

Bioresource Information Division

Kaoru FUKAMI

Senior Scientist, Head of Bioresource Information Division (July 2003 ~)

Yuichi OBATA

Senior Scientist, Head of Bioresource Information Division (~ July 2003)

Goal

Due to the recent advances in the genome analysis, various kinds of research resources such as genes, proteins, cells, and whole organisms have been produced. According as these bioresources are accumulated in the field of life science, they are coming to occupy more important positions in the field, and so is the information about the bioresources. It is thus a great contribution toward the advancement of the life sciences to make the information open to public in the form of a database together with a user-friendly retrieval system.

Grounded on this perspective, the Bioresource Information Division collects information on traits and locations of the bioresources preserved in RIKEN BRC, and other domestic and foreign organizations. The division is also working on constructing a database system for the information, linking with the related databases in and outside the country. By providing the research community with the database system, the division aims to promote the formation of a basis of life science research.

Activities

The Bioresource Information Division carries out the following projects.

I. Resource information assistance projects

- * Collection and management of resource information and analytical software.
- * Information distribution through the databases.
- * Assistance for resource information analysis.

II. Resource information technology development projects

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

Members

Senior Scientists, Heads of Bioresource Information Division

Kaoru FUKAMI, Ph. D. (2003.7 ~)

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

Research Scientists

Shigeru IWASE, Ph. D. (2002.1 ~)

Satoshi OOTA, Ph. D. (2003.10 ~)

Senior Technical Scientists

Mamoru NOGUCHI (2001.4 ~)

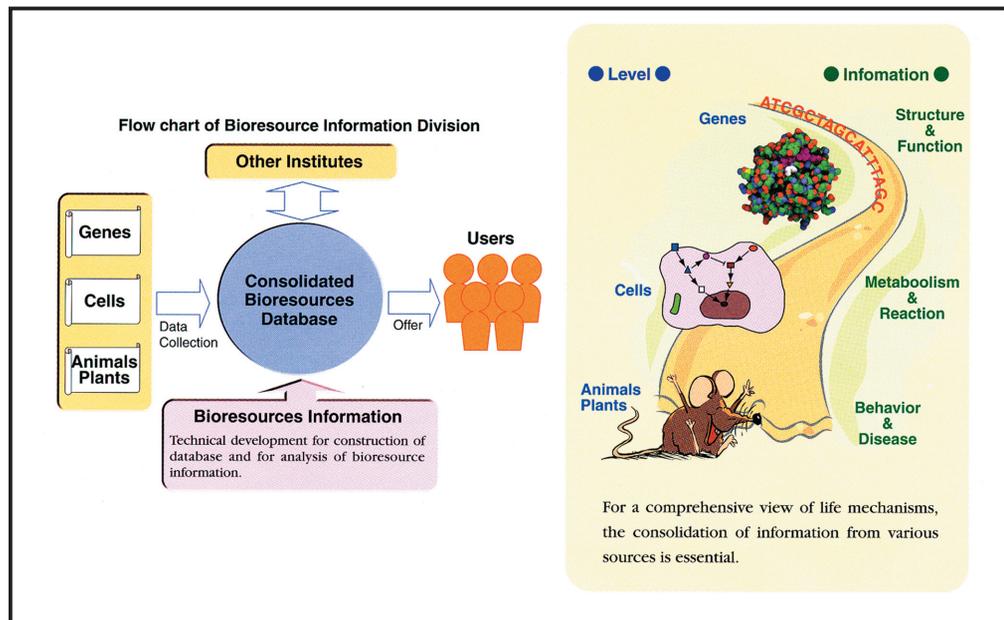
Toako USUI (2002.4 ~ 2003.3)

Senior Visiting Scientist

Yoshihiro UGAWA, Ph. D. (2001.11 ~)



