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GENOMICS R&D INITIATIVE

ANNUAL PERFORMANCE REPORT

2016-2017



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

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EXECUTIVE SUMMARY

The Genomics Research and Development (R&D) Initiative (GRDI) is a Government of Canada initiative that enables structured collaborations and common approaches in federal science departments and agencies in the field of genomics research to address issues that are important to Canadians. The GRDI has been funded for three-year cycles: Phase I (1999-2002), Phase II (2002-2005), Phase III (2005-2008), Phase IV (2008-2011), and Phase V (2011-2014). It was renewed in 2014 for five years (Phase VI, 2014-2019).

The Initiative has advanced significantly in the delivery of its overarching goal to apply high quality, genomics-based R&D solutions in federal laboratories to support regulatory, public policy, and operational mandates of Canada's government in socially and economically important areas such as health care, food safety, sound management of natural resources, a sustainable and competitive agriculture sector, and environmental protection, with strong collaborations with university and private sectors.

The fiscal year 2016-2017 was the third year of Phase VI of the GRDI. The Initiative continued to support mandated research in participating departments as well as a model of structured collaboration supporting two new highly coordinated interdepartmental projects along shared priorities and common goals: 1) Antimicrobial Resistance (the AMR project); and 2) Metagenomics Based Ecosystem Biomonitoring (the EcoBiomics project).

Considerable progress was achieved in 2016-2017, exemplified by the following highlights:

- A refined biomarker to identify genotoxic chemicals and a related software application were submitted to the US Food and Drug Administration biomarker qualification program;
- Incorporation of toxicogenomics data in the annual training session for regulators (Applied Genetic Toxicology for Regulatory Decision-Making);
- The new sequence typing for antibiotic resistance in *Neisseria gonorrhoea* (NG-STAR) enabled researchers to track the international spread of drug resistant

isolates of *N. gonorrhoeae*, and to identify AMR isolates that had not previously been characterised in Canada;

- A suite of bioinformatics tools to analyse bacterial whole genome sequences has been developed for more rapid and effective outbreak identification of foodborne pathogens such as *Salmonella*, *E. coli*, and *Campylobacter*;
- Next generation sequencing procedures and analytical tools to monitor the emergence of drug resistant variants of HIV have been transferred to public health laboratories in eight Latin American and Caribbean countries;
- More sensitive procedures were developed for public health investigators who track measles transmissions;
- Using whole genome sequencing, scientists were able to determine that the *Mycobacterium bovis* strain affiliated with the 2016 bovine tuberculosis outbreak in Alberta was not linked to earlier strains in Canada. This finding directed investigation and surveillance activities that aided the federal bovine tuberculosis eradication program;
- Scientists developed a web-based Genomics Portal that enables access to CFIA's database of bacterial genomes;
- Whole genome sequencing technology was successfully deployed in the CFIA's six food microbiology testing laboratories.

This Annual Performance Report for 2016-2017 follows the Performance Measurement Framework that was developed for Phase VI in 2015. It presents the GRDI profile and planned results, its links to departmental objectives and program alignment architecture, and its governance, coordination and accountability structures. It then reports on performance for 2016-2017 in terms of interdepartmental governance, R&D, and knowledge and networks. Appendix A presents summary statistics as well as a summary narrative account of R&D achievements for 2016-2017.



ACRONYMS

AAFC	Agriculture and Agri-Food Canada	HIV	Human Immunodeficiency Virus
ADM	Assistant Deputy Minister	IRIDA	Integrated Rapid Infectious Disease Analysis
ADM CC	ADM Coordinating Committee	MALDI	Matrix-Assisted Laser Desorption/Ionization
AMR	Antimicrobial resistance	NGS	Next Generation Sequencing
CABIN	Canadian Aquatic Biomonitoring Network	NG-STAR	Neisseria gonorrhoeae Sequence Typing for Antimicrobial Resistance
CFIA	Canadian Food Inspection Agency	NSERC	National Science and Engineering Research Council
CFS	Canadian Forest Service	NRC	National Research Council of Canada
CIPARS	Canadian Integrated Program for Antimicrobial Resistance Surveillance	NRCan	Natural Resources Canada
CITES	Convention on the International Trade of Endangered Species	PCR	Polymerase Chain Reaction
CNISP	Canadian Nosocomial Infection Surveillance Program	PHAC	Public Health Agency of Canada
CNPHI	Canadian Network for Public Health Intelligence	qPCR	Quantitative PCR
COSEWIC	Committee on the Status of Endangered Wildlife in Canada	R&D	Research and Development
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats	RNA	Ribonucleic Acid
DFO	Fisheries and Oceans Canada	S&T	Science and Technology
DNA	Deoxyribonucleic Acid	SGSA	Salmonella Genoserotyping Array
ECCC	Environment and Climate Change Canada	SNP	Single Nucleotide Polymorphism
eDNA	environmental DNA	SOPs	Standard Operating Procedures
FTE	Full Time Equivalent	SSC	Shared Services Canada
GRDI	Genomics Research and Development Initiative	STAGE	Strategic Technology Applications of Genomics in the Environment
HC	Health Canada	WG	Working Group

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GENOMICS R&D INITIATIVE – PROFILE



The GRDI was established in 1999 to establish and maintain core genomics R&D capacity in federal departments and agencies and provides \$19.9M/year to:

- 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);
- Public Health Agency of Canada (PHAC);
- National Research Council of Canada (NRC); and
- Natural Resources Canada (NRCan).

Projects funded under the GRDI are focused on departmental mandates and government priorities, and are strategically aligned with the objectives of the depart-

ments. They seek to uphold regulatory, public policy, and operational mandates in important areas such as health, food safety, sound management of natural resources, a sustainable and competitive agriculture sector, and environmental protection, with strong collaborations with university and private sectors.

The federal government has allocated \$393.3M to the GRDI between 1999 and 2019: \$55M for Phase I (1999-2002); \$59.7M each for Phases II (2002-2005), III (2005-2008), IV (2008-2011), and V (2011-2014); and \$99.5M for Phase VI (2014-2019). Phase V of the GRDI (2011-2014) introduced a model that mobilized resources for concerted research on issues that are beyond the mandates of single departments, supporting highly coordinated interdepartmental projects along shared priorities and common goals. Two new projects were launched in April 2016: 1) Antimicrobial Resistance; and 2) Metagenomics-Based Ecosystem Biomonitoring.

Resources

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 2016-2017 in support of GRDI projects, and demonstrates that non-GRDI funds

represented more than twice 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 2016-2017 (\$000)

DEPARTMENT/AGENCY	GRDI	NON-GRDI*	TOTAL
National Research Council Canada	4,440	12,204	16,644
Agriculture and Agri-Food Canada	4,440	9,249	13,689
Health Canada	1,600	3,062	4,662
Public Health Agency of Canada	1,466	1280	2,746
Natural Resources Canada	1,600	3,904	5,504
Environment and Climate Change Canada	800	1,575	2,375
Fisheries and Oceans Canada	720	1,386	2,106
Canadian Food Inspection Agency	720	3,437	4,157
SHARED PRIORITY PROJECT	GRDI	NON-GRDI	TOTAL
Antimicrobial Resistance	1,799	2,880	4,679
Metagenomics Based Ecosystem Biomonitoring	1,811	1,981	3,792
Coordination and Common Functions	370	16	386
Total	19,766	42,852	62,618

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

Planned Results

As reported in the NRC Departmental Report on Plans and Priorities Supplementary Table for the GRDI, the participating departments established a collective set of planned results for 2016-2017.

To deliver on these planned results, departments and agencies developed the following research plans and activities:

- 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.

To deliver on these planned results, departments and agencies developed the following research plans and activities:

Agriculture and Agri-Food Canada

GRDI investments at AAFC will focus on the priorities outlined in the Canadian Crop Genomics Initiative, and will be leveraged to enable industry to take advantage of new innovative opportunities. Activities will fall under three broad themes: 1) Biodiversity, gene mining and

functional analysis: to develop value-added traits (e.g. seed quality) for the highly competitive marketplace. Enhance the resiliency of Canada's crop production in the face of potentially catastrophic abiotic and biotic stresses to maximize profitability of the sector; 2) Bioinformatics and physical tools: ensuring that scientists can maximize the opportunities presented by genomics-based research such as identification and characterization of genes coding for desirable traits related to seed quality or disease resistance; and 3) Improved access to biological materials and data sets: to enhance the efficiency of plant breeding to lay the scientific foundation for major advances in the development and delivery of priority traits identified by industry.

Canadian Food Inspection Agency

At the CFIA, genomics research is focused on two thematic areas to enhance genomics capacity and capability to regulate pests and pathogens: "Detection and Isolation" and "Identification and Characterization." Under these themes, the CFIA's genomics research is aligned to its three business lines: animal health, food safety, and plant health. In animal health, genomics research activities are targeted to support management of public health risks associated with the transmission of zoonotic diseases as well as reportable and emerging animal diseases. For food safety, the genomic activities will enhance the CFIA in the areas of compliance testing, source attribution and risk profiling, while also enabling the enforcement of HC standards contributing to health risk assessment. Plant health genomics is focusing on further enabling early detection and rapid response, and informing regulatory decision-making for regulated plant pests and plant commodities within the agricultural and forestry sectors. Additionally, research is conducted horizontally to harmonize genomics activities across CFIA's three business lines with a focus to contribute to the improved transfer of technology and tools between CFIA business lines and to increase the accessibility to genomics tools for CFIA scientists.

Fisheries and Oceans Canada

Genomics-enabled research within DFO will continue to be aligned within the following themes: 1) Protecting fish species and enabling sustainable harvesting: to develop and apply leading-edge genomics tools to accurately identify species, populations and stocks for fisheries management and the conservation of vulnerable stocks, species at risk and aquatic biodiversity; 2) Safeguarding Canadian fish and seafood products: to 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 Canada's export markets for fish and seafood products; and 3) Maintaining healthy and productive aquatic ecosystems: to develop and apply new genomics tools to monitor, mitigate and restore aquatic ecosystems.

Environment and Climate Change Canada

ECCC will continue to deliver its GRDI funding under the Strategic Technology Applications of Genomics in the Environment (STAGE) program, with the following priorities for genomics research: 1) Ecotoxicology: to establish toxicology end points for microorganisms, chemicals of concern, and emerging stressors; and to predict the mode of action of chemicals of concern and their effects on organisms; 2) Wildlife conservation: to understand how genes are interacting in flora and fauna in response to environmental conditions and to track disease in wildlife; 3) Environmental monitoring: to develop indicators (e.g., gene expression profiles for key species) of ecosystem health in priority ecosystems (e.g., Great Lakes and St. Lawrence) and to track pathogen sources; and 4) Compliance and Enforcement: to analyze flora and fauna for individual species identification, parentage determination and ascertaining geographic origin. This work will enable the delivery of ECCC's obligation under the *Fisheries Act and the Canadian Environmental Protection Act*, and programs including the Chemicals Management Plan.

Health Canada

Genomics research will continue to focus on four priority investment areas to strengthen HC's regulatory role: 1) Supporting regulatory knowledge on therapeutics and biologics: to inform and support regulatory decisions throughout the biotherapeutic product life-cycle; 2) Supporting regulatory knowledge on food safety and nutrition: enabling detection and characterization of food-borne micro-organisms; characterization of health effects of food contaminants (e.g. fungal toxins, anthropogenic contaminants seafood toxins), food allergens, nutrients, novel foods/food ingredients, and pre- and pro-biotics; and development of 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; 3) Protecting human health from potential adverse effects of environmental contaminants, radiation, consumer products and pesticides; and 4) Research on socio-ethical impacts of genomics technologies, outputs and products: approaches for responsible integration of genomics for societal benefit, taking into account ethical, legal and socio-economic considerations.

National Research Council Canada

Investments from the GRDI at the NRC will support programs requiring genomics-related activities to help industry and government tackle strategic national priorities through mission-oriented research and technology deployment. In 2016-2017, these will be: 1) the NRC contribution to the Canadian Wheat Alliance, the goal of which is to improve the yield, sustainability, and profitability of wheat for the benefit of Canadian farmers and the economy. This will be achieved by improving breeding efficiency and reducing losses from drought, heat, cold and diseases, and improving nutrient use efficiency; and 2) the Biologics and Biomanufacturing program, the main objective of which is to cover all aspects of biologic development from discovery up to pre-clinical testing in collaboration with industrial partners. These programs were approved for implementation by the NRC Senior Executive Committee after undergoing a rigorous program approval and implementation process.

Natural Resources Canada

The Canadian Forest Service of NRCAN will focus on accelerating the translation of accumulated genomics knowledge into applications in support of Canada's forest sector competitiveness, including: 1) Forest generation: the development of innovative genomic applications will result in accelerated production of higher quality fibre, translating into economic and environmental benefits for Canada; and 2) Forest protection: the development of innovative genomic diagnostic tools will enable rapid detection and management of invasive insects and diseases which 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 to create new tools to enhance disease prevention and control. These technologies are providing methods to enhance: 1) the prevention and control of priority pathogens; 2) the response to antimicrobial resistant pathogens; 3) infectious disease surveillance; and 4) public health security measures. The knowledge generated from genomic approaches is supporting more detailed risk analyses, as well as the identification and development of new intervention points for the control and prevention of infectious diseases.

