



# Bioresource Information Division



Head

Kaoru FUKAMI-KOBAYASHI, Ph.D.

## Goal

Owing to the recent advances in genome analysis, various research resources such as DNA clones, cell lines, and genetically modified organisms have been and are still being exhaustively developed. Accordingly, with the accumulation of these bioresources in the field of life science, a huge amount of information about such resources is also accumulated, and none of this information can be utilized without information technology. It is thus indispensable for the formation of the basis of life science research to make bioresource information open to public in the form of digital contents, such as web pages, databases with user-friendly search engines, and ftp files.

Grounded on this perspective, the Bioresource Information Division collects information on the whereabouts and characteristics of bioresources preserved in RIKEN BRC, constructs databases, and offers bioresource information to research communities in the form of “bio-digital-contents” such as a web-based catalogs, linking them with related digital contents in and outside the country. By continuously providing up-to-date bio-digital-contents, the Bioresource Information Division aims to contribute to the advancement of life science.

## Activities

The Bioresource Information Division engages in the following projects.

### I. Resource collection/preservation/distribution projects

- \* Construction and management of bioresource databases
- \* Dissemination of bioresource information through databases and their search engines
- \* Support for bioresource distribution service

### II. Resource utilization promotion projects

- \* System development and maintenance for facilitating bioresource acquisition.
- \* Support for bioresource public relations.

### III. Resource information technology development projects

- \* Development of technology for consolidating bioresource databases.
- \* Development of technology for bioresource information analysis.
- \* Assistance/collaboration for bioresource information analysis

## Members

Head

Kaoru FUKAMI-KOBAYASHI, Ph.D. (2003.7~)

Senior Visiting Scientist

Yoshihiro UGAWA, Ph.D. (2001.11~2007.3)

Senior Research Scientist

Shigeru IWASE, Ph.D. (2002.1~)

Satoshi OOTA, Ph.D. (2003.10~)

Senior Technical Scientist

Mamoru NOGUCHI (2001.4~)

Technical Staff II

Naomi YUHARA (2005.4~)



Oota, Ichiishi, Iwase, Kiryu, Ueda  
 Yuhara, Amano, Sato, Ando, Endo, Fukutomi  
 Noguchi, Yokota, Fukami-Kobayashi, Honjo, Nakata

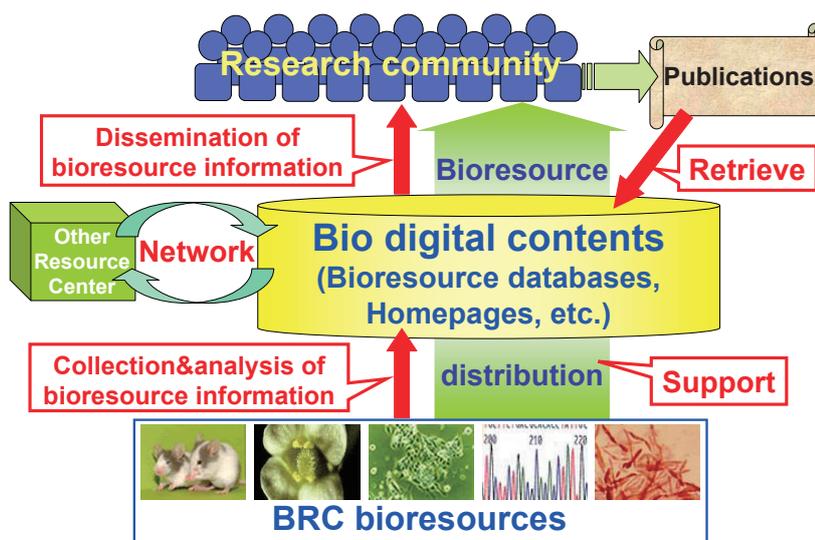


Figure 1. Bioresource Information Division is the hub of information in BRC.

