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Hot News from Abroad No. 21

- Visit to Indiana University -

Ryu UEDA, Prof. Invertebrate Genetics Laboratory,
National Institute of Genetics

Last October, I visited Indiana University (IU), Bloomington, Indiana, in the US. Here, I briefly report my observations and information obtained regarding the following organizations at IU.



1 Department of Biology : <http://www.bio.indiana.edu/>

IU comprises a total of 8 campuses over an extensive area of 1,400 ha. It is a massive organization comprising more than 90,000 undergraduate and graduate students combined. Of these, approximately 36,000 students live in Bloomington. The population of Bloomington is approximately 60,000, and thus, it is literally a university town. Although a large number of dormitories and apartments administrated by the university, are dispersed over the campus, the campus is so extensive that I walked to the lab everyday as if I were sauntering through a well-maintained park. The Department of Biology occupies the Jordan Hall (Fig. 1) and 2 other buildings adjacent to the hall. The number of laboratories is 50; 5 of which utilize *Drosophila* for research purposes. Further, 3 additional laboratories will be included by spring. One of the 3 buildings (Simon Hall) is newly constructed; and its completion ceremony was conducted during my stay; Mr. Simon graced the occasion with his presence (funds for the construction of most buildings have come partially from donations, and hence, the buildings are named after the donors). This practice of donations is truly enviable.



Fig.1

2 Drosophila Stock Center : <http://fly.bio.indiana.edu/>

The most active *Drosophila* stock center in the US is located in IU. Professor Kaufman at the Department of Biology is the PI. This center also administrates FlyBase, a famous database of *Drosophila*, as part of a consortium with Harvard University and the University of Cambridge. I had the opportunity to visit the center between my experiments and use it as a reference for NIG-Fly stock center, a sub-division of NBRP *Drosophila*. I will not discuss the stock center in detail since Professor Masatoshi Yamamoto at the Kyoto Institute of Technology, the core institute, has previously reported regarding the center. Currently, approximately 23,000 strains are maintained, and approximately 150,000 strains are distributed annually. Most requests are for deficiency strains with chromosome abnormalities that users do not maintain themselves and instead repeatedly request for each screening experiment. From one viewpoint, the center functions as a stockroom for each of these laboratories. The fees for the resources distributed by the center are charged by mailing a bill to the laboratories at the end of the year; however, most often, payments are received for only about half of these transactions, and managing the transactions is laborious. Therefore, the "credit card accounting system," which was developed by the Kyoto Institute of Technology last year, will be tested from January next year.



3 Center for Genomics and Bioinformatics (CGB):

<http://cgb.indiana.edu/>

CGB was established in 2000 and is owned by the Department of Biology. Currently, Peter Cherbas serves as its Director. During my recent visit, I found the modENCODE (model organism ENCODE) project, which CGB participates in, interesting. ENCODE project attempts to identify all the "functional elements" in the human genome and was initiated in 2003 (<http://www.genome.gov/10005107#1>). Although I am not aware of the details, modENCODE project (<http://www.modencode.org/>) was initiated this spring and *Caenorhabditis elegans* and *Drosophila melanogaster* were selected for analysis because of their relatively compact genomes. The focused research topics in *Drosophila* are as follows. Please refer to the abovementioned website for further details.



Prof. Ueda (Left)

1) Transcriptome:

For all the transcripts, start sites, polyA sites and splice sites will be determined by high-density microarrays, cDNA/RT-PCR sequencing, and RACE. Small non-protein coding RNAs will be validated by RNAi assays.

2) Regulatory Element:

All locations on the genome to which transcription factors (TFs) and DNA-binding proteins bind are identified by ChIP-chip. In addition to the investigation of existing antibodies, the TF whose examination is the most important is currently being decided using the ballot system on the website (<http://www.modencode.org/Vote.shtml>).

3) Chromosomal Proteins

The genome-wide binding and histone modification sites of 125 chromatin proteins will be identified by ChIP.



4) Small RNA and microRNA:

Small RNA libraries will be developed under normal and physiological stress conditions by using organisms, tissues, and cell lines at various developmental stages, and their sequences will be determined using the Solexa sequencer. Precursors of microRNA will be identified in the mutants of RNA processing by using tiling arrays. Novel transgenic organisms with mutant microRNA or small RNA will be developed, and their in vivo functions will be investigated.

5) Origin of Replication:

Components of the prereplication complex assembly (ORC1/2, MEM complex, etc.) will be analyzed by ChIP-chip. Moreover, the DNA copy number of various polytene tissues will be compared using custom arrays.

↳ To the next page

Although the *Drosophila* genome is the most thoroughly annotated, the recent discovery of non-coding RNA clearly demonstrates that it is still incomplete, particularly, with regard to the information at the 5'-end of transcribed regions. It appears that a considerably higher number of spliced products may exist if minor sequences are also considered. It is encouraging that the acquisition of this information is becoming technically feasible as a result of advances in microarray resolution and the development of next-generation sequencers; however, since the US is proficient at strategically promoting projects, it is among the first to enthusiastically implement these projects. Meanwhile, the data obtained by each approach will be meaningful only after it has been processed using informatics. From the viewpoint of program development, it may be difficult to elucidate the entire genome, unless a model organism with a compact genome (comprising limited information) is targeted.



