



**SPNHC**  
ADVANCING COLLECTIONS CARE

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7 September 2017

Dr. Paşca Palmer  
Executive Secretary, Convention on Biological Diversity  
Secretariat of the Convention on Biological Diversity  
United Nations Environment Programme  
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Dear Dr. Paşca Palmer,

Science has become a global endeavor as a result of shared goals, and there are increasingly more international and collaborative partnerships and organizations that span geopolitical boundaries. The Society for the Preservation of Natural History Collections (SPNHC) is an international society whose mission is to improve the preservation, conservation and management of natural history collections and the biological objects stored in them to ensure their continuing value to scientific research, education, and society. We are writing to comment on the Secretariat's 25 April 2017 Notification No. 2017-037 regarding information pursuant to paragraphs 2 of decision XIII/16 and NP-2/14 on "any potential implications of the use of digital sequence information on genetic resources for the three objectives of the Convention, and for the objective of the Nagoya Protocol, respectively."

Digital sequence data, such as standardized DNA-fingerprints or barcodes, DNA sequences, and full genome sequencing, has become an integral part of modern biodiversity research. Natural history objects in ex-situ collections are essential for biodiversity research and for the identification and conservation of the natural diversity on earth, either by traditional morphological or modern molecular means. The SPNHC membership distinguishes between the genetic materials we store and make accessible to the scientific community and the digital sequence data inferred analytically from it. Inferred digital sequence data is used as a comparison tool to define, differentiate, classify and explore the tree of life, which is vital for monitoring and achieving Goals B, C, and E of the 2011–2020 Strategic Plan for Biodiversity, as well as identifying threats to that biodiversity<sup>1</sup>.

The CBD has recognized that the information gained from taxonomic study is critical in the conservation of biodiversity and the sustainable use of its components, creating the Global Taxonomy Initiative to remove 'taxonomic impediment' from the implementation of the CBD. Strategic Action 8 of the Global Taxonomy Initiative aims to "improve the quality and increase the quantity of records on biodiversity in historic, current and future collections and make them available through taxonomic and genetic databases." More specifically, it is proposed that by 2020 all taxonomic barriers to the universal availability of scientific knowledge, data and information on biodiversity are removed. We are certain that imposing restrictions on the availability of digital sequence data will stop taxonomic progress, thereby preventing the global biosystematic community from fulfilling the CBD's goals.

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<sup>1</sup> <https://www.cbd.int/gbo/gbo4/publication/gbo4-en.pdf>

Digital sequence data in the public domain provides a key resource for the conservation of biological diversity and the sustainable use of its components. The International Nucleotide Sequence Database Collaboration (INSDC) is a long-standing initiative that links the three major databases of Europe (EMBL-EBI), Japan (DDBJ), and the United States (NCBI). Contributions of researchers and taxonomists to these public databases<sup>2</sup> are essential to monitor and conserve earth's biological diversity, which is a common concern of mankind. The submission of sequence data to public sequence databases increases transparency and reproducibility of scientific data and enhances traceability of utilized genetic resources. Free access to such data is a prerequisite for classification, identification and monitoring of the genetic diversity not only of wild species but also for domesticated livestock and cultivated plants, which are components of our cultural heritage (related to Aichi Target 13). Major population genetic data sets are the basis for the development of strategies to preserve the genetic diversity of wild relatives of cultivars and to minimize genetic erosion. To impose restrictions in sharing sequence data would impede taxonomy, as well as monitoring and preserving biological and genetic diversity worldwide by governments, local communities, and NGOs in Provider and User countries.

SPNHC wholeheartedly supports the objectives of the CBD and the Nagoya Protocol, agreeing that legal certainty and transparency are essential for the attainment of their objectives. Natural history collections anchor all associated information with specimens, and by linking permits, agreements, and other metadata to their specimens, there is increased transparency regarding their origins and use. We are extremely concerned that the motion to include digital sequence under the scope of the Nagoya Protocol would be counterproductive, making information unavailable for global scientific access and threatening basic progress regarding our understanding of the natural world. Freely accessible digital sequence information encourages progress through collaborative research and can allow users and providers to work together to fulfill the objectives of the CBD.

See Appendix 1 for examples of digital sequence data use that correspond with the objectives of the CBD and Appendix 2 for additional details regarding our society's history, membership, objectives, and available resources for the Nagoya Protocol.

