

ESA Submission

On

The Use of Digital Sequence Information and the benefits thereof for the three objectives of the Convention on Biological Diversity

- ✿ The CBD and the Nagoya Protocol apply to genetic resources. It is clear from the definitions used in the CBD¹ that the term ‘genetic resource’ covers tangible, functional nucleic acid molecules. Therefore, intangible digital sequence information cannot constitute a genetic resource as defined in the CBD and the Nagoya Protocol and is therefore out of scope.²*
- ✿ Keeping digital sequence information out of scope, therefore allowing access and use of publicly available digital sequence information without administrative burden, enhances innovation and creates a level playing field among public and private entities both in the developed and the developing world.*
- ✿ Maintaining digital sequence information out of scope also reduces the time needed to create new varieties and with that it allows for quicker responses to new challenges.*
- ✿ Keeping digital sequence information out of scope also supports sustainable use of genetic resources since it allows for more efficient use of all necessary resources, including genetic resources themselves.*
- ✿ Maintaining digital sequence information out of scope will maximize the advancement of the three objectives of the CBD.*
- ✿ Given the importance of using sequence information for ensuring food security, the global trend of exchanging and using sequence information should only be supported and not brought to a halt.*

The Food and Agriculture Organization of the United Nations forecasts that by 2050 the world’s population will have exceeded 9 billion people. This is an increase of 34% compared to the world’s population in 2009. The FAO also estimated food production would have to be increased by 70 %, due to the larger, more urban and richer population. Reduction of agricultural land adds further pressures and means that a large part of the increase in food production has to be realized by an increase in yield and cropping intensity. Varieties have to be adapted to local conditions and made more resilient to insects, diseases, viruses as well as more resistant to drought, temperature stresses, and weather extremes from climate change.

¹ According to Article 2 of the CBD “genetic resource” is defined as “genetic material of actual or potential value”; and “genetic material” is defined as “any material of plant, animal, microbial or other origin containing functional units of heredity.”

² ESA fully supports the position of ICC, the International Chamber of Commerce, on this matter.

In 2015 the FAO Commission on Genetic Resources for Food and Agriculture, emphasized in a publication³ that in order to maintain the capacity to respond to these future challenges, agrobiodiversity needs to be maintained *and* used. Access to Genetic Resources for Food and Agriculture (GRFA) is necessary to address the threats resulting from diseases, pests or changing climates. But in order to achieve and sustain food security, improving the capacity to actually use GRFA is critical. The Commission furthermore points out that 'maintaining GRFA is a global task that requires collaboration and cooperation at all levels between all relevant stakeholders'.

Collaboration and cooperation is also a recurring theme in the Convention on Biological Diversity and its Nagoya Protocol. For example, in article 10.e of the Convention, where Contracting Parties have committed themselves to encourage cooperation between its governmental organizations and private sector to develop methods for sustainable use of biological resources. In the Annex to the Nagoya Protocol, sharing of know-how, collaboration, cooperation and contribution in scientific research and development programmes are seen as a non-monetary benefit.

Good examples of such cooperation are the different public private partnership projects aimed at sequencing specific food crops⁴. With the (financial) support of the private sector, universities and research organisations generate sequence information, which after a short confidentiality period becomes available to the general public worldwide through publications and open access databases. This allows other researchers to apply and build upon these results in their own research, while also improving available sequence information that can generate more biological insights.

Ready access to sequence information allows a better understanding of the molecular basis of key agronomic traits, while knowledge of the structure and function of cultivated plant genomes ensures efficient use of limited funds, human resources and most importantly, genetic resources. Better adapted varieties become available in a shorter time frame. It eliminates the need to repeat steps done by others and also the unnecessary use of scarce genetic resources. It promotes food security world-wide as a global team effort. So, that the focus can be on generating new insights essential for the continued and speedy development of new varieties to meet the afore-mentioned challenges.

The importance of being able to use available scientific and technical information in research and breeding activities without any burden has clearly been recognized by the Contracting Parties to the CBD. In art. 17 of the CBD, the Contracting Parties to the CBD have committed themselves to facilitate the exchange of information, relevant to the conservation and sustainable use of biological diversity. With an explicit reference to results of technical and scientific research.

An example to illustrate that it has been practice to exchange DNA information for decades, is the National Center for Biotechnical Information⁵. The Center has as its mission to advance science and health by providing access to biomedical and genomic information. Researchers are encouraged to both submit and extract information from the different NCBI databases. Something which is clearly done on a frequent basis. A simple search entry for lettuce reveals already more than 77,000 DNA and RNA sequences. And for barley even 50 times more (over 3.5 million DNA and RNA sequences).

³ Genetic Resources for Food Security and Nutrition

⁴ For examples the Spinach Genome Sequencing Consortium (http://sbc.ucdavis.edu/Research_pages/Spinach/) or the Centre for BioSystems Genomics (<http://www.cbsg.nl/>) or the International Wheat Genome Sequencing Consortium (<https://www.wheatgenome.org/>).

