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

## Introduction to Resource Center No. 29

### Consolidation of Plant Research Infrastructure Advanced by *Arabidopsis Thaliana* Resources

Masatomo Kobayashi  
Experimental Plant Division, RIKEN BioResource Center

## Ongoing Column No.38

### “Xen”, A Server Virtualization Software Program: Overview



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- ◆ 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>

## Announcements (Details are available at <http://www.nbrp.jp/>)

- **The 2nd Workshop on Rat Resource Research**  
Date: January 30 (Fri), 13:00–17:00, 2009  
Place: International Conference Hall I, Clock Tower Centennial Hall, Kyoto University
- **RIKEN BRC International Symposium, “Bacteria as Research Resources”**  
Date: February 10 (Tue), 9:30–17:40, 2009  
Place: Hyatt Regency Tokyo (2-7-2 Nishi-Shinjuku, Shinjuku-Ku, Tokyo)
- **The 3rd International Biocuration Conference (IBC 2009)**  
Date: April 16–19, 2009, in Berlin, Germany  
Details are available at <http://projects.embl.org/Meeting2009>

## Introduction to Resource Center No.29

### Consolidation of Plant Research Infrastructure Advanced by *Arabidopsis Thaliana* Resources

Masatomo KOBAYASHI  
Head of Experimental Plant Division, RIKEN BioResource Center



The Experimental Plant Division, RIKEN BioResource Center (RIKEN BRC) is the core institute in charge of the project, “*Arabidopsis* / Cultured plant cells, genes,” which is a part of the National BioResource Project (NBRP) supported by the Ministry of Education, Culture, Sports, Science and Technology. Here, we introduce SABRE, a “crossover” database of plant genes that was developed in collaboration with the BioResource Information Division, RIKEN BRC, and released last year and ABRANA, a database of *Brassica* genes, which is under development.

Website:  
<http://www.brc.riken.jp/lab/epd/Eng>



## Background

The recent development of high-speed DNA sequencers accelerated the analysis of genome sequences of model crops in the world. The genomes of familiar crops such as beans, tomatoes, and napa cabbages have been successively sequenced and an enormous amount of information has accumulated in databases. In general, most crop research is aimed toward industrial applications such as the increase in the yield or the alleviation of damage by disease and pest. Thus, crop research in the post-genome era will involve the use of a reverse-engineering technique that relies on sequence information to predict gene functions in order to identify and utilize genes that are responsible for the growth of crops and regulation of responses to diseases and insect damage. However, in contrast to the case of *Arabidopsis thaliana*, whose genome has been almost fully sequenced, the genome analysis studies of most crops do not aim for “complete sequencing.” In addition, even if the genome has been sequenced, the consolidation of cDNAs is indispensable for the identification of coding regions.

Moreover, even if promising gene candidates were discovered by the genome sequence information and comprehensive cDNA analysis, the functional analysis of the genes by using crops is not straightforward: Effective transgenic or knockout strains cannot be developed for most crops and even if such strains are developed, a sufficiently large, closed greenhouse equipped with an advanced air-conditioner is required for cultivating the strains. Moreover, the production of seeds of the next generation occasionally requires over half a year. Hence, harnessing the research infrastructure of model test plants such as *A. thaliana* will be extremely helpful.



## “SABRE”, a consolidated database of plant genes



Currently, the functional analysis of all the genes in *A. thaliana* is included in the international project. More than half the genes, if not all, will presumably be experimentally annotated by 2010. Additionally, the knockout strains and full-length cDNA clones of approximately 95% and 70%, respectively, of all the genes are available at our institution and other resource centers in the US, EU, and Japan. Whether the highly consolidated resources and information of *A. thaliana* are utilizable is extremely important for promoting the research in plant genes. Even after the completion of the current international project in 2010, collaboration with crop research projects is expected to be the major task in the next *A. thaliana* projects.

