



COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE

Item 7 of the Provisional Agenda

INTERGOVERNMENTAL TECHNICAL WORKING GROUP ON AQUATIC GENETIC RESOURCES FOR FOOD AND AGRICULTURE

Third Session

1–3 June 2021

“DIGITAL SEQUENCE INFORMATION” ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE: INNOVATION OPPORTUNITIES, CHALLENGES AND IMPLICATIONS

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I. INTRODUCTION

1. The Commission on Genetic Resources for Food and Agriculture (Commission), at its Seventeenth Regular Session in 2019, took note of the *Exploratory fact-finding scoping study on “Digital Sequence Information” on genetic resources for food and agriculture* (Background Study Paper No. 68).¹ The study examined how “Digital Sequence Information” (“DSI”) on genetic resources for food and agriculture (GRFA) is currently being used, how it might be used in the future and what the implications of its use might be for the food and agriculture sector.
2. The Commission agreed that there is a need for further review of “DSI” on GRFA. It agreed to address, at its next session:
 - i. the innovation opportunities “DSI” on GRFA offers;
 - ii. the challenges of capacity to access and make use of “DSI”; and
 - iii. the implications of “DSI” for the conservation and sustainable use of GRFA and the sharing of benefits derived from GRFA.
3. The Commission requested its intergovernmental technical working groups on animal, aquatic, forest and plant genetic resources (Working Groups) “to consider these matters with regard to existing subsector-specific examples related to conservation, sustainable use and development of genetic resources, food security and nutrition, food safety, and efforts to combat crop and animal pests and diseases”.² The Commission further noted the importance of coordination with the ongoing processes under the Convention on Biological Diversity (CBD) and its Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity (Nagoya Protocol) and the International Treaty on Plant Genetic Resources for Food and Agriculture (Treaty).
4. This document aims to contribute to the discussion on “DSI” by reflecting on different options to define “DSI” (Section II). It considers the innovation potential “DSI” offers by providing, by way of example, a selection of actual and potential applications of “DSI” related to the conservation, sustainable use and development of GRFA, for review by the Working Group (Section III) and addresses some of the factors that determine whether this potential may fully be realized (Section IV). The implications of “DSI” for (research and development related to) the conservation and sustainable use of GRFA and, in particular, for the sharing of benefits derived from the utilization of GRFA will depend on the legal conditions for access and benefit-sharing (ABS) for “DSI” (Section V). The Working Group may wish to identify priorities for the Commission’s future work in light of the opportunities “DSI” offers, its implications and the challenges it poses (Section VI).

II. TOWARDS A DEFINITION OF “DIGITAL SEQUENCE INFORMATION”

5. There is no universally agreed definition for “DSI”. This is reflected in relevant decisions taken under the CBD and its Nagoya Protocol and the decision taken by the Commission in 2017 to establish a new work stream on “DSI”. As the Commission recognized at that time, “[...] there are a multiplicity of terms that have been used in this area (including, *inter alia*, “genetic sequence data”, “genetic sequence information”, “genetic information”, “dematerialized genetic resources”, “*in silico* utilization”, etc.) and [...] further consideration is needed regarding the appropriate term or terms to be used”.³
6. The World Health Organization’s (WHO) Pandemic Influenza Preparedness (PIP) Framework does not include a definition of “DSI”. However, it defines “genetic sequences” as: “the order of

¹ Heinemann, J.A., Coray, D.S. & Thaler, D.S. 2018. *Exploratory fact-finding scoping study on “Digital Sequence Information” on genetic resources for food and agriculture*. Background Study Paper No. 68. Commission on Genetic Resources for Food and Agriculture. Rome, FAO. (also available at <http://www.fao.org/3/CA2359EN/ca2359en.pdf>).

² CGRFA-17/19/Report, paragraph 23.

