Government of Canada | Gouvernement du Canada

Canada

GENOMICS R&D INITIATIVE

ANNUAL PERFORMANCE REPORT

2015-2016




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

TABLE OF CONTENTS

Appendices

Prepared by: Working Group for the Genomics R&D Initiative

For additional information: Dr. Anne-Christine Bonfils
Anne-Christine.Bonfils@nrc-cnrc.gc.ca




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.

Fiscal year 2015-2016 was the second 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 the last year of two highly coordinated interdepartmental projects along shared priorities and common goals that were initiated under Phase V: 1) Strengthening Food and Water Safety in Canada through an Integrated Federal Genomics Initiative (the FWS project); and 2) Protection of Canadian Biodiversity and Trade from the Impacts of Global Change through Improved Ability to Monitor Invasive Alien and Quarantine Species (the QIS project).

Considerable progress was achieved in 2015-2016, exemplified by the following highlights:

- The FWS project successfully generated promising phenotypic intelligence as well as analysis tools and functions that will be useful for enhanced source attribution and risk assessment (e.g., comparative genomic feature interpretation from divergent groups, molecular characterizations and protein expression analyses);
- The FWS project has developed the Integrated Rapid Infectious Disease Analysis (IRIDA) platform – an end-to-end system for the storage, management, analysis, sharing, and reporting of whole genome sequence data for genomic epidemiology;
- Molecular virulence in fusarium and unique resistance mechanisms in wheat and maize were defined to reduce fusarium mycotoxins in Canadian cereals;
- A guidance document was developed for prospective cell therapy product clinical trial sponsors, entitled 'Preparation of Clinical Trial Applications for use of Cell Therapy Products in Humans';
- The first Fit Chip was developed for multiple salmon species to assess salmon pathogens and their association with gene activation and disease development; and
- A simplified guidance document for regulators on the use of toxicogenomics in human health risk assessment was published (http://www.ncbi.nlm.nih.gov/pubmed/25944780).

This Annual Performance Report for 2015-2016 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 2015-2016 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 2015-2016.

ACRONYMS

AAFC	Agriculture and Agri-Food Canada
ADM	Assistant Deputy Minister
ADM CC	ADM Coordinating Committee
AMR	Antimicrobial resistance
CFIA	Canadian Food Inspection Agency
CFS	Canadian Forest Service
CNISP	Canadian Nosocomial Infection Surveillance Program
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
DFO	Fisheries and Oceans Canada
DNA	Deoxyribonucleic Acid
ECCC	Environment and Climate Change Canada
eDNA	environmental DNA
FTE	Full Time Equivalent
FWS	Food and Water Safety
GRDI	Genomics Research and Development Initiative
HC	Health Canada
HIV	Human Immunodeficiency Virus
IHNV	Infectious Hematopoietic Necrosis Virus
IRIDA	Integrated Rapid Infectious Disease Analysis
MALDI-TOF	Matrix-Assisted Laser Desorption/ Ionization Time-of-Flight
NCBI	National Center for Biotechnology Information
NGS	Next Generation Sequencing
NRC	National Research Council Canada
NRCan	Natural Resources Canada
PCR	Polymerase Chain Reaction
PHAC	Public Health Agency of Canada
QIS	Quarantine and Invasive Species
qPCR	Quantitative PCR
R&D	Research and development
RAD-seq	Restriction Site Associated DNA Sequencing
RNA	Ribonucleic Acid
S&T	Science and Technology
SE	*Salmonella* Enteritidis
SNP	Single Nucleotide Polymorphism
SOPs	Standard Operating Procedures
STAGE	Strategic Technology Applications of Genomics in the Environment
USDA	United States Department of Agriculture
VTEC	Verotoxigenic *Escherichia coli*
WG	Working Group

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 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 departments. 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 (2008-20011) 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 projects were developed: 1) Strengthening Food and Water Safety in Canada through an Integrated Federal Genomics Initiative; and 2) Protection of Canadian Biodiversity and Trade from the Impacts of Global Change through Improved Ability to Monitor Invasive Alien and Quarantine Species. Both projects continued to be supported in the first two years of Phase VI of the GRDI (2014-2016).

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 2015-2016 in support of GRDI projects, and demonstrates that non-GRDI funds represented more than 1.5 times the GRDI investments. Additional in kind investments included the sharing of technology platforms, materials, and expertise with a variety of collaborators in research areas that cut across traditional departmental sectors.

Table 2: Overall Investment in support of GRDI projects in 2015-2016 ($000)

DEPARTMENT/AGENCY	GRDI	NON-GRDI*	TOTAL
National Research Council Canada	4,440	10,991	15,431
Agriculture and Agri-Food Canada	4,440	9,249	13,689
Health Canada	1,600	2,918	4,518
Public Health Agency of Canada	1,600	1,252	2,852
Natural Resources Canada	1,600	3,355	4,955
Environment and Climate Change Canada	800	1,393	2,193
Fisheries and Oceans Canada	720	765	1,485
Canadian Food Inspection Agency	720	1,550	2,270
SHARED PRIORITY PROJECT	**GRDI**	**NON-GRDI**	**TOTAL**
Quarantine and Invasive Species	1,892	1,146	3,038
Food and Water Safety	1,784	3,413	5,197
Coordination and Common Functions	304	56	360
Total	**19,900**	**36,088**	**55,988**

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

Planned Results

As reported in NRC's Departmental Performance Report Supplementary Tables for the GRDI, the participating departments established a collective set of planned results for 2015-2016:

- 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;
- Genomic knowledge for the Canadian health regulatory system;
- Commercially-relevant advances in genomics R&D related to human health;
- Genomics knowledge to strengthen public health programs and activities related to the prevention and control of infectious disease;
- Genomics knowledge and advice for the sustainable management of fisheries and oceans;
- Genomic knowledge for forest generation and protection;
- Genomics-based tools and technologies for responsible environmental decision-making; and
- Concerted interdepartmental research along shared priorities and common goals on issues that are beyond the mandates of single departments.

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 Health Canada 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

Environment and Climate Change Canada 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 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 2015-2016, these will be:

1) NRC's 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 Subsequent Entry Biologics 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 NRC's 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 project Protection of Canadian Biodiversity and Trade from the Impacts of Global Change through Improved Ability to Monitor Invasive Alien and Quarantine Species (the QIS project) will design innovative protocols and build a comprehensive DNA barcode reference database that will inform federal regulatory and policy decisions to prevent and mitigate the impact of quarantine and invasive species, and provide the capacity to anticipate and respond quickly to emergencies. It is coordinated by AAFC and involves CFIA, DFO, ECCC, NRCan, and NRC.

The project Strengthening Food and Water Safety in Canada through an Integrated Federal Genomics Initiative (the Food and Water Safety (FWS) project) will develop the tools and infrastructure needed to apply genomics-based methods for pathogen isolation, detection and characterization from a variety of food, water and environmental matrices, focusing on verotoxigenic *Escherichia coli* (VTEC) and *Salmonella* Enteritidis (SE). It is coordinated by HC and involves AAFC, CFIA, ECCC, 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 asevidence-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 NRC was updated to reflect NRC's new industry-focus. It is aligned with Government of Canada's Strategic Outcomes and federal priorities and to NRC's business processes. NRC's performance reporting is aligned accordingly. The GRDI at 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 and subsequent entry 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 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 mandate of the WG 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 NRC. It provides GRDI-wide coordination, communication, networking and outreach support. This includes support to the ADM CC and the GRDI WG, transparent and effective communication to departments of the planning cycle, process requirements, financial administration and other project management requirements, and support for interdepartmental shared project planning and implementation. This function is also responsible for conducting studies and analyses to help establish GRDI-wide research priorities, providing management and administration support, as well as support for performance management, reporting, evaluation, and communications. It is funded through the shared priorities portion of the GRDI.

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 NRC for 2015-2016, the second 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. Five meetings of the ADM CC and nine meetings of the GRDI WG were held to allow for collaborative decisions. Leadership was provided to establish future strategic directions and develop project management plans for two Phase VI shared priority projects to be launched in April 2016: 1) Antimicrobial Resistance (the AMR project); and 2) Ecosystem Biomonitoring (the EcoBiomics project).

The implementation of Phase V shared priority projects continued to be supported for the last year: funding was made available to participating departments based on the approved Project Charters and bi-annual progress reports were presented to the ADM CC (November 2015 and March 2016). Guidance documents of the Innovation Management Strategy for shared priority projects were developed and endorsed by the ADM CC, including: general guiding principles; designing projects for enhanced end user engagement; open science; intellectual property guidance; material transfer guidance; sharing data guidance; open source software guidance; and authorship and publication. A community of practice of experts was engaged to finalize the documents and facilitate case by case implementation of the guidance.

The GRDI Performance Measurement Strategy was implemented with the finalization and approval by the ADM CC of the Annual Performance Report for 2014-2015, and input into NRC's Departmental Performance Report and Report on Plans and Priorities. The GRDI evaluation was launched under leadership of NRC's Audit and Evaluation group and the interdepartmental GRDI Evaluation Working Group.

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. Phase VI projects were selected based on their contribution to identified priorities where federal scientists had distinct expertise, using balanced portfolio approaches, and following formal approval processes.

Shared Priorities

Phase V shared priority projects were supported in the first two years of Phase VI of the GRDI (2014-2016). Formal Project Charters describe detailed governance structures to ensure seamless integration and clear roles and responsibilities. These include Management Advisory Committees, comprising senior managers from each participating department and agency, a Science Advisory Board with members representing academia, government and industry, theme leaders, dedicated project managers, and overall leadership by Scientific Project Coordinators. Ongoing open communication was established through conference calls, emails, presentations, and regularly scheduled meetings, to share updates and provide decision-making fora. Management Advisory Committees met to advise on the project directions and reviewing progress. Web-based SharePoint sites were used in both projects to host the most current versions of documents for access by all project participants and Advisory Boards.

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 2015-2016 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 2015-2016 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 Foottit, 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;
- Sean Walkowiak (AAFC) received the Natural Science and Engineering Research Council Canada Graduate Scholarships-Doctoral Award and the Significant Contribution to Science Outreach Award from Let's Talk Science;
- George Fedak (AAFC) received the 2015 AAFC Gold Harvest Award for First Canadian Biofungicide for Controlling Fusarium Head Blight in Wheat;
- Isobel Parkin (AAFC) received the AAFC Golden Harvest Team Award (Team Lead) for Brassica Genome Sequencing;
- Anas Eranthodi (AAFC), a PhD student in Nora Foroud's laboratory, was awarded "Best Student Oral Presentation" at the Plant Pathology Society of Alberta 2015 Annual Meeting;
- Ravinder Goyal (AAFC) was awarded (tied) for "Best Technical Oral Presentation" at the Plant Pathology Society of Alberta 2015 Annual Meeting;
- Anas Eranthodi (AAFC), a PhD student in Nora Foroud's laboratory, was awarded a "Graduate Student Scholarship" at the Plant Pathology Society of Alberta 2015 Annual Meeting;
- Guillaume Bilodeau, Marie-José Côté, Margaret Neuspiel, James Delano, and Michael Rott (CFIA) received the Science Branch Recognition Program 2016 in the category Partnership/Collaboration for their contribution to the QIS project;
- Ian Bradbury (DFO) was the recipient of a Cox Fisheries Scientist in Residence Award from Dalhousie University;
- Doug Crump (ECCC) received the Environmental Science & Technology best scientific articles second runner up award for 2015 in the field of Environmental Science (out of 1500 papers);
- Bruce Pauli (ECCC) won the first Place Platform Presentation and third Place Thesis Award at the University of Saskatchewan (Acute effects of exposure to oil sands-influenced sediments on the early life stages of Xenopus laevis);
- Carole Yauk's team (HC) received top five paper award for 2015 in the category 'Advancing the Science of Risk Assessment', from the Society of

Toxicology's Risk Assessment Specialty Section for a technical guidance for risk assessors using genomics;

- Carole Yauk's team (HC) received top paper of the year in 2015 by the Society of Toxicology's Risk Assessment Specialty Section for the research group's case study on the use of genomics in the risk assessment of benzo[a]pyrene;
- Sabah Bidawid and Nathalie Corneau (HC) received the Health Canada Deputy Minister's Award of Excellence in the category of Science and the Health Products and Food Branch Assistant Deputy Minister's Award for Excellence in the category of Science;
- Benjamin Hetman (PHAC) received the Best Oral Communication at the Canadian Society for Epidemiology and Biostatistics Annual General Meeting 2015 for presentation on the EpiQuant framework; and
- The PHAC Research Merit was awarded to the research team of Catherine Yoshida, Peter Kruczkiewicz, John Nash, and Eduardo Taboada for work on the Salmonella In Silico Typing Resource (PHAC).

