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GENOMICS R&D INITIATIVE

ANNUAL PERFORMANCE REPORT 2014-2015



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.

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EXECUTIVE SUMMARY

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

The Initiative has advanced significantly in the delivery of its overarching goal to apply high quality, genomicsbased 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 2014-2015 was the first year of Phase VI of the GRDI. The Initiative continued to support mandated research in participating departments as well as a model of structured collaboration supporting two 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; and 2) Protection of Canadian Biodiversity and Trade from the Impacts of Global Change through Improved Ability to Monitor Invasive Alien and Quarantine Species.

Considerable progress was achieved in 2014-2015, exemplified by the following highlights:

- A second generation microfluidic-based detection platform for food and water-borne pathogens was deployed in a front-line Canadian Food Inspection Agency (CFIA) regulatory testing laboratory. This system offers an 18 min turnaround time for the detection and identification of E. coli O157:H7 marker genes;
- An alpha version of a bioinformatics platform called IRIDA (Integrated Rapid Infectious Disease Analysis) was released to collaborators for storing, managing and sharing whole genome sequence data of pathogens;
- A molecular test for the highly disruptive Zebra Mussel has been developed, effectively increasing the window of opportunity for remedial actions to help reduce the severe economic and ecosystem consequences of this invasive species;
- A panel of primers that target specific DNA fragments has now been developed for Chinook Salmon. This will allow a wide array of stock identification applications, ensuring the sustainable harvest of one of the most valuable salmon species in Canada.

This Annual Performance Report for 2014-2015 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 2014-2015 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 2014-2015.

ACRONYMS

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AAFC	Agriculture and Agri-Food Canada	NEAFC	North East Atlantic
ADM	Assistant Deputy Minister		Fisheries Commission
ADM CC	ADM Coordinating Committee	NGS	Next Generation Sequencing
AMR	Antimicrobial resistance	NRC	National Research Council Canada
CFIA	Canadian Food Inspection Agency	NRCan	Natural Resources Canada
CHO	Chinese hamster ovary	OECD	Organization for Economic Cooperation and Development
CNISP	Canadian Nosocomial Infection Surveillance Program	PASKAL	Plant Abiotic Stress Knowledge
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats	PCR	Polymerase Chain Reaction
DFO	Fisheries and Oceans Canada	PHAC	Public Health Agency of Canada
DNA	Deoxyribonucleic Acid	PPEQ	Potato Post Entry Quarantine program
EC	Environment Canada	019	Quarantine and Invasive Species
eDNA	environmental DNA	aPCB	
FTE	Full Time Equivalent		Research and development
FWS	Food and Water Safety		
GRDI	Genomics Research and Development Initiative	RAD-seq	DNA Sequencing
нс	Health Canada	RNA	Ribonucleic Acid
HIV	Human Immunodeficiency Virus	S&T	Science and Technology
		SE	Salmonella Enteritidis
	Necrosis Virus	SNP	Single Nucleotide Polymorphism
ISO	International Organization for	SOPs	Standard Operating Procedures
	Standardization	STAGE	Strategic Technology Applications
IRIDA	Analysis	USDA	United States Department
MALDI-TOF MS	Matrix-Assisted Laser Desorption/		of Agriculture
	Ionization Time-of-Flight Mass	VTEC	Verotoxigenic Escherichia coli
	Spectrometry	WG	Working Group
MIKNA		WHO	World Health Organisation
NAFO	North Atlantic Fisheries Organization		

GENOMICS R&D INITIATIVE – PROFILE

The GRDI was initiated 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 Canada (EC); Fisheries and Oceans Canada (DFO); Health Canada (HC); Public Health Agency of Canada (PHAC); National Research Council Canada (NRC); and Natural Resources Canada (NRCan).

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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 (2008-2011) and V (2011-2014); and \$99.5M for Phase VI (2014-2019). Phase V of the GRDI (2011-2014) introduced a model that mobilized resources for concerted research on issues that are beyond the mandates of single departments, supporting highly coordinated interdepartmental projects along shared priorities and common goals. Two 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 continue 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 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 2014-2015 in support of GRDI projects, and demonstrates that non-GRDI funds represented almost twice the GRDI investments. Additional in kind investments included the sharing of technology platforms, materials, and expertise with a variety of collaborators in research areas that cut across traditional departmental sectors.

Table 2: Overall Investment in support of GRDI projects in 2014-2015 (\$000)

DEPARTMENT/AGENCY	GRDI	NON-GRDI*	TOTAL
National Research Council Canada	4,440	8,247	12,687
Agriculture and Agri-Food Canada	4,440	9,249	13,689
Health Canada	1,600	4,228	5,828
Public Health Agency of Canada	1,600	1.472	3.072
Natural Resources Canada	1,600	3,076	4,676
Environment Canada	800	1,987	2,787
Fisheries and Oceans Canada	720	808	1,528
Canadian Food Inspection Agency	720	1,488	2,208
SHARED PRIORITY PROJECT	GRDI	NON-GRDI	TOTAL
Quarantine and Invasive Species	1,910	3,062	4,972
Food and Water Safety	1,842	3,773	5,615
Coordination and Common Functions	228	42	270
Total	19,900	37,432	57,332

* 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 2014-2015:

- 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 infectious and chronic 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, enhancing the resiliency of Canada's crop production in the face of potentially catastrophic abiotic and biotic stresses and to maximize profitability for the sector; 2) Bioinformatics and physical tools: ensuring that scientists can maximize the opportunities presented by genomics-based research (e.g. 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 (e.g. disease resistance).

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.

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 Canada

Environment 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 support chemical and biological risk assessment; 2) Wildlife conservation: to support the management of species at risk and risk to flora and fauna; 3) Environmental monitoring: to develop indicators of ecosystem health; and 4) Compliance and Enforcement: to support EC's Enforcement mandate. This work will enable the delivery of EC'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 Health Canada'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 2014-2015, 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 Natural Resources Canada 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 Quarantine and Invasive Species (QIS) project) will continue to 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, EC, 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 continue to 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, EC, 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 the 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: 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 rapid detection of food pathogens, plant pests and animal disease agents; which in turn will enhance CFIA's capabilities to respond effectively to regulatory needs in food safety, ensuring compliance and maintaining consumer confidence, as well as minimizing 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 EC 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, GRDI-funded activities at EC contribute to the monitoring and understanding of Canada's ecosystem, help to assess risks posed by chemical pollutants to wildlife and migratory birds, and deliver practical applications that support regulatory compliance as well as evidence-based decision-making related to risk mitigation and conservation efforts.

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

The Program Alignment Architecture of 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 Economic Competitiveness and to the Program Activity Economic Opportunities for Natural Resources. 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 leadingedge 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 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 2014-2015, the first year of Phase VI, including timely secretariat support to GRDI departments and agencies and the implementation of updated GRDI governance, management and operating processes for Phase VI. Three meetings of the ADM CC and eight meetings of the GRDI WG were held to allow for collaborative decisions. Leadership was provided to establish future strategic directions for Phase VI shared priority projects to be launched in April 2016.

The implementation of shared priority projects was supported: funding was made available to participating departments based on the approved Project Charters and bi-annual progress reports were presented to the ADM CC (June and November 2014). The principles of the Innovation Management Strategy for shared priority projects was endorsed by the ADM CC and associated Guidance documents were developed and reviewed by the WG. A community of practice of experts was formed 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 2013-2014, input into NRC's Departmental Performance Report and Report on Plans and Priorities, as well as the continued implementation of the Management Response and Action Plan to finalize implementation of all recommendations from the 2010 evaluation.

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

Both shared priority projects have detailed governance structures in their Project Charters to ensure seamless integration and clear roles and responsibilities. These include Management Advisory Committees, comprising senior managers from each of the participating departments and agencies, 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 decisionmaking fora. 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. Both projects will continue to be supported in the first two years of Phase VI of the GRDI (2014-2016).

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 2014-2015 and quantitative indicators for performance evaluation are enumerated in Annex 2 by department/agency for: scientific contributions (key 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 2014-2015 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:

 Patrice Bouchard (AAFC) was the recipient of the C. Gordon Hewitt Award. One award is given annually by the Entomological Society of Canada for an early career scientist for contributions to entomology;

Knowledge and Networks

- Ed Topp (AAFC) received the Water Environment Association of Ontario Exemplary Biosolids Management Award;
- Carole Yauk's team (HC) received the EMGS Emerging Science Award for Best Student Poster Prize at the Annual Meeting of the Genetic Toxicology Association, Newark, Delaware, US;
- Genevieve Bondy (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;
- Gary Van Domselaar and Charles Shepard (PHAC) received a Science Award Nomination for Best Paper presented by the US Centers for Disease Control and Prevention; and
- Gary Van Domselaar (PHAC) received the James H Nakano Citation for Best Paper presented by the US Centers for Disease Control and Prevention, National Center for Emerging and Zoonotic Infectious Diseases.

