

Deciphering the walnut genome

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Credit: ARS

California produces 99 percent of the walnuts grown in the United States. New research could provide a major boost to the state's growing

\$1.6 billion walnut industry by making it easier to breed walnut trees better equipped to combat the soil-borne pathogens that now plague many of California's 4,800 growers.

In a new study, a team of scientists at the University of California, Davis, and USDA's Agricultural Research Service (ARS) used a unique approach to sequence the genomes of the English [walnut](#) and its wild North American relative by tapping into the capabilities of two state-of-the-art technologies: long-read DNA sequencing and optical genome mapping. The resulting genome sequences are believed to be of the highest quality ever assembled of any woody perennial.

"By sequencing the genome of a walnut hybrid, we produced complete genome sequences for both parents in the time normally required to produce the sequence of one genome," said Ming-Cheng Luo, leading genomics investigator on the project and a research geneticist in the Department of Plant Sciences at UC Davis.

This approach could be applied to genome sequencing of trees and many other woody perennials, opening the door to a better understanding of the genetic blueprints of almonds, pecans, pistachios and grapes.

"Like walnut, these other crops naturally cross-pollinate and are therefore highly variable," said Jan Dvorak, co-principle investigator and genetics professor at the Department of Plant Sciences at UC Davis.

"Variability has always greatly complicated our ability to produce a high-quality [genome sequence](#) for such crops, but these new technologies now make it possible," Dvorak added.

In California, walnuts are grown commercially using rootstocks chosen specifically for their ability to tolerate various soil-borne diseases.

"We chose to cross the widely used English walnut specifically with the

wild Texas Black walnut because of its native resistance to several soil-borne diseases and root nematodes, which are serious pests of walnut in California" said Dan Kluepfel, a USDA-ARS scientist and principal investigator of the walnut-rootstock development project.

The assembled [genome](#) sequences of the two walnut species also will now help researchers identify [genetic markers](#) that breeders can use to develop new varieties with improved pathogen and pest resistance.

More information: Tingting Zhu et al. Sequencing a *Juglans regia* × *J. microcarpa* hybrid yields high-quality genome assemblies of parental species, *Horticulture Research* (2019). [DOI: 10.1038/s41438-019-0139-1](https://doi.org/10.1038/s41438-019-0139-1)

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