³ CGRFA-16/17/Report Rev.1, paragraph 87.

nucleotides found in a molecule of DNA or RNA. They contain the genetic information that determines the biological characteristics of an organism or a virus". In addition, the PIP Framework makes reference to "genetic sequence data",⁴ a term that, however, it does not further define. The revised draft text of an agreement under the United Nations Convention on the Law of the Sea on the conservation and sustainable use of marine biological diversity of areas beyond national jurisdiction, issued on 18 November 2019, uses the terms "*in silico*", "Digital Sequence Information" and "genetic sequence data" without, however, offering a definition.⁵ The Governing Body of the Treaty has not yet decided on the official terminology for "Digital Sequence Information"/genetic sequence data and therefore decided at its last Session to use "DSI/GSD" until a new terminology has been agreed.⁶

7. A challenge these processes face in defining "DSI" or similar terms used is to decide on the scope or content of the term. While the term may be understood to embrace DNA and RNA sequences only, it could also cover amino acid sequences of proteins and/or information generated by cognitive processes applied to them or even information on the genetic resource, such as traditional knowledge or phenotypic data.⁷

Biological databases covered by Nucleic Acid Research

8. Background Study Paper No. 68 found that the scientific community notably does not use the term "DSI" and stressed that science is constantly evolving, making precise definitions potentially arbitrary or prescriptive. The authors, therefore, proposed an illustrative definition of "DSI": any kind of information that could be held by any existing or future database of the type collated by the scientific journal *Nucleic Acid Research* (NAR).⁸ NAR publishes the results of research into physical, chemical, biochemical, and biological aspects of nucleic acids and proteins involved in nucleic acid metabolism and/or interactions. The first issue of each year is devoted to biological databases.⁹

The degree of biological processing and the proximity to the underlying genetic resource as a basis to distinguish groups of "DSI"

9. The Conference of the Parties (COP) to the CBD, at its Fourteenth Regular Session, noted that the term "digital sequence information" may not be the most appropriate and therefore used it as a "placeholder". It also established a "science and policy-based process on digital sequence information on genetic resources" to, *inter alia*, "clarify the concept, including relevant terminology and scope, of digital sequence information [...]".¹⁰ As part of this process, it initiated broad consultations¹¹ as well as three studies, one of which focused on the concept and scope of "DSI" on genetic resources and how "DSI" on genetic resources is currently used.¹² The COP also established an extended Ad Hoc Technical Expert Group (AHTEG) to, *inter alia*, develop options for operational terms and their implications to provide conceptual clarity on "DSI" on genetic resources.

10. Building on the study *Digital Sequence Information on Genetic Resources: Concept, Scope and Current Use*, 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 "DSI". The three groups considered by the AHTEG as "DSI", as shown in Table 1, are cumulative (Group 2 includes all elements of Group 1, and Group 3 contains all elements of Groups 1 and 2).¹³ Associated

⁴ PIP Framework, see section 5.2.

⁵ A/CONF.232/2020/3.

⁶ IT/GB-8/19/Report, Resolution 9/2019.

⁷ Houssen, W., Sara, R. & Jaspars, M. 2020. *Digital Sequence Information on Genetic Resources: Concept, Scope and Current Use*. CBD/DSI/AHTEG/2020/1/3. p. 31. CBD. (also available at <https://www.cbd.int/doc/c/fe9/2f90/70f037ccc5da885dfb293e88/dsi-ahteg-2020-01-03-en.pdf>).

⁸ See See Heinemann, J.A., Coray, D.S. & Thaler, D.S. 2018. op. cit..

⁹ <https://academic.oup.com/nar>

¹⁰ Decision 14/20.

¹¹ For a synthesis of views, see CBD/DSI/AHTEG/2020/1/2.

¹² Houssen, W., Sara, R. & Jaspars, M. 2020. op. cit..

¹³ CBD/DSI/AHTEG/2020/1/7, Annex I, paragraph 9.

information, i.e. other than genetic and biochemical information, such as traditional knowledge associated with genetic resources, behavioural data and information on ecological relationships was not considered “DSI”. However, it is important to note that, in line with the Nagoya Protocol, ABS measures in many countries provide for ABS for traditional knowledge associated with genetic resources.

11. The AHTEG also identified multiple options for terminology to describe “DSI” on genetic resources but did not come to definite conclusions on this matter.¹⁴

Table 1. Clarifying the scope of “DSI” on genetic resources¹⁵

Group reference	Information related to a genetic resource			Associated information
	Genetic and biochemical information			
	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	<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.

