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Our monthly newsletter features a variety of information, highlightin current domestic and international issues concerning bioresources.

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National BioResource Project "Rice"

 Genetic and Genomic Resources of Rice Nori Kurata, Plant Genetics Laboratory, N IG



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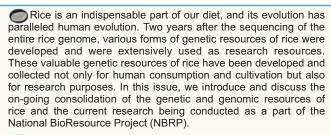
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Introduction to Resource Center No.18

National BioResource Project (Genetic and Genomic Resources of Rice"

Nori Kurata, Professor

Plant Genetics Laboratory, National Institute of Genetics



Similar to other biological species, diversity studies in rice were initiated as a new field of research subsequent to the sequencing of its genome; however, a number of varieties have not yet been analyzed as genetic resources. Natural mutations in rice have been acquired or selected in the course of evolution or cultivation. Genetic mutations necessary for conducting research and artificial mutant strains with tagged genomes have been constructed and collected.

I would like to focus on wild rice and introduce topics concerning the circumstances of the rice genetic resource project that are not thoroughly discussed in reports such as the characteristics and types of wild rice, the 2 centers for wild rice genetic resources in the world and problems in rice preservation.

Genetic Resources Indispensable for Researches in Evolution, Breeding, and Ecology [Strain Groups of Wild Rice]

Genetic resources of more than 140,000 strains of cultivated rice are known to exist worldwide. More than 35,000 strains are preserved in the Ministry of Agriculture, Forestry and Fisheries of Japan, and 11,000 strains are preserved in universities and research institutes in Japan. A large number of these resources have been collected and can be directly used for breeding.

In addition to these genetic resources, the NBRP also skillfully develops, preserves, and provides genetic resources of wild rice that are generally difficult to obtain for utilization as research materials (Fig. 1)

(Fig. 1).

Wild species resource of rice
9 genomes 21 speciess
1,700 accessions (NIG)

Seed stock
Vegetative stock

1,500
Vegetative stock

Vegetative stock

Under Development
Chromosome substitution strains
Species specific markers
New phylogenetic system

277 core collection (all species)
DNA samples
phynotypic characters (~20~)

Provided as research materials for evolutionary, developmental, physiology, and breeding studies, and for species differentiation.

photographs of characteristic phenotypes

Fig.1 _↑

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Other information on bioresources is available at

NBRP http://www.nbrp.jp/

SHIGEN http://www.shigen.nig.ac.jp/indexja.htm

WGR http://www.shigen.nig.ac.jp/wgr/

JGR http://www.shigen.nig.ac.jp/wgr/jgr/jgrUrlList.jsp

"2nd International Biocuration Meeting" October 25–28, 2007

at Dolce Hayes Mansion, San Jose, CA, USA Details are available at the following website: http://biocurator.org/Mtg2007/

Cell Technology initiated a new series entitled "Let's Use! BioResource". Bioresources in Japan will be introduced in a series of 14 volumes from November 2006 to December 2007.

Please refer to the section "wild rices" of the comprehensive rice database "Oryzabase" regarding the types of existing wild rice strains, their distribution in the world, and their morphological attributes.

Oryzabase — Database of National BioResource Project http://www.shigen.nig.ac.jp/rice/oryzabase/

Extensive information, such as images of the morphology of each strain, was added at the end of the previous fiscal year. These are viewable on the NBRP Rice website (Fig. 2).

Fig.2-A:Closely related wild-type rice (AA genome species)









Fig.2-B: Distantly related wild-type rice (non-AA genome species)

















Wild Rice Strains

Among the cultivated rice strains, Oryza sativa is grown in most farm lands worldwide and O. glaberrima is cultivated in some parts of Africa. The identified wild rice strains include 5 species that harbor the AA genome similar to cultivated species and 16 species with the BB, CC, BBCC,



CCDD, EE, FF, GG, or HHJJ genomes; these strains are grown in the tropical and subtropical regions of the world. However, the genomes and species of some strains have yet to be characterized, and many species have been renamed or have been assigned new names in the past 20-30 years. The classification of species harboring the BB, CC, BBCC, and CCDD genomes is still considerably ambiguous and sometimes produces unexpected results.