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 2014-2015 follow.

The FWS project provided training workshops on Unix and Microbial Whole-Genome Sequence Analysis to 22 Federal, Provincial, and Academic partners at the National Microbiology Laboratory in Winnipeg in May 2014. Its data analysis pipelines are being beta-tested off site at the BC Center for Disease Control and Simon Fraser University. 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 with collaborators from the USDA and 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. They are developing Standard Operating Procedures (SOPs) for NGS to be used in the Potato post entry quarantine program (PPEQ) for rapid detection, identification and characterization of plant viruses and that will be incorporated as CFIA Plant Health Diagnostics tools.

At Environment Canada, scientists participated in the Organization for Economic Co-Operation and Development (OECD) 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.

Health Canada's GRDI toxiogenomics research feeds into the US Environmental Protection Agency's Tox21/ToxCast program through a formal collaboration on a high-throughput genotox classification system, and an HC scientist serves as an expert advisor and co-author of the US EPA's NextGen report that supports the assessment of risks posed by environmental contaminants. In the context of emerging stem cell therapeutic treatments, outputs from GRDI funded research has led to the development of a new HC guidance document on the use of Cell Therapy Products in Clinical Trials. Furthermore, a lead HC scientist was invited to advise the Korean Food and Drug Administration on current Canadian regulations regarding the use of cell therapies in the clinic.

PHAC research projects are well networked to facilitate the translation of research 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. GRDI projects 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 the GRDI projects through the exchange of samples and knowledge; in addition, they facilitate the transfer of research outputs into practice. Internationally, PHAC GRDI projects are engaged with the World Health Organisation (WHO) 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 resistance human immunodeficiency virus. Work to enhance global surveillance of antibiotic resistance Gonorrhoea is also on-going in conjunction with WHO partners. GRDI supported researchers also collaborate with the Center for Disease Control, Atlanta, USA, to standardise detection technologies and to share approaches for the detection of emerging pathogens.

APPENDIX A- SUPPLEMENTAL PERFORMANCE DETAILS

Annex 1 – GRDI Projects and Funding Allocations from GRDI

GRDI FUNDS (\$) PROJECT TITLE

QUARANTINE AND	INVASIVE SPECIES									
1,909,593	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									
1,841,646	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										
88,000	Genome-wide mining and mapping of disease resistance genes - novel strategies to enhance wheat disease resistance breeding									
280,500	Using genomics to reduce fusarium diseases and mycotoxin hazards in Canadian grain									
82,500	Ethylene signalling and Fusarium Head Blight resistance in wheat									
125,000	Exploiting genomics to decipher hybrid vigour in Brassica napus									
140,000	Accessing adaptive ancestral avena alleles									
58,000	Using CRISPR to elucidate gene associated traits in wheat: Fusarium Head Blight resistance and yield capacity									
116,000	Genomics and genetics of Soybean Mosaic Virus-soybean interactions: next generation viral resistance									
33,630	Verification of plant defense genes against Sclerotinia sclerotiorum									
130,000	Effectors of Canadian Puccinia striiformis isolates									
32,000	Molecular tools for identification of stored-product insects and their symbionts for use in pest control.									
60,000	Cell-type specific chromatin dynamics in soybean hairy roots responding to water stress.									
159,998	Advanced genetic technologies for improvement of camelina and canola									
55,000	Mining legume genomes for attributes of sustainable nutrient (nitrogen) acquisition through symbiosis									
115,753	Exploiting wheat leaf rust fungus molecular resources to combat cereal rust diseases.									
63,200	Next-generation genomics for oat improvement									
2) Delivery of genor biological materia technologies	nics discoveries through bioinformatics and physical tools in order to improve access to both als and data sets, and to assist and accelerate the adoption and commercialization of new									
102,000	Development of genomics and bioinformatics tools enabling epigenetic analyses in oilseed crops									
102,000	Development of identification and analysis tools for amplicon-based metagenomics, focussing on high risk and regulated pathogens									
89,000	Exploring the applicability of new technologies and processes to the management and analysis of next generation sequencing data									

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3) Enhanced effici	iency of plant breeding
104,500	Development of genome editing technology in crop somatic cells using cell penetrating peptides
147,500	Process for making transplastomic cell and plant lines - tool for new trait development
172,000	Effector-based breeding tools and Quantitative Trait Locus discovery for management of root rot rot in soybean caused by <i>Phytophthora sojae</i>
38,360	Managing crop reproduction
63,200	Next-generation genomics for oat improvement
CANADIAN FOOD	INSPECTION AGENCY
70,000	Application of whole genome sequencing for molecular epidemiological investigations of bovine tuberculosis in Canada and for the high throughput discovery of novel diagnostic antigens for <i>Mycobacterium bovis</i> and <i>Brucella abortus</i>
130,000	Enhancing the CFIA's genomic capabilities for detection and characterization of high consequence known and unknown/unexpected animal viruses and their vectors/reservoirs
200,000	Whole genome sequencing technologies as tools for the detection, isolation, identification and characterization of pathogens in support of Canadian food inspection objectives
200,000	Detection and identification of plant pests and plants with novel traits using next generation sequencing
50,000	Development of diagnostic sequencing methods to monitor, detect and characterize RNA viruses of food, animals and plants, following viral contamination or infection
70,000	Development of infrastructure and bioinformatics tools to support genomics activities in CFIA's food, plant and animal business lines
ENVIRONMENT C	ANADA
33,250	Incorporating wood frog toxicogenomics into the adverse outcome pathways for environmental effects monitoring of oil sands industrial development and for regulatory activities
37,625	Avian toxicogenomics and adverse outcome pathways - new tools for risk assessment
73,938	Genomics research in support of <i>Canadian Environmental Protection Act</i> risk assessment for existing and new microbial substances
35,875	Molecular markers of exposure to parental and alkylated polycyclic aromatic hydrocarbons in birds and mammals
26,250	Population genetic structure of Canadian seabirds
78,750	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
61,250	Transcriptomic analyses of the ecotoxicological effects of nanomaterials on microorganisms
64,313	Assessing impacts of emerging contaminants in aquatic organisms using high resolution genomics
39,375	Multidisciplinary Rapid Assessment indicator of algal and bacterial community composition and harmful blooms
26,250	Aquatic ecotoxicogenomics of emerging contaminants: pharmaceutical, personal care products and algal toxins
87,500	Genomics to support effects based monitoring in the Ring of Fire
43,750	Application of genomics tools to identify fecal pollution source contaminating freshwater and marine ecosystems
51,800	Forensic DNA identification of iconic Canadian species
47,250	Analysis of Norovirus in sanitary effluents
52,176	Aligning and operationalising DNA-based bioassessment for regulatory monitoring of ecosystems
22,590	Integrating emerging genomic technologies into environmental protection and conservation

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FISHERIES AND OC	EANS CANADA
9,100	Rapid genomic screening for Atlantic Salmon aquaculture escapees and hybrids using Restriction Site Associated DNA Sequencing (RAD-seq) and a high throughput nanofluidic dynamic array
78,000	Genomic tools for salmon enhancement
36,800	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
56,000	Stock delineation of narwhals (<i>Monodon monceros</i>) from Baffin Bay and adjacent areas using novel genetic markers developed from genomic techniques
75,900	Assessing the spatial scale of dispersal and connectivity in non-indigenous Green Crab (<i>Carcinus maenas</i>) and commercial Sea Scallop (<i>Placopecten magellanicus</i>) in Canadian waters using RAD-seq and high throughput SNP genotyping
121,800	Bioinformatic support to develop "FIT-CHIP" for industry and salmon management applications
77,800	Integrating neutral and adaptive genetic information for addressing knowledge gap in redfish (<i>Sebastes</i> spp) population structure and its underlying mechanisms in Atlantic Canada: a genomic genotyping-by-sequencing approach of SNPs polymorphism
124,200	Parental-base tagging of chinook salmon
86,000	Detecting colonizing aquatic organisms using environmental DNA (eDNA) techniques
53,000	Discriminating capelin populations on the Northwest Atlantic: generational effects
HEALTH CANADA	
152,000	Application of an adjuvanticity assay to assess the effects of food chemicals of regulatory concern on the immune transcriptome
51,000	Safety of prebiotics in infants
75,000	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
210,000	Systems biology informed structure-activity-relationships to predict pulmonary pathology induced by nanomaterials
192,000	An integrated systems biology approach to investigate immunopotentiation induced by Respiratory Syncytial Virus vaccines
327,000	The coming revolution: next generation sequencing detection of de novo mutations in the offspring to identify germ cell hazards
243,000	Identification of biomarkers for the standardization and risk assessment analysis of mesenchymal stem cell based health products
200,000	Development of genomics biomarker to provide mechanistic context and data in support of human relevance for chemicals inducing cellular stress responses
NATIONAL RESEAR	CH 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