Matsuno, Noguchi, Ichiishi,
Iwase, Fukami, Oota



Specific aim

1) Resource information assistance projects

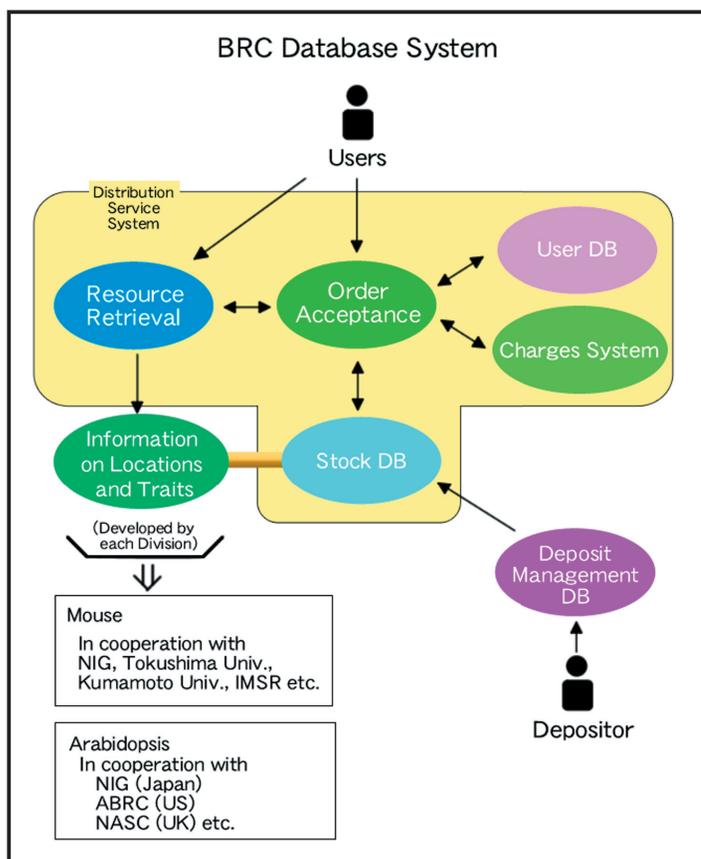
In addition to distribution of cell and genetic resources, BRC started distribution of laboratory animal and plant resources in the 2002-03 fiscal year. The Bioresource Information Division has been working on support for information management and development of software tools necessary to carry out the distribution of these bioresources. The division is also working on integration of these tools to develop a system with better information retrieval.

The division innovated a new system in information management of the distribution of cell resources on October 2002, and is now working on improvement of the system through its practical use.

Most bioresources collected by BRC have information on their biological features described by researchers, which is highly useful for execution of research. This is one of the advantages of BRC, where bioresource can be distributed along with their traits and other biological information. The division is planning to link the information derived from laboratory animal, plant, cell and genetic resources to obtain further information or biological findings.

2) Resource information technology development projects

The Bioresource Information Division is also working on development of a retrieval system, in collaboration with some organizations such as National Institute of Genetics, that searches locations of bioresources preserved in various organizations in Japan, by unifying their databases. The primary purpose of the development is to make the bioresources in Japan easier to retrieve: researchers will not need to access individual databases one by one if they are unified. The secondary purpose is to inspect consistency of the databases to be unified, resulting in improvement of the quality of individual databases. The unified database will provide us with better environment to survey information from various organisms and will facilitate extraction of biological significant findings. The division is now planning to unify mouse and Arabidopsis databases.



Publications

Original Papers (*Peer reviewed journal)

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2. Song J., Ugai H., Ogawa K., Wang Y., Sarai A., Obata Y., Kanazawa I., Sun K., Itakura K. and Yokoyama K. K.: "Two consecutive zinc fingers in Sp1 and in MAZ are essential for interactions with cis-elements", *J. Biol. Chem.* 276, 30429 - 30434 (2001).*
3. Tsujimura K., Obata Y., Matsudaira Y., Ozeki, S., Yoshikawa K., Saga S. and Takahashi T.: "The binding of thymus leukemia (TL) antigen tetramers to normal intestinal intraepithelial lymphocytes and thymocytes", *J. Immunol.* 167, 759 - 764 (2001).*
4. Fukami-Kobayashi, K.: "Getting functional information from your sequence by the use of protein signature databases", *Protein, Nucleic Acid and Enzyme* 46, 2098-2103 (2001).

5. Ota S, Li WH.: "NJML+: an extension of the NJML method to handle protein sequence data and computer software implementation", *Molecular Biology and Evolution* 18, 1983-1992 (2001).
6. Yasuda M., Takenoyama M., Obata Y., Sugaya M., So T., Hanagiri T., Sugio K. and Yasumoto K.: "Tumor-Infiltrating B Lymphocytes as a Potential Source of Identifying Tumor Antigen in Human Lung Cancer", *Cancer Res.*62, 1751-1756 (2002).*
7. Usui T.: "Inhibitory Glutamate Responses in Abdominal Muscles of the Larval Mealworm *Tenebrio molitor* L. (Coleoptera: Tenebrionidae)", *Jpn. J. Appl. Entomol. Zool.* 46, 153-158 (2002).*
8. Fukami-Kobayashi, K., Schreiber, D.R., Benner, S.A.: "Detecting compensatory covariation signals in protein evolution using reconstructed ancestral sequences", *Journal of Molecular Biology* 319: 729-743 (2002). *
9. Fukami-Kobayashi, K.: "How to make good use of CLUSTALW", *Protein, Nucleic Acid and Enzyme* 47, 1237-1239 (2002).
10. Yu N, Chen FC, Ota S, Jorde LB, Pamilo P, Patthy L, Ramsay M, Jenkins T, Shyue SK, Li WH., "Larger genetic differences within africans than between Africans and Eurasians", *Genetics* 161, 269-274 (2002).
11. 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).