

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/Lines | Comment |
| 11 | 21-32 | Advent of MinION, the world's "first and only nanopore DNA sequencer" is low cost technology that would sequence many genetic materials at very low cost and within a fraction of time. This may lead to development in more genetic information in digital form that could be utilized in synthetic biology for various purposes. |
| 13 | 4 th para | Many advantages of digital sequence information on genetic resources have been given in the executive summary but it is time to cite current and unforeseen disadvantages/demerits by utilization of sequence information in agriculture and other areas of science and technology. In agriculture, many countries are still not accepting GM crops for use in their own country then how come a large number of GM crops and other products originated from synthetic biology can be accepted in many countries. In another term what would be implications of over exploitation of synthetic biology on ecology, environment agriculture and human in future. Since vast microbial diversity exists in the India what would be implication of synthetically developed microbes/processes on the ecology of microorganisms and finally their impact on sustainability of biosphere. This should be discussed in the draft. |
| 19 | 9-27 | Various terminologies have used equivalent to "digital sequence information" by number of agencies and here the final document should give a single well justified and ratified terminology to remove all confusion in final draft. |
| 22 | 8-10 | Removal of "digital" word is justified because information/data can be in any form and would have same implication. |

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| 22 | 32 | A more accurate term “ <i>Biomolecular data</i> ” has been proposed for “ <i>digital sequence information</i> ” and it seems this term “ <i>Biomolecular data</i> ” includes sequence/composition of DNA, RNA, protein, carbohydrate, polyphosphate etc. |
| 23 | 1-23 | “ <i>Information</i> ” per se is <i>intangible</i> that may create problem in access benefit sharing due to confusion of its origin. It could be from nature and can be accessed from any region or country, or synthesized artificially. It seems “ <i>Data</i> ” is more appropriate word as it looks <i>tangible</i> . |
| 28 | 8-11 | “Smart Breeding” can possible through synthetic biology and but generation of numerous genetically modified crops may have devastating effects on wild /native biodiversity in the region and thus, it needs cautious use to save existing biodiversity of biosphere. |
| 35 | 22-34 | It is expected that bacteria collected from remote locations may have special traits but these locations are fragile and disappearing and thus synthetic biology can revolutionize and help developing new molecules utilizing molecular information of soil from your backyard field based on digital information of bacteria isolated from remote locations. |
| 36 | 35-39 | DNA Printer: A machine that allow creating genes, genetic element starting with digital sequence information. This innovation is first of its kind introduced by SGI-DNA and this may revolutionise future science and technology. This information in this document is very pertinent and useful to create awareness throughout the world on this frontier area of science. |
| 39 | 13-22 | In 2005, WFCC has developed a Global Unique Identifier (Guid) and TRUST System for tracking microorganisms in terms of utilization. This kind of tracking system may help implementation of ABS mechanisms in right spirit. |
| 43-45 | | Digital sequence information and biodiversity conservation: It deals with use of already available digital information in biodiversity conservation but there is need to develop “Global Repository of Sequence Information” as a platform to store and provide information to all the countries so to decide possible benefit sharing with right person/agency. |
| 47 | 37-40 | Labelling “ <i>natural</i> ” on synbio products such as vanillin, saffron, artemisin and stevia is not advisable and it is proposed to develop ‘ <i>global logo</i> ’ for synbio products to differentiate from natural products. If synbioproducts will label with natural tag it will jeopardise livelihood of small farming communities that are involved in such practices. |
| 54 | 30-33 | Possible mechanisms of valuation of “digital sequence information” are needed to be developed by debating/ consultation on this matter at various platforms worldwide and it should be reflected in the final draft of this document. |
| 56 | 15-21 | In one of the studies, it has been noticed that bacteria isolated from different niches of different hemispheres share 93% gene contents similarity and thus create complex situation for benefit sharing and thus matter of great relevance to examine such conditions under the ambit of Nagoya Protocol. |

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| General Comments | There should be a glossary of all terminologies used in the final documents. For example: digital sequence information, democratise science, biobrick, open innovation, nucleotide sequence information, synthetic biology, environmental genomic, biologic, smart breeding, swift compilation, foundries, DNA printer, biomonitoring, de-extinction, biological factories, synbioproducts, Protected common, dematerialization, synthetic gene, natural gene, single molecule sequencer, DNA barcode, gene/genome editing, citizen science sourcing, unfamiliar genes, reverse engineering, etc. |
| | This fact finding and scope draft is containing many issues with examples pertaining to digital sequence information on genetic resources that still need deliberation to formulate document that are to be relevant worldwide. |

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