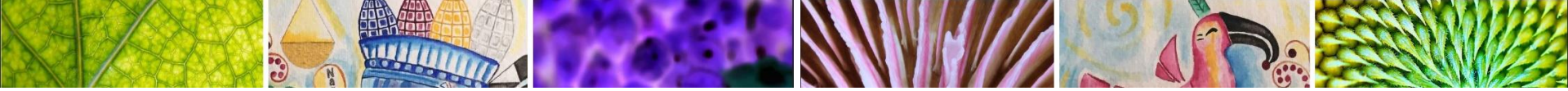
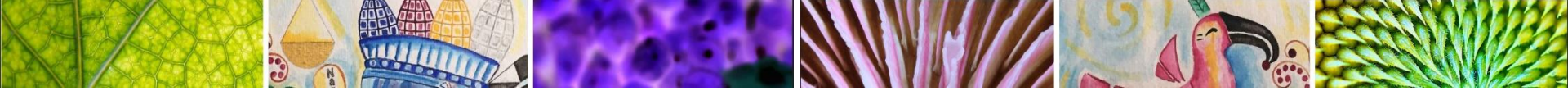


Outcomes related to digital sequence information on genetic resources under the CBD

Presentation of AHTEG Co-Chairs

25 YEARS Convention on Biological Diversity
SAFEGUARDING LIFE ON EARTH

2011-2020 United Nations Decade on Biodiversity

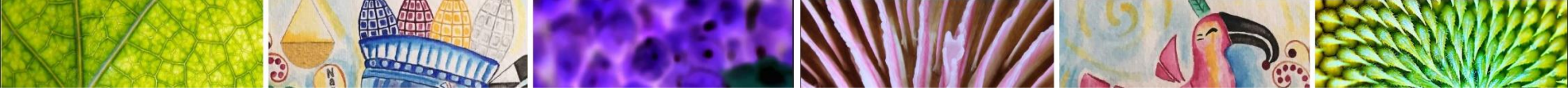


Contents

- AHTEG Participants
- Objectives of AHTEG
- Outcomes of AHTEG meeting
  - Scope and terminology
  - Implications arising from different groups
  - Key areas of capacity building

AHTEG Participants

Parties		IPLCs	International Organizations
Argentina	India	Andes Chinchasuyu (Ecuador)	African Union
Belarus	Japan	Society for Wetland Biodiversity Conservation (Nepal)	World Health Organization
Belgium	Norway		Secretariat pf the Commission on Genetic Resources for Food and Agriculture
Brazil	Philippines		Secretariat of the International Treaty on Plant Genetic Resources for Food and Agriculture
Bulgaria	Republic of Korea		World Intellectual Property Organization
Cameroon	Saint Lucia		CGIAR Centres
Canada	Senegal		Consortium of European Taxonomic Facilities
China	South Africa		International Chamber of Commerce
Costa Rica	Sudan		Peruvian Society for Environmental Law
Croatia	Uganda		Third World Network
Ecuador	United Kingdom		World Federation for Culture Collections
European Union			



Objectives of the AHTEG

(i) Consider the compilation and synthesis of views and information and the peer-reviewed studies

