

## Tomato genomics by JSOL

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The Solanaceae family includes important crops and model plants such as tomato (*Solanum lycopersicum*), potato (*Solanum tuberosum*), eggplant (*Solanum melongena*), pepper (*Capsicum annuum*), and petunia (*Petunia hybrida*). The Solanaceae Genomics Network (SGN; <http://sgn.cornell.edu>) is a rapidly evolving genetic and genomic resources for the plants of the Solanaceae family. One of the main goals of the SGN is to relate these species of the Solanaceae family to one another using a comparative genomics approach and to tie them to the other dicots and monocots through the fully sequenced genomes of *Arabidopsis* (*Arabidopsis thaliana*) and rice (*Oryza sativa*). The International Solanaceae Project (SOL) composed of over 30 countries was formed to address important questions in plant biology using the plant species in the Solanaceae family.

The Japanese SOL (JSOL) was established in March 2004 and has contributed to the international projects. Key activities of the JSOL include the sequencing of the entire euchromatic portion of the tomato chromosome VIII (Tabata group, Kazusa DNA Research Institute; Fukuoka group, National Institute of Vegetable and Tea Science), collection and sequencing of the tomato ESTs including cDNAs, and building databases for genomics of tomato (Shibata group, Kazusa DNA Research Institute), establishing extensive databases of phenotypic information for mutagenized tomato populations by EMS and gamma-irradiation (Ezura, Mizoguchi, Matsukura and Nishimura groups, University of Tsukuba; Kubo group, Okayama University; Mori group, Nagoya University; Imanishi group, National Institute of Vegetable and Tea Science; Shibata group, Kazusa DNA research Institute, Yamazaki group, National Institute of Genetics), developing tools for tomato functional genomics such as high-throughput genetic transformation protocol, TILLING platform and T-DNA tag line-based mapping platform (Ezura and Mizoguchi groups, University of Tsukuba), establishing a platform for comprehensive metabolite analysis (Shibata group, Kazusa DNA Research Institute), and providing technical workshop for Solanaceae community (Ezura and Mizoguchi groups, University of Tsukuba; Shibata and Tabata groups, Kazusa DNA Research Institute). Recently, the JSOL has made a good progress on these projects.

We therefore thought that it was timely to summarize the 1<sup>st</sup> 3 years' efforts on the international collaborations by the JSOL. We began to discuss on the possibility to publish a special issue on the recent progress on the tomato genomics in Japan with the chief editor, Prof. Hiroshi Sano, and other editors of the *Plant Biotechnology*. Actually we are very happy to make it and to step forward to the next phase. Also we thank Prof. Bouzayen (France), Prof. Choi (Korea), Dr. Carrari (Argentina), Prof. Mattoo (USA), and Dr. Samach (Israel) for their kind contributions to this special issue from the SOL.

This special issue includes both review and research articles on 1) genome sequencing (Asamizu pp 5–9; Lee et al. pp 11–16), 2) collection of ESTs and building databases for the tomato genomics (Yano et al. pp 17–25; Delalande et al. pp 27–31), 3) construction of extensive databases of phenotypic information for mutagenized tomato populations (Watanabe et al. pp 33–38; Matsukura et al. pp 39–44), 4) metabolomics (Carrari et al. pp 45–55, Srivastava et al. pp 57–70), 5) signal transduction and development (Asahina et al. pp 99–106; Liu et al. pp 117–126; Mizoguchi et al. pp 83–86; Niinuma et al. pp 87–97; Omura et al. pp 107–115; Samach and Lotan pp 71–82; Shiratake and Martinoia pp 127–133), 6) disease resistance (Arie et al. pp 135–147; Hikichi et al. pp 149–154). We hope the information in this special issue will be useful not only for researchers who are currently working on the plant species of the Solanaceae family, but also for young investigators who are planning to jump in the research area of the tomato genomics.

Finally, on behalf of the editors of this special issue, we would like to express our hearty thanks to Prof. Hiroshi Sano, the editor-in-chief of *Plant Biotechnology*, for continuous helping to preparing this special issue and also to Ms Kuniko Yasumi for her kind and efficient assistance.

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