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 2015-2016 follow.

The QIS project developed, validated and transferred Standard Operating Procedures (SOPs) to various user groups, which reported improved DNA extraction following the use of these procedures. Discoveries continue to be published in scientific journals by the QIS team and the SOPs will be used in the GRDI Phase VI shared priority EcoBiomics project.

The FWS project hosted an interactive two-day event that attracted 85 delegates from across Canada, including food industry representatives, researchers, regulators, public health officials and manufacturers of rapid diagnostic tools. The purpose of the workshop was to showcase some of the innovations of the FWS project, including new processes and tools that have the potential to significantly improve food safety in Canada. It fostered an environment of exchange and collaboration between researchers and end-users to boost the commercial uptake of publicly-funded R&D throughout Canada.

Scientists at AAFC shared their expertise relating to accurate identification of Next Generation Sequencing (NGS) data at lower taxonomic levels (i.e., species and strain) and have provided training to government collaborators, as well as to collaborators from the United States Department of Agriculture and from China.

Scientists at CFIA used newly acquired genetic information to confirm the presence of a highly pathogenic avian influenza virus on non-commercial farms in British Columbia's Fraser Valley.

Scientists at CFIA are developing SOPs for NGS to be used in the Potato Post Entry Quarantine Program for rapid detection, identification and characterization of plant viruses and to be considered as one of CFIA Plant Health Diagnostics tools. Additionally, CFIA scientists used whole genome sequencing based genotyping of 58 Canadian *Mycobacterium bovis* isolates to provide new information on the evolution of *M. bovis* strains associated with Canadian wildlife reservoirs and identified potential links between bacterial strains isolated in various Canadian and North American geographical areas.

2015-2016 has seen a dramatic increase in DFO's knowledge translation and mobilization activities, including 17 direct public communications products, primarily in the form of media interviews directly accessible to the Canadian public.

At ECCC, scientists participated in the Organization for Economic Co-Operation and Development technical committee on Molecular Screening and Toxicogenomics, and in the Committee for Nanotechnology. They also contributed to shellfish monitoring with the United States, and to the Saint Lawrence Action Plan Committee for pharmaceuticals and harmful algal blooms. In addition, scientists participated in the Genome Canada advisory committee for watershed microbiomes and co-founded the Wetland Ecogenomics Network.

Toxicogenomics research conducted under the GRDI at HC was used to define the first official 'genomics biomarker' of the United States Food and Drug Administration's Biomarker Qualification Program. 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, and the International Life Sciences Institute's Genetic Toxicology Technical Committee. In the context of emerging stem cell therapeutic treatments, outputs from GRDI funded research has led to the development and finalization of a new HC guidance document on the Use of Cell Therapy Products in Clinical Trials. A lead HC scientist was invited to present the outputs of GRDI research to end users, including a BIOTECanada group comprised of industry stakeholders that manufacture and distribute biologics in North America. In the area of food nutrition, GRDI research informs advice on dietary fibre labelling and its recommended intake for Canadians.

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. Researchers funded by the GRDI also collaborate with the Center for Disease Control, Atlanta, USA, to standardise detection technologies and to share approaches for the detection of biological toxins and emerging pathogens.

APPENDIX A– SUPPLEMENTAL PERFORMANCE DETAILS

Annex 1 – 2015-2016 GRDI Projects and Allocations from GRDI Funds

GRDI FUNDS ($)	PROJECT TITLE
QUARANTINE AND INVASIVE SPECIES	
1,891,864	Protection of Canadian biodiversity and trade from the impacts of global change through improved ability to monitor invasive alien and quarantine species
FOOD AND WATER SAFETY	
1,783,546	Strengthening food and water safety in Canada through an integrated federal genomics initiative
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	
102,000	Mining legume genomes for attributes of sustainable nutrient (nitrogen) acquisition through symbiosis
123,000	Using genomics to reduce fusarium diseases and mycotoxin hazards in Canadian grain
	Genome-wide mining and mapping of disease resistance genes - novel strategies to enhance wheat disease resistance breeding
301,152	Exploiting genomics to decipher hybrid vigour in *Brassica napus*
	Using genomics to reduce fusarium diseases and mycotoxin hazards in Canadian grain
84,000	Ethylene signalling and Fusarium Head Blight resistance in wheat
117,500	Exploiting genomics to decipher hybrid vigour in *Brassica napus*
113,500	Accessing adaptive ancestral avena alleles
70,000	Using CRISPR to elucidate gene associated traits in wheat: Fusarium Head Blight resistance and yield capacity
46,500	Verification of plant defense genes against *Sclerotinia sclerotiorum*
134,000	Effectors of Canadian *Puccinia striiformis* isolates
34,000	Molecular tools for identification of stored-product insects and their symbionts for use in pest control
62,000	Cell-type specific chromatin dynamics in soybean hairy roots responding to water stress
142,998	Advanced genetic technologies for improvement of camelina and canola
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	
120,000	Development of genomics and bioinformatics tools enabling epigenetic analyses in oilseed crops
96,000	Development of identification and analysis tools for amplicon-based metagenomics, focussing on high risk and regulated pathogens
183,131	Exploring the applicability of new technologies and processes to the management and analysis of next generation sequencing data
3) Enhanced efficiency of plant breeding	
84,600	Development of genome editing technology in crop somatic cells using cell penetrating peptides
153,129	Process for making transplastomic cell and plant lines - tool for new trait development

continued on next page

178,000	Effector-based breeding tools and Quantitative Trait Locus discovery for management of root rot in soybean caused by *Phytophthora sojae*
116,000	Genomics and genetics of Soybean Mosaic Virus - soybean interactions: next generation viral resistance
CANADIAN FOOD INSPECTION AGENCY	
70,000	Application of whole genome sequencing for molecular epidemiological investigations of bovine tuberculosis in Canada and for the high throughput discovery of novel diagnostic antigens for *Mycobacterium bovis* and *Brucella abortus*
130,000	Enhancing the CFIA's genomic capabilities for detection and characterization of high consequence known and unknown/unexpected animal viruses and their vectors/reservoirs
200,000	Whole genome sequencing technologies as tools for the detection, isolation, identification and characterization of pathogens in support of Canadian food inspection objectives
200,000	Detection and identification of plant pests and plants with novel traits using next generation sequencing
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 ENVIRONMENT AND CLIMATE CHANGE CANADA	
44,550	Incorporating wood frog toxicogenomics into the adverse outcome pathways for environmental effects monitoring of oil sands industrial development and for regulatory activities
41,250	Avian toxicogenomics and adverse outcome pathways - new tools for risk assessment
88,688	Genomics research in support of *Canadian Environmental Protection Act* risk assessment for existing and new microbial substances
35,888	Molecular markers of exposure to parental and alkylated polycyclic aromatic hydrocarbons in birds and mammals
19,800	Population genetic structure of Canadian seabirds
37,125	Polar bear conservation genetics: application of single nucleotide polymorphisms for the study of circumpolar population genetics, brown bear hybridization and genome wide association in polar bears
57.750	Transcriptomic analyses of the ecotoxicological effects of nanomaterials on microorganisms
58,163	Assessing impacts of emerging contaminants in aquatic organisms using high resolution genomics
51,975	Multidisciplinary Rapid Assessment indicator of algal and bacterial community composition and harmful blooms
24,750	Aquatic ecotoxicogenomics of emerging contaminants: pharmaceutical, personal care products and algal toxins
82,500	Genomics to support effects based monitoring in the Ring of Fire
43,725	Application of genomics tools to identify fecal pollution source contaminating freshwater and marine ecosystems
65,794	Forensic DNA identification of iconic Canadian species
50,325	Analysis of Norovirus in sanitary effluents
57,348	Aligning and operationalising DNA-based bioassessment for regulatory monitoring of ecosystems

continued on next page

FISHERIES AND OCEANS CANADA	
158,000	Rapid genomic screening for Atlantic Salmon aquaculture escapees and hybrids using Restriction Site Associated DNA Sequencing and a high throughput nanofluidic dynamic array
58,000	Genomic tools for salmon enhancement
94,400	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
17,800	Stock delineation of narwhals (*Monodon monceros*) from Baffin Bay and adjacent areas using novel genetic markers developed from genomic techniques
153,400	Assessing the spatial scale of dispersal and connectivity in non-indigenous Green Crab (*Carcinus maenas*) and commercial Sea Scallop (*Placopecten magellanicus*) in Canadian waters using Restriction Site Associated DNA Sequencing and high throughput SNP genotyping
149,200	Bioinformatic support to develop "FIT-CHIP" for industry and salmon management applications
87,300	Integrating neutral and adaptive genetic information for addressing knowledge gap in redfish (*Sebastes* spp) population structure and its underlying mechanisms in Atlantic Canada: a genomic genotyping-by-sequencing approach of SNPs polymorphism
HEALTH CANADA	
100,000	Application of an adjuvanticity assay to assess the effects of food chemicals of regulatory concern on the immune transcriptome
121,000	Safety of prebiotics in infants
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
209,000	Systems biology informed structure-activity-relationships to predict pulmonary pathology induced by nanomaterials
171,000	An integrated systems biology approach to investigate immunopotentiation induced by Respiratory Syncytial Virus vaccines
314,000	The coming revolution: next generation sequencing detection of de novo mutations in the offspring to identify germ cell hazards
210,000	Identification of biomarkers for the standardization and risk assessment analysis of mesenchymal stem cell based health products
225,000	Development of genomics biomarker to provide mechanistic context and data in support of human relevance for chemicals inducing cellular stress responses
NATIONAL RESEARCH COUNCIL	
3,552,000	Wheat improvement flagship (enhancing fusarium and rust tolerance; genomics-assisted breeding; abiotic stress; seed development)
888,000	Biologics and subsequent entry biologics: development of support technology

