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AD HOC TECHNICAL EXPERT GROUP ON
DIGITAL SEQUENCE INFORMATION ON
GENETIC RESOURCES
Montreal, Canada, 17-20 March 2020

REPORT OF THE AD HOC TECHNICAL EXPERT GROUP ON DIGITAL SEQUENCE INFORMATION ON GENETIC RESOURCES

INTRODUCTION

A. Background

1. The Conference of the Parties to the Convention on Biological Diversity adopted, at its fourteenth meeting, decision [14/20](#) on digital sequence information on genetic resources and noted the divergence of views among Parties regarding benefit-sharing from the use of digital sequence information on genetic resources, in which it decided to establish a science- and policy-based process towards resolving this divergence, including:

(a) An invitation to Parties, other Governments, indigenous peoples and local communities, relevant stakeholders and organizations to submit their views and information (para. 9):

- (i) To clarify the concept, including relevant terminology and scope, of digital sequence information on genetic resources and if and how domestic measures on access and benefit-sharing consider digital sequence information on genetic resources;
- (ii) On benefit-sharing arrangements from commercial and non-commercial use of digital sequence information on genetic resources;

(b) An invitation to Parties, other Governments and indigenous peoples and local communities to submit information on their capacity-building needs regarding the access, use, generation and analysis of digital sequence information on genetic resources, in particular for the three objectives of the Convention (para. 10);

(c) A request to the Executive Secretary (para. 11 (a)-(e)):

- (i) To compile and synthesize the views and information referred to above;
- (ii) To commission a science-based peer-reviewed fact-finding study on the concept and scope of digital sequence information on genetic resources and how digital sequence information on genetic resources is currently used building on the existing fact-finding and scoping study;
- (iii) To commission a peer-reviewed study on ongoing developments in the field of traceability of digital information, including how traceability is addressed by databases, and how these could inform discussions on digital sequence information on genetic resources;
- (iv) To commission a peer reviewed study on public and, to the extent possible, private databases of digital sequence information on genetic resources, including the terms and conditions on which access is granted or controlled, the biological scope and the size of

the databases, numbers of accessions and their origin, governing policies, and the providers and users of the digital sequence information on genetic resources, and encouraged the owners of private databases to provide the necessary information;

- (v) To commission a peer-reviewed study on how domestic measures address benefit-sharing arising from commercial and non-commercial use of digital sequence information on genetic resources and address the use of digital sequence information on genetic resources for research and development, taking into account the submissions provided by Parties, other Governments, indigenous peoples and local communities, relevant stakeholders and organizations;
- (d) The establishment of an extended Ad Hoc Technical Expert Group (AHTEG), involving participation from representatives of indigenous peoples and local communities (para. 11), and a request to the Executive Secretary to convene a meeting of the extended AHTEG (para. 11(f)) to:
 - (i) Consider the compilation and synthesis of views and information and the peer-reviewed studies referred to above;
 - (ii) Develop options for operational terms and their implications to provide conceptual clarity on digital sequence information on genetic resources, considering in particular the study on the concept and scope of digital sequence information on genetic resources and how digital sequence information on genetic resources is currently used building on the existing fact-finding and scoping study;
 - (iii) Identify key areas for capacity-building.

2. The outcomes of the meeting of the AHTEG are required to be submitted to the Open-ended Working Group on the Post-2020 Global Biodiversity Framework, established by the Conference of the Parties under its decision [14/34](#). The Working Group was requested to consider the outcomes and to make recommendations to the Conference of the Parties at its fifteenth meeting on how to address digital sequence information on genetic resources in the context of the post-2020 global biodiversity framework.

3. The Conference of the Parties serving as the meeting of the Parties to the Nagoya Protocol adopted, at its third meeting, decision [NP-3/12](#) on digital sequence information on genetic resources. In their decision, the Parties to the Nagoya Protocol welcomed decision 14/34 and decision 14/20 of the Conference of the Parties to the Convention. They requested the Working Group on the Post-2020 Global Biodiversity Framework to submit the outcome of its deliberations for the consideration of the Parties to the Nagoya Protocol at their fourth meeting.

4. With financial support from the European Union, the meeting of the Ad Hoc Technical Expert Group was held virtually from 17 to 20 March 2020.

B. Attendance

5. By notification 2019-053 of 12 June 2019, Parties, other Governments, indigenous peoples and local communities, relevant organizations and stakeholders were invited to nominate experts to the AHTEG.

6. The Secretariat received a total of 44 nominations from Parties to the Convention with more than 5 nominations from each region except Central and Eastern Europe, from which only 3 nominations were received. In addition, 25 nominations were received from organizations and two from indigenous peoples and local communities. The Secretariat selected 37 experts on the basis of their experience with and knowledge of digital sequence information on genetic resources, giving due regard to regional and gender balance.