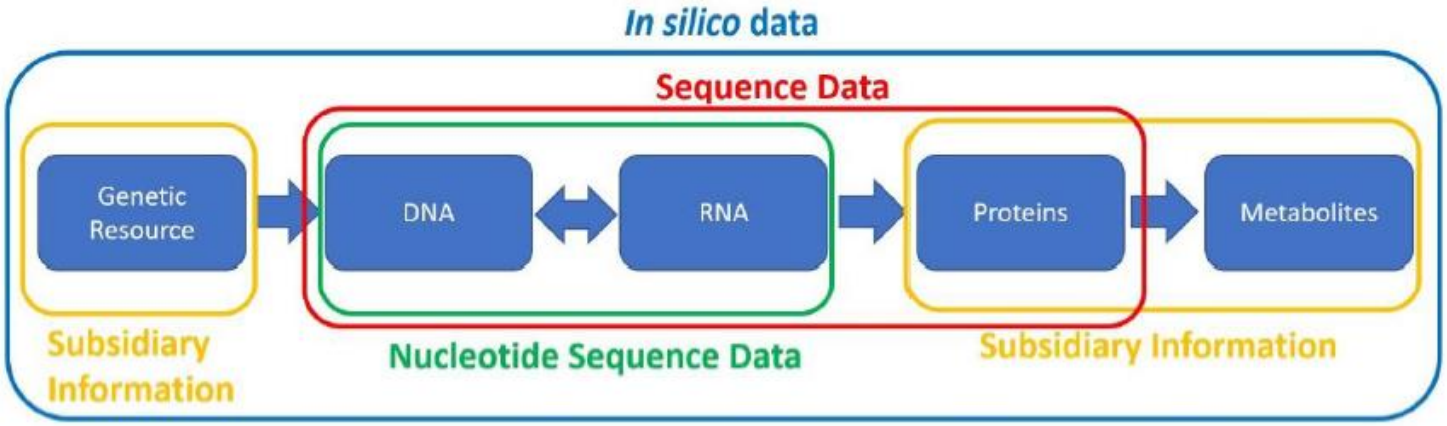
(ii) Develop options for operational terms and their implications to provide conceptual clarity on digital sequence information on genetic resources

(iii) Identify key areas for capacity-building.

Outcomes of the AHTEG: scope and terminology

'DSI' is a placeholder term for CBD negotiations

- There are different concepts of DSI, more or less inclusive in scope
  - From the simple order of nucleotides in a strand of DNA
  - To the structure of proteins for which the DNA is coding
  - To the biochemical composition of molecules produced within cells (metabolites)
  - To concepts such as 'natural information' or 'in silico' information



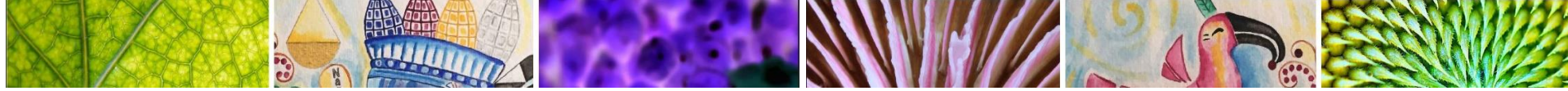
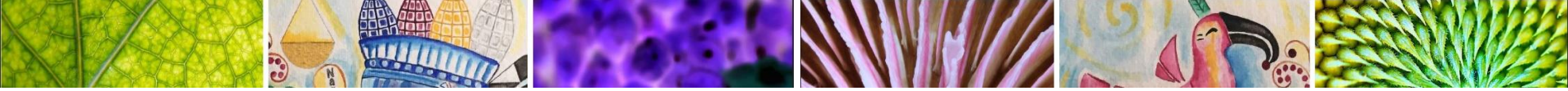


Table 1. Clarifying the scope of digital sequence information on genetic resources

	Information related to a genetic resource			
	Genetic and biochemical information			Associated information
Group reference	**Group 1**	**Group 2**	**Group 3**	
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	• 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.	• Amino acid sequences; • Information on gene expression; • Functional annotation; • Epigenetic modifications (for example, methylation patterns and acetylation); • Molecular structures of proteins; • Molecular interaction networks.	• Information on the biochemical composition of a genetic resource; • Macromolecules (other than DNA, RNA and proteins); • Cellular metabolites (molecular structures).	• 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.

