



youkihi

April 2006

 BioResource now! Vo2.No.4 is here

- Information on Resource-related Events :
- Introduction to Resource Center No. 8 :
 - Special Report on Drosophila
Masatoshi Yamamoto, Director of Drosophila Genetic Resource Center, Kyoto Institute of Technology
- Ongoing Column Vol. 13:
 - Bioinformatics in 10 minutes

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<http://www.shigen.nig.ac.jp/shigen/news/news.jsp>

Other information on bioresources is available at
 NBRP (<http://www.nbrp.jp/index.jsp>)
 SHIGEN (<http://www.shigen.nig.ac.jp/indexja.htm>)
 WGR (<http://shigen.lab.nig.ac.jp/wgr/>)
 JGR (<http://shigen.lab.nig.ac.jp/wgr/jgr/jgrUrlList.jsp>)

Information on Resource-related Events

- May 6, 2006
NBRP Symposium at Hotel Granvia Osaka "Post-Genome Research on Yeast and Bioresources"
- May 11-13, 2006
The Japanese Association for Laboratory Animal Science Panel Exhibition at the International Conference Center Kobe
"The Bioresources of Laboratory Animals: The Present Situation and Outlook" is in the planning stage
- May 22-23, 2006 FiMre at RIKEN BRC

Detailed information is available at <http://www.nbrp.jp/index.jsp>

Introduction to Resource Center No. 8

Recent Trends at the Drosophila Genetic Resource Center

Masatoshi Yamamoto
 Director of Drosophila Genetic Resource Center,
 Kyoto Institute of Technology



Drosophila Genetic Resource Center (DGRC)
<http://www.DGRC.kit.ac.jp/>

[1] Website Renewal

This website was launched immediately after the Drosophila Genetic Resource Center was established as a facility in the Kyoto Institute of Technology by the order of the Ministry of Education, Culture, Sports, Science and Technology (MEXT) in 1999 and has been regularly updated since then. In April this year, the website was renewed. Consequently, the "What's New" articles can be posted more rapidly and conveniently than before.

At the lower left corner of the homepage, there is a link to a website called "Flystock." This website contains an integrative database that lists the Drosophila strains maintained at the primary institute (Drosophila Genetic Resource Center, Kyoto Institute of Technology) and the secondary institutes (National Institute of Genetics, Ehime University, and Kyorin University), which promote the National BioResource Project (NBRP) "Drosophila." This database enables the search of Drosophila strains that are preserved at the major institutes in the country as well as receive orders for strains. Although this database currently does not cover all the maintained strains, a new, more efficient and powerful Drosophila database is under construction and will be launched soon.



[2] The Advantages of Actively Accepting Deposited Strains

The endeavor of this center and its collaborative institutes came to fruition due to NBRP. The Drosophila Genetic Resource Center has developed into a center with the biggest number of maintained strains (in fiscal year 2005) in the world, and we rank second only to the Bloomington Drosophila Stock Center at Indiana University in the United States with respect to the number of provided strains.

Many deposited strains that have been developed by domestic researchers are unique and useful, and most importantly, featuring excellent characteristics of the respective strains. In order to develop and expand as a genetic resource center on a global scale, genetic resources should be of high quality. In this regard, we deeply appreciate the support and consideration of the domestic researchers.

"The Drosophila Genetic Resource Center is an incubator for your lab." This statement is used to introduce our undertakings in supporting researchers and to clearly convey the objectives of this center. Our objective is to efficiently maintain the flow of providing strains to promote researches and facilitating the deposit of those research achievements back to the center so that it would contribute to other researches.

In order to ensure that generated or developed strains obtained as research achievements are used efficiently as genetic resources, we should actively welcome researchers to deposit strains. Our undertakings include requesting strain deposition and receiving the deposited strains as well as releasing and providing the deposited strains.

We plan to release information on the deposited Drosophila strains together with other related information such as journal articles which describe the development of the strains (on DGRC or Flystock). When searching for strains, the search result from the strain database will include literature references and allow users to order the strains. The user will then have sufficient information regarding the depositor's literature when requesting for the strains and therefore, when a research achievement is published as a journal article, the depositor's literature citations will increase. Thus, we are employing a method that would benefit the strain depositor by increasing the citation count of the literature.

[3] Completion of the Gakudo Hall and the Memorial International Symposium



As mentioned on the Drosophila Genetic Resource Center (<http://www.dgrc.kit.ac.jp/jp/nbrp/topics/000049.html>) website and on the public information website of NBRP, the Gakudo Hall was built on the Saga campus of the Kyoto Institute of Technology with contributions from Nippon Shinyaku Co., Ltd., and the completion ceremony was conducted on March 6, 2006. The description of the ceremony is available on the university's website (<http://www.kit.ac.jp/01/topics/2005/gakudou/gakudou060315.html>).



