african centre for biodiversity

Ms. Cristiana Paşca Palmer
Executive Secretary
Secretariat of the Convention on Biological Diversity
United Nations Environment Programme
E-mail: secretariat@cbd.int

Submission of 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. Pursuant to decision NP-2/14, paragraph 2, these submissions are also invited to include views and information relevant to the Nagoya Protocol.

and to

Food and Agriculture Organisation
Commission on Genetic Resources for Food and Agriculture
CGRFA@fao.org

Submission of information on the use of "digital sequence information on genetic resources for food and agriculture" and potential implications for the conservation and sustainable use of genetic resources for food and agriculture, including exchange, access and the fair and equitable sharing of the benefits arising from their use

30 August 2017

Dear Madam/Sir

We write to you from the African Centre for Biodiversity (ACB). The African Centre for Biodiversity (previously 'Biosafety') was established in 2003 and registered in 2004 in terms of the laws of the Republic of South Africa. ACB carries out research, analysis, capacity and movement building, and advocacy, and shares information to widen awareness and catalyse collective action and influence decision-making on issues of biosafety, agricultural biodiversity and farmer-managed seed systems (FMSS) in Africa. The ACB's work both informs and amplifies the voices of social movements fighting for food sovereignty in Africa.

We make these submissions based on our grave concerns about the implications stemming from the ability of corporate 'breeders' to use genetic engineering technologies such as Clustered regularly interspaced short palindromic repeats (CRISPR), which edit DNA, to access genetic sequence data pertaining to genetic resources, and convert this data back to

DNA or RNA and to use it in living organisms, and the risks this poses to the conservation and use of biological diversity and access and benefit sharing international and national regimes and agreements.

Genetic sequence data can be accessed on the internet or in an email, this means that it may no longer be a need to access and exchange of the physical genetic resources/biological materials. Crop traits can be accessed in this way as well as genes that encode for active compound in medical plants, and be used in the manufacture of pharmaceuticals. This gives rise to the possibility that genetic resources can be accessed without prior informed consent and in the absence of a benefit sharing agreement. This would thus undermine several international agreements, including in particular the 3rd objective of the Convention on Biological Diversity (Convention), the Nagoya Protocol on Access and Benefit Sharing (Protocol) and the International Treaty on Plant Genetic Resources for Food and Agriculture (Treaty). Indeed we will go so far as to say that current benefit sharing regimes may be rendered redundant as we go into the future particularly those of the Protocol and Treaty. The rationale underpinning objective 3 of the Convention, and the central imperatives underpinning the Protocol and the Treaty to prevent biopiracy or the misappropriaton of genetic resources will be totally eroded.

Today, what are commonly referred to as the "Big Six" mega seed and agrochemical corporations - namely: BASF, Bayer, Dow, DuPont, Monsanto and Syngenta - together control 75% of the global agrochemical market, 63% of the commercial seed market and over 75% of all private sector research and development (R&D) in the sector.

However, three mega-mergers in input supply underway between ChemChina and Syngenta, Dow and DuPont and Monsanto and Bayer are set to entrench the existing global oligopoly built on a cartel-like technological platform in biotechnology traits, commercial seed and patented agrochemicals. These mergers are indicative of broader processes and the threats they pose to economic participation, social equity and ecological sustainability.

These multinational corporations are making major strides in the new genetic engineering technology that will supersede 'aging' technologies such as transgenic crops: CRISPR, genome editing technology and synthetic biology, which are cheaper and quicker to develop, and for now, unregulated.

Recommendations

1. Parties and all other relevant stakeholders and interested parties to the Convention, the Protocol and the Treaty must ensure that a legally binding decision is taken to unequivocally require that sequence data be considered equivalent to its physical biological counterparts.

2. Sequence data in this regard, must be broadly defined, because it is not necessary to synthesize an entire genome in order for the data to be useful and profitable. Individual genes synthesized from data and inserted into living organisms can be of enormous commercial value, particularly in industrial and medical applications. Sequence data includes DNA, RNA and amino acid sequences as well as accompanying characterization information. Parties and all other relevant stakeholders and

interested parties to the Convention, the Protocol and the Treaty must thus pay attention to the scope of digital sequence data. The hereditary material of an organism is not just DNA but in some cases it is RNA. Since the complementarity between molecules, and their important functions, the sequences of both must be covered. The sequences of amino acids that nucleotides encode are similarly valuable and can be used to replicate and modify natural compounds and in design of biological systems. These sequences too need to be addressed with respect to benefit sharing, see below.

3. Further, Parties and all other relevant stakeholders and interested parties to the Convention, the Protocol and the Treaty must agree to measures to be taken at the national level, to ensure that access and benefit sharing laws and agreements not only apply to the physical transfer of biological material but also to sequence data. In this regard, the scope as mentioned above in point 2, must be broad enough to ensure that all relevant data is caught in the benefit sharing net.

4. Parties and all other relevant stakeholders and interested parties the relevant international agreements must ensure that a legally binding decision is made to require that repositories of sequences and databases in turn require their users to up front agree to benefit sharing as a pre-condition to accessing any sequence information. In this regard, Parties and all other relevant stakeholders and interested parties to the relevant international agreements must be asked to elaborate rules and procedures to govern such user agreements.

5. Turning to the first and second objectives of the Convention, we make the following submissions:

    5.1 The gene foundry and synthesis equipment industries are largely unregulated, and this creates risks to biodiversity. Since synthesis equipment does not care what it is synthesizing, and companies are generally not under any legal obligation to consider the safety of the nucleotide sequences they are producing, much less the ecological impacts, invasive and harmful organisms may be produced and thereby pose a risk to biodiversity. This needs urgent attention by the Parties and all other relevant stakeholders and interested parties to the Convention, including to take into account emerging newer equipment such as “digital-to-biological-converters” that are smaller, faster, cheaper, more portable and able to synthesize ever longer sequences.

    5.2 The misuse of sequence data may also impact negatively on the conservation of biological diversity. The ability to synthesize organisms, or modify organisms with synthesized genes (creating a new sub-species/strain) presents a serious and novel challenge to efforts to curb the negative effects of invasive species. While traditional efforts to prevent invasive species have focused on physically preventing introductions-e.g. phytosanitary measures and border protection-the use of genetic data can leapfrog these controls, resulting in the introduction of invasive species from within a country rather than from outside its borders.

    5.3 A link may be drawn between sequences and sustainable use of biological resources. The unregulated and free access to sequences of genetic resources such as natural medicinal compounds and "climate smart genes" (sequences conferring drought or salt tolerance for example) may harm communities and decrease the perception of the importance of maintaining and developing the resiliency of the genetic resources in situ and within context specific and appropriate ecological environments.

5.4 We make mention here that we do not accept that the recording of sequences in databases is sustainable use. The potential for the disruption or collapse of small farmers' markets particularly in Africa, where 80% of the food is produced by small-scale farmers farming on average of 2 ha, engendered by unfettered and unrestrained use, is a real and grave danger. This will have severe negative impacts on the conservation and sustainable use of biological diversity by economically and culturally undermining indigenous peoples and local communities conserving and sustainably utilizing a wide pool of biodiversity.

We trust that these comments will contribute to the further work by Parties and other stakeholders towards realizing the goals and objectives of all three international agreements referred to in this submission.

Kind regards

Mariam Mayet, Executive Director

African Centre for Biodiversity