Advancement and dissemination of rice genome research

~ Green Technology Project ~

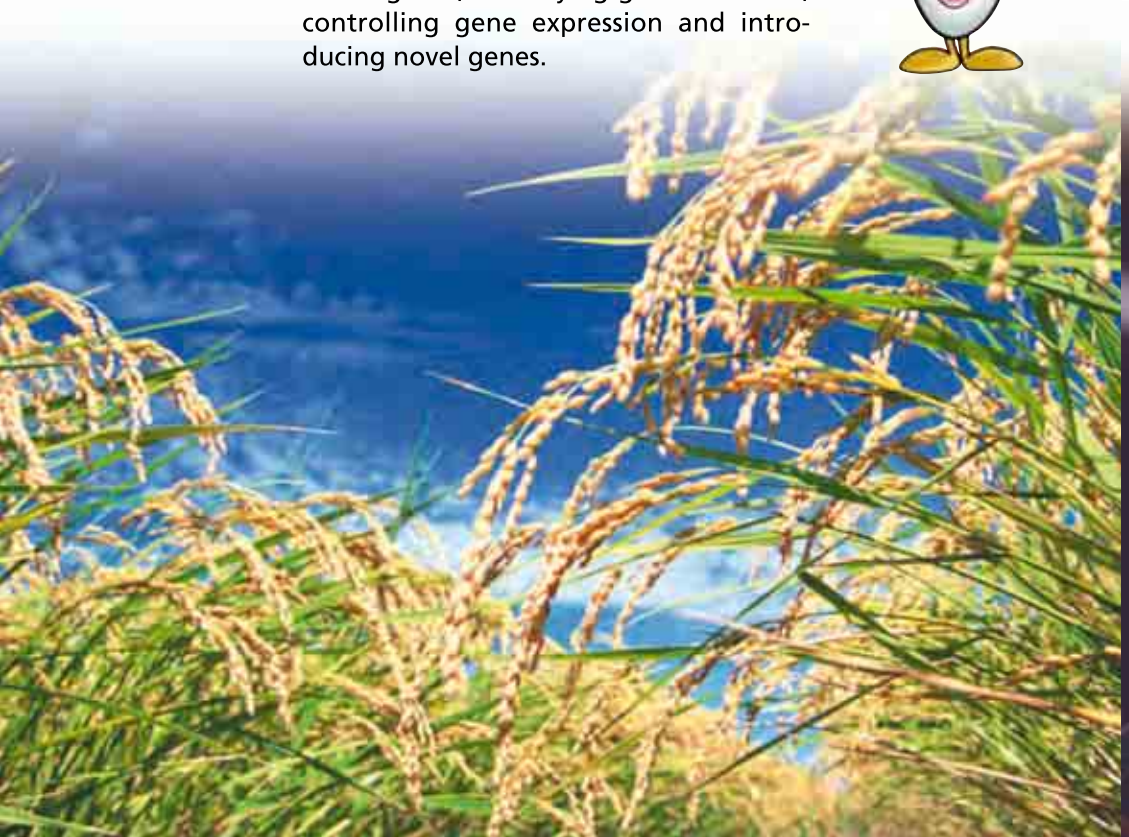
Rice power is mankind's future.

National Institute of Agrobiological Sciences

http://www.nias.affrc.go.jp/

The “Green Technology Project” aims to facilitate the breeding of strong, robust and nutritious rice varieties using the complete rice genome sequence.

The world population is expected to reach 9 billion in the middle of the 21st century, half of whom will depend on rice. Rice breeding is therefore crucial in maintaining a stable world food supply. The “Green Technology Project” is a core program for developing novel rice varieties through the advancement of basic and applied biotechnologies for finding useful genes, identifying gene functions, controlling gene expression and introducing novel genes.



The Green Technology Project is divided in three major areas.

Solving food shortages

Rice with high-yield potential
Using genes that increase number of seeds

Rice with tolerance to lodging
Using genes that control plant height and leaf shape

Preserving the environment

Rice with durable disease and pest resistance
Using disease and pest resistance genes

Rice with tolerance to environmental stress
Using genes for resistance to drought and cold conditions

Rice as potential source of biofuel
Developing crops for bioenergy production

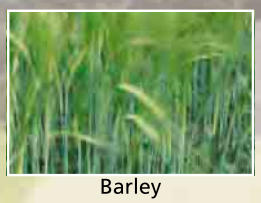
Promotion of human health

Rice with potential to help prevent diseases and keep people healthy

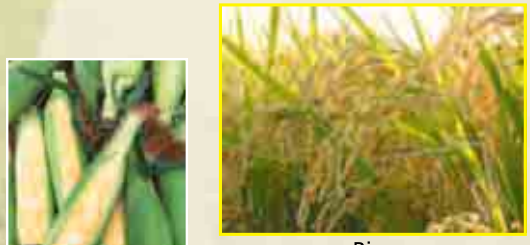
Objectives of sequencing the rice genome

Rice is a model for cereal crops.