Shared Priorities

The Antimicrobial Resistance project will develop a greater understanding of the critical activities that contribute to the development of antimicrobial resistance and critical exposure pathways by which antimicrobial bacteria reach humans, which could then be used to help validate economically sustainable technologies, practices, and policies to mitigate the development of antimicrobial resistance; it is a key component of the Federal Action Plan for Antimicrobial Resistance and Use in Canada. It is coordinated by AAFC and involves CFIA, HC, NRC, and PHAC.

Alignment with Government Priorities

The GRDI seeks to support increasingly complex federal evidence-based regulatory and policy decisions required by the respective mandates of participating departments and agencies, as well as the development of new policies and standards, within the realm of the specific role of federal research and focusing activities in areas where government is best able to deliver results. It also seeks to support the ability to anticipate and respond to the needs of Canadians in relation to areas of government responsibility for public health, the economy, agriculture and the environment.

Projects funded under the GRDI are focused on departmental mandates and government priorities, and are strategically aligned with the objectives of participating departments and agencies.

All research and innovation activities at AAFC (including those of the GRDI) directly support the achievement of prioritized research outcomes. The GRDI specifically contributes to the department's Strategic Outcome: An Innovative and Sustainable Agriculture, Agri-Food and Agri-Based Products Sector. Funding from the GRDI enables AAFC to develop and strengthen the Canadian Crop Genomics Initiative through investments in plant genomics and the formation of multi-disciplinary teams across Canada that focus on improving the sustainability and competitiveness of Canada's agriculture sector.

Activities of the CFIA under the GRDI support the agency's Strategic Outcome to Maintain a Safe and Accessible Food Supply and Plant and Animal Resource Base. Commodities and resources regulated under CFIA's Program Activities including the Food Safety program, Animal Health and Zoonotic program, and the Plant Resources program are all supported by genomics research outcomes. The GRDI program at the CFIA targets the development and application of genomics tools for the rapid detection of food pathogens, plant

pests, and animal disease agents. This enables the CFIA to respond effectively to regulatory needs in food safety, ensure compliance, maintain consumer confidence, and minimize animal and plant disease incursions.

National coordination for genomics research at DFO is provided by the Biotechnology and Genomics Program. The Biotechnology and Genomics Program supports genomics research for Economically Prosperous Maritime Sectors and Fisheries and Sustainable Aquatic Ecosystems, two of the three Strategic Outcomes of the department's Program Alignment Architecture. Genomics research is building the scientific knowledge base and expertise necessary to support priorities for fisheries and oceans management.

All GRDI-funded R&D activities undertaken at ECCC align with two of the three Strategic Outcomes: Canada's Natural Environment is Conserved and Restored for Present and Future Generations, and Threats to Canadians and their Environment from Pollution are Minimized. To this end, the STAGE genomic research priorities at ECCC contribute to the monitoring and understanding of Canada's ecosystem, help to assess risks posed by chemical pollutants to wildlife and migratory birds, and deliver practical applications that support regulatory compliance as well as evidence-based decision-making related to risk mitigation and conservation efforts.

Research funded by the GRDI at HC contributes to the generation of regulatory knowledge required for the appropriate management and communication of health risks and benefits associated with food, products, substances, and environmental factors. The knowledge and tools generated by genomics research ultimately support departmental efforts to respond to current and emerging health issues under the Program Activity: Canadian Health System Policy, and Strategic Outcome: A Health System Responsive to the Needs of Canadians.

The Program Alignment Architecture of the NRC was updated to reflect the NRC new industry-focus. It is aligned with Government of Canada's Strategic Outcomes and federal priorities and to the NRC business processes. The NRC performance reporting is aligned accordingly. The GRDI at the NRC supports the Strategic Outcome: Canadian Businesses Prosper from Innovative Technologies, the Program Technology Development and Advancement, and the Sub-Programs Aquatic and Crop Resource Development and Human Health Therapeutics. This is accomplished by contributing to research programs that focus on improving Canadian wheat, and on developing new biologics.

At the Canadian Forest Service of NRCan, the GRDI has developed the foundation for contributing to the Strategic Outcome Canada's Natural Resource Sectors are Globally Competitive and to the Program Activity Innovation for New Products and Processes. It contributes to the Intended Outcome: Advancing Forest Product Innovation. Resulting from this foundation are important amounts of data, infrastructure, and collaborations that are delivering practical applications.

Within PHAC, projects funded by the GRDI support the overarching strategic outcomes of promoting health, reducing health inequalities, as well as preventing and mitigating harmful consequences of infectious and chronic diseases. Researchers create innovative tools that apply genomic and bioinformatic technologies for more effective public health interventions. In addition, the GRDI generates leading edge scientific knowledge

to support public health decision-making and program development. By driving collaboration and knowledge exchange among public health professionals working in federal, provincial, territorial, municipal and non-government organisations, the GRDI facilitates the integration of reliable and current information into public health decision-making and interventions at all levels across Canada. The development and application of leading-edge public health science and of tools to provide specialized laboratory testing and reference services that will contribute to better public health and improved responses to emerging health risks, fall directly within the Program Activity of Public Health Infrastructure.

The federal science policy framework is currently provided by *Seizing Canada's Moment: Moving Forward in Science, Technology and Innovation* (hereafter referred to as the S&T Strategy), a strategy released by the federal government in December 2014 "as a commitment to keep science, technology and innovation at the forefront of government policy for years to come." This new strategy builds on the 2007 federal S&T Strategy, *Mobilizing Science and Technology to Canada's Advantage*. The GRDI contributes to the three pillars for Canada outlined in the S&T Strategy (people, knowledge, innovation) and supports the priorities of natural resources, health and life sciences, environment and agriculture. It informs good and sound decisions on public policy, regulatory responsibilities, and government priorities, congruent with the inherent value of federal research. It also supports technology commercialization efforts.

Governance, Coordination and Accountability

Departments are vertically accountable in terms of authority to deliver on their mandate and to spend resources. Accountability is thus often viewed as a challenge to the management of shared programs that have a collective sense of purpose. Indeed, programs involving more than one department to jointly pursue common objectives present unique complexities for setting priorities and sharing resources.

To ensure sound management of the GRDI, the interdepartmental governance framework established under the leadership of the NRC for previous phases of the GRDI continued to oversee the collective coordination of the GRDI. The governance structure for the GRDI includes three main elements: an Assistant Deputy Minister (ADM) Coordinating Committee, an Interdepartmental GRDI Working Group and a Coordination Function, with support from Ad Hoc Advisory Committees when particular needs for expert advice arise.

ADM Coordinating Committee (ADM CC)

An interdepartmental ADM CC is chaired by the lead agency (NRC) with membership at the ADM-level from each of the organizations receiving funding, and guest representatives from Industry Canada and Genome Canada. It is responsible for the overall strategic direction for the GRDI and approval of investment priorities. It ensures that effective priority setting mechanisms are established for the GRDI, and that government objectives and priorities are addressed. The Committee also ensures that common management principles are implemented and collaborations between organizations are pursued wherever relevant and possible. It typically meets three times a year at the call of the Chair, and more often when warranted by specific needs for decision-making.

Interdepartmental Working Group (WG)

An interdepartmental GRDI WG supports the work of the ADM CC. It is chaired by the lead agency (NRC) with membership at the Director level from all participating departments/agencies, and Industry Canada. The WG mandate is to provide recommendations and strategic advice to the ADM CC regarding strategic priority setting and overall management of the GRDI. The WG is responsible for providing direction to GRDI activities related to operational delivery, implementation planning and investment priority setting. The WG also supports evaluation and reporting requirements related to the GRDI. It meets about every two months, and more often when warranted by specific needs for recommendations and advice.

GRDI Coordination Function

The Coordination Function for the GRDI is housed at the NRC. It provides GRDI-wide program coordination, communication, networking and outreach support, including support to the ADM CC and the GRDI WG, transparent and effective communication to departments regarding the planning cycle, process requirements, financial administration and other project management requirements, and support for SPP planning and implementation. This function also helps establish GRDI-wide research priorities; facilitates interdepartmental project development and peer reviews; ensures SPP Project Management Plans and funding agreements are in place; and supports performance management, reporting, evaluation, and communications. It is funded through the funding envelopes set aside for shared priority activities.

Performance Measurement Strategy Framework

In fulfillment of 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), the Horizontal Performance Measurement Strategy that was developed for Phase V of the interdepartmental GRDI was updated for Phase VI. The updated version 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. An overview of the Performance Measurement Strategy Framework is provided in Appendix B, as well as the logic model that reflects the overall objectives for the GRDI, leading to the uptake and application of the knowledge and tools it generates for policy and regulatory decisions, key public policy priorities, and private sector innovation.

PERFORMANCE



Interdepartmental Governance

Coordinated Management Approaches

Ongoing coordination was provided by the NRC for 2016-2017, the third year of Phase VI, including timely secretariat support to GRDI departments and agencies and the implementation of updated GRDI governance, management and operating processes for Phase VI. Three meetings of the ADM CC and six meetings of the GRDI WG were held to allow for collaborative decisions. The launch of Phase VI shared priority projects was supported and funding was made available to participating departments based on the approved Project Management Plans. The GRDI Performance Measurement Strategy was implemented with the finalization and approval by the ADM CC of the Annual Performance Report for 2015-2016, and input into the NRC Departmental Results Report and Departmental Results Plan. The GRDI evaluation was completed under the leadership of the NRC Audit and Evaluation group and the interdepartmental GRDI Evaluation Working

Group. The Evaluation Report and a Management Response and Action Plan were approved by the ADM CC.

Mandated Research

Departments and agencies manage their GRDI activities within the scope of existing program areas aligned with their respective Strategic Outcomes, Activities, and Sub-Activities defined in their Program Alignment Architecture. Annex 1 lists the mandated research projects funded in 2016-2017.

Shared Priorities

Phase VI shared priority projects were launched, following approval by the ADM CC of formal Project Management Plans that describe detailed governance structures to ensure seamless integration and clear roles and responsibilities, and Science Plans that define study plans and deliverables for all project components at a more technical level.

Research and Development

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 are critical to ensuring impacts, and are thus included in the GRDI Performance Measurement Framework.

Direct scientific outputs for 2016-2017 and quantitative indicators for performance evaluation are enumerated in Annex 2 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); and research and technical personnel. Highlights of the results achieved in

2016-2017 against planned results are provided in Annex 3, and Annex 4 presents a list of research tools and processes developed under the GRDI.

Awards and prizes were awarded to several GRDI scientists to recognize the excellence of their research:

- The leadership teams of the GRDI shared priority projects were awarded the Public Service Award of Excellence for 2016 in the category of Scientific Contribution: Cathryn L. Abbott, DFO; Sabah Bidawid, HC; Guillaume Bilodeau, CFIA; Patrice Bouchard, AAFC; Nathalie Corneau, HC; Robert Footitt, AAFC; Morag Graham, PHAC; Siegfried Janz, NRC; André Lévesque, AAFC; James Macklin, AAFC; Franco Pagotto, HC; Michael Rott, CFIA; Edward Topp, AAFC; Gary Van Domselaar, PHAC; Teodor Veres, NRC;

- Guillaume Bilodeau, Marie-José Côté, Cheryl Dollard, Eliane Guillemette, and Steve Jones (CFIA) were awarded the 2016 International Seed Testing Association (ISTA) Seed Science Advisory Group Prize at the ISTA Seed Symposium in recognition for their poster presentation;
- Guillaume Bilodeau, Brittany Day, Cheryl Dollard, Vasily Grebennikov, Delano James, Wendy Laviolette, Philip Macdonald, Michael Rott, Donna Smith, and Graham Thurston (CFIA) were awarded the CFIA President's Award – Dr. Evans Award for Partnership and Teamwork for their contribution to the Barcode of Life with the University of Guelph;
- Guillaume Bilodeau, Marie-José Côté, Delano James, Margaret Neuspiel and Michael Rott (CFIA) were awarded the Science Branch Recognition Program 2016, in the category of Collaboration/Partnership for contribution to the Invasive Alien and Quarantine Species Genomics Research and Development Initiative project;
- Ian Bradbury (DFO) was the recipient of a Cox Fisheries Scientist in Residence Award from Dalhousie University;
- Alex Leclerc, an Honours student in Vimal Balakrishnan (ECCC)'s laboratory, was awarded the "Best Presentation Award" at the Gananoque Environmental Science Conference;
- Matthew Meier (HC) received 2nd place prize for Best Poster by a New Investigator at the 47th Annual Meeting of the Environmental Mutagenesis and Genomics Society;
- Sabina Halappanavar (HC) received the 2016 Assistant Deputy Minister's Award in the Category of Science for her work in nanotoxicology;
- Sabina Halappanavar (HC) received the 2016 Deputy Minister's Award for Excellence in Science for her work in nanotoxicology;
- Steve Brooks (HC) received Assistant Deputy Minister Award for Science;
- Steve Brooks (HC) received Deputy Minister Award for Science;
- Roger Johnson's (PHAC) coop student Ray De Villa received first prize in research poster competition at the Ontario Ministry of Agriculture, Food and Rural Affairs 2016 Food Safety Research Forum, Guelph, Ontario, on May 24, 2016.

