

**Current state of the use of digital sequence information on genetic resources
in the biodiversity field**

1. Access status of digital sequence information (DSI)

The “Open science” approach, under which anyone can enjoy access to research results without difficulty, has been promoted in recent years. Owing to this approach, both developed and developing countries are making use of these research results.

For instance, as a member of INSDC (International Nucleotide Sequence Database Collaboration) maintaining the international DSI database, we found that total of 172 countries were using the database during the period from 2014 to 2016 (Europe 46, Asia 43, South/Central America 35, Africa 32, Oceania 14, and North America 2: Website access 1,621,300) upon investigating the state of the use from outside Japan of DDBJ (DNA Data Bank of Japan) operated by National Institute of Genetics.

Furthermore, disclosure of data sets such as DSI has been required as a selecting condition for submitted papers in most international academic journals including “Science” and “Nature”.

2. The benefit of DSI usage to the objectives of the Convention on Biological Diversity

We believe that accumulation, open-access and free use of DSI will facilitate 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.

- (1) A comparison of DSI is considered to be one of the effective means to identify the current situation of ecosystem under specific circumstances. The DSI registered in the official database is used in such a comparison.

Species can be identified by analyzing DNA acquired from organisms or DNA samples (environmental DNA) collected from the environment including sea water and soil. The analysis of environmental DNA allows us to promptly identify species or populations of organisms such as living fish, microorganisms or soil organisms, without catching these lives. Through this method we can confirm ecosystem conditions, which has been difficult to address by conventional methods.

<Examples>

○ To restore degraded coral reef due to breaching through transplantation, we can judge the appropriateness of candidate places to reintroduce healthy coral by comparing DSI (genetic compositions) of different coral populations.

○ Environmental DNA analysis allows us to easily identify alien species' pathways and whether hybrids have been emerging or not, thus contributing to implement appropriate countermeasures against alien species.

○ Environmental DNA analysis on water samples from watering places in tropical forests enables us to detect survivals of endangered mammal species. Unlike conventional method to investigate wildlife with camera traps, this allows us to conduct more precise survey of wildlife, also being useful for species conservation.

(2) 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 process. Such technology is used all over the world to develop new varieties which 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 composed of public laboratories of 10 countries and regions^{*1}. The annotated sequences were released and made

available for public use*2. 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.

*1: Japan, the United States of America, China, Taiwan, France, India, Republic of Korea, Brazil, Thailand and the United Kingdom participated.

*2: 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), total of 1,312,614 pages accessed. (Jan 1 to Dec.31, 2016)

- (3) Toxicity and effective vaccines for plant or livestock pathogens or microorganisms which cause food poisoning often differ among different genotypes. Therefore, identification or detection by use of DSI allows increased effectiveness and safety in development and use of pharmaceutical agents. Furthermore, by identifying the action mechanism of medical agents against disease and pest, development of prevention and control technologies are facilitated.

<Example>

The genetic information on Foot and Mouth Disease (FMD) virus in various areas of the world, which was gathered by the Regional Reference Laboratories (e.g.: Pak Chong, Thailand) of the World Organization for Animal Health (OIE) and the World Reference Laboratory (Pirbright Institute in the UK), has been useful in selecting suitable vaccines in endemic areas, and in supplying vaccines for contingency planning for potential outbreak in free areas.