7. Following consultation with the Bureau of the Conference of the Parties, the composition of the AHTEG was announced in notification 2019-96 of 28 October 2019. The expert from the Plurinational State of Bolivia who was originally selected stepped down, and was replaced by an expert from

Argentina, following consultation with the Bureau. In addition, an expert nominated by the World Health Organization was later accepted to be a member of the AHTEG.

8. Due to the travel restrictions imposed in the light of the novel coronavirus (COVID-19) pandemic and in order to minimize risks to the safety and health of all participants, the Secretariat decided to convene the meeting of the AHTEG, scheduled from 17 to 20 March 2020, virtually using online technological solutions. The Bureau was informed of the change.

9. Experts nominated by the following Parties participated in the virtual meeting: Argentina, Belarus, Brazil, Canada, China, Costa Rica, Belgium, Bulgaria, Cameroon, Croatia, Ecuador, the European Union, India, Japan, Norway, the Philippines, the Republic of Korea, Saint Lucia, Senegal, South Africa, Sudan, Uganda, and the United Kingdom of Great Britain and Northern Ireland participated in the meeting remotely.

10. Experts nominated by indigenous organizations, namely Andes Chinchasuyu from Ecuador and the Society for Wetland Biodiversity Conservation Nepal, also participated in the virtual meeting.

11. Experts nominated by the following organizations also participated in the virtual meeting: The African Union, World Health Organization, Secretariat of the Commission on Genetic Resources for Food and Agriculture, Secretariat of the International Treaty on Plant Genetic Resources for Food and Agriculture, World Intellectual Property Organization, CGIAR Centres, Consortium of European Taxonomic Facilities, International Chamber of Commerce, Peruvian Society for Environmental Law, Third World Network, and World Federation for Culture Collections.

12. The expert from the European Bioinformatics Institute (EMBL-EBI) was unable to attend the meeting due to priority tasks related to COVID-19. The expert from Global Genome Biodiversity Network was also not able to attend the meeting due to unavoidable circumstances. The full list of participants is contained in annexed III.

ITEM 1. OPENING OF THE MEETING

13. The meeting was opened by the Acting Executive Secretary of the Convention on Biological Diversity, Ms. Elizabeth Maruma Mrema, at 8 am, Montreal Time, on Tuesday, 17 March 2020.

14. In her opening remarks, the Acting Executive Secretary thanked the experts for their understanding and flexibility to adapt to the circumstances imposed on everyone due to the COVID-19 pandemic and for making it possible to join the meeting remotely. She expressed her regrets for the inconvenience the last-minute changes in the format of the meeting created for those who had made preparation to travel to Montreal for the meeting as previously planned.

15. She stressed that the Convention had an exceptionally busy schedule in 2020, with a high number of important meetings, many of which were designed to feed into the discussions on the post-2020 global biodiversity framework and ultimately the meetings of the Conference of the Parties to the Convention and its protocols. Although there would likely be a need to reschedule a number of in-person meetings, she emphasized that the Convention could not afford to delay all of its meetings since that would jeopardize the overall process and, for that reason, the Secretariat, in consultation with the Bureau, had decided to conduct a number of smaller meetings through virtual means.

16. She took the opportunity to express thanks to the European Union and Norway for their financial support to the process established under decision 14/20.

17. She urged the experts to find a way forward to help overcome the divergence of views and polarization that the subject of digital sequence information generated, in order to usefully inform the political decision-making process.

18. She highlighted how the meeting of the technical experts was a crucial piece in the process of this “super-year” on biodiversity and noted the importance of the participants’ expertise and technical input to help advancing science-based discussions. She reminded participants that a number of organizations were looking at the process on digital sequence information under the Convention with a view to informing

their own relevant processes. According to the Acting Executive Secretary, the AHTEG therefore had the chance and opportunity to help shape the dialogue on digital sequence information globally and assist appropriate policymaking in due course.

ITEM 2. ORGANIZATIONAL MATTERS

19. The meeting of the AHTEG was conducted through a virtual real time meeting and an online discussion forum hosted on the ABS Clearing-House and the Biosafety Clearing-House platforms. The latter was intended to facilitate an in-depth discussion on issues raised during the virtual meeting sessions. The schedule of the meeting was readjusted in order to enable and facilitate the participation of all the experts who were based in different time zones.

20. Thus, sessions of the virtual meeting took place from 8 a.m. to 12 noon Montreal time from Tuesday, 17 March, to Friday, 20 March 2020, while the online discussion forums ran between 12.30 p.m. and 6 a.m. Montreal time, during the first two days of the meeting.

21. The discussion forum was designed as a closed forum which only members of the AHTEG and Secretariat staff had access to. Supplementing the discussions at the sessions of the virtual meeting, the outcomes of the discussions were summarized and used to contribute to the substantive part of the report of the meeting.

22. The AHTEG elected Mr. Christopher Lyal of the United Kingdom and Ms. Lactitia Tshitwamulomoni of South Africa as co-chairs.

