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

Research and Bioresources No.4

Genomic study on legumes

Satoshi TABATA

Department of Plant Genome Research, Kazusa DNA Research Institute

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Coming up in the next issue!
The next month's issue will be "Common marmoset."

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Genomic study on legumes



Satoshi TABATA Kazusa DNA Research Institute,
Head of Department of Plant Genome Research

Characteristics of leguminous plants

Legumes exhibit great diversity, comprising approximately 700 genera and over 18,000 species. Leguminous crops such as soybean, kidney bean, and red bean are cultivated in various regions all over the world, and are considered as second important crops after gramineous crops such as rice, wheat, and corn. Leguminous crops are consumed as foods and forages or used as raw materials for the production of various processed products such as oils, fats, and soy sauces.

Legumes have the ability of symbiotic nitrogen fixation that contributes to sustainable agriculture, thereby lowering the environmental burden. Symbiotic nitrogen fixation is a mutual phenomenon. Nodular bacteria (*i.e.*, soil bacteria) in the organ called a root nodule on the root of legumes, synthesize ammonia from atmospheric nitrogen and supply this ammonia to the host. In return, the host supplies these bacteria with carbohydrates and photosynthetic products (Fig. 1). Since legumes can grow in soil with less nitrogen content by performing symbiotic nitrogen fixation, they contribute greatly to the prevention of environmental pollution caused by excessive use of nitrogenous fertilizers and save the energy required to produce and transport nitrogenous fertilizers. Therefore, much effort has been directed toward introducing nitrogen-fixing ability in gramineous crops and industrial plants. Several domestic and foreign research groups are competing with each other to reveal the basic mechanism of symbiotic nitrogen fixation and the related genes, as the first step in introducing the nitrogen fixing ability in plants.

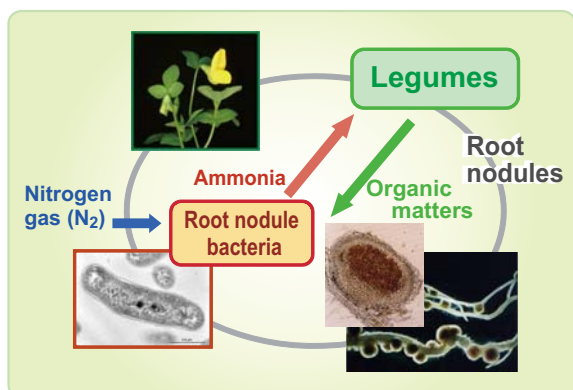


Fig. 1: Symbiotic nitrogen fixation by legumes

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• <http://www.shigen.nig.ac.jp/shigen/news/>

Other information on bioresources is available at

- ◆ NBRP <http://www.nbrp.jp/>
- ◆ SHIGEN <http://www.shigen.nig.ac.jp/>
- ◆ WGR <http://www.shigen.nig.ac.jp/wgr/>
- ◆ JGR <http://www.shigen.nig.ac.jp/wgr/jgr/jgrUrlList.jsp>

Genome sequencing of legumes

The genomes of legumes vary in size and ploidy types, which reflect the ecological, physiological, and morphological diversities of these plants (Table 1). For genetic analysis of processes that are observed specifically in legumes, such as symbiotic nitrogen fixation, "model materials" have been used in experiments instead of crops such as soybean. The model materials are more suitable than field crops in terms of growth rate, number of genes, plant size; further, transformation (DNA transfection) technology has facilitated the use of model materials for such studies. *Lotus japonicus* and *Medicago truncatula* can be cited as typical model legumes. These model plants have been used in molecular genetic studies such as isolation and functional analysis of mutant genes. Since 2000, the sequencing of the entire genome of *L. japonicus* and *M. truncatula* has been competitively undertaken by research teams in Japan (Kazusa DNA Research Institute) and in the US, France, and UK as a joint project, respectively. In addition, the genome sequencing of

soybean, one of the main legumes, has already been started with the support of DOE of US. Currently, the genome sequencing of 3 legume species is in progress simultaneously. All the genome sequencing projects are scheduled to be completed at around the same time, *i.e.*, by the end of 2009; the completion of these projects will provide us with the entire genome structures of the 3 legume species.