The view of the Gakudo Hall from the mulberry field located southward.

Gakudo Hall is named after "Gakudo Yojin (Hints on learning Buddhism)," which was taught by Dogen Zenji, in hopes that the hall will develop into a venue for international interaction where researchers who seek scientific facts can genuinely discuss their work and pursue their duties and social responsibilities. It is known that the propagation of Buddhism in Japan was initiated at Mt. Hiei; therefore, the Buddhist priest of the highest order, Ryusho Kobayashi, a retired executive of Enryakuji at Mt. Hiei, was asked to write the name on the name plate. He graciously accepted our request. His powerful spirit belies his age of 78 years. We would like to reiterate our appreciation to him. We can well understand the feeling of tension that he must have experienced in accepting our request because writing on a cypress board allows no room for mistakes, as opposed to writing on paper.

As inferred from the name, "Gakudo Hall," the then CEO of Nippon Shinyaku and the anonymous benefactors disliked the idea of naming the hall after the company. However, we wish to express our gratitude for their donation and therefore have considered using a logo that represents "Nippon Shinyaku's 14 selected herbs" (Yaku so juyon sen). Nippon Shinyaku Co., Ltd. declared that they have grown and developed because of the benefits offered by plants, and they selected 14 primary herbs to represent their company on their 80th foundation anniversary. As a token of our appreciation to Nippon Shinyaku, representative herbs were selected from these 14 herbs, and denoted on the room identification plates, adding colors to the insipid name plates. The herb designs were provided by the Institute for Botanical Research at Yamashina, Nippon Shinyaku Co., Ltd.



Ribbon cutting at the completion ceremony of the Gakudo Hall.

Kazuto Hatsuyama, President, Nippon Shinyaku Co., Ltd. (center); Mr. Shigeru Kure, Director of Genome Research, Life Science Division, Ministry of Education, Culture, Sports, Science And Technology (MEXT) (right of the center); and Yoshimichi Ejima, President of the Kyoto Institute of Technology (left of the center).



The Buddhist priest of the highest order, Ryusho Kobayashi (left), stands at the entrance in front of the stele on which "Toei Joubutsu" was engraved to have the honor of seeing the Konpon Chudo. February 24, 2006.



A tablecloth with the designs of the 14 selected herbs on it, and the room identification plates placed in Gakudo Hall; these were manufactured for the 80th foundation anniversary of Nippon Shinyaku Co., Ltd.

The 1st International Seminar at the Gakudo Hall



Three prominent Drosophila researchers were invited for the memorable international seminar. The first researcher to be invited was Distinguished Professor emeritus Thomas Kaufman from the Bloomington Stock Center at the Indiana University in the United States. It is practically the world's largest strain center and provides Drosophila strains which are trusted and utilized by all researchers. The Drosophila Genetic Resource Center and the Bloomington Stock Center mutually hold important strains and conduct discussions on future administrative plans as international strain centers. Thomas Kaufman is a prominent researcher of the homeobox genes in embryology, and he is currently conducting a research on the evolution of insects.

The second researcher to be invited was Professor Asa Rasumuson-Lestander. Prior to the approbation of the Drosophila Genetic Resource Center by MEXT in 1999, Umea University in Sweden faced difficulties in acquiring research funds from the EU and the stock center that had maintained numerous strains with chromosome aberrations was closed. In Japan, the public hearing of MEXT was still going on and the future prospects had not been envisioned yet. However, since the loss of the strains at Umea University would have been a substantial loss, I asked Professor Asa to somehow retain the strains for another year and promised to accept all the strains in Kyoto later. In addition to organizing the center within the budget, I had to make considerable efforts to obtain the certificate for the building and the facility of the center. Meanwhile, Professor Asa was maintaining the strains by utilizing her personal research fund. We were desperate to hold on to the strains; however, it is wonderful to reminisce about how we have developed a strong mutual trust in each other. The sustenance of our relationship can be credited to Professor emeritus Mel Green who played an important role in solidifying our mutual trust. Professor Mel and I have been discussing the necessity of having a strain center since 1990 and it was his consideration that facilitated the formation of a personnel foundation for accumulating information on the strain center from Umea University and Indiana University; this initiative enabled drafting of important documents for public hearing at MEXT.





The third researcher to be invited was Professor emeritus Dan Lindsley, the author of "The Bible," which is a must-have for Drosophila researchers. Together with "The Mutants of Drosophila melanogaster" by Bridges, "Genetic Variations of Drosophila melanogaster" and "The Genome of Drosophila melanogaster" are known as "The Red Book" or "The Bible." Later, these

books were digitized, and they became the basis for the construction of the current FlyBase. Currently, Professor Dan Lindsley is 80 years old. He had to return to his country immediately after the international symposium because he did not have an assistant who could observe the flies in his ongoing experiment; thus, he returned to continue and supervise his experiment.