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NATURAL RESOUR	RCES CANADA
69,031	Economic application for genomics R&D
150,948	Spruce Budworm eco-genomics: from population dynamics to population suppression
95,723	HApInomics: Host, Agrilus planipennis Integrative Genomics
195,127	Genomics-enhanced next generation forest disease diagnostic and monitoring
202,491	Applied genomics for tree breeding and forest health
48,782	Development of molecular tools to detect living fungi and fungus-like organisms of phytosanitary concern in wood
67,742	Genomic selection of disease resistance to White Pine Blister Rust in native Canadian white pine species
58,906	Toward predictive detection molecular assays for exotic pathogens – mining genomes of fungal pathogens for a signature of tree host affinity
75,198	Innovative land reclamation approaches in the oil sand sector: improving phytoremediation emphasizing tree-soil microbes mutual interactions
PUBLIC HEALTH A	GENCY OF CANADA
125,000	MALDI-TOF MS Identification of bacteria: the establishment of a national MALDI database to support diagnostic laboratories across Canada
50,000	Country-wide application of mass-spectrometry-based H antigen typing for E. coli and Salmonella
64,500	International validation of standard operating procedures for mass spectral diagnostic analysis of high consequence toxins: <i>Botulinum</i> neurotoxins
150,000	BioTools for the predictive genomics of priority foodborne pathogens
25,000	Closing the gaps in national surveillance of <i>Clostridium difficile</i> : epidemiologic and genomic characterisation of community-onset and recurrent <i>C. difficile</i> infections
161,000	Single nucleotide variant subtyping of Salmonella Enteritidis and Salmonella Heidelberg
75,000	The identification of <i>Mycobacterium tuberculosis</i> specific RNA molecules: An approach to improve accuracy and utility of currently used assays for latent tuberculosis infection
80,000	Neisseria gonorrhoeae sequence typing for antimicrobial resistance: a novel sequence-based antimicrobial resistance typing scheme for tracking the global dissemination of <i>N. gonorrhoeae</i>
190,000	The use of whole genome sequence analysis to support healthcare-associated outbreaks of carbapenem-resistant <i>Enterobacteriaceae</i>
100,000	Transfer of the validated <i>Salmonella</i> genoserotyping array into a PHAC reference laboratory and piloting the technology into the National Microbiology Reference Laboratory and targeted provincial health laboratories
190,000	Validation of metagenomics as a boni 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
90,000	Whole genome sequencing of measles virus of an effective molecular surveillance during measles elimination
90,000	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
150,000	Translational analytic infrastructure for emerging pathogen discovery

* Non-pay operating expenditures only

Scientific Contributions

Scientific contributions include scientific information and publications produced, accepted, in press, or published (including online) in 2014-2015. 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 2014-2015. They do not include submitted papers or publications in draft form, nor contributions that were reported in previous years.

KEY SCIENTIFIC CONTRIBUTIONS												
	AAFC	CFIA	DFO	EC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL	
Publications in refereed journals	40	4	3	64	12	44	30	13	17	5	232	
Publications in refereed conference proceedings	16	3	0	0	0	0	2	13	9	0	43	
Books (edited, written) and book chapters	5	0	0	3	1	0	0	1	0	0	10	
Invited presentations	41	4	6	6	8	3	14	13	15	6	116	
International conference presentations	21	2	0	25	6	56	14	13	8	12	157	
Editorial posts for national and international journals (excludes peer reviewers)	0	4	0	2	2	0	4	2	1	0	15	
New genomics related databases or libraries	1	1	0	2	0	0	19	5	0	0	28	
Awards, prizes	1	0	0	2	3	0	0	0	3	2	11	
Total	125	18	9	104	32	103	83	60	53	25	612	

Key Scientific Contributions Demonstrating Leadership

Other Scientific Contributions

NUMBER OF OTHER SCIENTIFIC CONTRIBUTIONS												
	AAFC	CFIA	DFO	EC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL	
Technical reports	0	2	3	3	0	0	5	3	0	0	16	
Other publications (ex. abstracts, notes, industry magazines, etc.)	1	2	0	5	1	0	1	1	1	0	12	
Poster presentations at conferences	11	1	1	12	13	78	6	10	18	11	161	
National conference presentations	20	0	1	10	5	57	3	5	3	2	106	
Deposits in genomics related databases or libraries	0	8	0	3	2	128	0	0	4	0	145	
Total	32	13	5	33	21	263	15	19	26	13	440	

Research tools and processes

Research tools and processes include those produced in 2014-2015, deriving from previous phases of the GRDI if produced in 2014-2015,

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	EC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL
Research tools	20	9	11	5	11	5	3	6	8	3	81
Research processes	2	8	3	5	2	4	1	2	2	0	29
Total	22	17	14	10	13	9	4	8	10	3	110

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	EC	НС	NRC	NRCan	PHAC	QIS	FWS	TOTAL
Participation in government meetings/seminars/advisory panels related to regulations or policy in Canada and internationally	10	5	6	11	16	0	4	19	0	0	71
Participations in national or international genomics-related committees	3	4	4	9	14	1	17	11	0	10	73
National or international genomics research peer review committees served on	10	0	3	3	1	0	6	3	0	0	26
Participation in national conferences	13	1	3	4	2	0	0	3	1	2	29
Participation in international conferences	16	6	1	19	5	5	2	0	1	12	67
Total	52	16	17	46	38	6	29	36	2	24	266

Collaborations

Collaborations by department/agency, expressed in terms of number of individual research collaborators in 2014-2015 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	EC	нс	NRC	NRCan	PHAC	QIS	FWS	TOTAL
Canadian universities	6	5	8	34	10	6	8	4	19	3	103
International universities	6	1	3	6	4	4	17	4	22	2	69
Other international research organizations	3	1	2	8	1	2	10	8	10	0	45
Other Canadian research institutions	0	0	0	2	0	28	2	1	7	0	40
Private sector	0	0	6	1	4	10	0	0	3	0	24
Other government departments	2	17	0	21	5	1	2	21	16	0	85
Other public sector organi- zations such as provinces, municipalities, and Non- Governmental Organizations	0	1	3	16	4	3	6	23	0	2	58
Total	17	25	22	88	28	54	45	61	77	7	424

Communications products

NUMBER OF COMMUNICATIONS PRODUCTS											
	AAFC	CFIA	DFO	EC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL
Media interviews	0	0	0	0	0	3	2	0	0	0	5
Press releases	0	0	0	0	0	3	1	0	0	0	4
Newspaper and magazine articles	3	0	0	0	0	2	6	1	0	0	12
Community presentations	0	0	0	1	0	3	2	0	0	1	7
Brochures, fact sheets, web pages	0	0	0	1	0	8	7	4	0	0	20
Total	3	0	0	2	0	19	18	5	0	1	48

End-User Engagement and Knowledge Transfer Activities

NUMBER OF OUTREACH	ACTIVIT	IES									
	AAFC	CFIA	DFO	EC	HC	NRC	NRCan	PHAC	QIS	FWS	TOTAL
End-user consultations	11	0	0	0	13	0	0	10	0	0	34
Public meetings	4	0	0	9		0	0	0	0	0	13
Science advice, including to senior management	5	0	0	0	9	0	2	26	0	4	46
Outward material transfer agreements	15	0	0	1	0	0	20	3	0	0	39
Transfer of standard operating procedures	1	1	0	0	1	0	0	8	24	1	36
Disclosures	0	0	0	0	0	0	0	1	0	0	1
Active patents, patent applications, patents issued	6	0	0	0	1	1	0	0	0	1	9
Licenses issued	0	0	0	0	0	0	0	0	0	0	0
New formal collaborative agreements / standard operating protocols	2	0	3	0	1	0	0	14	0	0	20
Knowledge transfer workshops with stakeholders/end-users	9	4	4	11	7	0	2	6	2	1	46
Requests for research results, papers, collaborations	26	1	2	5	1	0	1	6	0	1	43
Total	79	6	9	26	33	1	25	74	26	8	287