12. For each of the groups, the AHTEG identified different implications in terms of technical traceability of “DSI” to the source. Proximity of “DSI” to the underlying genetic resource and the biological process associated with the generation of the “DSI” determine if it is possible to technically identify or infer the genetic resource from which it is derived.¹⁶ The AHTEG concluded that different sectors relied to different degrees on the different groups of “DSI”.

13. As the relevance of defining “DSI” and the implications of the definition of “DSI” ultimately depend on the context/purpose for which the definitions will be used, the Commission and its Working Groups may wish to continue using “DSI” as a placeholder until there is more clarity on the context in which they wish to discuss “DSI” and the purpose for which it should be defined.

14. The term “digital sequence information on genetic resources for food and agriculture” obviously relates to “DSI” derived from GRFA. However, research and development on GRFA and “DSI” on GRFA may well involve genetic materials and “DSI” from non-GRFA organisms.¹⁷ Whether “DSI” on GRFA includes “DSI” from non-GRFA organisms (e.g. “DSI” on new traits

¹⁴ CBD/DSI/AHTEG/2020/1/7, Annex I, Table 2.

¹⁵ The table is taken from CBD/DSI/AHTEG/2020/1/7, Annex I, Table 1.

¹⁶ Houssen, W., Sara R. & Jaspars, M. 2020. op.cit, p. 32.

¹⁷ See Heinemann, J.A., Coray, D.S. & Thaler, D.S. 2018. op. cit. p.9.

derived from non-GRFA organisms), if used in research and development on GRFA, is an open question.

III. OPPORTUNITIES OFFERED BY “DIGITAL SEQUENCE INFORMATION” TO CONTRIBUTE TO THE CONSERVATION AND SUSTAINABLE USE OF GENETIC RESOURCES

15. “DSI” plays a fundamental role in environmental and biological research, contributing to the understanding of the molecular basis of life and evolution and of the ways in which genes can potentially be modified to provide new agricultural products, therapies and cures for diseases, new energy sources and other new products. It also plays important roles in taxonomy, identifying and mitigating risks to threatened species, tracking illegal trade, identifying the geographical origin of products, and conservation management.

16. “DSI” on GRFA contributes to food security and nutrition as a fundamental tool for characterization of GRFA, selection and breeding, creation of new products, food safety and traceability, and management of GRFA, including the development of veterinary medicinal products, such as vaccines. “DSI” is an essential component of technologies used for the characterization, conservation and sustainable use of GRFA¹⁸. It underpins a wide range of technologies involved in the analysis, synthesis and presentation of DNA, RNA and other molecules involved in heritability and trait expression for reproduction, growth and health. Synthetic biology is a relatively novel discipline, which is now making it possible to analyse and synthesize molecules such as DNA, RNA, proteins and even viruses *in vitro* and *de novo* using “DSI”.

17. “DSI” allows for the generation of benefits from a genetic resource based on digitized data and information and without access to the genetic resource. Background Study Paper No. 68 did not find significant actual or potential differences in the characteristics of technologies as they are applied in the different subsectors of GRFA. It found that “DSI” was used extensively in all subsectors of GRFA. “DSI” is a routine component of nearly all research in the biological sciences. Background Study Paper No. 68 concluded that “DSI” on GRFA is central to product development, including the improvement of GRFA, and its importance is expected to increase, especially as an increasing amount of “DSI” relevant to GRFA will become available. “DSI” can also be used to select reproductive/vegetative material for breeding, including artificial insemination, oestrus synchronization and *in vitro* fertilization, and cloning, or to monitor or test progeny. “DSI” is a critical element in innovating products and processes in green (agriculture), red (healthcare and medicine) and white (industrial) biotechnologies; it is expected to play an increasingly important role in blue biotechnology (fisheries/aquaculture).

18. “DSI” may also contribute to the sustainable use of GRFA by facilitating the discovery and design of new vaccines, pesticides, biofertilizers and probiotics. It is used to both diagnose diseases in all forms of GRFA and to design therapeutics for treatment. It may represent a critical element in the development of new products from GRFA to increase both income security and the financial sustainability of farmers.

