marker-assisted selection, gene pyramiding, association mapping and high-density genetic map generation. The genotyping platform is based on targeted resequencing strategies including the reduced exome capture for wheat, repetitive amplicon sequencing (rAMPseq) and a variation of region-specific extraction sequencing. It has decreased the costs of genotyping, improved accuracy and decreased bias.

Researchers collaborated with AAFC partners to establish a bread wheat nested association mapping (NAM) population. To generate the NAM population, the team crossed Stettler, a common reference line (Canada Western Red Spring variety), with 25 synthetic hexaploid wheat donor lines, which were developed at the International Maize and Wheat Improvement Center (CIMMYT; synthetic hexaploid wheat [SHW] Panel), and 25 historic and modern elite Canadian cultivars. The team generated 4,700 recombinant inbred lines within 50 subpopulations. A NAM population provides a valuable resource that promises to accelerate the introduction of beneficial changes to traits of interest to breeders and producers.

The team established a Galaxy platform to make computational biology accessible to researchers with no programming experience. To maximize the utility of genetic diversity in wild relatives, researchers have made significant progress in the development of genomic tools to enhance the frequency of meiotic recombination and clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9-based gene editing in wheat. Researchers created several valuable resources to allow breeders to incorporate trait-specific genes. This will improve the efficacy and speed of breeding by enabling breeders to achieve desirable allele combinations faster. Resources include a meiotic transcriptome atlas, a genotypic variation database, and genetic mutant stocks that can facilitate wide crossing with unadapted landraces and wild relatives. The team established a CRISPR/Cas9-based gene editing platform by developing a comprehensive toolkit comprising several components of gene editing. These components include WheatCRISPR, a web-based RNA design guide; a functional vector system; and a microspore-based haploid gene editing system.

Enhancing Fusarium *and rust resistance*

The Canadian what industry has a well-rounded research program for studying diseases and pests. Researchers have developed genomic resources (breeder-friendly genetic markers and quantitative trait loci [QTLs]) vital for dissecting the genetic architecture of complex traits in wheat, including *Fusarium* head blight (FHB) and rust disease resistance, abiotic stress tolerance and grain development. FHB and rusts are two major wheat diseases that together account for $200 million in annual losses in Canada.

Through its Enhanced Fusarium and Rust Tolerance (EFRT) pillar, the CWA has identified a number of potential gene targets and markers that increase FHB and rust resistance with little yield penalty. To date, hundreds of genetic markers of resistance and new lines of wheat showing increased FHB or rust resistance have been delivered to wheat breeders.

Researchers have also identified several novel gene and metabolite targets for future marker development. They have tested several combinations of resistance and adult plant resistance genes to identify novel combinations with synergistic (“booster”) effects on rust resistance. Following several years of testing in disease nurseries, researchers detected a few major effect QTLs on multiple chromosomes for various FHB-resistance component traits. The team has developed breeder-friendly markers to help introduce these QTLs into new Canadian varieties. Breeders are now using marker-assisted selection and rapid introgression methods developed at NRC to produce germplasm with increased FHB resistance.

Improving wheat productivity under conditions of abiotic stress

Scientists have developed genetic markers and advanced wheat lines for several abiotic stress-related genes, including traits for drought, heat and cold tolerance. They have also developed a framework map of markers associated with physiological traits affecting drought tolerance including root traits, photosynthesis and a number of yield-contributing traits. They established a standardized whole phenology platform and used it to discern genetic differences between wheat lines as well as identify superior lines with better root systems and greater photosynthetic efficiency.

Wax deposition is an important component of performance under drought conditions. Researchers identified a set of four key genes controlling the deposition of diketone waxes in reproductive stages of wheat. They implemented some promising biomarkers that were correlated with increased cold hardiness and heat tolerance, which researchers can use to select or develop valuable germplasm lines that offer unique molecular resources for winter hardiness and thermo-tolerance breeding.

Developing new wheat lines to improve performance and yield

Wheat as a crop faces several challenges, including yield gaps and low economic returns. To address these challenges, scientists at NRC have significantly advanced their understanding of the gene targets and regulatory networks that influence photosynthetic efficiency and grain development in wheat. They have established a comprehensive gene expression atlas for grain development. Scientists have also created new wheat lines with more tillers, high vegetative biomass, upright leaf architecture, high photosynthetic efficiency and several desirable spike traits, providing a unique resource for wheat improvement breeding programs.

Promoting beneficial biotic interactions

Researchers have developed a cost-effective microbial community profiling platform based on cpn60 gene Universal Target (UT) region polymerase chain reaction (PCR) amplicon sequencing. They initiated an on-farm study with A&L Biologicals to identify microbiome parameters associated with high- and low-productivity soils from farm fields. Using cpn60, 16S and ITS targets, scientists identified bacteria and fungi whose occurrence was significantly correlated with wheat productivity.

P-bacterium is a previously identified, putatively beneficial bacterium associated with wheat grown in soils under long-term phosphate fertilization in the absence of nitrogen fertilization. Researchers developed technical capabilities to isolate, culture and further characterize the P-bacterium and other new beneficial bacterial candidates. Analysis of wheat root microbial community profiling revealed significant correlations between root microbial community and wheat productivity.

Increasing the value of Canadian crops and agri-products

Genomics research is playing a key role in ensuring the continued profitability of the agriculture and agri-food sector. The GRDI at AAFC supports seven GRDI-mandated projects. Examples of results and outcomes from these projects follows.

Identifying new fungicide targets in cereals

Construction of a signalling network to regulate the mycotoxin deoxynivalenol (DON) has enabled AAFC to identify novel proteins involved in the DON biosynthesis pathway of the pathogen *Fusarium graminearum*. AAFC scientists have also identified proteins that may regulate secondary metabolism in other fungi.

The AAFC Ottawa Research and Development Centre has developed a platform to screen for novel adjuvants and fungicides that could be targeted against multiple pathogens relevant to the agricultural sector.

Breeding midge-resistant wheat and canola

The swede midge (SM), *Contarinia nasturtii*, is a serious pest of brassica vegetables and canola (*B. napus*) in Ontario, Quebec and now the prairie region. Crop losses due to SM infestations can be as high as 85% in Canada and 100% in Europe. The orange blossom wheat midge (WM), *Sitodiplosis mosellana*, is a major pest of Canadian wheat, accounting for annual losses

of $60–120 million. Since 2010, several varieties of resistant spring wheat have been released that carry *Sm1*, a resistance gene from winter wheat. *Sm1* is the only known WM-resistance gene, and the probability of resistance failure—where previously resistant plants become susceptible to the pest—is high.

These midge species share many common biological aspects, likely including how they interact with host plants. For this project, researchers conducted the most in-depth examination of the genomics of SM and WM to date and learned details of their interactions with host plants at the molecular level. Researchers collected midge larvae from the field and laboratory colonies and developed techniques to finely dissect SM and WM larval salivary glands. They used next-generation sequencing (RNA sequencing) to catalogue the entire suite of genes expressed in these glands. They are now using this information to identify genes encoding salivary "effector" proteins that may interact with host plants to modify their physiology (formation of feeding structures) and/or to initiate a defence response leading to host plant resistance.

Researchers also screened a *B. napus* diversity collection for SM interactions, which enabled them to identify several more tolerant lines. They used a genomics approach to understand the mechanisms underlying this phenotype.

Exploiting DNA diversity for AAFC cereal research

Understanding genetic diversity is essential for basic and applied genomic research. AAFC's objective is to develop a user-friendly database to support the rapid deployment of DNA assays for plant variety development and to provide a foundational resource for discovering the causal genetic factors of adaptive plant traits.

In the project's first year, AAFC researchers assembled and sampled more than 600 varieties of germplasm in wheat, oat and barley, representing diversity in wild and cultivated forms of each crop. The researchers used a method called "exome capture" to isolate and sequence the DNA from tens of thousands of genes from 200 of these varieties. They then developed a wheat database that provides access to DNA sequence differences in each gene. This database has enabled researchers to identify highly predictive DNA markers that will be used to improve disease resistance in Canadian wheat breeding programs.

In the second year of the project, AAFC scientists will sample and sequence genes from the remaining diversity collection, extend the database to incorporate oat and barley, and complete the analysis of genetic and epigenetic factors in a novel set of wheat germplasm. This research may help unravel why different wheat varieties flower at different times in response to their environment.

Capturing novel genetic diversity for oilseed crop improvement

Exploiting genetic variation is the central tenet of plant breeders' efforts to optimize crops for yield, quality traits and sustainable production in the face of disease and environmental stresses. However, plant breeding practices in canola have resulted in a general lack of genetic variation in current germplasm, limiting the ability of breeders to effectively address new production challenges. AAFC researchers are addressing this issue by working toward the following goals:

- define the genomic nature of available variation
- identify favourable gene variants and corresponding molecular markers for desirable traits
- develop and establish molecular strategies to accelerate combining of such traits in elite varieties
- facilitate targeted gene adaptation through gene editing technologies

By defining available genetic variation and providing genetic tools and foundational knowledge to expedite the establishment of desirable traits in canola, this project aims to accelerate the genetic improvement of the crop and secure the sustainable production and profitability of Canada's $19-billion canola industry.

Developing clean energy crops

While Canada's Clean Energy Strategy is currently under development, it will undoubtedly include biofuel crops. Camelina is marketed as a bio-diesel and aviation fuel

feedstock. Researchers are exploring camelina genetic variation and applying genomic solutions to address limitations in agronomic characteristics, seed and product quality. They are also conducting studies to better understand the economic opportunity for this emerging clean energy crop.

Researchers are exploiting world germplasm collections to enhance tolerance to abiotic stress, seed size, disease resistance, seedling vigour and seed protein quality. Wide adoption of camelina in Canada could extend oilseed production by more than 2 million hectares while offering significant economic and agronomic benefits such as reduced input costs and better crop stress tolerance.

Identifying virulence effectors that trigger cultivar-specific immunity to soybean root rot

Soybean root and stem rot caused by *Phytophthora sojae* is a major disease problem for Canadian growers. Pathogen virulence effectors that trigger immunity are strain-specific and evolve in response to cultivar-specific *Rps* genes. By studying the interaction between soybean and *P. sojae*, AAFC scientists have identified several immunity-triggering effectors from the pathogen that host *Rps* genes recognize. This work will assist pathogen diagnostics and soybean breeding.

Reducing the need for fertilization through a symbiotic microbiome

Mitigating the unintended consequences of excessive fertilization—such as increased air and water pollution, reduced biodiversity and increased human health risk—is considered one of the central societal challenges for the twenty-first century. In this context, it is essential to identify and exploit the most efficient natural systems for capturing and delivering nutrients to plants.

