Environment Canada Environnement Canada

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Ms. Cristiana Paşca Palmer
Executive Secretary
Secretariat of the Convention on Biological Diversity 413,
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September 8, 2017

Dear Ms. Cristiana Paşca Palmer:

In response to CBD notification 2017-037, requesting the submission of "views and relevant information on any potential implications of the use of digital sequence information on genetic resources for the three objectives of the Convention", Canada would like to provide the below list of examples of research projects that involve digital sequence information and directly support the objectives of the Convention on Biological Diversity.

More specifically, the below paragraphs will provide a number of specific examples of research conducted in Canada that require an unburdened access to sequence information (through GeneBank or other resources) of international origin. In this sense, this submission describes how access to sequence information is essential in order for these projects to support the three objectives of the CBD. This research contributes to abide to Articles 7, 9, 12, 15 and 17 of the CBD, as well as contributing to meeting reporting requirements as defined in Article 26. It also supports the delivery of the 2020 Biodiversity Goal C 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."

Examples of Research Using Openly Available Sequence Information

1. *Study of Soil and Water Microbiome: the EcoBiomics project*

Agriculture and Agri Food Canada (AAFC) is leading an interdepartmental Genomics Research and Development Initiative (GRDI) project 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 in order 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 conserving biological diversity. 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 define the biodiversity within a taxonomic, ecological and functional context. The ability to do this analysis is absolutely dependent on known sequence information from resources such as GenBank to identify the taxa in the sample 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 openly share this knowledge. This biomonitoring is essential to understand taxa and communities that may need conserving and thus potential regulatory actions. 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 invasives and functional changes that could damage productivity.

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

The fair and equitable benefits can only be realized through sharing of genomic sequence information. Without sharing, the reference sequences will be internalized and there will essentially be no libraries available to do identification and quality control. This would paralyze research on biodiversity, especially on microbial life, and thus have a ripple effect up to industry and the production systems they serve. Therefore, projects like EcoBiomics would no longer be possible without the essential openly available reference library of genetic sequences and associated annotations.

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 more efficient and effective crop pollinators. The documented alarming declines in both commercial honey bees and wild bee populations has led to increased fears that current agricultural productivity may be unsustainable without concerted efforts to maintain and enhance both wild and cultivated bee populations. AAFC conducts research focusing on documenting bee diversity in Canadian agricultural landscapes and studying the impacts of land-use, pesticides, and pathogens on bee populations. This work requires AAFC to sample large numbers of bees which all need to be identified to species level.

In order to efficiently and accurately identify species, AAFC often sequences various genomic regions of these bees and compare its sequences to those that have been made available in online databases through collaborative efforts of the scientific community for well over a decade now. Having access to sequences of bees from other countries is vital to be able to detect any newly introduced species that AAFC’s samples may be the first to detect in Canada. AAFC also makes use of worldwide 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. Equally as important are the sequences from the thousands of bees and pathogens that Canada has produced that represent 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, this was done through labour intensive hand weeding. Currently, there are over 450 weed species globally that have evolved certain levels of resistance to at least one, but often many, herbicides. Within Canada, just over 60 species are herbicide resistant and within the United States there are over 150, some of which are spreading or are at risk for spreading 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 for the farming community. Herbicide resistant weeds, whether they have evolved or have 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. Birdsrape, Brassica rapa).This creates herbicide resistant weeds that are difficult to control. In addition, if canola crops with different herbicide resistance genes are grown, it is possible for these traits to combine in the weed 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 AAFC to address this threat relies at every stage on free and open access to genomic resources. As a first step, AAFC uses the 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, AAFC uses 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 required by the Plant Biosafety Assessment Office within the Canadian Food Inspection Agency to facilitate informed, science based decisions on the unconfined release of enhanced cultivars. Finally, the availability of accessible published genomes allows AAFC 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 for AAFC to have an 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”, as mentioned at COP 13.

4. *Protection of Canadian Biodiversity by Monitoring Invasive 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 in Canada. AAFC conduct 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, AAFC scientists use DNA barcodes to identify invasive and pest insects of importance to agriculture and forestry. DNA sequences are a very important tool for the taxonomist and work well in combination with other characters systems (morphology, host plant identities and biogeographic patterns). DNA sequences allow 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 AAFC and other federal agencies working on alien invasive species, as it provide a diagnostic tool for the early detection (significantly lowering risk of establishment), surveillance and management of thousands of species, including alien invasive species.

5. *Biodiversity Institute of Ontario, University of Guelph and the International Barcode of Life Project:*

The Biodiversity Institute of Ontario (BIO) at the University of Guelph is the place of inception of DNA barcoding and the founding institution for the International Barcode of Life Project (ibol.org), housing the world's largest DNA barcoding analytical and informatics facility. Through its DNA barcoding operational and research arm – the Centre for Biodiversity Genomics, it coordinates an on-going international effort to maintain and expand the global reference library of DNA barcodes as an openly accessible online resource for DNA-based identification of living organisms – the Barcode of Life Data System (BOLD).

Genetic/genomic information has unquestionable value for improving our understanding of biodiversity and, through enhancing human knowledge of biodiversity through access to DNA sequence data, in advancing the CBD targets and objectives. Through a series of collaborative initiatives with the CBD Secretariat and in partnerships with research institutions, government agencies and other organizations worldwide, BIO has facilitated the dissemination of technological advances in this field of science among partner institutions; particularly in line with the following relevant CBD decisions:

- XI/29, on the Global Taxonomy Initiative;
- X/2, on the Strategic Plan for Biodiversity 2011-2020 and Aichi Biodiversity Targets;
- XIII/13, on invasive alien species; and\
- XIII/31, on key scientific and technical needs related to the implementation of the Strategic Plan for Biodiversity 2011-2020 and related research.

BIO's extensive, lasting collaborations with hundreds of researchers worldwide and the input received from thousands of BOLD users, have shaped its strong position in favour of free and open sharing of genetic sequence data.

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/), and most particularly Article 5 and paragraphs 5.1 and 5.2, as well as Article 6, paragraphs 6.2 points d, e and f;

•Implementation of NAPPO objectives. The North American Plant Protection Organization (NAPPO) has been created under International Plant Protection Convention (IPPC) to help achieve the goal of the IPPC to protect 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 WTO's SPS Agreements. The World Trade Organization (WTO) and its agreement on the application of Sanitary and Phytosanitary Measures (SPS Agreement) came into force in 1995. The WTO-SPS Agreement recognizes the 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 OECD's recommendations for Biological Resource Centres (BRCs) specifying that « [f]or 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. » WP6 will also address Informatics needs for Biological Resource Centres as specified in the OECD Best Practice Guidelines for Biological Resource Centres.

•Implementation of the DivSeek initiative (http://www.divseek.org/), of which AAFC is a partner. DivSeek brings together 69 founding organizations, including the Global Crop Diversity Trust, the CCGIAR Consortium, the International Treaty on Plant Genetic Resources for Food and Agriculture 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."

Overall, it is Canada's view that digital sequence information has the potential to bring numerous benefits to the Canadian and global society and we look forward to discussing this matter further in the context of the upcoming SBSTTA meeting.

Thank you and kind regards,

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