Bioresource Information Division

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Head (July 2003 ∽)
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Head (∽ July 2003)

Goal

Due to the recent advances in the genome analysis, various kinds of research resources such as DNA clones, cell lines, and genetically modified organisms have been and are still being exhaustively developed. According as the bioresources are accumulated in the field of life science, their information is also accumulated so enormously that we cannot utilize it without information technology. It is thus an indispensable part of the formation of a basis of life science research to make the bioresource information open to public in the form of digital contents, such as web pages, databases together with user-friendly search engines, ftp files, etc.

Grounded on this perspective, the Bioresource Information Division collects information on whereabouts and characteristics of the bioresources preserved in RIKEN BRC, constructs web-pages and database systems for the information, and provides the research community with the "bio-digital-contents", linking with the related digital contents in and outside the country.

"Bio-digital-contents" will soon equal or surpass "bio-papers" in importance of source of knowledge in the field of life science. By providing up-to-date "bio-digital-contents" continuously, the Bioresource Information Division aims to contribute to the advancement of life science.

Activities

The Bioresource Information Division carries out the following projects.

I. Resource information collection/analysis/distribution projects

* Distribution of resource information through BRC databases and web pages.
* Collection and update of resource information and software.
* Assistance of information technology to resource distribution service.

II. Resource utilization promotion projects

* Development of software to facilitate the utilization of the BRC bioresources.
* Assistance for resource information analysis.

III. Resource information technology development projects

* Development of technologies to construct consolidated resource databases.
* Development of technologies for resource information analysis.

Members

Senior Scientists, Heads of Bioresource Information Division

Kaoru FUKAMI, Ph. D. (2003.7 ～)

Yuichi OBATA, Ph. D. (2001.4 ～ 2003.7)

Senior Visiting Scientist

Yoshihiro UGAWA, Ph. D. (2001.11 ～)

Research Scientists

Shigeru IWASE, Ph. D. (2002.1 ～)　　Satoshi OOTA, Ph. D. (2003.10 ～)

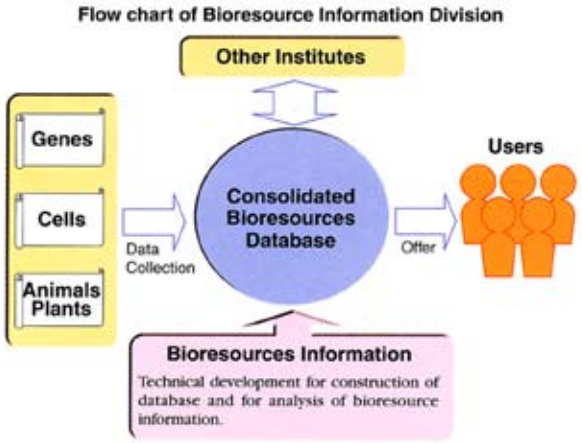
Senior Technical Scientist

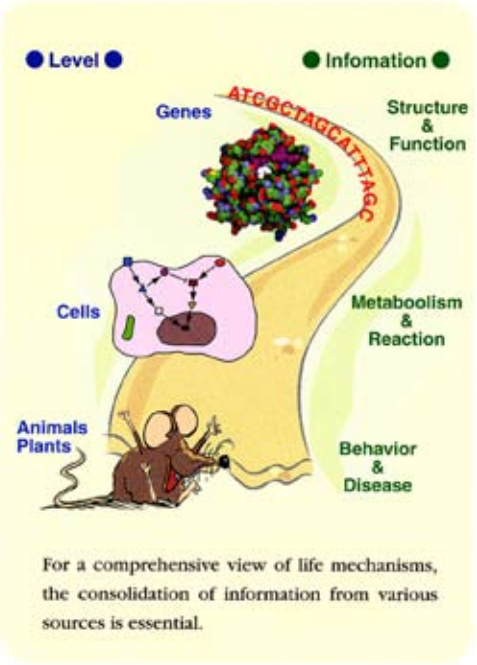
Mamoru NOGUCHI (2001.4 ～)

Technical Staff

Naomi YUHARA(2005.4 ～)

Nakano, Nakata, Noguchi, Ichiishi, Takahashi, Sugiyama, Matsuno, Nobayashi, Oota, Fukami, Uno, Iwase, Yuhara



