

NCP GB8-016 MYPoW/DSI

Submission of views and other information on “Digital sequence information”

(Deadline: 31 March 2019)

Terminology used

As reflected in CBD decision COP13/16 as well as COP14/20, the term “Digital Sequence Information” serves as a placeholder until an alternative term is agreed. The Scoping study commissioned by CGRFA¹, for example, explains that “genetic information” or “genomic information” is more common in scientific literature, whereas “DSI” is not commonly used.

“DSI” may consist of information on the whole genome of a genetic resource (Whole Genome Sequence Information) or only small parts of the genome like Single Nucleotide Polymorphisms (SNPs).

Germany emphasizes that terminology used in the research community evolves and corresponds to the rapidly evolving technologies and research fields (genomics, transcriptomics, proteomics etc.). Therefore, it might be difficult to agree on a definition of “DSI” that will be valid today as well as in the next 20 years. Germany is of the view, that “DSI” is part of a broader set of information related to genetic resources.

“DSI” within the Plant Treaty

Regarding “DSI” within the Plant Treaty, Germany would like to stress that besides passport data, phenotypic data and publications, genomic information (including “DSI”) is part of the Global Information System (GLIS) on PGRFA under Article 17 of the International Plant Treaty. As part of the GLIS it is already within the scope of the Plant Treaty. “DSI” is no physical material and therefore cannot be qualified as a genetic resource. For the same reason, access to “DSI” is not equivalent to “access to plant genetic resources for food and agriculture, or their genetic parts and components”, as mentioned in Article 12.3 (d) of the Plant Treaty text and Article 6.2 of SMTA. Germany is against any definition of genetic parts and components stating otherwise.

Types and extent of uses of DSI on PGRFA

“DSI” as such has limited value for use. To make use of “DSI”, data analyses and comparisons of data on a larger scale are often necessary. Important tools and methods that allow for targeted use are e.g. marker assisted selection (MAS), trait mapping (e.g. QTL mapping to develop targets for MAS), Genome Wide Association Studies (GWAS) among others.

Sequencing and the use of “DSI” are important for PGR related activities including but not restricted to

- **identification and characterization**, e.g. as an important step to prioritise target PGRFA for *in situ*, on farm or *ex situ* conservation
- **conservation**, e.g. by exploring population size and structure or to estimate relationships between populations, e.g. for classification of endangerment of species

¹ CGRFA **Background Study Paper No. 68** *Exploratory fact-finding scoping study on “digital sequence information” on genetic resources for food and agriculture* commissioned by CGRFA by Heinemann et al. (2018)

- **collection and gene bank management**, e.g. for the identification of duplicates, diversity assessment, establishment of core collections etc.
- **breeding and genetic improvements**, e.g. by identifying key agronomic traits

Although details on the generation and utilization of DSI in Germany are not available at the time being, Germany would like to state, that the abovementioned activities have impact to conservation management and dramatically advancement of research and substantially increased the efficiency of plant breeding in Germany already, and will continue to do so.

Relevance of DSI on PGRFA for food security and nutrition

PGRFA are the strategic reservoir of plant diversity on which all our food production depends. Germany emphasizes the importance of their conservation and sustainable use for the diversification of agri-food systems and the enhancement of food and nutrition security. In this regard, international collaboration and common efforts in research and development are essential to achieve the necessary quantity of food and the availability and affordability of nutrient-dense foods and improved dietary diversity worldwide. The relevance of DSI in this context has various dimensions.

For *ex situ* conservation of PGRFA in gene banks, “DSI” applications are an efficient tool to (i) identify gaps, to (ii) unequivocally identify accessions during acquisition, to (iii) monitor regeneration and multiplication, to (iv) eliminate duplicates and (v) to scrutinize and clarify taxonomic relationships. Systematic genotyping of collections allows gene banks to monitor the level of genetic variation within their collections and can ensure quality control, as well as proper maintenance, distribution, and use of gene bank collections.

Genetic sequencing and genomic technologies facilitate research on the genetic architecture of traits like disease resistance or important characteristics regarding the adaptation of crops to climate change and other challenges. With the use of genomic information, breeding processes can be and already have been enhanced, shortened and made more precise.

One important achievement in Germany was the development of reference sequences for important crop plants including wheat (*Triticum aestivum*) barley (*Hordeum vulgare*) and rye (*Secale cereale*) by the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) and its national and international collaborators. The publicly available sequence information will benefit the development of new and improved varieties that are better adapted to changing environmental and climatic conditions and more resistant to plant diseases.

Many crops that have been cultivated by humans in history, today could contribute to resilient and diverse agriculture, but are effectively neglected and receive limited research attention. Key research areas for future work on neglected and underutilised species (NUS) can be enhanced by genomic technologies and bioinformatics tools and include the genetic characterization of promising new species and making relevant information usable by farmers and breeders.

The past decade has seen breathtakingly advances in life-sciences that have greatly promoted our understanding of biological processes ranging from individual cells, via organisms up to populations and ecosystems. It is evident that these achievements have been based on the availability and free access to information including DSI. This asset needs to be carefully hedged as a common good. Stifling the free and unlimited availability of DSI is expected to massively hamper research on PGR and smother the international collaboration to improve the conservation management between gene banks.

Actors involved with DSI on PGRFA

Main actors and institutions involved with DSI on PGRFA are gene banks, universities and research institutions, breeding companies, DNA sequencing services, databases and bioinformatic networks. The way from generating sequence information out of a PGRFA, handling and storing of resulting data, publishing and making the resulting digital information accessible and available for targeted use is very complex. It involves different actors, collaboration at the national and international level and exchange of information at different points in time.

The value of DSI is leveraged by the interconnection of different actors. This has been facilitated by the rapid progress in bioinformatics, which have become an important backbone of making use of genomic technologies. As an example, the German Federal *ex situ* Genebank for Agricultural and Horticultural Crop Species based at IPK, nowadays uses DSI to assess the genetic diversity captured within its major collections. Through bioinformatics, IPK is developing ways of storing and analysing relevant data to facilitate informed access to its collections. This facilitates the use of the existing diversity in the gene bank collection for research and breeding.

Sequencing of genetic resources has been automated using sequencing machines. The proper management, analysis and assessment of large amounts of the resulting sequence data still seems to be challenging and is not standardized.

Germany therefore is convinced that a better understanding is necessary on how these processes work, interact and can be further advanced. Which steps are necessary from sequencing of PGR material and generation of DSI in research institutions to the transfer of sequence information in digital form? What are the steps to publish such data in international databases, such as those of the International Nucleotide Sequence Database Collaboration (INSDC) connected to the databases at the EMBL-EBI, NCBI and DDBJ for documentation or archiving in generally available form? How can we support open access to sequence information for research and breeding? What is needed for a more user-friendly provision of DSI, e.g. via so-called Application Programming Interfaces (API) or other means?

As mentioned above, the actors involved are inter-connected internationally, and we need common efforts in all countries to make use of the advantages that DSI offers to reach our common goals. Germany therefore fully supports the development, maintenance and increase of capacity in all countries to generate and use DSI.