The proposed groups are cumulative

Group 2 includes all elements of Group 1, and Group 3 contains all elements of Groups 1 and 2



Outcomes of the AHTEG: scope and terminology

	Information related to a genetic resource			
	Genetic and biochemical information			Associated information
Group reference	Group 1	Group 2	Group 3	
High-level description of each group	DNA and RNA	Group 1 + proteins + epigenetic modifications	Group 2 + metabolites and other macromolecules	

- AHTEG agreed that **groups 1-3** could be considered as **DSI**, while associated information, including associated traditional knowledge, is not considered DSI
- **But** the AHTEG recalled obligations to share benefits from the utilization of aTK under the Nagoya Protocol and the CBD
- Issue now back with the negotiators to make use of this clarification

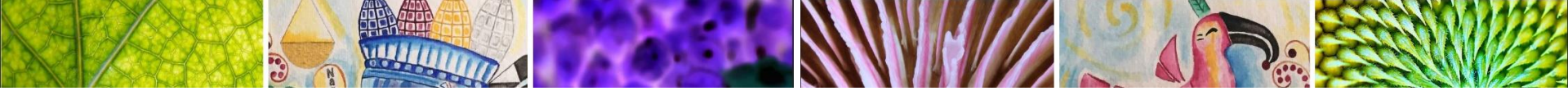
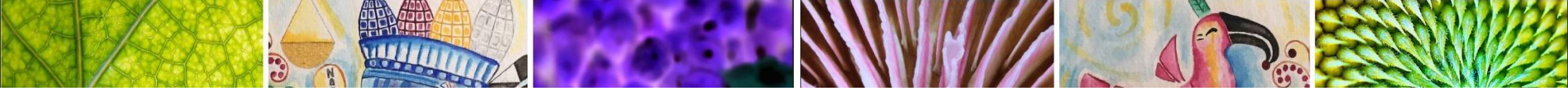


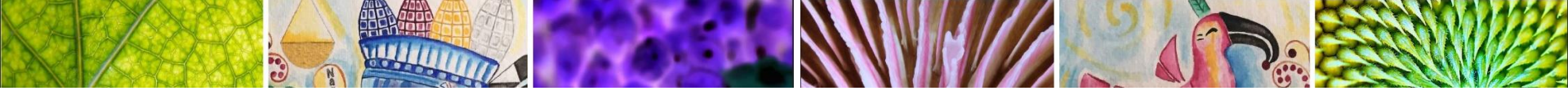
Table 2. Options for terminology to describe digital sequence information on genetic resources

Group reference	Group 1	Group 2	Group 3	Associated information
Category/term	• 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	• 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.	• 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.	• Associated information; • Contextual Information; • Subsidiary Information.
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 in silico				



Outcomes of the AHTEG: potential implications arising from the different groups

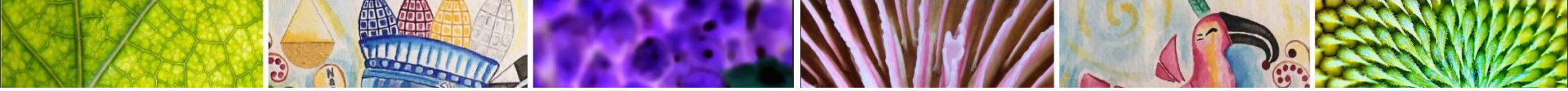
- For each group AHTEG discussed implications:
  - traceability;
  - INSDC on open exchange and use of DSI;
  - use of DSI and technologies enabled by DSI in life sciences research and innovation processes;
  - measures governing access, benefit-sharing and compliance.
- Discussions were preliminary
- Implications depend on benefit-sharing approach.
- Some potential implications not discussed in depth; could benefit from further information or consideration.