Considering these research backgrounds, we developed a database that associates cDNA clones of various model plants we administrate with the *A. thaliana* genome information and named it SABRE (Systematic consolidation of Botanical Resource) (Fig. 1). SABRE uses sequence information to associate the genome information released by the *Arabidopsis* Information Resource (TAIR), a core *Arabidopsis* information center, with the cDNA information of model plants. SABRE enables the users to refer to the newest information on *Arabidopsis* genome regarding any gene (cDNA) of interest simultaneously with the information on the cDNA clones of plants other than *Arabidopsis*. A highlight of the information in SABRE is that all the cDNA clones included in the database are stored at the resource center and are ready for research use. Currently, SABRE contains information on approximately 440,000 clones stored at RIKEN BRC. By obtaining the cooperation of affiliated institutions, we will soon be adding information on the full-length cDNAs that belong to various plant species and that have been developed and stored in the country.

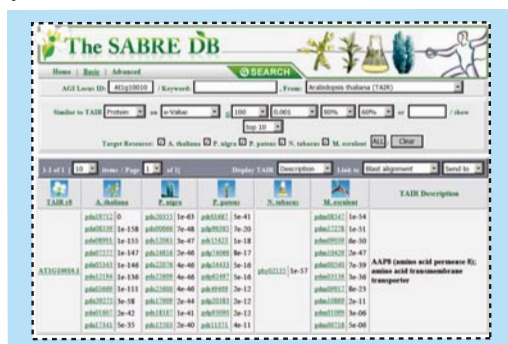


Fig. 1: The result screen of a search on SABRE

## "ABRANA", a model database for crop research

SABRE associates the *A. thaliana* genome information with plant genes (cDNAs) on the basis of sequence information and provides useful information on the functions of plant genes. However, many genes are present as gene families in plants; thus, the identification of the gene that is involved in a particular physiological function is difficult with only sequence information. Hence, RIKEN BRC is developing a database that enables the prediction of gene functions with high accuracy by appending the expression information of each cDNA contained in SABRE. For this purpose, with the support of the Bio-oriented Technology Research Advancement Institution, we isolated cDNAs of the stress response-related genes and developed a prototype microarray for diagnosing stress responses by using napa cabbage, which belongs to the same family (*Brassicaceae*) as *A. thaliana*, as a model plant. ABRANA (Arabidopsis-BRAssica Network Access), the database currently under development, will enable highly accurate association of stress response-related genes in *A. thaliana* with those in napa cabbages; this will be achieved by comparing the information obtained on napa cabbage cDNA with that on *A. thaliana* genes using a function of SABRE and incorporating the expression information obtained from microarray analysis (Fig. 2). In addition, the database can not only be used for molecular breeding studies but also be applied to various agricultural studies such as cultivar evaluation in terms of stress response or the assessment of immunoactive agents in plants. Even though ABRANA is still under development, this research method based on the cDNA resources and target-oriented microarrays is feasible with limited funding and human resources. Please contact the following email address if interested.

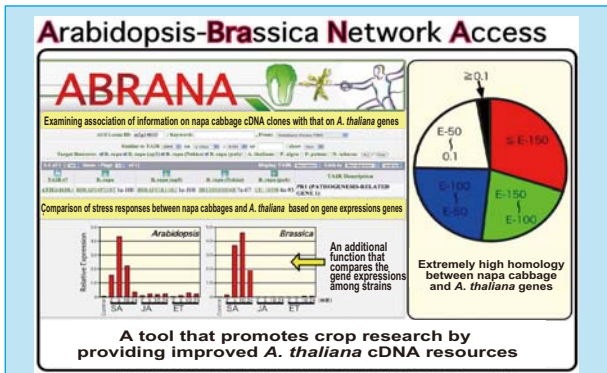


Fig. 2: Screen image of ABRANA

Website: <http://www.brc.riken.jp/lab/epd/Eng>  
Email address: [plant@brc.riken.jp](mailto:plant@brc.riken.jp)

### Plant resources distributed by RIKEN BRC

- *A. thaliana* seeds (transposon-tagged lines, activation-tagged lines, FOX lines, wild-type strains, and related species)
- Plant genes (full-length cDNAs of *A. thaliana*, *Physcomitrella patens*, *Populus nigra*, and *Manihot esculenta*)
- Cultured plant cells (*A. thaliana* T87 cells, Tobacco BY-2 cells, Rice Oc cells, *Lotus japonicus* Lj cells, and cell lines derived from other model plants)

### A Request to Researchers

We have a request to researchers who use our bioresources for their research.