(refer to Fig.3)

Characteristics of Wild Rice (refer [Wide Range of Ecological and Morphological Attributes and Difficulty in Cultivation]

The ecology and morphology of wild rice are considerably varied compared to those of cultivated rice. A common characteristic of wild rice species is rapid maturation after blossoming and almost complete seed dispersal within 10-20 days. In addition, wild rice



strains are highly allogamous and readily outcross. Because of these characteristics, during seed multiplication, the ears are covered with bags. Further, some perennial species exhibit strong vegetative reproductivity, produce few ears, and have low seed fertility (1-10%), making seed multiplication extremely difficult; thus, stock preservation is conducted. There are some strains that have been maintained by stock preservation for 30-40 years at the NIG, which is the core of the NBRP. Differences between the strains with regard to the blossoming (at predawn when the light intensity is mild, at noon when the light intensity is at its maximum, and in the evening when the light intensity diminishes) have been observed; reproductive isolations have also been observed among strains. A tetraploid species can grow twice as tall as a human being under suitable cultivation conditions, and some species can extend hundreds of roots or proliferate as creepers. In order to cultivate wild rice strains that grow naturally in tropical regions in Japan, a huge device that can be used for the application of a short-day treatment is essential. The simultaneous maintenance of 23 rice species with varied ecological and morphological attributes and the preservation of genetic resources in highly humid rice fields in the middle of summer are extremely laborious and demanding tasks, which would never have been successful without the support of the NBRP.



Fig. 3. Cultivation of Wild Rice

(A) Preparation of rice planting in a short-day farm field. 1,500 individual plants are cultivated in rice fields equipped with 7 devices that are used for the application of a short-day treatment. (B) A farm field where the ears were bagged after the short-day treatment. The bagging of ears prevents outcrossing and seed loss.

(C)Greenhouse cultivation of perennial rice strains. The strains are renewed annually by changing the pots. In order to maintain the strain for several decades, the plants are trimmed to adjust their size.

Genetic Resource Center for Wild Rice

There are two centers that function as genetic resource banks of wild rice in the world. The first is the International Rice Research Institute (IRRI; an international institute that is affiliated to the Food and Agriculture Organization of the



United Nations (FAO) established 49 years ago by the Rockefeller Foundation) and the second is the Genetic Strain Stock Center at the NIG. At the NIG, more than 2,000 strains have been collected from all over the world since the 1950s; at present, these strains have been consolidated into 1,700 strains excluding the strains that have yet not been characterized. Further, the classification and purification of highly heterogeneous strains is a major problem in the preservation of wild rice strains.

The IRRI collects, preserves, and distributes more than 3,000 wild-type rice strains; most strains are closely related and similar to cultivated rice strains, harboring the AA genome. Among the non-AA genome wild-type species, some of the IRRI primary wild rice strains comprised 200 or more distantly related wild-type rice strains (harboring non-AA genomes with many mutations) that were subdivided from the NIG in the 1980s. Fourteen species of wild rice at IRRI were used for the construction of a bacterial artificial chromosome (BAC) library; the project on the alignment of the AA genome conducted in the US for several years revealed that half of the species were originated from the NIG.



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However, the rice strains that were subdivided from the IRRI strains are tagged with strain numbers unique to the IRRI; therefore, cross-checking these strains from the NIG is difficult. In order to avoid confusion while using these strains, we held a meeting with IRRI's gene bank in 2006 and discussed the subject of mutually disclosing reference strain numbers.

