

## **The tomato genome sequence: an enabling platform for tomato biology**

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Sequencing the tomato genome is the cornerstone of “The International Solanaceae Genome Initiative” or “SOL Initiative”. The tomato reference sequence provides gene content and order, which are well documented to be similar to other Solanaceae genomes, thus making the phenotypic and evolutionary diversity in this family accessible for exploration at the sequence level. Because the Solanaceae represents a distinct and divergent clade of flowering plants, the tomato sequence will also prove to be a resource for investigating the forces of gene and genome evolution that may not be as readily addressed via other plant genomes. The Solanaceae (including pepper, potato and eggplant) is the most important vegetable family worldwide in terms of value and production and tomato is the primary model system for fleshy fruit biology. Tomato is the centerpiece of the Solanaceae family in terms of available and expanding genomic resources, is the source of public genetic markers used for developing comparative maps and breeding tools across this family and to related crops (e.g. coffee), is a primary crop target for translational biology (due to ease of transformation, diploid genetics, short growth cycle) and is an expanding model for systems biology.

In collaboration with other groups at Cornell and BTI (Steve Tanksley, Greg Martin, Joyce Van Eck, Lukas Mueller, Zhangjun Fei) in addition to Colorado State, the University of Oklahoma, the University of Arizona and TIGR, we have been involved in the coordinated development of an integrated set of experimental tools for use in tomato functional genomics. The resources developed are being used by our group to expand our understanding of the molecular events underlying fruit development and are being made available to the research community for analysis of diverse plant biological phenomena. These resources include deep EST collections, tomato microarrays, BAC, fosmid and cosmid genomic DNA libraries, a tomato physical map, a tomato genome sequence (part of an international consortium effort) and collections of microarray and RNA-seq based expression profiles. We are contributing to the U.S. component of the International Tomato Genome Sequencing Project which released the first public build of the tomato genome sequence in December, 2009 and an assembly frozen for publication earlier this year. This project involves 10 funded countries.

Our group is using the tomato genome sequence primarily to address question in fruit biology. It has helped us in rapidly closing positional cloning projects targeting fruit ripening loci including for the tomato *uniform (u)* mutation and a mutation we call *non-ripening ethylene insensitive (nei)*. We are also using the tomato genome sequence to map RNA-seq and Chip-seq reads for fruit development expression profiling and characterization of *RIN-MADS* interacting promoters, respectively. Our most recent efforts include characterization of the tomato epigenome during fruit development and ripening which will be the emphasis of this presentation.

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