September 7th, 2017

Dear Dr. Paşca Palmer,

Science is a truly global enterprise and many of the challenges facing us have a global dimension, not least of which are the threats to the World's biodiversity. One of the most important and obvious signs of this is the emergence, strength, and impact of scientific communities and organizations that transcend geopolitical boundaries to promote research and scientific inquiry for the benefit of humankind.

The Global Genome Biodiversity Network (GGBN) is one of these organizations, bringing together 65 members from 22 countries. This letter is GGBN's 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 the potential implications of the use of digital sequence information on genetic resources for the three objectives of the Convention on Biological Diversity, and for the objective of the Nagoya Protocol, respectively. GGBN is pleased to have the opportunity to share our views:

Currently, sequence information accessed from public databases is excluded from coverage by the Nagoya Protocol. We believe that exclusion should continue. Sequence data is not genetic material, nor is it a genetic resource. Sequence data is analytically derived information, or data that describe the order of nucleotides in DNA or RNA in genetic material (referred to by the CBD as "digital sequence information on genetic resources"). Our understanding is that the CBD and Nagoya Protocol explicitly cover genetic material, not information about this material. Our network and constituent members distinguish between the genetic materials we hold and make accessible to the scientific community and the information analytically inferred from genetic material. We note that it is essential to distinguish between these concepts and definitions.

We consider the sharing of digital sequence information (DSI) as equivalent to a Global Multilateral Benefit-Sharing Mechanism for information. Including DSI within the Protocol would bring challenges to users globally and potentially harm the implementation of the CBD. We also challenge the view that simple comparisons of sequence data for non-commercial uses can be considered "utilization". The existing sequence data play a major role in biodiversity conservation and sustainable management of natural resources. It is thus of vital importance for implementation of the Convention's objectives.

It is essential that the world's scientific community have open access to genetic sequence data. Rapid and unimpeded access to genetic sequence data is necessary for timely and accurate science required by the CBD. To date more than 2,311.8 billion bases are uploaded and available through the International Nucleotide Sequence Database Collaboration (INSDC) (see http://www.ebi.ac.uk/ena/about/statistics). This means that since 2015, this part of INSDC has almost doubled in size (Cochrane et al. 2016). The INSDC's policy, first published in 2002 (Brunak et al. 2002, http://www.insdc.org/policy.html), emphasizes the collaboration's mandate to uphold free, unrestricted access to all of the data records their databases contain, which is strongly supported by the scientific community. It is in the CBD's interest to support that access so that their objectives can be met. Limiting access will have a chilling effect on taxonomic progress, reducing the likelihood of achieving the 2020 goal of removing all taxonomic barriers to the universal availability of scientific knowledge, data and information on biodiversity.

Below we provide examples of uses genetic sequence data that correspond with the three objectives of the CBD. Future results such as these will be threatened unless sequence data is freely available.

CBD objective 1: Conservation of biological diversity

Use of DNA Sequence information is now integral to the process of taxonomy and of identification, and provides a cost-effective tool for global use. Open access to genetic sequence data enables essential research that supports the preservation of biodiversity, especially important as we develop models about the impact of climate change on species and their distribution, e.g., modelling and explanation of biodiversity patterns (e.g., Bacon et al. 20165). Comparisons of sequence data from known specimens and samples, such as those maintained in the world's museums and biorepositories allows the identification of cryptic and new species, while reducing the need for taking additional organisms and samples from wild populations.

Sequence data is essential to the identification of highly fragmented samples, such as the remains of birds, bats, and other animals recovered from airplane engines. These identifications are used to inform mitigation strategies at airports, targeting the practices and procedures to the unique behaviors and requirements of the most susceptible and frequently impacted animals. The identifications also aid in the design process for aircraft engines, making them less prone to damage caused by the most typically involved animals.

Conservation and sustainability of pollinators can be supported strongly through the use of genetic information. For example, the influential journal *Conservation Genetics* recently published an issue devoted to Conservation Genetics of Bee Pollinators (see https://link.springer.com/journal/10592/18/3/page/1).