Knowledge and Networks

To maximize the value of the GRDI and move that value to users for commercial and public good applications as the Initiative matures, knowledge translation and mobilization activities are required. These 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. Examples of knowledge and networks activities completed in 2016-2017 follow.

Scientists from CFIA established a reference genomic database of Canadian *Mycobacterium bovis* strains that played an important role in epidemiological investigations of the latest bovine tuberculosis outbreak (Alberta, 2016). These investigations demonstrated that the Alberta bovine *M. bovis* isolates were genetically different from *M. bovis* isolates recovered from Canadian domestic animals and wildlife between 1985 and 2015, and that they were recent introductions to Canada with a common ancestor from Mexico. A bioinformatics algorithm developed in collaboration with the United States Department of Agriculture was implemented at the Ontario Animal Health Laboratory for the *M. bovis*

genome data analysis. This promoted a harmonised approach for molecular epidemiological investigations of bovine tuberculosis outbreaks.

Through the GRDI-EcoBiomics project, Donald Baird (ECCC) participated in the European Union COST Action project: DNA AquaNet, which explores metabarcoding approaches to inform European legislation, including the Water Framework Directive and the Habitats Directive. He also collaborated on the UK Natural Environment Research Council Large Grant Project: Impacts of global warming in sentinel systems: from genes to ecosystems (Imperial College, London, UK).

Through the GRDI-AMR project, a material transfer agreement was signed with Les Aliments Breton Inc. to obtain swine fecal samples from diverse husbandry conditions. The project was also leveraged with funding from the National Science and Engineering Research Council (NSERC) to study the use of cranberries as an alternative to antibiotics in swine.

The NRC Wheat Flagship researchers contributed to: 1) the International Wheat Yield Partnership for research of photosynthetic efficiency in wheat; 2) the Wheat Initiative led by the Institut National de Recherche en Agronomie as part of an expert working group on adaptation of wheat to abiotic stress; and 3) the FusResis Consortium to develop enhanced Fusarium resistance in wheat.


Scientists funded by the GRDI at DFO focused on improving science advice to manage various fish stocks and aquatic resources, and disseminated scientific knowledge directly to managers, international partners, and communities whose livelihoods depend on the fisheries. They led or were involved in thirteen community meetings, three government advisory panels, three international and national genomics-related committees, and gave twenty-one media interviews to share the results of their research, and highlight the impacts of these results on long-term fisheries and aquatic resource management.

Scientists funded by the GRDI at ECCC participated in several international projects: 1) the DNA AquaNet project of the European Union Co-operation in Science and Technology Action, to explore the application of metabarcoding approaches within European legislation; 2) the 'Impacts of global warming in sentinel systems: from genes to ecosystems' Large Grant Project of the United Kingdom Natural Environmental Research Council; and 3) the international Daphnia Genomics Consortium. A scientist participated in the Organization for Economic Co-Operation and Development technical committee on Molecular Screening and Toxicogenomics, and in the Society of Environmental Toxicology and Chemistry Pellston Workshop for Advancing the Adverse Outcome Pathway Framework.

A lead HC scientist chaired an expert panel of the US National Institute of Environmental Health Sciences mandated to evaluate the use of genomics data in benchmark toxic dose modeling. A lead HC scientist also chaired the plenary session of the International Workshops on Genetox Testing (held every four years) in Tokyo on genetic toxicology assessments. These activities are expected to have major impacts on the procedures and strategies used for regulatory toxicology testing and risk assessment.

Data, signatures and algorithms produced by toxicogenomics research funded by the GRDI at HC were deposited in the National Institute of Environmental Health Sciences' Chemical Effects in Biological Systems Database, thus providing public access to gene toxicity prediction tools.

Several HC scientists serve as advisors for applying genomics technology to the risk assessment of chemicals for several international organizations, including the Organisation for Economic Cooperation and Development, the World Health Organization's International Programme on Chemical Safety, the Sustainable Nanotechnologies Project (SUN) Consortium, the International Life Sciences Institute's Genetic Toxicology Technical Committee, and the Horizon 2020 project consortium in the European Union.



In the area of food nutrition, a lead HC scientist provided expert advice and guidance based on GRDI results to companies wishing to add fermentable carbohydrates to infant formula.

Researchers at NRCan continued to develop tools to map and monitor the spread of forest invasive alien species, and transfer these tools to partners. They collaborated with CFIA and provided them with fully validated tools for the detection of Asian gypsy moth, and are building on this collaboration to develop detection tools for another important threat to Canadian forests, the Siberian moth.

Research projects at PHAC are well networked to facilitate the translation of results into practice and to enhance the exchange of knowledge with partners nationally and internationally. At the national level, PHAC projects are collaborating with colleagues in almost all provincial and territorial public health laboratories. These relationships provide for the exchange of samples, data, and knowledge, and provide the mechanism to support the validation and adoption of newly developed assays by front line clinical laboratories. Projects of the GRDI that are developing enhanced tools to prevent foodborne pathogens are also working in conjunction with established national surveillance networks, FoodNet Canada, and PulseNet Canada. Similarly, projects developing genomics-based tools for the control and reduction of antimicrobial resistance are working closely with national antimicrobial resistance (AMR) surveillance networks, the Canadian Nosocomial Infection Surveillance Program and the Canadian Integrated Program for Antimicrobial Resistance Surveillance.

The relationships developed between genomics researchers and the surveillance epidemiologists strengthen GRDI projects through the exchange of samples and knowledge; they also facilitate the transfer of research outputs into practice. Internationally, PHAC GRDI projects are engaged with the World Health Organisation and the Pan-America Health Organisation to share knowledge and technological approaches for the eradication of measles virus, and for the detection and response to drug resistant human immunodeficiency virus. Work to enhance global surveillance of measles virus and antibiotic resistant *Gonorrhoea* is also on-going with partners from the World Health Organisation.

APPENDIX A – SUPPLEMENTAL PERFORMANCE DETAILS



Annex 1 – 2016-2017 GRDI Projects and Allocations from GRDI Funds

GRDI FUNDS (\$)	PROJECT TITLE
SHARED PRIORITY PROJECTS	
1,799,316	Antimicrobial resistance (AMR)
1,810,860	Metagenomics Based Environmental Biomonitoring (EcoBiomics)
AGRICULTURE AND AGRI-FOOD CANADA	
1) Biodiversity, gene mining and functional analysis for the identification and extraction of genes for desirable traits, including mechanisms of plant resistance to biotic and abiotic stress and insect and pathogen virulence	
274,578	Accessing adaptive ancestral avena alleles
410,915	Advanced genetic technologies for improvement of camelina and canola
115,207	Cell-type specific chromatin dynamics in soybean hairy roots responding to water stress
245,776	Effectors of Canadian <i>Puccinia striiformis</i> isolates
163,211	Ethylene signalling and Fusarium head blight resistance in wheat
202,573	Exploiting genomics to decipher hybrid vigour in <i>Brassica napus</i>
232,335	Genome-wide mining and mapping of disease resistance genes – novel strategies to enhance wheat disease resistance breeding
195,853	Mining legume genomes for attributes of sustainable nutrient (nitrogen) acquisition through symbiosis
49,214	Molecular tools for identification of stored-product insects and their symbionts for use in pest control
572,199	Using genomics to reduce fusarium diseases and mycotoxin hazards in Canadian grain
138,249	Using CRISPR to elucidate gene associated traits in wheat: Fusarium head blight resistance and yield capacity
100,192	Verification of plant defense genes against <i>Sclerotinia sclerotiorum</i>
2) Delivery of genomics discoveries through bioinformatics and physical tools in order to improve access to both biological materials and data sets, and to assist and accelerate the adoption and commercialization of new technologies	
182,412	Development of genomics and bioinformatics tools enabling epigenetic analyses in oilseed crops
251,537	Development of identification and analysis tools for amplicon-based metagenomics, focussing on high risk and regulated pathogens
233,626	Exploring the applicability of new technologies and processes to the management and analysis of next generation sequencing data
3) Enhanced efficiency of plant breeding	
162,443	Development of genome editing technology in crop somatic cells using cell penetrating peptides

341,783	Effector-based breeding tools and Quantitative Trait Locus discovery for management of root rot in soybean caused by <i>Phytophthora sojae</i>
222,735	Genomics and genetics of Soybean Mosaic Virus - soybean interactions: next generation viral resistance
305,153	Process for making transplastomic cell and plant lines - tool for new trait development
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 <i>Mycobacterium bovis</i> and <i>Brucella abortus</i>
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
50,000	Development of diagnostic sequencing methods to monitor, detect and characterize RNA viruses of food, animals and plants, following viral contamination or infection
70,000	Development of infrastructure and bioinformatics tools to support genomics activities in CFIA's food, plant and animal business lines
ENVIRONMENT AND CLIMATE CHANGE CANADA	
55,000	Analysis of Norovirus in Wastewaters and Environmental Samples
13,000	Application of genomics to assess the impact of harvest and other mortality sources on vulnerable populations of North Atlantic murrelets
52,535	Development and validation of metabolomic techniques to evaluate impacts of large-scale environmental changes on stress responses in wildlife
95,960	Development of next-generation genomic tools to investigate cumulative effects of urban pollution and pathogens in two sentinel fish species
42,985	Environmental DNA - improving inference through validation studies
33,250	Genomics in support of effects based research
80,230	Hybrid data generation from traditional and DNA-based biomonitoring
43,665	Measuring Genome Health in Wildlife Populations
81,185	Metabolomics for predicting the mode of action of chemicals of concern in aquatic organisms
38,210	Metagenomic Profiling of River Water Quality for Watershed Protection
47,258	Rapid assessment of algal community composition and harmful blooms using DNA barcoding and remote sensing
57,310	Toxicogenomic solutions for assessing exposure and effects of environmental contaminants in wildlife
52,535	Transcriptomic analysis of the ecotoxicological effects of nanomaterials on microorganisms
66,860	Viable pathogen identification using DNA sequencing technology in microbial risk assessment
FISHERIES AND OCEANS CANADA	

176,000	A range wide single nucleotide polymorphism (SNP) baseline for improved genetic mixed stock analysis in Atlantic salmon in the northwest Atlantic: application to domestic and international fisheries
98,900	Assessing the spatial scale of dispersal and connectivity in non-indigenous green crab (<i>Carcinus maenas</i>) and commercial sea scallop (<i>Placopecten magellanicus</i>) in Canadian waters using Restriction Site Associated DNA Sequencing and high throughput SNP genotyping
144,200	Bioinformatic support to develop "FIT-CHIP" for industry and salmon management applications
42,500	Development and evaluation of environmental DNA (eDNA) based detection and biosurveillance tools for aquatic invasive species to inform management and policy decision making associated with shellfish
10,615	eDNA analysis of aquatic invasive species and species-at-risk field programs
70,000	Integrating neutral and adaptive genetic information for addressing knowledge gap in redfish (<i>Sebastes</i> spp) population structure and its underlying mechanisms in Atlantic Canada: a genomic genotyping-by-sequencing approach of SNPs polymorphism
145,450	Rapid genomic screening for Atlantic salmon aquaculture escapees and hybrids using Restriction Site Associated DNA Sequencing and a high throughput nanofluidic dynamic array
32,250	Stock delineation of narwhals (<i>Monodon monceros</i>) from Baffin Bay and adjacent areas using novel genetic markers developed from genomic techniques

HEALTH CANADA

185,000	An integrated systems biology approach to investigate immunopotentiality 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
240,000	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
134,000	Safety of prebiotics in infants
206,000	Systems biology informed structure-activity-relationships to predict pulmonary pathology induced by nanomaterials
360,000	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

56,870	Accelerating the discovery of insect volatile attractant molecules with genomics
77,284	An early detection tool for emerald ash borer and ash resource protection
181,173	Applied genomics for tree breeding
64,647	Development of metagenomic and bioinformatics tools to facilitate processing of trap captures
95,269	Developing molecular and environmental genomic approaches for microbial and invertebrate communities to assess ecosystem integrity in forest management
154,569	Developing the next generation biosurveillance tools for tracking and preventing forest pest invasions
53,467	Development of molecular tools to detect living fungi and fungus-like organisms of phytosanitary concern in wood
66,105	Genomics-assisted tree breeding for improving remediation of disturbed forest ecosystems
123,946	Innovative land reclamation approaches following oil sand mining: Improving phytoremediation tree-soil microbes interactions
69,507	Spruce budworm eco-genomics: from population dynamics to population suppression
79,000	Tools for enhanced molecular detection of Asian gypsy moth and identification of their geographic origins
PUBLIC HEALTH AGENCY OF CANADA	
137,255	BioTools for the predictive genomics of priority foodborne pathogens
140,000	Closing the gaps in national surveillance of <i>Clostridium difficile</i> : epidemiologic and genomic characterisation of community-onset and recurrent <i>C. difficile</i> infections
27,377	Field trials of Oxford Nanopore minion sequencing technology
70,000	Implementation of a next generation sequencing testing platform to support Pan American Health Organization drug resistance surveillance
50,000	Implementation of genome-based analyses to “One Health” surveillance of enteric disease
90,000	MALDI mass spectrometry identification of bacteria: the establishment of a national MALDI database to support diagnostic laboratories across Canada
50,000	<i>Neisseria gonorrhoeae</i> sequence typing for antimicrobial resistance: a novel sequence-based antimicrobial resistance typing scheme for tracking the global dissemination of <i>N. gonorrhoeae</i>
70,000	Proposal for a whole genome sequence-based genotyping approach for tuberculosis in northern Canadian communities
60,000	PulseNet Canada: Model framework development for genomic technology delivery in a laboratory network
146,322	Single nucleotide variant subtyping of <i>Salmonella</i> Enteritidis and <i>Salmonella</i> Heidelberg
190,000	The use of whole genome sequence analysis to support healthcare-associated outbreaks of carbapenem-resistant <i>Enterobacteriaceae</i>
124,652	Transfer of the validated <i>Salmonella</i> genosertotyping array into a PHAC reference laboratory and piloting the technology into the National Microbiology Reference Laboratory and targeted provincial health laboratories
70,000	Translational analytic infrastructure for emerging pathogen discovery
65,000	Validation of metagenomics as a <i>bona fide</i> laboratory approach for cost-effective enteric pathogen identification and subtyping
50,000	Whole genome sequencing of measles virus of an effective molecular surveillance during measles elimination
100,000	Whole genome sequencing of <i>Neisseria meningitidis</i> and its application to surveillance and understanding invasive meningococcal disease molecular epidemiology dynamics

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 2016-2017. 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 2016-2017. They do not include submitted papers or publications in draft form, nor contributions that were reported in previous years.