continued on next page

NATURAL RESOURCES CANADA	
41,728	Development of metagenomic and bioinformatics tools to facilitate processing of trap captures
84,000	Tools for enhanced molecular detection of Asian Gypsy Moth and identification of their geographic origins
71,325	Spruce budworm eco-genomics
61,136	Accelerating the discovery of insect volatile attractant molecules with genomics
182,438	Developing the next generation biosurveillance tools for tracking and preventing forest pest invasions
130,988	Applied genomics for tree breeding
53,373	Development of molecular tools to detect living *Phytophthora* spp. of phytosanitary concern in wood
77,633	Genomics-assisted tree breeding for improving remediation of disturbed forest ecosystems
83,941	An early detection tool for Emerald Ash Borer and ash resource protection
133,432	Innovative land reclamation approaches following oil sand mining: Improving phytoremediation tree-soil microbes interactions
101,893	Developing molecular and environmental genomic approaches for microbial and invertebrate communities to assess ecosystem integrity in forest management
PUBLIC HEALTH AGENCY OF CANADA	
90,000	MALDI-TOF mass spectrometry identification of bacteria: the establishment of a national MALDI database to support diagnostic laboratories across Canada
60,000	International validation of standard operating procedures for mass spectral diagnostic analysis of high consequence toxins: *Botulinum neurotoxins*
125,000	BioTools for the predictive genomics of priority foodborne pathogens
145,000	Closing the gaps in national surveillance of *Clostridium difficile*: epidemiologic and genomic characterisation of community-onset and recurrent *C. difficile* infections
160,000	Single nucleotide variant subtyping of *Salmonella* Enteritidis and *Salmonella* Heidelberg
60,000	The identification of *Mycobacterium tuberculosis* specific RNA molecules: An approach to improve accuracy and utility of currently used assays for latent tuberculosis infection
50,000	*Neisseria gonorrhoeae* sequence typing for antimicrobial resistance: a novel sequence-based antimicrobial resistance typing scheme for tracking the global dissemination of *N. gonorrhoeae*
190,000	The use of whole genome sequence analysis to support healthcare-associated outbreaks of carbapenem-resistant *Enterobacteriaceae*
90,000	Transfer of the validated *Salmonella* genoserotyping array into a PHAC reference laboratory and piloting the technology into the National Microbiology Reference Laboratory and targeted provincial health laboratories
65,000	Validation of metagenomics as a *bona fide* laboratory approach for cost-effective enteric pathogen identification and subtyping
60,000	Implementation of a next generation sequencing testing platform to support Pan American Health Organization drug resistance surveillance
80,000	Whole genome sequencing of measles virus of an effective molecular surveillance during measles elimination
70,000	Proposal for a whole genome sequence-based genotyping approach for tuberculosis in northern Canadian communities
50,000	Implementation of genome-based analyses to “One Health” surveillance of enteric disease
70,000	Translational analytic infrastructure for emerging pathogen discovery
60,000	PulseNet Canada: Model framework development for genomic technology delivery in a laboratory network
40,000	Whole genome sequencing of *Neisseria meningitidis* and its application to surveillance and understanding invasive meningococcal disease molecular epidemiology dynamics

* Non-pay operating expenditures only

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 2015-2016. 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 2015-2016. They do not include submitted papers or publications in draft form, nor contributions that were reported in previous years.

Key Scientific Contributions Demonstrating Leadership

KEY SCIENTIFIC CONTRIBUTIONS	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL
Publications in refereed journals	31	12	11	73	20	27	16	19	44	9	**262**
Publications in refereed conference proceedings	20	3	1	0	1	1	2	13	0	0	**41**
Books (edited, written) and book chapters	4	1	0	3	4	0	1	0	0	1	**14**
Invited presentations	11	22	7	11	19	3	21	18	10	2	**124**
International conference presentations	8	7	7	19	9	14	8	24	7	9	**112**
Editorial posts for national and international journals (excludes peer reviewers)	0	4	0	0	1	0	2	2	7	0	**16**
New genomics related databases or libraries	2	1	0	6	0	0	1	5	0	0	**15**
Awards, prizes	5	0	1	3	2	0	0	2	2	2	**17**
Total	**81**	**50**	**27**	**115**	**56**	**45**	**51**	**83**	**70**	**23**	**601**

Other Scientific Contributions

NUMBER OF OTHER SCIENTIFIC CONTRIBUTIONS	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL
Technical reports	1	6	5	3	0	20	3	4	0	0	**42**
Other publications (ex. abstracts, notes, industry magazines, etc.)	6	2	2	2	0	3	1	1	6	0	**23**
Poster presentations at conferences	11	6	2	7	15	64	2	14	8	18	**147**
National conference presentations	11	2	8	4	6	31	10	7	4	2	**85**
Deposits in genomics related databases or libraries	0	2	0	4	2	1	13	35	4	0	**61**
Total	**29**	**18**	**17**	**20**	**23**	**119**	**29**	**61**	**22**	**20**	**358**

Research tools and processes

Research tools and processes include those produced in 2015-2016, deriving from previous phases of the GRDI if produced in 2015-2016, 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	QIS	FWS	TOTAL
Research tools	8	6	13	5	13	19	3	16	11	3	**97**
Research processes	2	6	8	4	8	3	2	15	0	0	**48**
Total	**10**	**12**	**21**	**9**	**21**	**22**	**5**	**31**	**11**	**3**	**145**

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.

Contributions to Scientific Networks

NUMBER OF CONTRIBUTIONS TO SCIENTIFIC NETWORKS											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL
Participation in government meetings/seminars/advisory panels related to regulations or policy in Canada and internationally	9	6	9	10	19	0	2	22	0	0	**77**
Participations in national or international genomics-related committees	12	13	4	9	8	5	3	19	1	10	**84**
National or international genomics research peer review committees served on	25	0	1	2	1	1	4	1	0	0	**35**
Participation in national conferences	30	1	4	5	2	5	0	2	0	2	**51**
Participation in international conferences	35	1	5	19	3	33	2	0	1	9	**108**
Total	**111**	**21**	**23**	**45**	**33**	**44**	**11**	**44**	**2**	**21**	**355**

Collaborations

Collaborations by department/agency, expressed in terms of number of individual research collaborators in 2015-2016 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**	**QIS**	**FWS**	**TOTAL**
Canadian universities	22	4	15	39	10	3	12	16	27	3	**151**
International universities	16	0	4	9	4	1	14	5	33	2	**88**
Other international research organizations	7	0	2	11	8	2	7	22	18	1	**78**
Other Canadian research institutions	5	0	1	2	0	4	2	0	10	0	**24**
Private sector	6	0	4	1	4	10	3	0	5	0	**33**
Other government departments	18	12	0	22	5	4	4	10	37	0	**112**
Other public sector organizations such as provinces, municipalities, and Non-Governmental Organizations	2	1	8	10	4	3	8	25	6	4	**71**
Total	**76**	**17**	**34**	**94**	**35**	**27**	**50**	**78**	**136**	**10**	557

Communications products

NUMBER OF COMMUNICATIONS PRODUCTS											
	AAFC	**CFIA**	**DFO**	**ECCC**	**HC**	**NRC**	**NRCan**	**PHAC**	**QIS**	**FWS**	**TOTAL**
Media interviews	1	0	12	2	0	7	1	1	2	0	**26**
Press releases	0	0	1	0	0	8	0	4	0	0	**13**
Newspaper and magazine articles	1	0	2	3	0	6	0	1	0	0	**13**
Community presentations	15	0	2	13	0	2	1	0	0	2	**35**
Brochures, fact sheets, web pages	3	0	0	2	0	11	4	3	0	0	**23**
Total	**20**	**0**	**17**	**20**	**0**	**34**	**6**	**9**	**2**	**2**	110

End-user engagement and knowledge transfer activities

NUMBER OF OUTREACH ACTIVITIES											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL
End-user consultations	10	0	1	9	14	1	3	10	0	0	**48**
Public meetings	1	0	1	5	2	6	1	0	0	0	**16**
Science advice, including to senior management	28	0		0	4	2	6	26	4	2	**72**
Outward material transfer agreements	7	1	0	1	1	1	3	0	2	0	**16**
Transfer of standard operating procedures	11	2	0	1	1	4	1	6	7	1	**34**
Disclosures	0	0	0	0	0	3	0	0	0	0	**3**
Active patents, patent applications, patents issued	16	0	0	0	0	6	0	0	1	0	**23**
Licenses issued	1	0	0	0	0	0	0	0	0	0	**1**
New formal collaborative agreements / standard operating protocols	5	8	1	0	1	2	2	3	7	1	**30**
Knowledge transfer workshops with stakeholders/end-users	8	4	5	10	5	5	5	8	0	1	**51**
Requests for research results, papers, collaborations	79	2	1	2	2	4	4	16	2	2	**114**
Total	**166**	**17**	**9**	**28**	**30**	**34**	**25**	**69**	**23**	**7**	**408**

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 2014-2015, including but not exclusive to personnel financed through GRDI funds.

NUMBER OF RESEARCH AND TECHNICAL PERSONNEL											
	AAFC	CFIA	DFO	ECCC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL
Research scientists	35	28	9	10	19	66	20	24	20	42	**273**
Research professionals	5	8	14	25		18	12	36	24	17	**159**
Research technicians	45	23	11	15	19	134	24	19	24	24	**338**
Post-doctoral/visiting fellows	12	4	10	9	7	13	7	10	8	5	**85**
Graduate students	21	4	2	9	5	0	3	5	3	7	**59**
Undergraduate students	26	5	2	8	9	6	2	7	11	3	**79**
Administrative officers	0	0	0	3	0	0	1	2	1	0	**7**
Total	**144**	**72**	**48**	**79**	**59**	**237**	**69**	**103**	**91**	**98**	**1000**
Total Estimated Full Time Equivalents	68	19	18	26	26	86	30	31	36	45	385

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

Quarantine and Invasive Species (QIS) Project
Protection of Canadian biodiversity and trade from the impacts of global change through improved ability to monitor invasive alien and quarantine species

Participating Departments/Agencies:
AAFC, CFIA, ECCC, DFO, NRC, NRCan
Scientific Coordination: AAFC
Project Management: CFIA

The QIS project is a collaborative effort by 28 Principal Investigators from six departments and agencies, divided into five sub-projects and focusing on the protection of Canadian biodiversity and trade from the impacts of global change through an improved ability to monitor invasive alien and quarantine species. These species can cause millions of dollars in economic losses, result in trade disputes and border closures, cause irreversible environmental damage, and require vigilance and rapid responses when such a species is detected in Canada. The QIS project has gained domestic and international attention, and the number of collaborators and stakeholders continue to grow. By facilitating inter-sectoral collaborations, QIS promoted synergies that would have not otherwise occurred, therefore increasing efficiency and reducing the time required for specific tasks.

Sub-Project 1: Optimization and standardization of nucleic acid extractions

The objectives were to optimize and standardize methods for nucleic acid extraction for 1) preserved and archived tissues originating from the various federal collections and 2) bulk samples collected in the field for use in sensitive direct detection. Significant progress was made this fiscal year. Protocols for DNA extraction from various samples were developed and are available for specimens from different groups of organisms. Two new DNA extraction SOPs were transferred to user groups who saw improvement with DNA extraction as a result. A total of 27 protocols are now available on the QIS GCpedia page, and novel discoveries continue to be published in scientific journals by QIS collaborators. While the QIS project ends this year, work will continue to strengthen and implement the tools developed, and the GRDI Phase VI EcoBiomics project will build on tools developed by this sub-project.

Sub-Project 2: Barcoding of aquatic invasive species of highest risk to Canadian native fauna and trade

The objectives were to generate research outputs and outcomes that will 1) enable enforcement by DFO of impending Aquatic Invasive Species regulations that will be a part of a new or revised *Fisheries Act*; and 2) support EC's primary responsibility areas of Ecosystem Sustainability: Protecting National Capital, and Environment Protection: Understanding Cumulative Risks. The focus was to generate reference DNA sequence datasets for use in the development of accurate molecular detection tools that will enhance Canada's ability to prevent new aquatic invasions. Significant progress was made this fiscal year. A total of 906 specimens, representing all Canadian freshwater invertebrate species, were vouchered and sequenced. All the sequences are available on the Barcode of Life Database (BOLD). This rich and invaluable dataset will be essential to support decisions regarding the management, treatment and control strategies of alien species in the future as millions of aquarium fish and hundreds of thousands of live organisms are imported into Canada for food each year.