Sincerely,



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<sup>2</sup> Similar to Figure 19.1, <https://www.cbd.int/gbo/gbo4/publication/gbo4-en.pdf>

## Appendix 1. Examples of Digital Sequence Data Use that Correspond with the Objectives of the CBD.

### *CBD objective 1: Conservation of biological diversity*

According to Aichi Target 19, “All countries need information to identify threats to biodiversity and determine priorities for conservation and sustainable use,” However, this target should be considered a “commitment to increase the amount and quality of biodiversity relevant information and technologies as well as to make better use of it in decision making as well as to share it as widely as possible.” The rapidly growing number of individuals and species being sequenced, as well as the increasing depth of genomic coverage, plays a leading role in achieving this goal. Comparisons of sequence data available in public databases from specimens maintained in the world’s natural history museums forms a huge “reference library” in the public domain. Voucher based digital sequence records are the key for comparing and identifying specimens and for the discovery of cryptic and new species, reducing the need for taking additional animals and samples from wild populations. Bioportals, such as Barcode of Life Data Systems<sup>3</sup> or StainInfo<sup>4</sup>, that consolidate taxonomic information, sequences in public repositories, and literature references, as well as cover the costs for maintaining such data sets, are also key in achieving the conservation of biological diversity and monitoring progress associated with Aichi Targets 11 and 12.

### *CBD objective 2: Sustainable use of its components*

Active multilateral exchange of digital sequence information provides a useful resource for biodiversity conservation and sustainable management of natural resources, supporting the implementation of the CBD. Without widely available information on genetic composition, this goal, and particularly Aichi Target 13, would be compromised. One such example is the Fish Barcode of Life Initiative (FISH-BOL; <http://www.fishbol.org>), a global effort to coordinate an assembly of a standardized reference sequence library for all fish species that is derived from voucher specimens with authoritative taxonomic identifications. Natural resource managers and regulators can use DNA barcoding to monitor the illegal trade of processed fish products using, aiding in the control of over-harvesting these natural resources.

### *CBD objective 3 and Nagoya Protocol objective: fair and equitable sharing of the benefits arising out of the utilization of genetic resources*

No country holds sequence data for all of its biota, and genetic sequence data from species present in other countries may also be needed to identify biosecurity risks, such as invasive species that are intercepted by quarantine agencies. A multilateral system to control approximately 200 million sequences would certainly hinder the compilation of relevant data and information, and thus the delivery of (non-monetary) benefits to Providing Countries would be delayed. This has been demonstrated by the burdensome process established for genetic resources of the International Agricultural Resource Centers, which manages and controls information for only 64 food crops.<sup>5</sup>

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<sup>3</sup> Barcode of Life Data Systems currently hosts 2,869,168 referenced sequences cited in over 70,000 publications; <http://www.boldsystems.org/index.php/datarelease>

<sup>4</sup> StainInfo currently contains 699,352 strain numbers referenced to 1,387,8482 accession numbers cited in 142,948 publications; <http://www.straininfo.net/strains/search>

<sup>5</sup> <http://www.fao.org/plant-treaty/areas-of-work/the-multilateral-system/overview/en/>

## Appendix 2. The Society for the Preservation of Natural History Collections (SPNHC): History, Membership, Objectives, and Nagoya Protocol/ABS Resources.

SPNHC is a non-profit organization that was formed in 1985 to meet the concerns of a growing number of individuals involved with the development, management, and care of natural history collections. After more than 30 years of existence, the Society continues to be unique among natural history professional organizations, because of its international scope and multidisciplinary approach to collections management and care. Well curated collections are a critical foundation for scientific research, education, and society's general understanding of the natural world.

Our organization currently includes 686 members from 24 countries, including Africa, Asia, Australia, Europe, and North America.

The Society's objectives are:

- To provide and maintain an international association of persons who study and care for natural history collections
- To encourage research on the essential requirements for preserving, storing, studying and displaying natural history collections
- To publish a professional journal, Collection Forum, and encourage the dissemination of information about natural history collections
- To hold annual meetings and sponsor symposia and workshops to foster the exchange of ideas and information

SPNHC is making great efforts to advise its membership regarding the implications of the Nagoya Protocol and relevance to biodiversity collections. To date, there have been workshops and presentations at the annual meeting, as well as a best practices website page devoted to this topic ([http://spnhc.biowikifarm.net/wiki/Access\\_and\\_Benefit-Sharing\\_\(Nagoya\\_Protocol\\_and\\_the\\_CBD\)](http://spnhc.biowikifarm.net/wiki/Access_and_Benefit-Sharing_(Nagoya_Protocol_and_the_CBD))). To promote understanding, we are advising researchers who may be accessing genetic resources about obtaining Prior Informed Consent and establishing Mutually Agreed Terms. To ensure compliance, we are also communicating that those managing biodiversity collections must implement policies and procedures to track permits and benefit-sharing agreements to increase the transparency regarding the origins and use of collections.

For more information, go to: <http://www.spnhc.org>.