



July 2006

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### Information on Resource-related Events

- **September 25(Mon.) – 27(Wed.)**  
**The 78th Annual Meeting of the Genetics Society of Japan**  
 at Tsukuba International Congress Center  
 - Panel Exhibition: September 25 (Mon.)–27 (Wed.)  
 - Symposium: September 27 (Wed.), 1300–1800
- **October 28 (Sat) 9:00–11:00**  
**Progress in Fertilization Techniques of Rats** TERRSA Hall  
 at Kyoto TERRSA (Kyoto Citizen's Amenity Plaza, Shinmachi  
 Kujo Minami-ku, Kyoto, Japan)

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



### Hot News from Abroad No.12

#### Participation in the Plant Ontology Annotation Camp / Workshop

Hiroshi Fujii, National Institute of Fruit Tree Science,  
 National Agriculture and Food Research Organization

 I attended the Plant Ontology Annotation Camp/Workshop held at Cornell University, Ithaca, NY, USA, for three days from May 30 to June 1, 2006. Cornell University is a beautiful university where impressive school buildings are interspersed on its extensive campus and various plants are established. In addition, the city of Ithaca, where the university is located, has a truly wonderful environment surrounded by forests and lakes.



#### Cornell University :

I have never been to any university overseas and thus, was surprised by the huge campus and the magnificent buildings. There is a small lake, a river, and a waterfall on the campus.



The first time I learned about Plant Ontology (PO) was when I attended a lecture by Dr. Yukiko Yamazaki from the Center for Genetic Resource Information, National Institute of Genetics at the Gene Ontology Workshop of the Plant and Animal Genome XIV Conference held in San Diego, CA, USA this January. I am in charge of analyzing a massive amount of EST data of citrus and compiling them into a database. Recently, a large amount of EST data for fruit trees such as apples and grape has been published; this stimulated my interest in the comparative genomics of fruit trees. However, the description method of tissues and growth stages used to obtain the EST data of similar fruit trees are not consistent; hence, some strategy is considered necessary for the comparison of the EST data of different fruit trees. Listening to Dr. Yamazaki's lecture stimulated my interest in PO; being introduced to PO by her, I attended the Plant Ontology Annotation Camp/Workshop.



#### Workshop :

Participants conducted presentations in the room throughout the duration of the Camp/Workshop, except on the morning of the first day. In addition, the participants carried out PO annotation exercises by using computers allocated to each participant.



Besides the members of the organizer Plant Ontology Consortium (POC), approximately 10 researchers who construct the genetic database of rice, wheat, rye, corn, sorghum, tomato, and citrus participated in this Camp/Workshop. Many members deal with poaceous plants since a number of people who engage in the PO work on Gramene, which is a comparative genome database of Gramineae. It was the first time that a researcher involved in the study of dicot plants such as citrus attended the Camp/Workshop held by POC, and I was welcomed enthusiastically. Besides me, the Japanese participants were Dr. Kikuchi and Dr. Nagata from the National Institute of Agrobiological Sciences.

#### Vicinity of the University :

Ithaca city, where the university is located, is a small town with a population of approximately 30,000. It is adjacent to one of the Finger Lakes, Cayuga Lake, surrounded by forests and lakes. There appear to be a number of wineries around the lakes.



On the morning of the first day, the Camp/Workshop commenced with public lectures regarding the comparative morphology of plants by Dr. Kellogg from the University of Missouri, comparative genomics by Dr. McCouch from Cornell University, and use of plant ontology by Dr. Jaiswal, an organizer of the Camp/Workshop, at Emerson Hall, College of Agriculture and Life Sciences, Cornell University. In the afternoon, we moved to the computer room in Bradfield Hall where the workshop was conducted. There was a presentation session at the workshop during which all the participants sequentially presented their own research topics; it included a question and answer session. Workshops during which two factors of PO—"plant structure" and "plant growth and development stages"—were assigned to the cDNA library from which genes and ESTs of plants were obtained from journal articles, were successively conducted.



**Plant Ontology Consortium**  
<http://www.plantontology.org/>

I carried out the PO exercise of annotating the genes of citrus; however, it was not very simple. One of the reasons for this is that the terms have been coined with the central focus on Gramineae; thus, there are few examples that applied PO to arboreous perennial plants such as citrus. Another reason why I found the exercise complex is that although I had sufficient knowledge regarding the horticultural names of the structure of citrus, I lacked knowledge regarding the morphological terms of plant structure in PO. For example, the horticultural term for the inner white flocculate portion of the citrus skin is albedo, whereas a term of plant structure mesocarp (PO:0009087) should be assigned. There was a further problem in "plant growth and development stages." For example, in the case of rice, the "plant growth and development stage" of seeds can be approximately identified by the number of days after blossom, while in the case of citrus fruits, varietal differences are high and the relationship between the number of days and developmental stage is not necessarily uniform. Recently, I have started collecting and consolidating information regarding the development of citrus fruits by consulting with Dr. Jaiswal at POC and other domestic researches of citrus.

