TEMPLATE FOR COMMENTS

Contact information	
Surname:	Schigel
Given Name:	Dmitry
Government	
(if applicable):	
Organization:	Global Biodiversity Information Facility (GBIF)
E-mail:	dschigel@gbif.org
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**
11	5	not most
11	7	not true
11	21	Why only one platform mentioned?
11	22	add GBIF Data User Agreement https://www.gbif.org/terms/data-user
16	15	Add ”most notably GBIF”
16	28	GGBN is the only one mentioned, which is developing, but a project based initiative. GBIF needs to be mentioned here, too, as an intergovernmental data infrastructure
16	40	Discuss CC-BY-TC licenses here, including common misconceptions around
17	10	, and adds a valuable information layer, including new and complementary evidence of b provided at the planetary level by GBIF.
18	37	very little, unless top experts explain choice of respondents
23	38	in particular, this a new and very rapidly growing of biodiversity research with a huge potential and relevance for CBD mission
24	39	put together, next gen sequencing and barcoding work powerfully as metabarcoding – identification, and sometimes, quantification of organisms in the environmental samples of any origin from short fragments of DNA
29	24	add 3.1.6 on molecular biodiversity research
33		add lines on MIxS and GGBN data standards
63		Conclusions do not really conclude much – if authors are the chosen experts, they need to accept responsibility to give CBD clearer guidance. From the text it seems that authors lean towards the principle of openness of sequence data, with exceptions and species cases. If so, why not write it straight out? Nagoya is to regular transfer of physical material, sequences are data and CBD is recommended to support open data approach, sequence data included. This is will do much more to benefit sharing than erecting the legal walls that would be nearly impossible to defend

0	0	It is a very well prepared report and I admire depth of the analysis done in limited time. Number of respondents, coverage of data systems and data networks could be more comprehensive and detailed.

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