19. “DSI” contributes to species conservation. Small amounts of *DNA* collected from the water, for example, may allow scientists to identify more *species* of marine vertebrates than traditional *surveys* with nets. “DSI” is frequently used for identification of species and for assessing genetic diversity within and among species. It is also used to select material for genebank storage and can be used to test for viability and ensure purity over time.

20. “DSI” also plays an important role in food governance systems, including product labelling, and identification of food components, which can be important for the conservation of threatened species.

21. A selection of actual and potential applications of “DSI”, demonstrating its significant innovation potential, is provided in Table 2 for review by the Working Group.

¹⁸ See also CGRFA/WG-AqGR-3/21/Inf.16.

Table 2: Actual and potential applications of “DSI” for the conservation and sustainable use of genetic resources for food and agriculture

Animal genetic resources
<ul style="list-style-type: none"> • “DSI” is used to accurately identify and understand relationships between species from all over the world. For example, databases such as the Barcode of Life (https://ibol.org/) allow researchers to identify species, which allows for monitoring and conservation of biological diversity. “DSI” is also used for avoiding the further loss of threatened and endangered species. For example, researchers can use “DSI” to identify, understand and mitigate factors that threaten a wide range of populations of vulnerable species. • Use of “DSI” has facilitated improvements to the molecular characterization of breeds and contributed to the identification of genomic regions associated with both production traits and adaptive traits, such as heat tolerance and disease resistance, and to identify the variations responsible for numerous genetic defects. • “DSI” is used for <i>ex situ</i> collections, sampling strategies and evaluation of collections. “DSI” also allows cryoconservation to be improved by comparing the genotypes of animals with stored material to those of animals in live populations, followed by targeted collection of under-represented diversity. • It can be used to advance discovery and development of new livestock breeds, with enhanced outcomes for food security as well as determining adaptability to high altitudes and increasing tolerance to high ambient temperatures and humidity. • “DSI” is useful for disease diagnosis and prevention, and contributes to the conservation of threatened species, such as pollinators, contributing to improved food security and is therefore critical in preventing further loss of threatened and endangered species as well as in studying diversity. • Genomic analysis allows for the evaluation of long-term <i>in situ</i> conservation programmes. • Genomic selection, where genome-wide markers are used for predicting the breeding value of individual animals, is widely used in commercial breeding programmes. • For “DSI” of the rumen biome and its use in management of animal genetic resources, several significant metagenomic surveys of the rumen microbiome have been completed, creating “DSI” that is applied to the dual challenges of increasing feed efficiency and reducing greenhouse gas emissions.
Aquatic genetic resources
<ul style="list-style-type: none"> • “DSI” is used to characterize genes and identify genetic sequences, for the study of population genetics and for stock assessment. • DNA barcoding based on “DSI” has been used to support conservation of species, including those that might be illegally traded. • In aquatic genetic resources for food and agriculture “DSI” is most relevant for molecular markers, for example barcodes, omics and biotechnologies for disease diagnosis, and pedigree assignment in breeding programmes. • “DSI” contributes to reproductive technologies and detection of hybrids, and disease diagnosis and prevention. • “DSI” is used to support restoration of degraded coral reefs through transplantation, where the appropriateness of candidate places can be judged to reintroduce healthy coral by comparing “DSI” (genetic compositions) of different coral populations. • “DSI” can improve access to markets and consumer confidence in supply chains through traceability and identifying product substitution, and supporting product labelling and certification schemes.