The identification of invasive species benefits greatly from freely accessible sequence information, especially information shared globally. Invasives are, by definition, not native in the locality where they are captured. Rapid identification is essential to mitigation procedures, especially at ports of entry, making freely accessible sequence data of great importance to national authorities. The more sequences are available, the better the likelihood of accurate and useful rapid identification. Publicly-accessible databases are integral to developing tools for such rapid identifications.

CBD objective 2: Sustainable use of its components.

Publicly-accessible databases of sequence data serve as a "reference library" for comparing specimens and samples confiscated by law enforcement entities when investigating potential mislabeling of animals such as food fish, or trafficking of products made from controlled plants and animals. The same tools can be employed in biosecurity, for the identification of potential pests and pathogens (e.g. see case studies from the UK - http://www.nrcresearchpress.com/doi/full/10.1139/gen-2016-0010#.Wa0pHMiGPcs, Australia - https://link.springer.com/article/10.1071/AP03067, New Zealand - http://www.mpi.govt.nz/document-vault/1621, some EPPO standards – see https://www.eppo.int/STANDARDS/council2016.htm). Recent research by one of GGBN's members* found hidden diversity in a genus of ecologically and economically important giant South American catfish, with implications for protection policies and conservation plans. Fisheries agencies commonly use sequence data to define population stocks for management decisions.

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

GGBN member organizations frequently host students who participate in research expeditions and use ex-situ collections, thereby gaining valuable experience and professional knowledge. Those students take the benefits they have gained to their home institutions and countries. They publish research findings, including providing sequence data to publicly accessible databases. Every country needs access to genetic sequence data to answer questions related to identification, protection of biodiversity, or sustainable uses. Development of a system that limits access to the millions of sequences would prevent the equitable sharing of benefits.

Conclusion: Impact on science regarding availability of sequence data

The 21st century has been called the century of genomics, and sequence data permeate nearly every branch of modern biology. GGBN subscribes to the OECD Frascati Manual's definition of basic research as "*being experimental or theoretical research undertaken primarily to acquire new knowledge of the underlying foundation of a phenomenon and observable facts, without any particular application or use in view.*" While the majority of of research activities that take place in the Natural History collections-based institutions fall within this definition, an important number are explicitly aimed at collecting data with some application and use, especially design of management and protected areas, and to test efficacy of existing management policies. Regardless, all of this research relies upon openly accessible data, and in turn makes new data accessible thereby expanding the delivery of benefits.

To reiterate our most important comment**: Sequence data is not genetic material, nor is it a genetic resource.** GGBN and its members distinguish between the genetic materials we hold and make accessible to the scientific community and the data describing this material. We note that it is essential to distinguish between these concepts and definitions. We also challenge the view that simple comparisons of sequence data for non-commercial uses can be considered utilization; further, we are concerned that including digital sequence data under the scope of the Nagoya Protocol will have a severe limiting effect on essential global science by making data unavailable.

In closing, the Global Genome Biodiversity Network is committed to consistent, high quality standards for DNA and tissue collections, and to improving best practices for preservation and use of these collections for the preservation of the world's biodiversity. We support the legal certainty and transparency needed for attainment of CBD and Nagoya Protocol objectives. We strive to support the work of our large and growing member community in curating and understanding biodiversity. We support the aims of the Convention on Biological Diversity, and we welcome the opportunity to be part of on-going dialog regarding your objectives.