23. The AHTEG adopted the following agenda on the basis of the provisional agenda (CBD/DSI/AHTEG/2020/1/1) prepared by the Executive Secretary:

1. Opening of the meeting.
2. Organizational matters.
3. Consideration of the compilation and synthesis of views and information and the peer-reviewed studies.
4. Development of options for operational terms and their implications for the purpose of providing conceptual clarity on digital sequence information on genetic resources.
5. Identification of key areas for capacity-building.
6. Other matters.
7. Adoption of the report.
8. Closure of the meeting.

24. The AHTEG also agreed on the revised organization of its work as contained in annex II below.

ITEM 3. CONSIDERATION OF THE COMPILATION AND SYNTHESIS OF VIEWS AND INFORMATION AND PEER-REVIEWED STUDIES

A. Peer-reviewed studies

25. With financial support from Norway and the European Union, the Executive Secretary had commissioned the studies listed in paragraph 1(c) (ii) to (v) above. The drafts of all the studies were made available online for peer review as requested by the Conference of the Parties in its decision 14/20, paragraph 11.

26. The studies were finalized by the respective authors, taking into account the comments received within the timeframe allocated for the peer review of each study. The studies were made available for the consideration of the Ad Hoc Technical Expert Group as follows:

- (a) The study on concept and scope (CBD/AHTEG/DSI/2020/1/3);
- (b) The combined studies on traceability and databases (CBD/AHTEG/DSI/2020/1/4);

(c) The study on domestic measures (CBD/AHTEG/DSI/2020/1/5).

27. The full text of the peer-review comments received was made available online at <https://www.cbd.int/dsi-gr/2019-2020/studies/>.

28. Under this agenda item, the authors of each of the studies made a presentation which was followed by comments and questions for clarifications by the experts of the AHTEG. The presentations were focused on highlighting the major findings and elements that were considered to facilitate the deliberations of the AHTEG, mainly, under items 4 and 5 of its agenda. Accordingly:

(a) *Study on concept and scope*: The presentation focused on the flow of information associated with a genetic resource and provided an overview of the different groups proposed for digital sequence information, including the underlying rationale for the groups and a detailed description of the subject matter in each group. Potential terminology for each group was evaluated as well as additional issues which might be relevant to further clarify the concept and scope of digital sequence information;

(b) *Combined studies on traceability and databases*: The presentation focused on the International Nucleotide Sequence Database Collaboration (INSDC) as the central infrastructure for the exchange of nucleotide sequence data (NSD) and the rationale for limiting coverage in the study to NSD was explained. The presentation also covered the use of accession numbers and associated metadata for NSD across databases, its implications for traceability, and a breakdown of the information contained in INSDC databases (for example, species, geographic distribution). Finally, the presentation provided implications of observations on databases and traceability regarding digital sequence information other than NSD (for example, proteins, macromolecules);

(c) *Study on domestic measures*: The presentation provided an overview of existing domestic measures addressing digital sequence information, including terminology, access and/or benefit-sharing approaches, and implementation tools (for example, permits, contracts, benefit-sharing arrangements) used by countries.

29. Subsequent to each presentation, the experts were invited to ask clarification questions which were answered during the virtual meeting. Additionally, experts were invited to provide further comments and views on relevant issues raised by the studies in the online discussion forum. Experts were asked to focus their comments on the key observations arising from the study relevant to the mandate of the AHTEG. The outcomes of the deliberations concerning the studies in the virtual meeting and in the discussion forum are summarized in the report contained in annex I below.

B. Synthesis of views and information

30. As indicated in paragraph 1(c) (i) above, the Executive Secretary was requested to prepare a compilation and synthesis of the views and information submitted pursuant to paragraphs 9 and 10 of decision 14/20 of the Conference of the Parties to the Convention. The synthesis was made available as document CBD/DSI/AHTEG/2020/1/2 and the compilation of the full text of the submissions is available as document CBD/DSI/AHTEG/2020/1/INF/1.

31. The Secretariat presented key elements of the synthesis of views and information and the experts were invited to comment on the synthesis.

ITEM 4. DEVELOPMENT OF OPTIONS FOR OPERATIONAL TERMS AND THEIR IMPLICATIONS FOR THE PURPOSE OF PROVIDING CONCEPTUAL CLARITY ON DIGITAL SEQUENCE INFORMATION ON GENETIC RESOURCES

32. Under this agenda item, the AHTEG considered the technical and scientific scope of terms related to digital sequence information on genetic resources and developed options for operational scope, terms and their implications, to provide conceptual clarity.

33. In developing the options for operational scope, terms and their implications, the co-chair reminded the experts to consider the peer-reviewed studies, particularly the study on concept and scope

contained in document CBD/AHTEG/DSI/2020/1/3. To guide deliberations on this topic, the co-chair recalled the key elements of the study on concept on scope and introduced the document on salient points (CBD/AHTEG/DSI/2020/1/6) before introducing the various threads of the forum intended to facilitate the discussions on this item.