Table 1:
Genome sizes of legumes

• <i>L. japonicus</i>	470 Mb
• <i>M. truncatula</i>	470 Mb
• Red bean	540 Mb
• Kidney bean	588 Mb
• Soybean	1.1 Gb
• Pea	4.3 Gb
• Broad bean	13.1 Gb





Consolidation of genome information resources

A large amount of information on the structure, function, and location of genes can be obtained from genome sequence data. On the basis of this information, other useful genes have been screened and genome comparison analysis has been performed. This sequence information can be used to design DNA markers and for the rapid identification and isolation of mutant genes. Consequently, the identification of several genes related to symbiotic nitrogen fixation, synthesis of secondary metabolites specific to legumes, and disease-resistance is currently under way.

Regarding several other crop legumes that are not targeted for entire genome sequencing, projects involving large-scale development of DNA markers and construction of linkage maps of these plants have been initiated because of an increase in the speed and a decrease in the cost of nucleotide sequencing. These DNA markers can be used for genome comparison beyond the genera and for selective breeding; therefore, they are considered to contribute greatly to molecular breeding of various leguminous crops.

The information on the genome project of legumes and DNA markers can be obtained from the following websites.

Websites providing information on the genomes of legumes

 Lotus japonicus http://www.kazusa.or.jp/lotus/	 Soybean http://soybeanome.siu.edu/
 Medicago truncatula http://www.medicago.org/	 Soybean http://soybase.org/

Resources for *Lotus japonicus*

Numerous genome and biological resources are required to perform gene isolation and breeding using genome sequence information. Generally, these resources are personally maintained by researchers who have prepared or collected such information, and hence these resources can only be accessed on individual requests. However, regarding *L. japonicus*, Miyazaki University collects, maintains and provides resources that were developed and collected in Japan on a large scale with the support of NBRP (Fig.2: LegumeBase <http://www.legumebase.agr.miyazaki-u.ac.jp/>).

Genome and cDNA libraries are used as genome resources. Other biological resources include main experimental strains, recombinant inbred strains produced by interbreeding 2 experimental strains, domestic wild strains (n = 108), seeds of ethyl methanesulfonate (EMS) mutant strains, and a library of mutant root-nodule bacteria (*Mesorhizobium loti*) coexisting with *L. japonicus*. Moreover, the bioresources of soybean and wild soybean (*Glycine soja*) can be obtained through LegumeBase.

Accordingly, a large-scale genome sequencing project and an accompanying large-scale gene function analysis have been pursued for *L. japonicus*. To support these studies, a system for collecting and providing various resources has been developed. In the future, development of similar systems for other legumes might accelerate the breeding of leguminous crops. ■



Fig.2. LegumeBase



Erudite Lecture Series by Dr. Benno: No. 8

Piled up in women and run off in men

"I would like to ask Dr. Benno, who has been studying feces, to examine my feces." In light of the recent health boom, the media has approached me several times in search of something interesting. I apologize that I am beginning my talk with such a story, but allow me to explain my experience of examining extremely bad fecal samples in my laboratory.

In one case, immediately after opening a tightly wrapped container delivered by a cool-courier service, I was exposed to a very strong smell that cannot be described in words. The container contained multiple layers of feces with a very hard texture. In my talks, I generally introduce myself as the person who has seen the most human feces in Japan but this was the first time that I have seen such feces. I was also surprised by the contents of the feces. Generally, feces of healthy people have the consistency of a thick paste with a water content of around 80%. If the water content of the sample is 70%, the person might be severely constipated. The water content of the aforementioned fecal sample was as low as 60%. Moreover, this sample contained very few beneficial bacteria and an astonishingly large number of harmful bacteria.

This sample was of a 20-year-old woman who was living alone. She described her dietary habits as "I usually eat only confectionery products and drink packaged juice." She did not follow a fixed schedule. When hungry, she would eat only the available confectionery products. Indeed, her eating habits ultimately lead her to constipation and disregard toward the urge to defecate. It is noteworthy that the fecal samples of young women are generally malodorous and have a hard texture. It appears that the enteric environment of young women is currently undergoing radical changes.

On the other hand, most men do not exercise and are required to sit in front of a computer everyday for work purposes, and the resulting stress leads them to smoking. Men usually consume stamina foods that are high in calories. The dietary habits of men can be described as simple, quick, and irregular. Many male readers of this newsletter will relate to this fact. Then, let us now understand the characteristics of the feces of the "dad's generation?"