Forest genetic resources

- “DSI” is used for species, subspecies and hybrid identification; it assists in understanding phylogenetical information of species and population origin and profile; understanding of pleiotropic effect of gene expression and their morphological diversity; accelerating knowledge on heritability, ecophysiology and biology of forest tree species.
- “DSI” is contributing to the assembly of breeding populations in newly developed and advanced breeding programmes, as well as to selecting genetic material for storage or micropropagation.
- With the help of bioinformatics tools, “DSI” can give insight to the genetic make-up of individuals and populations, making real-time selection possible for progeny and breeding programmes; it has powerful potential for the breeding of forest trees as well as enhancing the productivity of plantation forests and judicious control of pest infestation.
- “DSI” has enabled the so-called “breeding-without-breeding” approach, which allows designing tree breeding programmes with affordable costs in many countries. This approach relies on “DSI” in the form of complete pedigree information from a subset of offsprings.
- Being an integral part of sustainable forest management, the conservation of forest genetic resources needs accurate information on genetic diversity among individuals and tree populations. Through barcoding and other fingerprint marker-based technologies coupled with “DSI”, better conservation strategies can be designed and implemented. “DSI” is also contributing to a more accurate delineation of species taxonomy.
- “DSI” can assist in maintenance of genetic diversity through the development of robust *ex situ* collections of at-risk species by identifying distinct natural populations and those with high diversity.
- “DSI” used in predictive genomics may help in the conservation of trees by identifying the environment suited to the genotype and by providing information for assisted migration.
- “DSI” can support complex biostatistics calculation of individual and population genetic diversity, targeting landscapes and areas of superior individuals important for further selection and conservation measures.
- Accumulated “DSI” enables comparison of large numbers of individuals and populations of the same and related species in order to identify the current distribution area and project changes to it due to climate change.
- Technologies that rely on “DSI” assist to identify the species and geographic origin of wood in order to detect illegal logging and trade.

Plant genetic resources

- “DSI” is critical for preventing further loss of threatened and endangered species. Conservation of plant genetic resources for food and agriculture tends to include increasing amounts of “DSI”, such as in the DNA Barcode of Life initiative, “local” initiatives such as the sequencing of genomes of an entire botanical garden, or major efforts from the Consortium of International Agricultural Research Centers (CGIAR) to “digitally curate” their collections.
- “DSI” supports the use of molecular markers, omics, cryopreservation, *in vitro* slow growth storage, wide crossing, somatic hybridization and micropropagation. Its use in biotechnologies for disease diagnosis is invaluable in molecular epidemiology and helps to trace the origin and evolution of pathogens.
- “DSI” can be used to advance discovery and development of new crop varieties, with enhanced outcomes for food security especially for production of drought- and pest-resistant crops, and crops altered for enhanced nutritional and economic value. Use of “DSI” has enabled researchers to rapidly identify markers for genes associated with drought tolerance in sorghum, maize, wheat and other crops.
- Access to DSI provides nowadays a fundamental basis for plant research and crop enhancement. Farmers and plant breeders use “DSI” to develop new crop varieties that are more productive, resilient and require fewer inputs such as water, fertilizers and pesticides. “DSI” also underpins marker-assisted selection in genomics-assisted breeding programmes.

- Continued access to “DSI” promotes research and development efforts to increase the sustainable use of plant genetic diversity, as well as understanding gene flow and pest management.
- “DSI” supports the maintenance of genetic diversity in plant breeding. Knowledge of genetic interrelationships of parental lines is a prerequisite for producing hybrids of maize, sorghum, sunflowers, and certain vegetable and fruit crops. Hybrid vigour in these crops results in yield and product quality that substantially exceed those of non-hybrid plants.