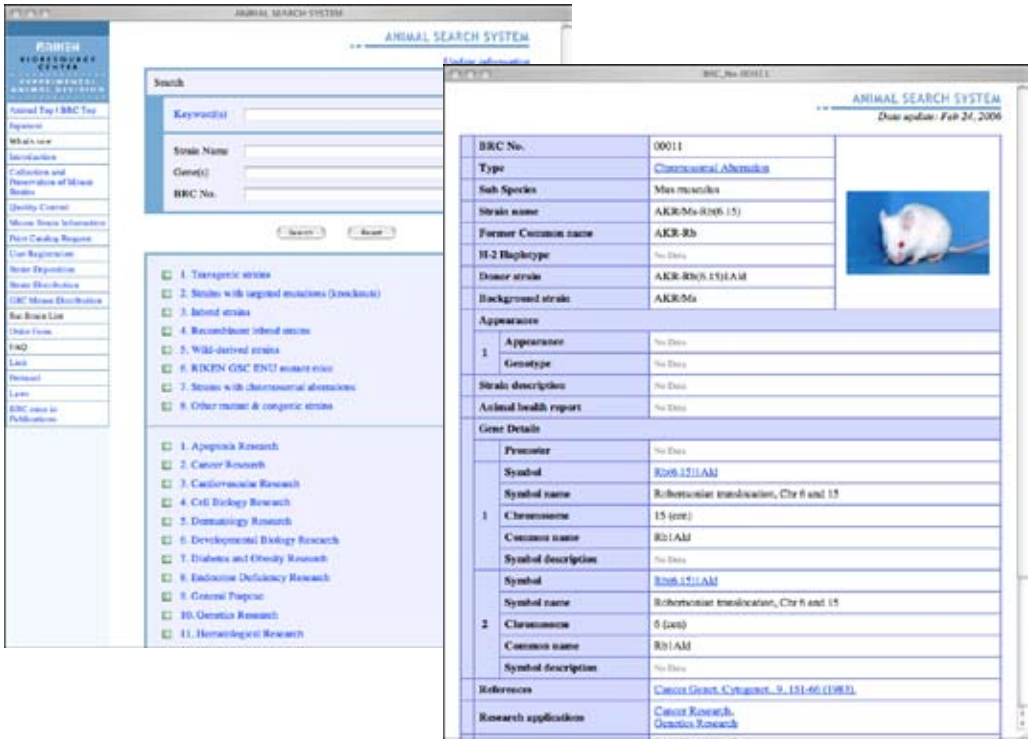


Specific aim

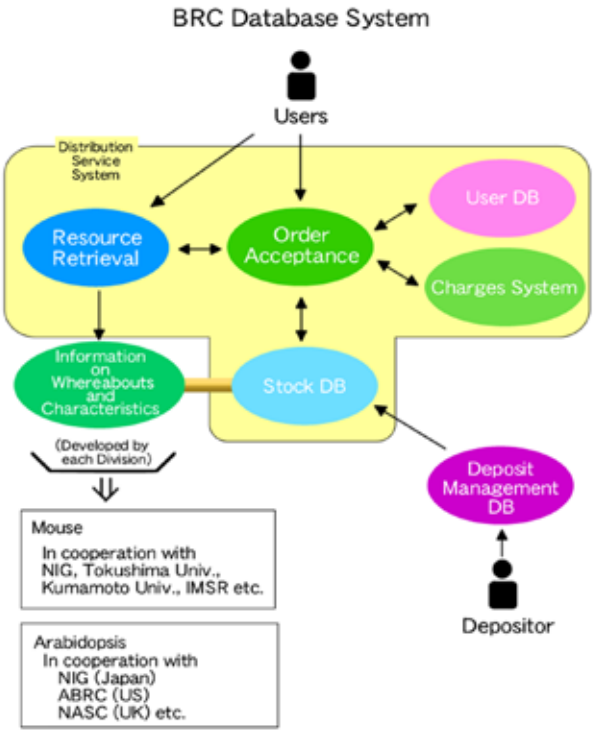
1) Resource information collection/analysis/distribution projects

To use bioresources effectively, information on their whereabouts and characteristics is necessary and indispensable. The Bioresource Information Division continuously provides the BRC users with the newest bioresource information in BRC in the form of on-line catalogues through web pages. The division delivers and updates information for obtaining the BRC resources, manuals, protocols, and announcements related to bioresources and BRC activities on the BRC web pages .

