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Views of Japan Bioindustry Association (JBA) on the issues of Digital Sequence Information on Genetic Resources

Dear Ms. Cristiana Paşca Palmer, PhD
Executive Secretary of the Convention of Biological Diversity

Concerning the notification 2017-037 (SCBD/SPS/DC/VN/KG/jh/86500) of 25 April 2017, Japan Bioindustry Association (JBA) greatly appreciates the opportunity for submission of our views and relevant information on the issues of digital sequence information on genetic resources as a relevant organization.

We would be most grateful if the Executive Secretary would take into consideration our views and relevant information given below, in the process of preparing documentation on the related agenda item for the meeting of the Ad Hoc Technical Expert Group on Digital Sequence Information on Genetic Resources.

1. Background

The thirteenth meeting of the Conference of the Parties to the Convention on Biological Diversity (hereafter the CBD) and the second meeting of the Conference of the Parties serving as the meeting of the Parties to the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefit Arising from their Utilization to the Convention on Biological Diversity (hereafter the Nagoya Protocol), respectively, adopted the decisions on digital sequence information on genetic resources (decisions XIII/16 and NP-2/14, respectively). These decisions invite Parties, other Governments, indigenous peoples and local communities, and relevant organizations and stakeholders to submit views and relevant information to the Executive Secretary on any potential implications of the use of digital sequence information on genetic resources for the three objectives of the CBD and the objective of the Nagoya Protocol.

2. JBA's views on digital sequence information under the CBD and the Nagoya Protocol

JBA supports the three objectives of the CBD and the objective of the Nagoya Protocol and has been actively engaged in contributing to the proper implementation of those objectives. And we believe that the legal certainty is essential for the implementation of those objectives of the CBD and the Nagoya Protocol.

Therefore, we would like to overview the relationship between digital sequence information on genetic resources and the CBD or the Nagoya Protocol, before we present our views and relevant information on the issues of digital sequence information on genetic resources.

First of all, the definition of "genetic resources" is "genetic material of actual or potential value" with "genetic material" being defined as "any material of plant, animal, microbial or other origin containing functional units heredity" (see Article 2 of the CBD). Furthermore, these definitions are also applied to the Nagoya Protocol (see Article 2 of the Protocol). Intangible digital sequence information on genetic resources does not fall within the definition of "genetic resources" under the CBD and the Nagoya Protocol, because "genetic resources" are tangible materials.

However, benefit-sharing relating to "digital sequence information on genetic resources obtained by utilizing accessed genetic resources" is not excluded from the CBD and the Nagoya Protocol. The conditions, including those for benefit-sharing, for dealing with such digital sequence information could be covered by the mutually agreed terms (MAT) between the provider and the user of the genetic resources.

3. JBA's views and relevant information on any potential implications of the use of digital sequence information on genetic resources for the objectives of the CBD and the Nagoya Protocol

3-1. Conservation of biological diversity

For the conservation of biological diversity in a certain area, the current state of biological diversity in that area must be monitored. Monitoring of biological diversity has traditionally relied on physical identification of species by, for example, visual surveys and counting of individuals in the field based on distinct morphological characters. However, such method depends on high level of expertise to distinguish between morphological characters and requires a lot of monetary cost, labor and time. Additionally, such techniques have sometimes resulted in being invasive on organisms or environment. Therefore, so far it has not been easy to obtain information proper and useful enough for the conservation of biological diversity.

In contrast, more recently, new techniques such as DNA barcode and DNA metabarcoding have been developed and applied to monitoring biological diversity[1]. They are powerful approaches to obtain information on species in environment by analyzing fragments of DNA extracted from environmental samples (environmental DNA, abbreviated as eDNA), such as water and soil sediment. It is possible to obtain information on species, populations and communities in environment by applying these approaches; for example, fishes by analyzing eDNA from sea water, animals based on eDNA from water holes, or soil organisms such as earthworms based on eDNA from soils.

Although there may be some room as well as limitation for the improvement of these approaches, they do not depend on high level of expertise to distinguish between morphological characters, resulting in achieving reduced cost, labor and time to monitor the state of biological diversity, in comparison with traditional techniques. This would enable more appropriate measures to be taken for the conservation of biological diversity.

Therefore, digital sequence information on genetic resources is expected to contribute increasingly to the conservation of biological diversity through these techniques of DNA barcode and DNA metabarcoding.

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[1] Thomsen, P.F., Willerslev, E., Environmental DNA — An emerging tool in conservation for monitoring past and present biodiversity, Biological Conservation 183, 4-18 (2015)

3-2. Sustainable use of the components of biological diversity

The contribution of digital sequence information on genetic resources to the conservation of biological diversity as mentioned above, would in turn drive the sustainable use of the components of biological diversity.

For example, particularly because of the cost-effectiveness of the approaches based on DNA barcode and DNA metabarcoding, the biological diversity in some appropriate areas could be periodically monitored. Such periodical monitoring would make it possible to obtain information on variation in, e.g., the population of specific components of biological diversity (e.g., some genetic resources). This would enable more proper plans for sustainable use to be developed and implemented.

Variation in some parts of DNA sequence can occur within the same species, for example, between wild species and domesticated or cultivated species. Such variation can also occur as a result of living in different habitats. Techniques are available to distinguish between, e.g., wild species from domesticated or cultivated species by using varied parts of DNA sequence as a marker (DNA marker)[2]. It would be possible to prevent overexploitation of a wild medicinal plant by monitoring whether a supply of such a medicinal plant on the market is wild species or cultivated one. And it would also be possible to prevent overexploitation of timber in some particular area if the original habitat of such timber could be deduced by such molecular technology.

As exemplified above, the use of digital sequence information on genetic resources could contribute to the sustainable use of the components of biological diversity in a number of ways.

3-3. Fair and equitable sharing of the benefits

Most of such digital sequence information is registered in publicly available databases, and any one in any country can freely access such data bases and use the information in her/his country for any purpose, including the conservation and the sustainable use of biological diversity.

Furthermore, to reiterate what we have mentioned at the beginning of this paper, benefit-sharing relating to "digital sequence information on genetic resources obtained by utilizing accessed genetic resources" is not excluded from the CBD and the Nagoya Protocol. The conditions, including those for benefit-sharing, for dealing with such digital sequence information could be covered by the mutually agreed terms (MAT) between the provider and the user of the genetic resources.

4 . Implications of digital sequence information on genetic resources for innovation

Digital sequence information on genetic resources is indispensable for research and development in modern life sciences and biotechnology. DNA barcode, DNA metabarcoding and DNA marker mentioned above in the context of the conservation and the sustainable use of biological diversity,

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[2] Lidder, P., Sonnino A., Biotechnologies for the Management of Genetic Resources for Food and Agriculture, Commission on Genetic Resources for Food and Agriculture, Background Study Paper No. 52, 2011

are fruitful results of such research and development. Furthermore, the value of digital sequence information on genetic resources is not limited to these, and covers a much wider area in academia, government and the private sector in a most fundamental and complicated way in our global society.

Advances in key areas (e.g. health, food & agriculture, environment) of our global society are supported by free accessibility to digital sequence information on genetic resources in publicly available databases. This is the crucial point. Regulatory interference with this aspect would be detrimental to entire human activity, including the conservation of biological diversity and the sustainable use of its components. Such interference should never occur.

Sincerely yours,

Yoshiaki TSUKAMOTO
Executive Director
Japan Bioindustry Association