Note: Examples have been taken from: ABS Task Force of the European Regional Focal Point on Animal Genetic Resources Submission on DSI, 2018; Canada Submission on DSI, 2018; German Submission on DSI, 2018; India Submission on DSI, 2017; Japan Submission on DSI, 2017; USA Submission on DSI, 2017; USA Submission on DSI, 2018; Heinemann, J.A., Coray, D.S. & Thaler, D.S. 2018. *Exploratory fact-finding scoping study on “Digital Sequence Information” on genetic resources for food and agriculture*. Background Study Paper No. 68. Commission on Genetic Resources for Food and Agriculture. Rome, FAO. (also available at <http://www.fao.org/3/CA2359EN/ca2359en.pdf>); Lidder, P. & Sonnino, A. 2011. *Biotechnologies for the management of genetic resources for food and agriculture*. Background Study Paper No. 52. Commission on Genetic Resources for Food and Agriculture. Rome, FAO. (also available at <http://www.fao.org/docrep/meeting/022/mb387e.pdf>); Clarke, R. 2010. *Private food safety standards: their role in food safety regulation and their impact*. Rome, FAO. (also available at <http://www.fao.org/docrep/016/ap236e/ap236e.pdf>); Sultana, S., Ali, M.E., Hossain, M.A.M., Asing, Naquiah, N. & Zaidul, I.S.M. 2018. Universal mini COI barcode for the identification of fish species in processed products. *Food Res. Internatl.*, 105: 19–28; El-Kassaby, Y.A., Cappa, E.P., Liewlaksaneeyanawin, C., Klápště, J. & Lstibůrek, M. 2011. Breeding without breeding: is a complete pedigree necessary for efficient Breeding? *PLoS One*, 6: e25737; Liu H., Wei J., Yang T., Mu W., Song B., Yang T. *et al.* 2019. Molecular digitization of a botanical garden: high-depth whole genome sequencing of 689 vascular plant species from the Ruili Botanical Garden. *Gigascience*, 8(4). 10.1093/gigascience/giz007; Halewood M., Lopez Noriega I., Ellis D., Roa C., Rouard M. & Sackville Hamilton R. 2018. Using genomic sequence information to increase conservation and sustainable use of crop diversity and benefit-sharing. *Biopreserv. Biobank*. 16: 368–376. 10.1089/bio.2018.0043; Laird, S.A. & Wynberg, R.P. 2018. *A fact-finding and scoping study on digital sequence information on genetic resources in the context of the Convention on Biological Diversity and the Nagoya Protocol*. 77 pp. (also available at <https://www.cbd.int/doc/c/e95a/4ddd/4baea2ec772be28edcd10358/dsi-ahteg-2018-01-03-en.pdf>); Spindel, J.E. & McCouch, S.R. 2016. When more is better: how data sharing would accelerate genomic selection of crop plants. *New Phytol.*, 212, 814–826. doi: 10.1111/nph.14174; Halewood, M., Chiurugwi, T., Sackville Hamilton, R., Kurtz, B., Marden, E., Welch, E. *et al.* (2018). Plant genetic resources for food and agriculture: opportunities and challenges emerging from the science and information technology revolution. *New Phytol.*, 217: 1407–1419. doi: 10.1111/nph.14993.

IV. CAPACITY TO ACCESS AND MAKE USE OF “DIGITAL SEQUENCE INFORMATION”

22. The importance of having access and being able to make use of “DSI” can hardly be overstated. The life sciences depend on the availability of the complete “DSI” datasets from different sources to compare with and understand new “DSI”.¹⁹

23. Many factors determine the capacity to access and make use of “DSI”. A significant amount of “DSI” is currently stored in an estimated worldwide 1 700 publicly accessible databases and repositories of biological and associated information. The databases include the DNA Data Bank of Japan at the National Institute of Genetics, the European Nucleotide Archive at the European Molecular Biology Laboratory's European Bioinformatics Institute and GenBank at the National Center for Biotechnology Information, United States of America. The three databases form the International Nucleotide Sequence Database Collaboration (INSDC), which is the core infrastructure

¹⁹ Oldham, P. 2020 *Digital Sequence Information - Technical Aspects*. (also available at https://ec.europa.eu/environment/nature/biodiversity/international/abs/pdf/Final_Report_technical_aspects_of_DSI.pdf); Scholz, A.H., Hillebrand, U., Freitag, J., Cancio, I. *et al.* 2020. *Finding compromise on ABS & DSI in the CBD: Requirements & policy ideas from a scientific perspective*. WiLDSI. (available at https://www.dsmz.de/fileadmin/user_upload/Collection_allg/Final_WiLDSI_White_Paper_Oct7_2020.pdf)

for sharing “DSI” connecting scientific databases and platforms. Little is known about “DSI” databases in the private sector.

