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Barley Varieties and Bioresources
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Research Institute for Bioresources, Okayama University

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Download the PDF version of this newsletter at
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/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.

Introduction to Resource Center   No.15

Barley Varieties and Bioresources

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Research Institute for Bioresources, Okayama University

Diversity in the heads of cultivated barley

Barley is an important crop that is used for brewing and human and animal consumption, and various genetic strains of wild type and cultivated species have been preserved. Cultivated barley is a diploid species, and numerous experimental strains with a focus on mutant strains have been developed. Recently, in addition to the bacterial artificial chromosome (BAC) library and a massive amount of expressed sequence tags (ESTs), 5,000 clones of full-length cDNA have been developed by the National BioResource Project (NBRP) for the first time in barley, which is a model plant of the wheat family, and will be released soon.

Through this project, we, the Research Institute for Bioresources at Okayama University preserve and distribute barley strains, BAC library, and cDNA clones, which we have independently collected or developed. Moreover, we have developed and are distributing filters to efficiently select BAC clones and pooled DNA samples for PCR. As part of the research on these genome resources, we have also been developing high-density maps of transcripts based on the sequence information of cDNA, their application to wheat, and GeneChip arrays. The aim of this project is to contribute to the analysis of genome and genes of barley and related plant species and the development of novel species by providing bioresources to researchers worldwide.

1 Preservation and Distribution of Strain Seeds

We preserve and distribute cultivated species, wild-type species, and experimental strains of barley. Currently, the number of preserved strains is more than 14,000 and the number of strains available for distribution has reached 6,478. This barley strain resource has been developed using experimental strains for genetic analysis and domestic species that have been collected from different parts of the world by the Research Institute for Bioresources at Okayama University (previously The Ohara Institute for Agricultural Research) since the 1940s. In particular, East Asian strains which grow in the eastern parts of India and are globally considered as valuable native species of barley are preserved in Okayama University. As an international genetic resource project on barley, Okayama University plays a role as a center for the International Barley Core Collection in Southeast Asia.

The Barley Database
http://www.shigen.nig.ac.jp/barley/

2 Preservation and Distribution of cDNA clones

We have released a database containing 135,000 ESTs and have specified 75,000 clones available for distribution. In addition, Okayama University has developed high-density maps of transcripts based on the sequence information of these cDNAs, their applications to barley, and GeneChip arrays. We are currently preparing to release full-length cDNA clones.

3 Preservation and Distribution of BAC clones and Development and Distribution of the Screening System

We have developed the second largest BAC library (approximately 300,000 clones) in the world and are distributing them along with the filters that are used for the effective selection of clones (16 per set) and pooled DNA samples for PCR (768 samples).

Packing of the BAC library copies for delivery to the United States.

4 Release of Strain Information and EST Data

The Barley Database includes the Barley Germplasm Database (database of barley strain information) and the Barley EST Database (database of ESTs in barley). Information on strain characteristics can be searched from the Barley Germplasm Database. The most recent updated contents include comparative maps of Poaceae crops and image data of genetic resources. The details are available at the website: http://www.shigen.nig.ac.jp/barley/ .

EST database   Comparative maps of *Poaceae* crops   Image data of genetic resources

5 Distribution Record

In the fiscal year of 2002, only strain seeds were provided. Later, we started distributing DNA resources too. In addition to universities, we provide the resources to public and private research institutes. It is also a characteristic of the barley bioresources to be distributed frequently to other countries, regardless of whether they are advanced or developing countries.

Barley harvest in
an experimental farm

Inside the seed storage room

6 Roles in the Genome Analysis of Barley and the Wheat Family

The International Barley Sequencing Consortium (http://barleygenome.org/) was organized in August 2006, and the sequencing of barley genome has been initiated. As a participant in the project, Okayama University plans to analyze the BAC clone sequences that are located on chromosome 3H by using full-length clones and BAC library that are specified by NBRP for distribution.

(http://brain.naro.affrc.go.jp/tokyo/marumoto/up/h18kadai/top.htm)

Chromosome 3H of barley is homologous to chromosome 3B of wheat, whose genome is currently being analyzed in France; thus, the genome sequences of both chromosomes can be comparatively analyzed. In addition, since these chromosomes are known to be homologous to chromosome 1 of rice, it is possible to identify genes by using the genomic information of rice. Many genes are known to be common to both barley and wheat; since barley is a diploid organism and thus easier to analyze, the genes of barley are being used as a model for identification of genes of wheat, an allohexaploid organism. Accordingly, the genome of the wheat family, which is a staple diet for humans, is being decoded.