NUMBER OF KEY SCIENTIFIC CONTRIBUTIONS											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	Total
Publications in refereed journals	4	22	10	20	24	33	21	32	18	9	193
Publications in refereed conference proceedings	35	10	0	0	0	0	0	18	2	1	66
Books (edited, written) and book chapters	12	2	0	0	2	0	1	1		1	19
Invited presentations	18	21	18	23	10	25	19	18	4	8	164
International conference presentations	26	5	6	14	11	14	12	21	0	11	120
Editorial posts for national/international journals (excludes peer reviewers)	24	13	3	2	2	0	4	4	0	3	55
New genomics related databases or libraries	2	1	0	4	2	0	0	6	0	0	15
Awards, prizes	6	4	1	1	5	1	0	1	2	1	22
Total	127	78	38	64	56	73	57	101	26	34	654

NUMBER OF OTHER SCIENTIFIC CONTRIBUTIONS

	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	Total
Technical reports		7	5	0	3	0	113	1	4	2	0
Other publications (ex. abstracts, notes, industry magazines, etc.)	22	2	0	1	2	3	1	3	0	2	36
Poster presentations at conferences		16	2	2	7	23	43	3	21	10	4
National conference presentations	31	8	3	3	3	11	4	3	1	1	68
Deposits in genomics related databases or libraries	165	0	0	1	2	0	20	44	3	0	235
Total	241	17	5	15	30	170	29	75	16	7	605

Research tools and processes

Research tools and processes include those produced in 2016-2017, deriving from previous phases of the GRDI

if produced in 2016-2017, 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	8	9	8	11	13	13	23	21	6	4	116
Research processes	1	2	11	5	6	5	8	12	2	0	52
Total	9	11	19	16	19	18	31	33	8	4	168

Knowledge Translation and Mobilisation

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.

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	15	18	9	13	20	4	2	21	0	0	102
Participations in national or international genomics-related committees	4	14	2	10	6	3	4	23	2	2	70
National or international genomics research peer review committees served on	7	3	1	2	2	2	4	0	0	0	21
Participation in national conferences	31	4	2	0	0	5	0	3	0	0	45
Participation in international conferences	32	1	0	3	6	45	1	2	1	0	91
Total	89	40	14	28	34	59	11	49	3	2	329

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	20	7	18	35	10	5	28	14	15	13	165
International universities	31	1	6	10	6	5	16	11	3	1	90
Other international research organizations	13	2	5	6	6	6	21	22	1	0	82
Other Canadian research institutions	6	0	0	0	0	8	1	0	2	0	17
Private sector	7	0	2	3	3	10	5	0	2	2	34
Other government departments	8	22	3	26	8	3	9	5	5	9	98
Other public sector organizations such as provinces, municipalities, and Non-Governmental Organizations	3	4	4	4	0	6	29	23	18	7	98
Total	88	36	38	84	33	43	109	75	46	32	584

NUMBER OF COMMUNICATIONS PRODUCTS											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	AMR	Eco-Biomics	Total
Media interviews	1	0	7	1	0	3	0	0	19	1	32
Press releases	0	0	1	6	0	6	0	4	1	1	19
Newspaper and magazine articles	1	0	18	20	0	4	0	1	0	0	44
Community presentations	3	0	9	13	0	3	0	0	0	0	28
Brochures, fact sheets, web pages	0	0	0	3	0	8	3	10	0	2	26
Total	5	0	35	43	0	24	3	15	20	4	149

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	10	1	6	31	14	12	0	0	0	0	74
Public meetings	0	0	2	1	1	0	0	0	0	0	4
Science advice, including to senior management	7	18	3	15	7	2	4	21	0	0	77
Outward material transfer agreements	19	0	0	0	1	3	2	0	0	0	25
Transfer of standard operating procedures	2	13	0	3	1	22	4	7	0	0	52
Disclosures	0	0	0	0	0	4	0	0	0	0	4
Active patents, patent applications, patents issued	0	0	0	0	0	8	0	0	0	0	8
Licenses issued	0	0	0	0	0	2	1	0	0	0	3
New formal collaborative agreements / standard operating protocols	2	0	0	1	0	6	1	4	0	0	14
Knowledge transfer workshops with stakeholders/end-users	4	4	0	6	15	6	1	7	0	0	43
Requests for research results, papers, collaborations	52	2	0	11	6	3	8	20	0	0	102
Total	96	38	11	68	45	68	21	59	0	0	406

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 2016-2017, 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	29	26	12	20	17	54	24	25	34	33	274
Research professionals	5	16	11	12	13	9	13	43	19	7	148
Research technicians	40	21	18	23	13	131	23	18	16	22	325
Post-doctoral/visiting fellows	15	2	6	7	6	21	5	7	3	4	76
Graduate students	20	3	2	8	3	0	5	7	12	1	61
Undergraduate students	20	7	2	6	8	9	5	5	6	4	72
Administrative officers	0	0	0	4	0	0	0	2	0	0	6
Total	129	75	51	80	60	224	75	105	90	71	962
Total Estimated Full Time Equivalents	61	16	19	31	23	91	38	31	36	24	370

Annex 3 - Highlights of Results Achieved in 2016-2017

Concerted interdepartmental research along shared priorities and common goals on issues that are relevant to the mandates of multiple departments

Metagenomics Based Ecosystem Biomonitoring (EcoBiomics) Project

Participating Departments/Agencies: AAFC, CFIA, ECCC, DFO, NRC, NRCan, PHAC

Scientific Coordination: ECCC, AAFC

Project Management: AAFC

Biodiversity is paramount in water and soil 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 develops 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 soil remediation for the oil and mining sectors. This project will enable a more comprehensive perspective of water and soil as living systems.

A significant milestone was reached with the establishment of the Bioinformatics Platform that enables the coordination of metagenomics analyses across seven federal departments and agencies. The Platform was established through close collaboration with Shared Services Canada (SSC). It includes significant high performance computing and data storage capacity online at the Dorval computing centre, and enhanced bandwidth capacity for participating departments and agencies.

Common methods were selected for collecting soil, water and invertebrate samples, and for nucleic acid extraction. A standardized approach was established for soil, water, and invertebrate metadata. Over 1500 soil, water, and invertebrate samples were collected across Canada for DNA sequencing and candidate genomic observatories were identified in collaboration

with end-user groups such as ECCC's National Water Quality Monitoring Program, and the Canadian Aquatic Biomonitoring Network (CABIN). Optimal PCR primers were selected to amplify DNA from bacteria (16S), fungi (ITS2), algae (18S), and invertebrates (CO1) for metabarcoding studies, and a centralized amplicon library preparation approach was set up for soil, water and invertebrate samples. A centralized approach was also established for DNA sequencing using the NRC Illumina MiSeq (metabarcoding) and HiSeq (metagenomics) platforms. Bioinformatics training was provided to 70 project participants, including for the SeqDB genomic management system and other software tools. A Project workflow was developed to coordinate all research and data management. Collaborations were initiated with a similar new initiative in the European Union (DNAqua-Net) and with the new Genome Canada ATRAPP Project (Algal Blooms, Treatment, Risk Assessment, Prediction and Prevention through Genomics).

Antimicrobial Resistance (AMR) Project

Participating Departments/Agencies: AAFC, CFIA, HC, PHAC and NRC

Scientific Coordination: AAFC

Project Management: AAFC

The development of resistance to antimicrobials by bacteria that were formerly sensitive is one of the most serious global health threats facing the world today. With no action, annual worldwide human deaths attributable to antimicrobial resistance could reach 10 million by 2050. The Antimicrobial Resistance project uses a genomics-based approach to understand how food production contributes to the development of antimicrobial resistance of human health concern, and explore strategies for reducing antimicrobial resistance in food production systems. It is a component of the Federal Action Plan for Antimicrobial Resistance and Use in Canada.

A description of strain collections has been compiled and a detailed plan for Whole Genome Sequencing (WGS) of bacterial isolates and metagenomes of targeted food and animal samples to understand the sources of clinical resistance. The metadata will initially be collected using available tools in the Canadian Network for Public Health Intelligence (CNPHI) while the sequence data is supplied directly to the Integrated Rapid Infectious Disease Analysis (IRIDA). Once a controlled vocabulary has been implemented for this metadata, it will be sanitized, transformed, and entered into the IRIDA system. Additional prospective sequence metadata will be entered directly into the IRIDA system. Training was provided to project participants for WGS data analysis. Over 1,500 human and non-human isolates have been sequenced to date.

For poultry, DNA from enterococci isolates was prepared and sent for sequencing, including from multi-antibiotic resistant *Escherichia coli* isolates and *Salmonella enterica* serovars (Enteritidis, Heidelberg, Kentucky, Typhimurium and Hadar). A formycin resistance gene (*fosA7*) was detected for the first time in Heidelberg. Feeding trials were conducted using feed supplemented with specific antibiotics, encapsulated essential oils (cinnamon and citral), pomaces from organic cranberry and wild blueberry and their ethanolic extracts to test their effectiveness against necrotic enteritis and coccidiosis in broiler chicken. A field experiment evaluating the persistence and transfer to crops of antibiotic resistance genes following application of poultry litter was undertaken on the AAFC London Research and Development Centre research farm.

For swine, an experimental study was conducted to compare the abundance of enteric bacteria showing resistance to antibiotics in feces from gilts and sows raised with or without antibiotics. From this study, 1910 bacterial isolates resistant to antibiotics were cultivated. The percentage of resistant Enterobacteriaceae was higher in gilts, but the abundance was similar among the groups. A total of 158 isolates were multi-resistant.

A total of 900 multi-drug resistant isolates of *Enterococcus faecalis* and *E. faecium* were isolated from beef cattle and their associated environment as well as from wastewater treatment plants and humans as part of

a “One Health” approach. Preliminary data suggests that there are distinct differences between isolates that are associated with cattle and their environment and those associated with humans.

The conceptual model for the AMR Integrated assessment model initially developed under a previous grant from the Ontario Ministry of Agriculture Food and Rural Affairs has been expanded to include data relevant to all of Canada. The model is being iteratively updated with new data and relationships as they are recognised or prioritised, and as additional pathways are populated.

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

Over several phases of GRDI support, the NRC has built an impressive target discovery and antibody development pipeline, primarily for oncology indications. Promising targets are identified based on their cancer-associated profiles. Hundreds of antibodies are then made against these targets and screened for specificity and function. NRC scientists are now adapting this pipeline to the latest immunotherapy modality: antibody-drug conjugates. The antibody components of these ADCs are being manufactured using the NRC Chinese Hamster Ovary cell production platform, creating a full development pipeline for therapeutic candidates. Combinations of genomic, proteomic, metabolomic and bioinformatic approaches are used for the following:

1. Target identification: To improve clinical efficacy and to overcome some limitations of first generation antibody-based therapeutics, the industry is currently shifting towards innovative and more powerful modalities such as antibody-drug conjugates, which offer the ability to deliver potent cytotoxic drugs specifically to tumor cells. The choice of therapeutic target is a critical success factor in this endeavor. The NRC continues to improve its target selection and prioritization approach, incorporating subtype classification, differential gene expression and subcellular localization data to the analysis of multiple types of cancer. Two rounds of antibody generation were carried out against over 40 new targets, yielding over 1000

clones, which are being functionally characterized. The NRC is partnering these assets with Canadian SMEs once they have completed *in vivo* validation.

2. Production platform: While improvements in Chinese Hamster Ovary-based recombinant protein titer and quality have been achieved by random cell-line mutagenesis and media optimization, efforts to engineer these cells greatly benefit from the application of a systems biology approach with an emphasis on genomics and metabolomics. This approach is accelerating our efforts in process intensification and is also providing a detailed molecular portrait of our proprietary cell line. This molecular characterization is being used in combination with metabolomic analysis to yield significant improvements in yield through optimization of media, especially in fed-batch mode. The composition of the media affects all aspects of metabolism, including key factors such as antibody production, cell density and cell viability that are critical for efficient production of high-quality biologics. Metabolomic analysis allows for the analysis of media composition during the different growth and production phases to understand nutrient utilization and inherent variations in metabolism. The NRC cell production platform is widely used for work with NRC clients and collaborators as well as for internal R&D.