24. Most scientific journals require that data underlying the results presented in a scientific article are made available in an open access repository before submission of the manuscript. The INSDC, which has a policy of open access, therefore serves as a unique registry of all publicly available “DSI”.²⁰

25. However, public availability of “DSI” does not mean that “DSI” is accessible for everyone in the same way. Substantial technical, institutional and human capacity is required to be able to access and make full use of the innovation potential of “DSI”. Though at varying degrees and depending on the status of technological development, many developing countries lack access to the necessary technical infrastructure, financial and human resources to fully exploit the potential “DSI” offers. Circumstances that may impact access to and use of “DSI” include shortage of trained bioinformaticians and limited computational expertise, educational and training opportunities, and scientific collaborations but also factors such as the lack of computing infrastructures, reliable electricity and high-speed Internet. To facilitate the use of “DSI” for research and development in developing countries, there is therefore a need to build or develop capacity, to support technology transfer, research collaborations and partnerships, to strengthen the scientific infrastructure and to make the necessary funds available.

26. Closely linked to the challenge of technical, institutional and human capacity required to access and make use of “DSI” are the challenges of storage, distribution and analysis tools. Given the exponential growth of genomic data, the infrastructure for the storage and distribution of “DSI” may well change in the future. While the cost of this infrastructure is currently predominantly met by public funds, such funding may not always be available and sufficient and alternative funding models may be considered. Such models could restrict access to “DSI”. However, they could also provide sustainable funding for the life science infrastructure without restricting access to “DSI”, take into account equity considerations and even provide the framework for benefit-sharing arrangements, for example through subscription fees, data deposit and access or membership fees.

V. IMPLICATIONS OF “DIGITAL SEQUENCE INFORMATION”

27. Given its scientific and economic significance, it is not surprising that “DSI” has raised the question if existing ABS measures for genetic resources address “DSI” adequately or, should this not be the case, if new rules should be established for “DSI”.

28. Most ABS measures might allow to address “DSI” as part of the agreement on mutually agreed terms (MAT) that are negotiated when genetic resources are made available for research and development. Whether “DSI” extracted from a genetic resource qualifies by itself as a “genetic resource” is subject to controversy and ultimately a question of law. Currently, treatment of “DSI” by domestic ABS measures varies from country to country. ABS measures of some countries, according to a recent study, seem to require prior informed consent (PIC) MAT before “DSI” may be accessed. These countries basically treat access to and the sharing of benefits derived from “DSI” like access to genetic resources and the sharing of benefits derived from them. Other countries, though not restricting access to “DSI”, require that benefits derived from the utilization of “DSI” are shared. Another group of countries requires neither PIC, nor benefit-sharing for the use of “DSI”.²¹ Thus, currently countries take different approaches to addressing “DSI” within their ABS measures, which ultimately could also affect the implementation and effects of ABS measures for the use and exchange of genetic resources, including GRFA.

²⁰ Arita, M., Karsch-Mizrachi, I. & Cochrane, G. on behalf of the International Nucleotide Sequence Database Collaboration. 2021. The international nucleotide sequence database collaboration, *Nucleic Acids Research*, 49(D1): D121–D124. <https://doi.org/10.1093/nar/gkaa967>

²¹ Bagley, M., Karger, E., Ruiz Muller, M., Perron-Welch, F. & Thambisetty, S. 2020. *Fact-finding 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*. CBD/DSI/AHTEG/2020/1/5. CBD. (also available at <https://www.cbd.int/doc/c/428d/017b/1b0c60b47af50c81a1a34d52/dsi-ahteg-2020-01-05-en.pdf>).

29. Between the two antipodes, treatment of “DSI” as a “genetic resource” for the purpose of ABS, on the one hand, and no ABS for “DSI”, on the other, multiple options for access to and the utilization of “DSI” are currently under discussion. Options include, but are not limited to:

- i. an agreement on the sharing of benefits derived from “DSI” based on standard MAT that are either nationally or internationally agreed;
- ii. the introduction of a pay-per-use or membership fee-based system for the use of “DSI”;
- iii. the establishment of a micro-levy, a small fee users of “DSI” and/or acquirers of relevant equipment for genomic research would have to pay; or
- iv. voluntary sharing of benefits for the use of “DSI.”

