Recommendation

The treatment of Digital Sequence Information with respect to the Convention on Biological Diversity and the Nagoya Protocol

January 22, 2018
Science Council of Japan

Genetic Resources Subcommittee: the committees of Basic Biology, Integrated Biology, Agricultural Science, and Basic Medical Science

Nagoya Protocol Implications on Agricultural Science Review Subcommittee: the committees of Agricultural Science and the Food Science

This published recommendation summarizes the findings of both the Genetic Resources Subcommittee – with the participation of the committees of Basic Biology, Integrated Biology, Agricultural Science, and Basic Medical Science – and the Nagoya Protocol Implications on Agricultural Science Review Subcommittee – with the participation of the committees of Agricultural Science and the Food Science.

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Summary

1 Background of the Recommendation

At the Science Council of Japan, joint meetings of the Genetic Resources Subcommittee and the Nagoya Protocol Implications on Agricultural Science Review Subcommittee were held to discuss the potential implications of including digital sequence information on genetic resources in the scope of the Convention on Biological Diversity and of the Nagoya Protocol. As a result of these meetings, we recommend the cooperation of academic institutions, researchers, and governments both domestic and foreign to: oppose the inclusion of digital sequence information; and establish a practical framework to achieve the objectives of the Convention and of the Protocol.

2 Present status and problems

(1) Arguments by resource provider countries in favor of including digital sequence information in the scope of the Convention on Biological Diversity and the Nagoya Protocol

Some signatory countries of the Convention on Biological Diversity and the Nagoya Protocol have presented the following three arguments for including digital sequence information in the scope of the Convention and the Protocol.

i) The meaning of “use of digital sequence information” cannot be distinguished from “use of genetic resources”.

ii) Making digital sequence information subject to the Convention on Biological Diversity and the Nagoya Protocol is in keeping with the objectives of the Convention and the Protocol and would support the promotion of science.

iii) A monitoring system is needed to ensure traceability of digital sequence information usage.

(2) Potential implications of including digital sequence information in the scope of the Convention on Biological Diversity and the Nagoya Protocol

There are serious concerns that inclusion of digital sequence information in the scope of the Convention on Biological Diversity and the Nagoya Protocol as promoted by the arguments listed above could have adverse impacts on achieving the objectives of the Convention and the Protocol and on the promotion of science and sustainable development of industries.

i) The scope of the Nagoya Protocol is specified to “genetic resources” and “traditional knowledge associated with genetic resources”. “Genetic resources” is defined as “genetic material” of actual or potential value, and “genetic material” is defined as any (tangible) “material” of plant, animal, microbial or other origin containing functional units of heredity. The wording “material” does not include digital sequence information, which is intangible.

ii) Open use of digital sequence information is indispensable for deepening our understanding of biodiversity, for the expeditious identification of pathogenic microorganisms in times of global epidemics, and so on; therefore, any restrictions on its use would impede the objectives of the Convention on Biological Diversity. Moreover, since digital sequence information comprises the principal foundation for life science research now and in the future, creation of new rules that restrict its use would become a major obstacle to research. Furthermore, there are various fields of sustainable research and development that are conducted based on the results of academic research, and any stagnation of such research would also negatively impact the advancement of these fields and the economic benefits that they create.

iii) Constructing a monitoring system that ensures traceability of access to and use of digital sequence information would be extremely difficult. Moreover, since in many cases economic benefits first arise from results obtained from cross-comparison of multiple similar sequence data made possible by the broad and open use of digital sequence information, it is extraordinarily difficult to monitor and objectively estimate the economic contribution of each item of information.

3 Recommendation

In order to achieve the objectives of the Convention on Biological Diversity and the Nagoya Protocol, prompt registration to public databases and the free utilization of digital sequence information is essential. From this perspective, we support the views of the Japanese Government submitted to the Secretariat of the Convention on Biological Diversity in September 2017 and make the following recommendations.