This project has used cutting-edge technologies to advance AAFC's knowledge of the mechanisms that promote interactions between plants and beneficial, nitrogen-fixing rhizobial bacteria. Specifically, researchers have examined the plant attributes that mediate the development of nodules, the root-derived accommodation structures of leguminous plants that host the symbiotic bacteria. AAFC researchers have used a forward genetic approach to identify and characterized a new locus that is essential for nodule organogenesis. This adds to understanding of the symbiosis by defining new, relevant plant loci and associated processes. It also advances the long-term goal of controlling rationally beneficial plant-microbe interactions to improve agricultural productivity and environmental preservation in Canada.

Enhancing forest generation and protection

Identifying genes that control desirable attributes in economically important tree species

Spruces contribute significantly to the Canada's forest sector and are the most reforested species in the country. Genomics tools are essential to achieving economic benefits much earlier than with conventional tree improvement programs, helping maximize the economic value of standing timber.

The GRDI-funded research on genomic selection of trees with desirable traits complements the Genome Canada-funded projects: Fast Tests for Rating and Amelioration of Conifers (FastTRAC), and Spruce-Up. GRDI researchers are working closely with federal, provincial and industry partners to deliver knowledge and applied genomic tools to significantly enhance conventional breeding programs and accelerate the development and deployment of genomics-improved spruce stock.

In 2017–2018, researchers conducted large-scale field collections involving multiple end users. They sampled more than 1,000 white spruce progeny and analyzed them for spruce budworm resistance. They also performed large-scale field experiments and collections to characterize the 100 "core trees" from a test site containing mature white spruce belonging to the Ministère des Forêts, de la Faune et des Parcs du Québec. Researchers used terrestrial Lidar to characterize the same 100 "core trees" for various dendrometric features. This work will contribute to assessing spruce resilience to biotic and abiotic factors (such as insects and drought) and to establishing connections between genotypes and phenotypes.

Increasing knowledge of genomics-based pest diagnostics and mitigation

Global trade and climate change increase the risk of introduction and establishment of unwanted insects and pathogens into Canada's forests. Early detection and rapid response are critical to mitigating this risk. GRDI research is contributing to early detection of multiple insect species. Scientists often use traps to inventory forest insects, but traditional identification of insects captured in traps is time consuming and costly.

A group of NRCan and Canadian Forest Service scientists started a project in 2015–2016 to develop metagenomics and bioinformatics tools for identifying insects caught in traps more quickly and at a lower cost. In 2017–2018, researchers sent libraries of identified insect specimens for metagenomics sequencing to generate DNA libraries and reference databases, and developed new bioinformatics software to analyze metabarcoding sequences.

Researchers have increased their understanding and refined techniques for combatting several pests:

Longhorn beetle

Traps used to inventory forest insects are baited with special chemicals—often pheromones—to better attract insects. In 2017–2018, GRDI researchers used novel molecular methods to identify candidate receptor proteins for the pheromone monochamol in three species of longhorn beetle. This work, along with the development of an insect cell line cultivated in vitro, was a crucial step in setting up a pheromone receptor identification platform, which will contribute to faster development of tools to monitor this economically important pest.

Asian gypsy moth

The European gypsy moth is found in Canada and is a relative of the Asian gypsy moth, an unwanted insect. The CFIA inspects marine vessels and their cargo—especially those arriving from the Far East—to ensure they are free of Asian gypsy moths. Vessels found to carry the insect, usually as eggs, must leave port and remove all evidence of the insect. In 2017–2018, researchers finished sequencing, assembling and analyzing the mitochondrial genomes of 10 geographic variants of the gypsy moth. This work enabled them to identify specific mitochondrial markers they could use to develop diagnostic assays to identify rare Asian gypsy moth specimens in bulk pheromone trap samples. The research team can now transfer these assays to CFIA for further validation and operational use to improve the accuracy of trap sample processing.

Researchers also began searching for the genomic determinants of flight capability in Asian gypsy moth females. Flight ability has important implications for a gypsy moth's ability to invade and spread. This work complements the Genome Canada-funded BioSurveillance of Alien Forest Enemies (BioSAFE) project and is invaluable for negotiating agreements with Canada's trading partners and for lowering the risk of detrimental introductions in North America.

Phytophthora

The fungus-like pathogens known as Phytophthora are a phytosanitary concern for Canada and its trading partners. Current molecular diagnostic methods that detect Phytophthora species cannot differentiate between positive results from living or dead organisms. Building on work begun in previous years, GRDI researchers have demonstrated that molecular methods to detect living Phytophthora can be used on wood infected with this pathogen. The researchers developed diagnostic assays to target four specific Phytophthora species of particular concern while excluding closely related species. This technology can confirm that forest exports meet regulatory standards and authenticate treatment effectiveness to prevent pathogen movement. It can also enhance Canada's ability to accurately inspect imports where infested material is difficult to detect (e.g., in living plants).

Forest invasive alien species

Early detection by testing imported material and conducting biosurveillance around points of entry is key to preventing colonization of forest invasive alien species (FIAS). If FIAS colonization does occur, tools are needed to map and monitor spread, and to identify expansion patterns that can inform management and eradication efforts. Over the last year, GRDI researchers have built up genomic collections of FIAS that

could damage Canadian forests. They have used this information to develop a suite of molecular detection tools to help prevent the introduction and spread of forest invasive pests and diseases in Canada. Specifically, researchers validated a suite of assays to detect fungal pathogens responsible for white pine blister rust and butternut canker. The genomics resources and expertise resulting from this research can be applied to any unwanted forest pest. The suite of genomic and analytic tools under development will increase confidence in Canada's phytosanitary certification processes and help maintain the country's access to international markets—not only for forest products but for all export industries that use wood-packing materials.

Spruce budworm

A spruce budworm outbreak is currently affecting large stands of forests in Quebec and is poised to spread into Ontario. Outbreak development forecast models will give forest managers another tool to support management decisions regarding this pest. GRDI researchers are applying a novel analytical approach to detect subtle genetic population structures that may exist in Ontario. This information will help assess the role of budworm genetic structure in outbreak behaviour.

Emerald ash borer

Ash trees make up a significant proportion of the deciduous forests that stretch from eastern Manitoba to the Atlantic provinces. Emerald ash borer (EAB) attacks are putting these trees at risk of disappearing from the landscape. This is due to the lack of an accurate and effective early detection tool and the absence of EAB resistance in native ash trees. GRDI researchers are working with public and private stakeholders (including affected municipalities) to understand the molecular response of ash trees to borer attacks. In 2017–2018, researchers sequenced and assembled the EAB genome to determine the genetic causes of this insect's success in its new environment and performed transcriptome analyses of susceptible ash trees in urban environments. Researchers identified more than 150 genes with altered gene expression following EAB infestation, which will enable them to develop a diagnostic test for affected ash trees.

White pine blister rust

The restoration of pines in the North American landscape requires trees that are resistant to white pine blister rust. Researchers are studying resistance mechanisms in western white pine, limber pine, whitebark pine and eastern white pine to improve ecosystem remediation. In 2017–2018, researchers discovered limber pine seed families originating in Canada with major gene resistance and identified a molecular mechanism that contributed to resistance in whitebark pine. Identifying genomic variation that contribute to host resistance can help breeding and genetic conservation programs by allowing managers to select for trees that are better able to adapt to environmental stressors.

Improving land reclamation following oil sands mining

Researchers are using genomics tools to conduct an industrial-scale pilot project to better understand tree-soil microbiome interactions at oil sands reclamation sites in Fort McMurray, Alberta. The results of the study will provide a picture of the above and belowground genetic diversity in sites under reclamation. This will enable researchers to understand how different reclamation strategies affect the dynamics of the whole biological system.

DNA metabarcoding of bacteria and fungi samples at reclamation sites has revealed that belowground microbiome diversity differs significantly among sites that have received different reclamation treatments. Because soil mycorrhizal communities are variable in both space and time, long-term monitoring is particularly important to better understand the ecological trajectory of these novel ecosystems. This will enable scientists to ensure that reclaimed plots will provide services to the ecosystem similar to those they provided before the disruptions. The data will provide new sustainable strategies for oil sands tailings reclamation and facilitate Canada-Alberta oil sands environmental monitoring.

Assessing ecosystem integrity in forest management

Researchers launched a project in 2015–2016 to develop metagenomics tools to assess ecosystem integrity and the sustainability of forest management practices. In 2017–2018, researchers completed all field sampling, DNA extraction and sequencing as well as bioinformatics and data analysis for the pilot study. The findings will enable them to enhance soil fauna gene libraries and improve sampling methodologies for soil invertebrates in forest management settings. Researchers also improved techniques for extracting DNA from deadwood and are currently working on better PCR protocols for the fungal deadwood community as part of a project assessing the effects on soil biodiversity of removing biomass from a site. These improved molecular techniques will help produce better data for forest integrity assessments.

Managing fisheries and oceans

The ability to decode large portions of complete genomes in non-model species has led to a paradigm shift in the way natural systems are studied. It has also opened up countless new applications and questions that researchers can now address quickly and at low cost. Not only can they identify genetic differences among individuals, populations and species, but they can also understand their functional significance and relationships with environmental drivers. As a direct consequence, genomics tools now offer broad-reaching potential to transform most aspects of aquatic conservation and management.

GRDI has supported several multi-year projects (through Phases I–VI from 2011 to 2019) that relate to how teams identify stocks or populations, manage mixed-stock fisheries, protect aquatic animal health, manage invasive species, protect threatened or endangered species, predict and plan for climate change impacts on species, design marine protected area networks and manage aquaculture. Examples of results and outcomes from these projects follows.

*Analyzing spatial stock structure of Arctic char (*Salvelinus alpinus*) in Labrador*

There is a long history of exploitation of Arctic char along the coast in northern Labrador, where these fish are caught at sea in both commercial and First Nations fisheries. The stock structure and composition of these fisheries remains unknown despite the cultural, economic and ecological importance of Arctic char in Labrador. However, quantifying population-specific exploitation is critical to ensuring effective management and stock conservation, particularly because these fisheries often target mixtures of stocks originating from different rivers.

With funding from the GRDI, scientists and collaborators began to characterize the Arctic char population structure in 2017 using genome-wide scans of thousands of single nucleotide polymorphisms (SNPs). The large SNP panels developed will provide a genetic tool for ongoing stock identification. Fisheries managers and DFO Conservation and Protection can use this tool to make decisions regarding potential violations in commercial or First Nations fisheries. Without this genetic information, scientists will not have a clear understanding of population structure. However, increased exploitation without this understanding could lead to a loss of adaptive diversity, thereby threatening species stability and persistence.