⁵ <https://www.ncbi.nlm.nih.gov/>

Taking into account the critical importance of wheat for food/feed production, nutritional value and food security (most widely grown crop worldwide on over 200 million ha), the International Wheat Genome Sequencing Consortium (IWGSC), with 1 800 members in 62 countries, is an international collaborative consortium, established by a group of wheat growers, plant scientists, and public and private breeders. Its goal is to make a high-quality genome sequence of bread wheat publicly available, in order to lay a foundation for research that will enable breeders to develop improved varieties. It is a global framework for linking genome and genetic analysis to practical breeding and making available new improved varieties for agricultural production.

To efficiently analyse and interpret the bulk of information, many software tools have already been developed, including multiple open-source tools⁶. These tools give researchers and breeders all over the world the possibility to benefit from previously performed research, even those scientists who do not have a lot of resources at their disposal. Expanding the scope of ABS legislation to include the sequence information included in such tools would change the worldwide scientific landscape and will have an immediate negative impact on food production and food security because it will no longer be widely available to all actors in the agriculture sector. Basically, it means going back 20 years in time. A time during which the development of a new variety took two to four times longer than nowadays. Without the wide availability of digital sequence information, suitable plant candidates for breeding activities can no longer be selected by using markers. Instead, a scientist will have to wait until the plants are fully grown to determine the characteristics. Which will have a significant effect on the availability of new varieties adapted to the new challenges and needs. This means that in case of a new disease, farmers and then consumers will have to wait significantly longer for a variety with a resistance to this disease.

In order to allow the sustainable use of genetic resources, these materials need to be characterised and evaluated. The development of genomic, phenotypic and other tools is playing a role in this characterisation and evaluation in order to allow the adaptation of the agriculture production to the challenges. The Nagoya Protocol recognizes the importance of genetic resources for food and agriculture and their special role for food security. Besides the fact that it would take longer to determine *if* a genetic resource is a suitable candidate for further research and breeding activities, it will also take more resources to determine *which* genetic resources are suitable candidates. In case of breeding for drought tolerance for example, many different genetic resources will be screened in the attempt to find suitable breeding candidates. Including digital sequence information in scope will limit availability of suitable markers. Meaning that such screening will need to be performed by setting up field trials, which again takes much more time and space.

Without the ability to screen different genetic resources quickly and cost efficiently, researchers and breeders will in many cases fall back on the genetic resources of which the characteristics are already known to them. Working with the same genetic resources over and over again will however negatively affect the genetic variation of a crop, narrowing its genetic base. While it is the genetic variation that enables plants and animals to adapt and survive in case of a changing environment⁷.

Keeping digital sequence information out of scope of ABS legislation creates a level playing field amongst the researchers and breeders in the world. The more limitations or administrative requirements that are imposed on the use of sequence information, the more it will be reserved solely for those researchers and breeders with sufficient funds and resources. Which goes counter to the objective of the CBD to take into account specifically the needs of developing countries.

⁶ https://en.wikipedia.org/wiki/List_of_open-source_bioinformatics_software

⁷ As mentioned in the 2015 publication of the FAO Commission on Genetic Resources for Food and Agriculture, 'Genetic Resources for Food Security and Nutrition'.

Considering the above, ESA is of the view that stretching ABS measures to digital sequence information would have significant negative impact on the three objectives of the CBD.

Impact on conservation:

Digital sequence information is essential for *ex situ* conservation, to identify and eliminate duplicates in collections and reduce cost as well as to ensure that material is being collected and conserved that represents the relevant diversity.

Digital sequence information is needed for *in situ* conservation, to measure genetic diversity and thereby ensure that we effectively conserve diversity in natural area and in/around the field, and to monitor how it evolves in response to environment changes.

Phenotype observation alone is tedious, expensive and does not provide complete information about diversity.

Keeping digital sequence information out of scope avoids the risk to conserve the wrong materials.

Impact on sustainable use:

Only a very small fraction of collected diversity for food crops is characterized. If society wants its scientists and breeders to develop climate resilient crops, or address other challenges in food production, more and better characterization of genetic resources is needed, and the facilitated use of digital sequence information is essential.

Impact on benefit sharing:

Extending ABS to digital sequence information for genetic resources for food and agriculture (GRFA) will hinder achieving the Sustainable Development Goals. Orphan crops, and less productive and less profitable market segments and agro-ecologies would be among the first to suffer from the complexities and uncertainties created. There will be even less innovation addressing the needs of resource-poor farmers.

Submergence tolerant rice is an example of innovation for resource-poor farmers, enabled by systematic characterization of genetic resources and use of digital sequence information: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3837307/> ; it may have not have been realized if ABS had applied to digital sequence information.

Impact on research activities:

It is valuable for researchers to be able to share their findings resulting from research projects. E.g. dissertations have to be published and if no DSI could be revealed research in such cases could not be realized anymore. And once the information is public, there is no manageable way to ensure the further flow of information.

In conclusion, for GRFA, expanding the scope of ABS legislation to digital sequence information adds an administrative burden and barrier to effective and beneficial use of such information. In effect, it will substantially and negatively impact conservation, sustainable use and benefit sharing. To reach the objectives of the CBD, any measures that stretch the scope to include digital sequence information should be avoided.