CANADA'S SUBMISSION TO THE FAO COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE

During its Sixteenth Regular Session held 30 January – 3 February 2017, the Commission on Genetic Resources for Food and Agriculture established a new work stream on "digital sequence information on genetic resources for food and agriculture" (Report, para.86). The Commission requested its Secretary (para.88) to invite Members to submit information on the use of "digital sequence information on genetic resources for food and agriculture" and potential implications for their conservation and sustainable use, including exchange, access and the fair and equitable sharing of the benefits arising from their use, and to compile and submit this information to the Executive Secretary of the Convention on Biological Diversity (CBD), as a timely contribution to the process set by decision CBD COP XIII/16.

The present document includes Canada's information on the use and potential implications of "digital sequence information" on genetic resources for food and agriculture.

Introduction

Agriculture, fisheries and forestry, as well as food and non-food product value chains, depend on living organisms; this includes pollinators, naturally-occurring organisms that support ecosystem services (e.g. soil microorganisms), and natural enemies that can be used as biocontrol agents to manage pests. Biodiversity is the pool of resources upon which production systems are based. A vast pool of genetic diversity has been developed under domestication and is in urgent need of effective conservation and sustainable use strategies around the world. Therefore, efforts to understand, preserve and utilize biological diversity for agriculture, forestry and fisheries have been and continue to be essential to bio-based industries and to sustain the enormous improvements science has brought to production, processing, conservation efforts and utilization of genetic resources.

The study of biodiversity has become central to Canada's research activities as science started uncovering the important interconnections between biodiversity, productivity and resiliency in agriculture, fisheries and forestry. The study of the biological diversity of crops, animals, forests, wild relatives, beneficial species, pests, invasive and alien species, and native species enables advances in areas such as genetic improvement of forest populations and breeds of farm animals, improvement of pest and nutrient management methods, development of new crops or crop attributes, threat identification and risk mitigation, and identification and management of invasive alien species. It supports resiliency of productive systems by enabling the development of beneficial management practices to manage the effects of intensive management practices on populations of beneficial organisms and the ecosystem services they provide.

Furthermore, in an increasingly globalized world, the movement of pests and diseases is a constant threat to production and could result in catastrophic losses of major economic importance for the agriculture, fisheries and forestry sector, as well as catastrophic damage to biodiversity. Therefore, the capacity to identify and characterize organisms that may threaten its ecosystems and biological resource base is vital.

The Government of Canada has committed to openness, transparency and information sharing through the Open Government Partnership and the Global Open Data for Agriculture and Nutrition initiative (GODAN - http://www.godan.info/). Since joining the Open Government Partnership, a multilateral initiative to foster greater transparency and accountability, Canada developed three national action plans aimed at enhanced access to information and expanded open data, among other things. The Ministry of Environment and Climate Change Canada is the federal lead on the Open Science element of Canada's 2016-2018 Action Plan on Open Government. Sharing data related to genetic sequences is not new – the GenBank initiative (https://www.ncbi.nlm.nih.gov/genbank/) has made genetic sequence data available worldwide since 1982. Full sequences of genotypes of various crops (wheat in 2012, soybean in 2010 and others) and annotations of animal genomes carried out by various countries (http://www.ensembl.org/info/about/index.html) have also been published and made available online.

As a federal government department, the Ministry of Agriculture and Agri-Food Canada (AAFC) is also committed to providing access to data produced, collected and used to the Canadian public, researchers and industry communities. AAFC is a contributor to the Government of Canada's Open Data Portal and more recently, in May 2016, joined the GODAN initiative, which supports global efforts to make nutritionally relevant data publically available for use worldwide. Joining GODAN makes AAFC's data accessible to an even wider audience and helps strengthen ties with key partner countries and organizations.

Given the importance to agriculture of understanding the various organisms at play, their life cycles and the conditions they need in order to thrive, the study of agrobiodiversity and bio-resources has always been a priority research area supported by Agriculture and Agri-Food Canada. Its scientific collections, as well as the biosystematic study of species important for agriculture, are as old as research in this department (128 years). Over the years, AAFC has built a critical mass of knowledge, expertise and science capacity to study taxa of importance for agriculture. AAFC shares information on its holdings of plant and animal genetic resources collections using Internet websites and other tools. Biodiversity in agricultural systems can be studied at the various levels of organization, and all these levels are important: alleles, genes, populations, species, communities in an agricultural landscape and the agro-ecosystem as a whole. This ranges from genetic variation that provides the basis for valuable traits in a crop or affects the behaviour of a pest species, to populations of soil microorganisms and their importance for nutrient or carbon cycling or productivity of agricultural crops dependant on pollinator populations.