Genomic knowledge for the Canadian health regulatory system

Safety of prebiotics in 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. It is important to assess the short-term and long-term effects of fermentable carbohydrates on the developing gut bacteria of young infants, given the large body of scientific literature linking these carbohydrates to gut bacteria composition, immunological function, and gastrointestinal disease.

In this project, HC researchers are studying the impact of dietary fermentable carbohydrates on the gut bacterial community of weaning rats, as well as the long term effects. 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 the weaning rats are reversed after two months of feeding them regular food. Further analysis will be required to determine how these changes may impact later intestinal function.

This project is already increasing awareness among HC regulators of the physiological outcomes that are potentially associated with consuming fermentable materials, especially as they apply to infant formula.

Identification and characterization of microRNA in serum and milk to measure the health effects of fungal toxins and chemical contaminants in food

MicroRNA (small, non-coding RNA) is important in the regulation of gene expression and their translation into protein products. In this project, 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 currently detected in foods. So far, they have 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 fungal toxin studies to determine the potential biomarkers of liver damage. The team has also completed benchmark dose-modeling of apical endpoints (e.g. toxicological effects involving body weight, liver lesions, organ weights, hematology endpoints, biochemistry endpoints) for specific types of flame retardant chemicals and fungal toxins.

This work will ultimately generate important regulatory toxicology data, thereby enhancing HC's ability to detect and respond to the presence of fungal toxins and chemical contaminants in food consumed by Canadians.

Genomics approach to predict pulmonary pathology induced by nanomaterials

Nanomaterials (tiny materials measuring less than 100 nanometres) can induce harmful effects in experimental animals. In a first study of its kind, HC researchers are combining toxicogenomics (the study of how genomes respond to toxic substances) and computational tools to identify and analyse the potential toxic effects of different classes of nanomaterials on lung cells and tissues. They conducted a comprehensive toxicogenomics analysis and compared the gene expression patterns in the lungs of mice exposed to different classes of nanomaterials, with the gene expression patterns from lungs showing respiratory diseases following exposures to infectious agents or chemicals. The researchers identified critical gene molecules responsible for lung pathology induced by nanomaterials. More recently, in a follow up study, they further demonstrated that carbon nanotubes-induced lung fibrosis involves a transcription factor that is also relevant for lung fibrosis in humans.

The results have been shared with HC's regulators and presented at international meetings and conferences involving the international regulatory community. The methods developed in the study can be used by HC to prioritize nanomaterials for further toxicological investigation and help in the rapid screening of nanomaterials that are potentially harmful. Future studies will test these methods on novel nanomaterials for which the toxicological data are scarce.

Genomics approach to understand the respiratory syncytial virus vaccine

A highly contagious virus that infects the respiratory tract of infants and young children, respiratory syncytial virus is the most common cause of bronchitis. To date, no vaccine has been approved for the prevention of infection although dozens of prototype vaccines have been under development for the last 50 years. The slow pace of respiratory syncytial virus vaccine development is largely due to a lack of both understanding of the disease and critical elements for evaluating the efficacy and safety of the vaccine.

This project aims to better understand candidate vaccines in relation to their safety and efficacy. Scientists are continuing Phase 1 animal studies on prototype vaccines; they have identified toxicity associated with certain forms of candidate vaccines and shed light on some of the underlying mechanisms. In addition, the researchers have developed methods to determine biomarkers pertinent to the safety and efficacy of candidate vaccines. The team has communicated its data to other government researchers and academics.

Next generation sequencing detection of 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.

Scientists from HC are using genomics technologies to analyse 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, a common environmental pollutant. The analysis of 300 samples has shown the presence of large scale duplications of DNA sequences in the offspring of exposed mice. Whole genome sequencing of six mouse families has shown a doubling of mutations in the offspring of exposed mice. 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. This spectrum will be used for sperm-offspring comparisons and heritability assessments.

Genomics approach for the standardization and risk assessment analysis of stem cell based health products

Stem cells have tremendous potential to treat diseases for which there are currently no cures – however, their use can be risky. In this project, HC researchers are developing diagnostic tools to enable a thorough evaluation of the risks and benefits associated with the therapeutic use of human mesenchymal stem cells, a type of adult stem cell. In 2016-2017, the research team collaborated with three world-renowned scientists in the field of cancer stem cells and hematology. The team also searched for potential protein biomarkers with the Thermo Fisher Scientific Group.

These collaborative efforts have led to numerous presentations at national and international conferences as well as various publications – including one study providing the first evidence that human mesenchymal stem cells have a direct effect on the outcomes of leukemia patients following treatment, which could lead to improved treatments for aggressive forms of leukemia. In addition, the team has generated a list of potential biomarkers to identify mesenchymal stem cells that are both safe and effective for treating immune disorders. These biomarkers are currently being tested to determine their capacity to discriminate human adult stem cells that can suppress an over-active immune response. These successfully validated biomarkers will be used to develop diagnostic tests for evaluating stem cell-based health products.

Development of practical toxicogenomics methods for hazard identification and risk assessment of environmental chemicals

The traditional toxicology tests used to evaluate the health effects of chemicals are both time consuming and expensive. In this project, 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 causes DNA damage or other adverse genetic effects.

In 2016-2017, the researchers advanced the application of genomics signatures (patterns of gene expression changes) to identify agents that cause various toxic effects. The team's major accomplishment was to complete the validation of a signature that predicts the ability of chemicals to cause DNA damage in cultured cells of relevance to humans. This work was submitted to the US Food and Drug Administration's Biomarker Qualification Program. The team also completed the development of a software tool that enables any laboratory in the world to apply the signature. Through several case studies, the team demonstrated how the signature can be integrated with both computational analysis of a chemical's structure and chromosome damage tests to predict the relevance of the chemical's responses to human health.

Genomics knowledge to strengthen public health programs

New methods to control and prevent food-borne illness

As food safety is a national priority, PHAC research addresses the critical need for scientific and technical innovation in pathogen detection and characterisation to improve the identification of outbreaks, and accurate and timely source attribution. The international validation of Standard Operating Procedures and an open analytic infrastructure support cross border surveillance and response. The *Salmonella* Genoserotyping Array (SGSA) is being validated and integrated into the PHAC *Salmonella* reference laboratory for the World Organisation for Animal Health, located in Guelph, Ontario. A rapid molecular subtyping method is under development for *Salmonella* Enteritidis and *Salmonella* Heidelberg, types of *Salmonella* that cannot easily be resolved into outbreak clusters using current methods. The validation and certification of these innovative methods will enable their use by provincial and national reference laboratories.

The surveillance programs run by FoodNet Canada and the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) monitor foodborne pathogens and the use and resistance to antibiotics

in the food chain. These programs monitor different points along the 'farm-to-fork' continuum: farms, surface waters, food production, and public health laboratories. Genomic epidemiology approaches applied to food safety are in development to support these programs in the identification of risk factors, sources of exposure, virulence factors, determinants of antimicrobial resistance, and transmission dynamics along the food chain of *Escherichia coli*, *Salmonella*, and *Campylobacter*.

GRDI researchers are working on the successful transition of enteric disease surveillance by the PulseNet Canada network from traditional molecular methods to whole genome sequencing. This will enable all network members to apply whole genome sequencing to foodborne disease surveillance and food safety. A translation framework to encompass all aspects of genomics in the context of PulseNet Canada has been designed, and implementation across Canada is proceeding on schedule.

New metagenomics sequencing approaches are being developed to characterize multiple pathogens in a single isolate without costly and labour intensive culturing conditions. They allow the rapid identification and subtyping of bacterial pathogens directly from complex clinical samples, such as stool, to ultimately improve the speed and accuracy of public health response to infectious disease outbreaks.

Detection and genomic epidemiology of priority pathogens

Researchers at PHAC continue to develop and apply modern technologies (e.g., genomics and mass spectroscopy) alongside advanced scientific computing to address the strategic need to advance the modernization and innovation of Canada's public health capacity for rapid identification of infectious pathogens.

Limited endemic outbreaks of measles are still occurring worldwide. The current genotyping marker used to indicate the absence of "Canadian" measles in circulation has become less effective to track increasingly identical isolates. A new method was developed to identify closely related isolates and track their occurrence to

support source attribution of emerging outbreaks. This will prepare Canada and the international community for the challenges of measles surveillance and elimination.

A national mass spectrometry database to support diagnostic laboratories across Canada has been established in collaboration with international colleagues in the United States and Europe. The mass spectroscopy identification of bacteria assists Canadian public health laboratories and hospitals in the identification of uncommon and rare bacterial pathogens and supports the implementation of new technology that is rapid, inexpensive and accurate for the identification of infectious disease pathogens.

Invasive meningococcal disease, caused by *Neisseria meningitidis*, has been endemic in Quebec for over 15 years. PHAC researchers have used whole genome sequencing to analyse the genetic epidemiology of 47 historical isolates. Their data demonstrates that a unique clone of this pathogen is circulating endemically within the province of Quebec. Notably, by characterising the presence of vaccine targets in the endemic clone, the data also predicts that an existing vaccine could be used to control the disease.

Antimicrobial resistance: supporting communities, hospitals and international response

Reducing the growing threat posed by AMR is one of PHAC's highest priorities because of the risk of losing our ability to manage infectious diseases in humans and animals. To that end, GRDI supported research is developing genomic-based technologies and methods to promote appropriate antibiotic usage and effective infection control procedures. In addition, new tools and procedures are being developed that will enhance our capacity to detect and track AMR pathogens. Together, these activities are designed to reduce the risk posed by antibiotic-resistant infections while supporting the management and treatment of infectious diseases.

Examples include:

- **Human Immunodeficiency Virus (HIV) Drug Resistance:** PHAC researchers have developed a next generation sequencing-based HIV drug resis-

tance testing technology that offers significantly enhanced detection sensitivity, data throughput and cost reduction in comparison to conventional approaches. Canada's National Microbiology Laboratory is collaborating with eleven national/ regional HIV reference laboratories in eight Latin America and Caribbean countries (Mexico, Brazil, Argentina, Chile, Colombia, Puerto Rico, Peru and Martinique) to transfer this drug resistance testing method activities to those labs. As a result, countries across Latin America will be able to independently and affordably perform enhanced HIV drug resistance surveillance and clinical monitoring. Better clinical management should in turn reduce HIV transmission by maintaining low viral loads in patients, and guiding the clinical response if drug resistant mutations emerge.

- ***Clostridium difficile***: Research is underway to minimize the burden of *C. difficile* in Canadian hospitals through the better understanding of transmission routes and recurrent cases in healthcare settings. Since infection and control prevention guidelines have focused mainly on patients within hospital settings, new information is needed on the emerging problem of community-onset infection and recurrent infections. Studies of risk factors for recurrent infection are directed at providing new clinical prediction tools to identify patients at highest risk of recurrent infection, which would allow for more targeted preventive and therapeutic interventions for patients with *C. difficile* infection.
- **Carbapenem resistance**: Carbapenem resistance has emerged in Enterobacteriaceae (a family of intestinal bacterial species) and is now causing large outbreaks at several Canadian hospitals. In collaboration with the provinces and hospitals, a standardized whole genome sequencing protocol is in development to support the control and prevention of healthcare-associated outbreaks of carbapenem-resistant Enterobacteriaceae. Single Nucleotide Variations between isolates and their relation to patient transmission patterns have been described. The development of this tool will inform strategies to apply a whole genome sequencing approach for

managing outbreak(s) on site; inform the Canadian Nosocomial Infection Surveillance Program (CNISP) and build capacity in provincial public health laboratories to assist in near real-time surveillance and control ongoing outbreaks.

- ***Neisseria gonorrhoeae***: A novel typing scheme has been developed to strengthen global surveillance of antibiotic resistance in *N. gonorrhoeae*. Known genetic mechanisms of resistance are being characterized to provide an internationally standardized nomenclature for *N. gonorrhoeae*. The standardization of molecular typing data associated with antibiotic resistance in *N. gonorrhoeae* allows public health practitioners around the globe to communicate in a common 'molecular language' enabling a more timely response to emerging drug-resistant strains of *N. gonorrhoeae*. Known as the Neisseria gonorrhoeae Sequence Typing for Antimicrobial Resistance (NG-STAR), this curated web-based user-friendly sequence typing tool based on antimicrobial resistance determinants in *Neisseria gonorrhoeae* is publicly accessible and will be available as a free online service for all scientists, enabling tracking and targeted responses.
- ***Mycobacterium tuberculosis***: Whole-genome sequencing of *M. tuberculosis* is being used to investigate highly homologous outbreak isolates found in Northern Manitoba and Nunavut. By developing an infrastructure for routine whole genome sequencing and genotyping, this study investigates the evolution of antibiotic resistance in previously sensitive strain populations and is leading to the identification of novel resistance mutations not detected by conventional methods. By increasing our knowledge of AMR determinants this study will assist public health officials in targeted surveillance, control and prevention.

