

Core knowledge of tree fruit expands with apple genome sequencing

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An international team of scientists from Italy, France, New Zealand, Belgium and the USA have published a draft sequence of the domestic apple genome in the current issue of *Nature Genetics*.

The availability of a genome sequence for apple will allow scientists to more rapidly identify which genes provide desirable characteristics to the fruit and which genes and gene variants provide disease or [drought resistance](#) to the plant. This information can be used to rapidly improve the plants through more informed [selective breeding](#).

An organism's genome is the total of all its genetic information, including genes. Genes carry information that determines, among other things, a plant's appearance, health, productivity and color and taste of the fruit.

The domestic apple is the main fruit crop of the world's temperate regions. Apple is a member of the plant family Rosaceae which includes many other economically important species, including cherry, pear, peach, apricot, strawberry, and rose, to name just a few.

The state of Washington accounts for approximately 60 percent of total apple production in the U.S. and Rosaceae [fruit production](#) is a multi-billion dollar industry in the state. Washington state scientists played an important role in the project.

Led by Washington State University horticultural genomicist Amit Dhingra, the Washington-based team sequenced and analyzed a unique version of the genome of the golden delicious apple in which all duplicated chromosomes are genetically identical. This information was used to validate the sequence of the more complicated "heterozygous" golden delicious apple (in which duplicated chromosomes are not identical).

"Before [genome sequencing](#), the best we could do was correlate traits with genes. Now we can point

to a specific gene and say, 'This is the one; this gene is responsible for this trait'. That trait of interest might be, for instance, a disease, which is why sequencing the human genome was such an important milestone. Or the trait might be for something desirable, like flavor in a piece of fruit. We are already working on finding physiological solutions to issues like bitter pit in current apple varieties with the gene-based information available to us and lay a foundation for improved varieties in the future through generation of sports (mutations) and breeding," Dhingra said.

The Washington state contribution to the sequencing work was a unique collaboration between the cross-state Apple Cup rivals of WSU and the University of Washington.

Microbiologist Roger Bumgarner's lab at the University of Washington provided the initial sequencing expertise and capability to the project, which was later complemented and replaced by sequencing expertise in the Dhingra genomics lab, who obtained the same DNA sequencing instrument used in Dr. Bumgarner's lab.

"UW is a world leader in medical research and WSU is a world leader in agricultural research," said Bumgarner. "Technological advancements and techniques initially used to study medically important genomes and problems can be rapidly applied to genomes and problems of agricultural importance. We both had something to contribute and to learn from one another. I think there are many more opportunities for such collaborations to develop in the coming years."

After the sequencing was completed, WSU computational biologist Ananth Kalyanaraman contributed to the analysis by comparing the apple genome with that of pear, peach and grape to identify the differences and commonalities that exist between these fruit crops.

While the apple genome provides a valuable resource for future research, one pressing question answered by the international team's paper in [Nature Genetics](#) was one of origin. Scientists have long wanted to know — and have for years argued vehemently about — the ancestor of the modern domesticated apple. The question is now settled: *Malus sieversii*, native to the mountains of southern Kazakhstan, is the apple's wild ancestor. Now that that question is settled, scientists will begin using the apple genome to help breed apples with desirable new traits, including disease resistance and, potentially, increased health-benefitting qualities.

"Having the apple [genome sequence](#) will greatly accelerate our ability to define the differences between apple cultivars at the genetic level," said Kate Evans, an apple breeder based at the WSU Tree Fruit Research and Extension Center. "This will allow us to exploit these differences and target areas of diversity to incorporate into the breeding program, resulting in improved cultivars for the consumers that are also better suited for long-term, sustainable production."

Dan Bernardo, dean of the WSU College of Agricultural, Human, and Natural Resource Sciences, said, "The Washington apple is an icon of quality around the globe. This is a natural home for the advanced science necessary to map the tree fruit genome and actively study how it functions."

Provided by Washington State University

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