Sub-Project 3: Barcoding of quarantine and invasive species in terrestrial ecosystems

The objective was to generate DNA barcode libraries that will provide baseline identifiers for confirmation of identities, focusing on species found in terrestrial ecosystems in Canada that are of quarantine significance and of economic importance to Canada. The sequencing of target insect and mite groups is complete with a combined total of 2300 sequences available on public databases including the National Center for Biotechnology Information (NCBI) and BOLD. Additionally 2056 dried herbarium specimens preserved in the National Mycological Herbarium were processed for DNA extraction, PCR and sequencing. A total of 1812 plant viral genomic sequences were also entered into the QIS database

SeqDB, representing over 100 viral species. Since the start of the project, workflows for assembling viral genomes has greatly improved, and the goal to generate as much viral genome sequence data as possible for grapevine, tree and small fruits has been achieved. Finally, for invasive plants, the QIS project has delivered more than the planned 9000 barcode sequences with 1618 raw specimens sampled and sequenced for four barcodes and 11631 raw sequences assembled for a total of 3663 consensus representing invasive plant species and relatives. Federal collections from this sub-project have been confirmed as essential sources of genetic material based on authoritatively identified specimens. This work will continue with AAFC's new funding to focus on the further development of DNA libraries.

Sub-project 4: Direct detection of quarantine and invasive species

The objective was to address real, practical needs to detect invasive species in matrices not previously considered useable or to radically improve and expand on current detection methods using NGS. Several themes were developed to evaluate the application of NGS methods for the detection of diverse groups of invasive species from bulk environmental samples.

Collection activities in this sub-project have led to the discovery of a new introduction in forest systems in British Columbia and range extensions for a number of exotic species in British Columbia and Alberta. Additionally, a complete workflow for the use of NGS for plant viruses has been developed, and the method has been validated with over 300 control samples and 110 additional samples with cost effective results. The application of NGS methods will be very important in the future and these new methods will assist in federal government monitoring, surveying and diagnostic testing.

Sub-Project 5: Bioinformatics

The objective was to create a cyber-infrastructure platform to manage and analyse data generated by the QIS project. High priority deliverables were completed, including several related to metagenomics data management, and support to the taxonomic project backbone and with reporting and tracking. Specimen data capture can now be completed by all GRDI participants, who have received training on AAFC infrastructure and secured Virtual Private Network (VPN) access. Additionally, more than 100,000 raw sequences and associated consensus sequences generated from thousands of specimens are available in the QIS database SeqDB. The knowledge and experience of the QIS bioinformatics sub-project will be invaluable to the success of future collaborations by federal departments and agencies on biodiversity issues.

Food and Water Safety (FWS) Project

Strengthening Food and Water Safety in Canada through an Integrated Federal Genomics Initiative

Participating Departments/Agencies:
AAFC, CFIA, ECCC, HC, PHAC and NRC
Scientific Coordination: HC
Project Management: HC

The FWS project is a collaborative effort by six departments and agencies to develop the tools and infrastructure needed to apply genomics-based methods for pathogen isolation, detection, characterization, and source attribution, focusing on two priority microbial pathogens: verotoxigenic *Escherichia coli* (VTEC) and *Salmonella* Enteritidis (SE). It includes the development of an integrated federal system to manage, store and provide open access to genomic data, genomic-based methods to increase the discrimination of risk assessment criteria and improved identification of pathogen sources. Activities are organised under three major themes: 1) *Isolation and Detection*; 2) *Information Generation;* and 3) *Bioinformatics*.

Sub-Project 1: Isolation and Detection

The main objective was to develop genomics-based tools for the rapid isolation and detection from a variety of foods, water and environmental matrices of O157 and six priority non-O157 VTEC strains. The detection and identification of pathogens in foods is highly dependent on the ability to extract and isolate them from highly complex food and environmental water matrices. To this end, scientists have aimed at isolating these pathogens either as whole intact cells or by extracting their nucleic acids. The project has reached important milestones, including delivery to stakeholders.

Using a variety of approaches, nucleic acid purification, antibodies specific to target VTEC and metabolic labelling technologies were applied to purify and/or partially remove target organisms from the ini-

tial matrix (food, soil, water). Much of the work has focussed on removing debris (i.e., new approach in food microbial diagnostics of removing the hay to find the proverbial needle). Significant advances in sample preparation using microfluidics technologies were achieved and can be combined with downstream detection technologies.

Sub-Project 2: Information Generation

Whole genome sequencing generated draft genomes for 549 VTEC & 246 SE by assembling short read sequences obtained at the central Winnipeg sequencing laboratory. Sequence polishing experiments were carried out to complete contiguous genomes for 20 preselected reference genomes (11 VTEC and 9 SE).

The FWS team also partnered with the National Center for Biotechnology Information to troubleshoot their cumbersome batch upload process and achieve more convenient public data archiving. As a result, the team validated a streamlined batch data upload procedure for enhanced 'direct-to-NCBI' data transmission from IRIDA. This validated direct upload function will greatly benefit all end users of genomic data, and will help promote open access to scientific data for broad use by stakeholders.

The FWS legacy genomes represent enhanced, publically available genomic resources for Canadian VTEC and SE that will continue to be hosted by the appropriate public data repository under the registered NCBI GRDI FWS BioProject (PRJNA287560), also mirrored at the DNA Data Bank of Japan (DDBJ) and the European Bioinformatics Institute (EMBL).

Lastly, tools were validated for VTEC microbial source tracking to achieve "attribution" to potential sources of fecal contamination and to inform VTEC risk assessment and risk modelling.

Sub-Project 3: Bioinformatics

Deliverables were centered on 1) the design and development of a computational platform for the storage, management, analysis, and reporting of microbial genomes and associated metadata; and 2) bioinformatics training workshops focusing on genomic epidemiology. Several important milestones have been achieved for the development of the Integrated Rapid Infectious Disease Analysis (IRIDA) platform. The IRIDA platform has been deployed to PulseNet Canada as part of its technology modernization program to transition to the use of next generation sequencing for molecular surveillance of foodborne diseases. The IRIDA development team collaborate with Torsten Seeman, developer of the Nullarbor pipeline to generate complete public health microbiology reports from sequence data. We are integrating the IRIDA system into the Nullarbor system that is expected to be used by Australia's public health system. The IRIDA system is being used as the base platform in the Phase VI GRDI shared priority AMR project. Discussion is ongoing with Public Health England to share FWS AMR sequence data using IRIDA as part of the Canada-United Kingdom partnership on AMR. With Genome Canada partners, members of the FWS project have spearheaded the creation of GenEpiO, an international consortium developing best practices for genomic epidemiology ontology.

Nineteen posters and 20 talks describing IRIDA have been presented at local, national, and international venues. Six scientific papers have published on various aspects related to IRIDA development, and several more are in preparation.

Important additional pieces of software have been created under this bioinformatics theme, including SigSeekr, a program to identify signature sequences for pathogens early in the sequencing cycle, the ARMI (Antimicrobial Resistance Marker Identification) pipeline to mine genomic data for the prediction of antimicrobial resistance compounds, and SISTR (Salmonella in *silico* Typing Resource for serotyping salmonella using a whole genome sequencing approach.

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

Over several phases of GRDI support, NRC has built an impressive target discovery and antibody development pipeline, primarily for oncology indications. Using a combination of genomic, proteomic and bioinformatic approaches, 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.

Antibody-drug conjugates are revolutionizing the field of cancer chemotherapy by combining the targeting specificity of antibodies with the killing potential of cellular toxins, thereby offering the promise of high efficacy and low toxicity. NRC is leveraging its target discovery, antibody generation, screening, and production platforms and adapting them for antibody-drug conjugates. In addition, the antibody components of these antibody-drug conjugates are being manufactured using NRC's Chinese Hamster Ovary cell production platform, creating a full development pipeline for therapeutic candidates. With support from the GRDI, NRC scientists continue to improve this critical platform, using genomic and metabolomic technologies to optimize its performance.

NRC is partnering with Canadian companies to advance unconjugated antibodies and antibody-drug conjugates through pre-clinical development and biomanufacturing, leading to human clinical trials. By working with the different actors of the Canadian biopharmaceutical ecosystem, including contract research and manufacturing organizations, NRC enables the advancement of this next generation of biotherapeutics. These interactions are stimulating the growth of the sector thereby creating jobs and increasing Canada's return on its innovation investments.

Of the traditional antibodies discovered by NRC through this pipeline, the one licensed to Montreal-based Alethia Biotherapeutics is the most advanced. In May 2015, the company announced the beginning of patient dosing in a Phase 1 (first in human) clinical trial for its fully humanized monoclonal antibody against cancer. The antibody AB-16B5 targets secreted clusterin, which plays an important role in cancer metastasis and progression, and was co-developed with NRC with support from the GRDI.

While antibody-drug conjugates are a more recent development at NRC, two candidates, one of which is derived from NRC's discovery pipeline, are being advanced in collaboration with Toronto's Formation Biologics. The first one, AVID100, an antibody-drug conjugate against solid tumours, has completed advanced preclinical studies.

Genomic knowledge for the Canadian health regulatory system

Genomic approach to assess effects of food chemicals on the development of allergies

The incidence of food allergy in Canada has been increasing for reasons yet unknown. In this project, HC researchers are aiming to develop genomics-based tools to assess chemicals for their potential to develop and enhance allergy and contribute to increased allergic diseases in Canada. Allergy-prone mice were fed food chemical contaminants and additives to screen for changes to their genes and proteins involved in the immune response to allergens. An assay for regulatory screening of chemical food additives and contaminants was developed and validated and is being applied to analyze selected food additives for their contribution to allergies. This is the last year for this project and overall, it has yielded data of interest to international toxicologists, regulators at HC as well as those under the Government of Canada's Chemicals Management Plan involved in the evaluation of novel food chemical contaminants and additives, including colouring agents and nanomaterials.

Safety of prebiotics in infants

Mothers' milk contains a wide variety of carbohydrates that are not digested in the small intestine, but pass into the large intestine where they serve as nutrients for the developing infant gut bacterial community. Some infant formulas contain fermentable carbohydrate oligomers/polymers to mimic this function. In Canada, three types of fermentable carbohydrates have been added to infant formula. Among these are fructooligosaccharides, which have been linked to increased inflammation in infants' guts. In this project, HC researchers are assessing the impact of fructooligosaccharides on infant gut bacterial community during weaning and over the long term in rats to develop genomics-based methods for assessing bacterial community composition associated with feeding fermentable materials in infant formula. The animal project has been completed where rats were fed fructooligosaccharides and the gut and tissue content samples have been stored

for analysis. New protocols have been established to monitor changes to the microbiome, and the intestinal and fecal samples have been prepared for sequencing. Metagenomic analysis of the colon cell response has begun, including preparation of the samples for analysis. Methodology to monitor gut barrier integrity and the microbiome metagenomics response has been developed. This project is already increasing awareness among HC regulators of the physiological outcomes potentially associated with feeding 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 is important in the regulation of gene expression and translation in protein products. In this project, HC researchers set out to identify and characterize microRNA in serum and milk associated with dietary exposure to fungal toxins and chemical contaminants currently detected in foods. HC researchers completed the microRNA isolation, analysis and profile from serum and liver from multiple flame retardant and fungal toxin studies to determine the potential biomarkers of liver damage. Bioinformatic analysis is currently underway. This work will enable the generation of important regulatory toxicology data to inform the risk assessment process, 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 can induce harmful effects in animals. As a first study of its kind in the area of nanotoxicology, toxicogenomics and computational tools are being used to analyze the effects of different classes of nanomaterials on pulmonary cells and tissues to screen for potential toxicities of novel nanomaterials. In 2015-2016, HC researchers exposed mice to carbon nanotubes. Lung samples from the mice were collected and analyzed to understand the physicochemical properties of these carbon nanotubes in the development of lung disease such as lung fibrosis. A thorough literature search was completed to review toxicogenomics studies related to lung and pulmonary disease. Based on the results, an Adverse Outcome Pathway detailing the toxicity pathways for lung fibrosis induced by nanomaterials was developed and submitted to the Organization for Economic Co-Operation and Development to support risk assessment activities.

