

# BioResource Now!

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Hot News <NO. 41>

# Model Plant Database that Connects Information with Resources: "SABRE2"

The SABRE<sup>2</sup>DB

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## From Bench to Bountiful Harvests

Humans have continuously selected plants possessing useful properties and created new plant varieties since the beginning of agriculture. Similar to Mendel's laws that were discovered from crossbreeding experiments with garden peas, the properties of plants are determined by genes. The creation of a new variety can be reworded as the creation of a plant line possessing a combination of useful genes. For this, the property of each gene must be sufficiently understood.



*Arabidopsis thaliana* with a plant length of approximately 40 cm can grow only with the light emitted from fluorescent lamps in a laboratory, and its "next-generation" seeds can be collected within approximately three months. Therefore, a characteristic of *A. thaliana* is that it is an easy-to-handle experimental plant. Because of this, *A. thaliana* has been actively used for basic research to understand various phenomena and functions of plants as a global-standard model plant. Another characteristic of *A. thaliana* is its small genome size. The whole genome of *A. thaliana* as a higher plant was sequenced for the first time in December 2000, prior to the completion of human genome sequencing. In 2001, the Arabidopsis 2010 Project was launched. This project aimed at investigating the functions of the approximately 27,000 genes found in total on the genome, and information on many genetic functions has already been obtained. In June 2010, the final year of the project, "from bench to bountiful harvests" was stated as the goal of *A. thaliana* research in the future. Since then, results of *A. thaliana* research have been applied to the studies on useful plants.

## Cross Search for Plant Genetic Resources in NBRP

There are difficulties in plant improvement. Thus, in order to use the findings of the *A. thaliana* research for the improvement of useful plants, the results of the *A. thaliana* research must be analyzed with regard to these difficulties to overcome them.

SABRE, the forerunner of SABRE2, is a cross-species database based on *A. thaliana* genes for searching clones possessing base sequences similar to those of *A. thaliana* genes. A clone searched in the SABRE database is displayed together with an *A. thaliana* gene possessing a base sequence similar to that of the searched clone and the annotation is added to the *A. thaliana* gene. By doing so, information on genetic functions, which has been abundantly obtained through *A. thaliana* research, can be used for research using clones. SABRE was developed in 2007, and it has been used for linking information on *A. thaliana* with clones (*A. thaliana*, *Physcomitrella patens*, cultured tobacco cells, *Populus nigra*, *Manihot esculenta*, halophyte *Thellungiella halophila*, halophyte *Striga hermonthica*, and *Brassica rapa*) provided by the RIKEN BioResource Center (BRC).

Recently, the SABRE database was improved to SABRE2 in cooperation with the National BioResource Project (NBRP) Information Center. In SABRE2, information on clones was added (*Triticum aestivum*, *Hordeum vulgare*, *Ipomoea nil*, *Lotus japonicas*, *Glycine max*, and *Solanum lycopersicum*), which was provided by the NBRP. Now, clones of 14 species can be searched at once in SABRE2 (Fig. 1). The linkage between information on *A. thaliana* and clones of model plants was reinforced; thus, SABRE2 can further contribute to the research and creation of useful plants.

## Great Improvement in the Interface

SABRE2 can search all plant genetic resources that are available from core institutions of the NBRP. The searched clone is linked to the database of each core institution; thus, detailed information can be obtained and the distribution can be ordered.

SABRE2 has information on more than 1.5 million plant clones, which is approximately 3 times that of SABRE. In order to easily search data, which have greatly increased qualitatively and quantitatively, the search screen and result display were drastically improved. For example, because the number of plant species to be handled increased, the search screen was changed so that users can select multiple plant species to be searched and obtain the results most relevant to them. The screen to enter a search keyword was changed so that the types of keywords that are useful for search, e.g., clone names and gene accession numbers, can be understood at a glance. When a keyword is entered, predictive text is displayed so that researchers other than those working on *A. thaliana*, e.g., those who develop new varieties of plants, can easily use the screen.

