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BioResource now !

Our monthly newsletter features a variety of information, highlighting current domestic and international issues concerning bioresources.

Introduction to Resource Center No.14

Resource Consolidation of Tomatoes, The Next-generation Model Plant

Hiroshi Ezura, Graduate School of Life and Environmental Sciences, University of Tsukuba

Hot News from Abroad No.16

Plant and Animal Genome XV Conference

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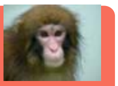
NBRP	http://www.nbrp.jp/
SHIGEN	http://www.shigen.nig.ac.jp/indexja.htm
WGR	http://www.shigen.nig.ac.jp/wgr/
JGR	http://www.shigen.nig.ac.jp/wgr/jgr/jgrUrlList.jsp

NBRP "Japanese Monkeys"



- A 5 year walk towards the future -

"The 5th RR2002 Symposium"
February 2 (Fri) , 2007
Nihon University Kaikan Daini Bekkan

※Detailed information is available at http://www.nbrp.jp/

Cell Technology initiated a new series entitled " Let's Use! BioResource ". Bioresources in Japan will be introduced in a series of 14 volumes from November 2006 to December 2007.

Introduction to Resource Center No.14

Resource Consolidation of Tomatoes, the Next-generation Model Plant

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1 From the resource consolidation of "staple food (plants that provide satiating food)" to the resource consolidation of "accessory food (plants that provide nutritious food that helps maintain a healthy body)"

Foods that are essential for life can be classified into staple food—grains (rice, wheat, corn, etc.), beans (soybean, etc.), and potatoes (Irish potato, sweet potato, etc.)—that satiate and accessory food—vegetables and fruits—that help maintain a healthy body. The analogy of this classification with a car indicates that the former food category corresponds to "fuel" and the latter corresponds to "lubrication oil" and an effective combination of the two results in satisfactory car function. Humans also lead a healthy daily life by consuming these 2 classes of foods in a well-balanced manner. The consolidation of plant resources has thus far been focused on the former class. However, from the viewpoint that a good diet is the basis of a healthy life, recently, it is again considered important to deepen our understanding of vegetables and fruits and the consolidation of these research resources was launched by organizing an international consortium.

A wide variety of vegetables and fruits are available as food and can be mainly classified into the following plant taxa: Solanaceae (tomato, eggplant, bell pepper, chili pepper, etc.), Cucurbitaceae (melon, cucumber, watermelon, pumpkin, etc.), Cruciferae (cabbage, napa, radish, broccoli, etc.), Compositae (lettuce, burdock, crown daisy, etc.), Umbelliferae (carrot, celery, Japanese parsley, etc.), Fabaceae (pea, pinto bean, black-eyed pea, etc.), Liliaceae (onion, green onion, garlic, asparagus, chive, etc.), Rosaceae (strawberry, apple, pear, etc.), and Chenopodiaceae (spinach, etc.).

Among these, Solanaceae resource consolidation focusing on tomato as a model plant has been initiated by employing the international consortium system.

2 Tomato—the focus of attention. Initiation of the International Solanaceae Genomics Project (SOL) in 2003.

Among the dicot plants, those belonging to Solanaceae are important candidates for resource consolidation, since they are evolutionarily distant from Arabidopsis thaliana (Cruciferae) or Lotus japonicus (Fabaceae) for which resource consolidation has already progressed. According to the results of expressed sequence tags (EST) analysis of Micro-Tom, approximately 30% of the expressed genes are actually not observed in A. thaliana and rice and are unique to tomato (Yamamoto et al. (2005) Gene, 356: 127–134). In addition, plants belonging to Solanaceae exhibit various features that are not observed in conventional model plants (A. thaliana and rice), hence the latter cannot be used for research. Tomato is thus considered to be a model plant for application research with regard to crops and for research in plant diversity and adaptive evolution. For example, during the process of evolution, the higher plants obtained the ability to bear fruits—an important crop trait.

For these reasons, the International Solanaceae Genomics Project (SOL), which is based on the international consortium, was initiated in 2003.