(1) The use of digital sequence information should not be included in the framework of the Convention on Biological Diversity and the Nagoya Protocol

As defined in the Convention on Biological Diversity, “genetic resources” refers to tangible material and does not include information. Changing of this definition should only be considered with great caution, since this would subsequently require a revision of the Convention itself thereby significantly affecting other frameworks as well.

(2) Restrictions should not be placed on publication and use of digital sequence information

If made subject to the Nagoya Protocol, registering of digital sequence information to public databases or using the information would require measures for things such as granting of permission and monitoring. The implementation of such measures would act as an obstacle to rapid registration and free use of digital sequence information, which would subsequently hinder the achievement of the Protocol’s objectives and impede the creation of shared benefits.

(3) Priority should be given to facilitating access to genetic resources

Access to genetic resources is indispensable for obtaining digital sequence information, but many provider countries of genetic resources are lagging behind in establishing the necessary access frameworks. In order to achieve the objectives of the Convention on Biological Diversity, priority should be given to making genetic resources available in a smooth and timely manner in all signatory countries to the Nagoya Protocol. Shared benefits cannot be created without establishing these frameworks.

(4) Scientists all over the world should join the discussion

If restrictions are imposed on the registration to public databases and the use of digital sequence information, implications will extend to publishing research papers when registration of this information is a required condition for publishing, consequently presenting great disadvantages to researchers of both provider and user nations. Researchers around the world should share the current status of the international discussion with the academic societies and other researchers in their respective countries, and join in the discussion from a scientific standpoint. As a representative of the scientific community of Japan, we will utilize this recommendation to cooperate with overseas researcher communities, and calls for the government's continuing involvement in this issue in line with the views expressed in the report it provided in September 2017. For its part, we will cooperate with the government and carry out such activities as the participation in international negotiations.

Contents

<Abbreviations>

AHTEG: The Ad Hoc Technical Expert Group on Synthetic Biology
COP: Conference of the Parties
INSDC: International Nucleotide Sequence Database Collaboration
ITPGRFA: International Treaty on Plant Genetic Resources for Food and Agriculture
MOP: Meeting of the Parties to the Protocol
SBSTTA: Subsidiary Body on Scientific, Technical and Technological Advice

1. Background of the recommendation

The Convention on Biological Diversity has three objectives, which are the conservation of biological diversity, the sustainable use of its components, and the fair and equitable sharing of the benefits arising from the use of genetic resources. The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity (herein referred to as the Nagoya Protocol) is a supplementary agreement that aims to implement the third objective of the Convention on Biological Diversity and prescribes measures to be taken by both provider and user countries of genetic resources (for example acquisition of prior consent from the provider country) when transferring genetic resources. It was ratified by Japan in August 2017. The Nagoya Protocol applies to genetic resources and traditional knowledge associated with genetic resources, however, the Conference of Parties (COP[1]) to the Convention on Biological Resources is currently debating whether to additionally include digital sequence information in the scope of the Nagoya Protocol. (Assumed to include nucleotide sequence information, the definition and scope of "digital sequence information" are as yet undecided.) At the Ad Hoc Technical Expert Group meeting (AHTEG[2]) on Synthetic Biology held in Montreal in September 2015, concern was raised that production by synthetic biology of useful materials such as enzymes using digital sequence information obtained from a wide range of genetic resources was tantamount to the usage of the genetic resources without prior consent of provider countries. This opinion was recorded in the AHTEG report. Following this, at the COP13 held in Mexico in December 2016 and at the second meeting of the Conference of the Parties to the Nagoya Protocol (MOP[3]2) it was decided that there would be a discussion regarding any potential implications for the three objectives of the Convention on Biological Diversity and for the objective of the Nagoya Protocol of the use of digital sequence information. (Convention Decision XIII / 16[1] and Protocol Decision NP-2/14[2]).

