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Digital sequence information on genetic resources

Synthesis of submission of views on possible new tools and models, such as databases, for making digital sequence information on genetic resources publicly available and accessible in a transparent and accountable manner to all Parties**

Note by the Secretariat

I. Introduction

1. In decision [16/2](#), the Conference of the Parties decided to explore possible new tools and models, such as databases, for making digital sequence information on genetic resources publicly available and accessible in a transparent and accountable manner to all Parties. The Conference of the Parties also requested the Subsidiary Body on Implementation to consider this information and to prepare a recommendation to the Conference of the Parties serving at its seventeenth meeting on this topic.
2. As such, the Secretariat issued notification [2024-115](#) inviting Parties other Governments, indigenous peoples and local communities and relevant organizations to submit their views on possible new tools and models, such as databases, for making digital sequence information on genetic resources publicly available and accessible.
3. A total of 18 submitters were received, nine from Parties (Brazil, Canada, Colombia, Egypt, European Union, India, Japan, Republic of Korea, and United Kingdom of Great Britain and Northern Ireland) and nine from observers (Alliance of University and Non-University Biodiversity Research with European and International Partners, Brazilian Bioinnovation Association, CGIAR Genebank Accelerator, DNA Data Bank of Japan, Digital Sequence Information Scientific Network, European Molecular Biology Laboratory European Bioinformatics Institute/European Nucleotide Archive, International Chamber of Commerce, Nascimento e Mourão Sociedade de Advogados, and Third World Network). All submitters can be found in notification No. [2024-115](#).
4. This submission of views is linked to the study requested to the Executive Secretary on options for making digital sequence information on genetic resources publicly available and accessible in a transparent and accountable manner (see CBD/SBI/7/5/Add.1 for the Executive Summary and

* [CBD/SBI/7/1](#).

** The present document is being submitted without formal editing.

CBD/SBI/7/INF/15 for the full study) and should be considered together by the Subsidiary Body on Implementation.

II. Synthesis of views

A. General observations and cross-cutting issues

1. Open data

5. All submitters recognize that open access to data is important for research and non-monetary benefits, with three Parties also emphasizing the need for equity and compliance with access and benefit-sharing compliance.

6. Several submitters presented the potential risk to open access to data that new tools and models may pose if not managed properly, calling instead for the improvement of existing open databases rather than new ones. The dominant view of the submitters is one of caution to not interfere with open science systems and to avoid fragmentation and inefficiencies. However, several Parties support open access to data but consider it is not sufficient to achieve equity, calling for an increased awareness of obligations, metadata improvements and integration of data systems. One Party and one observer consider open systems a failure and an enabler of data extraction without regulation and call for conditions on access to and use of digital sequence information, and a strong governance of databases and data tools to allow for traceability and compliance verification.

2. Capacity building

7. While capacity building was presented by some submitters as a tool to increase accountability and accessibility, it was strongly emphasized in the vast majority of submitters as the core solution to the fairness and equity gap, and in that sense goes beyond data accountability or accessibility.

8. The submitters presented four main categories of capacities:

9. Technical capacity, including: laboratory skills, sequencing and analysis of sequences, and bioinformatics skills. There was strong support in the submissions on the need for improved bioinformatic skills.

10. Infrastructure capacity, including: data storage, computational systems to support the analysis of the data, and database nodes. The need for database nodes, particularly in developing countries was mentioned.

11. Institutional and legal capacity, including: the ability to understand obligations across national and international fora, and the capacity to implement existing access and benefit-sharing frameworks.

12. Collaborative capacity including: the facilitation of partnerships and technology transfer, for some through research networks.

13. Capacity building was also presented by several Parties and observers as an enabler of compliance, with an empowerment of users and institutions through information as a way to avoid complex rules or the need for new databases.

3. Tracking and tracing of digital sequence information on genetic resources

14. Views diverged regarding traceability of digital sequence information on genetic resources. The majority of submitters, including Parties and observers, cautioned against introducing traceability systems, qualifying them as technically burdensome or unfeasible, and unnecessary as it would not add significant value and would hinder research and innovation. The submitters also state this would run contrary to decision [15/9](#) paragraph 5 which recognizes that tracking and tracing of all digital sequence information on genetic resources is not practical. On the other hand, two Parties and one observer strongly support the use of permit-based tracking systems linked to access and benefit-sharing frameworks stating this would avoid biopiracy and enable sovereignty. These views present both a full lifecycle traceability system from upload to commercialization, and a lighter

approach to trace some use of some data, possibly using blockchains. The latter approach was supported by another Party.

4. Data sovereignty and traditional knowledge in indigenous peoples and local communities

15. All submitters which addressed this topic recognized the legitimate rights and interests of indigenous peoples and local communities regarding digital sequence information on genetic resources, and that traditional knowledge requires specific governance approaches, stating that these are currently only partially addressed in existing systems. A divergence of views exists on whether new tools addressing these gaps should be voluntary and flexible or require stronger regulatory framework and legally binding conditions to data access and use.

16. Several submitters highlighted that indigenous peoples and local communities must be central to- and directly involved in-the governance of databases and data tools in order to reflect the diversity of knowledge systems and call for a flexibility of database structures around traditional knowledge. They encourage the use of traditional knowledge and attribution labels to ensure recognition without restricting access to data but cautioned against heavy regulatory systems.