Comparative analyses of major crops have shown that the genetic composition of the rice genome is similar to other cereal crops including maize and wheat. Since the genomes of maize and wheat are 6 and 40 times larger than that of rice, respectively, rice is the most suitable model plant for studying genetic information of cereal crops. The results obtained from sequencing the rice genome is anticipated to be the ultimate tool for isolating useful genes not only from rice but also from maize and wheat, and for breeding highly desirable varieties of rice and other crops.


Barley


Millet


Rice

Maize


Sorghum


Wheat

An innovative solution to problems on food, environment and health

With the aim of solving the problems associated with food shortage in the 21st century as well as problems associated with the environment, crops with high yields and ability to grow under harsh conditions will be developed. The project aims to promote the preservation of the environment by enhancing the inherent ability of crops to resist pests and insects, to sustain crop production using reduced amounts of insecticides and to increase biomass production. Crops will also be developed that promote human health and facilitate prevention of common diseases.

Rice genome research (about 32,000 genes)

Finding agronomically important genes
- Disease and pest resistance
- High yield etc.

Finding environmentally useful genes
- Environmental stress tolerance
- Biomass production

Genes for production of organic substances
- Peptide-containing rice
- Allergen-free rice

→ **To solve population / food supply problems**
- Developing technologies for stable production of diverse crops (rice, maize, wheat etc.)

→ **To contribute in environmental conservation**
- Developing rice that can grow in adverse environment
- Developing rice for production of biofuel

→ **To promote human health and welfare**
- Developing nutritious and disease-preventive rice

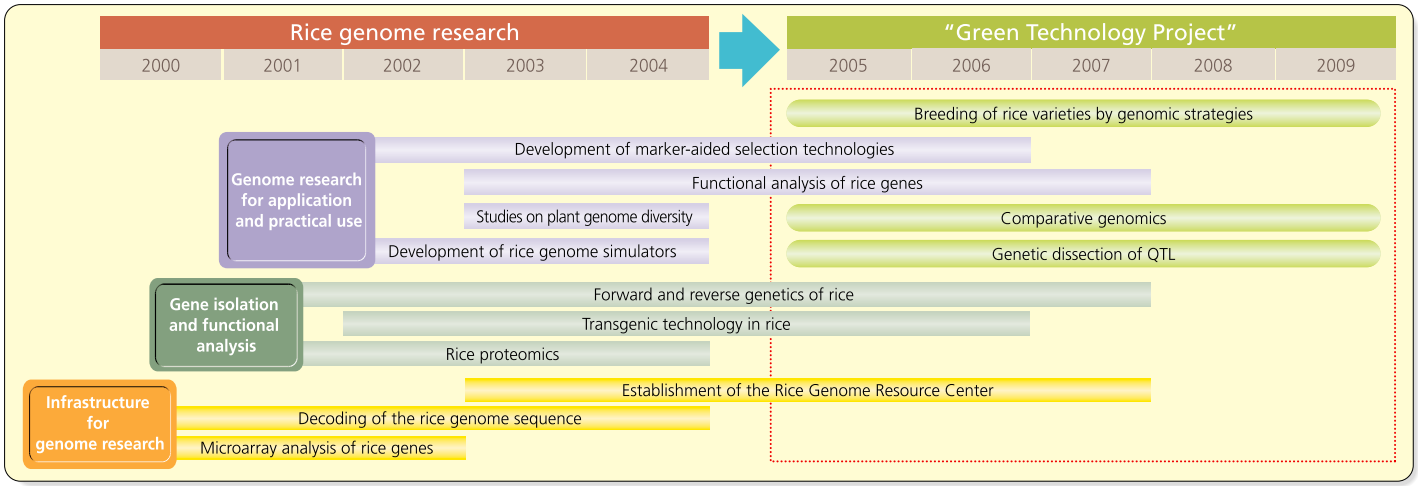
Timeline for rice genome sequencing

1998 Japan led the international sequencing consortium

Rice genome sequencing has been viewed as an indispensable endeavor for understanding the diverse genes of rice, ensuring a stable world food supply, promoting human health, and developing a sustainable agriculture. In 1998, researchers representing ten countries and regions organized the International Rice Genome Sequencing Project (IRGSP), with Japan playing the central role.