Using genomics to significantly increase Canada's share of global wheat production

The Canadian Wheat Improvement flagship program, funded in part by the GRDI, is the NRC contribution to a large-scale research alliance established to improve the yield, sustainability, and profitability of Canadian

wheat for the benefits of Canadian farmers and the economy. The Canadian Wheat Alliance 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. Highlights of scientific progress are as follows:

- 1. Genomics assisted breeding:** Work focuses on improving the necessary resources, including genomic sequences and annotation, large collections of genetic markers, high-throughput genotyping and the development of new populations for wheat breeding. A multiple genotyping and bioinformatics platform has been established to support Canadian wheat researchers and breeders for a range of applied genomic techniques including marker-assisted selection, gene pyramiding, association mapping, and the generation of high-density genetic maps. To maximise the utility of genetic diversity in wild relatives, significant progress has been made towards the development of genomic tools for enhancing the frequency of meiotic recombination and CRISPR/Cas9-based gene editing in wheat.
- 2. Enhancing Fusarium and rust resistance:** Fusarium Head Blight and rusts are two major wheat diseases that together account for \$200 million in losses annually in Canada. Marker-assisted selection and rapid introgression methods developed at the NRC are being employed to produce germplasm with increased resistance to these diseases. Scientists at the NRC have identified a number of potential gene targets and markers that impart increased resistance with little yield penalty. To date, 45 genetic markers of resistance and 35 new lines of wheat showing increased resistance have been delivered to wheat breeders. Additionally, hundreds of novel gene and metabolite targets have been identified for future marker development. Several combinations of resistance genes were tested to identify novel combinations with synergistic (“booster”) effects on rust resistance. Following multiple years of testing in disease nurseries, a few major effect quantitative trait

loci were detected on multiple chromosomes for various resistance component traits. Breeder-friendly markers were developed to facilitate the deployment of resistance into new Canadian varieties.

- 3. Improving wheat productivity under conditions of abiotic stress:** Genetic markers and advanced wheat lines were developed for several abiotic stress related genes, including traits for drought, heat, or cold tolerance. A framework map of markers associated with physiological traits impacting drought tolerance, including root traits, photosynthesis and a number of yield-contributing traits was developed. A standardized whole phenology platform was established and used to discern genetic differences between wheat lines and identify superior lines with better root system and greater photosynthetic efficiency. Wax deposition is an important component of the complex mechanism responsible for performance under water deficit. A set of four key genes controlling the deposition of diketone waxes in reproductive-stages of wheat were identified. Promising biomarkers found to have correlation with increased cold hardiness and heat tolerance were implemented to select or develop valuable germplasm lines that offer unique molecular resources for winter hardiness and thermo-tolerance breeding.
- 4. Targeting developmental pathways to improve performance and yield in wheat:** Wheat as a crop is facing several challenges including yield gaps and low economic returns. To address these challenges, scientists at the NRC have significantly advanced the understanding of gene targets and regulatory networks influencing photosynthetic efficiency and grain development in wheat. A comprehensive gene expression atlas for grain development has been established. New wheat lines with more tillers, high vegetative biomass, upright leaf architecture, high photosynthetic efficiency and several desirable spike traits have been developed which provide a unique resource for wheat improvement breeding programs.

Using genomics to improve 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 19 GRDI mandated projects covering three overarching themes: 1) Biodiversity, gene mining and functional analysis for the identification of genes for desirable traits; 2) Delivery of genomics discoveries through bioinformatics and physical tools to improve access to biological materials and datasets, and to assist and accelerate the adoption and commercialization of new technologies; and, 3) Enhanced efficiency of plant breeding. Projects highlights follow.

*Buried Treasure in our Oat Germplasm Collection: Accessing adaptive ancestral *avena* alleles*

Canada is the largest exporter of oats in the world. The oat industry brought \$430 million to the farm gate and exported \$620 million worth of high-quality oats in 2012. Wild oat species hold many secrets buried within their genetic makeup that can help improve cultivated oat. Oat breeders often go back to these ancestors and wild relatives to find useful traits such as disease resistance. Scientists are working on advanced methods to analyze the genetic variability that lies hidden in AAFC's collection of almost 30,000 varieties from 26 oat species. The research team grew, measured, and photographed 300 different seed samples from all available oat species and looked at their genetic information. This work has produced a major breakthrough in our understanding of the oat genome. Using genetic markers from a high-resolution map of oat chromosomes from cultivated oat, the team identified which wild oat species were the closest relatives of cultivated oat, and which specific oat chromosomes matched best with those from each wild species. These results provide important information about the evolution of oat, but they also have practical applications. The research helps to explain difficulties that breeders have experienced in crossing and recombining traits from different oat species. The new, high-resolution mapping results will provide guidance in choosing and selecting traits. The new information about oat's closest ancestors may even allow

us to create a new version of cultivated oat directly from its wild relatives. These results will provide new ways to access treasures that lie buried in our oat germplasm collections.

Next Generation Sequencing to Identify Pathogens: Development of identification and analysis tools for amplicon-based metagenomics, focussing on high risk and regulated pathogens

Scientists at AAFC play a key role to accurately scan, analyze and document pests that have a detrimental impact on import and export commodities. Of particular concern are pathogens that can either cause significant yield loss (e.g. bunts and smuts of cereal crops) or impose health risks to livestock and humans (e.g. mycotoxin producing fungi). Over 1,200 fungal species are currently regulated by 15 countries / regions, and 38 species in Canada and over 50 in the United States are under quarantine surveillance. Next Generation Sequencing (NGS) technologies are used by AAFC scientists to detect regulated pathogens at low levels. However, it takes a trained expert to avoid misinterpretation of NGS data. Most "off the shelf" tools for automated classification and analysis of NGS are based on sequence similarity and are not useful in detecting very closely related species. For many of these species, when only sequencing information of targeted DNA regions are available, the accurate assessment of samples for the presence of a regulated pathogen or its close relative(s) requires additional or customized software and knowledge. As NGS technologies become readily available to many international users who may not have the required scientific expertise, misinterpretation of NGS data may generate "false positive" results and create barriers to trade. To prevent false positives and any potential trade issues, AAFC experts trained in taxonomy and genomics are developing bioinformatics tools to help scientists make the best and most accurate science-based decisions using NGS technologies. For example, tools are being developed to differentiate between pathogenic and non-pathogenic species amongst those that are closely related. Another tool in development profiles the biodiversity of microbes and monitors pathogens present in commodities and dif-

ferent environments of the agri-ecosystem. This work involves close collaboration with the CFIA and the Canadian Grain Commission.

Genomic Tools for Pest Resistant Wheat: Genome-wide mining and mapping of disease-resistance genes - novel strategies to enhance wheat disease-resistance breeding

Wheat midge pests and rust diseases (including Ug99, a highly destructive strain that is not yet in Canada) can cause significant yield losses for wheat producers. By working with DNA markers linked to rust and midge resistance genes, AAFC scientists can detect multiple pest resistance in a wheat line. Without the use of DNA markers, it is difficult or impossible to detect multiple pest resistance. DNA markers for rust resistant genes have already been provided to Canadian wheat breeding programs, the markers for midge resistance will follow shortly. Further improvements in DNA markers will be possible once they are sequenced and will enable the development of new pest resistant, higher quality wheat cultivars for the benefit of Canadian producers.

Genomic knowledge for forest generation and protection

Identification of genes controlling desirable attributes in economically important tree species

The GRDI funded research on genomic selection of trees with desirable traits is complementary to the projects funded by Genome Canada: Fast Tests for Rating and Amelioration of Conifers (FastTRAC), and SMarTForests. Genomics tools are essential to achieve economic benefits earlier than with conventional tree improvement programs. To identify cell lines with favourable breeding values early on and thus maximize economic benefits, scientists at the Canadian Forest Service (CFS) of NRCan are currently analyzing a new protocol of somatic embryogenesis initiation with ten families. They have also provided to end-users genomic selection models for productivity traits in Norway spruce.

Increased knowledge of genomics-based pest diagnostics and mitigation

Global trade and climate change are two factors that increase the risk of introduction and establishment of unwanted insects and pathogens into Canada's forests. Early detection and rapid responses are critical in mitigating this risk. Traps are commonly used to inventory forest insects. These traps are baited with special chemicals, often pheromones, to attract insects. Sorting and identifying insects captured in traps is a time consuming and costly process. Metagenomics and bioinformatics tools are being developed to identify insects caught in traps, both faster and at a lower cost. Pilot studies to demonstrate proof of concept and optimize metagenomics and bioinformatics tools are ongoing and ahead of schedule. To bait the traps for the brown spruce longhorned beetle and the emerald ash borer, two key economically important insect pests, scientists identified candidate 'attractive' proteins and have begun the design and engineering of a cell-based insect odorant volatile screening tool. The project uses functional genomics data for pest insect surveillance, a novel approach within the government of Canada.

The European gypsy moth is found in Canada and is a relative of the Asian gypsy moth, an unwanted insect. The CFIA conducts inspections of marine vessels and their cargo, especially those arriving from the Far East, to ensure that they are free of Asian gypsy moth. Vessels that are found to carry the insect, usually found as eggs, must leave port and remove all evidence of the insect. Scientists analyzed DNA from eight populations of Asian gypsy moth from across its range and developed markers that can identify their geographic origin. The team provided CFIA with fully validated detection tools, along with Standard Operating Protocols for the detection of Asian gypsy moth and closely related species, whose introduction would have important economic impact in Canada. The team has also developed tools for the detection of the pathogens responsible for butternut canker, Annosum root rot, and ash dieback. The work is complementary to the project funded by Genome Canada: BioSurveillance of Alien Forest Enemies

(BioSAFE), and is invaluable for negotiating agreements with Canada's trading partners and to lower the risks of detrimental introductions in North America.

A spruce budworm outbreak is currently affecting large stands of forests in Quebec and is poised to spread into Ontario. Models that forecast outbreak development will provide forest managers, specifically the Ontario Ministry of Natural Resources, with another tool to support management decisions for this pest. GRDI scientists have processed close to 1000 spruce budworm samples from 20 sites to estimate the spruce budworm population at time "0" for forecasting models.

Ash trees are at risk of disappearing from the landscape due to emerald ash borer attacks. Research continued to study the factors influencing Emerald Ash Borer larval performance in various ash species to help identify resistance mechanisms and to support the development of a diagnostic test, in collaboration with the cities of Montreal and Ottawa. The project is an example of citizen science in action: it is integrated with TreeTaggr, a user-friendly Twitter-based tool that allows Canadians to report on pest infestations and help protect urban forests.

Prevention is the best strategy for forest health. Scientists continue to collect genomic information on pathogens and insects that may have deleterious impacts on Canadian forests, developing tools that can be used to 1) certify plant and tree material as free of unwanted pathogens; and 2) monitor potential invasive species in Canada. Current work is focused on poplars and pines, some of the most important tree species in the northern hemisphere. The research is complementary to the project funded by Genome Canada: BioSurveillance of Alien Forest Enemies (BioSAFE).

Trees that are resistant to white pine blister rust are required to restore pines on the North American landscape. Scientists are studying resistance mechanisms in western white pine, limber pine, whitebark pine and eastern white pine. A selection tool based on SNP markers was used for screening of resistance in western white pine breeding programs, and a major gene resistance locus was discovered in Alberta limber pine. Resistant stocks and genomics knowledge are avail-

able to stakeholders to support restoration of white pine in forest ecosystems that are disturbed by blister rust in Canada and across North America.

The fungus-like pathogens known as *Phytophthora* are a *phytosanitary* concern for Canada and its trading partners. Current diagnostic methods that detect *Phytophthora* species cannot differentiate whether a positive result is coming from living or dead organisms. Building on the work started last year, a method was developed to detect living *Phytophthora* in both pure cultures and infected wood. The research team also gained valuable knowledge of the stability of *Phytophthora* mRNA as a tool to test the efficacy of novel wood treatments.

Improving land reclamation following oil sands mining

An industrial-scale pilot project using genomics tools to better understand tree-soil microbiome interactions is ongoing at oil sands reclamation sites in Fort McMurray. The results provide a picture of the above and below-ground genetic diversity observed in sites under reclamation, to understand how different reclamation strategies affect the dynamics of the whole biological system. The project will define how phytoremediation could be used in Alberta to return to an ecosystem similar to natural forests, which would improve the industrial and environmental competitive advantage of the Canadian oil sands operators.

Ecosystem integrity in forest management

A project was initiated in 2015-2016 to develop metagenomics tools that assess ecosystem integrity and the sustainability of forest management practices. In 2016-2017, the team sequenced a gene library of boreal forest soil invertebrates and selected 18 sites along New Brunswick watersheds for collecting aquatic microbial samples. Further analysis is ongoing to identify critical riparian hotspots for sustaining ecosystem integrity and inform forest management guidelines. A meta-barcoding technique was developed to analyze the aquatic microbial community of critical riparian habitats and assess them as indicators of biological responses to water-

borne nutrients. The tool could be used by regulators, certification bodies and forest industry to assess the sustainability of forest management practices.

