



August 2006



BioResource now! Vo2.No.8 is here

- Information on Resource-related Events :
- Hot News from Abroad : No.14
 - **Compositae Genome Project**
National BioResource Project "Chrysanthemum"
Katsuhiko Kondo, Laboratory of Plant Chromosome and Gene Stock,
Graduate School of Science, Hiroshima University
- Ongoing Column : Vol. 16



Download the PDF version of this newsletter at
<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://www.shigen.nig.ac.jp/wgr/>
JGR <http://www.shigen.nig.ac.jp/wgr/jgr/jgrUrlList.jsp>

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.14

Compositae Genome Project

Compositae Whitepaper Meeting
 University of California at Davis August 17, 2006

National BioResource Project "Chrysanthemum"
 Katsuhiko Kondo, Laboratory of Plant Chromosome and Gene Stock,
 Graduate School of Science, Hiroshima University



Approximately two years ago, the Genome and Biomedical Sciences Facility was set up at University of California at Davis in the US (hereafter referred to as UC Davis), and the Genome Center was established in this facility for the purpose of integrating the common challenges encountered in agricultural, biological, and medical sciences. This opportunity was exploited by initiating the Compositae Genome Project as a significant action that was taken with the approval and collaboration of the community. It is vital to ensure the participation and consent of domestic universities and research institutes in order to manage extensive (several hundred million dollars) funding for the project. Further, it is essential to establish international cooperation, collaborative research, and the international standardization of research. These were the primary reasons for conveying the meeting.

Professor. Richard Michelmore, the director of the Genome Center at UC Davis is the representative of the Compositae Genome Project. The professor visited Tsukuba city to establish collaborations for research with the staff performing research in the field of plant molecular biology at the RIKEN institute in Japan and the Rice Genome Project of the Ministry of Agriculture, Forestry and Fisheries.



Conference:
 Director of Genome Center,
 Prof. Richard Michelmore



Unlike the Human Genome Project or Rice Genome Project that targeted a single species, this project focuses on chrysanthemum that includes one-tenth of the higher plants and is the most evolved species among dicot plants. Thus, this project targets an extensive variety of species. Particularly, among chrysanthemums, there are more than 40 species that warrant appreciation for their economic utilities as food, vegetables, oil (for food and biodiesel), medications, reagents, luxury grocery, grains, and ornamental plants; further, this genus includes 3,000 syntenic and affiliated species. Therefore, one of the initial challenges that we had to overcome was to include these species in this project. On the other hand, chrysanthemum is considered as an extremely harmful weed; it is also a well-known fact that a massive amount of money has been invested in eliminating the chrysanthemum weed. This was frequently discussed at the meeting since it is an important issue with economic implications.



Determining the base sequence of the chrysanthemum genome is definitely the most important task, and *Leontodon taraxacoides* spp. *Taraxacoides*, which has the smallest genome size among chrysanthemum species ($2n = 2X = 8$; the genome size is 1C 0.29/0.30 pg (unpublished data by Baak and Rieseberg) and a genome size that is approximately twice that of *Arabidopsis thaliana* genome (1C 0.16/0.16 pg) and smaller than that of rice (1C 0.49/0.50 pg)), was considered as the model plant. This chrysanthemum species is native to the mountainous regions in Europe; it was imported into the United States where it grew as a weed in 23 states between the Midwestern and Mideastern regions. Recently, in several prefectures in Japan such as Tokyo and Kanagawa have started to record this species as a naturalized weed. Using the basic data obtained from this project, economic species will be multilaterally selected for developing technology, and conducting innovative research, which are the most important objectives of chrysanthemum genome research. Moreover, using the resources available at the Seed Biotechnology Center at UC Davis, will enable the integration of genetic research and education regarding the chrysanthemum species including fundamental knowledge, particularly that regarding their breeding, molecular genetics, and genome analysis. Technical information such as gene manipulation, functional and comparative evolution, taxonomy, and weed science will also be integrated.



UC Davis :
 Genome and Biomedical
 Sciences Facility



It was strongly recommended that Professor Kondo, a researcher at the Laboratory of Plant Chromosome and Gene Stock, Graduate School of Science, Hiroshima University, attend the meeting because of the following reasons.

- (1) Our team conducts the largest scale collection, preservation, and study of the genus Compositae in Japan by focusing on the National BioResource Project.
- (2) Our facility publishes and provides numerous chromosome pictures such as those showing genomic in situ hybridization (GISH) and fluorescent in situ hybridization (FISH), which are the most striking features of the chrysanthemum species, and even researches the molecular phylogeny of the species. We have been informed that the construction of a physical map of chrysanthemum genome by fiber FISH is expected.
- (3) The possibility of the participation of a Japanese representative in the project was requested.



The meeting lasted from 9:00 to 17:00, it was held in a lecture hall at the Genome and Biomedical Sciences Facility at UC Davis. According to the official announcement, there were 55 participants; most of whom were researchers from US or Canadian universities. Besides the researchers from the US and Canada (all the foreign researchers and students in the two countries are considered as Americans or Canadians, respectively), there were other overseas participants, i.e., one researcher from each of the following countries: France, Holland, Argentina, United Kingdom, and Germany. They were introduced by their respective names at the beginning of the program.