These investigations will provide an unprecedented understanding of population structure to inform scientific decisions on the long-term sustainability of current fishing quota allocations. They will also enable researchers to consider the possibility of increasing allocations related to the exploitation of this valuable arctic species.

Using environmental DNA methods to detect and mitigate aquatic invasive species and monitor aquatic species at risk

Using environmental DNA (eDNA) in water samples to detect species can support traditional field surveys for aquatic species management and conservation, particularly for hard-to-find cryptic species. This project develops, evaluates and optimizes eDNA-based tests for more than 20 aquatic invasive species as well as for the at-risk Brook Floater. This will provide a rapid and

sensitive new tool for monitoring important aquatic species and creating distribution maps for the Brook Floater as well as ecologically and economically damaging invasive species. These resources will allow conservation workers to develop more efficient management and conservation strategies.

Using next-generation sequencing to investigate Atlantic cod population structure and connectivity in the western Atlantic

Recent advances in genomic research have made it possible to conduct fine-scale spatial analysis of cod stocks, populations and subpopulations to improve management. Atlantic cod fisheries used to have enormous commercial value, but overfishing led to depleted stocks. Despite management efforts, populations have not recovered.

This project aims to solve management issues by identifying factors involved in stock recovery. Researchers are surveying microscale movements of Atlantic cod populations within and out of the Gulf of St. Lawrence by sampling in the summer while adults are feeding and in the fall while adults may be migrating. Researchers will use next-generation sequencing (NGS) methods to develop a large number of genetic markers (i.e., 40,000 SNPs). Using this approach, they will provide DFO with an ultrafine-scale genetic baseline of western Atlantic cod of unprecedented quality and genomic coverage.

Atlantic cod populations are genetically characterized through a comprehensive sampling of spawning areas in Canada and the U.S. Population structures and connectivity are assessed at the Canada–U.S. border and the northern Gulf of St. Lawrence. This project will validate existing management units and may help to design alternate units to improve fishery management in both Canadian and American waters. It will also improve understanding of Atlantic cod stock dynamics and potential mixing that could have implications for the management of these stocks. It will also provide valuable information to DFO scientists involved in population dynamics modelling, specifically for framing DFO stock assessment data into biologically relevant units. Management modifications could significantly improve the models used to predict population dynamics and recruitment, and ultimately benefit management measures.

Using environmental DNA methods to detect aquatic organisms in the field

Scientists use newly developed, easy-to-use, portable qPCR instruments for eDNA analysis for real-time, in-the-field detection of aquatic invasive species, species at risk or other species important for fisheries. Scientists are developing methodologies for zebra mussel, a recent invasive species in Manitoba, and they will then test the transferability of these methods to other aquatic organisms (e.g., freshwater finfish). The work will be useful for programs with monitoring requirements in remote areas or for point-of-need locations (e.g., shipping ports, inspection sites), enabling community-based approaches to support government monitoring and managing of important aquatic organisms.

One important area that the mobile diagnostic eDNA detection instrument will target is zebra mussel monitoring and prevention programs. The invasive zebra mussel is currently a significant concern in Western Canada and the Northwestern U.S., as it is known to quickly colonize new habitats, disrupting ecosystems and local industry. GRDI funding has allowed DFO researchers to develop eDNA methods that can support existing dreissenid monitoring and prevention programs. With support from provincial and federal research partners, this work is contributing to our understanding of the efficacy of eDNA as an early detection tool for aquatic invasive species.

Using parentage-based tagging of Chinook salmon in British Columbia

Emerging genomics tools can support fisheries stock enhancement programs and help to manage mixed wild, enhanced and protected stocks. For example, the Salmonid Enhancement Program in the Pacific Region releases hundreds of millions of juvenile salmon every year that provide recreational, commercial and Aboriginal fishing opportunities and relieve fishing pressures off vulnerable stocks. Released hatchery-reared salmon form mixed-stocks with wild-born salmon

from B.C., as well as with released and wild-born fish from the U.S., including both healthy and at-risk wild stocks. Managing the mixed stocks involves determining how much each stock contributes to the fisheries and returns to spawn the next generation. The traditional assessment method is to implant released juveniles with coded-wire tags (CWTs) that can be recovered on their return to determine their age and release location. However, this method is costly (e.g., over $900,000 annually for Chinook salmon alone), requires killing the fish and, under current capacity, can only be performed on a small subset of released fish.

Using new DNA sequencing technologies, DFO scientists can determine the source of caught or returning fish down to the parent level. This is done by sequencing and assessing genetic markers called single nucleotide polymorphisms (SNPs) of all parents used in hatchery stock assessment. This innovative technique, known as parentage-based tagging (PBT), has shown 100% accuracy in stock identification for a number of species. It also provides concrete evidence regarding the stocks that are contributing to overall fisheries and populations. By using the PBT system, DFO can easily double its capacity for identifying caught or returned fish and obtain more specific information on each fish at a lower cost than the CWT system (estimated savings of $241,000 annually for the Chinook program alone).

DFO will adopt and expand this technology to better manage all mixed/enhanced fish stocks for maximum utilization of healthy stocks and better conservation of at-risk stocks. Combining this technology with other innovations in the future will provide test fisheries with hand-held field devices that will enable them to determine the identity of a fish down to the parent. This will provide much-needed information to enable DFO to respond to changing environments and future challenges to best manage Canadian fisheries.

Promoting responsible environmental decision-making

The 2016–2019 research cycle encourages projects focused on the development of genomics tools and approaches to support pollution prevention, regulatory compliance and enforcement, wildlife management and risk assessment of potentially toxic substances.

Descriptions of the four priority research areas follow.

Improving understanding of ecotoxicology

Researchers worked to improve the efficiency and accuracy of models to predict the effects of chemical exposure by improving understanding of the molecular mechanisms that underlie the toxicological effects of chemicals in wildlife and aquatic life. That includes developing genomics tools and approaches to examine the impact of existing and emerging chemicals (their transport, fate, effects and associated risks) on the biology and physiology of organisms as well as on biodiversity and ecosystem functions. Researchers focused on assessing the effects of exposure to chemicals of concern (including individual chemicals and complex mixtures) in avian, mammalian and aquatic species. A better understanding of chemicals' molecular modes of action significantly enhances the accuracy of models that contribute to improved risk assessment.

Monitoring ecosystems

Researchers also focused on understanding and monitoring aquatic and land-based ecosystems. For example, they looked at extending an established method for recovering biodiversity information from bulk environmental samples. In the Great Lakes, scientists are applying DNA barcoding to monitor algal community compositions for harmful blooms. They are also evaluating the ability of changes in microbial diversity to provide early warnings of adverse changes to aquatic ecosystem health. This work will increase understanding of cumulative environmental impacts and related risks associated with multiple stressors interacting over time.

Enhancing wildlife conservation

Scientists have developed genomic techniques to help them better understand wildlife species and how they respond to changes in their habitats due to disturbances, including climate change and natural resource development. For example, scientists are using genomics to study the impacts of cumulative stress associated with large-scale environmental changes (e.g., climate change and pollution) in wildlife populations such as arctic nesting eiders. They are also developing tools to delineate the geographical distributions of endangered, elusive or invasive species using analyses of material found in environmental matrices. These efforts will support wildlife species management and increase understanding of how populations adapt to changes in their environments.

Improving compliance and enforcement

Scientists are developing various innovative methods and tools to support regulatory enforcement and monitoring programs to protect the environment and wildlife from pollution, wildlife trafficking and other threats. That includes developing genomic markers to inform the harvest management of Murre colonies in the North Atlantic.

Improving food safety, animal health and plant protection

Characterizing foodborne pathogens through genomics databases

In 2017–2018, the CFIA focused on continuing to develop WGS technologies to analyze food pathogens, implementing them in support of regulatory food safety programs and expanding their deployment to front-line CFIA food testing laboratories. Scientists have completed WGS analyses of more than 1,600 foodborne bacteria, which have been added to a growing WGS database that will be useful for conducting trend analysis and surveillance activities. They also developed processes for managing data coming from other CFIA labs and business lines for improved integration into the food pathogen database.

Researchers improved and automated pipelines for the genomic analysis of pathogenic bacteria to provide a user-friendly interface for food microbiology analysts seeking to identify and characterize foodborne isolates. The GeneSippr and GeneSeeker pipelines have added functionalities that provide more precise identification of bacteria, virulence characterization, high-resolution typing and quality assurance. These methods have been validated to meet Microbiological Method Committee guidelines and are in the process of being transferred to CFIA testing laboratories, where they will support food microbiology inspection programs. These tools will provide highly informative results to underscore risk assessment and risk management decisions in food safety investigations.

Scientists also made significant progress using predictive genomics to inform the customization of selective enrichment procedures to improve the recovery of outbreak strains (e.g., shiga toxigenic *E. coli* [STEC]) from foods. They demonstrated the improved recovery of different model STEC strains from ground beef by clarifying their antibiotic resistance profiles using WGS for several classes of antibiotics that can be used as strain-specific selective agents. This novel approach will prove invaluable for the recovery of STEC strains during foodborne illness outbreak investigations.

Strengthening animal health diagnostic tools

This project aims to enhance the CFIA's ability to acquire, manage, analyze and use genomic data to identify pathogens and disease vectors/reservoirs important to animal health. Progress this fiscal year at the National Centre for Foreign Animal Disease (NCFAD) includes:

- establishing and certifying a new high-throughput sequencing facility at the Winnipeg containment level (CL) 3 laboratory, which included installing and networking new Ion Torrent instruments to facilitate sequencing of high consequence CL3 and CL4 agents
- installing a new high-performance bioinformatics computer, along with new bioinformatics tools
- developing new or improved protocols and SOPs

- sequencing a diverse collection of more than 400 diagnostic, surveillance, outbreak and archived samples including Ebola, Rift Valley Fever, foot-and-mouth disease, classical swine fever and influenza viruses
- improving sequence data handling, processing and annotation protocols
- implementing NGS as a complement to routine diagnostics

To date, NCFAD has sequenced more than 800 diagnostic, surveillance, archival and research samples representing more than 50 viral species, as well as the complete mitochondrial genomes of six Canadian mosquito and nine bat species. GRDI research has also supported avian and swine influenza surveillance activities, responded to a rabbit hemorrhagic disease outbreak and sequenced 39 samples containing unknown aetiological agents submitted by other collaborators, including PHAC's Centre for Biosecurity. In addition, the discovery of novel antigens for *Mycobacterium bovis* and *Brucella abortus* detection is a promising diagnostic biomarker for serological detection in infected animals.

