

Arabica coffee genome sequenced

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Credit: UC Davis

The first public genome sequence for *Coffea arabica*, the species responsible for more than 70 percent of global coffee production, was released today by researchers at the University of California, Davis.

Funding for the sequencing was provided by Suntory group, an

international food and beverage company based in Tokyo.

Now available for immediate use by scientists and plant breeders around the world, the new genome sequence has been posted to Phytozome.net, the public database for comparative plant genomics coordinated by the U.S. Department of Energy's Joint Genome Institute.

Details of the sequence will be presented Sunday, Jan. 15, at the Plant and Animal Genome Conference in San Diego.

Sequencing of the *C. arabica* genome is particularly meaningful for California, where [coffee](#) plants are being grown commercially for the first time in the continental United States and a specialty-coffee industry is emerging.

"This new genome sequence for *Coffea arabica* contains information crucial for developing high-quality, disease-resistant coffee varieties that can adapt to the climate changes that are expected to threaten global coffee production in the next 30 years," said Juan Medrano, a geneticist in the UC Davis College of Agricultural and Environmental Sciences and co-researcher on the sequencing effort.

"We hope that the *C. arabica* sequence will eventually benefit everyone involved with coffee—from coffee farmers, whose livelihoods are threatened by devastating diseases like coffee leaf rust, to coffee processors and consumers around the world," he said.

The sequencing was conducted through a collaboration between Medrano, plant scientists Allen Van Deynze and Dario Cantu, and postdoctoral research scholar Amanda Hulse-Kemp, all from UC Davis.

Friendly challenge leads to *C. arabica* sequencing

A few years ago, Medrano—born and raised in coffee-producing Guatemala—was urged by colleagues in Central America to consider introducing genomic technologies to improve *C. arabica*.

In 2014, researchers elsewhere sequenced the genome of *Coffea canephora*—commonly known as robusta coffee and used for making coffee blends and instant coffee. There has been, however, no publicly accessible genome sequence for the higher-value and more genetically complex *C. arabica*.

Medrano was intrigued with the challenge to sequence *C. arabica*, but as an animal geneticist was experienced in the genomics of livestock—not crops.

Undeterred, he quickly tapped the expertise of molecular breeder Van Deynze, director of research at the UC Davis Seed Biotechnology Center and associate director of the UC Davis Plant Breeding Center, as well as Cantu, a plant geneticist in the UC Davis Department of Viticulture and Enology.

Sequencing intersects birth of California coffee farming

Coincidentally, the UC Davis research team was introduced to farmer Jay Ruskey, who with the help of University of California Cooperative Extension farm advisor Mark Gaskell, was growing the first commercial coffee plants in the continental United States at his Good Land Organics farm north of Santa Barbara.

Coffee is a tropical crop, traditionally grown around the world in a geographic belt that extends no more than 25 degrees north or south of the equator. But at Ruskey's Central Coast farm, coffee trees are

producing high-quality coffee beans at a latitude about 19 degrees north of any other commercial coffee plantations.

Ruskey also has planted coffee trees on some 20 other farms stretching from San Luis Obispo south to San Diego, launching what he believes will become a new specialty-coffee industry for California.

Working with Ruskey, the UC Davis researchers collected genetic material—DNA and RNA samples—from different tissues and developmental stages of 23 Geisha coffee trees growing at Good Land Organics. Geisha, known for its unique aromatic qualities, is a high-value *C. arabica* variety that originated in the mountains of western Ethiopia.

Plant material from one of the trees—UCG-17 Geisha—was used for developing the *C. arabica* [genome sequence](#).

***Coffea arabica*'s complex genome**

C. arabica is a hybrid cross derived from two other plant species: *C. canephora* (robusta coffee), and the closely related *C. eugenioides*. As a result of that hybrid crossing, *C. arabica*'s complex genome has four sets of chromosomes—unlike many other plants and humans, which have only two chromosome sets.

Genetic secrets revealed in Geisha variety

Using sequencing technology developed by Pacific Biosciences of Menlo Park, California, the UC Davis researchers estimated that UCG-17 Geisha has a genome made up of 1.19 billion base pairs—about one-third that of the human genome.

The study used a combination of the latest technologies for [genome](#)

[sequencing](#) and genome assembly from Dovetail Genomics of Santa Cruz, California, revealing an estimated 70,830 predicted genes.

Going forward, the researchers will focus on identifying genes and molecular pathways associated with coffee quality, in hopes that these will provide a better understanding of the flavor profiles of Geisha coffee.

They have sequenced samples from 22 other Geisha coffee trees to obtain a glimpse of the genetic variation within that variety and among 13 other *C. arabica* varieties, which will also be important for developing plants that can resist disease and cope with other environmental stresses.

Genome sequencing crucial for global industry

Jose Kawashima, president and CEO of Mi Cafeto Co. Ltd. in Tokyo, a leading specialty coffee company in Japan, stressed the importance of the discovery for all levels of global coffee production.

"Having worked in the coffee industry for over 40 years and visited coffee farms around the world, I have never witnessed as many quality *C. arabica* coffee farms under duress due to deteriorating social issues and the impacts of climate change," said Kawashima, who was not directly involved in the [genome](#) sequencing effort.

"Therefore, it is urgent that this scientific discovery be used to implement practical improvements at the farm level to sustain the future of the coffee industry," Kawashima said. "If sustainability can be achieved at the coffee producer level, then coffee lovers in consuming countries can continue to enjoy quality coffee."

Sequencing effort funded by Suntory

Funding for the sequencing project was provided by the Suntory group, through its Suntory Global Innovation Center Limited, located in Kyoto, Japan.

The *C. arabica* sequencing was of particular interest for the Suntory group, whose many brands include coffee drinks, marketed in Japan.

"We anticipate that functional analysis of the genes identified by the *C. arabica* sequencing will lead to development of new, disease-resistant coffee varieties with enhanced flavor and aroma characteristics," said Yoshikazu Tanaka, senior general manager for Suntory Global Innovation Center Limited.

"The Suntory Group will continue its research and development efforts to identify formulas and raw materials for creating coffee beverages that have higher added value, with a focus on safety, security and good taste," Tanaka said.

Provided by UC Davis

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