Genomics approach to understand the Respiratory Syncytial Virus vaccine

Respiratory Syncytial Virus is a common and highly contagious virus that infects the respiratory tract of infants and young children, and is the most common cause of bronchitis. At this time, there is no vaccine available for the prevention of diseases induced by this virus due to a lack of understanding of the disease and critical elements for the evaluation of the efficacy and adverse reactions associated with the vaccine. This project aims to better understand vaccine-induced toxicity and establish regulatory tools to assess the safety of this vaccine. An animal study model has been established and analyses are being conducted to find biomarkers that may be pertinent to vaccine-induced toxicity. Preliminary research data has been communicated to HC regulators responsible for evaluating biological drugs in Canada.

Next generation sequencing detection of *de novo* mutations to identify germ cell hazards

De novo mutations are associated with a diverse array of genetic phenotypes and are increasingly being recognized as contributing to a wide range of human diseases. Evidence suggests that many environmental agents cause DNA damage, thus increasing the risk of inherited mutation and genetic disease in offspring. HC researchers are using genomics technologies to analyze chemically induced heritable mutations in animals and humans. Advanced genomic technologies have been applied to measure heritable large scale genome changes in mice offspring exposed to benzo(a)pyrene, a common environmental pollutant. About 300 arrays were analyzed indicating the presence of large scale duplications in the offspring of mice exposed to benzo(a)pyrene. Whole genome sequencing of six mouse families has been conducted to detect mutations in the offspring. A reference genome Muta™ Mouse was completed using whole genome sequencing and a bioinformatics pipeline has been implemented to establish the mutation spectrum in sperm of mice exposed to benzo(a) pyrene.

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, the use of stem cells is not without risk. 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 2015-2016, HC researchers collaborated with two world renowned scientists in the field of cancer stem cells. This collaboration has led to numerous presentations at national and international conferences as well as the publication of work in the prestigious journal Stem Cells which outlines the identification of two new biomarkers that could potentially be useful for evaluating the capacity of human mesenchymal stem cells to treat diabetes. In addition, the team has generated a list of potential biomarkers that identify mesenchymal stem cells that are both safe and effective for treating immune disorders. These biomarkers are currently being validated to determine their capacity to discriminate human adult stem cells that can suppress hyperactivated immune response. These successfully validated biomarkers will form the basis for the development of 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 time consuming and expensive. In this project, HC researchers are developing and validating timesaving and more cost effective risk assessment genomics-based methods to predict whether a chemical causes DNA damage or other adverse genetic effects. In 2015-2016, HC researchers focused on developing and advancing genomic tools to identify agents that cause toxicities in human cells in culture. Several peer review papers, reports, and a book chapter were published, describing the tools developed in this project and applying them to risk assessment. Data was provided to the Health and Environmental Sciences Institute for a submission to the United States Food and Drug Administration's biomarker qualification program to validate these genome tools. Significant contributions were made to the United States Environmental Protection Agency's Next Generation Risk Assessment publication on the application of genomics in human health risk assessment.

Genomics knowledge to strengthen public health programs and activities related to infectious and chronic disease

Enteric diseases: development of genomic technology in a laboratory network

As food safety is a national priority, PHAC research addresses the critical need for scientific and technical innovation in pathogen detection and characterisation that will improve the identification of outbreaks, accompanied by accurate and timely source attribution. International validation of Standard Operating Procedures and open analytic infrastructure provide a vehicle to support cross border surveillance and response.

Innovative molecular methods developed in earlier GRDI funding cycles are undergoing validation and integration into provincial and national reference laboratories (e.g., World Organisation for Animal Health *Salmonella* reference laboratory). The work is underway for Salmonellosis, a very common foodborne illness. Two projects are addressing Salmonella serovars, specifically Enteritidis and Heidelberg. Validation and certification of these innovative methods will enable provincial and national reference laboratories to uptake the technology.

The surveillance programs run by FoodNet Canada and the Canadian Integrated Program for Antimicrobial Resistance Surveillance provide surveillance of enteric pathogens and the use and resistance to antibiotics in the food chain. These programs cover different points along the 'farm-to-fork' continuum through monitoring of farms, surface waters, food production, and public health laboratories. Genomic epidemiology approaches applied to food safety are in development to define the risk factors and transmission dynamics of *Escherichia coli, Salmonella,* and *Campylobacter* collected through sampling activities of surveillance programs. A new metagenomics sequencing project is in development to further our ability to characterise multiple pathogens in a single isolate without costly and labour intensive culturing conditions.

Detection and genomic epidemiology of priority pathogens

To address the strategic need for rapid identification of infectious pathogens, PHAC continues to develop, validate and apply modern technologies (e.g., genomics and mass spectroscopy) alongside advanced scientific computing. This work supports the need to advance the modernization and innovation of Canada's public health capacity through genomic scientific evidence and methodologies. The selected infectious pathogens and their diagnostic and genomics epidemiology gaps are:

- Measles: Although measles has been eradicated from the America's, limited endemic outbreaks are still occurring internationally. The current genotyping marker used to indicate the absence of "Canadian" measles in circulation has become less effective to track increasingly identical isolates. To support public health interventions based on the source attribution of emerging outbreaks a new method for tracking is been developed. International and national isolates will be sequenced and through analysis of the whole genome a routine genotype will be developed to support measles surveillance.

- Mass spectrometry for diagnosis: In collaboration with international colleagues in the United States and European Union, a national mass spectrometry database to support diagnostic laboratories across Canada has been established. The mass spectroscopy identification of bacteria assists Canadian public health laboratories and hospitals in the identification of uncommon and rare bacterial pathogens and facilitates rapid and accurate identification of a pathogen in hospitals. This will enable clinicians to quickly target treatment and decrease costs. In addition, a mass spectroscopy procedure for the detection and analysis of Botulinum neurotoxins has been standardised and deployed in collaboration with the Centres for Disease Control (Atlanta) and the Royal Canadian Mounted Police National Security Investigations. The validation of this cutting-edge, rapid and cost effective technology across borders will enhance public health security and promote forensic analysis and information sharing between the USA and Canada.

- Bioinformatics: Canada's public health response capacity is being augmented by the development of Bioinformatics platforms across research programs to enhance the interpretation and quality of genomics and proteomic data obtained directly from clinical and environmental specimens. The data management and analytical tools efficiently process large comparative datasets for rapid pathogen identification from complex clinical specimens.

Antimicrobial resistance: supporting communities, hospitals and the international response

Reducing the growing threat posed by AMR is one of PHAC's highest priorities because of growing concern that we are losing our ability to manage infectious diseases in humans and animals because of AMR. To that end, GRDI supported research is developing genomic-based technologies and methods aiming 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 resistance 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 three national/regional HIV reference laboratories in Brazil, Mexico and Puerto Rico 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 recur-

rent 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. Single Nucleotide Variations between isolates and their relation to patient transmission patterns have been described. This will inform strategies to apply a whole genome sequencing approach for managing outbreak(s) on site and inform the Canadian Nosocomial Infection Surveillance Program (CNISP).

- *Neisseria gonorrhoeae*: A novel typing scheme is in development to strengthen international surveillance of antibiotic resistance in *N. gonorrhoeae*. Known genetic mechanisms of resistance are being characterized to provide an internationally standardized nomenclature for *N. gonorrhoeae*. When completed, the tool 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 the Northern Manitoba and Nunavut. By developing an infrastructure for the routine whole genome sequencing and genotyping, this study is investigating 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. In a related study, an approach for the detection of latent infection will be developed to improve upon current tests, which classify all persons that have had an immune response to *M. tuberculosis* as latently infected, including individuals that no longer carry the bacteria. The research aims to identify biological markers that are diagnostic for individuals that still harbour the bacteria M. tuberculosis, in other words who are truly latently infected. As a consequence the test will optimize clinical decision making by reducing unnecessary treatment and costs to the public health and health care systems.

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 NRC's 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 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**: A large scale array of SNPs specific to the nucleotide variation in Canadian wheat germplasm was developed and will be used to generate high density genetic maps and a Canadian wheat breeders' gene chip for breeding programs. An automated wheat DNA extraction platform and SNP genotyping platform were optimized to deliver high-throughput data at 1/8th the original SNP analysis cost, and is available to wheat breeders. Bioinformatics resources and tools continued to be developed to coordinate genomic and phenotypic data for wheat research. A large nested-association mapping population (4700 recombinant inbred lines) in wheat is currently in development and will become a key resource in the wheat research community.

2) **Enhancing Fusarium and Rust resistance**: Gene expression libraries have been created for both Fusarium- and Rust-infected wheat tissues. Different combinations of rust-resistance genes have increased the durability of rust resistance, and have given potential extended new use in breeding programs to previously defeated resistance genes. Cost effective SNP markers will accelerate Canadian wheat breeding and diversify the genetic base of resistance to Fusarium and rusts. In addition, metabolomics analysis of wheat infected by fungi has led to the identification of major metabolites involved in disease resistance, and given new leads on anti-fungal traits.

3) **Improving wheat productivity under conditions of abiotic stress**: Genetic markers were developed for several abiotic stress related genes, including traits for drought, heat, or cold tolerance. Bioinformatics was used to identify gene networks involved in improved tolerance to these stresses. Signalling factors for drought tolerance and water-use efficiency were discovered, and wheat lines with highly expressed signalling factor showed improved water-use efficiency phenotypes in controlled greenhouse conditions. A promising metabolic and genetic marker was found to have high correlation to cold tolerance in tolerant vs sensitive lines in winter wheat in collaboration between the University of Saskatchewan and NRC. Genes conferring heat tolerance in wheat are under further development, and show extreme heat tolerance under controlled greenhouse conditions.

4) **Targeting developmental pathways to improve performance and yield in wheat**: A gene expression atlas for genes involved in wheat seed development has been developed, including for embryo development stages. Photosynthetic efficiency is also related to grain filling and yield. Wheat lines highly expressing the gene target were shown to have improved photosynthetic efficiency under greenhouse conditions.

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. AAFC had 19 GRDI mandated projects in 2015 covering three overarching themes: 1) Biodiversity, gene mining and functional analysis for the identification and extraction of genes for desirable traits; 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; and, 3) Enhanced efficiency of plant breeding. Projects highlights follow.

Biodiversity, gene mining and functional analysis for the identification and extraction of genes for desirable traits

Using genomics to reduce Fusarium diseases and mycotoxin hazards in Canadian grain

Fusarium Head Blight in small grain cereals and Gibberella Ear Rot in maize are devastating diseases principally caused by *Fusarium graminearum*, resulting in low yielding, low quality, mycotoxin-contaminated grain, adversely affecting Canadian food safety and competitiveness. Although fungicide treatments and improved agronomic practices can possibly help to reduce Fusarium Head Blight and Gibberella Ear Rot in low to moderate infection years, Fusarium-resistant cereals are required to prevent devastating losses during epidemic years and to ensure safer mycotoxin levels in food and feed. There are few agronomically important and fusarium head blight resistant lines of wheat, barley, or maize available to producers and the molecular mechanisms of resistance have not been elucidated yet.