Sincerely,

Ole Seberg
Chair of the Executive Committee

Cc: *Executive Committee and Policy Task Force*

Appendix A. Overview of GGBN

The Global Genome Biodiversity Network (GGBN) (Droege et al. 2014, Seberg et al. 2016) is an international network of institutions that share an interest in long-term preservation of genomic samples representing the diversity of non-human life on Earth. GGBN is based on a Memorandum of Understanding and provides a platform for biodiversity biobanks from across the world to:

- Collaborate to ensure consistent quality standards for DNA and tissue collections
- Improve best practices for the preservation and use of such collections and
- Harmonize exchange and use of material in accordance with national and international legislation and conventions

The Global Genome Biodiversity Network has 65 members from 22 countries in North, Central, and South America, Europe, Africa, Asia and Australia. It provides its members with the primary benefit of making their DNA and tissue collections discoverable for research through a networked community of biodiversity biobanks. In doing so, GGBN provides trusted and transparent access to genomic samples for all, through an access and benefit-sharing framework.

One major goal of GGBN is to increase the number of sequence data that are vouchered. Deposition of voucher specimens in collections is crucial for all molecular research to enable verification and transparency of taxon identification.

GGBN does not itself produce sequence data, but the GGBN Data Portal (http://www.ggbn.org) cross-links to sequencing portals ((INSDC; International Nucleotide Sequence Database Consortium (http://www.insdc.org) and BOLD; the Barcode of Life Data System (http://www.barcodinglife.org)) to establish links between the stored samples and the sequence accession numbers related to the samples. Additionally the GGBN Data Portal stores information about the samples permit status. Thus, the GGBN Data Portal increases the visibility of samples and availability as well as any restrictions on their use. GGBN does not conduct research on or produce genetic sequence data.

GGBN serves its members by sharing a code of conduct and best practice tools that are compliant with the Nagoya Protocol as part of a responsible approach to making samples discoverable and accessible subject to any restrictions on their use, and when known, links to associated genetic sequence data.

GGBN has developed the GGBN Data Standard (Droege et al. 2016) to complement existing biodiversity standards such as Darwin Core or ABCD. The GGBN Data Standard is intended to provide a platform based on a documented agreement to promote the efficient sharing and usage of genomic sample material and associated specimen information in a consistent and open manner. It is a set of terms and controlled vocabularies designed to represent any, and all sample facts. This also includes vocabulary for permits and loans according to the requirements of the Nagoya Protocol. GGBN is working on a tool that enables tracking of parent and offspring use of samples.

GGBN proposes the GGBN Data Standard as the global biodiversity data exchange standard for fulfilling the Nagoya Protocol (Droege et al. in press) and is already in contact with INSDC, BOLD and GBIF to enable support of this standard in other global portals. GGBN seeks to make sure that all samples created since the ratification of the Nagoya Protocol will provide permit information by the end of 2020. Furthermore, we are working on automated submission pipelines to INSDC, which includes permit information. This is an example of transparency and accountability regarding permits.

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Breda Zimkus, Museum of Comparative Zoology, Harvard (2017-present)

Overview of Member Organizations:

Institution Full Name	Country	Date Of Joining	Member Status
Centre for Biodiversity Genomics	CA	2017-08-29	Associate
Missouri Botanical Garden	US	2017-08-11	Associate
China Biodiversity Conservation and Green Development Foundation	CN	2017-08-08	Observer
University of Alaska Museum of the North	US	2017-07-31	Associate
African Centre for DNA Barcoding, University of Johannesburg	ZA	2017-07-11	Associate
University of California, Berkeley, Museum of Vertebrate Zoology	US	2017-07-11	Associate
Centro de Ornitología y Biodiversidad	PE	2017-06-22	Associate