34. The discussions on this item were divided into two parts:

(a) First, the experts considered options to clarify (i) the scope of digital sequence information and (ii) the terminology for the different options. In clarifying the scope, the Group was asked to consider four incremental groups of subject matter potentially constituting digital sequence information, as proposed in the study on concept and scope, in order to evaluate the rationale for the different groups, as well as the subject matter of each of the options. In addressing terminology for the different options experts focused their discussions on terminology that is better suited for each of the different groups and to convey the concept and scope associated with digital sequence information on genetic resources;

(b) Secondly, the experts were asked to consider the implications arising from the different groups proposed for digital sequence information subject matter, concerning: (i) the traceability of different types of information; (ii) the use of digital sequence information and technologies enabled by digital sequence information in life sciences research and innovation processes; (iii) the International Nucleotide Sequence Database Collaboration (INSDC) in the open exchange and use of digital sequence information; and (4) measures governing access, benefit-sharing and compliance.

35. After very productive and valuable discussions on all issues during the virtual meeting, the deliberations continued in threads of the online forum intended to facilitate discussion on this item.

36. The outcomes of the deliberations of the virtual meeting as well as the online discussion forum for this item are contained in annex I below.

ITEM 5. IDENTIFICATION OF KEY AREAS FOR CAPACITY-BUILDING

37. In decision 14/20, paragraph 3, the Conference of the Parties to the Convention recognized that further capacity to access, use, generate and analyse digital sequence information on genetic resources was needed, and encouraged Parties and other Governments and relevant international organizations to support capacity-building and technology transfer, as appropriate, to assist in the access, use, generation and analysis of digital sequence information on genetic resources for the conservation and sustainable use of biodiversity and benefit-sharing.

38. Under this item, the experts were invited to identify key areas for capacity-building based on the information submitted, in accordance with paragraph 10 of decision 14/20, and as indicated in paragraph 1(b) above.

39. The Secretariat introduced elements related to this topic which have been drawn from the synthesis of views and information contained in document CBD/DSI/AHTEG/2020/1/2 as well as relevant developments on capacity-building processes under way in the Convention and its protocols. In considering key areas for capacity-building, the Secretariat provided the AHTEG with guiding questions for the further deliberations during the online discussion forum.

40. The outcomes of the discussions in the virtual meeting and in the online discussion forum are contained in annex I to this report.

ITEM 6. OTHER MATTERS

41. Participants noted that the virtual meeting posed certain challenges. The implications of limited availability of time for discussions and working in different time zones created a challenge; delays in responding to the discussions on the online forums were mentioned as an example. Participants stated that the virtual meeting had worked very well despite the challenges and expressed appreciation and thanks to the Secretariat for the quick turnaround in convening the meeting of the AHTEG virtually and servicing it so efficiently.

ITEM 7. ADOPTION OF THE REPORT

42. The co-chairs introduced the draft report of the Ad Hoc Technical Expert Group, which was adopted as orally amended. The report would be made available for consideration by the Open-ended Working Group on the Post-2020 Global Biodiversity Framework at its third meeting.

ITEM 8. CLOSURE OF THE MEETING

43. The experts expressed appreciation to the co-chairs for their extraordinary accomplishment in skilfully guiding and facilitating the meeting.

44. Following the customary exchange of courtesies, the virtual meeting of the Ad Hoc Technical Expert Group was closed at 6 p.m. on Friday, 20 March 2020, Montreal time.

*Annex I***OUTCOMES OF THE MEETING OF THE AD HOC TECHNICAL EXPERT GROUP ON DIGITAL SEQUENCE INFORMATION ON GENETIC RESOURCES**

1. The text below is a summary of the outcomes of the Ad Hoc Technical Expert Group (AHTEG) on Digital Sequence Information on Genetic Resources (hereinafter referred to as digital sequence information or “DSI”).

2. The experts recalled [decision 14/20](#), which notes that the term “digital sequence information” may not be the most appropriate term and that it is used as a placeholder until an alternative term is agreed.

I. SCOPE OF DIGITAL SEQUENCE INFORMATION ON GENETIC RESOURCES AND TERMINOLOGY

3. In clarifying the scope of digital sequence information, the AHTEG considered the four groups proposed in Study 1 on concept and scope (Figure 7 and Table 4 of the Study) and concluded that the four proposed groups were rational and helpful as a starting point for discussions. It noted that clearly defined groups would assist negotiators in the Convention process and other forums when discussing topics related to digital sequence information.

4. The experts discussed the distinction between “data” and “information”, noting that the latter could imply more processing than the former, and noting also that there is no clear boundary between the two.

5. In relation to the biochemical flow of information within a cell, the experts noted the ability to infer nucleic acid sequences from protein sequences (although imperfectly, because different DNA sequences may code for the same protein) and the current inability to readily infer nucleic acid or protein sequences from metabolites and macromolecules.

