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Transport, Energy and Communications DETEC

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Government of Switzerland Submission in response to CBD Notification 2017-037 - Digital Sequence Information on Genetic Resources

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Switzerland thanks the COP and the COP-MOP for the opportunity to express its views regarding potential implications of the use of digital sequence information on genetic resources for the three objectives of the Convention, and for the objective of the Nagoya Protocol according to decision CBD XIII/16 and decision NP-2/14.

Switzerland agrees that clarifying issues related to digital sequence information is highly relevant and is involved in and follows parallel discussions and studies on this topic in several other international fora (e.g. FAO CGRFA, FAO ITPGRFA, WHO PIP framework, CITES, IUCN). Switzerland deems it important that the processes undertaken by all these bodies be coordinated in order to ensure coherence and consistency in dealing with digital sequence information. Therefore, Switzerland invites the CBD secretariat to take a leading role in organizing regular exchange and coordinated planning between the Secretariats of the relevant agreements to facilitate mutual supportiveness of the work streams in these different bodies. Previous discussions revealed the general lack of an internationally agreed understanding or definition of what constitutes “digital sequence information”. A clarifying terminology may be important to determine and resolve questions at interfaces between different instruments as well as to further specify implications for the three objectives of the CBD and the objective of the Nagoya Protocol.

I. Implications of the use of digital sequence information on genetic resources for the first objective of the Convention (conservation of biological diversity)

Concerning the first objective of the Convention, Switzerland emphasizes the importance of digital sequence information for the conservation of biological diversity. For the protection and conservation of species and ecosystems, digital sequence information is particularly relevant in the fields of taxonomy and conservation ecology. A detailed description and characterization of populations, including digital sequence information, is key to distinguish populations that have similar morphological traits and consequently identify their ecological niches, enabling to better design adapted strategies for their management and effective protection. Therefore, it is crucial to encourage research on genetic diversity, its characterization and publication of the results.

II. Implications of the use of digital sequence information on genetic resources for the second objective of the Convention (sustainable use of its components)

Concerning the second objective of the Convention, Switzerland thinks that the use of digital sequence information can contribute to the sustainable use of the components of biological diversity but that it may also pose certain risks to biological diversity, depending on the context. On the one hand, sustainable use of biological diversity may be fostered by digital sequence information by using it as a tool for the management and protection of species and populations. Furthermore, the pressure on wild populations of endangered species may be reduced if artificial substitute products based on digital sequence information replace the natural product. In addition, conservation and sustainable use of genetic resources for food and agriculture (GRFA) are key for food security, nutrition and sustainable agriculture, e.g. with the growing interest in crop wild relatives and their potential implication in food security. On the other hand, new possibilities for biotechnological uses of components of biological diversity based on digital sequence information may pose risks to biological diversity, such as potential risks associated with the release of modified organisms into the environment or with the release of synthetic organisms with the aim of preventing extinction of endangered species or replacing extinct ones. Switzerland believes that the gained experience of environmental risk assessment procedures as conducted within the Cartagena Protocol for Biosafety may constitute a good example for assessing the risks due to the use of such engineered organisms.

III. Implications of the use of digital sequence information on genetic resources for the third objective of the Convention and the objective of the Nagoya Protocol (fair and equitable sharing of the benefits arising out of the utilization of genetic resources)

Switzerland has ratified the Nagoya Protocol on 11 July 2014. As a prerequisite for the ratification of the Nagoya Protocol in Switzerland, specific amendments to the Federal Act on the Protection of Nature and Cultural Heritage (NCHA) concerning the utilization of genetic resources were made. Subsequently, these provisions were detailed in the Ordinance on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilisation (Nagoya Ordinance, NagO), which came into force on 1 February 2016.

The adoption of the Nagoya Protocol, its ratification by Switzerland and the corresponding amendments in the Swiss legislation are bound to the wording and definitions given by the CBD and the Nagoya Protocol. Consistent with the definitions provided in the CBD, the Swiss Nagoya Ordinance defines “genetic resources” as “genetic material of actual or potential value”. Similarly, the term “genetic material” is defined as “any material of plant, animal, microbial or other origin containing functional units of heredity”. According to these definitions, the terms “genetic resources” and “genetic material” clearly refer to tangible matter. In contrast, intangible digital sequence information does not fulfil the criteria of the definitions of either “genetic material” or “genetic resources”. Therefore, “digital sequence information” is not covered by the definition of “genetic resources“.

The Nagoya Ordinance defines the term “utilization of genetic resources” as “conducting research and development on the genetic or biochemical composition of genetic resources, including through the application of biotechnology as defined in Article 2 of the Convention of 5 June 1992 on Biological Diversity”, which is in line with the definition provided in the Nagoya Protocol. Since research and development activities are not defined in the Nagoya Protocol, these terms are to be understood in context of the Nagoya Protocol (see IUCN Environmental Policy and Law Paper No. 83). It includes basic research activities, e.g. sequencing of DNA or characterization of the biochemical composition of a plant, as well as development activities, e.g. breeding of a new disease resistant crop variety (see http://www.news.admin.ch/NSBSubscriber/message/attachments/42239.pdf, “Erläuterungen zur Nagoya Verordnung”, p. 8-9, only in German). Although the CBD and the Nagoya Protocol do not explicitly address the issue of digital sequence information, research on the genetic or biochemical composition of genetic resources can generate different forms of digital sequence information, and thus, such information can play a role during the process of utilization of genetic resources. In the view of Switzerland, the technical procedure of sequencing of a genetic resource meets the criteria of the term “utilization of genetic resources”. Therefore, the application of this technology may fall under the scope of the Nagoya Protocol.

The specific conditions under which a particular genetic resource can be utilized, can be negotiated and defined in the mutually agreed terms (MAT) between the provider country and the user. This contract may also include provisions regarding digital sequence information resulting from the utilization of the particular genetic resource (e.g. provisions concerning the publication of digital sequence information on the genetic resource).

A potential redefinition of the terms “genetic material” and “genetic resources” to include not only tangible matter, but also digital sequence information would, in the view of Switzerland, extend the nature of what the term “genetic resource” refers to in the CBD and the Nagoya Protocol**.** In conclusion, the implications of such a redefinition on the existing legal framework in Switzerland remain difficult to assess because of the general lack of a common understanding of what constitutes “digital sequence information”.