In response to this decision, the Secretariat of the Convention on Biological Diversity called on the signatory countries to submit opinions and relevant information on the potential implications of making the use of digital sequence information subject to the Nagoya Protocol. In its report submitted to the Secretariat, the government of Japan expressed the opinion[3] that "the accumulation and disclosure of nucleotide sequence information for free public use promotes the development of science and technology … and contributes to the conservation and sustainable use of biological diversity. Such endeavors are likely to be hindered in the event

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[1] Conference of the Parties

[2] The Ad Hoc Technical Expert Group on Synthetic Biology

[3] Meeting of the Parties to the Protocol

that access to nucleotide sequence information is restricted." Various other governments and relevant organizations, particularly in Europe[4], have also raised serious concerns and objections to this trend. The Secretariat of the Convention on Biological Diversity published a report of the views expressed by the various governments and relevant organizations regarding this issue on 9 November 2017[4].

It is likely that in the coming year the debate on whether to make digital sequence information subject to the Conference on Biological Diversity and the Nagoya Protocol will further progress at the next AHTEG meeting scheduled to be held in Montreal in February 2018, at the Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA[5] 22) in July, and at the COP14 and the third Meeting of the Parties to the Protocol (MOP3) scheduled to be held in Egypt in November.

In light of this situation, the Science Council of Japan reviewed the potential implications of including digital sequence information in the scope of the Conference on Biological Diversity and of the Nagoya Protocol through the Genetic Resources Subcommittee and the Nagoya Protocol Implications on Agricultural Science Review Subcommittee.

Nucleotide sequence information, which comprises the majority of digital sequence information, is made freely available for worldwide access and usage by registering the information to a public database operated by the International Nucleotide Sequence Database Collaboration (INSDC[6]) jointly established by three organizations: the DNA Data Bank of Japan (DDBJ), The European Molecular Biology Laboratory – European Bioinformatics Institute (EMBL-EBI), and the National Center for Biotechnology Information (NCBI) in the United States. This kind of free usage of digital sequence information is contributing to the development of science and the resulting benefits such as the promotion of industry and improvements in medical care and welfare. It is also an important foundation for the two objectives of the Convention on Biological Diversity, which are the conservation of biological diversity and the sustainable use of the components of biological diversity. Furthermore, it also fulfills the responsibility of sharing non-financial benefits obtained through the use of genetic resources.

Taking all these into account, we have reached the conclusion that free access and unrestricted use of digital sequence information are indispensable for the development of science, the effective implementation of the original objectives of the Convention on Biological Diversity and the Nagoya Protocol, and also for the achievement of sustainable development goals for both resource provider countries and user countries. Therefore, we support the view presented in the report submitted by the government of Japan to the

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[4] REPORT OF THE AD HOC TECHNICAL EXPERT GROUP ON SYNTHETIC BIOLOGY
https://www.cbd.int/doc/meetings/synbio/synbioahteg-2015-01/official/synbioahteg-2015-01-03-en.pdf

[5] Subsidiary Body on Scientific, Technical and Technology Advice

[6] International Nucleotide Sequence Database Collaboration

Secretariat of the Convention on Biological Diversity in September 2017. In consideration of the anticipated acceleration of the movement to include digital sequence information related to genetic resources in the scope of the Convention on Biological Diversity and the Nagoya Protocol at the relevant meetings and conferences scheduled to be held in the coming year, we, in cooperation with relevant academic organizations and researchers here and abroad, and with the government of Japan, issues a recommendation opposing the inclusion of digital sequence information in the scope of the Convention on Biological Diversity and the Nagoya Protocol and requests the establishment of an effective framework to achieve the objectives of the Convention and the Protocol.

2. Present status and problems

(1) Arguments by resource provider countries in favor of including digital sequence information in the scope of the Convention on Biological Diversity and the Nagoya Protocol

Some signatory countries of the Convention on Biological Diversity and the Nagoya Protocol have presented the following arguments concerning the use of digital sequence information.

i) The meaning of “use of digital sequence information” cannot be distinguished from “use of genetic resources”

This argument asserts that using digital sequence information such as nucleotide sequence information, being no different in the end than using the genetic resources that are the source of that information[7], is subject to (fair and equitable) benefit sharing and thus subject to the Convention on Biological Diversity and the Nagoya Protocol. Therefore, the argument is that “genetic resources” may naturally be interpreted to include digital sequence information, and that digital sequence information should also be interpreted more broadly to include not only nucleotide sequence information, but also amino acid sequence information and so on.