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	EC	НС	NRC	NRCan	PHAC	QIS	FWS	TOTAL
Research scientists	23	39	16	12	16	44	16	23	22	42	253
Research professionals	47	12	10	23	22	16	10	28	4	16	188
Research technicians	32	20	15	22	12	103	15	14	2	29	264
Post-doctoral/visiting fellows	11	4	1	7	8	25	9	5	7	7	84
Graduate students	14	2	2	10	3	1	5	4	0	12	53
Undergraduate students	23	5	5	8	17	15	2	10	14	4	103
Administrative officers	1	0	0	3	0	0	2	2	1	0	9
Total	151	82	49	85	78	204	59	86	50	110	954
Total Estimated Full Time Equivalents	49	18	13	28	27	64	31	25	46	49	350

Annex 3-Highlights of Results Achieved in 2014-2015

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, EC, DFO, NRC, NRCan Scientific Coordination: AAFC Project Management: CFIA

The QIS project is a collaborative effort by 22 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.

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

The objectives are 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. Multiple DNA extraction SOPs were transferred to user groups and follow-up with end users has demonstrated improvement with DNA extraction results. A manuscript on assay development for DNA extraction from bulk insect samples has been accepted for publication. To resolve the issue of amplifying barcodes that target DNA of phytoparasite chloroplasts, work was initiated to

develop alternate markers that would differentiate and identify species for the phytoparasites genera. Primers amplifying an area of a chloroplastic gene have been tested with specimens from parasitic herbaceous plants and have shown promising results.

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

The objectives are 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. Significant progress was made this fiscal year. The focus is 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. Fifteen species were contributed to the Royal Ontario Museum collection, and issues with the preservation of samples and with the loss of traceability between previously submitted barcodes and vouchers have been identified. The development of a DNA sequence database to enable detection of aquatic invertebrate invaders directly from environmental samples is progressing well and the collection now contains over 2900 specimens that are being assessed for quality assurance. Over 2500 high risk nematode specimens were sent for extraction and subsequent sequencing for two genes and will be used to create a reference DNA database for species identifications.

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

The objective is 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. Significant accomplishments include: samples of 37 genera and 29 species of economically important nematodes in agriculture and forestry were collected from Canada, USA, China and Turkey, and were identified and characterized using morphological and molecular approaches; 742 rust specimens have been extracted, processed and were used to barcode a rust pathogen of highbush cranberry; all tree-fruit and grapevine samples have been analyzed for known viruses and the viral genomes have been assembled; new hybridization array have been designed to detect and type *Phytoplasma* spp. in plant and insect samples of known status; and protocols for barcoding certain target plant genera (from the Least Wanted Plant list) have been transferred and used successfully by the CFIA Botany Laboratory to help with the identification of plant species.

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

The objective is 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. A strategy was designed to test the sensitivity of DNA sequencing to detect rare beetles (i.e., one beetle specimen in a sample size of 2000). Work is ongoing to determine strategies to detect beetle associates, which include blue-stain fungi that include significant plant pathogens. A bioinformatics workflow was developed and incorporated in Galaxy workflows for automation and reuse. Significant progress is being made on the development of NGS for plant virus diagnostics and comparison of NGS to conventional diagnostic methods.

Sub-Project 5: Bioinformatics

The objective is to create a cyber-infrastructure platform to manage and analyse data generated by the QIS project. The team reviewed and prioritized all project deliverables based on overarching priorities. High priority deliverables were completed, including several related to metagenomics data management, provision of support for editing the Taxonomic project backbone and with reporting and tracking. To date, all available GRDI DNA sequences have been loaded into AAFC's SeqDB database, representing an increase of 22 new workbooks, 6,218 Specimens and 29,890 DNA sequences since the last reporting period. Bioinformatics training was provided to a cross-section of CFIA users, and a joint USDA-AAFC training activity related to metagenomics data analysis was successfully held.

A number of bioinformatics research tools were produced, relevant to groups dealing with DNA barcoding and microbe identification.

Food and Water Safety (FWS) Project Strengthening Food and Water Safety in Canada through an Integrated Federal Genomics Initiative

Participating Departments/Agencies: AAFC, CFIA, EC, 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 genomicsbased 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 is 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 the contaminant 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. A number of isolation approaches have been investigated: filtration devices based on size exclusion or positively-charged membrane captures; metabolic labelling; monoclonal antibodies; a microfluidic-based device designed to isolate whole bacterial cells from food matrices; and comparison of DNA extraction methods from soil and water samples. Work on enhancing the rapidity and sensitivity of detection of targeted food and waterborne microbial agents has resulted in the development of novel technologies (quantitative Polymerase Chain Reaction (PCR) assay;

metagenomics sequencing in leafy greens; arraybased photonic wire evanescent field instrument; microfluidic-based platform) that will significantly strengthen Canada's capacity to address food contamination threats. The microfluidic-based platform, which fully automates all of the steps required to carry out a Cloth-based Hybridization Array System procedure for the identification of *E. coli* O157:H7, has been deployed in a front-line CFIA regulatory testing laboratory for a rigorous assessment of its performance.

Sub-Project 2: Information Generation

Work on whole genome sequence analysis continued to close the FWS reference genomes (11 VTEC and 9 SE) to generate curated and consistently annotated full genome sequence resources for future use. Data of sequenced genomes of 374 non-O157 VTEC strains were added to the FWS database for analysis, bringing the total to date to 586 strains (including in-kind VTEC genomes contributions). The total number of strains of Salmonella sequenced under the FWS project has now reached 80. Environment and food surveillance activities for VTEC and Salmonella Enteritidis are also generating a pan-Canadian awareness of pathogen type, prevalence, and sources, as well as of the factors contributing to their presence and persistence. New genomic-based tools are being validated for microbial source attribution and tracking. Analyses are being performed for VTEC risk assessment and risk modelling. Comparative genomic analysis is expected to identify unique genetic markers and protein features relevant for pathogen detection, for attribution to potential sources of contamination, and to aid in the selection of the best methods for VTEC identification in various sample types. Ongoing environmental and food surveillance activities are generating a pan-Canadian vision of what VTEC and SE pathogens are where, when and why, representing the most comprehensive sampling of non-O157 VTEC genomes to date within Canada's borders.

Sub-Project 3: Bioinformatics

Deliverables are 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. A system for storing, managing and sharing whole genome sequence data is complete and under end-user testing. The FWS principal investigators and trainees continue to publicize IRIDA internationally, and other project members are participating in global community initiatives such as Global Microbial Identifier, the Canadian Advisory Committee for the Global Alliance for Genomics and Health, The Global Coalition for Regulatory Science Research, the Global Health Security Action Group, and the European Food Safety Authority. Members of the FWS project attended and played a leadership role at key international meetings on whole-genome sequence-based infectious disease outbreak investigations, including the Global Summit on Regulatory Science held in Montreal in August 2014; the Global Microbial Identifier meeting held in York, United Kingdom, in September 2014 and in Beijing in May 2015; the International Meeting on Microbial Genomics, Lake Arrowhead, California; and the 31st Chilean Congress of Infectious Diseases. Further development of the FWS platform and visualization tools were enthusiastically received and additional contacts were formed with researchers interested in utilizing the IRIDA project across Canada and internationally. National and international interest and support has been universally expressed for the project. Training workshops on Microbial Genomics and Bioinformatics were held, training over 100 persons on the application of whole genome sequencing in modern microbial genomics analysis. Training materials are being adapted for online self-directed leaning. This will provide public health workers with the ability to analyze whole genome sequence data for infectious disease tracking, outbreak response, pathogenomics, and population dynamics.