## "Many Doors Are Open" to SABRE2

\* <http://saber.epd.brc.riken.jp/sabre2/SABRE2.cgi>

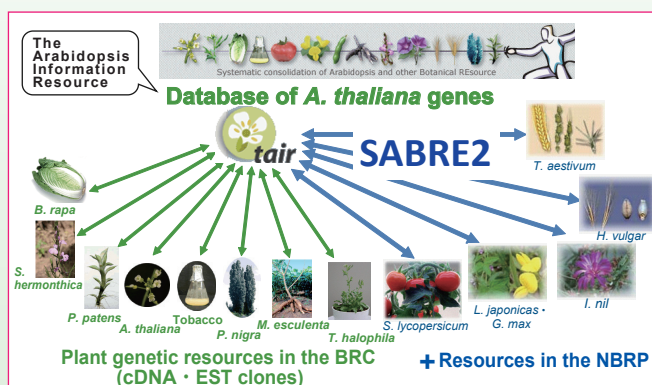


Fig. 1. Use of information on *A. thaliana* for plant genetic resources in the NBRP (<http://saber.epd.brc.riken.jp/sabre2/SABRE2.cgi>)

In an environment where the Internet is available, everybody can easily access SABRE2 at the above URL\* using personal computers and smartphones.

By using an Application Programming Interface (API), the functions of SABRE2 can be used from other websites and databases.

→ To the next page

The search box displayed on the homepage of SABRE2 is an example of this (Fig.2). A box similar to this box can be easily inserted into other websites by embedding a few lines of codes into the html of a webpage. This box was already introduced into the comprehensive search site of the NBRP (<http://resourcedb.nbrp.jp/>). When a keyword is entered in the entry field, a new window opens and the search results obtained in SABRE2 are displayed.

If you are interested in an introduction of the Search Box, please contact us.


**Contact us** <http://saber.epd.brc.riken.jp/sabre2/SABRE2.cgi?cmd=h#contactus>

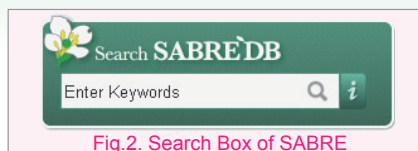


Fig.2. Search Box of SABRE

## “Many Doors Are Open” to Applied Research

A unique feature of SABRE2 is the link between information and bioresources. Due to the recent improvement, the role of linking experimental plants with actually cultivated plants and basic research with applied research was reinforced. We hope that this database is widely used,

resulting in making the most use of information obtained in the *A. thaliana* research in various research fields, creating new useful plants, and increasing food production.

SABRE2 was developed as the “integration of plant databases based on genomic information” (representative: Satoshi Tabata, Deputy Director, Kazusa DNA Research Institute) supported by the Database Integration Coordination Program, the National Bioscience Database Center, the Japan Science and Technology Agency.

## Comparison and Synchronization of Folders and Files

The National BioResource Project (NBRP) makes various types of data files available in text format, such as lists of resources. Have you ever been in a situation in which you have downloaded the same text or CSV file after a certain period of time, and were unsure which part of the two files had been changed? In this edition, I would like to introduce a tool called WinMerge that can be used to compare folders and files.

This tool can not only identify the differences between files and folders but also be used to make copies of folders or files; therefore, it can serve as a tool for backing up folders.

WinMerge, as the name suggests, is a tool for Windows. Those using a Mac can perform similar comparisons using a tool such as FileMerge.

### Let's try using WinMerge (comparison tool for Windows)

First, you must prepare WinMerge for use. You can download the Japanese version of WinMerge from (<http://www.geocities.co.jp/SiliconValley-SanJose/8165/winmerge.html>) as a zip file. You should extract the zip file contents and create a shortcut to the executable file on your desktop.

After launching the executable file, WinMergeU.exe, you must specify the file or folder that you would like to compare (Fig. 1). Alternatively, you can drag-and-drop the files you wish to compare onto the WinMergeU shortcut.

If you launch the tool through the drag-and-drop method, however, you cannot select the option to compare subfolders, and subfolders will thus not be displayed. You must therefore be careful when attempting to compare folders using the drag-and-drop method.

