

## Scientists' tomato genome-mapping project provides key to unlocking improved flavor

Scientists from the U.S. Agricultural Research Service (ARS) and the Boyce Thompson Institute (BTI) may have pinpointed a gene responsible for improved flavor profiles for tomatoes, thanks to their recent genome-mapping project.

For the study, molecular biologist James Giovannoni with the ARS Plant, Soil and Nutrition Research Laboratory and BTI bioinformatics scientist Zhangjun Fei constructed the pan-genome for the cultivated tomato and its wild relatives, mapping almost 5,000 previously undocumented genes.

A genome is a biological map of an organism's genes and their functions. But a genome is usually of a single variety, which then acts as a reference genome for the rest of the species.

This pan-genome includes all of the genes from 725 different cultivated and closely related wild tomatoes, which revealed 4,873 genes that were absent from the original reference genome.

While cultivated tomatoes have a wide range of physical and metabolic variation, there have been several extreme bottlenecks during its domestication and breeding. This means today's tomatoes have a narrow genetic base.

The pan-genome helps identify what additional genes beyond the reference might be available for crop breeding and improvement.

In modern times, breeders have concentrated on traits such as yield, shelf life, disease resistance and stress tolerance – traits that have been economically important to growers.



“One of the most important discoveries from constructing this pan-genome is a rare form of a gene labeled TomLoxC, which mostly differs in the version of its DNA gene promoter. The gene influences fruit flavor by catalyzing the biosynthesis of a number of lipid (fat)-involved volatiles—compounds that evaporate easily and contribute to aroma,” explained Giovannoni.

In addition, the researchers found a new role of TomLoxC. It also facilitates the production of a group of apocarotenoids – organic chemicals that work as signaling molecules influencing a variety of responses in plants including environmental stresses.

The compounds also have a variety of floral and fruity odors that are important in tomato taste.

The rare version of TomLoxC was found in only 2% of older or heirloom cultivated large tomato varieties, although the version was present in 91% of currant-sized wild tomatoes, primarily *Solanum pimpinellifolium*, the wild predecessor of the cultivated tomato.

It is becoming more common in newer varieties, suggesting the industry’s shift in focus.

“It appears that there may have been strong selection pressure against or at least no selection for the presence of this version of TomLoxC early in the domestication of tomatoes,” Giovannoni added.

“The increase in prevalence of this form in modern tomatoes likely reflects breeders’ renewed interest in improved flavor.”

With the availability of this wide array of specific genetic information, breeders should be able to work quickly to increase the flavor of store-bought, mass production tomatoes while preserving the traits that make them an economically advantageous crop, noted the United States Department of Agriculture (USDA).

“These novel genes discovered from the tomato pan-genome added substantial information to the tomato genome repertoire and provide additional opportunities for tomato improvement. The presence and





absence profiles of these genes in different tomato populations have shed important lights on how human selection of desired traits have reshaped the tomato genomes,” said Fei.

The scientists expect the addition of nearly 5,000 genes to the tomato genome repertoire will provide additional opportunities for improvement as their roles in tomato biology and fruit quality are determined.

Their research involved collaboration with the University of Florida, The Pennsylvania State University, the University of Valencia, the University of Georgia and the Chinese Academy of Sciences, with support from the USDA’s Agricultural Research Service, U.S. National Science Foundation, BARD, the U.S.-Israel Binational Agricultural Research and Development Fund, and Vaadia-Bard Postdoctoral Fellowship Award.

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