

Consortium of European Taxonomic Facilities

DIGITAL SEQUENCE INFORMATION (DSI) OF GENETIC RESOURCES

Executive Statement



*Exploring and documenting
diversity in nature*



PREAMBLE

Currently, the vast majority of published research results, including Digital Sequence Information (DSI), are also publically available. The fact that especially genomic data are freely available has raised concerns that such data could be acquired and commercialised without triggering an obligation to share benefits with the countries from where the genetic resources were originally sourced. Although CETAF understands the position of some *Providers* who would like to introduce some sort of governance model to address this concern, the CETAF community wishes to highlight the enormous number of non-monetary benefits which are shared by taxonomists and biosystematics, and which actively contribute to and support the objectives of the Convention on Biological Diversity (CBD) by having DSI publicly accessible as well as the negative impacts such a decision would have on biodiversity sciences.

CETAF is committed to benefit-sharing and has developed a **CETAF Access and Benefit Sharing Code of Conduct and Best Practices** for its members to facilitate their scientific activity. For DSI, specifically, CETAF understands that a functional common set of technical standards to provide data on a global basis for the common good is more than enough, instead of developing new systems that will be both difficult and expensive to implement, and that will create a potentially huge negative impact on science globally, and particularly on CBD implementation.

COMMENTS

1. Significance of Digital Sequence Information

Different forms of biodiversity information — including DSI — **are valuable to inform decisions** on conservation and sustainable use of resources, for biodiversity research and other scientific and implementation activities, as well as for research and development of novelties. In the light of this, ensuring that the (entire) information is **available globally** is an essential tool for CBD implementation and is in line with Aichi Target 19.¹

2. Use of DSI in implementing the CBD and meeting the Biodiversity Strategy Targets

For the CETAF community, the use of DSI relates to research activities with non-commercial benefits, for example taxonomic and biosystematics research in biodiversity sciences. DSI is widely used in many areas, to **understand, monitor and safeguard the genetic diversity of organisms on Earth** as well as **to document and understand the diversity of life on Earth**.

In fact, DNA sequence information is vital in implementing the CBD. Our understanding of migrations and changes in genetic diversity, the analysis of effects on genetic diversity after habitat loss, or the ensuring of pollinator conservation are only some of the numerous fields where DNA sequence information has proven to be essential in protecting organisms and finding equitable conservation solutions. Such strong, direct and diverse evidence indicates the potential impairment for conservation planning and implementation of the Convention that would be created if the availability of DSI were to be restricted. Successful implementation is underpinned by and relies on the **free access to and use of DSI by research teams** as well as on their **scientific output (results, conclusions and recommendations)**.

DNA sequences (such as, but not limited to, DNA barcodes) are widely and increasingly used for the identification, classification, description, comparison and monitoring of organisms. Use of DSI is integral for taxonomy and biosystematics, and provides a cost-effective tool for global use. However, the tool is only useful and relevant if it is backed-up by as many DNA sequences as possible, and is accessible as easily as possible: this is the system that has been created by the scientific community and their publicly accessible databases.

¹ cf. GBO4, Fig. 19.1



3. Need to maintain publicly available DSI

DSI is generated by researchers all around the globe, and to keep that information publicly available, traceable and searchable, a select number of public databases manage, archive and offer access to DSI in an operational, accessible and equitable way. Three major global databases host publicly available DSI — they are known as the International Nucleotide Sequence Database Collaboration (INSDC), which are identified as key actors in decision IX/22 of the Conference of the Parties (COP) to the CBD² for enabling the exchange of daily information and to mediate data on more than 200 million sequences.³

These data are published for the use of the entire research community in *Provider* and *User* countries at zero marginal cost, maintained under testable quality procedures and standardised quality norms of the global research community. Accessibility to DSI creates an **invaluable global resource which generates high scientific value** because published scientific research results are free to be used by the informed public.

4. Risks from introducing a control to public access

Changes to the existing protocols for using DSI from public databases would immediately create risks to CBD implementation and to scientific progress more generally.