Researchers made significant progress in 2017–2018 using high-quality genome sequences produced from *Mycobacterium bovis* strains collected in Canada since 1985. These genetic sequences provided reference information to model epidemiological relations between bovine tuberculosis outbreaks in Canadian wildlife and agriculture animal populations, develop new rapid strain differentiation molecular diagnostic tests, and design and develop new immunological tests with improved sensitivity and specificity.

Detecting and identifying invasive plants, plant pests and plants with novel traits

The CFIA is developing its capacity for DNA barcoding and NGS to enhance its ability to detect and identify invasive plants, regulated plant pests and pathogens, and plants with novel traits. Researchers have acquired materials and reagents as planned and are using appropriate samples and bioinformatics tools to create sequencing data storage. They are continuing to develop methods for the targeted sequencing of plants with novel traits. They have also analyzed metagenomic sequencing data from spore and insect traps, pollen sampling, and baiting plates to detect potential FIAS and plants with potential weed seeds.

The development of new tools and field protocols has enabled researchers to detect and genotype target organisms. They have also been working on developing a pipeline for genome assembly among the multiple themes of the project and their ongoing activities such as detecting viruses, insects, invasive plant species and plants with novel traits.

Through this research, the CFIA is developing more specific and higher-throughput tools for monitoring the environmental presence and release of invasive plants, plant pests and plants with novel traits. This includes the use of pipelines to sequence and assemble the genomic regions of different organisms to help them develop markers for detection and identification. Researchers established new detection marker regions for identification and genotyping, and conducted WGS on different plant pests. They evaluated metagenomics for a pilot project on the use of the methods in different sample types and developed bioinformatics pipelines for WGS, metagenomics and identification of plants with novel traits. Some applications were transferred to diagnostic labs to improve their testing capacity. NGS revealed various tree fruit viruses, including quarantine viruses.

Developing genomics and bioinformatics tools

Recent developments in the field of genomics have led to the increased application of these technologies to CFIA's regulatory science activities. Researchers in CFIA's food, plant and animal business lines have developed a number of methods and applications in parallel. This project is intended to harmonize genomics activities, including method development, bioinformatic analysis of genomic data and the provision of training on bioinformatic tools.

A number of research groups in the plant and food business lines have developed collaborations with AAFC to address bioinformatics support needs. This project builds on these existing collaborations while enhancing

agency-wide access to these tools. The use of common platforms for genomics/bioinformatics work ensures that efforts are not duplicated and that resources can be reallocated to ensure emerging genomics technologies can be integrated into CFIA's mandated activities.

CFIA's list of regulated pests includes many RNA viruses responsible for infecting plants and animals. Several of the latter are zoonotic by a number of foodborne viral agents, and thus pose human health risks. This research is focused on using novel RNA sequencing genomic technologies to detect, identify and characterize RNA viruses found in various matrices such as plants, animal tissues or food. This project facilitates joint efforts by scientists in all three of CFIA's business lines to develop, improve, adapt and harmonize NGS methods and pipelines for identifying and characterizing known and unknown RNA viruses for CFIA. Similarly, CFIA regulates bacterial organisms in food, animal and plant business lines because they pose human health risks and are infectious to both plants and animals. The Agency will implement automated bioinformatics tools for analyzing bacterial genomes from diverse sources developed under this project into its diagnostic arsenal.

Annex 4: Research tools and processes produced by the GRDI

Research tools

- Metabarcoding approach: Sequencing of natural DNA samples in order to identify aquatic microbes using different biomarkers (16S, 18S) (EcoBiomics);
- Accurate interpretation of metabarcodes using Automated Oligonucleotides Design Pipeline (AODP): Zahariev, M., C. A. Levesque, W. Chen (2016). The Automated Oligonucleotides Design Pipeline (AODP) version 2.4.6.2, available at: https://bitbucket.org/wenchen_aafc/aodp_v2.0_release (2017/02/24) (EcoBiomics);
- Illumina –MiSeq facility in-house NHRC-Saskatoon: NGS applications in ecotoxicological studies applying microbial community end points, isolation of mRNA from complex environmental samples (EcoBiomics);
- Automated amplicon metagenomics pipeline released to the project and the public https://github.com/AAFC-BICoE/snakemake-amplicon-metagenomics (EcoBiomics);
- Articulated Blade microfluidic platform for extraction and purification of genetic material from soil samples (EcoBiomics);
- All-plastic microfluidic cartridge and automated protocol for extraction and purification of genetic material from soil samples (EcoBiomics);
- Streamlining DNA extraction using the BioMek NXP instrument (EcoBiomics);
- Automation of DNA library preparation for Illumina sequencing using the Illumina Neoprep (EcoBiomics);
- Functional screening tool for phytoremediation purposes using poplars (EcoBiomics);
- CO1 Classifier: A CO1 reference set that can be used with the RDP classifier to make high throughput CO1 metabarcode taxonomic assignments (EcoBiomics);
- Developed an efficient homogenization method for the handling of ~1L of solid material. Aliquots of 250mg can be processed for DNA extraction following the PowerSoil protocol (EcoBiomics);
- A multiplex PCR assay for detection of AmpC-like beta-lactamase blaCMY-2 and glutathione S-transferase fosA7 genes conferring resistance to cephalosporins and fosfomycin (AMR);

- A visual heat map analysis tool (in-house programming with SAS software) was developed, using the data generated by screening over 8000 isolates with the pin replicator technique (based on the initial number of isolates per sample, the relative importance of the four antibiotics used and the resistance or susceptibility criteria), to determine hotspots of ESBL enterobacteria in the swine production continuum (sows, suckling piglets, weanling piglets, growing pigs, finishing pigs and carcasses from the longitudinal study on conventional and antibiotic-free farms) (AMR);
- Integrated Assessment Model of Antimicrobial Resistance (IAM.AMR) (AMR);
- Quantitative Microbial Risk Assessment of Ceftiofur-resistant Salmonella Heidelberg in broilers (AMR);
- EpiQuant 2.0: an R-based framework that enables users to compute the epidemiological concordance of clusters in a population, enabling mapping of salient ecological features associated with distinct subgroups in a population and enhanced visualizations of genomic and epidemiologic correlates (AMR);
- Generation of 60 nalidixic acid resistant mutants of Salmonella enterica (10 strains each from serovars Kentucky, Enteritidis, Heidelberg, Typhimurium, Newport, and Infantis) (AMR);
- Ectyper: Software for predicting serotype in E. coli from whole genome sequences. Ectyper can be used in the identification of AMR-associated serotypes (AMR);
- Spfy: An online platform for performing real-time identification of AMR, virulence and subtype markers as well as testing for epidemiological associations between AMR phenotypes and E. coli populations (AMR);
- Phylotyper: Software for preforming accurate prediction of subtypes from gene sequences, including AMR gene subtypes or molecular subtypes associated with resistant strains (AMR);
- QIIMEgraph: Redmine automation tool for generating user-defined graphics of 16S rRNA-based microbial profile derived from QIIME2.0 analysis (AMR);
- QIIMETaxReport: Redmine automation tool for generating user-defined taxonomic composition table derived from QIIME2.0 analysis (AMR);
- crowBAR: a tool for Bayesian Allele Recovery of missing allelic data for genome-based Multi Locus Sequence Typing in incomplete genome assemblies (AMR);
- MOB-suite: Software tools for clustering, reconstruction and subtyping of plasmids from draft genome assemblies (AMR);
- Plasmid Profiler: software to characterize plasmids from large data sets directly from sequence reads (AMR);
- IRIDA: end-to-end sequence data management, analysis, sharing, and visualization platform (AMR);
- Ceftiofur-resistant Salmonella Heidelberg Risk Profile (AMR);
- Carbapenemase and extended-spectrum beta-lactamase (ESBL) containing Enterobacteriaceae in retail seafood Risk Profile (AMR);
- AMR Threat Assessment (AMR);
- Identification of gain of virulence changes and mutations in the soybean root rot pathogen Phytophthora sojae (AAFC);
- Updated high-density consensus map of oat; novel software based on haplotype-based population filtering (AAFC);
- The first full exome capture design for use in diploid, tetraploid, and hexaploid oat (AAFC);
- Full exome captures in approximately 200 varieties of oat, wheat, and barley (AAFC);
- Development of material from reciprocal crosses between elite Canadian wheat lines and four selected synthetic wheat line form from crosses between Aegilops tauschii and T. turgidum (AAFC);
- Development of 1 x capture arrays designed to specific genomic regions (AAFC);
- Chromosomes conformation capture array for wheat (AAFC);

- Reference database in wheat containing DNA sequence variants in captured genes (exons) and adjacent regions (AAFC);
- Complete de novo transcriptome developed for swede midge, Contarinia nasturtii, third instar larvae useful for the identification salivary effector proteins involved in host plant interactions leading to resistance (AAFC);
- De novo salivary gland transcriptome from second and third instar wheat midge larvae, Sitodiplosis mosellana (AAFC);
- Identification of germplasm lines from nested-association mapping population of Brassica napus for swede midge host plant resistance. Levels of susceptibility determined from moderate to highly susceptible. These lines may be further investigated for use in plant breeding for swede midge resistance (AAFC);New plant locus essential for nitrogen fixation, which mitigates need for N-fertilizer inputs (AAFC);
- New family of plant genes that mediate root nodule formation, the plant organ that host nitrogen-fixing bacteria (AAFC);
- Produced Toolbox components for CRISPR/Cas9 gene editing, including production of purified Cas9 and Cas9N enzymes in-house, vector construction and genome editing event screening based on genotyping technology (AAFC);
- Identified short list of candidate wheat genes located within the 5AS and 2DL FHB resistance QTLs (AAFC);
- Identified five wheat lines still strongly resistant to FHB carrying an approximately 40 MB 7EL fragment from a wild wheat relative (AAFC);
- Germplasm with pyramided stem rust genes shared with numerous AAFC breeding programs (AAFC);
- Identified and annotated 301 MAP kinases from wheat, barley, rye and triticale (AAFC);
- Development of a resistance gene-like database for cereals used to construct a DNA capture array of 52,777 probes (120-mers) covering 2.78 Mbp (AAFC);
- Identified sources of tan spot and yellow rust resistance through the screening of 206 T. intermedium lines (AAFC);
- Enablement of gene editing (CRISPR) technology in C. sativa (AAFC);
- Fully Automated Multiplex Detection of Foot and Mouth Disease Virus, Vesicular Stomatitis Virus, Swine Vesicular Stomatitis Virus, Classical Swine Fever Virus, African Swine Fever Virus (ASFV) genome on a microfluidic platform (CFIA);
- Fully Automated Neuraminidase Subtyping of avian influenza virus on a microfluidic platform (CFIA);
- Fully Automated Detection and Hemagglutinin Subtyping of avian influenza virus on a microfluidic platform (updated and improved) (CFIA);
- Protocol for sequence assembly from ampliseq data (CFIA);
- Whole Genome Sequencing data reference library and culture collection bacterial isolates (CFIA);
- Nematode Species Identification Using Molecular Techniques (CFIA);
- A bioinformatics script (GMOSeqr) for capturing genetic elements commonly used in constructing transgenic plants from NGS sequence data was improved with the expansion of the reference database (CFIA);
- Fusarium sporotrochioides qPCR assays (CFIA);
- The AutoROGA software tool was developed to automatically parse complex bioinformatics output and produces a simplified report to be provided to CFIA stakeholders (CFIA);
- The CFIA Ottawa Laboratory Carling Sequence Analysis Portal (COGSAP) allows for uploading and analysis of genomic sequence data with an easy to use graphical user interface, greatly simplifying the data analysis process for many common bioinformatics tools (CFIA);
- Panel of Chinook salmon primers that produces 390 amplicons in a single polymerase chain reaction (DFO);