Outcomes of the AHTEG: potential implications arising from the different groups

Traceability:

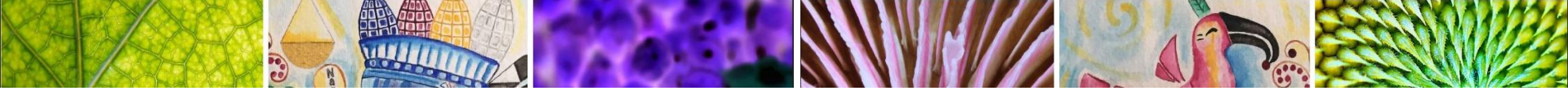
- reiterated value of open access
  - some experts noted “open” does not necessarily mean “free and unrestricted” access
- Ways to improve traceability discussed, including linking IRCCs
- easier for Group 1;
- More or less relevant depending on benefit sharing approach i.e. bilateral vs. multilateral
- Important to receive information from INSDC



Outcomes of the AHTEG: potential implications arising from the different groups

Sectors and life sciences: further discussion needed

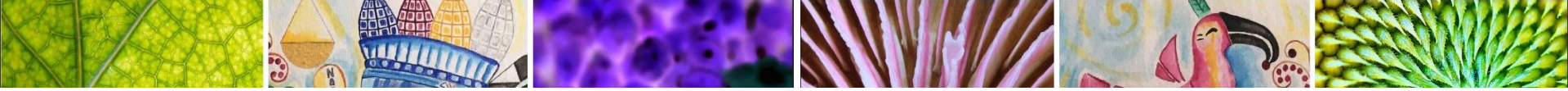
ABS and compliance: further discussion needed



Outcomes of the AHTEG: capacity building needs

Capacity building discussed as form of non-monetary benefit sharing

- capacity-building critical for DSI
  - capacity of countries to develop endogenous research and identify, understand, monitor and manage their own biodiversity.
- could be integrated in broader capacity-building initiatives/strategies.
- emphasis on need for appropriate funding and support for development and maintenance of scientific infrastructure.

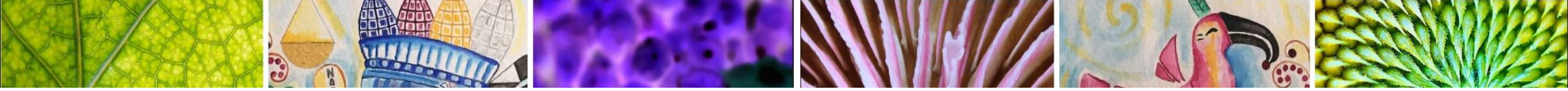


Outcomes of the AHTEG: capacity building needs

Capacity building discussed as form of non-monetary benefit sharing

Key areas:

- General understanding of issues related to DSI including the economics of information
- Understanding the R&D steps along values chains based on GRs and DSI
- Analysis and processing of big data related to DSI
- Access and use of international databases
- 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.



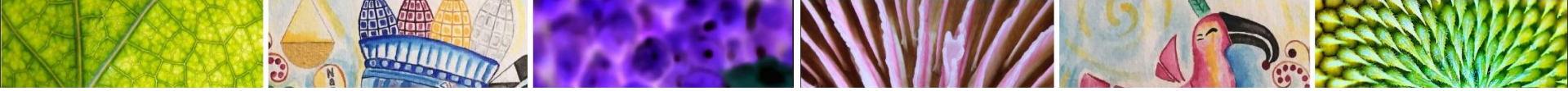
Outcomes of the AHTEG: capacity building needs

Key stakeholders:

- need to build capacity of national focal points and regulators/legislators as well as indigenous peoples and local communities to understand issues related to DSI;

- ensuring engagement and collaboration among different governmental agencies at domestic level;

- 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 DSI.



Outcomes of the AHTEG: capacity building needs

Capacity building modalities:

- On-site and/or virtual courses/workshops
- Case studies, exchange of information and experiences, and sharing of lessons learned
- Joint scientific research, technology transfer, scientific visits, partnerships and collaborations including through regional networks;
- Support for development of scientific infrastructure, including through regional approaches (for example, CGIAR centres);
- Intercultural dialogue through face-to-face meetings for indigenous peoples and local communities
- Integration in academic curricula;
- Integration in regional and international development agendas.

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Thank you

For more information on DSI :
https://www.cbd.int/dsi-gr/