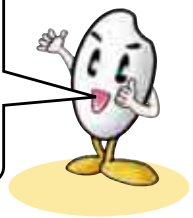
The consortium aimed to promote sharing of resources, information and technologies in order to accelerate the sequencing efforts and provide researchers around the world with the high-quality sequence of the rice genome. Japan led the international consortium and was in charge of sequencing six chromosomes, which correspond to half of the genome.

Projects for sequencing the genomes of organisms usually involve the cooperation of many countries and regions. The rice genome sequencing project is the first large-scale genome project in which Japan played a major part. In this effort, the National Institute of Agrobiological Sciences (NIAS) collaborated with the Institute of the Society for Techno-Innovation of Agriculture, Forestry and Fisheries (STAFF) through the Rice Genome Research Program (RGP) to facilitate the sequencing of approximately 200 million bases of the entire genome.



IRGSP

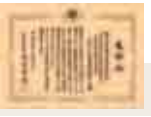
- Japan
- USA
- China
- France
- Taiwan
- India
- Thailand
- Korea
- UK
- Brazil



2002 Completion of draft sequencing

A ceremony was held to celebrate the completion of the sequencing of the rice genome. The announcement was made by then Prime Minister Junichiro KOIZUMI.

2004 The entire rice genome was decoded



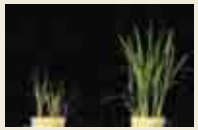
In December 2004, the international consortium announced the completion of the entire rice genome sequence thereby achieving its ultimate goal. The results were presented to then Agriculture, Forestry and Fisheries Minister Yoshinobu SHIMAMURA on December 13, 2004. A comprehensive analysis of the genome sequence was published in the internationally renowned journal, Nature (Vol. 436, August 11, 2005). Obtaining the complete sequence of the genome was one of the core objectives of the program for rice genome research, and this achievement serves as the basis for the "Green Technology Project".

The rice genome sequence data was handed over to then Minister of Agricu ture, Forestry and Fisheries (right) Certificate of appreciation from the MAFF minister (eft)

The results of rice genome analyses are deposited in public databases which can be accessed from various research institutes. DNA materials, seeds and mutant lines obtained in the process of genome research are stored and made available for distribution.

Mutant library for elucidating gene functions

http://tos.nias.affrc.go.jp



Resistance to virus

Dwarfism
(Two p ants on the right are dwarf)

Panicle sprouting

Mutant for cellulose synthesis
(Leaves and stems are vulnerable to breaking due to reduced cellulose content.)

Rice genome database constructed

Rice annotation database

(Left)
The database provides information on the analysis of entire genome including the functions of predicted rice genes.

http://rapdb.dna.affrc.go.jp/

Database of rice expressed genes

(Right)
The database provides information on the sequence and function of 32,127 expressed genes of rice.

http://cdna01.dna.affrc.go.jp/cDNA/

Rice Genome Resource Center established

http://www.rgrc.dna.affrc.go.jp/jp/

●Storage, management and access to genome resources

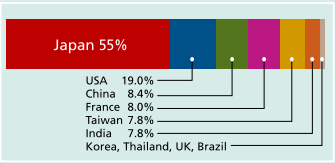
●Support to researchers
An open laboratory for researchers to conduct microarray analysis

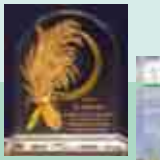
Japan's contribution in sequencing the rice genome has been widely recognized.

Japan played the leading role in the international sequencing consortium and made a major contribution in the overall sequencing effort. Approximately 55% of the entire genome sequence was sequenced by Japan's Rice Genome Research Program (RGP). This contribution was highly acclaimed by the international scientific community.

For these efforts, RGP received the Golden Sickle Award from the Kingdom of Thailand, and one of its papers entitled "The Genome Sequence and Structure of Rice Chromosome 1" (published in Nature Vol. 420, November 21, 2002) won the first prize in the Global Scientific Contest in conjunction with the celebration of the International Year of Rice.

Contribution to rice genome sequencing





Golden Sickle Award

"Green Technology Project" opens up the future of mankind.