6. Building on the rationale proposed in Study 1, the AHTEG considered that the degree of biological processing and the proximity to the underlying genetic resource provide a rationale to group information that may comprise digital sequence information. The proposed groups are cumulative (Group 2 includes all elements of Group 1, and Group 3 contains all elements of Groups 1 and 2).

7. A distinction was made between genetic and biochemical information as included in Groups 1 to 3 indicated in paragraph 6 above and associated information related to a genetic resource, such as traditional knowledge associated with genetic resources, and other information, variously described as contextual, associated, or subsidiary information (see table 1 below).

8. The AHTEG discussed the importance and relevance of associated traditional knowledge to the utilization of digital sequence information on genetic resources and recalled that there are obligations to share benefits from the utilization of traditional knowledge associated with genetic resources under the Nagoya Protocol and the Convention.

9. In clarifying the scope of digital sequence information, the AHTEG agreed that the first three groups proposed in Study 1 could be considered as digital sequence information, while associated information previously assigned (in the study) to Group 4, including traditional knowledge associated with genetic resources, is not digital sequence information (see table 1 below).

Table 1. Clarifying the scope of digital sequence information on genetic resources

	Information related to a genetic resource			Associated information
	Genetic and biochemical information			
Group reference	<i>Group 1</i>	<i>Group 2</i>	<i>Group 3</i>	
High-level description of each group	DNA and RNA	Group 1 + proteins + epigenetic modifications	Group 2 + metabolites and other macromolecules	
Examples of granular subject matter	<ul style="list-style-type: none"> • Nucleic acid sequence reads; • Associated data to nucleic acid reads; • Non-coding nucleic acid sequences; • Genetic mapping (for example, genotyping, microsatellite analysis, SNPs, etc.); • Structural annotation. 	<ul style="list-style-type: none"> • Amino acid sequences; • Information on gene expression; • Functional annotation; • Epigenetic modifications (for example, methylation patterns and acetylation); • Molecular structures of proteins; • Molecular interaction networks. 	<ul style="list-style-type: none"> • Information on the biochemical composition of a genetic resource; • Macromolecules (other than DNA, RNA and proteins); • Cellular metabolites (molecular structures). 	<ul style="list-style-type: none"> • Traditional knowledge associated with genetic resources • Information associated with digital sequence information Groups 1, 2 and 3 (for example, biotic and abiotic factors in the environment or associated with the organism) • Other types of information associated with a genetic resource or its utilization.

10. Further, during the discussion regarding the scope of digital sequence information, the experts noted the following:

(a) That using the groups proposed for describing digital sequence information and associated information can provide conceptual clarity;

(b) Achieving conceptual clarity regarding digital sequence information is important to ensure legal clarity in all circumstances, and some experts noted that the distinction among different groups might be more important for certain approaches to benefit-sharing (for example, bilateral approaches) than others (for example, multilateral approaches);

(c) The importance and value of passport data in traceability (such as the provider country,¹ where the biological sample was collected, coordinates of sample collection, sample collection date, accession number or other unique identifiers, collector, etc.) as exemplified by the minimum information about a genome sequence (MIGS) specification by the Genomics Standards Consortium;

(d) That technological innovations might add to the granular subject matter and that this could be taken into account to accommodate future technological developments.

11. In addressing terminology, experts discussed a variety of terms as potentially appropriate for each of the Groups. Table 2 below summarizes potential terminology for the proposed groups.

¹ In accordance with the Convention on Biological Diversity, provider country hereinafter is understood as the country of origin of the genetic resource or the Party that has acquired the genetic resource in accordance with the Convention.

Table 2. Options for terminology to describe digital sequence information on genetic resources

Group reference	Group 1	Group 2	Group 3	Associated information
<p>Category/term</p>	<ul style="list-style-type: none"> • Nucleotide sequence data (NSD); • Genomic sequence information; • Genomics information; • Nucleotide sequence information (NSI); • Genetic Resource Sequence Data (GRSD); • Digital sequence data (DSD); • Data on the genomic DNA (or RNA) of a sample genetic resource 	<ul style="list-style-type: none"> • Genomic and proteomic sequence information; • Genomic and proteomic sequence information • Nucleotide sequence information (NSI); • Genetic information (GI); • Sequence data; • Nucleotide and amino acid sequence data (NASD); • Nucleotide and amino acid sequence and structural information (NASSI); • Nucleotide and amino acid sequence, structural and functional information (NASSFI); • Functional digital information of NSD; • Proteomic data; • Genomic and proteomic sequence information; • Data on the macromolecular composition of a sample genetic resource. 	<ul style="list-style-type: none"> • Genomic, proteomic and metabolomic information; • Genetic and “omic” information; • Metabolomic data; • “Omic” information • Genomic, proteomic and metabolomic information; • Data on the biochemical and genetic composition of a sample genetic resource. 	<ul style="list-style-type: none"> • Associated information; • Contextual Information; • Subsidiary Information.
<p>Other terms were additionally discussed, including the following: digital sequence information, natural information, digital genetic resource information, digital genetic resource data and information, genetic resource data and information, genetic information, all data on a sample (genetic resource) and <i>in silico</i>.</p>				

II. POTENTIAL IMPLICATIONS ARISING FROM THE DIFFERENT GROUPS

12. For each of the groups considered above, the AHTEG discussed implications: (a) concerning traceability of different types of information; (b) concerning the use of digital sequence information and technologies enabled by digital sequence information in life sciences research and innovation processes; (c) of the International Nucleotide Sequence Database Collaboration (INSDC) on the open exchange and use of digital sequence information; and (d) concerning measures governing access, benefit-sharing and compliance.