Forests are the most diverse ecosystems on land, containing the majority of the world's terrestrial species. Timber, pulpwood, firewood, cash crops, fish and medicinal plants from forests provide livelihoods for hundreds of millions of people worldwide. Unlike agricultural plants, forest trees are largely undomesticated and highly heterozygous, due to their outcrossing breeding systems.

In Canada, genetic sequence data is used to generate molecular markers which are important tools for forest trees and associated forest species (e.g. caribou) contributing to areas such as: (1) the assembly of breeding populations in newly developed and advanced breeding programs, and (2) species conservation activities such as the proper delineation of species taxonomy for management issues associated with conservation. Integrative approaches are being implemented within Canada to address the impacts of abiotic and biotic stressors. An example of this is where future climate modeling has been very successful in uncovering potential threats of declines in genetic diversity and the distribution of forest tree species, so that timely precautions to conserve the species can be undertaken.

Canada has developed the National Forest Information System (https://ca.nfis.org/index_eng.html) in 2000 as a collaborative effort with Natural Resources Canada, Canadian Forest Service and the Canadian Council of Forest Ministers to provide access to the most current, consistent and reliable forest resources information, integrating information across jurisdictional boundaries. This system contains data that allows for an accurate picture of Canadian forest practices and forest biodiversity, including assessing genetic conservation requirements of native tree species of Canada, information concerning threats to genetic diversity (e.g. invasive alien species), species biology and ecology (https://pfc.cfsnet.nfis.org/CAFGRIS/home.jsp).

Nonetheless, characterising biodiversity can be challenging. For example, the soil microbiome is composed of microscopic organisms that are in many cases very challenging to isolate, making downstream analysis complex. Other examples include the identification of very similar species or detection of alien invasive species over a vast territory. Genomics has provided very powerful solutions, which allow the identification of specimens without having to isolate them. This highlights the importance of genetic sequences for biodiversity in bio-based resource sector science.

Terminology

Canada is not comfortable with the term “digital sequence information” to characterize this data. First, the sequences in question are genetic sequences, not (for example) mathematical sequences or sequences of events. Therefore, to avoid confusion, the word “genetic” should be part of the term identifying this issue.

Second, the fact that genetic sequences can be conveyed digitally is of secondary importance; the “digital” aspect only refers to a particular mode of storage or mode of transmission. Genetic sequences listed on a sheet of paper would still be genetic sequences. Therefore “digital” should be removed from the term.

Third, the term “information” is not appropriate. “Data” would be more accurate, because data can be codified and is transmissible, which is the case for genetic sequences, but not always the case for information.

Therefore, Canada would prefer to use the term “genetic sequence data” (GSD), which we shall use in the rest of this document.

Genetic Sequence Data are not Genetic Resources

It has been proposed that GSD should be treated as if they were genetic resources. Canada does not agree; we are of the view that GSD are not genetic resources.

The definition of genetic resources in three legally-binding international instruments makes that clear.

In the Convention on Biological Diversity, Article 2:

> *"Genetic resources"* means genetic material of actual or potential value
>
> *"Genetic material"* means any material of plant, animal, microbial or other origin containing functional units of heredity.

In the International Treaty on Plant Genetic Resources for Food and Agriculture, Article 2:

> "Plant genetic resources for food and agriculture" means any genetic material of plant origin of actual or potential value for food and agriculture.
>
> "Genetic material" means any material of plant origin, including reproductive and vegetative propagating material, containing functional units of heredity.

In the Nagoya Protocol on Access to Genetic Resources and Benefit-Sharing, Article 2:

> The terms defined in Article 2 of the Convention shall apply to this Protocol.

These definitions are consistent and aligned. They state clearly that genetic resources "contain" "functional units of heredity" like DNA. The functional units of heredity are not themselves genetic resources, and even less so the base sequences within these functional units. Genetic sequence data, by their nature, do not and cannot contain functional units of heredity like DNA. Genetic sequence data do not accord with the legal definition of genetic resources in these international instruments. They therefore provide no legal basis to treat GSD like genetic resources.

There are also risks incurred in treating GSD as genetic resources. Genetic sequence data are not permanent and would change over the years; the sequences will be modified by punctual, random mutations. It is also evident in other articles of these instruments that they were not intended to relate to genetic sequence data. For example, provisions in these international instruments to conserve genetic resources certainly do not apply to strands of DNA.

