

Views and Other Information on Digital Sequence Information from Japan to the Eighth Session of the Governing Body

The Government of Japan would like to submit the following information on views and other information on digital sequence information (DSI) to the Eighth Session of the Governing Body, as a reply to Notification NCP GB8-016-MYpoW/DSI, based on Resolution 13/2017 of the Treaty.

The “open science” approach, under which anyone can freely access scientific research results, has been promoted in recent years, enabling all countries, both developed and developing, to leverage such results. According to the International Nucleotide Sequence Database Collaboration (INSDC), which maintains the international DSI database, as many as 172 countries were using the database between 2014 and 2016¹.

The disclosure of DSI has been required as a selection criteria for publishing research in most international academic journals including *Science* and *Nature*. This type of disclosure and open use of DSI have been instrumental to innovations in science and their sustainable use. Any attempts at regulating the use of DSI would put a halt to such innovations and sustainable use.

Our input on each category of information to be submitted are as follows:

1. Terminology used in this area

We think that “Genetic Sequence Data” is the most appropriate terminology, as it is widely used, and considered to be a clear term in the scientific community.

2. Actors involved in DSI on PGRFA

Researchers in Ecology and Breeding

3. The types and extent of uses of DSI on PGRFA, such as: characterization; breeding and genetic improvement; conservation; identification of PGRFA;

We believe that accumulation, open-access and free use of DSI will facilitate the development of science, and will benefit conservation and sustainable use of biological diversity as explained below. The following activities could be hindered if open-access and free use of DSI are to be restricted.

By using DNA markers which identify differences in sequences, it has become possible to efficiently select individuals with the useful gene(s) associated with the target traits from progeny in plant breeding processes. Such a technology is used worldwide in order to develop new varieties that meet various needs.

<Example>

Rice was the first crop whose whole genome sequence was decoded completely and precisely. The decoding was accomplished by a consortium comprising of public laboratories in various parts of the

¹ (Europe 46, Asia 43, South/Central America 35, Africa 32, Oceania 14, and North America Website access: 1,621,300 page views)

world². The annotated sequences were released and made available for public use³. This information is widely used to isolate important genes or to develop DNA markers, as well as to provide the basis for genome analysis of other crops in the Poaceae family, such as maize and wheat.

4. The relevance of DSI on PGRFA for food security and nutrition

There are increasing concerns that global strains in the balance of food supply and demand may occur in the medium to long term, due to an increase in global population, projected economic growth in developing countries, the chronic malnutrition in such countries and increasing weather abnormality. Such conditions render it increasingly necessary to promote sustainable agricultural production activities, especially in developing countries.

In order to establish stable and sustainable production of agricultural crops in developing countries that are vulnerable to climate change, drought, high salinity and poor soil, Japan International Research Center for Agriculture Sciences (JIRCAS) is now working on development of breeding materials and basic breeding technologies for highly productive crops adaptable to such adverse environments through the use of DSI. Specific examples are as follows:

(1) Rice and Soybeans

For rice, JIRCAS is developing breeding materials which have high temperature resistance, drought tolerance, phosphate deficiency resistance and high nitrogen use efficiency. For soybeans, JIRCAS is developing breeding materials which are tolerant to drought and high salinity.

(2) Guinea yam (*Dioscorea rotundata*)

Guinea yam (*D. rotundata*) is an important staple food crop especially in West Africa. To improve breeding efficiency, JIRCAS attempted to generate fundamental genomic information and test the applicability of molecular tools. In the whole genome sequence of *D. rotundata* (594 Mb), 26,198 genes were forecasted, and a DNA marker for sex discrimination was developed, using genomic and phenotypic information. This marker enables breeders to examine the sex of their materials at the young seedling stage. It also demonstrates the potential of using genomic information to further improve breeding efficiency in yam.

(3) Quinoa

Quinoa, a pseudocereal originating from the Andes region of South America, is emerging as an important crop with the potential to contribute to global food security due to its high nutritional value and ability to tolerate adverse environments. However, molecular analysis of quinoa is limited by its genome complexity derived from allotetraploidy and its genetic heterogeneity due to outcrossing. Through the use of DSI, JIRCAS established the inbred quinoa accession Kd, presented the draft genome

² Japan, U.S., U.K., China, Taiwan, France, India, Republic of Korea, Brazil, Thailand

³ The database for this sequencing project (Rice Annotation Project Database) which is operated by the National Agriculture and Food Research Organization of Japan, was accessed by total of 143 countries other than Japan (Europe 47, Asia 22, South/Central America 24, Africa 31, Oceania 2, North America 2, Middle East 15). A total of 1,312,614 pages were accessed. (Jan 1 to Dec.31, 2016)

sequence of Kd using next generation sequencing, and constructed the free- access Quinoa Genome DataBase. Thus, these findings from the use of DSI provide insights into the mechanisms underlying the agronomically important traits of quinoa.