ii) Making digital sequence information subject to the Convention on Biological Diversity and the Nagoya Protocol is in keeping with the objectives of the Convention and the Protocol and would support the promotion of science

This argument asserts that the potential impacts on biological diversity of using digital sequence information in synthetic biology cannot be predicted. For example, genetic resources and related materials such as vanillin (the main aroma component of vanilla) and artemisinin (an anti-malaria drug) are manufactured through synthetic biology using digital sequence information. The argument contends that the manufacture of such products without the prior consent of resource provider countries precludes the fair and equitable sharing of benefits, which is the third objective of the Convention. In addition, new biomass crops born of synthetic biology technologies such as genetic recombination and genome editing risk bringing about changes in land use and replacement of conventional crops resulting in the reduction and loss of biological diversity; therefore, it is argued that making digital sequence information subject to the Convention and the Protocol is a matter of course. As such, the argument maintains that new regulations would not impede the promotion of science, but rather facilitate the successful implementation of the objectives of the Convention and the Protocol.

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[7] AHTEG on Digital Sequence Information on Genetic Resources
https://www.cbd.int/abs/dsi-gr/ahteg.shtml

iii) A monitoring system is needed to ensure traceability of digital sequence information usage

Concerning digital sequence information, in spite of no physical materials being transferred, the transfer of genetic resource sequence information over the internet and the use of that information through synthetic biology can yield the same results as using genetic resources without the prior consent of provider countries. Digital sequence information therefore presents a loophole to the use of genetic resources, and as countermeasures to address this, the argument asserts the need for thorough reporting of the location where the original source of the genetic resource was obtained whenever sequence information is registered to a database and also for the establishment of a monitoring system to ensure traceability of access and utilization of the information.

(2) Potential implications of including digital sequence information in the scope of the Convention on Biological Diversity and the Nagoya Protocol

There are serious concerns that inclusion of digital sequence information in the scope of the Convention on Biological Diversity and the Nagoya Protocol as promoted by the arguments listed above could have adverse impacts on achieving the objectives of the Convention and the Protocol and on the promotion of science and sustainable development of industries.

i) Inconsistency in the definition of the scope of the Nagoya Protocol

The scope of the Nagoya Protocol is specified to "genetic resources" and "traditional knowledge associated with genetic resources". "Genetic resources" 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. Although the scope of the Nagoya Protocol based on the interpretation of this wording leaves room for discussion, at least the current wording of "material" does not include digital sequence information, which is intangible. Strictly speaking, since the issue of redefining (the word) "material" is one that would require revision of the Convention itself, to equate the use of digital sequence information to the use of genetic resources through changes in interpretation threatens to significantly damage the legal stability of the existent Convention on Biological Diversity and Nagoya Protocol. Furthermore, the issue must be taken under very careful consideration so as to ensure consistency with other frameworks related to the use of genetic resources, such as the ITPGRFA[8], as they would also be affected.

ii) Making digital sequence information subject to the Convention on Biological Diversity and the Nagoya Protocol would have adverse impacts on

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[8] International Treaty on Plant Genetic Resources for Food and Agriculture

achieving the objectives of the Convention and the Protocol and on the promotion and sustainable development of science

(a) Adverse impacts on achieving the objectives of the Convention on Biological Diversity and the Nagoya Protocol