13. The experts noted the preliminary nature of the discussions and that the implications would depend on the nature of the benefit-sharing approach. They also noted that some of the potential implications were not discussed in depth as others and could benefit from further information or consideration.

A. Potential implications of different groups concerning traceability and INSDC

14. In discussing the peer-reviewed Study 2 on databases and traceability, the following key observations were made, as follows.

15. The experts discussed implications of publicly accessible databases in relation to digital sequence information. They reiterated the value of open access, with some experts noting that “open” does not necessarily mean “free and unrestricted” access, and noted that publicly accessible databases are functioning using differing terms and conditions of use.

16. Experts noted potential ways to improve traceability, such as:

- (a) Enhancing the inclusion of relevant passport data (for example, by requiring the provider country field entries when uploading relevant records to the databases);
- (b) Including information regarding the genetic resource in databases;
- (c) Linking journal publications with genetic resources stored in *ex situ* collections.

17. Some experts also considered:

- (a) Including disclosure of the provider country in patent applications;
- (b) Enhancing bioinformatic tools to support traceability, for example by direct comparison of sequences;
- (c) Explore the feasibility to link internationally recognized certificates of compliance (IRCCs) to genetic sequences uploaded in INSDC, including through interoperability.

18. With respect to the traceability of the different groupings, experts considered that Group 1 with the narrowest scope would in theory be the easiest to trace and verify, while Groups 2 and 3 would be progressively more difficult.

19. It was noted that traceability could be more or less relevant depending on the approach to benefit-sharing followed, and the related monitoring and compliance requirements. For example, in the case of a multilateral approach to benefit-sharing, traceability of digital sequence information to the provider countries and monitoring its use along the value chain may not be required.

20. Related to this, experts noted the potential complexity and cost of developing systems that could be used to trace and monitor the use of digital sequence information along the value chain.

21. With regard to the implications for INSDC, experts noted that it would be important to receive direct input from INSDC on this issue.¹ Experts noted that more consistent use of INSDC country tags and enhanced passport data could enhance traceability.

¹ The expert nominated by INSDC was not able to attend the meeting.

22. Experts noted that standard ST.26² under the World Intellectual Property Organization (WIPO) on machine readability of nucleotide sequence listings may facilitate data consistency between patent information systems and INSDC, and therefore facilitate comparison of patent information and accessions in INSDC.

B. Potential implications of the different groups for technologies and/or sectors in the life sciences

23. Experts, on the basis of Study 1, on concept and scope, considered the coverage of the technologies enabled by digital sequence information and the use of digital sequence information in the different sectors in the life sciences. In the discussions, experts indicated that table 3 of Study 1, providing an overview of the reliance of different sectors on digital sequence information, was particularly useful.

24. Experts noted that discussions on implications for life-science sectors was of a preliminary nature and that evaluating the implications of the different groups for the scope of digital sequence information would benefit from a deeper discussion, including:

- (a) Considering the implications of the groups for different technologies, as opposed to sectors;
- (b) Considering the benefit-sharing implications resulting from the different Groups;
- (c) Considering the implications of the use of digital sequence information by public and private scientists resulting from the different groups;
- (d) The shift in bioprospecting from testing of natural products to screening of chemical libraries.

25. In its limited deliberations on the implications for sectors in the life sciences, the AHTEG noted:

- (a) Challenges regarding traceability and enforceability which arise inherently from the inability to readily infer from metabolites their underlying DNA, RNA or proteins;
- (b) That data and information concerning metabolites, as proposed in Group 3, is important for research in the healthcare and pharmaceutical sector;
- (c) The extent of processing across the different groups is indicative of the correspondingly higher amount of effort required to realize value from a genetic resource and this may be a consideration for traceability and/or benefit-sharing, which may require a sector-based approach.

26. Experts highlighted the importance of having legal certainty regarding usage of digital sequence information for all sectors therefore any approach to benefit-sharing should provide legal certainty, incentivize the use of digital sequence information and decrease unnecessary burden in monitoring, tracing, and tracking requirements.

C. Potential implications of the different groups or options concerning measures governing access, benefit-sharing and compliance

27. In considering the study on domestic measures, experts acknowledged that some countries are currently regulating digital sequence information, others may be waiting for international consensus on this issue under the Convention and in other forums, and others have stated that they do not intend to regulate it at all.