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

Chinese hamster ovary (CHO) cells are the primary expression system used by industry to produce biologics. The CHO production platform of NRC includes many proprietary improvements that facilitate the expression and purification of biologics. With support from the GRDI, NRC scientists continue to improve this critical platform, using genomic and metabolomic technologies to optimize its performance. This CHO production system is already enabling the development of a new generation of biotherapeutics by Canadian private companies



such as Formation Biologics, Zymeworks and Alethia Biotherapeutics. NRC aims to transfer the platform to Canadian biomanufacturers to foster a thriving biomanufacturing sector thereby creating jobs and increasing Canada's return on its innovation investments.

In addition to industrial applications, the platform also has benefits in the area of public health. Canadian scientists have developed antibodies that show great promise in treating Ebola. Two of the three antibodies found in the experimental treatment ZMapp were initially developed by PHAC; PHAC has requested NRC's assistance to increase production capacity for their anti-Ebola antibodies. NRC's expertise in the development of CHO cell lines and related bioprocesses has enabled the production of research-grade antibodies for PHAC.

In February 2015, Alethia Biotherapeutics submitted a Clinical Trial Application with Health Canada to initiate a Phase I (first in human) clinical trial of a fully humanized monoclonal antibody against cancer. The antibody, AB-16B5, was co-developed with NRC with support from GRDI and licensed to Alethia. AB-16B5 targets secreted clusterin to inhibit the epithelial to mesenchymal transition, which plays an important role in cancer metastasis and progression.

Formation Biologics (formerly AvidBiologics) continues to advance the preclinical validation of its lead candidate, AVID100, an antibody-drug conjugate against solid tumours. This antibody-drug conjugate is being developed in collaboration with NRC and includes biomanufacturing scale-up using NRC's CHO production platform. The promising results have enabled the company to close its second financing round and begin the preparation of a Clinical Trial application for 2016.

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 genomicsbased 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 system suppression during allergy development. Methods for analyzing complex protein mixtures have been developed and validated and are currently being applied to analyze selected food additives for their contribution to allergies. Overall, this project has yielded data of interest to toxicologists as well as regulators 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

Mother's 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. Preliminary work to optimize the methods for next-generation sequencing has been completed, and methods for assessing gut integrity have been studied.

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

MicroRNA (miRNA) is important in the regulation of gene expression and translation in protein products and thus response of the genome. In this project, HC researchers set out to identify and characterize miRNA in serum and milk associated with dietary exposure to fungal toxins and chemical contaminants currently detected in foods. In the first year, HC researchers completed the miRNA isolation, analysis and profile from serum. This work will enable the generation of important regulatory toxicology data to inform the risk assessment process, enhancing our 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 develop methods to screen for potential toxicities of novel nanomaterials. In 2014-2015, HC researchers exposed mice to six different types of nanomaterials and analyzed the physical-chemical properties of these nanomaterials. 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 OECD to support risk assessment activities.

Genomics approach to understanding 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 the vaccine-induced toxicity and establish the regulatory tools for the safety assessment of this vaccine. An animal study model has been established to be used to study vaccine-induced toxicity. Methodologies have also been developed to analyze biomarkers that may be pertinent to vaccine-induced toxicity.

Next generation sequencing detection of de novo mutations in the offspring 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. In the first of its kind, 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 common environmental pollutant, benzo(a)pyrene. An experimental and analytical pipeline has been developed to apply high-throughput sequencing approaches to identify mutations occurring in a specific gene in mice sperm to allow for sperm-offspring comparison and assessment of heritability. Preliminary results show that benzo(a)pyrene induces similar types of mutations in the sperm of exposed males that differ from those observed in the bone marrow of the same animals.

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. A contract has been put in place with a world renowned scientist in the cancer stem cells' field that will enable the accomplishment of all of the research objectives, as well as a letter of agreement has been established for the transfer of materials to be analyzed by mass spectrometry. This letter of agreement has already led to some preliminary research that will be presented at the American Society for Mass Spectrometry meeting in June 2015. 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 now 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 the first year, two papers were published that detail the development of these methods, and validation exercises have shown that the methods are effective across different laboratories and cell lines. These two papers formed the foundation for the use of toxicogenomics data for the first time in the HC assessment of a chemical contaminant in drinking water. Additionally, the method is currently being integrated with the US Environmental Protection Agency's ToxCast program for use as a high-throughput genotoxicity classification system. Furthermore, data generated from this research has been incorporated into training materials for the OECD and a course given to HC regulators involved with human health risk assessments.

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 subtyping to improve the management of contaminated products through 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.

The development of innovative molecular methods (e.g. SNPs, metagenomics) developed in earlier GRDI funding cycles are undergoing validation and integration into provincial and national programs (e.g. National Microbiological reference, World Organisation for Animal Health reference laboratory, and International Organization for Standardization (ISO) certification). This work is underway for Salmonellosis, a very common foodborne illness. Two projects are addressing Salmonella serovars Enteritidis and Heidelberg specifically (with a panel of 12 Single Nucleotide Variants and a Salmonella Genoserotyping Array developed in Phase V). Validation and certification of these innovative methods will enable provincial and international reference laboratories to uptake the technology. A countrywide validation of a new E. coli H antigen assay using matrix-assisted laser desorption/ionization

time-of-flight mass spectrometry (MALDI-TOF-MS) is providing an easier platform for most clinical microbiology labs to address this underreported subtype.

To further our ability to subtype multiple pathogens in a single isolate without the costly and labour intensive culturing conditions a new metagenomics sequencing project is in development. 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 complementary 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 E. coli, Salmonella, and Campylobacter collected through sampling activities of surveillance programs.

Detection and Genomic Epidemiology of Priority Pathogens

To effectively address the strategic need for rapid identification of priority pathogens, PHAC has endeavored to develop, validate and apply modern technologies (e.g., genomics and mass spectroscopy) alongside advanced scientific computing. This work provides the scientific evidence and methodologies to support the modernization and innovation of Canada's public health capacity. The selected priority 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 as we approach worldwide elimination.
- Mass spectrometry for diagnosis: In collaboration with international colleagues in the United States and European Union, a national Matrix Assisted

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Laser Desorption/Ionization- Time of Flight Mass spectrometry database to support diagnostic laboratories across Canada has been established. The mass spectroscopy identification of bacteria will be of great benefit to Canadian public health laboratories and hospitals in the identification of uncommon and rare bacterial pathogens and facilitate rapid and accurate identification of an organism at the local level. This will in turn enable clinicians to target treatment and decrease costs. An additional common SOP for the analysis of Botulinum neurotoxins is in development in collaboration with the Centres for Disease Control and the Royal Canadian Mounted Police National Security Investigations. The validation of this cutting-edge, rapid and cost effective technology across borders will support public health security and increase forensic analysis for participating nations.

 Bioinformatics: Canada's public health response capacity is further augmented with the development of Bioinformatics platforms across research programs to enhance the interpretation and quality of metagenomics/metaproteomic data. The data management and analytical tools efficiently process large comparative datasets for rapid pathogen identification from mixed clinical specimens.

Antimicrobial Resistance: Supporting Communities, Hospitals and the International Response

We are losing our ability to manage infectious diseases in humans and animals because of AMR and this complex problem requires effective collaboration across jurisdictions locally, nationally and internationally to provide standardized protocols for AMR surveillance. PHAC is committed to providing world renowned expertise to support action to reduce the spread of AMR and reduce public health risk. In addition, research undertaken and technologies / methodologies developed serve to influence antibiotic usage and infection control procedures. Together, these activities contribute to a reduction in antibioticresistant organisms and disease burden. The AMR research has been prioritised based on the pathogens presenting the greatest threat to public health infrastructure. They are:

 Human Immunodeficiency Virus (HIV) Drug Resistance: In collaboration with the Pan-America Health Organization, 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. Three national/regional HIV reference laboratories from Brazil, Mexico and Puerto Rico have been enrolled and a series of technology transfer activities to participating labs will enable independent affordable and accountable HIV drug resistance surveillance and clinical monitoring.

