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Colorado State University Professor's Team among Group of International Scientists Who Sequenced DNA of the Tomato Genome

FORT COLLINS – Tomatoes could be reengineered to get tastier and survive droughts and pests now that a Colorado State University professor's team and some 300 other scientists from around the globe have sequenced the crop's DNA.

CSU Professor Stephen Stack and lab members Lindsay Shearer, Lorinda Anderson, Song-Bin Chang, and Suzanne Royer in the Department of Biology are part of the Tomato Genome Consortium (TGC) that includes scientists from 14 countries. The TGC –sequenced the tomato genome and wrote the cover story describing the results of a decade of work that appears in the journal *Nature* this week.

The sequence reveals the structure and order of tomato's roughly 35,000 genes. This knowledge will be fundamental to future improvements in tomatoes, such as taste and storage of fruits, as well as pest and drought resistance.

Since 2000, Americans have been eating an average of about 19 pounds of fresh tomatoes per person each year, according to the U.S. Department of Agriculture.

"We're not making a better tomato – that's not what we're doing - but there are people who will," said Stack, who has studied tomato chromosomes at CSU since 1978. "There are very few organisms that have had this kind of sequencing done – you can just about count them on one hand.

"This wasn't a quick and dirty shotgun sequence," he said of the scientific consortium's work. "It's a gold standard sequence." The work in Stack's and the other US labs involved is supported by the National Science Foundation (NSF).

Fresh market tomatoes were worth an estimated \$1.3 billion to U.S. growers last year, making it the nation's highest ranked fresh market vegetable in terms of total revenues. Processed and fresh tomatoes together account for \$2 billion in sales annually. Many colonial Americans believed the brightly colored fruit was poisonous, but tomatoes were an established part of the American diet by the mid 1800s.

The tomato belongs to the Solanaceae or nightshade family, the world's most important plant family for vegetable crops including tomatoes, potatoes, peppers and eggplants, and many plants used for spices, medicines, drugs, and ornamentals, such as tobacco, belladonna, mandrake, and petunia. The tomato genome sequence is a reference sequence for the whole family and as such will contribute to improvements in the other species as well.

Analysis of the tomato sequence indicates that the ancestral genome "triplicated" suddenly about 60 million years ago, close to the Cretaceous Boundary Event that resulted in mass extinctions, most notably disappearance of the dinosaurs. During subsequent evolution, most of the triplicated genes were lost, but some of the genes survived and specialized to control important features of the tomato, such as fruit characteristics including ripening time, firmness, and red pigmentation.

The genome sequence and related resources are freely accessible on the website <http://solgenomics.net>.

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