- Collection and genotyping of all Chinook Salmon hatchery brood parents spawned in 2016 where CWTs are applied to juveniles released from hatcheries for stock identification and assessment (DFO);
- Thermal stress Biomarker panel with TaqMan assay efficiencies, species amplifications, and preliminary validations completed. Ultimately to be included in Fit Chip application (DFO);
- Hypoxia stress Biomarker panel with TaqMan assay efficiencies and species amplifications determined. Ultimately to be included in Fit Chip application (DFO);
- Biomarkers associated with imminent Mortality identified and TaqMan assays developed and efficiency tested and applied across multiple tracking and holding studies. Ultimately to be included in Fit Chip application (DFO);
- Development of an eDNA field sampling protocol for aquatic invasive species (AIS) monitoring by DFO scientists and biologists (DFO);
- Development of an eDNA field sampling protocol for aquatic species at risk (ASAR) detection to be used by environmental non-governmental organizations (DFO);
- Species-specific qPCR assays (6) for AIS to be used by the DFO AIS monitoring group (DFO);
- Species-specific qPCR assays (6) for sensitive detection and monitoring of ASAR by Parks Canada and DFO Species-at-Risk Branch (DFO);
- Production of a SNP catalogue for economically important redfish (Sebastes spp.) using a reference genome, we now have around 20K SNPs that can be used to discriminate populations and species (DFO);
- SeaScape Map of economically important redfish species that supports research for commercial species used by scientists and managers from DFO for fish stock assessments and management (DFO);
- Tissue archive containing tissue samples from >850 Atlantic cod collected throughout the eastern Atlantic Ocean (DFO);
- DNA archive containing genomic DNA extracted from >900 Atlantic cod collected throughout the eastern Atlantic Ocean (DFO);
- Raw genomic data archive containing 746 gigabytes raw genomic data generated from 1050 Atlantic cod captured in 11 Northwest Atlantic Fisheries Organization (NAFO) zones (DFO).
- Curated genomic data archive containing 2.6 terabytes of trimmed and de-mulitplexed genomic data aligned to the Atlantic cod genome, collected from 1,307 Atlantic cod captured in 11 NAFO zones (DFO);
- Panel of diagnostic SNPs capable of distinguishing cod populations north and south of a temperature cline offshore from Halifax (DFO);
- Development of zebra Mussel/Dreissena qPCR environmental DNA assays (DFO);
- Water filtration device for collecting environmental DNA samples in extreme remote areas (DFO);
- A bioinformatic software designed to exploit the high information content of mass spectra data (ECCC);
- Next generation sequencing (NGS) to detect microbial species within an artificial microbial blend (ECCC);
- Custom designed 4 X 44K microarrays for S. tropicalis (Agilent Technologies, California, USA) to perform high quality gene expression analysis (ECCC);
- ToxChip PCR array for a Pacific coastal seabird species used to screen chemicals and complex environmental mixtures analysis (ECCC);
- A novel screening technique, which uses whole liver slice cultures to screen for chemical effects in wild and domestic species (ECCC);
- Double-crested cormorant embryonic hepatocyte culture(ECCC);
- Microsatellite mutation assay for river otters used by environmental and chemical risk assessors to assess the genetic health of animals exposed to genotoxic agents(ECCC);
- Microsatellite mutation and blood micronucleus assay for double crested cormorants(ECCC);

- DNA methylation assay for bank swallows (ECCC);
- Development and implementation of captive feeding studies in an avian model (ECCC);
- Mini-rotating annular reactors for controlled exposure and growth of microbial communities (ECCC);
- Specimens put in culture using specific culture media and growth conditions that are controlled in growth chambers (ECCC);
- Collection of arthropod samples to improve precision of biodiversity monitoring (ECCC).
- Screening method for regulators to detect and identify microRNA changes in tissue exposed to fungal toxins and anthropogenic chemicals (HC);
- Data analysis tools and bioinformatics algorithms for regulators to screen nanomaterials with the potential to induce lung disease (HC);
- Software to analyze genetic material (HC);
- Method for extracting miRNA from feces and separating it from ribosomal RNA1 (HC);
- Animal models and assays for the evaluation of adverse reactions resulting from the exposure to the Respiratory Syncytial Virus for human health risk assessment (HC);
- Isolation methods for human mesenchymal stem cells (HC);
- Bioinformatics pipeline for applying Next Generation Sequencing to simultaneously sequence large numbers of barcoded mutant genes for comparing mutagenic mechanisms of various agents among tissues and enabling improved evaluation of genotoxins (HC);
- Bioinformatics pipeline for applying next generation sequencing for analysis of complex and large genomic data for DNA changes in tissues exposed to toxins for human health risk assessment (HC);
- Refined biomarker to distinguish between genotoxic (DNA damaging) and non-genotoxic chemicals for human health risk assessment (HC);
- BMDExpress Data Viewer: toxicogenomics tool for human health risk assessment of chemicals, to be used as a prototype for future models at the US National Institute of Environmental Health Sciences (HC);
- High-Throughput Genotyping platform for wheat capable of simultaneously profiling SNP markers (NRC);
- Breeder friendly diagnostic markers for Rust-resistance genes (NRC and AAFC);
- Two Breeder-friendly fusarium head blight-resistance molecular markers developed (NRC);
- Genes exhibiting extreme heat tolerance when highly expressed in wheat in growth chamber conditions (NRC);
- Identified markers for glaucousness, root proliferation, height, and seed size in wheat (NRC);
- Signalling factors involved in abiotic stress response in wheat for drought, heat, or cold tolerance (NRC);
- Gene targets for photosynthetic efficiency in wheat (NRC);
- Gene expression atlas for wheat seed development (NRC);
- Galaxy Bioinformatics platform for wheat sequence data analysis (NRC);
- Genomic tools for enhancing the frequency of meiotic recombination and CRISPR/Cas9-based gene editing in wheat (NRC);
- Pan genome sequencing of Canadian wheat - Genome sequence assembly of Stettler, a popular Canadian wheat variety (NRC);
- A bread wheat NAM (nested association mapping) population– a valuable genetic and germplasm resource for wheat improvement (NRC);
- Valuable pre-breeding germplasm for future Canadian wheat breeding programs (NRC);
- A breeder-friendly gene editing platform for crop plants (NRC);

- An integrative wheat bioinformatics portal as a primary access point for information and bioinformatics resources developed in-house and from 3rd party (NRC);
- An RNAseq data analysis workflow in the Galaxy platform; Meiotic transcriptome atlas in wheat (NRC);
- Pairing homoeologous 1 (Ph1) – deletion mutants (NRC);
- Genomic resources (breeder-friendly genetic markers and quantitative trait loci) vital for dissection of genetic architecture of complex traits in wheat (NRC);
- Limber pine genetic map positioning 9,500 functional genes (NRCan);
- Molecular approach to identify the geographic origins of gypsy moth samples using a panel of SNP markers (NRCan);
- Molecular assay to detect Asian gypsy moths in bulk pheromone trap samples (NRCan);
- Molecular assay to detect Caucasian gypsy moths in individual samples (NRCan);
- Detection assays for the 50 most unwanted Canadian forest pathogens (NRCan);
- Detection assay for the butternut canker pathogen (NRCan);
- Protocols for the extraction of nucleic acids from field and bulk samples (NRCan);
- New sets of primers for barcodes for forest Coleoptera (NRCan);
- Functional screening tool for phytoremediation purposes using poplars (NRCan);
- Tree genotyping markers for evaluation of land reclamation practices using Aspen (NRCan);
- Transcriptomic profiling (RNA-seq) to identify ash EAB responsive genes (NRCan);
- Terrestrial soil faunal community meta-barcoding analysis tool (NRCan);
- Metabarcoding tool to assess microbial communities (NRCan);
- HomopRemover: A program designed to effectively remove sequences containing long homopolymers (NRCan);
- Illumicut: A program specially designed to efficiently detect and remove forward and reverse sequencing primers in paired-end reconstructed sequences (NRCan);
- The Salmonella In Silico Typing Server (SISTR) (http://lfz.corefacility.ca/sistr-app) a bioinformatics resource for multiple rapid Salmonella subtyping required for epidemiological analysis (PHAC);
- Panseq (http://lfz.corefacility.ca/panseq) for the pan-genomic analyses of closed and draft genomic sequences (PHAC);
- SuperPhy (http://lfz.corefacility.ca/superphy) online predictive genomics platform for near real-time analyses of thousands of genome sequences (PHAC);
- Spfy (https://lfz.corefacility.ca/superphy/spfy/) for near real-time analyses of thousands of genome sequences with results that are understandable and useful to those in the fields of clinical medicine, epidemiology, ecology, and evolution (PHAC);
- Phylotyper (https://github.com/superphy/insilico-subtyping) to predict biological subtypes from gene sequence data (PHAC);
- Ectyper (https://github.com/phac-nml/ecoli_serotyping) to predict serotype from genomic sequence, and identify known Escherichia coli virulence factors within whole-genome sequence data(PHAC);
- Feht (https://github.com/chadlaing/feht) a commandline program to automatically identify markers predictive of groups (PHAC);
- BIO-HANSEL, an in silico analytical tool to subtype S. Enteritidis and S. Heidelberg strains using raw Illumina sequencing data or unfinished genomic sequences (PHAC);

- Application of the RNAse-H dependent PCR (IDT Inc.) for detection of single nucleotide variants of S. Heidelberg strains using raw Illumina sequencing data or using unfinished genomes (PHAC);
- EpiQuant for comparisons of the strength of epidemiological and genetic relationships between bacterial isolates (PHAC);
- crowBAR v.0.9 to support pathogen characterisation from unfinished data (PHAC);
- N. meningitidis Bacterial Isolate Genome Sequence database (BIGSdb) to upload whole-genome sequencing data to the online system and interrogate against data stored in this public database enabling investigation of N. meningitidis local epidemiology and outbreaks (PHAC);
- Pipelines for emerging pathogen detection developed using ultrafast k-mer based methods (PHAC);
- Neptune: a bioinformatics tool for rapid discovery of signature sequences in pathogen genomes (PHAC);
- National MALDI Database (NMD): a database containing the spectra of rare and unusual, but clinically relevant bacteria, as well as those species that are under-represented in the commercial Bruker Daltonic databases, providing fast, accurate and cost-effective identification of those pathogens locally, rather than having to be sent to a reference centre (PHAC);
- Quasitools for analyses of any viral next generation sequencing data for varied purposes (PHAC).

