



Convention on Biological Diversity

Distr.
GENERAL

CBD/WG2020/3/INF/9
8 November 2021

ENGLISH ONLY

OPEN-ENDED WORKING GROUP
ON THE POST-2020 GLOBAL
BIODIVERSITY FRAMEWORK
Third meeting (resumed)
Geneva, Switzerland, 12-28 January 2022
Item 5 of the agenda*

INFORMATION FROM THE COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE RELATED TO DIGITAL SEQUENCE INFORMATION ON GENETIC RESOURCES

Note by the Executive Secretary

1. At its Eighteenth Regular Session, the Commission on Genetic Resources for Food and Agriculture of the Food and Agriculture Organization of the United Nations requested its Secretary to bring 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) to the attention of the Open-ended Working Group on the Post-2020 Global Biodiversity Framework.¹
2. The Commission also requested its Secretary to submit the content of a table on digital sequence information on genetic resources (DSI) to the Convention on Biological Diversity “in order to provide information on the potential future importance of DSI for the characterization, conservation, sustainable use and fair and equitable benefit-sharing and its importance and potential implications for [genetic resources for food and agriculture].”²
3. The Secretary of the Commission conveyed this information to the Executive Secretary of the Convention in November 2021. Accordingly, the information is being made available for the resumed third meeting of the Open-ended Working Group on the Post-2020 Global Biodiversity Framework.
4. The table lists selected examples of actual and potential applications of DSI relevant to the conservation and sustainable use of genetic resources for food and agriculture. The table can be found in the annex below and is made available in the form and language received by the Secretariat.
5. The ABS Elements may be accessed in the six official languages of the United Nations at: <https://www.fao.org/documents/card/en/c/CA5088EN/>.

* CBD/WG2020/3/1.

¹ See para. 28 of the Report of the Commission on Genetic Resources for Food and Agriculture, Eighteenth Regular Session, available at <https://www.fao.org/3/nh331en/nh331en.pdf>.

² See para. 34, *ibid.*

Annex

Selected examples of actual and potential applications of “digital sequence information” relevant to the conservation and sustainable use of genetic resources for food and agriculture³

Common to all genetic resources
<ul style="list-style-type: none"> • DSI is used to accurately identify and understand genetic 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 disease diagnosis and prevention, for management of breeding programmes and for avoiding the further loss of genetic diversity between and within species. For example, researchers can use DSI to identify, understand and mitigate factors that threaten a wide range of populations of vulnerable species. • DSI is used for monitoring <i>in situ</i> conservation programmes and for the development and optimization of <i>ex situ</i> collections, sampling strategies and evaluation of collections.
Animal genetic resources
<p><i>Characterization:</i></p> <ul style="list-style-type: none"> • 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. <p><i>Sustainable use:</i></p> <ul style="list-style-type: none"> • DSI allows the maintenance of genetic variability within populations for sustainable use of animal genetic resources. Different methods have been developed to manage inbreeding while increasing genetic gain. • It can be used to advance discovery and development of new livestock breeds, with enhanced outcomes for sustainable and resilient livestock systems and food security. • DSI can improve the rapid understanding of traits of interest for adaptation to new breeding conditions, particularly in the context of climate change, such as adaptability to high altitudes and increasing tolerance to high ambient temperatures and humidity. • DSI is useful for disease diagnosis and prevention. • 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. <p><i>Conservation:</i></p> <ul style="list-style-type: none"> • DSI contributes to the conservation of threatened species, such as endangered breeds or 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. • DSI 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 underrepresented diversity.

³ This table has been extracted from the document *Digital sequence information on genetic resources for food and agriculture: Innovation opportunities, challenges and implications*, [CGRFA-18/21/5](#).

- Genomic analysis allows for the evaluation of long-term *in situ* conservation programmes. By genomic analysis, information about breed history and about genetic diversity within and between breeds or populations is available for mating plans.

Aquatic genetic resources

Characterization:

- DSI is used to characterize genes and identify genetic sequences, for the study of population genetics and for stock assessment.

Sustainable use:

- 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 can improve access to markets and consumer confidence in supply chains through traceability and identifying product substitution, and supporting product labelling and certification schemes.

Conservation:

- DNA barcoding based on DSI has been used to support conservation of species, including those that might be illegally traded.
- 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.

Forest genetic resources

Characterization:

- 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 morphological diversity; accelerating knowledge on heritability, ecophysiology and biology of forest tree species.

Sustainable use and management:

- 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.
- Technologies that rely on DSI assist to identify the species and geographic origin of wood in order to detect illegal logging and trade.

Conservation:

- 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.

Plant genetic resources

Characterization:

- Increasingly, various types of molecular markers – usually developed based on DSI – are used either alone or as complements to morphological traits to identify and/or analyse heritable variations in germplasm accessions.
- The continuing development and use of next generation sequencing increase significantly the throughput for the generation of DSI, which coupled with the significantly reduced costs and time for molecular assays, including whole genome sequencing, is resulting in the increasing use of genotyping by sequencing (or GBS) to analyze the variations, i.e. characterize, germplasm accessions. A widespread use of GBS will enhance significantly the efficiency of genebank operations as duplicate accessions would be identified reliably and removed from the holdings.

Sustainable use:

- Based on DSI, the sequences of DNA or even a new organism that perform novel functions are created from scratch; this increasingly growing interdisciplinary endeavor is known as synthetic biology.
- Molecular markers are used to establish the identity of crop varieties.
- Molecular markers are used for disease diagnosis in molecular epidemiology and help to trace the origin and evolution of pathogens.
- Access to DSI provides nowadays a fundamental basis for plant research and crop enhancement. DSI can be used to advance the development of new crop varieties, with enhanced outcomes for food security especially for production of drought- and pest-resistant crops, crops that require fewer inputs of water or fertilizers, 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.
- 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.

Conservation:

- 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 molecular characterization data, such as in the DNA Barcode of Life initiative, or “local” initiatives such as the sequencing of genomes of an entire botanical garden.

Note: A previous version of this table has been produced based on examples taken from the literature below. The table has been revised in the light of comments and inputs received from the Commission's Working Groups and Commission Members. CGRFA-17/19/4/Inf.1; Heinemann, J.A., Coray, D.S. & Thaler, D.S. 2018. op. cit.; 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., Fu, Y. *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., Michiels, F. *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.