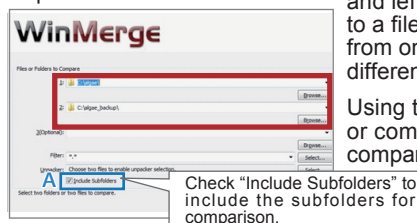


Fig. 1. File or folder selection dialog

### Let's try a comparison

Let's look at the file comparison screen. Differing lines are highlighted in orange. You can merge a changed line by right-clicking on the line and selecting “Copy to Right” or “Copy to Left,” or you can edit the files directly (Fig. 2).

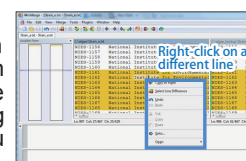


Fig. 2. File comparison screen

Next, let's look at the comparison screen that appears when you have selected two folders to compare. Files that appear in both folders but are different are highlighted in orange, and files that are only present in one of the folders are highlighted in grey (Fig. 3A).

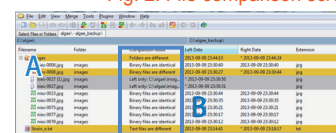


Fig. 3. Folder comparison screen

If you check the “include subfolders” option (Fig. 1A) upon launching the tool, WinMerge can also indicate whether the contents in the subfolders are different.

Refer to the “Comparison results” column for a detailed outcome (Fig. 3B).

Comparison results of “Right only” or “Left only” refer to the right and left folder locations shown in the header, respectively. Similar to a file comparison, you can right-click on a folder to copy the files from one folder to another. Furthermore, you can double-click on a different file and open up a new file comparison screen.

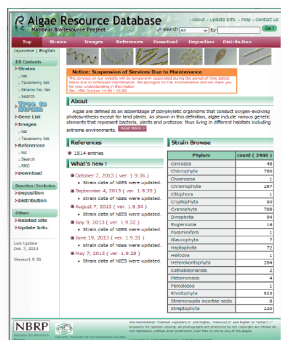
Using this tool, you can quickly and accurately compare large files or complex folder structures. It's easy to use, so why not try it to compare your files?



(Hiroki Watanabe)

## Database of This Month

### National BioResource Project “Algae”



- Number of strains: 2,999
- Number of genes: 183 (675 strains)
- Number of published papers: 1,500 (as of August 2013)

**Comment from a practicing developer:** NBRP Algae is a database, in which information on strains conserved in the National Institute for Environmental Studies (microalgae) and Kobe University (macroalgae) is integrated. Conserved strains can be searched not only by general keyword search but also by using a dendrogram, “Tree to Strain,” which is displayed in the menu on the left side of the homepage. Data on conserved strains, images, and published papers are updated once a month. Images of algae are unmissable. Please feel free to use the database and do not hesitate to express your comments, questions, or opinions.

DB name : Algae  
URL : <http://www.shigen.nig.ac.jp/algae/>  
Language : Japanese, English  
Contents :

- Conserved strains (scientific names, collection information, conservation forms, culture conditions, images, characteristics, sizes, and published papers)
- Information on genes whose sequencing has been completed
- Tree to Strain (a dendrogram provided by Takeshi Nakayama, Lecturer, University of Tsukuba)
- Files to be downloaded

**Features :** Strains conserved in the National Institute for Environmental Studies and Kobe University can be searched in the block. Conserved strains can be accessed from the dendrogram.

Cooperative DB : NIES, KU-MACC  
DB construction group : NBRP Algae, NBRP Information Management organization : Genetic Resource Center, NIG  
Year of DB publication : 2004 Year of last DB update: 2013

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### Editor's Note

This month, a new version of an integrated database of plant genome resources, which has been recently released, was introduced. I heard that many people started using the SABRE2 search box soon after it was included into the comprehensive search site of NBRP. In addition, resources can be used beyond the species barrier. I thank the authors for providing hot topics (Y. Y.).

### BioResource Information

(NBRP) [www.nbrp.jp/](http://www.nbrp.jp/)  
(SHIGEN) [www.shigen.nig.ac.jp/](http://www.shigen.nig.ac.jp/)  
(WGR) [www.shigen.nig.ac.jp/wgr/](http://www.shigen.nig.ac.jp/wgr/)  
(JGR) [www.shigen.nig.ac.jp/wgr/jgr/jgrUrlList.jsp](http://www.shigen.nig.ac.jp/wgr/jgr/jgrUrlList.jsp)