17. Also, two Parties and one observer advocated for stronger control over: data access to support data sovereignty, compliance with prior informed consent, and conditions of data use. One observer proposed legally binding access and use agreements enforced by user logs, time-limited data retention, and intellectual property policy as a combination of tools to prevent biopiracy and ensure benefit-sharing.

18. Finally, two observers promoted the adoption of data sharing and stewardship frameworks by databases, as well as the integration of indigenous peoples and local communities' rights and traditional knowledge labels. The observers noted this can be achieved via improved metadata fields and labels and doing so would be an example of using technology to enhance the rights and sovereignty of indigenous peoples and local communities over their data in databases.

B. Views on models and tools, including databases

1. CBD-hosted database for digital sequence information on genetic resources

19. Two Parties and one observer supported or proposed the development of a database-hosted by the Convention on Biological Diversity in order to improve compliance with access and benefit-sharing frameworks, transparency in the use of the digital sequence information on genetic resources, and equitable benefit-sharing. A permit-based tracking system integrated with the Convention on Biological Diversity's Clearing-House Mechanism and increased involvement of the provider countries of genetic resources were all mentioned as methods to improve existing database systems.

20. However, the majority of submitters opposed or strongly cautioned against the creation of such a database. Both Parties as well as observers from the scientific community and the private sector pointed to the existing global public database infrastructure, in particular the International Nucleotide Sequence Database Collaboration, arguing this already ensures open access to data and supports transparency and accountability. Further, submitters acknowledged that recent efforts have been made to improve existing gaps, notably regarding geographical origin of the genetic resources from which the sequences are extracted. Key concerns were raised regarding the creation of a new database, these include concerns relating to the duplication of existing systems, which would lead to unjustified and high financial and technical cost, thereby diverting resources from much needed capacity building on the use of genetic and genomic data; increased fragmentation of the global sequence data ecosystem, and a lack of incentives for data submission from the scientific community. These concerns were considered counter to the principles in decision 15/9 of not hindering research and innovation (paragraph 9(e)) and being efficient, feasible and practical (paragraph 9(a)).

21. Additionally, some submitters proposed that such a database could instead support an increased interoperability between decentralized or federated systems, and existing databases and platforms. They noted the potential role for the Secretariat of the Convention in aligning frameworks

and protocols between databases and regional or national nodes, allowing them to retain their independence.

22. Finally, two Parties did not oppose the creation of a Convention on Biological Diversity-hosted database but called further analysis of cost, administrative and intellectual property considerations.

2. Other tools and models

23. Most submitters converged on the need to strengthen existing databases, often in place of replacing existing ones.

(a) Improvement of existing global databases

24. This was the dominant proposal in many submitters of both Parties and observers, centered around the strengthening of the International Nucleotide Sequence Database Collaboration with improved metadata fields (such as country of origin; traditional knowledge; legal compliance declaration; biocultural labels; and self-declaration compliance systems), better information sharing on access and benefit-sharing obligations and expectations, and attribution tools for countries, institutions, and traditional knowledge.

25. Several of the submitters also advertised linkages and interoperability between databases as a way to benefit from some specialized databases while preventing a fragmentation of the data itself. Tools serving this purpose evolved around the use of standardized metadata, ontologies and digital object identifiers.

(b) National databases

26. However, three submitters encouraged the creation of national databases, but linked to global systems, in order to impose national access conditions and manage data sovereignty. These national databases are envisioned to use unique identifiers not only for the data but also the users in order to track digital sequence information on genetic resources access and use, linking sequences to products. This was strongly opposed by many as technically infeasible, costly and hindering for research and innovation.

(c) The Clearing-House Mechanism of the Convention on Biological Diversity

27. Three submitters presented the potential for the Clearing-House Mechanism to play a central role for data governance, and to track permits and proofs of compliance with access and benefit-sharing frameworks. One Party submission added that the Clearing-House Mechanism could also track and monitor the use of digital sequence information on genetic resources, and cross-reference sequences with national permits, communicating with provider countries through notifications.

28. However, the most widely shared position is a moderate use of the Clearing-House Mechanism as a facilitation and coordination tool for non-monetary benefit sharing, an information and awareness hub for access and benefit-sharing obligations and legal frameworks, and as a monitoring tool for the purpose of the evaluation of the Multilateral Mechanism.

29. Finally, several submitters implicitly suggested to limit the role of the Clearing-House Mechanism to capacity-building and suggested to improve its efficiency but not expand its current functions.

(d) Artificial Intelligence

Artificial intelligence was addressed in a few submissions and was regarded as an enabler of compliance and education, and something that databases should include and adapt to, not restrict. One Party remarked that researchers are increasingly relying on artificial intelligence models rather than raw sequences, potentially reducing direct interaction with databases in the future. The submission continued to state that in order to make the Multilateral Mechanism future-proof, data governance models should not focus on data access but adapt to new technologies. One submission indicated that advanced analytics are part of an evolving ecosystem which is needed to make data

increasable usable while another submission expressed concern, suggesting that the increased use of artificial intelligence tools could lead to a widening of a capacity gap and increased inequality.