Examples of Research Using Openly Available Genetic Sequence Data

In this section, we provide examples of research done in Canada that require simple and ready access to genetic sequence data of Canadian and international origin. They will, in particular, demonstrate that the use of GSD is not limited to substituting for genetic resources. We will also describe how access to GSD is important for these projects to support the objectives of the CBD. This research contributes to implement Articles 7, 10, 12 and 17 of the Convention on Biological Diversity, and contributes to meeting reporting requirements as defined in Article 26. It also supports the delivery of one of the 2020

Biodiversity Goals for Canada: “By 2020, Canadians have easy access to adequate and relevant information about biodiversity and ecosystem services to support conservation planning and decision-making”, and in particular Target 14: “By 2020, the science base for biodiversity is enhanced and knowledge of biodiversity is better integrated and more accessible.” (http://www.biodivcanada.ca/default.asp?lang=En&n=9B5793F6-1&offset=3#target_14);

1. *Study of soil and water microbiome: the EcoBiomics project*

Agriculture and Agri-Food Canada is leading a federal interdepartmental Genomics Research and Development Initiative (GRDI) that aims to develop new knowledge to improve water quality and soil health by comprehensively characterizing aquatic microbiomes, soil microbiomes, and invertebrate zoobiomes, and testing hypotheses to enhance environmental monitoring, assessment and remediation activities. It also aims at establishing comprehensive biodiversity baselines for assessing future changes to water and soil biodiversity at important long-term environmental monitoring sites in Canada.

The EcoBiomics project directly supports the objective of identifying biological diversity for conservation. This project uses metagenomics approaches to profile microbial and invertebrate communities in varying habitats tied to water and soil including pristine natural areas, agricultural, forestry and fishery systems, oil sands, and lakes and rivers. The result of the sampling in these locations based on standardized molecular approaches will identify the biodiversity within a taxonomic, ecological and functional context. The ability to do this analysis is absolutely dependent on known genetic sequence data from sources such as GenBank to identify the taxa in the samples and potentially their role in the ecosystem being studied. This project may also contribute to the identification and naming of taxa that are not known to science and to share this knowledge openly. This biomonitoring is essential to understand taxa and communities that may need conserving and thus potential regulatory action. There is also a strong economic tie to the production systems involved as maintaining diversity is typically correlated to healthy systems, and thus production as well as monitoring for alien invasive species and functional changes that could damage productivity.

The objectives of EcoBiomics also directly support the sustainable use of the components of biological diversity, as the production systems rely on sustainable biodiversity-based ecosystem services to be productive. The biomonitoring will produce metrics to assess sustainability. It should also indicate what remediation in terms of soil or water diversity is necessary to allow ecosystems to return to “normal” function.

Fair and equitable benefits of this project can only be realized through sharing genomic sequence data. Without sharing, the reference sequences will be internalized and there will essentially be no libraries available to carry out identification and quality control. This would obstruct research on biodiversity, especially on microbial life, and have a ripple effect to industry and the production systems they serve. Projects like EcoBiomics would no longer be possible if access to reference libraries of genetic sequence data and associated annotations becomes complicated and expensive.

2. Studying pollinator diversity and understanding threats to their populations

At least 35% of global crop production, and the majority of fruits, depend on bees and other insects for pollination services. While most interest in insect pollinators has focused on commercial honey bees, there is growing understanding that native bees are also efficient and effective crop pollinators. Alarming declines in both commercial honey bees and wild bee populations have led to increased fears that current agricultural productivity may be unsustainable without concerted efforts to maintain and enhance both wild and cultivated bee populations. Agriculture and Agri-Food Canada conducts research focussing on documenting bee diversity in our agricultural landscapes and studying the impacts of land use, pesticides, and pathogens on bee populations. This work involves sampling large numbers of bees which all need to be identified to species level.

In order to efficiently and accurately identify species, we often sequence various genomic regions of these bees and compare our genetic sequences to those that have been made available in online databases through collaborative efforts of the scientific community for well over a decade. Having access to genetic sequences of bees from other countries is vital to be able to detect any newly introduced species that our samples may be the first to detect in Canada. We also make use of worldwide genetic sequences of pathogens known to negatively impact bees in other parts of the world, in order to screen bees sampled in Canada for these pathogens. Importantly, the genetic sequences from the thousands of bees and pathogens that we have produced are invaluable tools for other researchers worldwide.