- 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 admitted symptomatic patients, new information acquired on the emerging problem of communityonset infection and recurrent infections. Studies of risk factors for recurrent infection are in development to provide 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 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 further international surveillance of antibiotic resistance in N. gonorrhoeae. Known genetic mechanisms of resistance are being characterized to provide an internationally standardized, uniform and consistent 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 in development to investigate highly homologous outbreak iso-

lates found in the Northern Manitoba and Nunavut. The investigation describes the evolution of antibiotic resistance in heretofore sensitive strain populations; the identification of novel resistance mutations not captured by traditional approaches; and the development of infrastructure for the implementation of whole genome sequencing for routine genotyping. In addition the detection and treatment of latent infection will be developed to complement current tests which simply identify exposed individuals, but not necessarily infected with *M. tuberculosis*. The distribution of biological markers will provide an accurate and reliable indication about the presence of active infection with M. tuberculosis to 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 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:

- Genomics Assisted Breeding: The wheat genome survey sequence was significantly improved with mate-pair data, and in collaboration with the International Wheat Genome Sequencing Consortium, an advanced version of this resource will be available shortly. A SNP genotyping platform for marker-assisted selection in breeding was developed using Fluidigm technology. A novel method was developed for genotyping single wheat microspores.
- 2) Enhancing Fusarium and Rust Resistance: Genomic analysis of rust isolates show that rusts are rapidly evolving and new forms of resistance need to be identified for wheat. Stacking of wheat R and Adult-plant resistance alleles led to very strong rust resistance. Four new Quantitative Trait

Loci that affect Fusarium Head Blight resistance have been identified on wheat chromosomes 1A, 3D, 2B, and 4B.

- 3) Improving Wheat Productivity under Conditions of Abiotic Stress: The genes responsible for cuticular wax deposition in wheat were identified, and are being evaluated for use as droughtresistance markers for breeding. A fatty acid marker for improved LT50 freezing tolerance in wheat was identified, and may be predictive of winter kill rates in winter wheat lines. Diverse winter wheat lines are being field tested and genotyped to determine the level of correlation of the metabolite vs cold tolerance. The Plant Abiotic Stress Knowledge Application and Library (PASKAL) database and bioinformatics tools (knowledge, sequence data, mathematical modelling) were developed for analysis of abiotic stress in wheat and related plant species.
- 4) <u>Targeting Developmental Pathways to improve</u> <u>Performance and Yield in Wheat</u>: RNAseqbased transcriptomics has identified 65-70% of genes involved in wheat seed development. Combined with SNP analysis, these genes were further mapped to their respective AA, BB, or DD genomes in diploid, tetraploid, and hexaploid species. The Target-of-Rapamycin gene, a key gene in photosynthetic efficiency and complex wheat yield and seed development pathways, was cloned from both wheat and Brachypodium.

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. Twenty-one projects were initiated at AAFC during the first year of GRDI Phase VI. Projects highlights follow.

Variation in plant populations is very important for plant breeders. Plant breeding is aiming at high yield, high quality and quantity, extension of adaptation ability to climate and soil conditions and tolerance or resistance to pests and diseases of cultivated food crops. Domesticated crops represent only a fraction of the genetic variation contained within the original wild germplasm. There are many cases where selective introgression of wild material has led to improved agronomic quality. Breeders acknowledge that wild

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relatives of crop species contain useful genetic diversity, essential to address current and future challenges in food production.

AAFC has identified a core set of 95 wild and cultivated oat accessions to be grown and characterized in order to determine their potential to contribute to new traits incorporated into cultivated oats. The genetic material is coming from the Plant Gene Resources of Canada located in Saskatoon. A new direct-genome-sequencing approach is applied to characterize these accessions and a new genotyping database is generated and linked to the oat accessions. The transferability of useful traits from wild oat germplasm to cultivated oats is assessed and will serve as pre-breeding material for future oat improvement. The impact is to increase the use of exotic oat germplasm preserved within PGRC and to provide genomic tools and new phenotypic information to better use the existing genetic diversity in breeding cultivated oats with new traits incorporated from wild germplasm that will meet future requirements of the oat industry. To date, phenotypic characterization is mostly complete and DNA samples have been prepared.

Under the GRDI, AAFC scientists work to identify new resistance genes to specific crop diseases, understand the genetics and biology of resistance and virulence, and deploy these resistance genes into cultivars/hybrids. The pathogen Fusarium graminearum, which causes Wheat and Barley Head Blight and Corn Ear Rot, has been one of Canada's most devastating diseases over the past 30 years due to its negative impacts on the health and safety of consumers (mycotoxin contaminated grains), animal health, and farm income, affecting Canadian food safety and competitiveness. Although fungicide treatments and improved agronomic practices can possibly help to reduce Wheat and Barley Head Blight and Corn Ear Rot in low to moderate infection years, Fusarium-resistant cultivars are required to prevent devastating losses during epidemic years and to ensure safer mycotoxin levels in food and feed. Previously, genomic researchers had co-authored the genome sequence of the pathogen and had mined the Fusarium gene expression database to elucidate novel toxin biosynthesis and regulation. However, little is known about the molecular mechanisms of resistance. The new knowledge generated by this project will significantly increase our understanding of how wheat and corn defend themselves against

Fusarium, the mechanisms used by the fungus to cause disease in the host, and the shifting of pathogen ecosystem. Knowledge of the hostpathogen interactions will greatly improve our ability to combine natural resistance strategies and design novel ones in crop germplasm, or interfere with pathogenesis, using sustainable crop management protocols. During the first year of the project, very good progress has been made towards dissecting the mechanism of resistance found in wild grass introgressed into wheat, and also in surveying the diversity of Canadian F. graminearum strains, acquiring new information on the biosynthesis and regulation of mycotoxins and impact of fungal competition, and defining other pathogenicity mechanisms.

Rusts, as fungal diseases, are threatening the Canadian wheat industry. They produce prodigious amounts of spores in a short period of time, which are rapidly wind-dispersed over a large area causing up to 40% yield loss of cultivated wheat crops. Stripe rust (Puccinia striiformis) has become a major threat to the wheat industry in Western Canada due to emergence of newly aggressive races since the year 2000 that are more and more resistant to massively applied fungicides in recent years. The rapid ability of the pathogen to defeat single resistance genes has led to the solution of pyramiding genes into new cultivars. To optimize this gene deployment and to maintain their efficacy, it is critical to study and understand how the organism adapts so quickly which relates directly to its genome organization and gene expression and mutation. A few partial reference genomes are available hence comparative genomics among many races and genetic lineages are powerful approaches to answer these questions. The main goal of the research project is to obtain a better physical genome and gene organization for stripe rust. This was achieved this year by obtaining very good quality DNA and a genome coverage of 20X from PacBio long read sequencing data to complement Illumina sequencing data. The project will also study gene regulation in stripe rust and identify effectors in different rusts.

Current breeding practices use crosses between elite inbreds to generate hybrids that exhibit higher and more stable yields than either of the contributing parents. These strategies have been widely adopted in most crops, but for corn, gains made through hybrid vigour have stagnated relative to the improvements shown in elite inbreds. Similar limitations are expected for other crops as beneficial alleles are fixed in contributing inbreds. There is considerable scientific interest in unveiling underlying genetic mechanisms conferring hybrid vigour through the development and application of associated molecular tools in order to better predict the optimal inbred parents maximizing their combination's ability. With access to fully sequenced genomes, more readily available due to the recent and substantial cost decrease of next generation sequencing and high density marker arrays, there is an opportunity to understand some of the current limitations in canola breeding, to determine combining ability of novel germplasm and to identify molecular markers associated with heterotic potential, all of which could contribute to Brassica crop improvement. AAFC scientists have proposed to identify current limitations in canola breeding and are providing knowledge and tools for the development of germplasm that overcome the limitations and generate varieties with sustainable and enhanced yield under Prairie conditions. The initial objective of assessing regions of the *B. napus* genome that have been selected through breeding in spring type *B. napus* is complete. The outputs from this project will have a beneficial impact for Canadian producers through the development of germplasm with enhanced yield. It is expected that this genomic knowledge will be used by industry partners to contribute to the continued success of the canola industry in Canada.

Genomic knowledge for forest generation and protection

Identification of genes controlling desirable attributes in economically important tree species

Research continued to focus on understanding how to efficiently build the forest of the future by using trees from today's forests that have desired traits. The desired traits relate to fibre quality and forest sustainability, such as: phenology and growth; wood quality characteristics; resistance to biotic and abiotic factors; and adaptation to environmental change. Central to this project is the creation of genomic profiles that help identify and select trees at an early age. The research project is complementary to two Genome Canada funded projects, SMarTForests and Fast Tests for Rating and Amelioration of Conifers (FastTRAC). Together, the projects will see the transfer and uptake of genomic tools by end users that will provide accurate predictions of wood and growth traits in young trees.

Increased knowledge of genomics-based pest control and diagnostics

Research on genomics-based pest control products for species that are of economic importance involves searching for active ingredients, target sites, and new or improved approaches for the development of environmentally benign pest control methods.

