Researchers uncover the hidden complexity of the Montmorency tart cherry genome

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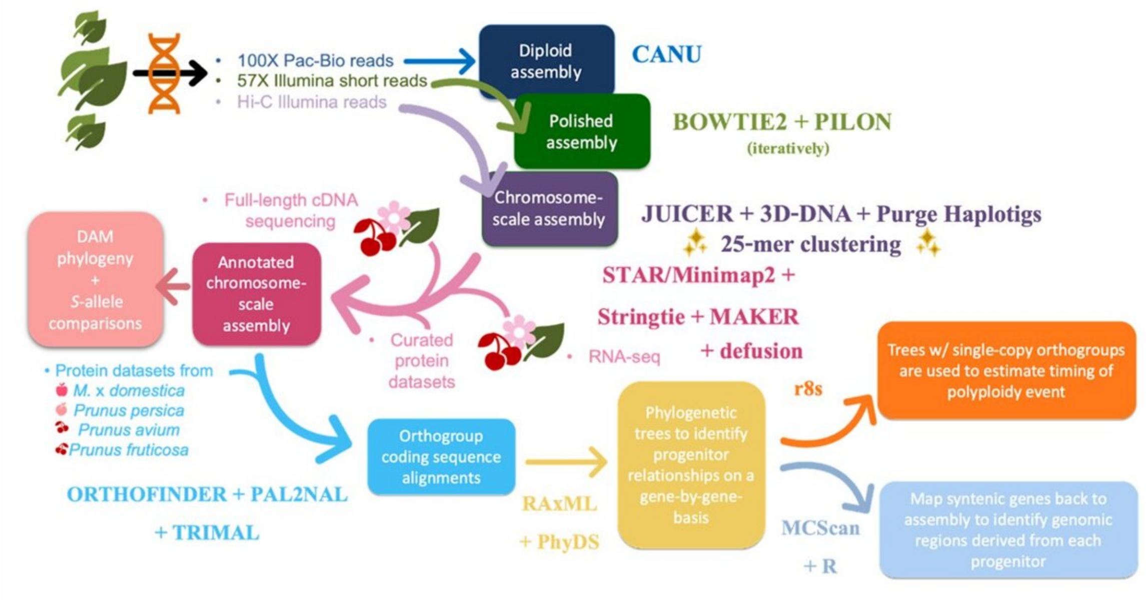

Workflow for the assembly and annotation of the P. cerasus 'Montmorency' genome and subsequent analyses. Credit: *Horticulture Research* (2023). DOI: 10.1093/hr/uhad097/7159687

Since Michigan is the nation's leading producer of tart cherries, Michigan State University researchers were searching for the genes associated with tart cherry trees that bloom later in the season to meet the needs of a changing climate. They started by comparing DNA sequences from late-blooming tart cherry trees to the sequenced genome of a related species, the peach. However, in a surprise to the researchers, the genetic discrepancies between the species outweighed the similarities. This led the team to create the first annotated Montmorency tart cherry genome and identify the DNA segments that code for each gene.

The research was published in the journal *Horticulture Research*.

"I naively thought that this would be an easy endeavor; we would simply sequence a few early and late-blooming cherry trees and align the sequences to the peach genome and get an answer in just a few weeks," said Courtney Hollender, an assistant professor in the College of Agriculture and Natural Resources at MSU. "I couldn't have been more wrong."

Genomes contain all the genes and genetic instructions for an organism's development. Sequencing it provides a map for researchers when they are trying to—for example—grow a cherry tree that will bloom later in the season. For Hollender's doctoral candidate, Charity Goeckeritz, an exercise in frustration piqued her curiosity.

"I was trying to align the tart cherry DNA sequences with the peach genome and they just weren't aligning very well," said Goeckeritz. "I was complaining about it to everyone and, finally, one of my friends suggested we just sequence the tart cherry genome."

Hollender and Goeckeritz teamed up with Amy Iezzoni, MSU professor emerita and the nation's only tart cherry breeder; Kathleen Rhoades, Iezzoni's doctoral student; Bob VanBuren, an assistant professor in the Department of Horticulture and MSU's Plant Resilience Institute; Kevin Childs, director of the MSU Genomics Core; and Patrick Edger, an associate professor in MSU's Department of Horticulture. Together they found that the Montmorency tart cherry genome was more intricate than they originally thought.

The complexities come from the tart cherry's parental plant chromosomes. Tart cherries are allotetraploids, meaning instead of having two sets of chromosomes like humans, they have four sets from at least two different species.

"Not only does tart cherry have four copies of every chromosome, but it also is the product of a natural cross between two different species," said Goeckeritz, "the ground cherry, Prunus fruticosa, and the sweet cherry, Prunus avium, that may have happened almost two million years ago."

While Goeckeritz is using the genome to study bloom time, Rhoades, who conducted the RNA sequencing or gene expression analysis for the project, is working to identify genes that are associated with specific fruit traits, such as color and firmness.

Having the Montmorency tart cherry genome sequence opens the possibilities for a tremendous amount of future research that will ultimately benefit the industry and the consumer by growing more trees that can withstand varying spring weather and produce more cherries.

"Before this genome, there were some sequences for tart cherries but it wasn't a complete picture, and I just wanted to have the genome for research and breeding purposes," said Hollender. "Now we have a complete picture, and this research will have a major impact on all future tart cherry research and breeding efforts worldwide."

More information: Genome of tetraploid sour cherry (Prunus cerasus L.) 'Montmorency' identifies three distinct ancestral Prunus genomes, *Horticulture Research* (2023). DOI: 10.1093/hr/uhad097/7159687.
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Provided by Michigan State University

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