

Potential implications of the use of “digital sequence information on genetic resources”

Submitted by *Ethiopia*

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Context

In Notification SCBD/SPS/DC/VN/KG/jh/86500 dated 25 April 2017 (see <https://www.cbd.int/doc/notifications/2017/ntf-2017-037-abs-en.pdf>) the Executive Secretary of the CBD invites Parties, other Governments, indigenous peoples and local communities, and relevant organizations and stakeholders to submit views and relevant information on any potential implications of the use of digital sequence information on genetic resources for the three objectives of the Convention, including information relevant to the Nagoya Protocol. The current document presents preliminary views from African biodiversity negotiators on this topic. It is submitted without prejudice to future African negotiating positions.

Perspective

The issue under discussion is largely driven by an exponential increase in global information technology capacity, which makes it possible to:

- Isolate, analyse and sequence any naturally occurring substance;
- Store and share the resulting information;
- Interrogate (“data mine”) very large sets of information; and
- Utilise the information to reconstitute natural substances in original and altered structures.

This creation and utilisation of a wide variety of naturally occurring information has expanded to an extent that was hardly imaginable 30 years ago, when the CBD was negotiated. This increased capacity to manipulate naturally occurring information is the result of virtually unlimited computing power, cheap digital storage and ubiquitous fast information transfer, coupled with next-generation sequencing techniques, advanced data mining capacities, and new disruptive technologies such as gene printing, gene editing and other tools of synthetic biology.

- We believe that there is an emerging global consensus on the need to consider and regulate as appropriate the implications of these technologies for biodiversity governance.

Terminology

Without prejudging ongoing discussions about the best terminology to use when discussing this topic, we submit that while the term “digital” currently describes some key characteristics of data generation and storage, it may become obsolete in the future. The mathematical and electronic models currently used for encoding information might be overtaken by information technology developments (e.g. quantum computing, “DNA chips” etc.) in the medium term. What is relevant is the information itself, the fact of storage and world-wide accessibility and the modes of reconstitution and utilisation. Any outcome of the current discussion must be open for revision with regard to technological advances.

We further submit that the term “genetic” is open to misinterpretation in this context, because it tends

to obscure rapid developments in other relevant “-omics” (e.g. proteomics, metabolomics etc.). We note that it is clarified through the definition in the Nagoya Protocol that utilisation of genetic resources refers not only to the genetic molecules (i.e. DNA and RNA) but to any naturally occurring component contained in the analysed biological material (i.e. proteins, metabolites and other molecules). The term “genetic” should therefore be avoided when choosing language to describe the subject matter and provide legal clarity about it. To avoid a situation in which emerging biodiversity governance policy is (again) overtaken by rapid technological innovation and change we favour the use of a neutral and wide term like “natural information”, while remaining open to discussing the possibility that different types of natural information might eventually be subject to different governance regimes.

We further submit that the term “sequence” is open to misinterpretation as well, because it might be misunderstood as referring to nucleic acid sequences only. With regard to the definition of utilisation, it is understood that the term “digital sequence information” covers the information contained in any natural substance, described through the sequence of e.g. nucleic acids in DNA, amino acids in proteins, or atoms in biochemical compounds.

- In our view, the outcome of the current exercise should be to clarify that utilisation of naturally occurring information is equivalent to utilisation of genetic resources.
- In our view, it is crucial to apply the term “digital sequence information” in a way that fully recognizes and incorporates the definitions of the CBD and the NP.

Implication for the objectives of the CBD

We see the three objectives of the CBD as inextricably intertwined: fair and equitable benefit sharing provides incentives for sustainable use, which leads to good conservation outcomes. If the emerging technologies under discussion undermine any one of these pillars, they undermine all of the CBD.

