

Preface

The 8th Joint Conference on Solanaceae Genomics (SOL) and the 2nd International Cucurbit Genomics Initiative (ICuGI) were held in Kobe, Japan, from 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 began 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 2012, and the information and related tools are available through the SOL Genomics Network (<http://solgenomics.net/>). The ICuGI was initiated after the meeting in Barcelona, Spain, on June 30–July 1, 2005, as an international collaboration to establish genomic information and functional genomics tools for Cucurbit crops. Reference sequences of the cucumber (2009), melon (2012), and watermelon (2013) have been obtained. This information is available through the Cucurbit Genomics Database (<http://www.icugi.org/cgi-bin/ICuGI/index.cgi>).

The *Solanaceae* and *Cucurbitaceae* families include many edible vegetable crops that are among the most widely represented horticultural species. The conference provided many opportunities for scientists to interact with colleagues working in different and related areas and guided us toward elucidating the evolutionary history of, and the genetic diversity between, *Solanaceae* and *Cucurbitaceae*. We also believe that the joint conference provided us with approaches to addressing questions such as “What is the next step for plant genomics research?,” “What can we learn from large volumes of sequencing data?,” and “How can we use this information for plant improvement?” Thanks to the latest technical advancements in sequencing equipment and bioinformatics, we are now able to determine the genome sequences of cultivars, variations, and wild species and to investigate comprehensive gene fluctuations using whole-transcriptome shotgun sequencing (also called RNA-seq). The genome sequencing

projects of several key members are ongoing. One of the major goals of the conference was to explore the ideas, strategies, and methodologies by which we can use this information in our studies and eventually benefit human lives by improving global food security.

More than 300 delegates from over 22 countries attended the joint conference, and more than 200 presentations were made. These numbers were amazing for us when considering our situation after the disaster on March 11, 2011, in Japan. We believe the Joint Conference uplifted Japanese scientists and even Japanese society. Drawing from the presentations and related research, we invited several authors to prepare review chapters and prepared this volume for the book series.

I thank the authors of the chapters in this volume for their contributions and thoughtful insights regarding the current research and developments in this field. I hope that these chapters will serve as a valuable resource for advancing our basic and technical knowledge on *Solanaceae* and *Cucurbitaceae* research and breeding. Finally, I thank Prof. Toshiyuki Nagata, the Editor-in-Chief of this book series, for providing the timely opportunity to prepare this volume. The editing of this book was supported by my coeditors, Tohru Ariizumi (University of Tsukuba, Japan), Jordi Garcia-Mas (IRTA, Spain), and Joclyn K. C. Rose (Cornell University, USA).

Tsukuba, Japan

H. Ezura



<http://www.springer.com/978-3-662-48533-0>

Functional Genomics and Biotechnology in Solanaceae
and Cucurbitaceae Crops

Ezura, H.; Ariizumi, T.; Garcia-Mas, J.; Rose, J. (Eds.)

2016, VIII, 165 p. 6 illus., 5 illus. in color., Hardcover

ISBN: 978-3-662-48533-0