2005

The program for rice genome research achieved the ultimate goal of decoding the entire rice genome sequence. The functions of each gene and breeding applications will be investigated in the future. The "Green Technology Project" was launched in 2005 in order to focus on practical utilization of the results of extensive rice genome analysis for agricultural purposes.

The Green Technology Project includes researches on isolation of useful genes, analysis of gene functions, and breeding new rice varieties using genetic recombination technologies and DNA markers. The rice genome sequence information has been very useful for studying the diversity of plant genomes in wild rice species and understanding crops other than rice, such as barley and wheat.

Research achievements

●Rice with improved yield

With the aim of developing high-yielding rice varieties, studies are being conducted on plant hormones, morphology, photosynthesis etc.

Ordinary rice (left) and high-yielding rice (right)

●Rice with low shattering rate

A japonica variety "Nipponbare" cultivated in Japan is less vulnerable to seed shattering than an indica variety "Kasalath". Using the rice genome data, a gene (*qSH1*) involved in seed shattering has been isolated.

Comparison of seed shattering character (left: Nipponbare, right: Kasalath)

●Rice with insect pest resistance

Rice with durable resistance to insect pests is being developed.

Brown planthopper
(Nilaparvata lugens)

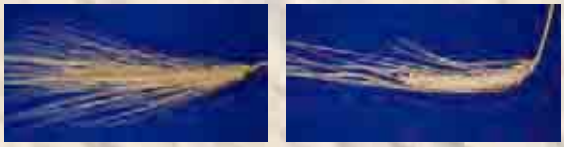
●Health-promoting rice

Rice with potential to help prevent diseases is being developed to keep people healthy.

Rice containing cedar pollen peptides

●Gene determining the number of rows of barley grain heads

Barley has two types of grain heads with grains arranged in either two or six rows. Using the rice and barley genomic information, the gene responsible for determining the number of rows in grain head was isolated.



Hordeum vulgare
(six-row barley)

Hordeum distichum
(two-row barley)

●Early flowering rice

The genes involved in the timing of the onset of flowering have been clarified in rice. Using this information, Koshihikari lines with various flowering times have been developed.

Left: Early flowering

●Disease resistant rice

Rice blast is a disease that has long been a major concern of farmers. Studies are being conducted on genes involved in developing durable resistance to the pathogen.

Strong ◄——► Weak
Rice blast

These are just some of the results obtained from the Green Technology Project. On-going researches aim to understand the functions of rice genes and ensure a stable food supply for mankind in the future.

Rice Genome
Q & A

Q: What is the "genome"?

A: The genome is the set of all genetic information of an organism. In rice, this complete set of genetic materials corresponds to the twelve chromosomes, which are chains of DNA located within the cell. The genome of rice contains about 32,000 genes.

Q: What can we learn from genome research?

A: By studying the genome, we can understand when, how, and in which organ each gene becomes active. We can also understand the differences between two species and between individuals of the same species by comparing their genomes. The results of rice genome research can also be used to understand the mechanism of plant stress resistance, and thus facilitate the breeding of varieties with enhanced resistance to various diseases and pests.

Q: What is the "Green Technology Project" and it's goals?

A: The world population is expected to reach 9 billion in the middle of the 21st century. Because half of the population depends on rice as source of food, studies on rice are crucial to ensure a stable world food supply. The "Green Technology Project" was started in 2005 with the aim of efficiently applying the rice genome sequence information for advancement of agriculture. The project encompasses studies on the functions of genes using the genomic information and effective development of new cultivars to sustain productivity.

Q: How can we access the data from rice genome research?

A: The genome sequence data can be accessed through the Japan DNA Data Bank (DDBJ) and is now widely used by many researchers. Several databases have also been constructed as part of various projects on rice genome analysis (RAP-DB at http://rapdb.dna.affrc.go.jp/, KOME at http://cdna01.dna.affrc.go.jp/cDNA/, etc.) .

Q: Is the rice genome information useful for studying other plants?

A: Yes, the rice genome information has been used for studying other crops, such as maize and wheat. In the near future, the genome information could also be a useful tool for studying crops to induce production of biofuels.

Q: How is the information commonly used?

A: DNA markers are now widely used for cultivar identification (for example to distinguish Koshihikari from other rice varieties) and for breeding superior rice varieties. In the case of Koshihikari, more desirable characteristics such as shorter plant height, variable flowering time and increased resistance to diseases are now being targeted.

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