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IUCN Briefing for negotiators

Marine Genetic Resources, Part II

Key messages: MGR from the ocean in ABNJ is a global commons issue. Scientists and businesses from different countries can build on MGR to develop monetary and non-monetary benefits: new knowledge, and, ultimately, products that may be protected by IP or trade secrets and from which there may be product sales or fees in respect of IP and know-how. Reflecting the commons nature of MGR and the different opportunities and contributions that different people, communities, and states make to the development of these benefits, it is appropriate that these benefits should be shared in a fair and equitable manner. This is consistent with norms of scientific research, international regimes relating to human rights and sustainable development, and flexibility offered in the WTO TRIPS regime for intellectual property (IP).

The term “Marine genetic resources” (MGR) needs to be defined broadly to include “metadata” and “derivatives” to understand the environmental context and reduce the need for further sampling, and to advance consistency with the Nagoya Protocol.

1. Define “marine genetic resources” broadly to include associated data and “derivatives”

Why? The “metadata” associated with a sample is important to enable subsequent users to know where and from what conditions the marine genetic resource (MGR) was collected. Including derivatives (e.g. biochemical compounds) in the MGR definition is important so these compounds can be accessed and reproduced in the laboratory for applications in pharmaceuticals, amongst others, without the necessity for further sampling. Including derivatives is also important for ensuring consistency with the Nagoya Protocol on Access and Benefit Sharing of Genetic Resources under the Convention on Biological Diversity (CBD):

CBD Article 2 "Genetic material" means any material of plant, animal, microbial or other origin containing functional units of heredity. "Genetic resources" means genetic material of actual or potential value.

Nagoya Protocol Article 2 “Derivative” means a naturally occurring biochemical compound resulting from the genetic expression or metabolism of biological or genetic resources, even if it does not contain functional units of heredity.

How? Use genetic resource (GR) definitions from Article 2 of the Convention on Biological Diversity and that of derivatives in Article 2 of the Nagoya Protocol, and use geographical scope to ensure it applies to GR from ABNJ. Article 8 should apply to “MGR and associated data”:

BBNJ Article 1 [8. “Marine genetic material” means any material of marine plant, animal, microbial or other origin containing functional units of heredity.]

[9. Alt. 1. “Marine genetic resources” means **marine genetic material** any material of marine plant, animal, microbial or other origin, [found in or] originating from areas beyond national jurisdiction and containing functional units of heredity with actual or potential value of their genetic and biochemical properties.]

[9. Alt. 2. “Marine genetic resources” means marine genetic material of actual or potential value.]

BBNJ Article 8 [1. The provisions of this [Part][Agreement] shall apply to: [(a) Marine genetic resources, **their associated data and derivatives**, insofar as they are collected for the purpose of conducting research into their genetic properties;]

2. Use the term “digital sequence information” recognizing that this is a placeholder term under the CBD

Why? The requirement that access to digital sequence information (DSI) must be provided is considered critical to prevent fragmentation of databases as the value rests with the compilation of information, not individual sequences. If agreement on how to handle DSI were not reached, states might decide to create their own separate databases which would reduce the value of the current system where data is shared openly in a large single database. The CBD is developing a definition of DSI that will likely include collection metadata, DNA/RNA sequence data and protein sequence data (“group 2” see CBD/DSI/AHTEG/2020/1/3 and the decision based on this CBD/DSI/AHTEG/2020/1/7). The timeline for adoption of a definition of DSI by the CBD is uncertain. Any definition of DSI made in the BBNJ agreement risks confusion if the CBD or the DSI community adopts a different one.

How: Do not define DSI under the BBNJ Agreement, but rely on the definition that is eventually adopted for the CBD.

3. Treat DSI and specimens separately and share DSI multilaterally using open access principles

Why? DSI is essential to biodiversity conservation, biotechnology and medicine, amongst others. The majority of DSI (most publicly funded and some commercially funded) is currently shared via open access databases. A multilateral benefit-sharing solution that does not impede scientific and applied work using DSI is essential. Multiple instruments are dealing with DSI (CBD, WHO, FAO, UNCLOS) and a unified solution is necessary to ensure the databases remain open-access and collate data from multiple sources (animal, plant, bacterial etc.).

How? DSI should be shared openly following current scientific norms. Several solutions to DSI benefit-sharing have been proposed but the most workable one can be found in this short article by Scholz et al, 2022, on “[Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation](#)”). It proposes five principles on which such an approach should be based: i) remain open access to enable DSI to be interpreted and applied; ii) avoid regulatory complexity so that access rules do not impede access to DSI; iii) globally harmonized, given the high stakes and multiple instruments involved; iv) support biodiversity conservation; and above all v) fair, creating a level playing field for all who contribute to and use DSI.

Article 10(2) States Parties shall take the necessary legislative, administrative or policy measures, as appropriate, to ensure that *in situ* [collection of] [access to] marine genetic resources within the scope of this Part shall be subject to:

(d) The deposit of samples, data and related information in open source platforms, such as databases, repositories or gene banks;

Article 10(4) States Parties shall take the necessary legislative, administrative or policy measures, as appropriate, to ensure that access to [~~marine genetic resources in silico~~][~~and~~][digital sequence information][~~genetic sequence data~~] is facilitated [subject to articles 11 and 13]

4. Build traceability on existing global scientific infrastructure

Why? Creating a new system for track and trace of MGR from ABNJ would be expensive and ineffective. We should move away from a one size fits all system as different uses/applications of MGR require different types of traceability and sharing of benefits. Current traceability mechanisms have been created by states under the Nagoya Protocol but are ineffective when it comes to tracing movement of GR across borders.

How? Propose the use of unique scientific identifiers that have “persistence” (assurance of availability of the identifier long-term), “resolvability” (the identifier itself can be used to directly discover the data objects), “discoverability” (identifiers can be discovered within and across systems), and “authority” (refers to curation and standardization of the identifier, important so that they remain viable long-term). Many such identifiers exist such as in the Global Biodiversity Information Facility (for specimens) and also sequence databases such as the International Nucleotide Sequence Data Collaboration (INSDC). The concept of unique scientific identifiers can be introduced as in this example:

Article 13 [3. States Parties shall take the necessary legislative, administrative or policy measures, as appropriate, to ensure that:

~~[(a) A unique identifier is assigned to marine genetic resources [collected] [accessed] in situ. In the case of marine genetic resources accessed ex situ [and in silico] [[and] [as digital sequence information] [as genetic sequence data]], such an identifier shall be assigned when databases, by repositories and gene banks and submitted to the clearing house mechanism the list mentioned in article 51 (3) (b) to the clearing house mechanism;]~~

For more information, see:

[BBNJ Knowledge Series | IUCN](#) (all resources are compiled here)

WCC Resolution 128 "Acting for the conservation and sustainable use of marine biological diversity in the ocean beyond national jurisdiction" 2021 IUCN Congress in Marseille, France.

IUCN comments on revised draft text February 2020

M Jaspars and A Brown, 2021. “Benefit sharing: combining intellectual property, trade secrets, science and an ecosystem-focused approach” in Myron H. Nordquist and Ronán Long, *Marine Biodiversity of Areas beyond National Jurisdiction* (Brill, 2021)

Scholz et al, 2022, [Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation](#), Nature Communications <https://doi.org/10.1038/s41467-022-28594-0>

DOSI, 2021 [070-DOSI-Policy-brief-Intellectual-Property-Rights-V2-web1.pdf](#) (dosi-project.org)

DOSI, 2022i [MGR-Traceability-BBNJ-Policy-Brief.pdf](#) (dosi-project.org)

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