CONVENTION ON BIOLOGICAL DIVERSITY (CBD) NOTIFICATION 2017-037

Digital Sequence Information on Genetic Resources

Submission by Australia

Australian Government

<u>NOTE</u>: All information provided in this response has been drawn from Australian Government agency input only.

Notification 2017-037 - Digital Sequence Information on Genetic Resources

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Australia thanks the Secretariat for the invitation to submit 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 and the Nagoya Protocol, as communicated in notification 2017-37 Ref.:SCBD/SPS/DC/VN/KG/jh/86500 of 25 April 2017.

Key Points

The objectives of the Convention are:

1. the conservation of biological diversity;
2. the sustainable use of its components; and
3. the fair and equitable sharing of the benefits arising out of the utilisation of genetic resources.

"*Genetic resources*" as defined under the Convention and the Nagoya Protocol means genetic material of actual or potential value.

"*Genetic material*" as defined under the Convention and the Nagoya Protocol means any material of plant, animal, microbial or other origin containing functional units of heredity.

Digital Sequence Information on genetic resources is not defined under the Convention. For the purposes of this submission Australia defines "*digital sequence information on genetic resources*" as electronically held sequence information which represents the biological composition of "*genetic material*" as defined under the Convention.

Australia considers digital sequence information on genetic resources and the physical genetic resources and material as distinct entities. This distinction aligns with the outcome of lengthy debate in the establishment of the Nagoya Protocol. To consider digital sequence information a genetic resource under the Convention and the Nagoya Protocol would require a renegotiation of the Convention and the Nagoya Protocol to redefine 'genetic material' noting information does not contain 'functional units of heredity' or genes.

Australia does consider that digital sequence information on genetic resources has a role in supporting Parties to meet the objectives of the Convention in line with Articles 3, 15(6) and 15 (7).

> ***3*** *States have, in accordance with the Charter of United Nations and the principles of international law, the sovereign right to exploit their own resources pursuant to their own environmental policies, and the responsibility to ensure that activities within their jurisdiction or control do not cause damage to the environment of other States or of areas beyond the limits of national jurisdiction.*
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> ***15(6)*** *Each Contracting party shall endeavour to develop and carry out scientific research based on genetic resources provided by other Contracting Parties with the full participation of, and where possible in, such Contracting Parties.*
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> ***15(7)*** *Each Contracting Party shall take legislative, administrative or policy measures, as appropriate, and in accordance with Articles 16 and 19 and, where necessary, through the financial mechanism established by Articles 20 and 21 with the aim of sharing in a fair and equitable way the results of research and development and the benefits arising from the commercial and other utilization of genetic resources with the Contracting Party providing such resources. Such sharing shall be upon mutually agreed terms.*

There is a broad range of types and quality of sequence information relating to genetic resources that may be stored and/or transmitted digitally. Different types of sequence information include DNA, RNA and protein sequences as well as information on epigenetic factors such as methylation and glycosylation sites. The quality of information can range from raw sequence data through to fully annotated, characterised and codon optimised sequences complete with information on relationships to other sequences, including from multiple source organisms.

Open access to digital sequence information deposited in the public domain is the common standard in the global scientific community. Digital sequence information is found in many publicly available databases that can be considered data hosts not data owners. For example, GenBank (including Barcode of Life database of reference sequences from vouchered specimens of species) is an open access sequence database that contains nucleotide sequences for more than 300,000 organisms with supporting biological and bibliographic annotation.

Access to, and use of, digital sequence information is fundamental to modern biotechnology. The identification of useful information from within raw sequence data relies upon vital contextual information provided through existing public databases of characterised and annotated digital sequence information.

The generation and open sharing of digital sequence information on genetic resources provides benefits through increased scientific information and discovery that enable Parties, to meet the objectives of the Convention and the Nagoya Protocol. The use of digital sequence information on genetic resources increases the value of biological diversity and enables scientific progress and innovation.

Australia finally notes a number of multilateral discussions are in progress regarding whether and how regulatory mechanisms that apply to physical resources should be extended to digital sequence information. Outside the Convention and Nagoya Protocol discussions include:

- Multilateral System of the International Treaty for Plant Genetic Resources in Food and Agriculture (genomic sequence of germplasm);
- World Health Organisation (genetic sequence data from influenza viruses with pandemic potential); and
- Biodiversity Beyond National Jurisdiction discussions under the UN Convention on Law of the Sea (digital information from marine genetic resources).

Co-ordinated and non-duplicative consideration of this crosscutting issue is required to ensure consistency across these fora. We call on the CBD Secretariat to ensure the continuation of this collaboration as we consider this to be critical to inform the work being progressed through the CBD.