The southern side of the huge training room in the Gakudo Hall has glass windows, and the room has a high ceiling. During the symposium, the room was bright with a pleasant atmosphere, and the symposium received an enthusiastic response.

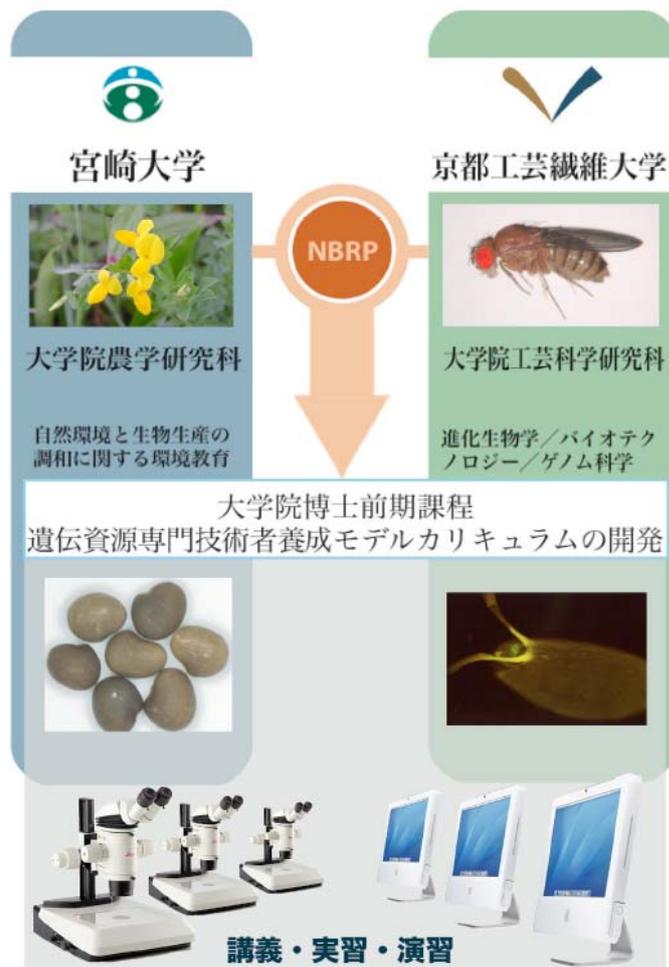
[4] Program for Genetic Resource Education and Development



The goals of NBRP are maintaining genetic resource and controlling their quality, and also establishing a system to supply reliable strains whenever they are required. When such a system is established, it is common for researchers who are in a hurry to begin their study to utilize the strains obtained from the resource center immediately without inspecting them. However, this is a precarious situation, and a fundamental feature of biology, which is that organisms continuously undergo mutation, may be forgotten. The consolidation of the genetic resources tends to reduce the number of human resources with detailed knowledge of genetic resources. Due to the competitive environment in the scientific research community, which has recently been in question, the priority is to accomplish results by utilizing any useful tool as soon as possible. Naturally, maintenance and control of high-quality genetic resources should be expected. However, researchers should recognize the fact that organisms do change and inspect research materials before using them for experiments. If the researchers provide feedback on the state of the resource that they received, that would aid the maintenance of strains at a higher quality.

Under such circumstances, the Graduate School of Science and Technology at the Kyoto Institute of Technology have collaborated with the Graduate School of Agriculture at the University of Miyazaki since 2006 to initiate the "Program for Genetic Resource Education and Development" to develop a model curriculum for training skilled professionals.

Kyoto Institute of Technology and University of Miyazaki are the primary institutes of NBRP for *Drosophila* and *Lotus japonicus*, respectively; these are experimental animal and plant models with distinctive small-sized features. With the objective of producing skilled engineers, lectures on biological resources, biodiversity and environment and their related regulations that aim to cover fundamental topics necessary for the handling of extensive organism species are incorporated into the curriculum. Seminars on animal genetic resource are conducted at the Kyoto Institute of Technology while seminars on plant genetic resource in University of Miyazaki. Students move around the concerned universities to attend the seminars.



Curator is a person in charge of important preserved materials and research resources at a museum, art gallery, or a research institute and denotes a skilled professional such as the director or a responsible museum attendant.