Research processes

- In-depth evaluation of sequencing coverage requirements, and development and validation of bioinformatics analysis pipeline to determine the microbiome and resistome of a wide variety of environmental metagenomes (AMR);
- After pin replication (tool optimized by Topp's lab) of 8228 isolates on solid media supplemented with antibiotics, presumptive ESBL species were selected with the aid of the heat map analysis tool combined with frequency analysis, for validation of resistance using the Sensititer profiling of 300 multidrug resistant isolates and for subsequent (next year) whole genome sequencing (AMR);
- Whole Genome Sequencing, using the Oxford Nanopore MinION technology on selected isolates showing resistance to third generation cephalosporins and carbapenems, is in progress (AMR);
- Assessment of publicly available tools for the extraction of predicted AMR determinants (e.g. ARIBA, ABRicate, CARD, Resfinder) (AMR);
- Comparison of data mining techniques for plasmid identification (e.g. ABRicate, PlasmidFinder) (AMR);
- Assessment of population structure using increasingly higher resolution genomic techniques (MLST, cgMLST, BioHansel, SNVPhyl) (AMR);
- Procedures for visualizing population structure with associated plasmid and AMR determinant results (PHYLOViZ, Grapetree) (AMR);
- Genomic characterization of a Canadian Vibrio parahaemolyticus isolate with unique mobilizing capacity (AMR);
- Established a mouse model for studying horizontal transfer of antimicrobial resistant genes in the intestine (AMR);
- Phenotypic and genotypic analysis of Salmonella antibiotic resistance genes (AMR);
- Culture based method for the isolation of 3GC resistant Enterobacteriaceae from retail meat and seafood (oysters, mussels, imported shrimp) (AMR);
- High-through put procedure to confirm phenotypic resistance of bacterial isolates (AMR);
- Rapid identification of bacterial isolates through the use of the Brucker MALDI Biotyper (AMR);
- Optimized protocol for solid phase mating of diverse Salmonella serovars (AMR);
- Identification of characteristic phenotypes (metabolite utilization, pH range) using machine learning to predict host range and serotype in E. coli (AMR);

- Method for the identification of genomic markers that are predictive of species, subspecies, serovars or other taxonomic levels (AMR);
- Schema for Whole Genome Multi-Locus Sequence Typing for Salmonella enterica was developed (collaboration with EFSA-funded INNUENDO consortium) (AMR);
- Neighbourhood Adjusted Wallace Coefficient was developed for measuring the stability of bacterial population clusters for the development of standardized nomenclatures for global genomic epidemiology (AMR);
- Improvements in scale and yield of rapid barcoding for multiple samples on the Nanopore sequencing instrument (AMR);
- Automatic closing of complete chromosomes and plasmids using Nanopore and Illumina hybrid assemblies (AMR);
- Associating resistance genes to mobile genetic elements using MOB suite and refiner (AMR);
- Data Standardization tool kit: Set of tools for specimen data clean up and standardization (AMR);
- Validation of haplotype-based genotyping-by-sequencing analysis for genomic selection and gene association analysis (AAFC);
- Characterization of the chromatin structure of Chinese Spring using ChIP (AAFC);
- Characterization of the methylome of Chinese Spring using WGBS (AAFC);
- Generation of nucleosome positions in Chinese Spring using Mnase-Seq (AAFC);
- Genotyping of parental diploid, tetraploid and synthetic hexaploid material using the wheat SNP array (AAFC);
- Phenotypic characterization of the diploid, tetraploid and synthetic hexaploid wheat assessing morphology and flowering time (AAFC);
- Protocols and pipeline for de novo transcriptome assemblies of Cecidomyid midges (AAFC);
- Transcriptome analysis of swede midge and wheat midge larvae using next-generation sequencing (AAFC);
- Constructed a DON protein interaction network involving 197 Fusarium proteins (AAFC);
- Transcriptome analysis of a plant mutant affected in nitrogen fixation, using next-generation sequencing (AAFC);
- Optimized production of gramillins (Fusarium cyclic lipopeptides) and improved purification process (AAFC);
- Standardized a Confocal laser scanning microscopy (CLSM) method to follow development of Fusarium graminearum on inoculated wheat heads, using Alexa Fluor 488 and propidium iodide staining (AAFC);
- C. sativa lines expressing engineered lysine feedback inhibition-insensitive dihydrodipicolinate synthase with increased seed lysine levels (AAFC);
- C. sativa lines expressing engineered high lysine-high methionine seed proteins (AAFC);
- C. sativa line deficient in major seed storage protein (cruciferin) production (AAFC);
- C. sativa line expressing feedback inhibition insensitive phosphoenolpyruvate carboxylase with altered amino acid levels and increased seed size (AAFC);
- Broad spectrum viral capture enrichment method for Next Generation Sequencing of vertebrate viruses (CFIA);
- Targeted probe-capture enrichment method for whole genome sequencing of African Swine Fever Virus and Classical Swine Fever Virus (CFIA);
- Targeted whole genome amplicon sequencing of Seneca A virus, influenza virus using Illumina Nextera XT on MiSeq (CFIA);
- Highly automated ampliseq method for whole genome sequencing of Zika virus and Zaire Ebolavirus, Classical Swine Fever Virus, Foot-and-Mouth Disease Virus (CFIA);

- Targeted cDNA method for whole genome sequencing of Vesicular Stomatitis Virus, Swine Vesicular Disease Virus, Foot-and-Mouth Disease Virus, Nipah/Hendra Virus, Epizootic Hemorrhagic Disease Virus, Rabbit Hemorrhagic Disease Virus (CFIA);
- High throughput cloning of full-length Open Reading Frames (ORFs) from M. bovis and B. abortus for cell free expression of recombinant proteins (CFIA);
- Isolation of Viral RNA from allantoic fluid and cell culture using triphasic reagents (CFIA);
- Amplification of Seneca virus A Whole Genome Sequencing using 2-step RT-PCR (CFIA);
- Generation of Avian Paramyxovirus cDNA for Next Generation Sequencing (CFIA);
- A series of TaqMan Assays that can identify Asian Gypsy Moths and/or Asian Gypsy Moth introgression based on diagnostic CO1 and FS1 genetic markers, respectively, in various simplex and duplex reactions (CFIA);
- Genome Quality Assessment with Machine Learning (GenomeQAML) uses machine learning to extract values of parameters that are characteristic of excellent-, good-, or poor-quality assemblies from a well-curated dataset. The program is able to use these values to categorise the assembly quality of new strains, removing the inherent subjectivity of manually categorising the quality of genome assemblies (CFIA);
- sField experiment protocols for metabarcoding eDNA sampling, extraction, and bioinformatics to be used for field surveys for aquatic invasive species and species at risk management (DFO);
- 220K salmon SNP array as a genetic tool to inform domestic and international fisheries and conservation of Atlantic salmon (DFO);
- 49 SNP-type assays to inform management of Atlantic salmon stocks (DFO);
- A 6K Redfish SNP catalogue, to support research informing commercial stock assessment (DFO);
- Optimized protocol for Atlantic salmon genotyping on 96 SNP x 96 individual platform, for use in determining aquaculture introgression effects on wild populations, to inform management of aquaculture and conservation of wild stocks (DFO);
- A scallop panel of SNP-type assays for fisheries stock assessment (DFO);
- A green crab panel of SNP-type assays for aquatic invasive species assessment (DFO);
- Gill-tissue specific Fit Chip for non-lethal measurement of salmon health indices to be used to inform salmon enhancement programs and fisheries management (DFO);
- Ion Torrent workflow for next generation sequencing of narwhal and beluga for population metagenomics investigations to inform marine mammal stock management (DFO);
- Narwhal mitogenome sequence analyzed and assembled for stock assessment information (DFO);
- High quality Chinook salmon SNP panel is applied to produce amplicons of interest (DFO);
- All hatchery broodstock of Chinook salmon juveniles released are genetically marked enabling identification of hatchery and year of release, potentially replacing the Coded Wire Tag marking system, which is applied to develop fishery regulations and policy (DFO);
- Discovery of optimized protocol for to significantly enhance eDNA capture in the freshwater environment by increasing the amount of extracellular DNA binding to the water filter, which in turn increases detection sensitivity (DFO);
- Standard Operating Procedure (SOP) for DNA isolation, library preparation and double digest restriction enzyme associated DNA (ddRAD) sequencing to be used for future Atlantic cod sequencing projects. (DFO);
- SOP for processing of raw Atlantic cod genome sequence reads; a modified STACKS protocol has been developed containing standardized quality thresholds (DFO);

