



Biodiversity Institute of Ontario

September-5-17

Dear Dr. Cristiana Paşca Palmer,
CBD Executive Secretary

Please find below a statement from the Biodiversity Institute of Ontario, University of Guelph in response to the request for input to CBD Notification 2017-037 on potential implications of the use of digital sequence information on genetic resources for the three objectives of the Convention¹. The above document refers to the corresponding Decisions of the Convention (XIII/16)² and the Nagoya Protocol (NP-2/14)³ which note that “digital sequence information on genetic resources is a cross-cutting issue” that may concern the objectives of the Convention on Biological Diversity and of the Nagoya Protocol and also note the urgency of addressing this matter, given the “rapid advances arising from research and development in biotechnology regarding the use of digital sequence information on genetic resources”.

The Biodiversity Institute of Ontario at the University (BIO) 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)⁴. 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;

¹ <https://www.cbd.int/doc/notifications/2017/ntf-2017-037-abs-en.pdf>

² <https://www.cbd.int/doc/decisions/cop-13/cop-13-dec-16-en.doc>

³ <https://www.cbd.int/doc/decisions/np-mop-02/np-mop-02-dec-14-en.doc>

⁴ <http://boldsystems.org>

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- 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.

In addressing your inquiry, it is important to note that 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. Nonetheless, this document will focus on the keystone question that has been raised by CBD Parties and actively discussed during CBD's COP13 (December 2016) and the preceding SBSTTA meetings.

For the sake of clarity, the phrase “digital sequence information **on** genetic resources” is interpreted here as “digital sequence information **derived from** genetic resources”, thereby addressing the keystone question of whether *digital [DNA] sequence information* should become the purview of the Nagoya Protocol in the same way as it currently governs the transfer and utilization of *genetic resources*.

BIO's extensive, lasting collaborations with hundreds of researchers worldwide and the input received from thousands of BOLD users, as well as its obligations as a Canadian institution whose operations are chiefly supported through taxpayer-funded grants have shaped its strong position in favour of free and open (=unrestricted) sharing of genetic sequence data. It is becoming increasingly apparent that the biodiversity community should take guidance from and follow the best practices established for human genomic information by the Bermuda Principles⁵ and the Fort Lauderdale Agreement⁶ which, in their time, have set the bar for open access publishing in biomedical research.

Unfortunately, the biodiversity community today has yet to adopt similar standard principles, but imposing additional layers of bureaucratic overhead on the process of data [pre]publication would further hamper the process.

Using the terms of Decision 2/14, it should be argued that “digital sequence information on genetic resources” should not be included in the objective of the Nagoya Protocol in its current

⁵ http://web.ornl.gov/sci/techresources/Human_Genome/research/bermuda.shtml

⁶ <https://www.genome.gov/pages/research/wellcomereport0303.pdf>

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form. In other words, the existing ABS provisions and mechanisms for controlling the transfer and use of genetic resources (=anything containing DNA) should not be expanded to DNA sequence information (possibly, 90% of what biological science is now working with), without a thorough review of the impact that the Nagoya Protocol and its established procedures have had on biodiversity research since its ratification in 2014.

There is a growing body of published evidence that ABS provisions have done little to address the fair and equitable sharing of benefits between providers and users of genetic resources but are beginning to impose unbearable legal overhead on basic biodiversity research which increasingly relies on DNA sequence information, e.g., to facilitate fast and accurate taxonomic identifications. Furthermore, biodiversity research may be particularly stifled in biodiversity-rich countries where decline and extinction of species are a more imminent concern.

In practical terms, the adoption of a centralized ABS mechanism governing all non-human DNA sequence information can be considered as:

1. Unfeasible – given the amount of digital sequence data already in existence and its exponentially growing volume, it would be computationally impossible to implement a tracking mechanism for monitoring/policing the transfer of digital genetic sequence information, e.g., through a centralized Clearing House Mechanism. Although exact data are not available at the moment, an indirect indicator could be the number of IRCC's issued so far by the CHM for genetic resources since 2014 *versus* the number of published studies using such resources.
2. Impractical – there is no clear indication that any such attempts to impose a complex clearance procedure would do anything to address the concerns of certain Parties about data piracy. At least, there are no indications that the implementation of NP *per se* has done much to curb biopiracy (not counting the growing voluntary conscience of researchers and increasingly collaborative vs 'colonialist' nature of international research projects).
3. Counterproductive – such measures will create unnecessary barriers to science – particularly basic science and especially areas of application of DNA sequence information in characterizing and surveying biodiversity, e.g., the Global Taxonomy Initiative. See above regarding the possible impact of NP on research already.

Unfortunately, the stable flow of CBD national reports on the status and trends of biodiversity



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create a false impression that humanity has a pretty good idea of what is happening. By contrast, the recent influx of digital sequence information provides a clear indicator of how little we know about even the very basic parameters, e.g., number of species in a given ecosystem. In order to get closer to a true assessment, the volume of digital sequence data on natural biodiversity has to increase by orders of magnitude and DNA-based diagnostic technologies have to become part of the standard toolkit of any researcher or practitioner dealing with biodiversity. And it needs to be done fast, before too much diversity is lost unknowingly. This can only be done in a nurturing and supportive environment. As mentioned above, the ramifications of the NP in its current form on basic biodiversity research are highly debatable and it is questionable whether expanding it to cover DNA sequence information would improve the situation.

In summary, digital DNA sequence information should be an important topic at the CBD discussion table, but the tone of the discussion should change from that currently taken. Rather than debating ways to restrict and control access to genetic resources and derived information, the international community should do more to establish legally robust provisions for free and unrestricted data sharing, including possible legal restrictions on proprietization of genetic resources and derived information by private or corporate entities, particularly where such proprietization may lead to unfair or inequitable sharing of benefits or to stifling/hampering of scientific enquiry. Also, more needs to be done to support developing country researchers in generating and publishing digital sequence information from their respective national genetic resources.

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