AAFC has proposed to apply its extensive expertise and resources in genetics, genomics, proteomics, molecular pathology, and mycotoxin chemistry to study host plant resistance and susceptibility, Fusarium infection mechanisms and intra- and inter-specific fungal competition to ultimately develop durable resistance in crops to combat this serious threat to Canadian agriculture. Since the project started, in 2014, AAFC's scientists have made excellent progress regarding the understanding of cereal resistance/susceptibility and fungal infection mechanisms. Many genes associated with Fusarium Head Blight resistance have been identified in wheat and maize and are being characterized further. To understand Gibberella Ear Rot resistance mechanisms, AAFC's scientists have conducted transcriptome analysis of resistant and susceptible maize and have identified 14 differentially expressed genes mapping very close to Gibberella Ear Rot resistance quantitative trait loci. Throughout 2015, AAFC's scientists have found an unexpected diversity in gene content between Fusarium genomes, and have identified many Fusarium genes affecting fitness and pathogenicity.

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

Development of identification and analysis tools for amplicon-based metagenomics, focussing on high risk and regulated pathogens

1,207 fungal species are being regulated by 15 major countries / regions; among which, 38 species in Canada and over 50 in the United States are under quarantine surveillance. These pathogens can either cause significant yield loss or impose health risk to livestock and humans. AAFC continues to develop the best science-based approach to accurately scan, analyze and document such economically important pests in import and export commodities to maintain its leadership in protecting trade and reducing risks to Canadian and North American agriculture industry.

Deep sequencing using amplicon-based NGS technologies allows the detection of regulated pathogens at low levels, but at the same time misinterpretation of NGS data can also carry risks to Canadian trade. The misinterpretation reside in gaps in coverage of reference sequences, some of these are being addressed by the Quarantine Barcode Of Life (QBOL) in Europe and the Quarantine and Invasive Species project from the Canadian QIS project.

Building on the QIS project results, the overall goal of this project is to develop new bioinformatics tools/packages to facilitate the classification of NGS data and statistical analyses for hypothesis testing at lower taxonomic levels (e.g. species and strain-levels), focussing on quarantine species.

So far in this project, AAFC has developed a combined phylogenetic and signature oligonucleotides database for 215 fungal/oomycetes genera containing 248 plant pathogens regulated by 15 countries worldwide. The research team has also initiated several new collaborative projects associated with plant and/or soil microbiomes with Canadian industries and academia in Canada, France and China.

Enhanced efficiency of plant breeding

Genomics and genetics of Soybean Mosaic Virus-soybean interactions: next generation viral resistance

Among 67 viruses that infect soybean, Soybean Mosaic Virus is the most prevalent pathogen that impedes soybean production in Canada as well as all other soybean-producing countries. This seed-borne aphid transmitted virus causes severe reductions in plant growth, seed quality and lower yield. Current genetic resistance is found to be very fragile and it can be easily overcome by Soybean Mosaic Virus isolates. New durable genetic resistance is highly demanded to protect soybean production from possible catastrophic Soybean Mosaic Virus outbreaks.

During the previous GRDI cycle, AAFC has generated a soybean mutant population consisting of approximately 5,000 lines to develop novel genetic resistance to Soybean Mosaic Virus, and has identified two essential soybean genes required for Soybean Mosaic Virus infection. To further this work, AAFC has proposed this new project to screen the existing mutant population for Soybean Mosaic Virus resistance by the genomic approach.

As of February 2016, AAFC has screened over 1,500 mutant lines for Soybean Mosaic Virus resistance by mechanical inoculation of Soybean Mosaic Virus endemic in Ontario. The team of researchers has identified two lines showing hypersensitive response and nine lines displaying resistance to Soybean Mosaic Virus. The next step will be to test if the resistance is stably inheritable to next generation.

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 Genome Canada funded project, Fast Tests for Rating and Amelioration of Conifers (FastTRAC). This work integrates end-users to maximize the successful transfer and uptake of the genomic tools in an operational context. In 2015-2016, NRCan-CFS researchers completed the DNA extraction of both Norway and white spruce and the samples were sent for sequencing. The team also examined different tree compounds which may be involved in the tree's defense mechanisms against insect and pathogen attack.

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 our forests. Early detection and rapid responses are critical in preventing potential damage to our forests.

Traps are a common tool used to inventory forest insects, to facilitate management decisions and the subsequent implementation of management approaches. These traps are baited with special chemicals that attract and capture insects. Sorting and identifying insects captured in traps is a time consuming and costly process. In 2015-2016, a group of NRCan-CFS scientists started a project to develop metagenomics and bioinformatics tools to identify insects caught in traps, both faster and at a lower cost. The first milestone achieved involved processing and identifying field collected insects using traditional methods, such as a microscope and diagnostic keys, and generating DNA libraries of the identified species.

As mentioned above, traps are baited with special chemicals, often pheromones. Pheromones are chemicals released by one individual which when perceived by another of the same species, elicits a behavioural or physiological response. The identification of pheromones is a long process where odorant molecules are tested for their "attractiveness". NRCan-CFS researchers are using a non-traditional approach to determine which molecules are found to be "attractive" in key economically important insect pests, the brown spruce longhorned beetle and the emerald ash borer, by identifying the candidate proteins to which they bind.

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. A newly started project, which is complementary to the Genome Canada funded project, Protecting Canada's Forests against Invasive Alien Species by Next Generation Biosurveillance, will go beyond the development of genomic tools to distinguish between the different species. In 2015-16, DNA was extracted from eight populations of Asian Gypsy Moth from Russia and Asia to North America and by using SNPs, markers are being developed to identify geographic origin of unknown gypsy moths. This information is valuable in negotiating agreements with our trading partners.

Spruce budworm is considered by many to be one of the greatest insect threats to our forests. An outbreak is currently affecting large stands of forests in Quebec and it 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 use when making management decisions for this pest. Researchers at NRCan-CFS have processed close to 1000 spruce budworm samples from 20 sites, providing essential data towards an estimation of the spruce budworm population at time "0" which will in turn be used in the forecasting model.

Ash trees are at risk of disappearing from the landscape from Emerald Ash Borer attacks. Research continued at NRCan-CFS in the development of potential management tools against the insect. 2015-2016 saw the sequencing and assembly of the Emerald Ash Borer genome. Also, the team not only identified genes in ash trees that are associated with the presence of Emerald Ash Borer but also in the insect, two digestive enzymes that are involved in host exploitation and could be used to control larvae.

Prevention is the best strategy for forest health. NRCan-CFS scientists continued to collect genomic information on pathogens and insects that may have deleterious impacts on Canadian forests. The project is developing tools that can be used to 1) certify plant and tree material as being free of unwanted pathogens; and 2) monitor potential invasive species in Canada. The research on pathogens supported by GRDI funds is complementary to the Genome Canada funded project, Protecting Canada's Forests against Invasive Alien Species by Next Generation Biosurveillance.

Trees that are resistant to white pine blister rust are integral in restoring pines on the North American landscape. NRCan-CFS scientists are furthering our understanding of resistance mechanisms in western white pine, limber pine, whitebark pine and eastern white pine. Markers to be used in selecting trees that are resistant to white pine blister rust are being transferred to breeding programs for field trials and validation.

The fungus-like pathogens known as *Phytophthora* are a phytosanitary concern for both Canada and our 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, important information when testing the efficacy of novel wood treatments.

Improving land reclamation following oil sands mining

The project started in 2014-2015 examining the dynamics of tree and plant community establishment on oil sand mined sites continued. DNA metabarcoding of soil samples from disturbed, reclaimed and natural sites was completed. Differences in microorganism communities show that sites reclaimed with peat moss show lower levels of certain organisms important for sustainable tree development.

Ecosystem integrity in forest management

A new project was initiated to develop metagenomics tools that assess ecosystem integrity and the sustainability of forest management practices. In 2015-2016 NRCan-CFS scientists began building invertebrate gene libraries for key forest soil species from a site where forest biomass is being removed for bioenergy. The other site, a riparian zone, was characterized and microbial DNA was extracted from the aquatic samples. Community analyses of the microbes are underway.

Genomics knowledge and advice for the management of fisheries and oceans

For Phase VI of the GRDI, ten genomics research projects are funded at DFO, seven of which are multiple year ventures with ongoing investigations into the 2015-2016 year that continued to: increase capacity for generating genome wide data of Sea Scallops and Green Crab to directly address management and conservation needs; provide a rapid and cost effective solution for salmon species identification, information for stock specific exploitation, and stock identification all in a single accessible test; 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; analyze the level of straying and introgression from Chinook Salmon enhancement facilities into surrounding wild spawning habitats; and produce a predictive "FIT-CHIP" tool to assess a variety of external stressors, pre-existing conditional states and important physiological impacts on salmon stocks.

Examples of the emerging results and outcomes of DFO's genomics research projects from the previous GRDI phase include the following:

A genomics approach to measuring Atlantic Cod population structure and its relationship with Marine Protected Area effectiveness

The Gilbert Bay Atlantic Cod population, which is safeguarded by a Marine Protected Area, has excessively high genetic variation (a well-known indicator of a healthy population) in comparison to fish from the offshore Labrador and the Newfoundland shelf. Telemetry results have shown that Gilbert Bay cod migrate outside the Marine Protected Area and mix with other Atlantic Cod. However, the extent of mixing between Gilbert Bay cod and other cod is unknown. A spatial survey using a genomics approach was conducted in order to quantify the extent of diversity among those populations. Identification of Gilbert Bay cod from other Atlantic Cod caught commercially demonstrated the usefulness of genomic tools in conservation and resource management. Predicting the behaviour pattern (Gilbert Bay cod are believed to return to a specific location in Gilbert Bay to overwinter) of individuals genetically and then testing these predictions using acoustic telemetry served to improve the value of management advice from genetic and telemetric tools.

Stock delineation of Redfish in the Northwest Atlantic

The geographic distribution of Deepwater Redfish (*Sebastes mentella*) is essentially continuous across the North Atlantic. Therefore, sustainable management of this resource demands a good understanding of the population structure not only within Canadian waters, but also across the North Atlantic. Using genetic and shape analysis of archived otoliths from Redfish caught in the Northwest Atlantic, this project described the genetic structure of the Redfish stocks straddling the North Atlantic Fisheries Organization and the North East Atlantic Fisheries Commission management areas, providing in-depth species and population identification. This helped to determine the connectivity of Canadian Redfish stocks from the Labrador Sea and Newfoundland's Grand Banks with

those in the Irminger Sea and western Greenland, as well as with Redfish from Davis Strait and Flemish Cap. A precise description of the stock that lies within Canada's harvestable waters will ensure sustainable exploitation of one of the most lucrative groundfish fisheries in Atlantic Canada.

Genomics study of the role of Infectious Hematopoietic Necrosis Virus infection in Sockeye Salmon populations

Sockeye Salmon is arguably the most iconic of the Pacific salmonids and one of the most famous Sockeye runs is the Fraser River which at times has seen returns of up to 30 million fish. However, this run has experienced declines in productivity since the 1990s and disease has been identified among a list of factors that may be responsible. Amongst many known sockeye pathogens, infectious hematopoietic necrosis virus (IHNV) is recognized as a lethal contagion but key questions remain about IHNV regarding the origins, transmission and impact of the virus across salmonid species and stocks. To start answering these questions, researchers developed a new, highly sensitive IHNV diagnostic tool which was used to track the presence of IHNV in Sockeye Salmon after being exposed to the virus. This led to the discovery that a small percentage of those fish surviving IHN virus exposure still showed the presence of the virus despite the absence of disease. It was found that these persistent virus infections were linked to a unique brain profile that suggested an ongoing adaptive immune response. The capacity of IHNV to reside in hosts that show no symptoms supports a virus carrier hypothesis and if proven infectious, could have significant consequences towards maintaining and spreading IHNV among susceptible hosts, bringing the potential for deleterious effects on Sockeye Salmon populations with it. Improved understanding of the virus' action and responses within a Sockeye host will better enable a comprehensive management approach and securing Sockeye stocks for future generations.