- SOP for the detection of diagnostic Atlantic cod genomic variants containing standardized quality thresholds (DFO);
- Optimized protocols for the sequencing of complete narwhal mitogemones using Ion Torrent next generation sequencing (DFO);
- Operating procedures for environmental DNA (eDNA) collection and sample preservation in remote Arctic areas for research groups and resource managers using eDNA techniques to detect aquatic organisms (DFO);
- Data acquisition of thousands of differently expressed genes and analysis of this data using bioinformatics software (ECCC);
- Development of a protocol to multiplex more genetic samples in one single sequencing lane (ECCC);
- Research processes for preparing complex mixtures from passive samplers deployed in the oilsands area or from sediment cores that contain variable concentrations of polyaromatic hydrocarbons (ECCC);
- Yellow perch used to asses health and rainbow trout used to asses cumulative effect of contaminants and climate change (ECCC);
- A novel and rapid process by which complex extracts are prepared (containing all organohalogen contaminants) from wild bird eggs (ECCC);
- A process/SOP for developing Avian ToxChip PCR arrays for any species of bird (ECCC);
- NGS applications in ecotoxicological studies applying microbial community end points, isolation of mRNA from complex environmental samples (ECCC);
- Animal model and assay protocols to analyze the immune response and adverse reactions resulting from the exposure to the Respiratory Syncytial Virus for vaccine regulation (HC);
- Standardized method for assessing microbiome composition (HC);
- Transfection method for human mesenchymal stem cells (HC);
- Transcriptomics data from human mesenchymal stem cells derived from normal and leukemic patients (HC);
- SNP discovery approaches for wheat, including an automated DNA extraction and SNP analysis platform (NRC);
- Data analysis pipeline that integrates quantitative trait locus and expression quantitative trait locus mapping methods (NRC);
- Metabolomics methods for experimental analysis of wheat infected by fungi (NRC);
- Marker-assisted selection and rapid introgression methods to produce wheat germplasm with increased fusarium head blight resistance (NRC);
- Optimised methods for gene editing (NRC);
- Pan genome of Canadian wheat; mapping structural variation (NRC);
- Optimized method for single cell sequencing in plants (NRC);
- A well-rounded research program to study diseases and pest in wheat (NRC);
- A cost-effective microbial community profiling platform based on cpn60 gene UT region PCR amplicon sequencing (NRC);
- Standard operating procedures for the collection of field insect samples (NRCan);
- Standard operating procedures for curating and identifying insect samples (NRCan);
- Standard operating procedures for processing and identifying insect samples with metagenomics and bioinformatics tools (NRCan);
- Standard operating procedures for the maintenance of insect cell lines (NRCan);
- Improved analysis of whole genome sequencing data from highly clonal bacterial pathogens (PHAC);

- A knowledge translation pathway to provide comprehensive training and ongoing support to provincial public health and federal food safety labs that will introduce whole genome sequencing into routine surveillance and outbreak response by the PulseNet Canada network (PHAC);
- A process for quantifying the strength of epidemiological relationships between bacterial isolates enabling the use of genomic data by federal and provincial epidemiologists working to track the source of infectious pathogens (PHAC);
- Salmonella and Campylobacter cgMLST pipelines that allow for rapid phylogenetic analysis of draft whole genome sequencing assemblies and rapid assessment of assembly quality (PHAC);
- A framework for assessing the stability of clusters of isolates in bacterial populations used to identify stable clusters for tracking of strains of interest in genomic epidemiology and to identify clusters that are undergoing diversification such as in the case of outbreaks (PHAC);
- An analytical process to analyse N. meningitidis genomic epidemiology using Bacterial Isolate Genome Sequence database (BIGSdb) (PHAC);
- A process for shotgun metagenomics sequence library preparation was developed for various complex biological specimens and target pathogen types (PHAC);
- A rapid mass spectroscopy method for the identification of 7 toxins from five bacterial groups, enabling clinical diagnostic laboratories to more rapidly and accurately identify bacterial toxins in patients (PHAC);
- Methodologies to rapidly obtain S. pneumoniae genome sequence data from clinical specimens including data on drug resistance and pathogenicity (PHAC);
- A genomic typing method for H. influenzae to support genomic epidemiology and identification of antibiotic resistant clones (PHAC);
- A method for the PCR amplification of seasonal and pandemic influenza A viruses (PHAC);
- A multiplex RT-PCR protocol for IFVs that enables routine influenza A surveillance (PHAC);
- Long-range PCR amplification of hepatitis C virus genomes from patient (PHAC);
- A method for Hepatitis-C virus next generation sequencing by capture probe enrichment (PHAC);
- A method for Hepatitis-A virus next generation sequencing by capture probe enrichment (PHAC);
- A method for Hepatitis-B virus HBV next generation sequencing by amplicon-based sequence analysis (PHAC);
- Protocols for PCR amplification and NGS sequencing of HIV-1 protease, reverse transcriptase and integrase genes have been fully validated and implemented in HIV resistance analysis for both research and surveillance purposes (PHAC);
- An improved method for measles virus whole genome sequencing using enrichment of virus nucleic acids (PHAC);
- A new MeV sequence analysis protocol had been developed for distinguishing endemic MeV transmission from separate MeV importation events (PHAC).

APPENDIX B: GENOMICS R&D INITIATIVE: PERFORMANCE MEASUREMENT FRAMEWORK OVERVIEW

A horizontal Performance Measurement Strategy was developed for Phase VI of the GRDI. This document covers fiscal years 2014–2015 to 2018–2019 and formalizes the roles and responsibilities of the eight departments and agencies involved in the Initiative to support effective monitoring and evaluation activities.

The logic model presented in Figure 1 reflects the overall objectives for the GRDI:

> *Through the GRDI, eight federal science departments and agencies collaborate in the field of high-impact genomics research to address biological issues that are important to Canadians, focusing on the innovative and regulatory role of federal government research and operational mandates in important areas such as safe guarding health, food safety, sound management of natural resources, a sustainable and competitive agriculture sector, and environmental protection.*

A number of activities are conducted to reach this objective, focused on: R&D activities; coordination of research, reporting and management activities; collaboration among stakeholders to access world-class research infrastructure and networks; and dissemination and transfer of research results and translation of knowledge into commercial and public good applications.

These activities will generate outputs such as rigorous management processes for interdepartmental collaborations, scientific information and publications, research tools and products, and a highly skilled workforce. As immediate outcomes, these outputs will provide: structured collaboration mechanisms among participating departments and agencies; enhanced scientific leadership to support governmental mandates and priorities; knowledge, tools and advice for policy and regulatory decisions, as well as for the development of innovative tools and processes.

Intermediate outcomes consist in positioning federal science departments and agencies as genomics research leaders; use of research results by government policy makers and regulators for better informed evidence-based regulatory, policy, and resource management decisions; and use of research results by stakeholders to support innovation in Canada. Ultimately, the GRDI would be one of the factors contributing solutions to issues that are important to Canadians, and to the Government of Canada Outcomes: Healthy Canadians; Strong economic growth; An innovative and knowledge-based economy; and A clean and healthy environment.

The GRDI comprises three important program elements:

- **Interdepartmental governance**—While good management is an important aspect of any government program, it is particularly important for the GRDI because of the number of departments and agencies involved and the diversity of their respective mandates. It is thus important that practices put in place support effective departmental and interdepartmental coordination and provide a well-structured framework to clarify expectations and foster strategic approaches. It is critical that departmental and shared priorities be well defined so that the projects are selected to ensure government-wide priorities for genomics research information are addressed. Phase V of the GRDI demonstrated the viability of a truly interdepartmental approach and the ability of GRDI participating departments/agencies to work together, foster synergies, and add value to existing departmental resources. Phase VI builds on this successful model.

- **Research and development**—Research and development is the central component of this Initiative to respond to priorities, support governmental mandates, inform policy and regulatory decisions, and foster innovation. All activities surrounding the actual conduct of R&D; reporting and management activities; building a highly qualified work force to ensure enhanced scientific leadership in support of government mandates and priorities; collaboration to access world-class research infrastructure and expertise, and dissemination and transfer of research results are all critical to ensuring progress towards outcomes

Table 4 outlines the performance indicators, sources and responsibility for the outcomes outlined in the logic model (Figure 1) which should be reported upon, either in the annual performance report or at the time of evaluation as appropriate. Evaluations will not attempt to measure the contribution of the GRDI to the Government of Canada Outcomes, as attribution becomes challenging. Rather, it will focus on the achievement of immediate and intermediate outcomes, and assess whether it is reasonable to expect that the achievement of these outcomes would contribute to the Government of Canada Outcomes.

As this is a horizontal Initiative including several departments and agencies, some descriptive information is also included in the Framework related to projects, financial support and stakeholders and end-users. This is intended to support consistent collection and reporting on GRDI activities within individual departments and agencies, and are not included as indicators of performance.

Figure 1: Logic Model for the interdepartmental Genomics Research and Development Initiative Phase VI

Through the GRDI, eight federal science departments and agencies collaborate in the field of high-impact genomics research to address biological issues that are important to Canadians, focusing on the innovative and regulatory role of federal government research and operational mandates in important areas such as health care, food safety, sound management of natural resources, a sustainable and competitive agriculture sector, and environmental protection.