 General knowledge lectures were conducted in the morning from 9:00 to 11:30, the topics were as follows: (1) Greetings, and the aim and goals of the meeting introduced by Professor Richard Michelmore, the representative of the meeting and the director of the Genome Center at UC Davis, (2) a lecture by Professor Lowell Urbatsch of Louisiana State University titled "Phylogenic Overview and Species Diversity", (3) Lecture by Professor Richard Michelmore titled "Genome Project", (4) Lecture by Professor Steve Knapp from University of Georgia titled "Biochemical Genomics", (5) Lecture by Professor Loren Rieseberg from University of British Columbia in Canada titled "Ecological Genomics", and (6) Lecture by Professor Simon Hiscock from Bristol University in the UK titled "Reproductive Biology and Species Differentiation".

 A poster exhibition focusing on specific areas was organized from 10:00 to 10:30 and 11:30 to 13:00. Since a major portion of the poster exhibition was related to studies on sunflower and lettuce and this a favored field led by the Professor Michelmore, it was inferred and reconfirmed that these two species would be the research goal of the project. In addition, 2,420 species of North American chrysanthemum belonging to 418 genera were consolidated and published in the June issue of Flora of North America in Vols. 19, 20, and 21; these publications were introduced and advertised extensively throughout the meeting. I also presented a poster regarding the research conducted by the National BioResource Project on Compositae and by the Laboratory of Plant Chromosome and Gene Stock, Graduate School of Science, Hiroshima University. At this time, I learnt that researchers at Miami University, Akron, OH, USA, were conducting an analogous research in which they used the North American species of chrysanthemum, which are completely different from ours, to cross genera and analyze the resultant hybrid species.



Poster Exhibition

 Between 13:00 and 15:00 in the afternoon, as a part of the group discussions, we split into the following four groups—(1) taxonomy, (2) genetics and allelic diversity, (3) sequencing and genome properties, and (4) functional analysis and secondary metabolism. We discussed the following preassigned themes regarding chrysanthemum research: applications of recent and future genome data, usability of model plant data, chrysanthemum properties having strong implications, novel researches, researches that lost momentum, demanded resources, short-, medium-, and long-term essential tasks and operations, the method of research collaboration among chrysanthemum researchers, integration of diverse chrysanthemum researches, necessity of a conventional steering committee, necessity of a resource database, modification of terms used for the database search, methodology of the whole genome base sequencing and its timing, choice of an agricultural product with a high economic value, a weed, or a model plant with a small genome size for the whole genome base sequencing, funds available for research, competent researchers who can acquire research funds and political context, primary researchers of chrysanthemum, creative use of bioenergy, and other themes including those necessary for the white book were discussed.



Reception at the Prof. Michelmore's Home after the Meeting

 The generalized session was conducted from 15:30 to 17:00. The results of each group discussion were presented and summarized to identify the common issues among each discussion. The meeting closed after a general discussion. During the meeting, as a part of the team conducting the National BioResource project on chrysanthemum, we advertised that the reserved plants are available as resources for research. Subsequently, we submitted a set of documents to the representative Professor Michelmore, and explained its contents, and won his approval.



NBRP Chrysanthemum
<http://www.shigen.nig.ac.jp/chrysanthemum/>



Reprinting and reduplication of any content of this newsletter is prohibited. All the contents are protected by the Japanese copyright law and international regulations.

Information Technology

Vol.16



"CMap (Comparative Map Viewer)"

Does everyone know about GMOD? GMOD is the abbreviation for Generic Software Components for Model Organism Databases, which is a US website that provides an open-source tool shared by the database groups of model organisms (<http://www.gmod.org/home>). Numerous tools such as a genome browser, GBrowse, and Textpresso for text searching can be downloaded for free. CMap is a newly included tool. It is a comparative map viewer that can compare multiple map information on the website. It has been used on Gramene, a comparative genome database of grains, and GrainGenes, a database of wheat.



In our lab, CMap is used on the wheat database (KOMUGI), (<http://map.lab.nig.ac.jp:8080/cmap/>, Fig.A). The Japanese version of the tutorial was prepared; those interested may please access it by visiting the site. The main functions of CMap are as follows: (1) construction of a map image, (2) identification of markers, (3) the establish links among multiple maps, and (4) matrix representation of markers that are common among maps.



Fig. A : CMap on Wheat DB

The advantage of the tool is that the links among the multiple maps selected by a user are optimized and intelligently displayed. Display switching and customization features are also provided. Further, functions such as scaling up and down of the maps as well as partial cutting and inversions can be easily performed. Fig. B shows an initially selected map in the center, one on the left, and two more on the right. The number of markers displayed will be optimized according to the size.

Although I used this tool for the first time, in my opinion, those who can read English and are familiar with knowledge regarding relational databases and Unix/Linux can construct the maps relatively easily because the information was well developed. The development of a tool that exhibits similar functions from the beginning is considerably tedious, and I cannot think of any reason to not use it.

(Rie Tsuchiya, Genetic Informatics Laboratory, Center for Genetic Resource Information)

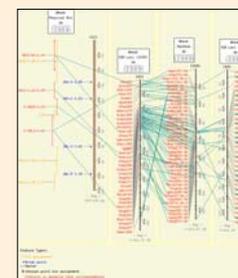


Fig. B : Example Linkage Map

Google Sitemap will be introduced next time.

Editor's Note: Dr. Kondo generously provided an interesting hot topic, i.e., the international chrysanthemum genome project. I appreciate his gesture considering his busy schedule immediately after his arrival from overseas. Chrysanthemum is the representative flower of our country, and it is believed that the production of chrysanthemum is the highest among all the flowering plants. Moreover, the number of chromosomes is $2n = 4-90$; thus, chrysanthemums include an extremely diverse variety of plants that are considerably unique. The time for chrysanthemum blossom in Japan is coming soon! (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