3. Understanding gene flow related to herbicide resistance

Since the beginning of agriculture, controlling weeds has been a major concern for farmers. Initially these were managed through labour intensive hand weeding. Currently, over 450 weed species globally have evolved resistance to at least one, but often many, herbicides. Within Canada, just over 60 species are herbicide resistant and in the United States there are over 150, some of which are spreading or will spread into Canada. Furthermore, with the introduction of crops modified to have herbicide resistance, the genes that confer these traits could move into wild relatives, providing additional challenges for weed management on the farm. Herbicide resistant weeds, whether they evolved or received this resistance through gene flow, are a clear threat to agricultural production within Canada and globally. Within the *Brassicaceae*, it has been documented that transgenes for herbicide resistance can move from crops (e.g. canola, *Brassica napus*) into weeds (e.g. Bird rape, *Brassica rapa*).This creates herbicide resistant weeds that are difficult to control. Further, if canola crops with different herbicide resistance genes are grown, it is possible for these traits to combine resulting in weeds with multiple resistances. As a result, it is important to assess the potential of transgenes escaping from *Brassicaceae* crops

The research conducted at Agriculture and Agri-Food Canada to address this threat relies at every stage on free and open access to genomic resources, including genetic sequence data. As a first step, we use freely available information on genes from species around the world to determine which weed species are most closely related to novel crops and, therefore, most likely to receive transgenes. This enables efficient allocation of resources to where the risk of gene flow is the highest. Second, we use similar information to develop molecular markers to detect hybrids between crops and their wild relatives, allowing determination of the rate at which this hybridization is likely to occur. This information is needed by the Plant Biosafety Assessment Office at the Canadian Food Inspection Agency to make informed, science-based decisions on the unconfined release of enhanced cultivars. Finally, the availability of accessible published genetic sequence data allows us to create the tools needed to dissect the consequences of hybridization so that an informed risk benefit analysis can be made including: 1) pinpointing the potential frequency of this hybridization in nature, 2) determining the portions of the genome that are most likely to be exchanged, and 3) quantifying how quickly a transgene may spread once introduced. For example, a glyphosate resistant (e.g. Roundup resistant) ecotype of the weed *Kochia scoparia*, has recently invaded Canada from the USA and the gene that confers this resistance is spreading through Canadian populations. This species has the potential to cause devastating losses in wheat and soybean. Its genome has just been made available allowing us unprecedented ability to understand how seed and pollen movement contribute to the spread of these genes through populations. This information will contribute to the development of more effective and sustainable weed management strategies for this species.

This work supports the mainstreaming of biodiversity in agricultural production, and the promotion of "awareness, use and sustainable use of agricultural ecosystems; improve its productivity and diversification; integrate positive incentives for biodiversity in field production and reduce agricultural pollution".

4. *Protection of Canadian biodiversity by monitoring invasive alien species*

Every year, new and emerging insect pests arrive in Canada and threaten Canadian biodiversity as well as production of agricultural crops. Chemical pesticides are often the primary short-term solution for crop protection against invasive insects. However, alternative pest management solutions are urgently needed as public concern over pesticide use continues to rise, and as many pesticide chemistries are phased out. Canada conducts research to identify organisms from all life stages through the development of new genomics tools for efficient detection of quarantine and invasive species; thus substantially bolstering Canada's operational strategy for both prevention and effective eradication or mitigation of new invaders.

To make this work possible, scientists use DNA barcodes to identify invasive and pest insects of importance to agriculture and forestry. Genetic sequences are a very important tool for taxonomists and work well in combination with other systems of characterization (morphology, host plant identities and biogeographic patterns). Genetic sequences allow scientists to rapidly distinguish species that are potentially invasive and harmful from those that are beneficial and part of natural ecosystems. Globally, this project is central for Canada's work on alien invasive species, as it provides a diagnostic tool for early detection (significantly lowering risk of establishment), surveillance and management of thousands of species, including alien invasive species.

A project funded by Genome Canada is involved in the protection of Canadian biodiversity through biosurveillance of Alien Forest Enemies (BioSAFE). It is led by researchers from Canadian universities in collaboration with the Canadian Food Inspection Agency. This national level project will enable forest health professionals to track and identify forest invasive pests and diseases using a genomics based approach. This project will enable the development of DNA-based diagnostic tests to identify and monitor these pathogens quickly (within hours) and accurately, which will then be used as a decision support tool to mitigate threats. The success of this project requires the availability of open access to GSD of known pathogens for identification.