Future of Wild Rice Resources



The characteristics of the 5 species harboring the wild-type AA genome and the other 16 species that are distantly related wild-type rice species are still largely unknown. Wild rice species, with the exception of those harboring the AA type genome, cannot be used for hybridization with cultivated rice strains to acquire even the seeds of the next generation. Although genetic research is difficult, some groups in the US are planning to conduct a broad-scale genome analysis of wild rice from the viewpoint of genome information. The NBRP aims to develop even more useful genetic resources of wild rice by consolidating polymorphism and morphology markers of the wild-type rice genome in the 2nd stage of the project. In addition, other projects will attempt to introduce chromosomes from wild rice into cultivated rice. Thus, considerable progress is expected to be achieved at the end of the 2nd stage of the NBRP.

★ Hot News from Abroad No.18

Discussion of MTA at the AUTM 2007 Annual Meeting (2)

[Session on the Regulation of Corporeal Property]

Mutsuaki Suzuki, Director Intellectual Property Unit, National Institute of Genetics

The MTA sectional meeting at the AUTM 2007 Annual Meeting was introduced in a previous issue (in Vol. 3, No. 5). A discussion regarding MTA, which will be introduced in this issue, was conducted at the session on the regulation of corporeal property.

This session dealt with the topic of the administration on corporeal property of research achievements. Catherine E. Vorwald, University of Maryland, was the moderator. Thomas Mercolino from the section of technology transfer at Johnson & Johnson, Julia Brill from Johns Hopkins University, and Jesus Soriano from American Type Culture Collection (ATCC) were the panelists.

The session began with a lecture by Thomas Mercolino on the transfer of compounds from corporations to academic institutes. According to him, transfers usually occur during these 2 instances: (1) when researchers at academic institutes want to prove their hypotheses and (2) when corporations want to test the compounds using the developer's model system. In order to avoid reaching a dead end with regard to the allocation of intellectual property rights, these 2 points should be separately considered. It is also important to understand that corporations are primarily concerned about confidentiality while academic institutes are more concerned about publications. He emphasized that the MTA should facilitate productive negotiation.

J. Brill from Johns Hopkins University then gave a lecture titled, "Extermination Administration of MTA Dragons." According to J. Brill, some

MTAs provide a license for the use of the developed materials under certain conditions; however, some MTAs are very strict in that they waive the right of user's invention or prohibit the modification of materials.

The MTA is associated with several problems—a severe shortage of officials trained to handle MTAs, the nonrecognition of MTA as a license, the absence of an assessment method for evaluating the quality of the developed materials, and the lack of a standard handling process of MTA. The shortage of officials, in particular, is a serious problem. In one of the 8 institutes investigated, an official handled a maximum of 575 cases of MTA

In this situation, a comprehensive analysis of "values," "risks," and "benefits" is very essential; thus, the clarification of the accepted range of MTA and the standardization of waivering process are important. In the end, J. Brill described that MTA should be considered as only the first step toward introducing a new technology and alternative ideas for intellectual property

transfer should be encouraged to achieve mutual cooperation between the research community and industry.



The session concluded with a lecture by J. Soriano from ATCC on administration challenges of bioresource centers. According to J. Soriano, ATCC functions as a bioresource center and provides products, services, and information to

researchers. A bioresource center is different from a simple preservation institute or a culture collection center, and factors such as accuracy, reliability, productivity, storage stability, distribution, product development, information distribution, business management, intellectual property, and correspondence with regulations, are very important. Further, the importance of bioresource centers in technology transfers and the stringent internal administration required for the distribution of research samples was introduced, and the significance of corporeal property administration was described.

From the three above-mentioned person's lecture, the US seems to have the same problems as Japan but I felt that they are a step ahead to deal with these issues since the corporeal property administration of MTA is more widespread in the US. It is important to have a group that continuously discusses the corporeal property administration of MTA in Japan.

The cable car which runs near the hall of AUTM200



near the hall of AUTM2007

Editor's Note: Although the completion of the whole genome sequencing of rice gave the impression that we have reached the peak of one of the mountains, Dr. Kurata's article made me feel that we still stand at the bottom of Mt. Fuji. Please visit the Oryzabase website. Dr. Suzuki's discussion on MTA conveyed the enthusiasm of ATCC who can take pride in their history of over 80 years. (Y.Y.)

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