International Barley
Sequencing Consortium

INTERNATIONAL
BARLEY
SEQUENCING
CONSORTIUM

Interesting Websites

WikiProfessional   http://www.wikiprofessional.info/

Dr. Barend Mons (SHARED http://www.shared-global.org/) used the Wikipedia approach to successfully create a community website for all researchers, in which multiple life science databases are integrated into a single resource. This website is scheduled to be released in March and only has a few resources available at this moment. However, the beta version allows access to Swiss-Prot, Gene Ontology, PubMed and disease information from the National Library of Medicine. This website is highly anticipated by project members such as Dr. Amos Bairoch of Swiss-Prot and Dr. Michael Ashburner of Flybase and looks like it will attract a lot of attention. (Nature 445, February 15, 691p (2007))

Allen Brain Atlas   http://www.brain-map.org/
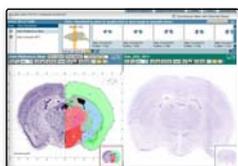
Since it appeared on the cover of Nature 445, 11th January 2007, many of you may have already known about it. This is a digital atlas developed at the cell-level resolution by systematically analyzing the expression patterns of approximately 20,000 genes in the mouse brain. The Multiple Image Viewer of this atlas has a high level of completion and I am impressed with its user-friendly functions.   (Yukiko Yamazaki)

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10 minutes

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Firefox Search Plug-In

How convenient it would be if we could use the search function of a website that we frequently visit without having to access the site every time? Plugins that incorporate the search function of Google, Yahoo, or Amazon in your internet browser are available. Once we install these plugins, a toolbar that enables quick searching will appear in our browser (Fig. 1).

Fig. 1

Then, would it be impossible to use the search function of websites that do not provide such plugins? Actually, it can be easily done with a browser called Firefox2. Here, I would like to talk about how to customize your quick search toolbar.

Let's try out Google Scholar's quick search function!

① **Writing the Plugin -----**

```
 1 : <?xml version="1.0" encoding="UTF-8"?>
 2 : <SearchPlugin xmlns="http://www.mozilla.org/2006/browser/search/">
 3 : <ShortName>Google Scholar</ShortName>
 4 : <InputEncoding>UTF-8</InputEncoding>
 5 : <Image width="16" height="16">data:image/xxx</Image>
 6 : <Url type="text/html" method="GET" template="http://scholar.google.com/scholar">
 7 :       <Param name="hl" value="ja"/>
 8 :       <Param name="lr" value=""/>
 9 :       <Param name="q" value="{searchTerms}"/>
10 : </Url>                            Fig. 2:Sample.xml
11 : </SearchPlugin>
```

The quick search plugin of Firefox2 is developed in XML (Fig. 2). First, create a file named xxx.xml with a text editor. Lines 1 and 2 are the XML declaration and the code for Google Scholar is just 9 lines. Line 3 indicates the name shown on the toolbar, line 4 indicates the character encoding and line 5 indicates the URL of the icon. Line 6 – 9 is the actual code for the search function. The value of the "template" attribute of the <URL> tag specifies the search URL for Google Scholar. The <Param> tags specify the required parameters and "value={searchTerms}" in line 9 indicates that input from the textbox in the toolbar will be used as keywords. Lastly, write the end tags in lines 10 and 11 and we are done.

② **Placing the Plugin -----**

Put the plugin file that you have written into the "searchplugins" folder as indicated below.

{Path to the "Program Files"}\Mozilla Firefox\searchplugins

③ **Using the Plugin -----**

After you have placed the plugin file into the appropriate folder as stated above, restart Firefox2. If the Google Scholar option appears in the quick search toolbar, then you have successfully installed the plugin. Select Google Scholar from the list, type a keyword into the textbox and press the Enter key. Your browser should then display the results of your search.

With a little effort, this is how you can customize your quick search toolbar and make it even more convenient for yourself. Please, do give it a go during your coffee break!

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"translated by ASL translatiaon service and proofread by Sharoh Yip"

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