

THE ITALIAN CONTRIBUTION TO THE INTERNATIONAL TOMATO GENOME PROJECT

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Tomato (*Solanum lycopersicum*) is an economically and nutritionally valuable crop and constitutes a model plant for genetic research of the *Solanaceae* family. Its genome encodes approx. 35.000 genes, which are largely grouped in contiguous euchromatic regions corresponding to approx. 25% of the total 950 Mb genome. An international project is currently under way to sequence the euchromatic DNA of this species on a BAC-by-BAC strategy with Italy undertaking chromosome 12. BACs have been selected *via* genetic (Introgression Line) or cytogenetic (FISH) mapping. Each sequenced anchor BAC serves as a seed from which to radiate out into the minimum tiling path. Identification of the flanking BACs is performed by molecular validation along with analyses based on the use of bioinformatic platforms developed for the project. To date, sequences of 50 BACs representing more than 40% of the euchromatic region of Chromosome 12 are available. A bioinformatic platform has been built in-house to provide a preliminary annotation of the tomato genome. Sequencing and subsequent annotation of tomato genome are providing a reference enabling comparative genomics and systematics amongst higher plants.