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APPROACHES TO SEQUENCING THE SHORT ARM OF TOMATO CHROMOSOME 12

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The Solanaceae is the third most economically important plant taxon that includes more than 3000 species. The International Solanaceae Genome Initiative is a project aimed to sequencing the tomato genome and to link it to the Solanaceae molecular map, exploiting the very high microsynteny conservation among the genomes of tomato, potato, pepper and eggplant. Tomato was selected as a reference since it provides the smallest diploid genome (950 Mb) with simple diploid genetics, short generation time, routine transformation technology, and availability of rich genetic and genomic resources. The tomato genome encodes approx. 35,000 genes, which are largely sequestered in contiguous euchromatic regions corresponding to less than a 25% of the total DNA in the tomato nucleus (220~250 Mb of gene rich regions). A physical map was constructed integrating FPC (Fingerprint Contig Physical) and overgo hybridization data at Cornell University. Selected "seed" BACs for each chromosome were distributed to the nine countries participating to this effort.

We have received 320 seed BACs anchored to 33 markers on chromosome 12. Fourteen seed BACs located on the short arm of chromosome 12 with insert size >100Kb are being analyzed. Molecular analyses were performed in order to verify the identity and the location of BACs. In particular, specific PCR based markers were developed according to sequence database reported at SGN (Solanaceae Genomic Network) website and FPC analysis/BAC-ends sequencing were performed. The position of BACs identified through PCR-marker association was confirmed by means of SNPs identified in *L. pennellii* ILs (introgression lines). Moreover, a mapping effort based on FISH was also initiated and FISH mapping of five clones is in progress, since FISH facilities are being set up at the University of Naples and CNR-IGV. Out of five BAC clones initially selected, two were completed sequenced and are being submitted to phase III on SGN register; the other three are still in the sequencing pipeline. Identification of additional clones to extend sequencing area in FPC contigs using BAC-ends overlapping approach has begun.

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