

# Scientists complete more comprehensive genetic analysis of domesticated grape

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Flame Seedless grapes. Photo by Patrick Tregenza.

(PhysOrg.com) -- U.S. Department of Agriculture (USDA) scientists have completed the most comprehensive genetic analysis to date of the domesticated grape, applying new technology to uncover a surprising degree of genetic diversity and fine-tune genetic markers that may lead to grapes better equipped to resist pests and pathogens that now prompt repeated spraying of grape crops.

The study, published in the [Proceedings of the National Academy of Sciences](#), shows that although wine and table grapes (*Vitis vinifera*) were domesticated up to 8,000 years ago in the Near East, they still have enough [genetic diversity](#) to offer untapped potential for developing

desirable traits, according to lead author Sean Myles, now a postdoctoral research scientist at the Stanford University School of Medicine.

"Grapes are one of the world's most economically important [fruit crops](#), and this study shows not only the potential for developing new approaches for improving existing varieties, but also the genetic relationships between many common varieties," said Edward B. Knipling, ARS administrator. ARS is the chief intramural scientific research agency of USDA.

The researchers say their results show that when breeders developed a successful wine or table [grape](#) variety, they were likely to continue planting it or its close relatives for centuries. As a result, grapes have experienced less intense breeding than other crops over the last millennia. That relative absence of crossbreeding has made grapes a natural target for many pests and pathogens, the researchers say. Many grape growers spend thousands of dollars each year spraying fungicides just to control powdery and downy mildews.

Grapes are woody perennial vines that take three years to mature from seedling to a fruit-bearing plant, so traditional breeding of new grape varieties is expensive and time-consuming. With the recent development of genomic tools for plant breeding, scientists worldwide have been searching for genetic markers associated with desirable traits in grapes. Scientists can use these markers to accelerate the development of grape varieties that are better equipped to resist diseases and pathogens, tolerate cold and drought, and offer the right mix of taste, maturity and other desirable traits.

In their study, the researchers found that domesticated grapes are likely to be sufficiently diverse to address many of the challenges faced by growers.

The researchers used a DNA microarray—a technology commonly used in genomics—equipped with 9,000 genetic probes to examine patterns of variation among pieces of DNA known as single nucleotide polymorphisms (SNPs) in 950 grape samples, also known as "accessions." Similar microarrays also have been developed to analyze the genomes of horses, cattle, sheep, corn and rice.

With the information generated from the custom microarray, the scientists developed a chart that outlines the genetic kinship of dozens of the grape accessions that produce some of the world's most popular wines, including Riesling and Pinot Noir.

The results also addressed confusion created by centuries of grape breeding and vegetative propagation. Over the years, when a grape variety sprouted a unique mutant trait or characteristic, such as a different fruit color, that new mutant was often vegetatively propagated and given a new name by a breeder. There are currently more than 10,000 names for grape cultivars worldwide but, from a genetic standpoint, some of the mutants that were named as new varieties were identical to their parents, or so nearly identical that genetic tests cannot distinguish between the mutant offspring and the parent, the researchers say.

As a result, Myles and his colleagues found that 58 percent of the 950 vinifera accessions they examined were so closely related that they appeared to be clones of at least one other accession.

**More information:** [www.pnas.org/](http://www.pnas.org/)

Provided by USDA Agricultural Research Service

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