TEMPLATE FOR COMMENTS

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Title of document reviewed:	The Emergence and Growth of Digital Sequence Information in Research and Development: Implications for the Conservation and Sustainable Use of Biodiversity, and Fair and Equitable Benefit-Sharing – A Fact-Finding and Scoping Study Undertaken for the Secretariat of the Convention on Biological Diversity

Comments on the draft fact-finding and scoping study		
Page #	**Para #**	**Comment**
0	0	Missing aspect: the study talks mostly about DSI in the public domain. Besides this, is it common practice to sell DSI in private databases, e.g. from one company to the other?
0	0	Issues of scope associated with terminology are very important with regard to implications of the use of digital sequence information for the third objective of the Convention and the Nagoya Protocol. On page 19 para 1 it is stated that these were not part of the terms of reference for this study, however, decisions XIII/16 and NP-2/14, respectively, demand for a study to clarify terminology and concepts and to assess the extent and the terms and conditions of the use of digital sequence information on genetic resources *in the context of the Convention and the Nagoya Protocol*. Therefore, some elaborations of issues of scope associated with terminology in this specific context would have been useful for the further discussions. Moreover, while the discussion on the scope of the Nagoya Protocol is largely lacking in this study, the authors already anticipate the assumption that there is a general obligation for benefit-sharing for digital sequence information. However, in order to justify this assumption, a discussion on the scope would be required first.
0	0	The provision of a summary of the previous work and negotiations to this and related subjects (digital sequence information, derivatives, temporal scope, …) in the history of the CBD and Nagoya Protocol negotiations would be important in order to obtain a comprehensive picture on this topic. This could also include an overview of how existing regulations deal with digital sequence information.
0	0	The structure of the study is unclear and confusing at some points. It is not intuitive what line the report is following. It should be more clearly structured, e.g. by type of utilization or by sector. Under each section the same topics and questions should be addressed to provide a comprehensive, structured and comparable overview.

0	0	A general overview of the nature of what digital sequence information refers to would be helpful and essential in the beginning (rather than starting off the discussion of the uses of digital sequence information in the various sectors). This should elaborate on different types of digital sequence information (e.g. non-coding vs. coding DNA sequences, regulatory sequences, conserved sequences, genes that encode specific traits, etc.). The following sections could then refer to particular types of sequence information, their uses in the various sectors as well as potential implications for benefit-sharing.
0	0	Missing aspect: the study does not address the role of digital sequence information on genetic resources in the context of "big data" applications, in which not the information of a specific sequence is relevant, but rather general trends across a multitude of sequences or datasets.
0	0	Missing aspect: the potential link of digital sequence information to traditional knowledge associated with genetic resources may be relevant in the context of the Nagoya Protocol.
10	38	Where is the information in this paragraph coming from? Reference is missing.
11	5	Where is the information in this paragraph coming from? Reference is missing.
11	17	This paragraph needs an addendum. Material is and will still be important as reference in the future for any research and development activities. As a researcher, you will not want to work with e.g. a DNA sequence for years and find out in the end that it was somehow wrong – e.g. from belonging to another species or simply containing errors. Since it is so cheap our days to sequence organisms, I guess most people would verify the digital sequences of the material they are working with before they invest in large investigation projects about it.
11	23	How reliable is this sequence data?
11	31	How affordable are these new technologies? If it is becoming extremely cheap, maybe there is not so much North-South inequality regarding the technical equipment for research anymore. If basically everyone can easily generate DSI from the genetic resources because the new techniques are so affordable, it might questionable why there should be benefit sharing on the data itself.
13	6	The study lacks a discussion.
18	3	A lot of information for this study was gathered through interviews with a wide range of stakeholders and experts. Some explanations on the procedure to select these stakeholders would be helpful to understand the approach, as well as to potentially underline the comprehensiveness and unbiasedness of the study. In many instances, it is difficult to assess the value of these statements, because quantitative information or references to such information is lacking.
22	3	The sentence *"…it is unclear whether a partial coding sequence or a DNA sequence that regulates gene expression constitutes a functional unit of heredity, and so qualifies as a "genetic resource", …*" is misleading, because "genetic resources" are not solely defined by *constituting functional units of heredity*, but as genetic *material*, which in turn is defined as any *material* of plant, animal, microbial or other origin containing functional units of heredity. Therefore, digital sequence information would by definition not qualify as "genetic resource".
23	2	The term "*intangible materials*" does not make sense.
23	3	The sentence *"… it is argued that the term runs the danger of extending the scope of ABS to artificial sequences…"* is misleading, because it implicitly states that "natural sequence information" (in contrast to "artificial sequence information") would be within the scope of ABS.
26	6	It is not clear how "industrial biotechnology" is different from other "biotechnology" activities and why these processes and products are often neither sold nor patented (if this is the case).
32	4	How do database managers know that many datasets are not entered into international public databases? Some further explanations should be provided.

34	4	This paragraph and the following give the impression that the collection and sequencing of physical samples are rather an exception and most people work with digital sequence information that is already in databases. This, however, stands in contrast to the exponential growth of data uploaded into databases.
39	4	While the discussed approaches that attach conditions to the use of digital sequence information may be important to consider for benefit-sharing, it is important to note that this will only be the case if there will be a benefit-sharing obligation for digital sequence information.
40	11	Additionally, the legal status is unclear.
43	1	In this section it should be emphasized that in biodiversity conservation and sustainable use research often requires physical material besides digital sequence information.
43	4	It is not clear, why in particular the “genetic sequences of microorganisms” are highlighted in this section.
44	4	The sentence could be amended as follows: “*For example, using sequence information, researchers can calculate the likelihood of a non-native species becoming invasive in an ecosystem by determining their source populations, and thus their introduction pathways,* <u>and the evolutionary history of the invasive genotypes</u>.”
51	27	This is an extremely important conclusion from our point of view and should be emphasized even more.
56	3	It should state: “*Conserved sequences* <u>may</u> *create complexities for benefit-sharing, …”*
57	6	The term “*’dematerialization’ of genetic resources*” does not make sense, as genetic resources are defined as material, thus, they cannot be dematerialized (this would change the definition of genetic resources).
63	2	While it is true that there are “*significant opportunities for non-monetary, and possible monetary, forms of benefit-sharing*”, it should also be noted that there is currently no general benefit-sharing obligation for digital sequence information according to the Nagoya Protocol.

Please submit your comments to secretariat@cbd.int or by fax at +1 514 288 6588.