Acquisition of digital sequence information is indispensable for "understanding of biodiversity", which provides the basis for “the conservation of biodiversity” – the first objective of the Convention on Biological Diversity. The sequencing of diverse organisms has been made possible by dramatic advances in DNA sequencing technology in recent years, and the practical realization of portable DNA sequencing is expected to precipitate a rapid increase in sequence analysis within resource provider countries as well. Researchers concerned with taxonomy and ecology in both genetic resource provider countries and user countries have established international research collaborations and are conducting on-site investigations for biodiversity research. As a result of this research and the published findings, information on biodiversity is disseminated allowing for the advancement of still more biodiversity research creating a cycle of positive feedback through which research findings also lead to economic applications of genetic resources. However, if digital sequence information is made subject to the Nagoya Protocol, it will be necessary to manage and monitor the digital sequence information. Resulting restrictions on the disclosure and use of sequence information will greatly impact biodiversity research, whose results depend on comparative analysis of genetic information such as nucleotide sequences. In addition, without being able to compare digital sequence information it will no longer be possible to determine which sequence information originated from a genetic resource endemic to a particular country nor to distinguish which resources are useful. Clearly this would have negative implications for both resource provider countries and user countries. For these reasons, the global and open sharing of digital sequence information is fundamental to implementing the objectives of the Convention on Biological Diversity and the Nagoya Protocol. Expenses for these purposes in the case of nucleotide sequence information is provided by the collaborating nations of the INSDC – Japan, Europe, and the United States – and all signatory countries, including resource provider countries, have already enjoyed significant non-financial benefits.

The acquisition of digital sequence information is also essential for the sustainable use of the components of biological diversity – the second objective of the Convention on Biological Diversity. Analysis of nucleotide sequences – the principal data of digital sequence information – is useful among other things for monitoring illegal trade of processed products whose origins are difficult to trace by other means. As a result illegal outflow of biodiversity can be prevented thus supporting the sustainable use of biodiversity. Such analysis is also essential when dealing with pathogens and health emergencies. In recent years for example, in the case of not only human infections but also of infectious diseases affecting crops, forests, livestock, fishery products, etc., the identification and comparison of the genomic sequences of the pathogenic microorganisms and their vectors (insects etc.) have enabled the accurate execution of pathological and epidemiological surveys leading to the swift enactment of effective countermeasures. Making digital sequence information subject to the Nagoya Protocol would result in delays in the release of information from each country giving rise to a situation where the prompt identification of pathogenic microorganisms is hindered resulting in failure to prevent global epidemics. If the use of digital sequence information of pathogens is affected, there is real concern that threatens the lives and food supplies of people around the world. Such impacts would be felt most strongly by resource provider countries. In these ways, restrictions on the use of the digital sequence information may be a serious obstacle to achieving the objectives of the Convention on Biological Diversity and the Nagoya Protocol with respect to the sustainable use of genetic resources as well.

Annex 1 lists the specific provisions of the Convention on Biological Diversity that are likely to be affected by the inclusion of digital sequence information.

(b) Adverse impacts on the promotion of science and sustainable development

Digital sequence information comprises the principal foundation for life science research now and in the future. Research based on the acquisition and use of digital sequence information is conducted and advancing in a wide variety of fields including: the basic sciences of taxonomy, ecology, genetics, evolutionary biology and developmental biology; environmental science (e.g. environmental conservation, the influence of alien and native species); agriculture (e.g. breeding, plant conservation and veterinary medicine); and health science (e.g. emerging and re-emerging infectious diseases, drug development). Digital sequence information obtained in Japan, especially nucleotide sequence information, has been made widely available to the world through the DDBJ. The DDBJ has collaborated with the NCBI in the United States and the EMBL-EBI in Europe to establish the INSDC and has been contributing to international sharing of nucleotide sequence information. Moreover, the submission guidelines of the major academic journals require submitters to register with the DDBJ, the NCBI or the EMBL-EBI and obtain an accession number as a condition for review whenever nucleotide sequence information is reported in a paper. Research based on registered nucleotide sequence information can be performed without restriction, and substantial benefits have already been shared internationally. Research based on nucleotide sequence information will undoubtedly continue to rapidly expand due to revolutionary advances in techniques for acquisition of digital sequence information. The creation of new rules obstructing the free use of nucleotide sequence information will become a major obstacle to the promotion of science including multinational collaborative research and development.