According to the results of a survey conducted by a pharmaceutical company, the toilet gave off a very bad odor after being used by elderly or middle-aged male members of the family. Around 80% of men who are fathers reported that they were blamed for leaving a bad odor in the toilet. The poisonous substances produced by harmful fecal bacteria are responsible for the bad odor. Moreover, the incidences of diarrhea have been reported to be high in men who are stressed. This phenomenon is called the irritable bowel syndrome. Because of everyday stresses, the mucosa of the large intestine is damaged to a great extent, and consequently, the diarrhea cannot be stopped. The bodily rhythm is lost, and water retention is adversely affected.

The term "piled up in women and run off in men" conveys an idea about the lifestyle of modern people. It is a clear indication of lifestyle-related diseases. Hence, if you do not improve your lifestyle immediately, you may encounter severe problems.



10 minutes

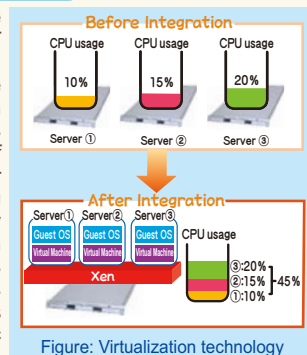
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Green IT

What do you think of when you hear the term green IT? This term refers to the measures taken for reducing the amount of carbon dioxide emission, including reducing power consumption of IT equipment and saving power with IT equipment.

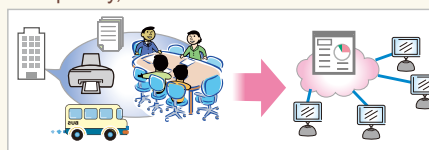
Reducing power consumption of IT equipment

It is important to reduce the electric power consumed by IT equipment. For instance, several servers and network devices are used to manage the information center in the Genetic Informatics Laboratory, National Institute of Genetics. At such centers, power saving can be achieved by reducing the electric power consumed by each machine. The virtualization technology introduced in this series (Vol. 4 No. 12 and Vol. 5 No. 1) has been used in the Genetic Informatics Laboratory to reduce the electric power consumed by servers.



Power saving IT equipment

This concept can be interpreted in 2 different ways. First, electric power consumption of other devices can be reduced by using IT equipment. For instance, improved performance of temperature sensors in an air conditioner can effectively control room temperature and consequently reduce the excessive power consumption of the air conditioner. Second, carbon dioxide emissions can be reduced by using IT equipment. A video conference can be cited as an appropriate example for this approach. If a video conference is held between 2 remote locations through television or the Internet, the participants are not required to travel by cars or buses, and consequently, the amount of carbon dioxide emission is reduced. In



NBRP, this approach has been referred to as the computerization of the material transfer agreement (MTA).

Trends in the IT industry

After the Kyoto Protocol has come into effect, Japan is obliged to reduce the amount of carbon dioxide emission by 6% between 2008 and 2012, with respect to the level recorded in 1990. After the proposal of the green IT initiative by the Ministry of Economy, Trade and Industry, the IT industry has actively pursued the reduction in power consumption. In May 2009, an exhibition was held on the topic of green IT for the first time in Japan. I will share with you some information from the exhibition about a data center.

A data center is a facility where a large number of servers are operated at a single location. Such centers face difficulty in reducing the electric power consumed by equipment other than the servers. Particularly, the electric power required to cool the servers is the main concern. Aisle capping can be cited as the latest method to effectively cool the servers. In this method, the air used for cooling the servers is completely separated from the heat released from the servers. Implementation of this method in the data center helped to achieve a power usage effectiveness (PUE) value of 1.4-2.0. The ideal PUE value is 1.0 and the PUE values of general data centers are within the range of 2.3-2.5. (Tohru Watanabe)

※PUE value: Obtained by dividing the total power consumption by power consumed by the IT equipment.

Editor's Note The groups performing genome research in Japan have given a tough competition to other international competitors; especially, the group headed by Dr. Tabata who has independently pursued the sequencing of the entire genome of *L. japonicus* and has been in the forefront in the international league. Dr. Tabata, who is also the deputy director of Kazusa DNA Research Institute, has been highlighting the importance of data disclosure and public access to bioresources for a long time and he has supported the bioresource project. I am grateful to Dr. Tabata for writing this manuscript in spite of his busy schedule. (Y.Y.)

Contact Address:

1111 Yata, Mishima-shi, Shizuoka 411-8540, Japan
Center for Genetic Resource Information, National Institute of Genetics
Tel: 055-981-6885 (Yamazaki)
E-mail: brnews@chanko.lab.nig.ac.jp

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