Genomics knowledge and advice for the management of fisheries and oceans

In 2016-2017, GRDI funded the final phase of six multi-year projects as well as two new research projects to:

- increase capacity for generating genome wide data of commercial sea scallop and invasive green crab populations to directly address management and conservation needs;
 - develop a genomics-based test for stock analysis to inform domestic and international Atlantic salmon fisheries;
 - develop new molecular marking tools for narwhal stock and population assessment for effective national and international allocation of the harvest;
 - identify adaptive mechanisms structuring and maintaining redfish genetic diversity in Atlantic Canada, while addressing knowledge gaps in redfish population structure;
 - quantify the genetic impacts of farmed escaped Atlantic salmon on wild salmon populations and the frequency of interbreeding in the wild;
 - produce a predictive “FIT-CHIP” tool to assess a variety of external stressors, pre-existing conditional states and important physiological impacts on salmon stocks; and
 - develop environmental DNA (eDNA) tools for detecting key aquatic invasive species as well as species at risk as a non-invasive monitoring technique to inform management.
- Examples of results and outcomes from DFO’s GRDI-funded genomics research projects from 2016-2017 include the following:

Impact of escaped farmed fish on wild Atlantic salmon populations

It is estimated that up to two million farmed domesticated Atlantic salmon escape annually on a worldwide basis, often in areas where farmed caged salmon vastly outnumber wild populations. GRDI funding allowed DFO scientists to develop tools to examine the genetic interactions among escaped farmed salmon and wild populations in Newfoundland to better understand the impacts of aquaculture on wild populations. Results from this study directly support decisions related to DFO’s Aquaculture Policy Framework, the implementation of DFO’s Wild Atlantic Salmon Conservation Policy, and is informing decisions on whether to expand aquaculture in key areas, and allow farming of non-native aquaculture strains in Canadian waters. This will improve sustainable and low-impact aquaculture production and wild population conservation in Canada.

Development of salmon “FIT-CHIPS” to rapidly determine health and condition of salmon

Scientists from DFO have developed a series of “salmon FIT-CHIPS,” a novel monitoring tool to predict salmon health. It identifies rapidly and inexpensively the presence of stressors (e.g. temperature, hypoxia), disease (viral, bacteria), and the state of preparedness for salinity shifts associated with migration. The application of these chips will: 1) optimize salmon hatchery culture and release strategies to improve salmon enhancement programs, 2) increase accuracy of marine survival estimates for harvest stock assessment by including information on health and impact of stressors, and 3) increase survival of salmon through the identification and mitigation of stressors. Results provide data to support science advice to managers in fisheries, aquaculture, enhancement, or environmental and university organizations. Outcomes of this research support DFO’s Economically Prosperous Maritime Sector and Fisheries Plans and Priorities, and results are being made available to policy makers in the Aquaculture Management Division.

Stock delineation of narwhals for conservation and traditional fisheries

Narwhal is an Arctic whale considered of Special Concern by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC). It is also an important cultural and subsistence resource harvested by Inuits in Canada, providing needed revenue of \$5M annually for northern communities. Under the Convention on the International Trade of Endangered Species (CITES), scientific evidence to support findings of non-detrimental impacts on the at-risk species is required to obtain permission for international trade. GRDI funding allowed DFO scientists to develop narwhal specific genetic markers and determine the differences among narwhal stocks, survey new and existing (archived) narwhal samples, and integrate this new genetic data with existing data. Results for this research allow managers to assess and update narwhal hunt boundaries and contribute directly to the ongoing development of Integrated Fisheries Management plans. Improved health and sustainable harvest of narwhal populations will directly impact the health and economic prosperity of Nunavut communities that depend on them, in a challenging and changing environment.

Assessing scale of dispersal and connectivity of the invasive green crab

The European green crab is a high impact aquatic invasive species and predator with large commercial and ecosystem consequences. It is inflicting serious damage on both the Atlantic and Pacific coasts. Green crabs compete with native crabs and lobster for food and shelter and can harbour pathogens to native decapods, reduce invertebrate and fish diversity, can destroy shellfish beds (quahog, oyster, clam and scallop), thereby threatening shellfish aquaculture, and damage eelgrass beds, essential habitats for many species. In GRDI funded projects, DFO scientists developed genomic markers and identified two different lineages of green crab, their invasion pathways and lineage-specific environmental tolerances, as well as the role of hybridization in the expansion of invasive populations. This information was used to determine likelihood of range expansion, and update risk assessment for temperate and northern

(Arctic) locations in Canada. The research contributes to understanding climate-associated adaptations, risk management strategies for invasive species, and legislation, regulation and compliance measures to prevent unwanted invasive species introductions and limit impacts post-invasion.

Integrating adaptive and population structure genetic information in redfish fisheries

The term redfish refers to a collective group of different *Sebastes* species that are a major commercial groundfish, with landings worth over \$40 million in 2015. The various redfish species and populations are difficult to distinguish, and those that are listed as threatened or endangered under COSEWIC are threatened by their inclusion in a single non-differentiated fishery. Two GRDI-funded projects at DFO have used current and archived redfish samples to genetically distinguish among different species and populations, examined how the populations have changed over time, identified adaptive mechanisms influencing genetic diversity and local adaptations, and spatially delineated some species and populations. This knowledge has led to the development of separately managed redfish fisheries where not previously possible, including species- and population-specific Total Allowable Catch and allocation rules, as well as the designation of one population as 'threatened' under COSEWIC with separate precautionary-approach conservation management strategies implemented. The research also facilitated a partnership with redfish harvesters, to establish the first industry-led monitoring program for redfish species.

Improved mixed-stock analysis for domestic and international Atlantic salmon fisheries

Regional stock identification for Atlantic salmon includes populations at various stages of risk of extinction, as well as populations originating from domestic and international waters. This project combined existing and new genomics resources to create an informative group of genetic markers to enable rapid and cost-effective genetic analysis. Results have clarified fine-scale and evolutionary population structure as well as individual fish sex and stock identification. This work directly informs Canadian policy regarding domestic (e.g. First

Nations fisheries) and international fisheries agreements (i.e. International Council for the Exploration of the Sea/ North Atlantic Salmon Conservation Organization), decisions related to the implementation of DFO's Wild Atlantic Salmon Conservation Policy, and the protection of genetic and geographic diversity needed for conservation of mixed stock fisheries. The tools developed will also be used for species and stock identification by DFO's Conservation and Protection for making decisions regarding potential violations in salmon subsistence and recreational fisheries.

Genomics-based tools and technologies for responsible environmental decision-making

In 2016-2017, ECCC began a new research cycle (2016-19) in the development of genomics tools and approaches to support pollution prevention, regulatory compliance and enforcement, wildlife management, and risk assessment of potentially toxic substances.

The four priority research areas are described below.

Ecotoxicology

Efforts were undertaken to improve the efficiency and accuracy of models to predict the effects of chemical exposure by building a better understanding of the molecular mechanisms underlying the toxicological effects of chemicals in both wildlife and aquatic life. For instance, genomics tools and approaches are in development to examine the impact of existing and emerging chemicals (i.e., their transport, fate, effects, and associated risks) on the biology and physiology of organisms as well as on biodiversity and ecosystem functions. Research 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 the molecular mode of action of chemicals significantly enhances the accuracy of models that contribute to improved risk assessment.

Environmental monitoring

Activities also focused on understanding and monitoring aquatic and land-based ecosystems. For example, research focused on extending an established method for recovering biodiversity information from bulk envi-

ronmental samples. In the Great Lakes, DNA barcoding is being applied to monitor algal community compositions for harmful blooms, while changes to microbial diversity are being evaluated for their ability to provide early warnings of adverse changes to aquatic ecosystem health. The application of this work will increase our understanding of cumulative environmental impacts and related risks associated with multiple stressors interacting over time.

Wildlife conservation

Genomic techniques were developed to better understand wildlife species and how they are responding 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. Tools are also being developed to delineate the geographical distributions of endangered, elusive, or invasive species using analyses of material found in environmental matrices. These efforts will support the management of wildlife species and increase our understanding of how populations adapt to changes in their environment.

Compliance and enforcement

Scientists are developing various innovative methods and tools to support the enforcement of regulations to protect the environment and wildlife from pollution, wildlife trafficking and other threats, and to support regulatory monitoring programs. For example, genomic markers are under development to inform the harvest management of murre colonies in the North Atlantic.

Using genomics for food safety, animal health and plant protection

Characterizing food-borne pathogens through the creation of genomics databases

Scientists from CFIA have created a database of food-borne pathogens and new tools to enhance the capacity to detect the presence of microbial haz-

ards in food. More than 3000 pathogens that include strains of *Salmonella*, *Listeria*, *Escherichia coli*, *Shigella*, *Staphylococcus* and infectious bacteria related to food-borne illnesses have been fully sequenced and added to the database. Metagenomic sequence data from beef, pork and produce samples have been mined to inform the development of improved methods for pathogen detection. Automated bioinformatic processes for rapid sequence analysis have been developed to ensure data reliability.

Strengthening animal health diagnostic tools

This project aims to enhance the CFIA's capability in the acquisition, management, analysis and utilization of genomic data. New wet bench methodologies and bioinformatics pipelines for the acquisition, assembly and annotation of the genomic sequences of known high priority, unknown or unexpected pathogens and differentiation of disease vectors from closely related species are being established. To date, this project has sequenced approximately 300 isolates of diagnostic, surveillance, archived and research samples representing 12 diverse viral families and 21 viral species. The CFIA created the reference genomic database of *Mycobacterium bovis* strains isolated between 1985 and 2016 from Canadian livestock and wildlife, and harmonised epidemiological investigations of bovine tuberculosis outbreaks with the USDA. Through the development of new, user-friendly methods for rapid detection and typing of high priority pathogens and vectors, this project is working to enhance CFIA's capability to prepare for and respond to high priority, new, emerging, and re-emerging animal health threats.

Detection and identification of invasive plants, plant pests, and plants with novel traits

The CFIA is developing DNA barcoding and next generation sequencing to enhance its plant health regulatory capacity in the areas of detection and identification of invasive plants, regulated plant pests and pathogens, and plants with novel traits. Genomic regions from different organisms were sequenced and assembled for the development of markers to be used for identification and detection. Preliminary analyses of field samples have identified a putative new member of the rare genus

Idaeovirus that may be the causal agent of an uncharacterized disease in *Ribes*. Whole genome analysis of bacteria provided evidence to reclassify *Clavibacter michiganensis* subspecies at the species level.

Comparative genomics analyses led to the identification of pathogenicity islands in soft rot bacterial isolates from potatoes. Genetic markers were selected and validated to sequence a number of nematode genera, including *Pratylenchus*, *Meloidogyne*, *Xiphinema*, and *Ditylenchus*. Plant with Novel Trait (PNT) mapping and junction analyses were conducted for transgenic soybean, potato and corn samples. Asian gypsy moth and Asian long-horned beetle mitochondrial and nuclear regions were sequenced to rapidly and accurately identify species, population origins and genes associated with specific traits.

Development of genomics and bioinformatics tools

The overarching goal of this project is to harmonize genomics activities across CFIA's three business lines, focusing on bacterial genome analysis. A web-based Genomics Portal has been developed to enable access to CFIA's databases of bacterial genomes. This portal includes a bioinformatics pipeline for genome assembly, a marker selection feature, tools for PCR primer verification, and tools for the detection of genes that confer antimicrobial resistance. Methods to analyze Single-Nucleotide Variants (SNVs) have also been incorporated into the portal. Another important activity undertaken by this project was an evaluation of bioinformatics processes and procedures to ensure that activities met quality assurance requirements for the Agency. The use of bioinformatics tools for diagnostic purposes is a new area for the CFIA, and it is important that strategies and procedures for data analysis, data management and data curation meet quality requirements. The CFIA leads an international working group on the development of quality assurance guidelines, which were published in the consensus standards Journal of Association of Official Analytical Chemists (AOAC) International. Documents describing how the CFIA is currently implementing these guidelines are under development.