In 2004 fiscal year, the division enhanced the retrieval systems of mice and DNA clones in order to offer more addressed and detailed resource information to the BRC users. It also enhanced the retrieval system of RIKEN Arabidopsis full-length cDNA (RAFL) clones to deal with clones whose 3'- or 5'-sequence is available. It developed the retrieval systems of the newly released bioresources, human mesenchymal stem cells (HMS), human cord blood stem cells (HCB) and human B lymphocytes transformed by Epstain-Barr Virus (HEV). The SENDAI Arabidopsis Seed Stock Center (SASSC) was transferred from the National Institute of Genetics and started its operation in BRC. In 2005 fiscal year, the division developed the retrieval system of poplar full-length cDNA clones, and added characteristics information of GSC mice and PCR protocol data to the mouse database and sequence data to the DNA clone database respectively. In parallel with



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



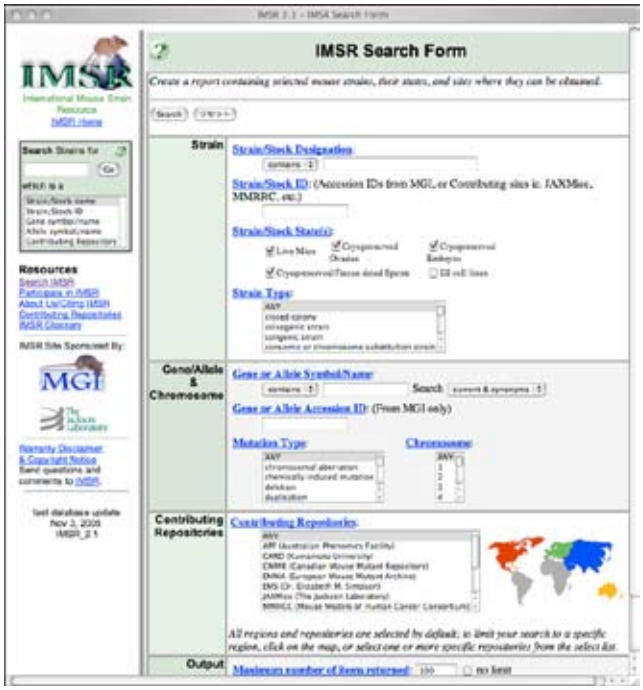
The Bioresource Information Division also develops database systems for resource distribution service from BRC. The system is continually refitted to catch up with alteration of the service process and addition of new resources in BRC. In 2004 fiscal year, the division improved the data structure of the cell distribution system, and then integrated information of mice and DNA clones to the system in order to use it for their distribution and develop the BRC database system. The information of stem cells was also integrated into the system along with the start of their distribution from BRC. In addition, as JCM (Japan Collection of Microorganisms) changed its affiliation to BRC, integration of information on microorganism distribution service was conducted. The BRC database system was transferred to a new server on March 2005 because of the replacement of the computer system of Tsukuba Institute.

2) Resource utilization promotion projects

The Bioresource Information Division develops software tools to reduce the burden on the BRC users when they obtain the BRC bioresources. In 2004 fiscal year, an order support system was developed for the plant resource. In 2005 fiscal year, a similar system was developed for the DNA resource. The division also developed a system to fill in the forms necessary to resource distribution such as MTA (material transfer agreement) with user information registered through the User Registration System .

3) Resource information technology development projects

The Bioresource Information Division works on developing one-stop-shop in cooperation with other domestic and foreign organizations. In 2004 fiscal year, participation to JMSR (Japan Mouse Strain Resources) and IMSR (International Mouse Strain Resource) was accomplished. JMSR and IMSR are consolidated databases that searches whereabouts of mouse resources preserved in various organizations in Japan, and in the world, respectively. By using these databases, researchers will not need to access individual databases one by one. Now the division keeps on sending updated data regularly to these databases. In addition, the division works on developing new technology to extract biologically significant information from various experimental data obtained from many kinds of bioresources.



Publications

Original Papers (* Peer reviewed Journal)

1. Fukami-Kobayashi, K., Tateno, Y., Nishikawa, K.: “Parallel evolution of ligand specificity between LacI/GalR family repressors and periplasmic sugar-binding proteins”, Molecular Biology and Evolution 20, 297-277 (2003).*

2. Watanabe H, Fujiyama A, Hattori M, Taylor TD, Toyoda A, Kuroki Y, Noguchi H, BenKahla A, Lehrach H, Sudbrak R, Kube M, Taenzer S, Galgoczy P, Platzer M, Scharfe M, Nordsiek G, Blocker H, Hellmann I, Khaitovich P, Paabo S, Reinhardt R, Zheng HJ, Zhang XL, Zhu GF, Wang BF, Fu G, Ren SX, Zhao GP, Chen Z, Lee YS, Cheong JE, Choi SH, Wu KM, Liu TT, Hsiao KJ, Tsai SF, Kim CG, OOta S, Kitano T, Kohara Y, Saitou N, Park HS, Wang SY, Yaspo ML, Sakaki Y; DNA sequence and comparative analysis of chimpanzee chromosome 22. Nature. 2004 May 27; 429(6990): 382-388. *