28. The experts noted that the multiplicity of different ABS national frameworks addressing digital sequence information on genetic resources poses challenges for users, including those involved in basic non-commercial research, academic research and small and medium-sized enterprises.

² WIPO Standard ST.26, "Recommended Standard for the Presentation of Nucleotide and Amino Acid Sequence Listing Using XML (Extensible Markup Language)", of which version 1.3 was approved on 5 July 2019. WIPO ST.26 will take effect on 1 January 2022.

29. It was noted that digital sequence information on genetic resources may result, directly or indirectly, from utilization of genetic resources.

30. In this regard, the importance of a concerted and cost-effective international approach to digital sequence information on genetic resources was highlighted, and experts noted possible approaches, including measures at the time of access (noting, for example, flat-fee access or creative commons licensing approaches, database access agreements), open access with benefit-sharing triggered by utilization or commercialization, and a possible multilateral approach.

31. The experts noted that the discussion on potential implications for the different groups concerning measures governing access, benefit-sharing and compliance was of a preliminary nature, and it was noted that this issue would benefit from further discussion. In general, experts noted that the implications of the different groups concerning measures governing access, benefit-sharing and compliance would depend on the different approach to benefit-sharing that might be taken. For example, it was noted that access measures would be unnecessary in a bounded openness model and other multilateral approaches in which utilization or commercialization would trigger benefit-sharing.

III. IDENTIFICATION OF KEY AREAS FOR CAPACITY-BUILDING

32. The experts highlighted that capacity-building was critical for digital sequence information on genetic resources, including the capacity of countries to develop their endogenous research and to identify, understand, monitor and manage their own biodiversity.

33. It was suggested that capacity-building to utilize genetic resources and digital sequence information should be integrated in broader capacity-building initiatives/strategies, adapted and tailored to the needs of each country and research institutions, and take into account the needs and specificities associated with carrying out research in different types of environments (for example, marine versus terrestrial).

34. The need to secure appropriate funding and support for development and maintenance of scientific infrastructure was emphasized.

35. Experts discussed capacity-building as a form of non-monetary benefit-sharing. It was noted that capacity-building initiatives intended as a form of benefit-sharing should take into account the socioeconomic contexts of provider countries and be designed to contribute to enhancing the endogenous research capacities of these countries.

36. In discussing key stakeholders for capacity-building related to digital sequence information, experts agreed:

(a) On the need to build the capacity of national focal points and regulators/legislators as well as indigenous peoples and local communities to understand issues related to digital sequence information;

(b) On the importance of ensuring engagement and collaboration among different governmental agencies at the domestic level;

(c) On the need for universities, *ex situ* collections, research institutions, the private sector, and institutions working on bioinformatics to play a role in capacity-building related to digital sequence information.

37. Experts identified the following key areas for potential capacity-building:

(a) General understanding of issues related to digital sequence information, including the relevance of the economics of information to better understand links between access and benefit-sharing and digital sequence information;

(b) Understanding of the steps involved in the research and development of different products along value chains based on genetic resources/digital sequence information;

(c) Analysis and processing of big data related to digital sequence information;

(d) Reinforcement of the effectiveness of access to and use of international databases by the research community in all countries, including developing countries;

(e) Taxonomy, molecular biology applications for DNA/RNA extraction from genetic resources, PCR and/or sequencing, digital sequence information processing and uploading to databases, bioinformatics, database management.

38. Experts discussed the potential for model contractual clauses, frameworks, and models for addressing digital sequence information in mutually agreed terms to avoid divergent approaches creating obstacles and complexities.

39. Finally, experts also raised different modalities for capacity-building activities, such as:

(a) On-site and/or virtual courses/workshops in all the official languages of the United Nations;

(b) Case studies, exchange of information and experiences, and sharing of lessons learned in the official languages of the United Nations;

(c) Joint scientific research, technology transfer, scientific visits, partnerships and collaborations including through regional networks;

(d) Support for development of scientific infrastructure, including through regional approaches (for example, CGIAR centres);

(e) Intercultural dialogue through face-to-face meetings for indigenous peoples and local communities following culturally appropriate tools and methodologies in indigenous languages which could include dialogue between scientists and traditional knowledge holders;

(f) Integration in academic curricula;

(g) Integration in regional and international development agendas.