There are various fields of research and development such as pharmaceutical development, agribusiness, and biomass production that are conducted based on the results of academic research, and any stagnation of such research will inevitably have adverse impacts on the advancement of these fields and the economic benefits that they create. Stagnation of research and development will result in the loss of creation of benefits for sharing among the signatory countries. Various fields of research and development that are based on digital sequence information are indispensable for the implementation of the "17 Sustainable Development Goals" established by "the 2030 Agenda for Sustainable Development" adopted at the United Nations Headquarters. However, making digital sequence information subject to the Convention on Biological Diversity and the Nagoya Protocol would obstruct free acquisition, registration, disclosure and use of digital sequence information. As a result, it will not be possible to conduct the necessary research and development making it very difficult to implement the goals for sustainable development.

iii) Problems with establishing a monitoring system to ensure traceability of access to and usage of digital sequence information

Building a new monitoring system that ensures traceability of access to and usage of digital sequence information will inevitably change the current information management system in use by the INSDC resulting in the risk of negative impacts such as increasing the cost of database management and delaying of technological innovation. The reality is that identical genetic resources are commonly distributed across national borders, and in many cases it is not realistically feasible to identify the origin of the genetic resource that provided the digital sequence information that eventually leads to any economic benefits. This is particularly prominent in the case of microorganisms. Furthermore, since in many cases economic benefits first arise from results obtained from cross-comparison of multiple similar sequence data made possible by the broad and open use of digital sequence information, it is extraordinarily difficult to monitor and objectively estimate the economic contribution of each item of information. Therefore, there are so many issues concerning the methods of calculation and economic benefit-sharing that it is extremely difficult to reach international consensus in a short period of time. As stated above, there is great concern that new regulations on digital sequence information will hinder scientific research and obstruct the achievement of the objectives of the Convention on Biological Diversity and the Nagoya Protocol.

（３）Future direction

Many countries, including Japan, have already ratified the Nagoya Protocol, but it is still difficult to say whether all of the signatory countries have established systems for the provision and use of genetic resources. In order for any benefits to be produced that form the basis for the fair and equitable sharing of benefits as indicated in the objectives of the Convention on Biological Diversity and the Nagoya Protocol, quick and unhindered access to genetic resources should first be provided. In addition, since such a system allowing quick and unhindered access to genetic resources is also required to obtain digital sequence information, all signatory countries must be encouraged from a scientific standpoint to develop a sufficient framework for access to genetic resources before discussing whether digital sequence information should be made subject to the Nagoya Protocol. Both the Convention on Biological Diversity and the Nagoya Protocol will greatly influence the future advancement of life science. However, in the course of revising such critical contents, concerns related to diplomatic negotiations tend to take precedence, therefore special steps must be taken to ensure that the concerns of the scientific community are sufficiently considered. The government of Japan has adopted an attentive stance to the appropriate academic viewpoints, but arguments from numerous other countries tend to reflect non-academic viewpoints, in particular countries that are mainly providers of genetic resources.

A continuing effort must be made by the various academic societies of Japan to encourage international academic organizations to share the current situation with researchers from genetic resource provider countries and user countries and ask that arguments from all countries be made from a scientific viewpoint. In Japan as well, there is still insufficient awareness among researchers of the issues concerning digital sequence information. Together with raising awareness, it is extremely important that researchers make real efforts to encourage their overseas counterparts to call on the negotiators from each nation to present arguments from a scientific standpoint. In order to promote the above, as a representative of the scientific community of Japan, we will utilize this recommendation to cooperate with overseas researcher communities, and calls for the government's continuing involvement in this issue in line with the views expressed in the report it provided in September 2017. For its part, we will cooperate with the government and carry out such activities as participating in international negotiations.

3. Recommendation

In order to achieve the objectives of the Convention on Biological Diversity and the Nagoya Protocol, prompt registration to public databases and the free utilization of digital sequence information (particularly nucleotide sequence information) is essential. From this perspective, concerning the current international argument on the treatment of digital sequence information with respect to the Convention on Biological Diversity and the Nagoya Protocol, we support the views of the Japanese Government submitted to the Secretariat of the Convention on Biological Diversity in September 2017 and makes the following recommendations.