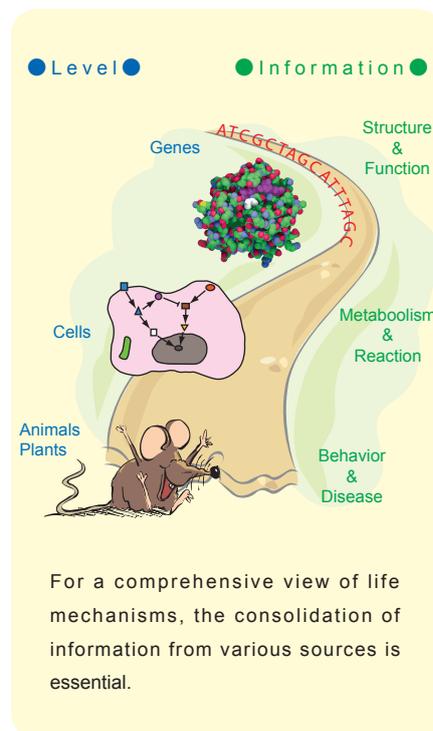


Figure 2. Biological levels and their associated information

## Specific Aims

### 1. Resource collection/preservation/distribution projects

To use bioresources effectively, information on their whereabouts and characteristics is necessary. The Bioresource Information Division continuously provides BRC users with the newest information on BRC bioresources in the form of bio-digital-contents such as web-based catalogs, which can be updated at any time if necessary, in collaboration with the other divisions of BRC. The division also delivers and updates information for obtaining BRC resources, manuals, protocols, and announcements related to bioresources and BRC activities on the BRC web pages. (Fig.3)

In addition, to carry out a large number of resource distributions from BRC efficiently and smoothly, the Bioresource Information Division has developed a database system for resource distribution service, which it also manages. The system is continually refitted to catch up with changes in the service process and additions of new resources to BRC. (Fig.4)

In the 2005 fiscal year, the division developed a retrieval

system of poplar full-length cDNA clones, and added characteristic information of GSC mice and PCR protocol data to the mouse database, and sequence data to the DNA clone database.

In the 2006 fiscal year, the division opened the mouse phenotyping data (i.e., blood chemistry, blood hematology, and morphology measure) and image data of cell lines to the public from the web pages of the Experimental Animal Division and the Cell Engineering Division, respectively. It also developed a BLAST search system for plant cDNA/EST clones (i.e., Arabidopsis, moss, poplar, and tobacco) and retrieval systems of newly released bioresources, namely Arabidopsis transposon-tagged line homozygous seeds, CD34-positive human cord blood stem cells (HCH) and EBV-transformed B cell lines derived from Mongoloid Minority Groups in South America (Sonoda-Tajima Collection: HSC). The distribution service system was modified to introduce a special discount for large-volume orders of microbial cultures. In the 2007 fiscal year, the division developed the RIKEN BRC Mouse Phenome Database (RMPD) to provide mouse phenotyping data in a more visual and comprehensible form.



Figure 3. BRC homepage  
(<http://www.brc.riken.jp/inf/en/index.shtml>)

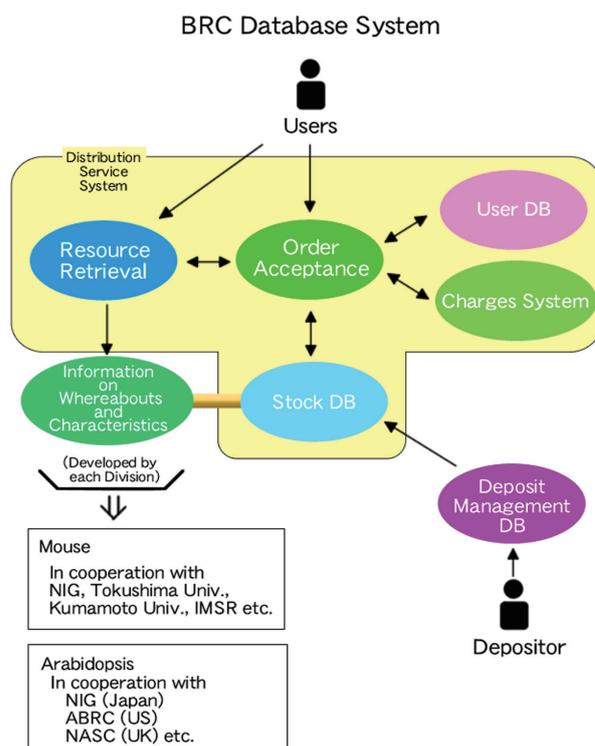
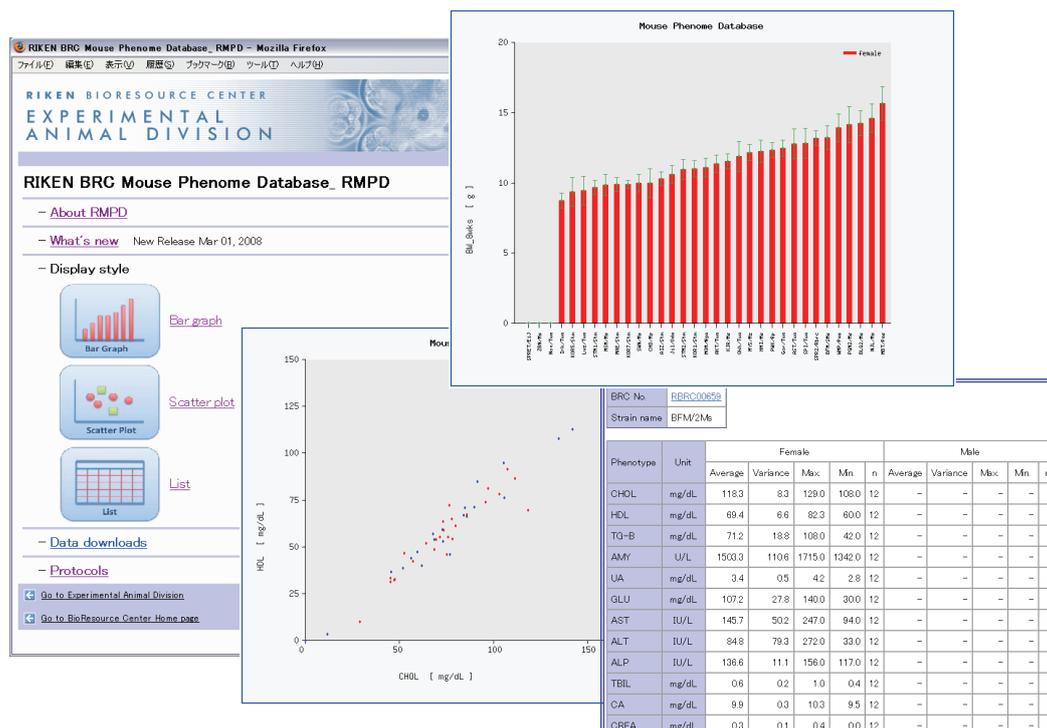