Annex II

REVISED ORGANIZATION OF WORK

<i>Date/time</i>	<i>Agenda item</i>	<i>Virtual meeting (live)</i>	<i>Online forum discussions</i>
Tuesday, 17 March 2020			
8 to 8.30 a.m.	Item 1. Opening of the meeting	Opening statements and introductions	
8.30 to 9 a.m.	Item 2. Organizational matters	Election of the co-chairs, proposed organisation of work, and adoption of the agenda	
9 a.m. to 12 noon	Item 3. Consideration of the compilation and synthesis of views and information and the peer-reviewed studies	Study 1 (CBD/DSI/AHTEG/2020/1/3): Presentation and questions and answers by the authors (1 h) Study 2 and 3 (CBD/DSI/AHTEG/2020/1/4): Presentation and questions and answers by the authors (1 h) Study 4 (CBD/DSI/AHTEG/2020/1/5): Presentation and questions and answers by the authors (1 h)	Discussions on the studies in three different threads (discussion threads will be open from 12.30 p.m. until 6 a.m.) Moderated by Co-chairs
Wednesday, 18 March 2020			
8 to 8.30 a.m.	Item 3. <i>Continued</i>	Synthesis (CBD/DSI/AHTEG/2020/1/2): Presentation and brief comments (30 min)	
8.30 to 11.30 a.m.	Item 4. Development of options for operational terms and their implications for the purpose of providing conceptual clarity on digital sequence information on genetic resources	Document on salient points (CBD/AHTEG/DSI/2020/1/6) <ul style="list-style-type: none"> • Section II, A: Scope- (1 h) • Section II, B: Potential implications of the different options (1 h) • Section II C: Terminology (1 h) 	Threads will be created for each topic. (discussion threads will be open from 12.30 p.m. until 6 a.m.) Moderated by Co-chairs
11.30 a.m. to 12 noon	Item 5. Identification of key areas for capacity-building	Document on salient points (CBD/AHTEG/DSI/2020/1/6). Section III <ul style="list-style-type: none"> • Introduction by the Secretariat 	A thread will be created. (thread will be open from 12.30 p.m. until 6 a.m.) Moderated by co-chairs

<i>Date/time</i>	<i>Agenda item</i>	<i>Virtual meeting (live)</i>	<i>Online forum discussions</i>
Thursday, 19 March 2020			
8 to 9 a.m.	Item 3: <i>Continued</i>	Presentation of summary by the co-chairs and discussions	
9 to 11 a.m.	Item 4: <i>Continued</i>	Presentation of summary by the co-chairs and discussions	
11 a.m. to 12 noon	Items 5: <i>Continued</i>	Presentation of summary by the co-chairs and discussions	
Friday, 20 March 2020			
8 a.m. to 12 noon	Item 6. Other matters Item 7. Adoption of the report Item 8. Closure of the meeting.	Other matters, adoption of the report and closing statements	

Annex III

LIST OF PARTICIPANTS

Experts nominated by Parties		
Africa		
1	Aurélie Taylor Patience Dingom	Cameroon
2	Mame Nahé Diouf	Senegal
3	Lactitia Tshitwamulomoni	South Africa
4	Nada Babiker Hamza	Sudan
5	Samson Gwali	Uganda
Asia and the Pacific		
6	Jiang Chang	China
7	Chirra Achalender Reddy	India
8	Nobuyuki Fujita	Japan
9	Eizadora T. Yu	Philippines
10	Myounghai Kwak	Republic of Korea
Latin America and the Caribbean		
11	Patricia Gadaleta	Argentina
12	Henry de Novion	Brazil
13	Melania Muñoz García	Costa Rica
14	Efren German Santos Ordóñez	Ecuador
15	Jannel Gabriel	Saint Lucia
Central and Eastern-Europe		
16	Galina Mozgova	Belarus
17	Nikolay Kirilov Tzvetkov	Bulgaria
18	Tamara Čimbora Zovko	Croatia
Western European and Others		
19	Hendrik Segers	Belgium
20	Kathryn Davis	Canada
21	Alicja Kozłowska	European Union
22	Gaute Voigt-Hanssen	Norway
23	Christopher H. C. Lyal	United Kingdom
Experts nominated by indigenous peoples and local communities' organizations		
24	Kamal Kumar Rai	Society for Wetland Biodiversity Conservation Nepal
25	Yolanda Teran	Indigenous Organization Andes Chinchasuyu from Ecuador

Experts nominated by relevant organizations		
26	Manuel Ruiz Muller	Peruvian Society for Environmental Law (SPDA)
27	Daniele Manzella	Secretariat of the International Treaty on Plant Genetic Resources for Food and Agriculture
28	Edward Hammond	Third World Network
29	Dan Leskien	Commission on Genetic Resources for Food and Agriculture (CGRFA)
30	Kevin McCluskey	World Federation for Culture Collection (WFCC)
31	Dirk Neumann	Consortium of European Taxonomic Facilities (CETAF)
32	Dominic Muyldermans	International Chamber of Commerce (ICC)
33	Shakeel Bhatti	World Intellectual Property Organization (WIPO)
34	Noelle Anglin	CGIAR Centres
35	Pierre du Plessis	African Union
36	Vasee Moorthy	World Health Organization (WHO)

Additional attendees on 17 March 2020

Amber Scholz (presenter of study)

Marcel Jaspars (presenter of study)

Margo Bagley (presenter of study)

Elizabeth Karger (co-presenter of study)