Spruce budworm is considered by many to be one of the greatest threats to our forests due to the periodic nature of its outbreaks, which can cause devastating damage and severe economic losses. Modeling their dispersal and the development of novel control options could offer forest managers new tools in the management of this pest. Provincial governments rely on decision support systems to inform their forest managers on how to proceed with the management of insect pests. Researchers at NRCan have created genomic resources including genetic markers that will assist in the management of spruce budworm.

Few control options exist for spruce budworm. Researchers at NRCan examined genes involved in overwintering in an effort to disrupt this process. These genes are responsible for the creation of anti-freeze proteins, essential for budworm winter survival.

Researchers at NRCan are also using genomics to develop potential management tools for the emerald ash borer, a wood boring beetle originally from Asia that causes severe economic and ecological damage to native ash trees. To further understand and mitigate the threat, scientists examined ash tree molecular responses to larval feeding for the development of a diagnostic test for infestation. Digestive enzymes of the emerald ash borer were also studied to understand how the pest exploits ash trees.

Future forests will benefit from having trees that are resistant to pests and pathogens, especially in this era of changing climate and increased global trade. Research by NRCan scientists focused on identifying and understanding the genes in fungi responsible for tree infection and the genes in trees that resist fungal attack. Work focused on two fungal diseases, white pine blister rust and poplar leaf rust. Genomic tests for resistance to white pine blister rust are ready to be transferred to breeding programs. In 2014-15 work began on developing a genomic tool that differentiates between live versus dead fungi and fungus-like pathogens of phytosanitary concern. The same tool will provide a method to measure the effectiveness of wood treatments applied before export, to assure our trading partners that Canadian wood is pest/ pathogen free.

Prevention is the best strategy for forest health. Less than 10% of the world's estimated 1.5 million fungal species have been described, therefore the potential for unidentified emerging pathogens finding their way to Canada and establishing themselves could be overwhelming. The research on pathogens supported by GRDI funds is complementary to two Genome Canada funded projects, TAIGA and Protecting Canada's Forests against Invasive Alien Species by Next Generation Biosurveillance. Building on previous years' research successes, 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. Another goal of the project is to develop and validate pathogen detection tests with improved accuracy for Canada's most unwanted pathogens. These tests are being transferred to end-users for application. The genomic resources developed through this project can be applied to other pests and pathogens.

Improving land reclamation following oil sands mining

A new project started in 2014-2015 examines the dynamics of tree and plant community establishment on oil sand mined sites. Genomic approaches were used to compare tree microbe inventories present in disturbed, reclaimed and natural sites. This research provides the necessary baseline data for future work that will allow the assessment of successful reclamation trajectories.

Economics analysis of forest genomics R&D

While forest genomics research has been conducted for many years, analyses of the economic considerations and impact from that research is only just beginning. Economists at NRCan examined the current GRDI projects to provide an economic perspective. A quantitative economic analysis was not completed due to the lack of data; however potential applications and commercialization opportunities were examined.

Genomics knowledge and advice for the management of fisheries and oceans

For Phase VI of the GRDI, ten genomics research projects are underway at DFO to: develop test-case eDNA assays that will be able to detect and eventually monitor distribution of colonizing organisms of management concern such as Zebra Mussel, Dolly Varden, Chum Salmon and Pink Salmon; 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, stock specific exploitation information, 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; confirm population structure of primary Capelin stocks to improve stock management and determine variation of species attributable to generational effects; identify adaptive mechanisms structuring and maintaining Redfish genetic diversity in Atlantic Canada, while addressing knowledge gaps in Redfish population structure; genetically 'mark' (genotyping) hatchery broodstock as a new method of monitoring the migration patterns and returns of Chinook salmon; 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:

<u>A genomics approach to measuring Atlantic Cod</u> 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 North Atlantic Fisheries Organization (NAFO) and North East Atlantic Fisheries Commission (NEAFC) 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 2014-2015, EC 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 biodiversity and ecosystem functions. In particular, related research focused on assessing the effects of exposure to chemicals of concern (including polyclic aromatic hyrdocarbons and organic flame retardants) in avian, mammalian and aquatic species. Better understanding molecular mode of actions of chemicals significantly enhances the accuracy of the models which contribute to improved risk assessment.

Environmental Monitoring

Environment Canada 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 cromate 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 results to increase remediation efforts. 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, EC 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 that data quality and control is being aligned to regulatory monitoring programs. DNA sequencing of iconic Canadian species, including polar bears and moose, was also undertaken this year to support the management and protection of wildlife populations. These efforts will ensure that genomics results deliver accurate and reliable results that can be used in ensuring that the Canadian environment and wildlife are being protected from pollution and other threats.

Using genomics for food safety, animal health and plant protection

Characterizing food-borne pathogens through creation of genomic databases

This project aims to develop genomics databases of known pathogens that will allow CFIA to deliver a highly responsive, risk-based food inspection system. In this project, CFIA scientists are working to create a database of food borne pathogens and creating new tools with enhanced capacity to detect the presence of microbial hazards in food supply. In the first year of the project to characterize food-borne pathogens, more the 700 strains of *Salmonella*, *Listeria* and *Escherichia coli*, and an additional 210 bacteria species related to food-borne illnesses, have all been fully sequenced and added to the regulatory genomic database.

Strengthening Animal Health diagnostic tools

The creation of a reference library of information relating to the genetics of viral pathogens such as bovine virus, will allow for the development of novel diagnostic tools that can be used for rapid detection and identification of high priority animal viruses. For instance, the genetic information of the bovine virus Mycobacterium bovis has been isolated from Canadian livestock and wildlife reservoirs and is being used to create protein-based diagnosis that can be used on wildlife and domestic species for characterization and identification. Further, this research project coincided with the recent outbreak of the avian influenza in British Columbia's Fraser Valley where the CFIA used the newly acquired genetic information to confirm the presence of a highly pathogenic H5N1 and H5N2 avian influenza virus on non-commercial farms. The GRDI supported research, conducted within the National Centre for Foreign Animal Disease laboratories, was instrumental in providing rapid insights into this developing outbreak.

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. For instance, in the area of plant virus detection and identification, researchers are using NGS to develop a cost-effective procedure that will be used in the Potato Post Entry Quarantine program (PPEQ) for rapid detection, identification and characterization of plant viruses. By propagating potato viruses/viroids in potato microplants and extracting RNA from these virus containing samples, a complementary DNA library has been constructed. This library will be used to develop a standard NGS protocol with optimized conditions that will then be used as tool in the CFIA Plant Health Diagnostics.

Development of genomics and bioinformatics tools

The CFIA's list of regulated pests includes many RNA viruses responsible for infection of plants and animals; human health risks are posed by several zoonotic animal viruses. This research is focused on using novel RNA Sequencing genomic technologies to detect, identify and characterize RNA viruses found in various matrices such as plants, animal tissues or a variety of foods. This project is facilitating joint efforts by scientists in all three of CFIA's business lines, to develop, improve, adapt and harmonize NGS methods and pipelines for identification and characterization of known or unknown RNA viruses for CFIA. These genomic tools will be integrated into the Agency's diagnostic arsenal.

Recent developments in the field of genomics have led to the increased application of these technologies to CFIA's regulatory science activities. A number of methods and applications have been developed in parallel in the food, plant and animal business lines. This project is working to harmonize genomics activities, including method development, bioinformatic analysis of genomic data and the provision of training on the use of bioinformatic tools. Currently, a number of research groups in the plant and food business lines have developed collaborations with AAFC to address needs for bioinformatics support. This project is building on these existing collaborations, while enhancing agency-wide access to these tools. The use of common platforms for genomics/bioinformatics work will ensure that efforts are not duplicated and that resources can be re-allocated to extend capacity for integration of emerging genomics technologies into CFIA's mandated activities.