Figure 4. BRC resource database system



**Figure 5. RMPD (the RIKEN BRC Mouse Phenome Database) provides mouse phenotyping data (i.e., blood chemistry, blood hematology, and morphology measure) in a visual and comprehensive form.**

(Fig.5) It also prepared web-based catalogs for newly released bioresources, i.e., *Xenopus tropicalis* EST clones, cassava full-length cDNA clones, gene-trap mouse ES cell clones and a mouse iPS cell line; increased the number of images of mouse strains and cell lines available in the web-based catalogs of these resources; and completely reformed the retrieval system of mouse strains to improve its efficiency. As for ISO9001:2000, whose certification was delivered to the Cell Engineering Division and Microbe Division in August 2007, the division contributed to the achievement with the installation of a document server and its participation in internal audits.

In parallel with the above developments, the division continually updates information on the whereabouts and characteristics of BRC bioresources in order to offer their latest information to BRC users and ensure the reliability and sustainability of the BRC resource project.

## 2. Resource utilization promotion projects

The Bioresource Information Division develops software tools to reduce the burden on the BRC users when they obtain BRC bioresources. In the 2005 fiscal year, the division developed an order support system for DNA resources. It also developed a system for filling in forms necessary to resource

distribution such as MTA (Material Transfer Agreement) with user information registered through the User Registration System. Regarding the order support system for plant resources, the division added a function for downloading the MTA form in the 2006 fiscal year, and expanded its target to domestic users in the 2007 fiscal year. It also developed an order support system for domestic users of mouse resources, and is now developing a similar system for overseas users. Moreover, it developed a system for presenting on a web page a miniquestionnaire, which started operation on the web pages of the Cell Engineering Division. Answers to the questionnaire are summarized every month and made public on its web page.

In parallel with the above developments, the division provides technical support for bioresource public relations such as web page update, dispatch of BRC general catalogs and monthly delivery of e-mail news from the other divisions of BRC.

## 3. Resource information technology development projects

The Bioresource Information Division works on developing a one-stop shop in cooperation with other domestic and overseas organizations. The division keeps on sending updated data regularly to JMSR (Japan Mouse Strain Resources) and