Maintained Resources



DGRC (Kyoto Institute of Technology)	14,492 strains
Basic strains	4,001
NP Lines (Gal4 enhancer trap)	1,973
GS Lines (Gene Search System)	4,572
Protein Trap Lines	369
LA Gene- induce (with y+ marker)	938
Others	2,639
NIG-Fly (National Institute of Genetics)	5,633 strains
NP Lines (Gal4 enhancer trap)	2,715
RNAi strains	2,037
Mutant strains	881
EHIME-Fly (Ehime University)	488 strains
Wild type Drosophila from Japan	53 species 412 strains
KYORIN-Fly (Kyorin University)	459 strains
Wild-type strains : 255 strains	
Drosophila melanogaster species group	
Drosophila ananassae species subgroup	
Subgenus Drosophila	
Genus Chymomyza	
Mutant strains : 204 strains	
Drosophila. ananassae species subgroup	
Drosophila auraria complex	
Drosophila hydei	

(from Flystock)



Announcement of the Next Issue



Special edition on Yeast !
Faculty of Sciences,
Osaka City University



Editor's Note :

Drosophila is possibly one of the biological resources that have been used for the longest time. The individual size of Drosophila is small, the generation time is short (approximately two weeks), and breeding is relatively easy; thus, Drosophila are particularly appropriate for hybridization experiments that are necessary in genetics. In genetics, knowledge gained using Drosophila led to the development of molecular biology, neural biology, and developmental biology. Another factor that supports the Drosophila research community is that the community has created a research environment wherein researchers can easily obtain the necessary resources. The Kyoto Institute of Technology is a part of this community, and it plays an important role as a representative institute in Japan.

Another characteristic of Drosophila research in the 21st century is its contribution in bioinformatics. The database for Drosophila, namely, Flybase is a famous integrative database of model organisms known to all biologists. Recently, the activities in bioontology that enables the utilization of interspecies information have progressed. Drosophila, as the forefront life science, will continue to fly into the future. I would like to sincerely thank Dr. Yamamoto for contributing in spite of his busy schedule. (Y. Y.)

Contact Address:

1111 Yata, Mishima-shi, Shizuoka 411-8540, Japan

Center for Genetic Resource Information, National Institute of Genetics

Tel: 055-981-6885 (Yamazaki)

E-mail: BRnews@chanko.lab.nig.ac.jp

Information Technology

Vol. 13



"Bioinformatics"

"Sequence Manipulation using Cygwin (Windows)"

In the previous issue, I have demonstrated the use of a terminal window on Mac OS X which might not have been useful to Windows users. In this issue, I will explain the use of a terminal or a UNIX-like environment on Windows. Cygwin enables us to experience UNIX or LINUX on Windows machines.

1

Download the installer (setup.exe) from <http://www.cygwin.com/> and double-click on the icon. After that, click as instructed to complete the installation. (The installation process takes some time. For detailed descriptions of the installation procedure, please type the keyword cygwin on search engines such as Google, and refer to the numerous websites that contain detailed descriptions.)

2

Once the installation is complete, double-click the "Cygwin" icon (a shortcut) that appears on the desktop to initiate it. A black screen will be displayed.

3

Type the following on the black screen and press Enter.

```
$mkdir test
```

4

Type the following on the black screen and press Enter.

```
$ls
```

Then, the word typed in step 3, "test," along with some other words will be displayed. Here, the words displayed indicate a file or a folder. The previous command "mkdir test" will create a folder named "test".

5

Type the following on the black screen and press Enter.

```
$cd test
```

The command cd is a command to move to another directory, and in this case, it implies moving into the "test" folder. Now, you are located in the "test." folder. The question that arises is where is this "test" folder located? Go to My Computer→Local Disc (C:)→Documents and Settings→"your user name" and check if the folder, "test," has been created.

6

Next, as indicated in the title of this bioinformatics section, let us try to manipulate a base sequence. Open the "test" folder and right-click on New→Text Document to create a new text document. Once the file is created, change the file name to "sequence." In the "sequence" file, copy an arbitrary base sequence (in one byte Roman characters) (no line feed or space should be added). Now the file is ready for use.

7

Now, let us count the number of bases in the base sequence that we have saved in the "sequence" file. Type the following and press Enter. The number of bases (letters) will be shown.

```
$wc -c sequence.txt
```

8

Finally, let us excise a part of the base sequence (5th to 10th letter). Type the following on the black screen and press Enter. The 5th to 10th letters will be shown.

```
$cut -c 5-10 sequence.txt
```

In the previous and current series, we have tried working in a UNIX- or LINUX-like environment. Currently, UNIX or LINUX is used frequently in bioinformatics. In addition, it is considered that the researchers currently working on wet experiments (conducting experiments using actual biological materials) will require knowledge of the dry experiments (conducting experiments or data processing using computers). It would be great if these series sparked interest in UNIX or LINUX and encourage readers to explore the field of bioinformatics. (Shingo Sakaniwa)