(1) The use of digital sequence information should not be included in the framework of the Convention on Biological Diversity and the Nagoya Protocol

As defined in the Convention on Biological Diversity, “genetic resources” refers to tangible material and does not include information. An item that does not meet that definition should not be included in the framework of the Convention and the Protocol. Changing of this definition should only be considered with great caution, since this would subsequently require a revision of the Convention itself thereby significantly affecting other frameworks as well.

(2) Restrictions should not be placed on publication and use of digital sequence information

If included in the framework of the Nagoya Protocol, registering of digital sequence information to public databases or using the information would require measures for things such as granting of permission and monitoring. The implementation of such measures would not only be extremely difficult but would also act as an obstacle to rapid registration and free use of digital sequence information. This would subsequently hinder the achievement of the Protocol’s objectives and impede the creation of shared benefits.

(3) Priority should be given to facilitating access to genetic resources

Access to genetic resources is indispensable for acquiring digital sequence information, but many provider countries of genetic resources are lagging behind in establishing the necessary access frameworks. In order to achieve the objectives of the Convention on Biological Diversity, priority should be given to making genetic resources available in a smooth and timely manner in all signatory countries to the Nagoya Protocol. Shared benefits cannot be created without establishing these frameworks.

(4) Scientists all over the world should join the debate

If restrictions are imposed on the registration to public databases and the use of digital sequence information, implications will extend to publishing research papers and findings when registration of this information is a required condition for publishing, consequently presenting great disadvantages to researchers of both provider and user countries. Researchers around the world should share the current status of the international debate with the academic societies and other researchers in their respective countries, and join in the discussion from a scientific standpoint. As a representative of the scientific community of Japan, we will utilize this recommendation to cooperate with overseas researcher communities, and calls for the government's continuing involvement in this issue in line with the views expressed in the report it provided in September 2017. For its part, we will cooperate with the government and carry out such activities as the participation in international negotiations.

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Provisions of the Convention on Biological Diversity affected by the inclusion of digital sequence information in the scope of the Convention on Biological Diversity and the Nagoya Protocol.

Article 12. Research and Training
(b) Promote and encourage research which contributes to the conservation and sustainable use of biological diversity, particularly in developing countries, …

Article 13. Public Education and Awareness
(a) Promote and encourage understanding of the importance of, and the measures required for, the conservation of biological diversity, as well as its propagation through media, and the inclusion of these topics in educational programs; and …

Article 15. Access to Genetic Resources
1. Recognizing the sovereign rights of States over their natural resources, the authority to determine access to genetic resources rests with the national governments and is subject to national legislation.
2. Each Contracting Party shall endeavour to create conditions to facilitate access to genetic resources for environmentally sound uses by other Contracting Parties and not to impose restrictions that run counter to the objectives of this Convention.
5. Access to genetic resources shall be subject to prior informed consent of the Contracting Party providing such resources, unless otherwise determined by that Party.
7. Each Contracting Party shall take legislative, administrative or policy measures, as appropriate … with the aim of sharing in a fair and equitable way the results of research and development and the benefits arising from the commercial and other utilization of genetic resources with the Contracting Party providing such resources. Such sharing shall be upon mutually agreed terms.

Article 16. Access to and Transfer of technology
1. Each Contracting Party, recognizing that technology includes biotechnology, and that both access to and transfer of technology among Contracting Parties are essential elements for the attainment of the objectives of this Convention, undertakes subject to the provisions of this Article to provide and/or facilitate access for and transfer to other Contracting Parties of technologies that are relevant to the conservation and sustainable use of biological diversity or make use of genetic resources and do not cause significant damage to the environment.

Article 17. Exchange of Information

1. The Contracting Parties shall facilitate the exchange of information, from all publicly available sources, relevant to the conservation and sustainable use of biological diversity, taking into account the special needs of developing countries.

Article 18. Technical and Scientific Cooperation

1. The Contracting Parties shall promote international technical and scientific cooperation in the field of conservation and sustainable use of biological diversity, where necessary, through the appropriate international and national institutions.