International Solanaceae Genomics Project (SOL)
http://www.sgn.cornell.edu/index.pl

Tomato is a fruit vegetable that is most abundantly produced in the world and is a crop that is greatly associated with our diet. In addition, tomato contains functional ingredients that are important for maintaining health as the proverb goes "a tomato a day keeps the doctor away,"; and has thus received considerable attention from the industry. On the other hand, tomato is advantageous as a research material since its genome size is relatively small (950 Mb), it exhibits various features that the conventional model plants lack (such as fructification and neutral sensitivity to photoperiod), its quantitative trait loci (QTL) analysis has progressed, and considerable research has been conducted on it. Therefore, tomato was selected as a model plant for Solanaceae plant research and genome sequencing, and other resource consolidations are being conducted in the countries affiliated to the consortium. The international consortium has set the sequencing of the 12 chromosomes of tomato as a common research theme, and the participant countries have been cooperatively deciphering the chromosomes. Moreover, the participant countries also consolidate the resources independently. A workshop is conducted every year to exchange information. In 2007, the workshop will be held on Cheju Island in Korea.

The 4th Solanaceae
Genome Workshop 2007
http://www.solanaceae2007.org/

3 Activities of Japan Solanaceae Consortium (JSOL) — internationally-acclaimed Solanaceae genome research

As described previously, tomato is the "next-generation model plant" that holds the combined importance of being both a research as well as an industrial resource. Accordingly, in response to the initiation of the international activity of SOL, affiliated researchers in the country gathered at the workshop hosted by the Kazusa DNA Research Institute in March 2004 and organized the Japan Solanaceae Consortium (JSOL). The Kazusa DNA Research Institute and University of Tsukuba subsequently assumed a leading role and initiated the resource consolidation of tomato research as a "grassroots activity." The JSOL has organized symposiums at related conferences in the country and original international symposiums to disseminate information. As a result, the expectations from academic and industrial communities regarding the resource consolidation of tomato research have been raised. In December 2005, the 178th Committee on Plant Molecular Design was established as an academic-industrial cooperative research committee of the Japan Society for the Promotion of Science to provide opportunities for exchanging research information related to this next-generation model plant and to support these research activities.

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↱ The primary activity, assignment, and status of the JSOL are as described below. JSOL conducts resource consolidation using Micro-Tom (Fig. 1), a dwarf tomato breed, as a standard breed. The Micro-Tom plant is small with a length of approximately 15 cm, and many individual plants can be grown in a small space. In addition, since Micro-Tom can be grown under relatively weak illumination conditions such as a fluorescent light, it is easily cultivable even in a completely closed environment. Moreover, the generational shift from seeding to fruiting is approximately three months, and this short generation time is advantageous for genetic research.

Fig. 1: Micro-Tom as a system for next-generation model plants

Rock wool cube (5cm per side)
It grows up under the same conditions as *Arabidopsis thaliana*.

1 . Genome Sequencing

1) Sequencing of the 8th chromosome (Kazusa DNA Research Institute, National Institute of Vegetable and Tea Science)
(Status：http://www.sgn.cornell.edu/about/tomato_sequencing.pl)

2) EST and full-length cDNA sequencing and database development (Kazusa DNA Research Institute)
(Reference：http://www.kazusa.or.jp/jsol/microtom/indexj.html)

2 . Developing Tools for Functional Analysis of Genome

1)
- Development of mutant strains
  (Approximately 4,000 strains mutagenized by ethyl methan sulfonate (EMS) and approximately 5,000 strains mutagenized by gamma irradiation)
- Selection of mutants (358 strains as of 2007/01/01)
- Database development
  (TOMATOMA, tomato mutant archives (Fig. 2), data accumulation)

(University of Tsukuba, National Institute of Genetics, Okayama University, Nagoya University, National Institute of Vegetable and Tea Science, and Kazusa DNA Research Institute)

Fig. 2: Mutant database of Micro-Tom
TOMATOMA-Tomato mutants Archive

2) Development of high-efficiency transformation technology
(Reference: Sun et al. (2006), Plant Cell Physiol., 47:426–431)
(University of Tsukuba)

3) Development of TILLING platform
(DNA pool under construction from mutant strains) (University of Tsukuba)

4) Development of easy mapping technology using T-DNA tag lines
(T-DNA tag lines under construction) (University of Tsukuba)

3 . Popularization of the Consolidated Information and Technology (Kazusa DNA Research Institute and University of Tsukuba)

1) Implementation of courses in array
2) Implementation of courses in transformation technique
3) Implementation of training courses in biotechnology technique

