

# Tomato genome fully sequenced

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For the first time, the genome of the tomato, *Solanum lycopersicum*, has been decoded, and it becomes an important step toward improving yield, nutrition, disease resistance, taste and color of the tomato and other crops. The full genome sequence, as well as the sequence of a wild relative, is jointly published in the latest issue of the journal *Nature* (May 31, 2012).

Specifically, the genome was sequenced from the "Heinz 1706" tomato.

The publication caps years of work by members of the Tomato Genomics Consortium, an [international collaboration](#) between Argentina, Belgium, China, France, Germany, India, Israel, Italy, Japan, the Netherlands, South Korea, Spain, United Kingdom, United States and others.

James Giovannoni, a scientist at the Boyce Thompson Institute for Plant Research, located on the campus of Cornell University, and the U.S. [Department of Agriculture](#), lead the U.S. tomato sequencing team, which includes researchers at several institutions. The wild tomato (*Solanum pimpinellifolium*) [genome sequence](#) was developed at Cold Spring Harbor Laboratory.

Consortium researchers report that tomatoes possess some 35,000 genes arranged on 12 chromosomes. "For any characteristic of the tomato, whether it's taste, natural [pest resistance](#) or [nutritional content](#), we've captured virtually all those genes," says Giovannoni.

The sequences of these genes and their arrangement on the [chromosomes](#) are described in the Nature article, "The tomato genome sequence provides insights into fleshy fruit evolution," which is information that allows researchers to move at a quicker pace and plant breeders to produce new varieties with specific desired characteristics.

"Tomato genetics underlies the potential for improved taste every home gardener knows and every supermarket shopper desires and the genome sequence will help solve this and many other issues in tomato production and quality," says Giovannoni.

Now that the genome sequence of one variety of tomato is known, it will also be easier and much less expensive for seed companies and plant breeders to sequence other varieties for research and development, he added. Whereas the first tomato genome sequence came at a cost of millions of dollars, subsequent ones might only cost \$10,000 or less, by building on these initial findings.

To provide access to the gene sequences of the tomato and related species, Boyce Thompson Institute scientist Lukas Mueller and his team have created an interactive website ([www.solgenomics.net](http://www.solgenomics.net)). In the

United States, Boyce Thompson Institute scientists Zhangjun Fei and Joyce Van Eck contributed to the sequence and its analysis. Other U.S. institutions involved: Cornell University, Colorado State, University of Florida, University of Oklahoma, University of Georgia, University of Arizona, University of Delaware, Montana State, University of Tennessee, Cold Spring Harbor Laboratory and the USDA.

The sequencing of the tomato genome has implications for other plant species. Strawberries, apples, melons, bananas and many other fleshy fruits, share some characteristics with tomatoes, so information about the genes and pathways involved in fruit ripening can potentially be applied to them, helping to improve food quality, food security and reduce costs.

"Now we can start asking a lot more interesting questions about fruit biology, disease resistance, root development and nutritional qualities," Giovannoni says. Tomatoes represent a \$2 billion market in the United States alone. The USDA estimates that Americans consume, on average, more than 72 pounds of tomato products annually.

The sequencing would not have been possible without the work of Cornell's Steven Tanksley and Boyce Thompson's Greg Martin in the 1990s. Tanksley, Martin and other Ithaca scientists developed genetic maps and other molecular tools for tomatoes to study mechanisms of [disease resistance](#), and those tools ultimately paved the way for the consortium's sequencing efforts.

**More information:** The tomato Genome Consortium; Tomato genome sequencing and comparative analysis reveal two consecutive triplications that spawned genes influencing fruit characteristics, *Nature*, 2012.

The genome sequence and related resources can be accessed at the [Solgenomics website](#).

Provided by Cornell University

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