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## Editorial

### From randomly to inevitable: Accelerating tomato breeding by comprehensive tools and information

Tomato (*Solanum lycopersicum* L.) is an important crop in the fresh produce and food-processing industry, with one of the highest production yields for edible crops in the world. Due to the variation in consumer palatability and preference, tomato cultivars are diverse in terms of shape, color, taste and functional materials compared to major cereal crops. Accordingly, rapid and efficient breeding technologies for tomato are required.

Tomato belongs to the Solanaceae family and is a model species for investigating fleshy fruit development. In 2003, the International Solanaceae Project (SOL), comprising over 30 countries, was formed to address important questions in plant biology using plant species in the Solanaceae family. The consortium initiated the full-genome sequencing of tomato using the inbred tomato cultivar Heinz 1706, and the high-quality genome sequence was recently published (The Tomato Genome Consortium 2012). The Japanese SOL (JSOL), co-chaired by Dr. Hiroshi Ezura at the University of Tsukuba and Dr. Daisuke Shibata at the Kazusa DNA Research Institute, was established in March 2004 and began developing unique and comprehensive tools and resources to accelerate tomato research and breeding.

JSOL has used an inbred miniature tomato cultivar, Micro-Tom, as the core genetic background due to its many advantages as an experimental material. The key activities of JSOL include the following: collection and sequencing of tomato ESTs, including full-length cDNAs; building databases for tomato genomics; establishing extensive databases of phenotypic information for tomato populations mutagenized with EMS and gamma-irradiation (Saito *et al.* 2011); developing tools for such tomato functional genomics as high-throughput genetic transformation protocol (Sun *et al.* 2006), a TILLING platform (Okabe *et al.* 2011) and a T-DNA tagline-based mapping platform; establishing a platform for comprehensive metabolite analysis and providing technical workshops for the Solanaceae research community.

In 2007, a portion of the JSOL activities was funded by the Ministry of Education, Culture, Sports, Science and Technology (MEXT), Japan (Yamazaki *et al.* 2010) as the National BioResource Project (NBRP) tomato, with aims to collect, propagate, maintain and distribute tomato bioresources to promote studies of tomato functional genomics (Ariizumi *et al.* 2011). Under NBRP tomato, the sequencing of full-length cDNAs (Aoki *et al.* 2010) and BAC end-sequencing (Asamizu *et al.* 2012) have been performed, and the information is available for the research community. In addition, the resequencing of the Micro-Tom genome has

been completed, and the high-quality genome sequence will soon be released. In association with these NBRP tomato activities, the development of other tools and information useful for tomato research and breeding is in progress by the tomato research community. These tools and resources will contribute to the rapid and efficient breeding of tomato and also to fleshy fruit research.

This special issue of *Breeding Science* highlights some of the recent progress and current challenges in accelerating tomato research and breeding. Five review articles of note represent the exciting frontier of the development of comprehensive tools and information for tomato research and breeding. These review articles cover the discovery of genes responsible for tomato yield (Ariizumi *et al.* 2013), tomato functional genomics (Aoki *et al.* 2013), DNA markers (Shirasawa *et al.* 2013), omic approaches for tomato breeding (Kusano *et al.* 2013) and tomato mutant resources and the TILLING platform (Okabe *et al.* 2013). Taken together, these review articles report the comprehensive tools and information that are changing tomato breeding from a random effort to inevitable research.

I appreciate the authors of the articles featured in this issue for their contributions and thoughtful insight on the current developments in this field of research. I hope that these review articles will serve as a valuable resource for advancing our technical knowledge on tomato research and breeding. Finally, I would like to thank Dr. Masaru Iwanaga, the Editor-in-Chief, and Dr. Kenji Katayama, the Managing Editor of *Breeding Science*, for providing the timely opportunity to prepare this special issue.

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