Institution Full Name	**Country**	**Date Of Joining**	**Member Status**
University of Kansas Biodiversity Institute	US	2017-06-21	Observer
Biodiversity Research and Teaching Collections, Texas A&M University	US	2017-04-03	Associate
Bernice Pauahi Bishop Museum	US	2017-03-23	Observer
Denver Botanic Gardens	US	2017-03-01	Core
Museum of Comparative Zoology, Harvard University	US	2017-01-09	Associate
Global Biodiversity Information Facility	DK	2016-12-28	Observer
Vietnam National Museum of Nature	VN	2016-12-16	Associate
Colciencias, Departamento Administrativo de Ciencia, Tecnología e Innovación	CO	2016-09-29	Observer
International Society for Biological and Environmental Repositories	CA	2016-09-29	Observer
European, Middle Eastern & African Society for Biopreservation and Biobanking	FR	2016-09-29	Observer
Entomological Collections Network	US	2016-08-05	Observer
Korean National Research Resource Center	KR	2016-07-27	Observer
Carnegie Museum of Natural History	US	2016-03-24	Associate
National Marine Biodiversity Institute of Korea	KR	2015-12-14	Observer
Royal Ontario Museum	CA	2015-12-04	Associate
Rio de Janeiro Botanical Garden	BR	2015-11-09	Associate
Museum of Southwestern Biology	US	2015-09-21	Associate
Royal Botanic Garden Edinburgh	UK	2015-08-18	Associate
Institute of Vertebrate Biology, The Czech Academy of Sciences	CZ	2015-08-10	Core
Royal Museum for Central Africa	BE	2015-07-15	Associate
BCCM Belgian Coordinated Collections of Microorganisms	BE	2015-06-17	Observer
BCCM/DCG Diatoms Collection	BE	2015-06-17	Observer
BCCM/IHEM Biomedical Fungi and Yeasts Collection	BE	2015-06-17	Observer
BCCM/ITM Mycobacteria Collection	BE	2015-06-17	Observer
BCCM/LMBP Plasmid Collection	BE	2015-06-17	Observer
BCCM/LMG Bacteria Collection	BE	2015-06-17	Observer
BCCM/MUCL Environmental and Applied Mycology	BE	2015-06-17	Observer
BCCM/ULC Cyanobacteria Collection	BE	2015-06-17	Observer
Museo de Zoología, Pontificia Universidad Católica del Ecuador	EC	2015-06-03	Core
Naturhistoriska riksmuseet	SE	2015-05-05	Observer

Institution Full Name	**Country**	**Date Of Joining**	**Member Status**
Senckenberg Görlitz	DE	2015-04-18	Associate
Denver Museum of Nature & Science	US	2015-03-15	Associate
Natural History Museum of Oslo	NO	2014-10-31	Core
Charles University in Prague	CZ	2014-09-18	Core
Universidade Estadual de Campinas	BR	2014-06-26	Associate
Institute of Botany of the Academy of Sciences	GE-AB	2014-06-12	Associate
Association for Farmers Rights Defense	GE	2014-04-24	Associate
Hungarian Natural History Museum	HU	2014-03-10	Associate
Museum für Naturkunde	DE	2014-02-10	Core
Royal Botanic Gardens, Kew	UK	2013-09-25	Core
Ruder Boskovic Institute	CR	2013-08-16	Core
Museum Victoria	AU	2013-07-25	Associate
South Australian Museum	AU	2013-06-20	Associate
Senckenberg Frankfurt and BiK-F	DE	2013-05-28	Core
Ocean Genome Legacy	US	2013-04-21	Core
Beijing Genomics Institute-Shenzhen	CN	2013-04-15	Associate
Natural History Museum London	UK	2011-10-11	Core
National Museum of Natural History	US	2011-10-11	Core
American Museum of Natural History	US	2011-10-11	Associate
Australian Museum	AU	2011-10-11	Associate
Commonwealth Scientific and Industrial Research Organization	AU	2011-10-11	Associate
Alexander von Humboldt Institute for Research on Biological Resources	CO	2011-10-11	Associate
Natural History Museum of Denmark	DK	2011-10-11	Core
National Research Foundation - National Zoological Gardens of South Africa	ZA	2011-10-11	Associate
Smithsonian Tropical Research Institute	PA	2011-10-11	Associate
AIT Austrian Institute of Technology GmbH	AT	2011-08-29	Core
New York Botanical Garden	US	2011-02-24	Core
Zoological Research Museum Alexander Koenig	DE	2007-06-01	Core
Leibniz Institute DSMZ	DE	2007-06-01	Core
Botanic Garden and Botanical Museum Berlin-Dahlem	DE	2007-06-01	Core