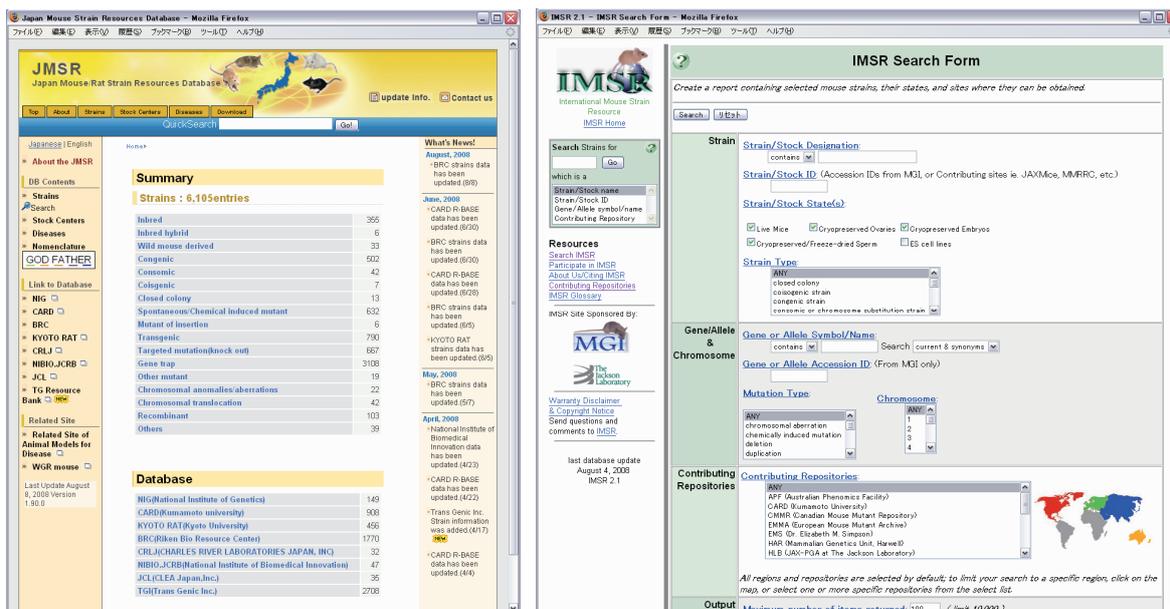


Figure 6. JMSR (Japan Mouse/Rat Strain Resources Database) and IMSR (International Mouse Strain Resource) web pages

IMSR (International Mouse Strain Resource), to which BRC participated in the 2004 fiscal year. JMSR and IMSR are consolidated databases that search the whereabouts of mouse resources preserved in various organizations in Japan and in the world, respectively. By using these databases, researchers will not have to access individual databases one by one. (Fig.6)

In the 2005 fiscal year, the division started to develop a system for collecting literature information published using BRC bioresources. Now the division surveys, analyzes and releases such literature information on the web pages of respective resource divisions in collaboration with the other divisions of BRC, while improving the system for faster and more efficient retrieval. As one of the quality controls of BRC cell lines, the division started to analyze genetic polymorphism among the cell lines by the Short Tandem Repeat-Polymerase Chain Reaction (STR-PCR) method in collaboration with the Cell Engineering Division. The analysis is continuously carried out and the latest results are made available on the web pages of the Cell Engineering Division. In the 2007 fiscal year, the division developed SABRE (Systematic consolidation of Arabidopsis and other Botanical Resources), where BRC plant gene resources are determined of their relation to TAIR (The Arabidopsis Information Resource) gene models and of their annotations through their sequence similarities. (Fig.7)

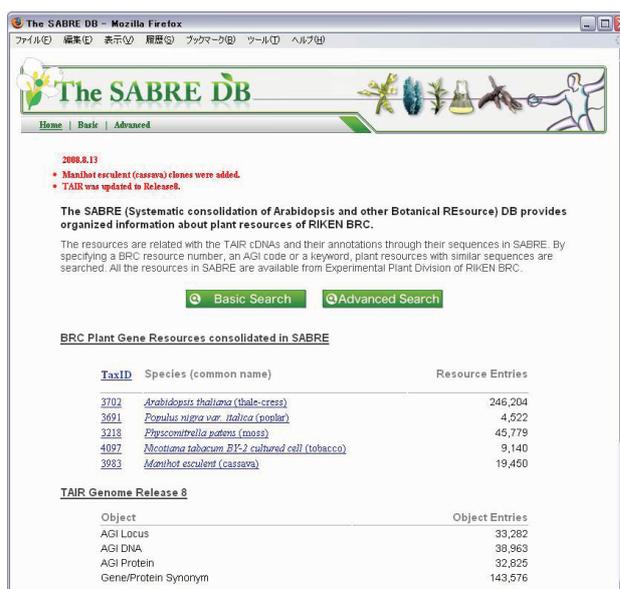


Figure 7. SABRE (Systematic consolidation of Arabidopsis and other Botanical Resources) homepage