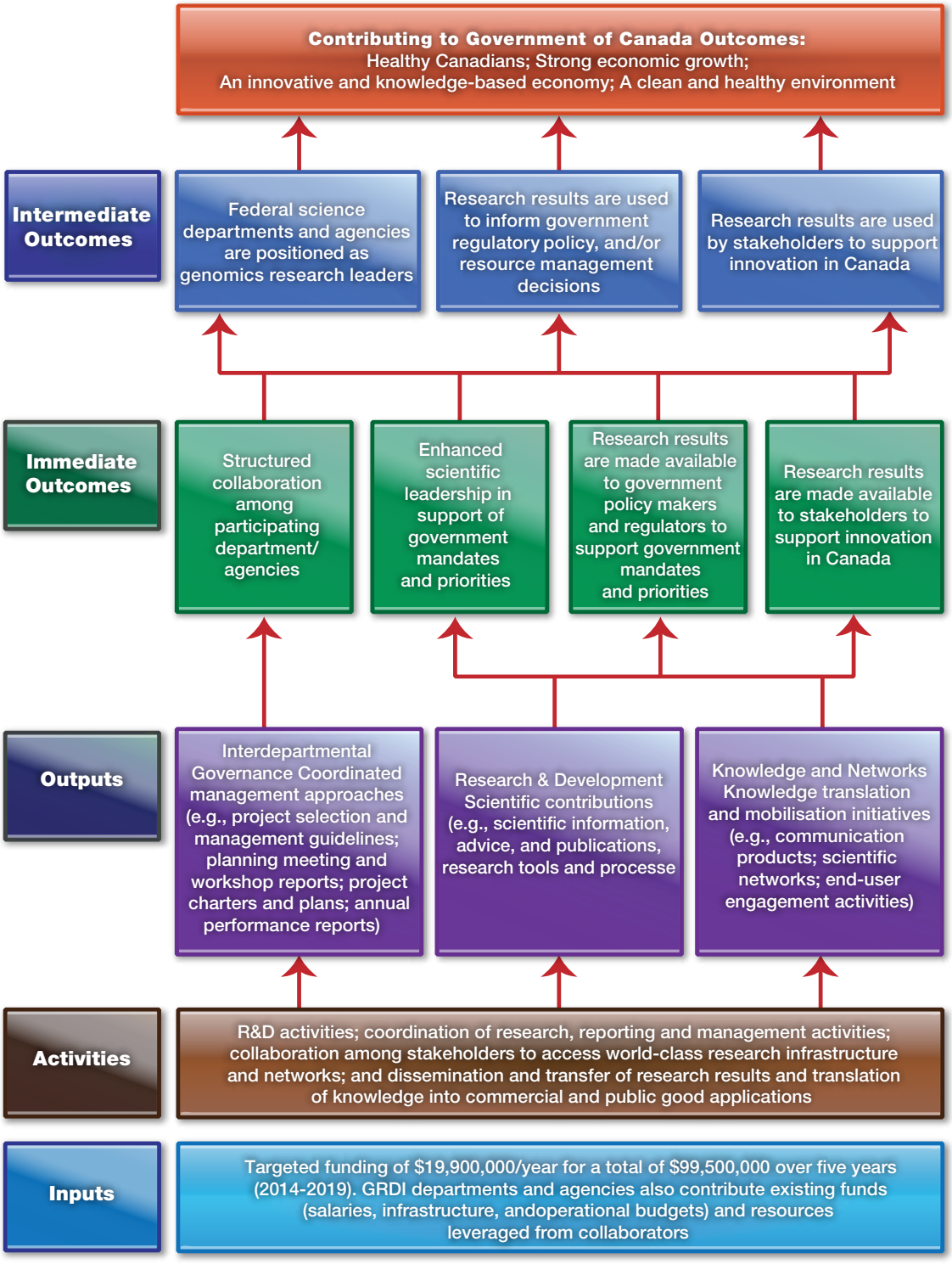
Contributing to Government of Canada Outcomes:
Healthy Canadians; Strong economic growth;
An innovative and knowledge-based economy; A clean and healthy environment
Intermediate Outcomes
Federal science departments and agencies are positioned as genomics research leaders
Research results are used to inform government regulatory policy, and/or resource management decisions
Research results are used by stakeholders to support innovation in Canada
Immediate Outcomes
Structured collaboration among participating department/ agencies
Enhanced scientific leadership in support of government mandates and priorities
Research results are made available to government policy makers and regulators to support government mandates and priorities
Research results are made available to stakeholders to support innovation in Canada
Outputs
Interdepartmental Governance Coordinated management approaches (e.g., project selection and management guidelines; planning meeting and workshop reports; project charters and plans; annual performance reports)
Research & Development Scientific contributions (e.g., scientific information, advice, and publications, research tools and processe
Knowledge and Networks Knowledge translation and mobilisation initiatives (e.g., communication products; scientific networks; end-user engagement activities)
Activities
R&D activities; coordination of research, reporting and management activities; collaboration among stakeholders to access world-class research infrastructure and networks; and dissemination and transfer of research results and translation of knowledge into commercial and public good applications
Inputs
Targeted funding of $19,900,000/year for a total of $99,500,000 over five years (2014-2019). GRDI departments and agencies also contribute existing funds (salaries, infrastructure, andoperational budgets) and resources leveraged from collaborators

Table 4: Program Performance Measurement Strategy Framework

Project Information developed by all participating departments/agencies towards the start of every phase (Descriptive, within departments/agencies)

- Project titles and summary descriptions (key objectives and impact areas)

Financial Information reported annually by all participating departments/agencies (descriptive)

- Internal $ leveraged from A-base resources
- Other funding by collaborators (OGDs; universities; international organizations; private sector; etc.)
- In-kind contributions by collaborators

End-users determined by all participating departments/agencies at project planning stage (descriptive)

- List of stakeholders and end-users available for each research project (including contact information)

OUTPUTS						
Area	Indicator	Methodology/Source	Frequency	Target[1]	Date to achieve target	Responsibility
Interdepartmental Governance Coordinated management approaches	% of processes, templates and guidelines for interdepartmental shared priority projects approved by ADM CC	Processes (e.g., for collective decisions on priorities and projects) and documents (e.g., Project Charter template and annexes) approved by ADM CC. Source: meeting minutes	Once per phase	100%	March 2016	NRC secretariat and departments / agencies
	% of departments / agencies sharing information on manage-ment approaches for mandated research projects	Departmental processes in place and shared in GRDI Best Practices Document	Once per phase	100%	September 2014	Departments / agencies
	% of publicly available GRDI-level annual performance reports completed	GRDI Annual Performance Report approved by ADM CC and published online	Annual	100%	September of following fiscal year	NRC secretariat
	% of project performance reports completed for internal management	Project performance reports produced according to department/agency requirements	Annual	100%	September of following fiscal year	Departments / agencies

OUTPUTS						
Area	Indicator	Methodology/Source	Frequency	Target[1]	Date to achieve target	Responsibility
Research and Development Scientific contributions	# of key scientific contributions by type demonstrating leadership	Annual reporting in project reports (e.g., publications in refereed journals, publications in refereed conference proceedings, book chapters, invited presentations, etc.)	Annual	Within the range recorded for Phase V (1472, avg. 490/yr.)[1]	By end of phase	Departments/ agencies
	# of other scientific contributions by type	Annual reporting in project reports (e.g., technical reports, poster presentations, deposits in genomics related databases or libraries, etc.)	Annual	Within the range recorded for Phase V (1445, avg. 482/yr.)[1]	By end of phase	Departments/ agencies
	# of research tools produced # of research processes produced	Reporting of tools and processes produced in project reports	Annual	Within the range recorded for Phase V (283, avg. 94/yr.)[1]	By end of phase	Departments/ agencies
Knowledge and Networks Knowledge translation and mobilisation initiatives	# of contributions to scientific networks by type	Annual reporting in project reports (e.g., participation in meetings related to regulations or policy, participation in national or international research committees, etc.)	Annual	Within the range recorded for Phase V (252, avg. 84/yr.)[1]	By end of phase	Departments/ agencies
	# of research collaborations by organization type	Annual reporting in project reports (e.g., universities (Canadian and international), other research organizations, private sector, etc.)	Annual	Within the range recorded for Phase V (1,101, avg. 367/yr.)[1]	By end of phase	Departments/ agencies
	# of communications products by type	Annual reporting in project reports (e.g., media interviews, press releases, newspaper and magazine articles, brochures, web pages, etc.)	Annual	Within the range recorded for Phase V (241, avg. 80/yr.)[1]	By end of phase	Departments/ agencies
	# of projects that included end-user engagement activities	Annual reporting in project reports	Annual	100%	By end of phase	Departments/ agencies

IMMEDIATE OUTCOMES						
Area	Indicator	Methodology/Source	Frequency	Target[1]	Date to achieve target	Responsibility
Structured collaboration among participating departments/ agencies	% of GRDI shared priority projects managed using interdepartmental governance structures	Meetings of project management teams and ADM CC, decisions recorded in meeting minutes	Once per phase	100%	By end of phase	NRC Secretariat and Departments/ agencies
	% of resources allocated to interdepartmental collaborations	Funding allocations approved by ADMCC and transferred by NRC to participating departments/agencies according to formal Project Charters	Annual	20%	By end of phase	NRC Secretariat
	# of departments involved in shared priority projects	Shared priority project planning meetings, Project Charters	Once per phase	At least three per project	By end of phase	Departments/ agencies
Enhanced scientific leadership in support of government mandates and priorities	# of research and technical personnel	Annual reporting in project reports (e.g., research scientists and professionals, post-doctoral fellows, students, etc.)	Annual	Within the range recorded for Phase V (2,410, avg. 803/yr.)[1]	By end of phase	Departments/ agencies
Research results are made available to government policy makers and regulators to support government mandates and priorities	% of projects leading outreach activities for disseminating results to identified end-users	Annual reporting in project reports (e.g., end-user consultations, workshops, transfer of methods and protocols, science advice, etc.)	Annual	100%	By end of phase	Departments/ agencies
Research results are made available to stakeholders to support innovation in Canada	# of transfer activities by type	Annual reporting in project reports (e.g., collaborative agreements, workshops, material transfer agreements, standard operating procedures, disclosures, patents, etc.)	Annual	Within the range recorded for Phase V (398, avg. 133/yr.)[1]	By end of phase	Departments/ agencies

INTERMEDIATE OUTCOMES						
Area	Indicator	Methodology/Source	Frequency	Target[1]	Date to achieve target	Responsibility
Federal science departments and agencies are positioned as genomics research leaders	Scientific production and impact in genomics	Evaluation	Every 5 years	On par or better than other genomics researchers in Canada	By end of phase	Evaluators
Research results are used to inform government regulatory, policy, and/or resource management decisions	Case analysis of examples where risk assessment, regulatory, policy, and resource management decisions have been informed by GRDI research (federal, provincial, municipal)	Evaluation	Every 5 years	n/a (qualitative/ descriptive)	By end of phase	Evaluators
Research results are used by stakeholders to support innovation in Canada	Case analysis of examples where innovative tools and processes have been adopted in Canada based upon GRDI research (# of people interviewed who have used GRDI research)	Evaluation	Every 5 years	n/a (qualitative/ descriptive)	By end of phase	Evaluators

[1] Quantitative targets have been established based on GRDI Phase V Annual Performance Reports between 2011 and 2014.

ACRONYMS

AAFC	Agriculture and Agri-Food Canada
ADM	Assistant Deputy Minister
ADM CC	Assistant Deputy Minister Coordinating Committee
AMR	antimicrobial resistance
ARG	antimicrobial resistance gene
BaP	benzo(a)pyrene
CFIA	Canadian Food Inspection Agency
CL	containment level
CRISPR	clustered regularly inter-spaced short palindromic repeats
CWT	coded-wire tag
DFO	Fisheries and Oceans Canada
DNA	deoxyribonucleic acid
EAB	emerald ash borer
ECCC	Environment and Climate Change Canada
EcoBiomics	Metagenomics-Based Ecosystem Biomonitoring
eDNA	environmental DNA
FHB	Fusarium head blight
FIAS	forest invasive alien species
GPSC	General Purpose Science Cluster
GRDI	Genomics Research and Development Initiative
HC	Health Canada
HIV	human immunodeficiency virus
ICVF	International Council on Viruses and Other Graft Transmissible Diseases of Fruit Crops
IRIDA	Integrated Rapid Infectious Disease Analysis
MGE	mobile genetic element
NAM	nested association mapping
NGS	next-generation sequencing
NRC	National Research Council Canada
NRCan	Natural Resources Canada
PBT	parentage-based tagging
PCR	polymerase chain reaction
PHAC	Public Health Agency of Canada
qPCR	quantitative polymerase chain reaction
QTL	quantitative trait locus
R&D	research and development
RNA	ribonucleic acid
SM	swede midge
SNP	single nucleotide polymorphism
SOP	standard operating procedure
SPP	Shared Priority Project
SSC	Shared Services Canada
STAGE	Strategic Technology Applications of Genomics in the Environment
STEC	shiga toxigenic E. coli
WGS	whole-genome sequencing
WM	wheat midge