3. Kashiwagi K, Fukami-Kobayashi K, Shiba K, Nishikawa K; Construction and characterization of chimeric proteins composed of type-1 and type-2 periplasmic binding proteins MglB and ArgT. Biosci Biotechnol Biochem. 2004; 68(4): 808-813. *

4. Imanishi T, Itoh T, Suzuki Y, O'Donovan C, Fukuchi S, Koyanagi KO, Barrero RA, Tamura T, Yamaguchi-Kabata Y, Tanino M, Yura K, Miyazaki S, Ikeo K, Homma K, Kasprzyk A, Nishikawa T, Hirakawa M, Thierry-Mieg J, Thierry-Mieg D, Ashurst J, Jia L, Nakao M, Thomas MA, Mulder N, Karavidopoulou Y, Jin L, Kim S, Yasuda T, Lenhard B, Eveno E, Suzuki Y, Yamasaki C, Takeda J, Gough C, Hilton P, Fujii Y, Sakai H, Tanaka S, Amid C, Bellgard M, Bonaldo Mde F, Bono H, Bromberg SK, Brookes AJ, Bruford E, Carninci P, Chelala C, Couillault C, de Souza SJ, Debily MA, Devignes MD, Dubchak I, Endo T, Estreicher A, Eyras E, Fukami-Kobayashi K, Gopinath GR, Graudens E, Hahn Y, Han M, Han ZG, Hanada K, Hanaoka H, Harada E, Hashimoto K, Hinz U, Hirai M, Hishiki T, Hopkinson I, Imbeaud S, Inoko H, Kanapin A, Kaneko Y, Kasukawa T, Kelso J, Kersey P, Kikuno R, Kimura K, Korn B, Kuryshev V, Makalowska I, Makino T, Mano S, Mariage-Samson R, Mashima J, Matsuda H, Mewes HW, Minoshima S, Nagai K, Nagasaki H, Nagata N, Nigam R, Ogasawara O, Ohara O, Ohtsubo M, Okada N, Okido T, OOta S, Ota M, Ota T, Otsuki T, Piatier-Tonneau D, Poustka A, Ren SX, Saitou N, Sakai K, Sakamoto S, Sakate R, Schupp I, Servant F, Sherry S, Shiba R, Shimizu N, Shimoyama M, Simpson AJ, Soares B, Steward C, Suwa M, Suzuki M, Takahashi A, Tamiya G, Tanaka H, Taylor T, Terwilliger JD, Unneberg P, Veeramachaneni V, Watanabe S, Wilming L, Yasuda N, Yoo HS, Stodolsky M, Makalowski W, Go M, Nakai K, Takagi T, Kanehisa M, Sakaki Y, Quackenbush J, Okazaki Y, Hayashizaki Y, Hide W, Chakraborty R, Nishikawa K, Sugawara H, Tateno Y, Chen Z, Oishi M, Tonellato P, Apweiler R, Okubo K, Wagner L, Wiemann S, Strausberg RL, Isogai T, Auffray C, Nomura N, Gojobori T, Sugano S; Integrative annotation of 21,037 human genes validated by full-length cDNA clones. PLoS Biol. 2004 Jun; 2(6):856-875. *

5. Mise-Omata S, Obata Y, Iwase S, Mise N, Doi TS; Transient strong reduction of PTEN expression by specific RNAi induces loss of adhesion of the cells. Biochem Biophys Res Commun. 2005;328(4):1034-1042.

6. 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. 2005;15(4):463-474.

7. 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. 2005 Jun 28;102(26):9230-4. *

Oral Presentation

1. Satoshi Oota, Kiyoshi Ezawa, Kuniya Abe, Hideki Noguchi, Toshihiko Shiroishi, Kaoru Fukami-Kobayashi, Kazuo Moriwaki, Hidemi Watanabe, Yoshiyuki Sakaki, Asao Fujiyama, Naruya Saitou.`' Compositional evolution within/between human, chimpanzee, mouse and rat'. HUGO's 10th Human Genome Meeting Kyoto, Japan (18-21 April 2005).