## Publications

### 【Original Papers】 (\*Peer reviewed journals)

- Mise-Omata S., Obata Y., Iwase S., Mise N., Doi T. S.: "Transient strong reduction of PTEN expression by specific RNAi induces loss of adhesion of the cells." *Biochem Biophys Res Commun.* 328(4):1034-1042 (2005).
- Kiyosawa H., Mise N., Iwase S., Hayashizaki Y., Abe K.: "Disclosing hidden transcripts: mouse natural sense-antisense transcripts tend to be poly(A) negative and nuclear localized." *Genome Res.* 15(4):463-474 (2005).
- Fukami-Kobayashi K., Shiina T., Anzai T., Sano K., Yamazaki M., Inoko H., Tateno Y.: "Genomic evolution of MHC class I region in primates." *Proc Natl Acad Sci U S A.* 102(26):9230-9234 (2005).\*
- Yoshino K., Iimura E., Saijo K., Iwase S., Fukami K., Ohno T., Obata Y., Nakamura Y.: "Essential role for gene profiling analysis in the authentication of human cell lines." *Human Cell* 19, 43-48 (2006).\*
- Ezawa K., Oota S., Saitou N.: "Genome-wide search of gene conversions in duplicated genes of mouse and rat." *Mol Biol Evol.* 23, 927-940 (2006).\*
- Amano K., Nakamura H., Numa H., Fukami-Kobayashi K., Nagamura Y., Ichikawa H., Natsuo Onodera N.: "Self-organizing clustering: non-hierarchical clustering for large scale DNA sequence data." *IPSI Transactions on Bioinformatics.* 48, 49-53 (2007).\*
- Fukami-Kobayashi K., Minezaki Y., Tateno Y., Nishikawa K.: "A Tree of Life Based on Protein Domain Organizations." *Mol Biol Evol.* 24, 1181-1189 (2007).\*
- The Rice Annotation Project (Itoh T et al.) Curated Genome Annotation of *Oryza sativa* ssp. *japonica* and Comparative Genome Analysis with *Arabidopsis thaliana*. *Genome Res* 17 (2), 175-183 (2007).\*
- Matsuya, A. et al.(35 authors): Evola: "Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees." *Nucleic Acids Res* 36 (Database issue), D787-792 (2008).\*
- Rice Annotation Project (Tanaka, T. et al.) The Rice Annotation Project Database (RAP-DB): 2008 update, *Nucleic Acids Res* 36 (Database issue), D1028-1033 (2008).\*

## Oral Presentations

### 【International Conferences】

- Oota S., Ezawa K., Abe K., Noguchi H., Shiroishi T., Fukami - Kobayashi K., Moriwaki K., Watanabe H., Sakaki Y., Fujiyama A., Saitou N.: "Compositional evolution within/between human, chimpanzee, mouse and rat." HUGO's 10th Human Genome Meeting, Kyoto, Japan, Apr. (2005).
- Ezawa K., Oota S., Saitou N.: "Statistical analysis of gene conversion in mouse and rat genomes." HUGO's 10th Human Genome Meeting, Kyoto, Japan, Apr. (2005).
- Amano K., Nakamura H., Numa H., Nagamura Y., Ichikawa H., Fukami-Kobayashi K.: "Frame-Cluster Mapping: Genomewide Analysis for Detection of Localized Signal Regions." GIW2006, Yokohama, Japan, Dec. (2006).
- Kobayashi M., Abe H., Iuchi S., Kabayashi T., Tamura T., Oota S., Fukami-Kobayashi K.: "Current status of plant resource project in RIKEN BRC" 18th International Conference on Arabidopsis Research, Beijing, China, Jun. (2007).
- Oota S., Mekada K., Arai F., Obata Y., Fukami-Kobayashi K., Yoshiki A.: "FOUR-DIMENSIONAL QUANTITATIVE ANALYSIS ON THE GAIT OF

MUTANT MICE BY USING THE MOTION CAPTURE TECHNOLOGY.” 21st International Mammalian Genome Conference, Kyoto, Japan, Oct. (2007). (<http://www.imgc2007.com/>).

6. Oota S., Mekada K., Arai F., Fujita Y., Kawamura K., Obata Y., Fukami-Kobayashi K., Yoshiki A.: “Construction of a musculoskeleton model of mutant mouse hind limb for quantitative analysis on the gait pattern.” 31st Annual Meeting of the Japan Neuroscience Society, Tokyo, Japan, Jul. (2008).

**【Domestic Conferences】 Total 14**