4 Challenges for the Future

Consequent to the release of information related to the Micro-Tom-based resource that has been consolidated by the "grassroots activity" of JSOL which has been conducted for 3 years since 2004, the expectations from within and outside the country are being raised. As a consequence of introducing the activities of JSOL at an international workshop on tomato genome research held in Hyderabad, India, in November 2006, particularly high expectations have been placed on the international consortium regarding the support of genome sequencing technology; the release of full-length cDNA information, mutant strains, mutant databases and the TILLING (targeting induced local lesions in genomes) platform; and the popularization of transformation technology. However, in order to respond to these expectations, the sequencing of all the collected full-length cDNAs; proliferation of mutant strains; consolidation of information such as the cultivation properties of each mutant strain; enforcement and release of the DNA pool for the TILLING platform; and immediate consolidation of a diffusion system is necessary. The consolidation of these systems and the release of resources to the global academic and industrial communities hold promise for the development of an international hub for tomato resources in the country.

Workshop in India

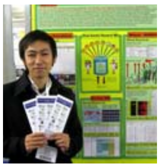
Hot News from Abroad No.16

Plant and Animal Genome XV Conference

PAG is an international conference held annually in January and this year was its 15th session. I was participating in the conference for the third year. The temperature was slightly lower than usual this year and warm clothing was needed.

This year, I presented a poster regarding BioResource World (http://resourcedb.nbrp.jp/) entitled, "Genetic Resource Databases in Japan". Approximately 1,000 posters and company exhibits were displayed at the venue, and the number of company exhibitions appeared to have increased compared to the previous year. People from various countries actively exchanged opinions at the workshop that was organized on each day of the conference, and I was particularly interested in the workshop regarding Blast2GO (http://www.blast2go.de/). Blast2GO is a software that is used to perform gene ontology (GO) annotation using BLAST to identify homologous base sequences and is a desktop application. (The software uses Java Web Start and is initiated by clicking on a link on the website. It takes some time to start if you are using it for the first time.) The software not only annotates GO but also supports the display of KEGG maps of related enzymes and the visualization of interactive GO trees and the input and output of files; further, the overall percentage of completion appears high. (Shingo SAKANIWA)

At the PAG, I exhibited a poster entitled "Plant Genetic Resource Databases," which described the latest contents of Oryzabase(http://shigen.lab.nig.ac.jp/rice/oryzabase/), KOMUGI (http://shigen.lab.nig.ac.jp/wheat/komugi/), and Barley (http://www.shigen.nig.ac.jp/barley/). The Oryzabase, in particular, drew considerable attention, and most of the questions were regarding the work on plant ontology and the coordination with other Rice databases, which was helpful to recognize the needs of the user. There were questions regarding the virtual display in KOMUGI and regarding the type of resources included in the algae database. In addition, 100 copies of pamphlets that introduced the activities of NBRP were distributed to promote the project. Since I generally do not get many opportunities to speak to foreign users of these databases, it was a good opportunity to test my English conversation skills, which I had started to learn. It was a great pleasure for me to communicate in English with others. Based on the experience I gained this time, I would like to further facilitate the activity of NBRP in future. Furthermore, I attended the InterPro/UniPro/IntAct hosted by the European Bioinformatics Institute (EBI), GBrowse training for beginners, and several database (DB) sessions, and as a whole it was a highly productive meeting. (Tohru WATANABE)



This was my first year of participation in the PAG, which is an international conference, and I assimilated relevant information from the GO workshop, the demonstration of GBrowse, and from various poster presentations. The GO workshop began with a discussion regarding basic information on GO followed by the significance of GO and the annotation method. The talk was subsequently expanded to the introduction to AmiGO, GO Slim Mapper, and GO Term Finder to conveniently utilize the massive amounts of annotated data. The interpretation was provided in a simplified manner, thus engaging my interest.

Researches using other ontologies that are not covered by GO were also described at the poster presentation. I was able to obtain knowledge in various projects such as protein ontology, the description of proteins and their interactions; plant ontology, the description of the structure and phenotype of plants; and mammalian phenotype ontology, the description of the phenotype of mammals. Accordingly, I could envisage a promising future for ontology. (Gaku KIMURA)

Editor's Note: In our country, the research community that studies tomato—a member of the Solanaceae taxon—is larger than expected and is enlivened with surprisingly numerous young people. The international tomato groups participate in the development of plant ontology and are interested in the Micro-Tom mutant project and the full-length cDNA project in Japan. Thus, the future development of this resource is promising. (Y.Y.)

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