Arctic fish genomics as 'sentinels' of ecosystem integrity and change

Many northern fish species, particularly chars and whitefishes, support large freshwater and coastal aboriginal subsistence fisheries in the western Arctic. Other fish species are valuable components of the food web and sustain other larger animals, including seals and beluga whales. These fish species are adapted to Arctic environments and are vulnerable to man-made stressors such as climate change. Unfortunately, climate change also raises the risk of colonization of Arctic habitats by sub-Arctic species. Colonizers potentially affect resident species through hybridization, direct competition or predation, disease and parasite introductions. The genomics focus in this project was on profiling key sentinel colonizer species like Bull Trout (as a sentinel fish species in the Mackenzie Valley), Pacific salmons (as sentinel colonizers of coastal Canadian Arctic rivers), and Pacific Cod (as a sentinel of Beaufort Sea ecosystem change). Profiling the genetic variety of these potential colonizers provided a baseline of their genetic makeup. When placed in the context of the diversity of Arctic species, potential hybridization with resident species was determined. The project also examined expectations regarding the potential source populations and consequences of their colonization of the area.

Investigations into climate induced selection and mixed stock genetics of Atlantic Salmon in the Northwest Atlantic

There is growing recognition that mortality during the marine stage in Atlantic Salmon represents a dominant cause of declines in salmon abundance. Sources of this mortality include those associated with climatic variation as well as exploitation due to subsistence harvests. In fact, a majority of salmon populations in the northwest Atlantic are now threatened or at risk of extinction and estimates of the impact of climate change and subsistence harvests are central to rebuilding and recovery strategies. By identifying genes associated with climate change and genetic adaptation in Atlantic Salmon, this work provided an opportunity to discover the overall role of climate change in the decline of Atlantic Salmon, the strength of genetic selection and potential to adapt to the impacts of climate change on salmon health (heat tolerance in particular). This project also helped to quantify the exploitation of specific populations in the subsistence harvests of Atlantic Salmon in the northwest Atlantic. The combination of precise molecular markers with specific statistical approaches provided a unique opportunity to explore catch composition, movements, and mortality of Atlantic Salmon in Canadian waters.

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

In 2015-2016, ECCC developed genomics tools and approaches to support pollution prevention, regulatory compliance and enforcement, wildlife management, and risk assessment of potentially toxic substances. This was achieved by building environmental genomics capacity based on the four priority research areas 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 were developed 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. In particular, related research focused on assessing the effects of exposure to chemicals of concern (including polycyclic aromatic hydrocarbons and organic flame retardants) in avian, mammalian and aquatic species. Better understanding the molecular mode of action of chemicals significantly enhances the accuracy of models that contribute to improved risk assessment.

Environmental monitoring

ECCC continued to focus its R&D activities on understanding and monitoring aquatic and land-based ecosystems. For example, research focused on increasing the understanding of the effects of metals (including chromate and copper) on fish species living in recipient waters downstream of mining and smelting activities. In the Great Lakes, DNA barcoding is being applied to monitor algal and bacterial community compositions for harmful blooms, while metagenomics is being evaluated for its ability to assess and enhance water quality monitoring programs by providing microbial source tracking. 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, ECCC scientists are using genomics to study the contemporary genetic structure of polar bear populations in order to support the management of populations and to identify populations possessing unique adaptive genetic variations. Population genetic variation was also examined using genomic tools to define population units of priority seabirds, including Northern Gannets and Razorbills in Atlantic Canada, where natural resource development is occurring. These efforts will support the management of wildlife species and increase our understanding of how populations adapts to changes in their environment.

Compliance and enforcement

Environment Canada's scientists developed various innovative methods and tools to support the compliance and enforcement of regulations to conserve and protect the environment from pollution and threats. R&D activities focused on the operationalization of DNA-based bioassessments to ensure data quality and control for regulatory monitoring programs. DNA sequencing of iconic Canadian species, including polar bears, was also undertaken this year to support ECCC's regulatory enforcement mandate. These efforts will ensure that genomics deliver accurate and reliable results that can be used to protect Canada's environment and wildlife from pollution, wildlife trafficking and other threats.

Using genomics for food safety, animal health and plant protection

Characterizing food-borne pathogens through the creation of genomics databases

This project aims to develop genomics databases of known foodborne pathogens to enable CFIA's highly responsive, risk-based food inspection system. In the second year of this project, more the 1,683 pathogens including strains of *Salmonella, Listeria, Escherichia coli, Shigella, Staphylococcus* and infectious bacteria related to foodborne illnesses have been fully sequenced and added to the regulatory genomics database. This project has also: sequenced 172 metagenome samples including beef, pork and produce; developed a pipeline for rapid quality assessment; and curated the collection to ensure the highest data reliability.

Strengthening animal health diagnostic tools

The creation of a genetics reference library for viral pathogens such as bovine viruses will support novel diagnostic tools that can be used for the rapid detection and identification of high priority animal viruses. The recent development of new methods for whole genome sequencing (WGS) has supported the CFIA's National Centre for Foreign Animal Disease response capacity with the detection of pathogens. The establishment of in vivo cloning of a target gene was a key accomplishment. Bioinformatics training was also completed for molecular epidemiology investigations. The CFIA acquired new information on the evolution of *Mycobacterium bovis* strains from the WGS genotyping of 58 Canadian M. bovis, which will serve to better protect wildlife reservoirs in various Canadian and North American areas. This project has also sequenced the full genomes of 33 avian swine influenza virus isolates to support traditional diagnostic tests, and developed protocols for Bluetongue Virus, Foot and Mouth Disease Virus, and Seneca Valley Virus, along with other high priority viruses.

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

The CFIA is developing capacity for DNA barcoding and Next Generation Sequencing to enhance CFIA regulatory plant health responsibilities in the areas of detection and identification of invasive plants, regulated plant pests and pathogens, and plants with novel traits. Researchers have acquired materials and reagents as planned and appropriate samples and bioinformatics tools are being used to create sequencing data storage. Plant with Novel Trait mapping and junction analysis were conducted and metagenomic sequencing data from spore and insect traps were analysed for the detection of potential forest invasive alien species. The development of new tools and field protocols has assisted in the detection and genotyping of target organisms such as viruses, insects, and Plants with Novel Traits.

Development of genomics and bioinformatics tools

The overarching goal of this project is to harmonize genomics activities across CFIA's three business lines. CFIA's labs have collectively demonstrated success with the HiSeq 2500 instrument and have developed a process for sequence-independent amplification and a pipeline using CLC Genomic Workbench to process data. Recent developments include improvements to the Virtool to provide a more malleable workflow, and steps towards its implementation. This project is focused on using novel RNA sequencing technologies to detect, identify and characterize RNA viruses in their various hosts. The activities completed to date will contribute to the improved transfer of technology and tools between CFIA business lines and increased accessibility to genomics tools for CFIA scientists.

Annex 4 – Research tools and processes produced by the GRDI

Research tools

- SNVPhyl pipeline for genomic epidemiology, regulatory, research, public health and outbreak investigations (FWS);
- Neptune Pipeline for target signature identification and diagnosis (FWS);
- The Salmonella In Silico Typing Resource (SISTR) (FWS);
- Molecular detection assays for tree pathogens of Canadian importance (QIS);
- Generation of a positive control for assay development through the generation of DNA of a rust pathogen of sugarcane *Puccinia melanocephala* (QIS);
- Sequence motifs for cyptic species within three anisakid nematode genera (*Aniskais, Pseudoterranova, Contracacecum*) (QIS);
- New set of primers and optimized PCR conditions for invasive eel swimbladder nematode (*Anguillicola*) (QIS);
- Mitochondrial marker capable of species identification and phylogenetic inference of Gyrodactylidae (QIS);
- Taxonomic framework allowing for the coupling of biodiversity assessments (QIS);
- Sets of primers and probes for specific detection of 13 aquatic invasive freshwater finfish (QIS);
- A series of assays capable of detecting and quantifying phytoplasma in plan and insect samples, including qPCR/ddPCR, Luminex and LAMP assays (QIS);
- Pipeline for the characterization of known invasive species as well as genes involved in the synthesis of several cyanotoxins (*sry, aoa, mcy, stx gene clusters*) (QIS);
- VirTool: workflow for plant virus detection of known virus species (QIS);
- NuVs: workflow for novel plant virus detection (QIS);
- Identifying homozygous lines that allow the capture of meristem, guard cell and stress responding cells using INTACT technology (AAFC);
- Custom bioinformatics tools have been developed and can be implemented into analyses pipelines (AAFC);
- Bioinformatics tools have been developed to allow the efficient analysis of sequence data derived from RNA-seq, ncRNA-seq, Bisulfite-seq, MNase-seq and ChIP-seq;
- Develop Automated Oligonucleotide Design Pipeline and Oligo-Fishing Pipeline for accurate recognition of DNA signatures for multiple regulated pathogens in NGS metagenomic data (AAFC);
- Screened over 1,500 mutant lines for Soybean Mosaic Virus resistance by mechanical inoculation of Soybean Mosaic Virus endemic in Ontario (AAFC);
- Four new plant transformation constructs generated expressing two alternative gRNAs targeting either the camelina or Arabidopsis herbicide pathway gene (AAFC);
- PacBio long read sequencing data to complement Illumina sequencing data (AAFC);
- Several plant transformation vectors with novel gene expression and selection components (AAFC);
- *Mycobacterium bovis* whole genome sequence assembly and phylogenetic tree construction (CFIA);
- Comparative genomics and bioinformatics analysis of the whole genome sequences of *M. bovis* and *Brucella abortus* to identify ORFs coding for potential diagnostic antigens (CFIA);
- High throughput cloning of all the identified ORFs (up to 1000 ORFs per species) into the pIVEX2.3d or pIVEX2.4d vector (CFIA);
- *In vitro* transcription/ translation of all identified ORFs for the high throughput production of recombinant proteins (CFIA);