ModENCODE is owned by the consortium, and Peter participates in transcriptome project. As mentioned previously, there is a stock center in IU. When I visited the center, the scientists were in the midst of developing fly samples that could be used for the entire modENCODE. In addition, cell lines are distributed as research resources from Peter's lab. A post-doctoral researcher was absorbed in extracting total RNA and confirming its quality by northern blot analysis. These RNA samples will be stock-preserved and distributed to the participants of the project according to their requirements.

I also visited the genomics laboratory of CGB; it was an extremely plain room with a 454 sequencer, 2 array readers, and approximately 20 thermal cyclers. The informatics section provides various services. Further, the section manages the construction of web pages. Moreover, the PCs in the CGB labs were in a thin-client environment. It is a system in which a server provides all the software and stores data, while only small terminals are provided on each desk. Each individual is not required to purchase expensive software. This is convenient since it eliminates the need for software installations and users do not have to be concerned with securities and backups. The software programs that are used in this environment are also developed by the informatics section.



4

Drosophila Genomics Resource Center (DGRC): <https://dgrc.cgb.indiana.edu/>

The DGRC at IU was established in 2000 as a section of the CGB (the DGRC of the Kyoto Institute of Technology was established in 1999). This organization is independent from the previously introduced *Drosophila* stock center and distributes various vectors, microarrays, and cell lines. Recently, exhaustive analysis of gene functions has been conducted by performing RNAi experiments in cell lines. In this case, it is obvious that the type of cell lines used is crucial. Accordingly, gene expression profiling of various cell lines was conducted using microarrays, and the resource information is under preparation to be published. In future, we will use feeder cells to establish cell lines from various sources.



IU administrates not only a stock center of flies but also the information on FlyBase as well as a genomics resource center; the common thread binding these facilities is being considered as an "ideal" resource center for conducting fundamental research using the fly. This visit made me reconsider the importance of "integration" and "division."

※ The picture was provided by Prof. Ueda.

Report on the BMB2007

- **BMB2007 (Annual Meeting of the Molecular Biology Society of Japan & the Japanese Biochemical Society)**
December 11–14, 2007 : at Pacifico Yokohama
- **Special plan for the "National BioResource Project":**
A panel exhibition with realia—"Complete Array of BioResources"



The focus was on the 37 biological organisms and resources available in NBRP; they were introduced using the realia at the exhibition site of the conference. Among the conference participants, almost 2,000 people visited us at the exhibition site.

Editor's Note: I requested Prof. Ueda, who visited the US for technical assistance, to write this travel report for us. In his report, he has reported the reality of "robust research fundamentals" that support top-level research in *Drosophila*, one of the most versatile model organisms, so that we could understand the concept better. BioResource now! will be celebrating its 4th year. Look forward to reading reserved topics on bioresources, which will continue to be provided even next year. Wish you a happy new year! (Y.Y.)

10 minutes

Information Technology - 28-



Let's use Wikipedia!



Wikipedia has been established as an encyclopedia that anyone can edit and is apparently used by many people. Thus, as a step away from the user's viewpoint and toward the editor's perspective, I will introduce the watchlist and contributions in Wikipedia. Since a Wikipedia account is necessary to use these functions, let us begin by opening an account.

URL: <http://en.wikipedia.org/wiki/>

1. Open an account and login

Click the "Log in / create account" link displayed at the top right of the Wikipedia website to login or create a new account. (Fig. 1).

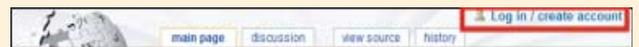


Fig. 1: Top page of Wikipedia

Click "Create one" and fill in the necessary information to open an account and register. Once the registration is completed, go back to the original page, type the user name and password, and click the login button.

The notification of successful login and change in the menu located on the top right as shown in Fig. 2 indicates completion of the login process.

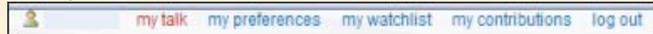


Fig. 2: User's Menu

2. Watchlist

Once logged in, the watchlist will be available for use. If the Wikipedia pages of your interest are registered in the watchlist, you will be notified at each update. Let us test this function by adding the NCBI page to the watchlist.

URL: <http://en.wikipedia.org/wiki/NCBI>

Open the NCBI page and click the "watch" tab displayed on the right edge of the tabs on the page (Fig. 3). The registered watchlists can be edited from the "my watchlist" in the user's menu.

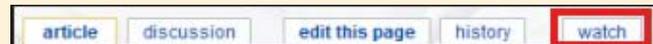


Fig. 3: Watchlist tab

Wikipedia does not support RSS and thus this watchlist is useful in managing the articles of your interest. The registered page can be deleted from the "Edit watchlist" page (Fig. 4).



Fig. 4: Watchlist

3. Contributions

In "my contributions" in the user's menu, you can check the contributions that you have made. As a general rule, anyone can edit; however, the editing of the content in which you are directly involved, is restricted. To edit the page, please read through the "Editing Wikipedia" in the help section and do it with care.

I have briefly explained about creating a Wikipedia account and the user's menu. Using the user's menu will further enhance the usefulness of Wikipedia. Why don't you take this opportunity to try it?

(Tohru WATANABE)

Next year's January issue will be "MOUSE", since it is the year of the mouse according to the Chinese zodiac.

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