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);
- Web-based server prototype for in silico typing of Salmonella (FWS);
- Protocols for the extraction of nucleic acids from marine vertebrates and invertebrates(QIS);
- Protocols for the extraction of nucleic acids from field and bulk samples (QIS);
- New set of degenerate PCR primers for amplifying and sequencing specific DNA regions in parasitic flatworms (digeneans and cestodes) (QIS);
- Novel PCR assay to detect the cpn60 gene of Phytoplasma spp (QIS);
- New set of primers for barcodes of several plant families (QIS);
- Canadian Biodiversity Information Facility web portal (QIS);
- SeqDB: GRDI project database(QIS);
- Gene candidates and diagnostic markers for wheat leaf rust (Lr16), stem rust (SrCad) and midge (sm1) (AAFC);
- Potential R genes candidates from the three genomes (A, B, and D) of hexaploid wheat (AAFC);
- Gene sequence information for *Puccinia striiformis* isolates (AAFC);
- Vagrant-seqdb: Tool for versatile and automated deployment in-house developed database application (SeqDB) (AAFC);
- Vagrant-galaxy: Tool for versatile and automated deployment of the Galaxy data analysis and workflow system (AAFC);

- Gbif-ipt-vagrant: Tool for versatile and automated deployment of the IPT platform (AAFC);
- PacBio long read sequencing data to complement Illumina sequencing data (AAFC);
- Camelina sativa lines developed with altered seed protein profiles (AAFC);
- Brassica napus (canola) lines developed with altered DNA recombination potential (AAFC);
- Several plant transformation vectors with novel gene expression and selection components (AAFC);
- Genome sequences of two Canadian *Fusarium* avenaceum strains deposited at the National Center for Biotechnology Information GenBank in the Whole Genome Shotgun database (AAFC);
- Gene expression dataset submission to NCBI Gene Expression Omnibus (GEO) for Arctic Mesorhizobium (AAFC);
- Gene expression dataset submission to NCBI Gene Expression Omnibus (GEO) for wheat lines susceptible and resistant to fusarium head blight (AAFC);
- Collection of trangenic Arabidopsis lines for isolating individual cell-type nuclei from root tissue (AAFC);
- Automated Oligonucleotide Design Pipeline (AAFC);
- Oligo Fishing Pipeline (OFP beta) and validation script (AAFC);
- R for Amplicon-Sequencing-based Microbial Ecology (RAM) (AAFC);
- Genome sequence for Camelina sativa (AAFC);
- Optimized procedure for high quality DNA purification from *Mycobacterium bovis* (CFIA);



- Tools that use Python programming language and R statistical computing language for assay designs and analysis tasks (CFIA);
- SPAdes de novo assembly pipeline that assembles and performs preliminary characterization of Fungi genomes from fastq files generated by Ion Torrent PGM (CFIA);
- Optimized next generation sequencing technology for detection/identification of mixed seed species (CFIA);
- Protocols for the extraction of nucleic acids from individual nematodes (CFIA);
- DNA extraction protocols for archived Atlantic salmon (*Salmo* salar) scales (DFO);
- DNA markers for genotyping wild and farmed Atlantic salmon (Salmo salar) (DFO);
- Complete mitochondrial genome sequencing from each of the five beluga (*Delphinapterus leucas*) Canadian populations (DFO);
- Database of highly polymorphic region (HPR) types of Infectious Salmon Anaemia Virus (ISAV) from different strains of Atlantic salmon (*Salmo salar*) (DFO);
- High throughput methodology for monitoring
 45 different microbes relevant to fisheries, aquaculture and salmon enhancement facilities (DFO);
- Optimized protocol for the extraction of high molecular weight DNA from tissue sample for genotyping-by-sequencing analyses (DFO);
- Sequences for 22 primer pairs for the amplification of tetramer microsatellite loci in narwhals (DFO);
- Microsatellite dataset for wild and hatchery Chinook Salmon (DFO);
- Hatchery Brood Full Parental Microsatellite
 Genotyping of Puntledge River Summer Chinook
 Salmon parents spawned in 2014 (DFO);
- Enzyme-linked immunosorbent assay (ELISA) of Bacterial Kidney Disease infection levels (DFO);
- Amplicon panel of primers (targets 445 amplicons containing 650 single nucleotide polymorphisms) for Chinook Salmon (DFO);
- eDNA qPCR assays to detect zebra mussel, Dolly Varden, Chum Salmon, and Pink Salmon (DFO);

- DNA markers for genotyping (Improved resolution of allelic variation in 6 microsatellite loci) (DFO);
- Data repository of capelin genotypes (DFO);
- SNP microarray for transcriptomic and genomic SNP's in polar bears and brown bears (EC);
- RAD sequencing library for razorbill species (EC);
- Mini-rotating annular reactor for controlled exposure and growth of microbial communities for ecotoxicological testing (EC);
- P53 gene sequence for the double-crested cormorant genome (EC);
- qPCR procedures for detecting and quantifying DNA from canines, humans, ruminants, and seagulls in water samples for microbial source tracking (EC);
- 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 miRNA 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);
- 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);
- Improved software tools (NRC);
- Plant Orthology Browser: http://nrcmonsrv01.nrc. ca/pob/ (NRC);
- Orthology & gene order analytics: stand-alone scripts/programs (NRC);
- Fungal culture collection (NRCan);
- Bioinformatics pipeline for assay development workflow using genomic sequences (NRCan);
- Enhanced SISTR: (http://lfz.corefacility.ca/sistrapp) 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);
- Enhanced single nucleotide variant-based tool for subtyping of S. Enteritidis (PHAC);
- MiSeq-based HIV drug resistance testing platform developed to enable the PAHO surveillance program (PHAC);
- HyDRA- an internet-based HIV DR data processing web server (PHAC);
- EpiQuant server developed to compare the strength of epidemiological and genetic relationships between bacterial isolates (PHAC).

Research processes

- Standard Operating Procedure for the sequencing (barcoding) of plant DNA using one to four gene areas (QIS);
- Galaxy genomic workflow tool customized for use on the project High Performance Computing cluster (QIS);
- Standard Operating Procedure for the extraction of herbarium plant DNA (QIS);
- Bioinformatics pipeline package for efficient identification of Reference Gene Associations applicable to any crop species and a wheat RGA database for public access (AAFC);
- Bioinformatic based approach for performing DNase hypersensitive sites sequencing using limited nanogram quantities of chromatin (AAFC);
- OpenStack Framework (AAFC);
- Data grid software (iRODS) (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);
- High-throughput sequence analysis (AAFC);
- High-throughput functional assay system (AAFC);
- Systems to modulate meiotic recombination frequency (AAFC);
- Genotyping of *M. bovis* isolates using whole genome sequencing (CFIA);
- High throughput discovery of novel diagnostic antigens for M. bovis and B. abortus (CFIA);
- Standard operating procedure for the use of NGS technology for detection and identification of contaminating seeds species (CFIA);
- Standard operating procedure for generating whole genome sequences for influenza A virus isolates directly from swab specimens (CFIA);

- Standard operating procedures for generating COX-1 and ITS sequences from *Culicoides* midges (CFIA);
- Optimization protocols for genotyping of capelin using microsatellite DNA markers on an Applied Biosystems sequencer (DFO);
- Multiplexing protocols for eDNA qPCR assays (DFO);
- Hatchery Broodstock Full Parental Genotyping (DFO);
- Diagnostic Y-linked SNPs in polar and brown bears (EC);
- Population genetic structure for the razorbill species (EC);
- NGS application in microbial community for ecotoxicological end-points (EC);
- Method for the assessment of DNA in doublebreasted cormorant liver and lung tissue (EC);
- Method to amplify microsatellite markers in wildlife species, including moose and polar bears (EC);
- 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);
- SNP discovery approaches (NRC);
- Parallel mate-pair library approach and assembly approaches (NRC);
- Data analysis pipeline that integrates quantitative trait locus and expression quantitative trait locus mapping methods (NRC);
- Three RNA sequence processing pipelines (NRC);
- Viral Induced Gene Silencing for wheat (NRC);
- Six SOP for the maintenance of insect cell lines (NRCan);
- Improved annotation and assembly of whole genome sequences (PHAC);
- Novel HIV drug resistance testing platform (PHAC);
- Illumina MiSeq-based HIV drug resistance testing protocol and associated sequencing library to enable the integration into surveillance program (PHAC);
- Botulinum neurotoxin activity detection by an endopeptidase-MALDI-TOF mass spectrometry assay transferred to Canadian Federal Laboratories for validation (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 worldclass 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 toolsproduced# of research processesproduced	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)	Outputs (continued)											
Area	Indicator	Methodology/ Source	Frequency	Target ¹	Date to achieve target	Responsibility						
Knowledge and Networks Knowledge translation and mobilisation	# 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						
initiatives	# 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 Outcom	ies											
Area	Indicator	Methodology/ Source	Frequency	Target ¹	Date to achieve target	Responsibility						
Structured collaboration among participating departments/ acencies	% 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 Outco	omes									
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.