

A junction of *Solanaceae* and *Cucurbitaceae* researches: SOL&ICuGI2011

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The Joint Conference on the 8th Solanaceae Genomics (SOL) and the 2nd International Cucurbit Genomics Initiative (ICuGI) was held in Kobe, Japan on November 28 to December 2, 2011, organized by the 178th Committee on Plant Molecular Design, University-Industry Research Cooperation Societally Applied Scientific Linkage and Collaboration of Japan Society for the Promotion of Science (<http://plantmdc.gene.tsukuba.ac.jp>).

The annual SOL genomics workshop has been commenced after the meeting in Washington DC, USA on November 3, 2003 to initiate an international collaboration entitled “The International Solanaceae Genome Project.” The SOL achieved the whole genome sequencing of tomato cv. Heinz 1706 in 2010, and the information and the related tools have been provided through the SOL Genomics Network (<http://solgenomics.net/>). The ICuGI was initiated after the meeting in Barcelona, Spain on June 30-July 1, 2005 to establish genomic information and functional genomics tools for Cucurbit crops as an international collaboration. Reference sequences of cucumber, melon and watermelon have been obtained. Currently the information has been provided through the Cucurbit Genomics Database (<http://www.icugi.org/cgi-bin/ICuGI/index.cgi>).

Families of *Solanaceae* and *Cucurbitaceae* include many edible vegetable crops that are the most represented horticultural species. The conference provided many opportunities for scientists to interact with people working on different/related areas, and guided us to reveal the evolutionary history and genetic diversity between *Solanaceae* and *Cucurbitaceae*. We also believe that the joint conference have given us future prospect on “what is the next step of plant

genomics research?” and “what can we learn from large volumes of sequencing data?”. Thanks to the latest technical advancement of sequencing equipments and bioinformatics, we are now able to determine genome sequences of cultivars, variations, and wild species, and to investigate comprehensive gene fluctuations using whole transcriptome shotgun sequencing (also called RNA-seq). Genome sequencing projects of several key members are ongoing. One of the major goals of the conference was to explore the idea, strategies or methodology how we make these information benefit for our studies, as well as for human lives to solve the global food securities.

More than 300 delegates from over 22 countries attended to the joint conference and more than 200 presentation were made. It was an amazing number for us when considering our current situation after the disaster on March 11, 2011 in Japan, and a high exchange rate of yen. We believe the Joint Conference boosted up Japanese scientists and even Japanese society. Among the presentations, we invited several authors to prepare original or review manuscripts, and prepared this special issue of this journal.

I appreciate the authors of the articles featured in this issue for their contributions and thoughtful insight on the current researches and developments in this field. I hope that these articles will serve as a valuable resource for advancing our basic and technical knowledge on *Solanaceae* and *Cucurbitaceae* research. Finally, I would like to thank Dr. Taku Demura, the Editor-in-Chief of *Plant Biotechnology*, for providing the timely opportunity to prepare this special issue. The editing of this special issue was supported by guset editors, Hiroshi Ezura and Tohru Ariizumi (University of Tsukuba), and Koh Aoki (Osaka Prefecture University).