5. *Inventorying forest genetic diversity*

Canada has a long history of forest research that generates genetic sequence data and utilizes open access GSD. Research has been conducted through diverse collaborative efforts involving the federal government (Natural Resources Canada, Canadian Forest Service), jurisdictional governments (e.g. British Columbia, Alberta, Ontario, Quebec and New Brunswick), academia (e.g. University of British Columbia, Laval University) and industry. This research has included assessing the genetic diversity in natural and managed forest tree populations and in identifying the geographic scale for capture of diversity, and for the conservation of rare forest tree species. Research of this type contributes directly to *ex situ* and *in situ* forest conservation activities and tree improvement programmes.

Improving the understanding of genetic diversity is recognized as important for the sustainable management of forest genetic resources. It is recognized that monitoring changes below the species level provides necessary information for ensuring that adaptive potential is maintained so that species can evolve in response to changing environmental conditions. Ensuring that species can respond to environmental change continues to be priority for much of the forest research conducted within Canada.

Other implications for the Government of Canada

Further to supporting the three objectives of the CBD, the above-mentioned research activities also contribute to support other Canadian international engagements such as:

- Meeting Canada's obligations regarding the stewardship of plant genetic resources for food and agriculture based on the *International Treaty on Plant Genetic Resources for Food and Agriculture* (http://www.planttreaty.org/). Art.13.2(a) identifies exchange of information as a benefit of the Multilateral System, including information on technologies, and results of technical, scientific and socio-economic research, including characterization. Genetic sequence data are a tool in the sustainable use of plant genetic resources, as per Article 6, paragraphs 6.2 (b), (c), (d), and (f) and in monitoring their degree of genetic variation as per Article 5.1(f);

- Implementation of NAPPO objectives. The North American Plant Protection Organization (NAPPO) was created under the International Plant Protection Convention (IPPC) to help achieve the goal of protecting the world's cultivated and natural plant resources from the spread and introduction of plant pests while minimizing interference with the international movement of goods and people. The regional mandate for NAPPO was formalized by Canada, the United States and Mexico in a Cooperative Agreement signed in 1976 at the Minister/Secretary of Agriculture level.

- Implementation of the World Trade Organization (WTO) Sanitary and Phytosanitary (SPS) Agreements. The World Trade Organization and its agreement on the application of the SPS Agreements came into force in 1995. The WTO-SPS Agreement recognizes the International Plant Protection Convention (IPPC) as the relevant international organisation for the elaboration of science-based International Standards for Phytosanitary Measures (ISPMs) to help ensure that phytosanitary measures are not used as unjustified barriers to trade. Regional Standards for Phytosanitary Measures (RSPMs) are often established before the international ones by organizations such as NAPPO or the European Plant Protection Organization (EPPO).

- Supporting the recommendations of the Organization for Economic Cooperation and Development (OECD) for Biological Resource Centres (BRCs) which specify that “for networking of BRCs to be truly successful, technology for co-ordinating and combining catalogues and databases to meet the requirements of science in the post-genomics era will have to be implemented.” Informatics needs for Biological Resource Centres are specified in the OECD Best Practice Guidelines for Biological Resource Centres.

- Implementation of the DivSeek Initiative (http://www.divseek.org/), of which Agriculture and Agri-Food Canada is a partner. DivSeek brings together 69 founding organizations, including the Global Crop Diversity Trust, the Consortium of the Consultative Group on International Agricultural Research (CGIAR), the Beijing Genomics Institute and the Global Plant Council. Its aim is to “unlock crop diversity” by extracting genetic information from samples of crop varieties and wild relatives stored in gene banks. The overall aim is to accelerate development of “climate-ready, high-yielding and nutritious crops”, which is a global good and benefits everyone.

Concluding Remarks

The various applications of genetic sequence data make important contributions to the utilization of genetic resources for food and agriculture, and to practical market-based or producer-oriented options that can enhance improvement of crops, farm animals, forests and fisheries, and facilitate their effective conservation.

Restricting the dissemination of genetic sequence data would limit the benefits that can be generated from the use of genetic resources and jeopardize their efficient conservation. Sharing information on genetic sequences is the corner-stone of entire scientific disciplines such as phylogeny, phylogenetics, molecular biology, molecular genetics, and many more, contributing to the global understanding of life in all its forms. Understanding diversity within a species is needed to maintain the viability of ecosystems and ecosystem services. Genetic sequence data are not genetic resources and should not be treated as such.

Genetic sequence data has the potential to bring numerous benefits to Canadian and global society. In this document, we provided examples of research projects that directly support the objectives of the international agreements on biodiversity and genetic resources. Such projects require a flow of genetic sequence data among countries that is not complicated or expensive in order to advance these objectives.

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