- Optimisation of a Next Generation Sequencing technology for the detection/identification of mixed seed species (CFIA);
- Establishing and Optimisation of a Next Generation Sequencing technology for the detection/identification of potato viral and bacterial species (CFIA);
- 220K array Atlantic salmon SNP data for Labrador and Maritimes: baseline data for stock and population identification (DFO);
- GENEPOPEDIT: R package for the manipulation of large Atlantic Salmon SNP datasets (DFO);
- Atlantic salmon SNP panel: Optimized panel of SNP-type assays for 144 Atlantic salmon SNPs (DFO);
- Parallel_Newhybrids: R package for efficient parallel identification of Atlantic Salmon hybrids and hybrid classes (DFO);
- HYBRID_DETECTIVE: R package for the statistical treatment of Atlantic Salmon hybrid identification, simulation of hybrids, estimates accuracy and efficiency of putative panels, and determines the hybrid origin of experimental data (DFO);
- Wild vs Farm baseline samples: Baseline SNP allele frequencies for wild and farmed Atlantic salmon from both Newfoundland and Maritimes (DFO);
- Green crab SNP panel: Optimized panel of SNP-type assays for 96 green crab SNPs (DFO);
- Scallop SNP-type assays: Over 96 scallop working SNP-type assays (DFO);
- A new SNP-based tool for the genotyping of Sebastes species: designed for analysing SNPs associated with RADseq (DFO);
- A high throughput microbe monitoring platform, containing 45 microbes known or suspected to cause disease in salmon (DFO);
- Validation of molecular assays for genes most highly associated with a mortality related signature (associated with poor migratory survival in some sockeye salmon stocks) (DFO) ;
- First Fit Chip with salmon microbes and diverse immune-related genes (DFO);
- Mini-rotating annular reactors for controlled exposure and growth of microbial communities (ECCC);
- Developed eDNA sequencing and data analysis pipeline with collaborator at the University of Guelph as an additional tool to get more source tracking information out of water samples (ECCC);
- New pipeline for extraction, processing, sequencing and analysis of DNA sequences using DNA metabarcoding for use in biomonitoring applications (ECCC);
- RAD sequencing library for gannets species (ECCC);
- US patent for the STEAMER virus to market for the detection of steamer in soft cell clams (ECCC);
- Genomics and proteomic tools for regulators to identify immune pathway biomarkers related to chemical immunosuppression and/or allergy (HC);
- Assay for regulators to screen chemical food additives and contaminants for their ability to activate the immune system and increase the risk of food allergies (HC);
- Screening method for regulators to detect and identify microRNA changes in tissue exposed to fungal toxins and anthropogenic chemicals (HC);
- Adverse Outcome Pathway mapping the toxicity pathways for lung fibrosis induced by nanomaterials to support human health risk assessment (HC);
- Data analysis tools and bioinformatics algorithms for regulators to screen nanomaterials with the potential to induce lung disease (HC);
- Software to analyze genetic material (HC);
- 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);
- Data and bioinformatics algorithms for predicting lung disease induced by nanomaterials (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 integration with multiple platforms and cell lines for human health risk assessment (HC);
- BMDExpress Data Viewer: toxicogenomics tool which works with an open source software (http://sourceforge.net/projects/bmdexpress/) to visualize the dose-response change in tissues for human health risk assessment of chemicals (HC);
- High-Throughput Genotyping platform for wheat capable of simultaneously profiling 24 SNP markers thereby reducing overall cost per marker compared to the standard method (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 drought response in wheat were identified which confer drought tolerance in wheat (NRC);
- Gene targets for photosynthetic efficiency in wheat were identified and showed improved efficiency in greenhouse conditions (NRC);
- Gene expression atlas for wheat seed development (NRC);
- Galaxy Bioinformatics platform for wheat sequence data analysis (NRC);
- Asian Gypsy Moth detection assays (NRCan);
- TreeTaggr, Twitter based application to report the presence of tree pests such as Emerald Ash Borer (NRCan);
- Enhanced SISTR: (http://lfz.corefacility.ca/sistr-app) a bioinformatics resource for multiple rapid Salmonella subtyping (PHAC);
- Enhanced Panseq: (http://lfz.corefacility.ca/panseq) for the pan-genomic analyses of closed and draft genomic sequences (PHAC);
- Enhanced SuperPhy: (http://lfz.corefacility.ca/) for epidemiological and comparative inquiries by users with and without bioinformatics training (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* (PHAC);
- An on-line 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);
- Illumina MiSeq next gen 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);
- EpiQuant server developed to compare the strength of epidemiological and genetic relationships between bacterial isolates (PHAC);
- WGS pipeline for *Neisseria meningitidis* draft genome data (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

- Optimisation of retron gene targeting technology (AAFC);
- Development of high quality DNA that enable us to obtain PacBio and Illumina Pair Mates sequencing information (AAFC);
- Improvement of standard DNA extraction protocol for Pst (AAFC);
- Validation the in silico RGAs for important wheat diseases, such as yellow/leaf/stem rusts and Fusarium Head Blight (AAFC);
- Optimization of membrane protein purification methods (AAFC);
- Developed methods for the analysis of soybean plants infected with four different root rot diseases (AAFC);
- Determination of efficiency of Systemic Gene Silencing for High-throughput screening (AAFC);
- High-throughput sequence analysis (AAFC);
- High-throughput functional assay system (AAFC);
- Integrated Rule-Oriented Data-management System (iRODS) (AAFC);
- *In silico* RGA identification and comparative genome analysis (AAFC);
- Next generation sequencing methods (AAFC);
- Plant gene silencing: methods and protocols (AAFC);
- Systems to modulate meiotic recombination frequency (AAFC);
- WGS-based high-resolution genotyping of highly clonal Canadian strains of *M. bovis* (CFIA);
- Protocols for amplification, sequencing, sequence assembly and analysis of Chiropteran disease reservoirs (CFIA);
- Metagenomic and genomic analysis of plant pathogens using next generation
- Sequencing and development of detection assay for detection and identification (CFIA);
- Fusion primers sequenced developed were transferred to a AAFC lab with a research agreement (CFIA);
- Developed bioinformatics pipeline using well-established tools for junction analysis in transgenic plants (CFIA);
- A unique R-scripted bioinformatic pipeline to discover and validate biomarkers associated with stressors across multiple microarray studies (DFO);
- Mapping of 5 salmon microarray platforms to the Atlantic Salmon genome (cGRASP 16K and 32K, Koop 44K, Traits, SIQ) (DFO);
- Targeted enrichment with Agilent SureSelect to resequence portions of genes represented by probes on different microarry platforms (DFO);
- Identification of 158 genes highly associated with smoltification processes across species and study systems (DFO);
- Identification of 139 genes highly associated with thermal response and tolerance across species and study systems (DFO);
- Identification of 40 of genes predictive of salmon morbidity (emminent mortality) (DFO);
- Optimized protocols for the sequencing of complete narwhal mitogenomes using Ion Torrent next generation sequencing (DFO);
- Assignment of hatchery Chinook and Coho Salmon to parental broodstock to provide stock (hatchry) origin and age of fish (DFO);
- NGS applications in ecotoxicological studies applying microbial community end points, isolation of mRNA from complex environmental samples (ECCC);
- Scoping of DNA sequence library (cytochrome oxidase gene regions) specifically relating to macroinvertebrate species commonly encountered in routine biomonitoring samples across Canada (ECCC);
- Interrogation of major gene sequence repositories (GenBank, Barcode of Life Database) to quantify the occurrence and quality of deposited sequences, as a backbone for future widespread use of DNA metabarcoding in CABIN biomonitoring studies (ECCC);
- RT-qPCR method for detecting murine spike-in virus in sewage samples (ECCC);
- Animal model and assay protocols to analyze the immune response and adverse reactions resulting from the exposure to the Respiratory Syncytial Virus (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);
- DNA extraction protocols for spore on silicone-coated rods (NRCan);
- Validated Standard Operating Procedure for the detection of botulinum neurotoxin activity by an endopeptidase-MALDI-TOF mass spectrometry assay ("Endopep MS" assay) (PHAC);
- 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*.
- Typing and tracking of *N. gonorrhoeae* via in silico antibiogram (PHAC);
- A pipeline for the isolation, library construction, WGS generation, and SNP analysis for use during a hospital outbreak 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);
- 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);
- 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 validated pipeline for pre-processing of WGS data; a process that allows users to take raw sequencing reads and perform QC, assembly, gene prediction and annotation of WGS data in order to prepare it for downstream analyses (PHAC);
- *Salmonella* and *Campylobacter* cgMLST pipelines that allow for rapid phylogenetic analysis of draft WGS assemblies and rapid assessment of the quality of these assemblies (PHAC);
- Analytical process for the identification of non-vertical genes (horizontally acquired by homologous recombination) (PHAC); and
- A set of methods (and method guidance) to optimize the extraction, preparation, analysis of DNA from a newly emerged pathogen towards its identification (PHAC).

APPENDIX B

Genomics R&D Initiative: Performance Measurement Framework Overview

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

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

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

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

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

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

The GRDI comprises three important program elements:

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

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

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

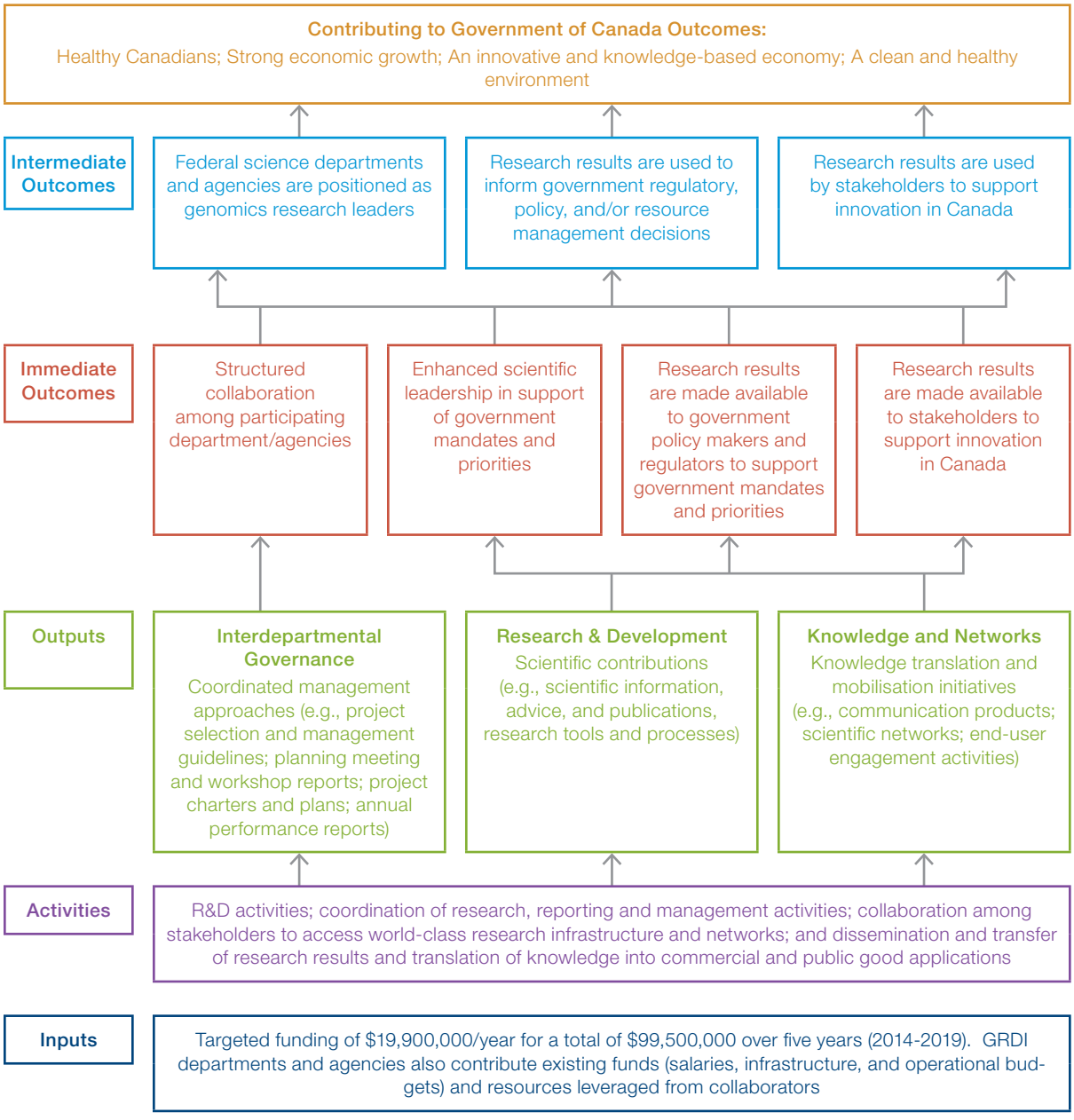

Table 1: Program Performance Measurement Strategy Framework

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 interde-partmental 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
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

Outputs (continued)						
Area	**Indicator**	**Methodology/ Source**	**Frequency**	**Target[1]**	**Date to achieve target**	**Responsibility**
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 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

Immediate Outcomes (continued)						
Area	**Indicator**	**Methodology/ Source**	**Frequency**	**Target[1]**	**Date to achieve target**	**Responsibility**
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.