If changes prevent scientists from having access to data, they will certainly cease to work on the biota of the countries concerned

which will ultimately lead to a loss of non-monetary benefits in those countries, a lack of information being generated on their genetic resources, and a rapid deceleration in the progress made in documenting and understanding native biodiversity. It will also hinder the global resource that is already being used by Parties. Moreover, if scientific information were treated solely in a bilateral benefit-sharing manner, as could be proposed, countries would not benefit from information generated about, among others, non-endemic species or *ex-situ* collections.

Furthermore, each Party maintaining its own national database would have to bear significant costs and cope with the difficult issues of standardisation. Especially in the context of sustainability and data curation in individual repositories, it is worth noting that enormous amounts of publicly available DSI are surprisingly fragile, may be subject to inattention or lack of appropriate data preservation strategies, or shortages of funding for maintenance.

Any novel multilateral system to manage DSI thus faces major risks: (i) difficulty in managing the very large volume of transactions, including application of conditions; (ii) loss of input from researchers following the transition to a different database model; (iii) unsecured sustainability.

Creating a new system that aims to regulate and control access to and the use of over 200 million sequences, and millions of genomic libraries containing terabytes and terabytes of DSI in a sustainable way will be very difficult, to say the least. This would create a huge impediment to scientific progress and would also be extremely — if not prohibitively — costly.

Finally, **restricting access to and uses of common knowledge sources “diminishes research opportunities, retards innovation and tends to lower actual returns over time”⁴.**

5. Evaluation of risks and benefits

Biodiversity information, including DSI, that is held in public databases, and which has in the most part been funded by public money and obtained in collaboration with the *Providers* according to current regulations, where the information is shared openly and any Party can access it, are clearly part of the non-monetary benefits arising from such an exchange.

If the coverage of the CBD is to include DSI and the existing

model is changed as to operate in a bilateral manner, with Parties holding rights to published sequence data originating from specimens accessed within their borders, the existing effective, smooth and globally beneficial process will be dramatically hampered. Certainly, if it were necessary to reach an agreement with a providing country before any sequence was accessed on a database, the system would inevitably fail as it would entail enormous logistical and administrative operations. If countries prohibit publication of the data (currently such publication is a requirement and scientific norm) they are likely to reduce non-commercial research on their biodiversity, and thus the available information they have in hand will be radically affected.

CONCLUSIONS

Biodiversity scientists all over the globe, whom are usually publicly funded, increasingly make the data on which they base their research results publicly available. In fact, providing open access to research publications and to research data is now, more often than not, a requirement of the funding bodies themselves. These data, including DSI, are maintained to the standardised quality norms

of the global research community and available for use in *Provider* and *User* countries at zero marginal cost. In this context, the CETAF scientific community supports the objectives of the CBD and the Nagoya Protocol, agreeing that legal certainty and transparency are essential for the attainment of their objectives, but it also supports full and open access to DSI in the recognition that restricting access to such data would be deleterious, if not catastrophic, for biodiversity-based research and thus the implementation of the CBD. Natural history collections anchor all associated information to specimens, and by linking permits, agreements, and other metadata to their specimens, there is increased transparency regarding their origin and use. **Freely accessible DSI encourages progress through collaborative research and can allow Users and Providers to work together to fulfil the objectives of the CBD.** To include DSI under the scope of the Nagoya Protocol has the potential to be counterproductive and not only hamper deliverance of benefits but also risk failure to reach the global biodiversity targets, and the first two objectives of the CBD. We foresee that such a decision would also create a huge impediment to future progress in documenting and understanding biodiversity on Earth.

² <https://www.cbd.int/decision/cop/?id=11665>

³ Currently, a typical genomic library of 96 samples for a phylogeny in a taxonomic study contains up to 67,200,000 sequence reads.

⁴ Reichman et al. 2016. *Governing Digitally Integrated Genetic Resources, Data and Literature: Global Intellectual Property Strategies for a Redesign Microbial Research Commons*. Cambridge University Press, Cambridge.



SIGNATORIES



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Natural History Museum of Crete

GREECE



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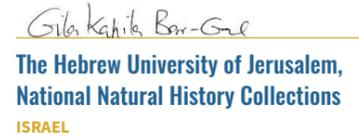
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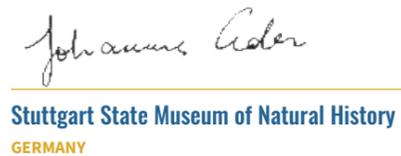
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