

# Plant geneticists find veritas in vino

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Viticulture, the growing of grapes (*Vitis vinifera*) chiefly to make wine, is an ancient form of agriculture, evidence of which has been found from the Neolithic and Early Bronze Ages. We have a detailed understanding of how nurture affects the qualities of a grape harvest leading to the concept of terroir (the range of local influences that carry over into a wine).

The nature of the grapes themselves has been less well understood but our knowledge of this is substantially increased this week by the publication in the open-access journal PLoS ONE of a high quality draft genome sequence of a Pinot Noir grape by an Italian-based multinational consortium.

The genome of the grape is spread over 19 pairs of chromosomes and is around 504.6 megabases in length. The team of researchers, led by Dr Riccardo Velasco of the Istituto Agrario di San Michele all'Adige, used a shotgun sequencing approach, which has resulted in 10.7X coverage, 4.2X using pyrosequencing and 6.5X by Sanger sequencing. At the same time, the genome of the grape chloroplast was also sequenced and, remarkably, this was found to be identical to an independently determined sequence from a different strain of Pinot Noir that was published last year.

The grape, therefore, has a relatively small genome for a crop plant, similar to that of rice or poplar trees and much smaller than that of wheat or maize. Nevertheless, sequencing the genome was complicated by the degree of heterozygosity between pairs of chromosomes, some

11.2% of the sequence differing between homologous regions. There was so much variation, in fact, that Velasco describes it as like being “in the presence of two genomes.”

Moreover, the team discovered more than two million single nucleotide polymorphisms (individual letter changes in the grape’s genetic blueprint) in 87% of the 29,585 identified genes. While this made sequencing the genome difficult, it now provides a massive library of inherent variation with which to investigate which genes influence which characteristics of the growing plant and in what ways. “It is a treasure trove,” says Brian Dilkes of the University of California, Davis Genome Center, “as detailed a description of a plant genome sequence as I have seen in a ‘first’ paper”.

The genome can also provide clues to the evolution of grapes. Many plant genomes, especially those of crop plants, have been produced by at least one duplication of a smaller ancestral genome. Whether this was true for grapes had been controversial but this study clearly shows that ten of the 19 chromosomes resulted from a duplication that occurred shortly after the lineage of grapes diverged from that of the model plants *Arabidopsis* and poplar.

The breeding of grape vines is difficult because they take several years to grow to maturity and domesticated grapes tend to have very low fertility. For this reason, grapes are usually propagated by cuttings or graftings so that vineyards are filled with hundreds of thousands of genetically identical clones. This leaves grapes highly susceptible to the emergence of aggressive microorganisms, such as phyloxera, which devastated European grape production in the 19th and early 20th century, and powdery mildew, which continues to threaten American harvests to this day.

The Pinot Noir genome will provide an invaluable tool for creating grape

varieties resistant to such diseases without altering the quality of the resulting wine. Velasco and his colleagues have identified a large number of genes related to disease-resistance, 289 of which contain one or more SNPs. In spite of this, Pinot Noir remains susceptible to several fungi, bacteria and viruses possibly due to a defective system for recognition pathogen. Many of these disease-resistance genes are present in clusters whose associations with resistances or tolerances of different grape varieties to specific diseases can now be investigated. Also Pinot Noir can be crossed with many wild grapespecies providing a large reservoir of disease-resistancegenes, which can be exploited with the aid of this genome road map.

“This description of the grape genome presents an opportunity to direct genetic improvement or disease resistance,” says Brian Dilkes. “The genome sequence simultaneously identified hundreds of genes, which correspond to enzymes that produce flavor and aroma compounds. This will allow breeding for diseases resistance to proceed without disturbing the biochemistry of taste and grape quality. When I told sommelier Andrew Meadows about this recently, his reaction was, ‘Good! I would love to offer a decent Pinot for less than \$30’.”

This grape genome may also have implications beyond viticulture. Grapes can be both genetically transformed and micropropogated to produce hundreds of identical clones. With the sequencing of its relatively small genome, it is well placed to become a model organism for fruit trees in general. It is, however, in the safeguarding and improvement of grape stocks that the effects of this genome will be felt most strongly. “The sequence of the grape genome,” says Velasco, “together with the large arsenal of SNP loci, now offers a tool to open a new era in the molecular breeding of grapes.”

Source: Public Library of Science

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