Annex 4 – Research Tools and Processes Produced by the GRDI

Research tools

- Galaxy cluster in the cloud deployment tool (AAFC);
- Galaxy tools for iRODS data grid integration (AAFC);
- RAM: R for Amplicon-Sequencing-Based Microbial-Ecology, version 1.2.1.7 (AAFC);
- Deposited 454 pyrosequencing demultiplexed data of 97 samples to Sequence Read Archive (AAFC);
- High-density marker profiling for ancestral genomes of *Avena* species and hexaploid oat (AAFC);
- Genes associated with the 2DL QTL locus for *Fusarium* head blight resistance (AAFC);
- Transcriptomic evidence for the control of soybean root isoflavonoid content by regulation of overlapping phenylpropanoid pathways (AAFC);
- Database and bioinformatics pipeline to identify sequences for the detection and identification of unknown plants with novel traits using next generation sequencing technology (CFIA);
- High-throughput method using barcoded adapters for whole genome sequencing of influenza A virus isolates from swab specimens (CFIA);
- Standardized method using next generation sequencing technology to generate barcode libraries of Avian Paramyxovirus-1 from isolates (CFIA);
- Standard procedures for whole genome sequencing of *Mycobacterium bovis* (CFIA);
- Bioinformatics pipeline for the analysis of fungi and oomycete from spore and insect traps (CFIA);
- Bioinformatics pipelines for the analysis of food-borne pathogen isolates (CFIA);
- Bioinformatics pipeline for the analysis of crop seed amplicon for the detection/identification of contaminated seeds (CFIA);
- Next generation sequencing procedure to detect regulated and quarantined pests in the potato post entry quarantine program (CFIA);
- Bioportal that houses a number of tools for processing whole genome sequencing data, including GeneSipp, PCR verifier, AMR detector, and other tools (CFIA);
- R program (genepopedit) published as a simple and flexible tool for manipulating multilocus molecular data in R, broad genetic applications (DFO);
- Parallel_Newhybrids: R package developed and published for efficient parallel identification of Atlantic salmon hybrids and hybrid classes (DFO);
- Validation of Viral Disease Development Biomarker panel for incorporation into salmon FIT-CHIPs to assess health status to inform management of salmon stocks (DFO);
- Smoltification Biomarker panel developed with TaqMan assay efficiencies species amplifications, and preliminary validations completed for incorporation into salmon FIT-CHIPs to assess migration-readiness (DFO);
- Thermal stress Biomarker panel with TaqMan assay efficiencies and species amplifications, and preliminary validations for incorporation into salmon FIT-CHIPs to assess stress history and preparedness (DFO);
- Hypoxia stress Biomarker panel with TaqMan assay efficiencies and species amplifications determined for incorporation into salmon FIT-CHIPs to assess stress history and preparedness (DFO);
- Biomarkers associated with imminent Mortality identified and TaqMan assays developed and efficiency tested and applied across multiple tracking and holding studies to be incorporation into salmon FIT-CHIPs (DFO);
- eDNA sampling protocol developed for aquatic invasive species biosurveillance to be used in shellfish transfers in British Columbia (DFO);

- 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);
- Growth chambers for cyanobacteria and algal cultures (ECCC);
- ToxChip PCR array for a Pacific coastal seabird species (ECCC);
- A novel screening technique, which uses whole liver slice cultures to screen for chemical effects in wild and domestic species (ECCC);
- endpoint PCR and qPCR assays for detecting human, dog, ruminant, cow, and seagull fecal contamination in water (ECCC);
- qPCR array assay based on newly published human gut microbiome information to more comprehensively detect and characterize human fecal contamination in water samples (ECCC);
- eDNA sequencing and data analysis pipeline as an additional tool to get more source tracking information out of water samples (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);
- Glass-Agar Sandwich Reactive Oxygen Species assay (ECCC);
- Complete sequence of common murre genome (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);
- 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);
- Software to analyze genetic material (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);
- BMDEpress 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 expression atlas for wheat seed development (NRC);
- Gene targets for photosynthetic efficiency in wheat (NRC);
- Galaxy Bioinformatics platform for wheat sequence data analysis (NRC);

- A nested-association mapping (NAM) population of 4,700 RILs for dissecting genetic architecture of complex traits (NRC);
- Genomic tools for enhancing the frequency of meiotic recombination and CRISPR/Cas9-based gene editing in wheat (NRC);
- Integrated genomics approach for use in genetic mapping of economic traits in trees with complex genomes (NRCan);
- A novel SNP-based selection tool for use in resistance screening in western white pine breeding programs nationally and internationally (NRCan);
- Novel limber pine germplasm with major gene resistance for use in breeding program nationally and internationally (NRCan);
- Molecular approach to the identification of the geographic origins of gypsy moth samples intercepted at Canadian ports using SNP markers (NRCan);
- 12 validated molecular detection assays (qPCR) for Asian gypsy moth (NRCan);
- Molecular detection assays for the Canadian 50 most unwanted forest pathogens (NRCan);
- Asian gypsy moth and related species collection containing over 800 specimens (NRCan);
- Increased adoption of TreeTaggr, Twitter based application to report the presence of tree pests such as emerald ash borer (NRCan);
- Protocols for the extraction of nucleic acids from field and bulk samples (NRCan);
- New sets of primers for barcodes for forest Coleoptera (NRCan);
- Meta-barcoding tool to assess the terrestrial soil faunal community component of ecological integrity (NRCan);
- Meta-barcoding technique to assess aquatic microbial communities as indicators of biological response to water-borne nutrients from critical riparian habitats in an effective and cost-effective way (NRCan);
- SISTR: (<http://lfz.corefacility.ca/sistr-app>) a bioinformatics resource for multiple rapid *Salmonella* subtyping (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 provides near real-time analyses of thousands of genome sequences (PHAC);
- Phylotyper: <https://github.com/superphy/insilico>-subtyping; predicts biological subtypes from gene sequence data (PHAC);
- Ectyper: https://github.com/phac-nml/ecoli_serotyping: predicts serotype from genomic sequence, and identifies 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);
- Development of protocols for the extraction of nucleic acids from *C. difficile* in 96 well format (PHAC);
- Application of targeted PCR and amplicon sequencing of SNVs of SE for identification of serotypes of *S. enterica* (PHAC);
- Application of the RNase-H dependent PCR (IDT Inc.) for detection of SNVs of *S. Heidelberg* strains using raw Illumina sequencing data or using unfinished genomes (PHAC);
- An online sequenced-based molecular antimicrobial resistance typing tool for tracking the global dissemination of *N. gonorrhoeae* strains (PHAC);
- A curated database of antimicrobial resistant gene sequences from Canada combined with publicly available alleles from around the globe (PHAC);
- A SNP-based pipeline for WGS analysis in the context of a hospital outbreak and antimicrobial resistance (PHAC);
- Illumina MiSeq next generation sequencing and the analysis of results using National Microbiology Laboratory IRIDA platform and BioNumerics software (PHAC);

- Salmonella Genoserotyping Array (SGSA) for high throughput Salmonella typing (PHAC);
- HIV DR analysis (HyDRA) pipeline and web server (PHAC);
- Illumina MiSeq-based HIV DR typing protocol (PHAC);
- High resolution measles genotyping method for outbreak investigation (PHAC);
- The Salmonella In Silico Typing Server (SISTR): allows users to upload draft WGS assemblies and performs serovar prediction, cgMLST analysis, with meta-data driven interactive visualizations for phylogenetic and epidemiological analysis that allow the user to examine the phylogenetic, spatial, and temporal distribution of strains (PHAC);
- Methods for extraction of nucleic acids of priority pathogens from common clinical samples (PHAC); and
- Web application for rapid analysis of metagenomics sequence data for the identification of novel pathogens (PHAC).

Research processes

- High resolution mapping of the stem rust resistance gene SrCad (AAFC);
- Evaluation of RGAugury as an integrative bioinformatics tool for large scale genome-wide identification of resistance gene analogs (AAFC);
- Using Haplotag software for haplotype-based genotyping-by-sequencing analysis (AAFC);
- Protocols for generating WGS for Seneca Valley Virus from swabs (CFIA);
- Field 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 SNPtype 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);
- Metabarcoding protocols developed for aquatic invasive species biosurveillance to be used in shellfish transfers in BC (DFO);
- RT-qPCR method for detecting norovirus GI and GII in waste water treatment plant samples (ECCC);
- NGS applications in microbial ecology studies applying microbial community end points, isolation of DNA from complex environmental samples, amplification of 16S cyanobacterial and 16S chloroplast (eukaryotic algae) RNA using specific designed primers and sequencing (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);

- Protocol to multiplex more genetic samples in one single sequencing lane (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);
- Mitochondrial DNA to identify novel gypsy moth ecotypes (NRCan);
- Updated Standard Operating Procedures (SOPs) for the maintenance of insect cell lines (NRCan);
- SOPs for the use of the Asian gypsy moth assays by end-users (NRCan);
- User Guide for the development and validation of real-time PCR assays (French and English versions) (NRCan);
- A new DNA extraction protocol for spore on silicone-coated rods (NRCan);
- Standard operating procedures (SOPs) for the collection of field insect samples (NRCan);
- SOP for curating and identifying insect samples (NRCan);
- SOP for processing and identifying insect samples with metagenomics and bioinformatic tools (NRCan);
- Optimized protocols for the extraction of nucleic acids from *C. difficile* in 96 well format suitable for WGS (PHAC);
- Improved analysis of whole genome sequencing data from *S. Heidelberg* (PHAC);
- Typing and tracking of *N. gonorrhoeae* via in silico antibiogram (PHAC);
- A knowledge translation pathway of synthesis, iterative tailoring, and application to provide comprehensive education, training and ongoing support for genomics to provincial public health labs and federal food safety partners that will introduce WGS into routine surveillance and outbreak response by the PulseNet Canada network (PHAC);
- Standard Operating Procedures for SGSA testing of Salmonella isolates (PHAC);
- The MiSeq-based HIV drug resistance testing platform (PHAC);
- A pipeline for the isolation, library construction, WGS generation, and SNP analysis for use during a hospital outbreak situation. The analysis pipeline includes specific analysis for SNPs within Tn4401, a transposon that carries the *Klebsiella pneumoniae* carbapenemase to track its movement between plasmids (PHAC);
- A novel pipeline for the rapid identification of plasmids from WGS data to rapidly identify the types of plasmids found in clinical isolates including those that harbour the KPC gene (PHAC);
- Protocol for generation of sequencing libraries for use in next generation sequencing of *Mycobacterium tuberculosis* (PHAC);
- A process for quantifying the strength of epidemiological relationships between bacterial isolates (PHAC);
- A set of methods (and method guidance) to optimize the extraction, preparation, and analysis of DNA from a newly emerged pathogen (PHAC); and
- A validated pipeline for pre-processing of WGS data, a process that allows users to take raw sequencing reads and perform assembly, gene prediction and annotation of WGS data in order to prepare it for downstream analyses (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.

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.

Knowledge and Networks: To maximize the value of the GRDI and move that value to users for commercial and public good applications as the initiative matures, knowledge translation and mobilization activities are required. These 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.

Table 1 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 R&D 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.

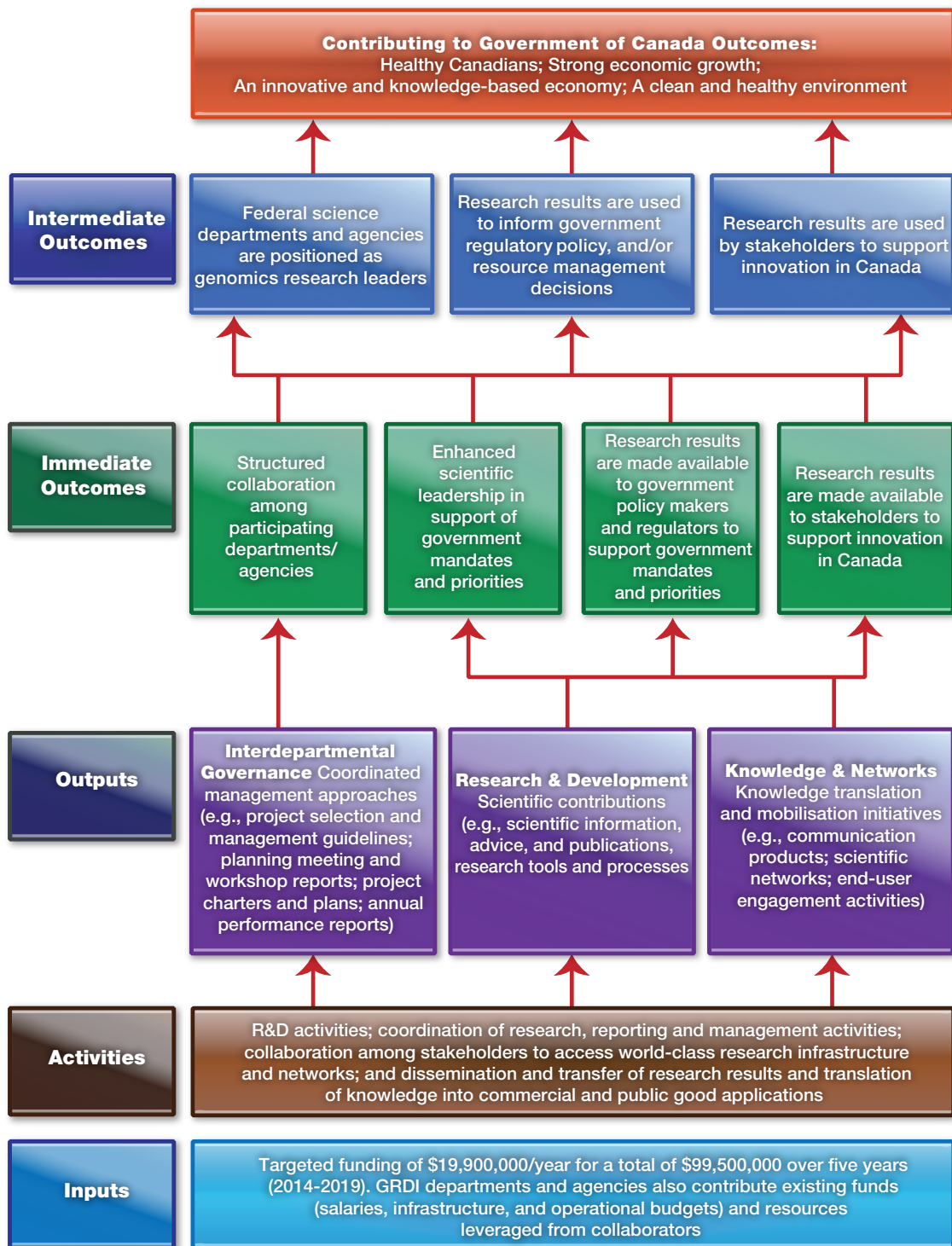


Table 1: Program Performance Measurement Strategy Framework

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 management 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.