30. Benefits could either be shared bilaterally or be pooled in and disbursed through a multilateral mechanism; they could be established dependent on or irrespective of the (extent of) use of “DSI” or the geographical origin of the original gene sequence. Benefit-sharing could be mandatory or voluntary, monetary and/or non-monetary.²²

31. Depending on the option chosen, ABS for “DSI” may have different implications, including with regard to transaction costs, the need to trace the country of origin of the original genetic resource, the user-friendliness of the system and, ultimately, the characterization, conservation and sustainable use of genetic resources, including GRFA. While the options to address “DSI” and their implications resemble to quite some extent previous discussions on ABS for genetic resources, regulating ABS for “DSI” faces an additional challenge, which is to avoid a “two-tier DSI/genetic resources bureaucracy”²³ that could develop if ABS for “DSI” is addressed through additional, rather than existing, legal, administrative or policy measures.

VI. OPTIONS FOR FUTURE WORK

32. Given the ongoing discussions in other fora, it seems pertinent for the Commission and its Working Groups to continue monitoring relevant developments in these fora, to reflect upon the implications of these developments for the access to, use of and the sharing of benefits derived from GRFA and to identify, as appropriate, key aspects that should be taken into consideration in addressing “DSI” on GRFA.

33. The Commission’s *Elements to Facilitate Domestic Implementation of Access and Benefit-Sharing for Different Subsectors of Genetic Resources for Food and Agriculture – with explanatory notes* (ABS Elements),²⁴ in their latest edition, do not address the issue of “DSI”. The ABS Elements are non-descriptive and aim to assist governments considering developing, adapting or implementing ABS measures to take into account the importance of GRFA, their special role for food security and the distinctive features of the different subsectors of GRFA, while complying, as applicable, with international ABS instruments. The Working Groups and the Commission could consider updating or complementing the ABS Elements by adding a section that reflects, or at least references, the ongoing discussions around “DSI”.

34. There is still a lack of awareness of the significant and increasingly important role “DSI” may play for research and development and for the sharing of benefits, including in the food and agriculture sector. The policy implications of “DSI” and their impact on the use and exchange of GRFA and, more broadly, on the food and agriculture sector, are still largely unexplored and have not been considered in any depth by the Commission and its Working Groups. The Working Group may therefore wish to recommend that an intersessional workshop be held to raise the awareness of relevant stakeholders of the role of “DSI” for research and development related to GRFA and the food

²² For an overview of these and other options, see: <https://www.cbd.int/abs/DSI-webinar/Dsi-Webinar3-Policy-options.pdf>

²³ Scholz, A.H., Hillebrand, U., Freitag, J., Cancio, I. *et al.* 2020. *op cit.*

²⁴ FAO. 2019. *ABS Elements: Elements to facilitate domestic implementation of access and benefit-sharing for different subsectors of genetic resources for food and agriculture – with explanatory notes*. FAO, Rome. 84 pp Licence: CC BY-NC-SA 3.0 IGO. (also available at <http://www.fao.org/3/ca5088en/ca5088en.pdf>).

and agriculture sector in general. The workshop could be co-organized with relevant instruments and organizations, such as the CBD, the Treaty and WHO.

VII. GUIDANCE SOUGHT

35. The Working Group may wish to:

- (a) review the relevant section of Table 2; and
- (b) recommend that:
 - i. the Commission request FAO to analyse the effects that the different options of ABS for “DSI” may have on research and development in the food and agriculture sector, for review by the Working Groups and the Commission;
 - ii. the *Elements to Facilitate Domestic Implementation of Access and Benefit-Sharing for Different Subsectors of Genetic Resources for Food and Agriculture – with explanatory notes* (ABS Elements), be complemented by a section on “DSI” reflecting or referencing the ongoing discussions and their potential implications for GRFA;
 - iii. an intersessional workshop be held, in collaboration with relevant instruments and organizations, to raise awareness of relevant stakeholders of the role of “DSI” for research and development related to GRFA, and the food and agriculture sector in general;
 - iv. the Commission request FAO to support countries in building the necessary technical, institutional and human capacity to utilize “DSI” on GRFA for research and development; and
 - v. the Commission continue monitoring developments relevant to “DSI” in other fora, to consider the implications of these developments for the access to, use of and the sharing of benefits derived from GRFA, with a view to identify, as appropriate, key aspects that should be taken into consideration in addressing “DSI” on GRFA.