**CBD Notification 2021-063 - Submission of views and new information on policy approaches, options or modalities for digital sequence information on genetic resources from CAB International 29 September 2021:** [**https://www.cabi.org/**](https://www.cabi.org/)

CABI is an international not-for-profit organization with 49 Member Countries that uses genetic resources in its mission to improve people’s lives by providing information and applying scientific expertise to solve problems in agriculture and the environment. This is achieved through knowledge sharing and the application of scientific research to improve global food security and safeguard the environment. CABI has implemented practices to ensure compliance with the Nagoya Protocol on Access and the Fair and Equitable Sharing of Benefits and has implemented policy to ensure compliance and best practice. CABI continues to believe that amendments to the Nagoya Protocol are not necessary in respect to Digital Sequence Information (DSI) and are happy to see it treated at a Country level. However, this would mean that countries will take their own position on this, potentially making international collaboration and usage difficult. To avoid this, it would be helpful to have a common agreement on the generation of DSI and how it can be used so as not to impede innovation in the life sciences.

**CABI’s general response to the document CBD/WG2020/3/CRP.1** of 31 August 2021 available at <https://www.cbd.int/conferences/post2020/wg2020-03/documents>. A report of the OPEN-ENDED WORKING GROUP (OEWG) ON THE POST-2020 GLOBAL BIODIVERSITY FRAMEWORK, Third meeting Online, 23 August – 3 September 2021 entitled *Digital sequence information on genetic resources*.

*The OEWG draft recommendation to the Conference of the Parties (the text has not been negotiated or agreed) to create a practical system to ensure fair and equitable sharing of the benefits arising from the use of digital sequence information on genetic resources and associated traditional knowledge.*

CABI agrees that there is the need to continue working on those aspects that could link digital sequence information on genetic resources with associated traditional knowledge. CABI does not see the need for regulating access to digital sequence information on genetic resources, and supports open access to digital sequence information on genetic resources. It is the use of DSI in products and tools for the market that should result in benefit sharing. CABI agrees that any approach to address digital sequence information on genetic resources should not prevent access to digital sequence information.

CABI agrees that the technical capacity to generate, access and use digital sequence information on genetic resources is still low in some developing countries and therefore the “benefits of having open-access” are not fairly or equitably available to all at present. However, there are not many countries that are not generating and using DSI in their research programmes.

CABI also agrees that a further review of the efficiency and efficacy of the current modality, including how digital sequence information on genetic resources is currently used is considered necessary and that mechanisms for traceability of digital sequence information on genetic resources are needed. Any approach needs to consider that open access to DSI in public databases should give legal certainty, be practical and have a multilateral approach. CABI feels strongly that innovation based on digital sequence information on genetic resources is essential for sustainable use and conservation of biodiversity.

CABI agrees that capacity-building is necessary, including through technology transfer in mutual collaboration. CABI is sharing such benefits through its current work through research collaboration, training, technology co‑development and more. Although there may be other potential mechanisms for achieving this there is potential for a multilateral benefit-sharing‑ mechanism, depending on how it is built and ensuring that it focuses on benefits for utilisation of DSI and not its generation and its role in identifying and cataloguing biodiversity.

CABI’s stated position on DSI is provided in annexe 1 below and remains unchanged. We agree that the use of DSI should result in benefit sharing. However, its generation and publication are a requirement for the taxonomic description and cataloguing of a country’s biodiversity to facilitate monitoring and conservation of it. This in itself is the benefit that is shared and it is independent of who does this (i.e. the country holding the genetic resource or those accessing it from outside the country). If material is accessed by foreign researchers, sequenced and the data is placed in the public domain this is the act of providing appropriate benefit sharing for this use. The comparison of data against this resource to enable its identification is part of this process. The capacity to do this is becoming universal although it is agreed that there is a need for capacity building to make this more uniform. Funding to achieve this could come from a multilateral benefit sharing mechanism that includes appropriate benefits arising from the exploitation of DSI through placing income generating products on the market and NOT its generation and publication.

Traceability follows from the mandatory inclusion of DSI metadata with each deposit of data in the public databases. However, using this data for comparison purposes to gain a name or taxonomic position for an inventory of biodiversity or to identify an unknown should not be subject to further benefit sharing if the result goes into the public domain.

CABI agrees that there are several possible approaches and that should all possible modalities include all the elements listed in paragraph 11 (points a – h) of the document CBD/WG2020/3/CRP.1. CABI believes that any such approach should refrain from applying monetary benefit sharing to DSI generation, publication and comparative genomics for description, identification or taxonomic purposes. As with genetic resources themselves, access and use permissions and terms and conditions (PIC and MAT) for DSI are a matter for negotiation with provider countries. CABI agrees that any appropriate share of benefits resulting from DSI utilisation as mandated under Nagoya Protocol or national provisions to implement it, or ABS agreements with individual countries, should be paid into a multi-lateral mechanism (i.e. the global biodiversity fund) and this mainly used to support capacity building and conservation activities.

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**Annexe 1. CAB International’s (CABI) position regarding Digital Sequence Information**

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CABI continues to believe that amendments to the Nagoya Protocol are not necessary in respect to Digital Sequence Information (DSI) and are happy to see it treated at a Country level. However, this would mean that countries will take their own position on this, potentially making international collaboration and usage difficult. To avoid this, it would be helpful to have a common agreement on the generation of DSI and how it can be used so as not to impede innovation in the life sciences.

**CABI position**

* Generating and publishing sequence data is considered as the production of descriptive information on the organism and therefore not utilisation. As such, it should be out of Nagoya Protocol regulatory scope.
* Publishing the sequence as electronic data is an act of sharing such descriptive information and thus meets any benefit-sharing commitment required.
* DSI can be used at many non-exploitative levels: for example, its use to confirm identification, this is an observation, not research; in most cases the resulting sequence data are published.
* If DSI is used for financial benefit then this should be considered utilisation and the full benefit sharing aspect would be negotiated with the provider country as would be done for access to the organism itself. Such use and its implications should be made clear on terms and conditions of use of public databases containing DSI.
* The generation and use of DSI must be considered when negotiating access, i.e. be expressed in the Mutually Agreed Terms (MAT) and presented in any Material Transfer Agreement (MTA) to give clarification on what can and cannot be done regarding DSI (at least until clarification is given by the Conference of the Parties and reflected [if needed] in guidance or regulation).

**Rationale:** Selected DSI such as barcodes are becoming standard tools for identification and phylogenetic characterisation of species and populations: The real power of this approach becomes most obvious when sequences from multiple individuals and sources (countries) are freely shared and duly acknowledged. Whole genome sequencing will, without any doubt, have a similar impact on taxonomy. We argue strongly that DSI generated for taxonomic or descriptive purposes needs to be freely shared in the public domain to help address the taxonomic impediment that the CBD recognises, as well as to meet the needs of agriculture and other sciences. Indeed, we suggest that such generation and publishing of DSI should be considered as part of a country’s responsibilities under Article 7 (Identification and Monitoring) and 17 (Exchange of Information) of the CBD.