TEMPLATE FOR COMMENTS

Contact information	
Surname:	Ye
Given Name:	Wang
Government	
(if applicable):	
Organization:	Foreign Economic Cooperation Office, Ministry of Environmental Protection of China
E-mail:	wang.ye@mepfeco.org.cn
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	Terminology: It is suggested using the terminology of “sequence information on genetic resources” instead of “digital information on genetic resources’, since “digital’ would mislead people focus on digitized information (e.g. data from network database), while ignore such sequence information in print media, though which could be digitized as well. And “digital” may overemphasize the digitized information, there by the key point of ABS would be partial to the interaction between the principal parts of sequencing or sequence publishing and the users (they are both the users of genetic resources), rather than the genetic resources providers and users. The “information” is not only restricted to data of certain genetic material itself, but the understanding after comprehensive analysis including the functions and others.
0	0	The main content of ABS: The main content of ABS on sequence information should be how to face the challenge of ABS when the users benefit from the published sequence information, while don’t need to acquire the physical materials, such as certain plant leaves. The perspective of discussion in the report was focused on the providers and users of sequences, deviated from what the Nagoya Protocol talked about.
0	0	Monitoring: One of the key points of monitoring the sequence information utilization is to guarantee that the disclosure of the sources of sequence information accurately and objectively by users.
10	1	There’s a surplus brackets.
44	29	It is suggested to add the sentence of “Transcriptomic information is used to study species interaction and coexistence in existing plant communities (Han et al. 2016).” before “ The science is still evolving”. Han BC, Umaña MN, Mi XC, Liu XJ, Chen L, Wang YQ, Liang Y, Wei W, Ma KP. 2017. The role of transcriptomes linked with responses to light environment on seedling mortality in a subtropical forest, China. Journal of Ecology 105: 592-601.
47	23	It is suggested to add the sentence of “however, it is challenging to‘ re-create’ a genetically diverse population.” at the end of line 24.
22	23	‘and’ should be gone?

0	0	Further analysis is expected on what extend the sequence information could replace the material itself.
		Additional rows can be added to this table by selecting “Table” followed by “insert” and “rows below”

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