Please include information of the bioresources in Materials & Methods or Acknowledgement when you publish your research journals. In addition, please contact the facility who provided those bioresources to you.

NBRP has opened a registration website for research journals. You can easily submit the information of your journal at the address provided below.

<http://rrc.nbrp.jp/>



Coming up in the next issue!  
The special topic on resources in the next month's issue will be "Xenopus."

## 10 minutes Information Technology - 38 -



### "Xen," A Server Virtualization Software Program: Overview

#### What is server virtualization and what is it used for?

This time, we introduce "Xen," a server virtualization software program. These software programs can virtually run multiple operating systems (OS) on a server; they mainly enable the effective use of central processing units (CPU) and the memory of the server and reduce the cost of server administration. Server virtualization software programs are becoming increasingly popular owing to the recent improvements in the server performance, such as the development of the quad-core CPU (a CPU packaged with 4 processor cores) and reduction in the price of servers.

Xen is a software program that enables server virtualization and was originally developed as a research project at the Univ. of Cambridge and is currently freely available as an open-source software program. Xen enables the simultaneous operation of different types of OS such as Linux and Windows on a single server (Fig. 1).

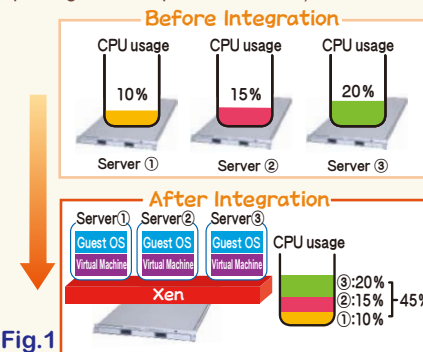


Fig. 1

#### Types of Virtualization (Merits of the Hypervisor type)

There are 2 types of server virtualization software programs: **host-OS type** and **hypervisor type** (Fig. 2). Typical host-OS type software programs include the famous VM Ware and Virtual PC. Even though the host-OS type software program is easy to install, the overhead is high and the guest OS performance is significantly reduced; thus, the host-OS type software program has limited usage such as in testing environments. In contrast, recently developed mainstream hypervisor-type software programs such as Xen directly interchange information between the guest OS and the hardware as virtual machine monitors, thus minimizing the overhead. The currently available server virtualization software programs, Oracle VM released by Oracle and Sun xVM Server released by Sun Microsystems, are based on the source code of Xen.

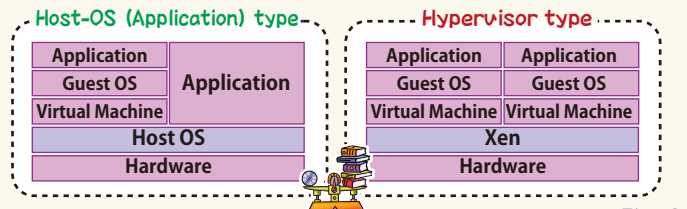


Fig. 2

#### Installation of Xen

Previously, Xen had to be installed by using the command line of Linux, and thus, required some knowledge of the UNIX system. However, since Xen is now bundled with the Version 5 of CentOS (an open-source OS compatible with Red Hat Enterprise Linux), the graphical user interface can be used for installation and settings.

Owing to space limitation, we will introduce the "Installation and Settings" of Xen on the CentOS 5 in the next issue.

(Takehiro YAMAKAWA, Center for Genetic Resource Information)

**Editor's Note** Fortunately, we could release all our newsletters up to the December issue this year. We thank all the authors who provided us with information on the current topics. Although the world economy is in a significant downturn, our National BioResource Project would be able to "soft-land" with the support of research subsidies from the next fiscal year. All the staff members are excited about continuing to update the readers on current topics.

We wish everyone good luck for the coming year! (Y.Y.)

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