We acknowledge and appreciate the immense potential of these technologies to contribute to conservation (through e.g., genetic taxonomy, DNA barcoding, targeted bio-banking etc.) and to sustainable use (through e.g. less invasive/destructive bioprospecting methods, better characterisation and protection of genetic diversity within populations, etc.). First and foremost, however, we are concerned about the potential implications of these technologies for the third objective – fair and equitable sharing of the benefits arising from utilisation.

Precisely because of their potential power for good, these technologies are poised to elevate the benefits of utilisation to a completely different level. However, because of their technological complexity, relative inaccessibility to developing countries and typically high levels of intellectual property protection, they also threaten to widen existing technology and capacity gaps and thereby undermine efforts for conservation and sustainable use. Conversely, were these technologies to be made more widely available and accessible through benefit sharing measures such as information exchange, technology transfer and capacity development, they hold substantial promise of boosting the transition to a green economy and hastening the universal achievement of truly sustainable global development.

- The policy and governance models that emerge from the current discussions should aim to maximise the potential of the technologies under consideration while also preventing an inadvertent undermining of the purpose and objectives of the CBD.
- Because the principle of fair and equitable sharing of benefits arising from utilisation is established by the CBD and only elaborated in the Nagoya Protocol, and because the CBD applies to all its Parties while the NP currently applies only to a subset of the CBD Parties, the policy

measures that emerge from the current discussion must primarily be embedded in the CBD, through a CoP decision clarifying the matter, before specific ABS implications are elaborated under the auspices of the NP.

Relevance to the Nagoya Protocol

In the context of the NP and user measures in national ABS regulations, the utilisation of natural information instead of the genetic resource itself potentially undermines benefit sharing and bypasses compliance measures. According to our analysis, existing user measures will not lead to a monitoring of the utilisation of sequence information in the country where utilisation occurs. This implies that providers will be forced to use their national access legislation (PIC) and utilisation agreements (MAT) in an attempt to control such utilisation and ensure appropriate sharing of benefits (e.g. by explicitly prohibiting sequencing natural compounds contained in genetic resources unless agreed in MAT and connected to benefit sharing).

In our view, it would be an unfortunate outcome if this situation resulted in undue restrictions being placed on the harvesting, sharing and utilisation of natural information in all its many forms. Data become more valuable for the attainment of the CBD objectives and other purposes, when available for comparison, and information inherently involves flows and exchanges; attempting to restrict these is likely to be both very difficult and counter-productive. We believe that the main task to hand is designing measures to ensure fair and equitable sharing of benefits; if this is achieved there will be little need for controlling access, and monitoring compliance will be simplified and facilitated.

- Trying to control access to natural information is likely to be difficult and to produce sub-optimal outcomes for humanity.
- Finding creative ways to guarantee benefit sharing will allow open access to and sharing of natural information to flourish, with positive outcomes for the global community.
- We think the Global Multilateral Benefit Sharing Mechanism foreseen in Article 10 might help parties to arrive at beneficial solutions.

Observations on Scope

In the early discussions around this topic there have been some voices denying that natural information is within the scope of the CBD and NP, because “genetic resources” are defined as “genetic material of actual or potential value”. According to these arguments information is not material and therefore out of scope. But the CBD and NP define “genetic material” as “any material of plant, animal, microbial or other origin containing functional units of heredity” (with “functional units of heredity” left undefined). We submit that the phrase “or other origin” was originally included in the definition as clear and agreed language signalling that “functional units of heredity” can be contained in non-biological material. This reflects the reality that the essence of a “functional unit” is its ability to convey the information necessary to encode the hereditary trait. To the best of our knowledge there is nothing in the known Universe that is not “material” in some sense; certainly there is no known way of transmitting information except through material means. We acknowledge that different rules might well be applied to accessing information alone (e.g. for comparative data analysis, gene mining, taxonomy etc.) compared to using the same information to establish a heritable trait in an organism or population (through gene printing, gene editing, synthetic biology, marker assisted breeding etc.), but we nevertheless maintain that be any standards of logic the utilisation of such information is clearly within scope, at the very least when the information is utilised to effect heredity.