

Current Progress in the Tomato Chromosome No. 2 Sequencing

Doil Choi, Sung-Hwan Cho, Dal-Hoe Goo, Hong-Seok Park, Cheol-GooHur and SanghyeobLee

Plant Genome Research Center, KRIBB, Yusung, P.O. Box 115, 305-600, Republic of Korea

As a member of the international consortium, we are on the way of sequencing the complete euchromatic region of tomato chromosome No.2. Sequencing will proceed by minimum tiling path on the basis of BAC by BAC. Each sequenced BAC will serve as a seed from which to radiate out into the minimum tiling path. Identification of the correct next BACs in the euchromatin minimum tiling path for sequencing is based on the use of a BAC-end sequence (BES) database that is created as part of this project, as well as a fingerprint contig physical map that had been constructed. A bioinformatics portal will be created for this project that will be mirrored at several locations around the world and provide a mechanism by which researchers in different locations can develop and contribute bioinformatics tools and information to the project. Currently over 30 seed BACs of chromosome No. 2 were selected by marker-anchored BACs overgo probe hybridization and FISH. All of seed BACs sequences were finished and the initial stage of annotation was performed. More than 30 next BAC clones were also selected by BAC-end sequence BLAST and co-FISH with the seed BACs. Currently, we finished over 80 BAC clones that altogether cover about 7 Mb span of the tomato chromosome No. 2. The strategies and current progresses of tomato chromosome No. 2 sequencing will be presented in the meeting.