 It is presumed that commercially growing fruit trees have common characteristics such as hypertrophy of fruits or accumulation of sugars. Further, there are common gene groups across their taxonomic distances. On the other hand, a massive amount of expressed sequence tag (EST) data for fruit trees such as citrus, apples, and grapes has recently been published on international base sequence databases, as mentioned previously. It is expected that the comprehensive annotations of the ESTs using PO and comparison of expressed genes performed by taking into consideration "plant structure" and "plant growth and development stages" will lead to the elucidation of fruit tree-specific gene groups and a gene-level understanding regarding the cultivation of fruit trees.



**McClintock Shed :**  
A commemorative photo was taken in front of a cabin that was used by Dr. Barbara McClintock who won a Nobel Prize for Physiology or Medicine in 1983 for her discovery of McClintock Shed transposons for the investigation of cornfield.



## Hot News from Abroad No.13

### Participation Report of the 3rd GO Annotation Camp

Hajime Ohyanagi, Laboratory for DNA Data Analysis,  
Center for Information Biology and DNA Data Bank of Japan

I participated in the gene ontology (GO) annotation camp, for the third time this year, as a representative of the Rice Annotation Project (RAP). Last year, the camp was held at Stanford University, CA, USA; this year, it was conducted at the Tresidder Union near the center on the campus for three days—from July 12 to 14. There were a total of approximately 50 participants, mostly from Europe, and the chairperson was Dr. Karen Christie, a senior scientific curator of Saccharomyces Genome Database (SGD) at Stanford University. The content of the camp included "Overview lecture of GO" and "GO annotation workshop (while actually reading journal articles)".

On the first day of the "GO annotation workshop," participants assigned GO terms and evidence codes to genes listed in two journal articles while reading them. This assignment was repeated on the second and third days by groups of five or six people using a total of 10 journal articles; each exercise was followed by a discussion with all the participants.

In fact, I could understand the rough scheme of GO annotation through the lectures and exercises; however, I believe that some experience is necessary to correctly assign GO terms and evidence codes. In addition, the GO framework is closely related to language, and thus, it appears that the Japanese, for whom English is not a native language, face some difficulties; I was the only Japanese participant this time.

The participants also actively interacted during events other than the GO workshop including dinner at the downtown Palo Alto and the free self-introduction time of each participant for a few minutes in the morning. Most of the participants were annotators or curators of databases for model organisms; I found these 3 days extremely significant since during this time, I could strengthen my relationship with many people playing active roles in the development of various databases overseas. The infrastructure of Stanford University was convenient not only for the university affiliates but also for visitors; the university guesthouse was equipped with wireless LAN, and the stay was comfortable.



※The group picture can be viewed at the URL below.

[http://www.geneontology.org/photo\\_GO\\_Annotation\\_Camp\\_20060714.shtml](http://www.geneontology.org/photo_GO_Annotation_Camp_20060714.shtml)

## Information Technology Vol.15

Useful web services are emerging simultaneously worldwide. Currently, Google Analytics is one among the numerous services being introduced. People with their own websites might be aware that Google Analytics is a website analysis tool provided by Google. Administrators of websites can identify whether or not the user is satisfied with the websites by understanding user behaviors. Results of the analysis will provide valuable information to modify and improve websites.

Google Analytics is multifunctional and presumably, it can be applied not only to individual websites but also to small- to medium-scale websites. The following are the main features:

- Available for free and simple to install
- Comprehensible analysis results at a single view due to graphical display
- Finding the regions from where the visited users accessed your websites
- Trailing other websites where the visited users moved over from your websites



## "Google Analytics"

Those who have read up to this point might like to use Google Analytics; however, it is not possible to use the service immediately. Since Google Analytics is extremely popular, a user is required to input his/her name and mail address at the URL ([http://www.google.com/analytics/ja-JP/sign\\_up.html](http://www.google.com/analytics/ja-JP/sign_up.html)) and wait until the receipt of an invitation via mail from Google.

Once the mail is received, those who do not have a Google account need to create an account at the URL (<https://www.google.com/accounts/NewAccount>). Those who do have an account should input the invitation code at the URL (<https://www.google.com/analytics/home/>).

Subsequently, click the "Create Account" button, and type the URL of your website, account name, time zone, family name, phone number, and country or region. After agreeing to the user contract, a tracking code (a code necessary to track the behavior of the visited user) is added to the source of your websites to complete the process. After approximately 1 hour, the data required to analyze the access is received, and one is able to analyze the behavior of a user per hit. (Gaku Kimura, Genetic Informatics Laboratory, Center for Genetic Resource Information)

**Editor's Note:** In this month, the topic of two ontology camps was opportunely provided. I am grateful to Dr. Fujii and Dr. Ohyanagi for providing valuable reports. I felt that the bioontology community in Japan had expanded to some extent. (Y.Y.)

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