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Compendium of Plant Genomes

Life Sciences : Plant Genetics and Genomics

Cantu, Dario, Walker, M. Andrew (Eds.)

The Grape Genome

- Describes the best practices to resolve and annotate grape genomes and transcriptomes
- Provides a uniquely comprehensive description of grapevine genetic diversity and its application in modern breeding programs
- Explains how domestication shaped the grape genome
- Links the grape genome composition and expression to viticulture traits and grape berry quality

This book describes the current state of international grape genomics, with a focus on the latest findings, tools and strategies employed in genome sequencing and analysis, and genetic mapping of important agronomic traits. It also discusses how these are having a direct impact on outcomes for grape breeders and the international grape research community. While *V. vinifera* is a model species, it is not always appreciated that its cultivation usually requires the use of other *Vitis* species as rootstocks. The book discusses genetic diversity within the *Vitis* genus, the available genetic resources for breeding, and the available genomic resources for other *Vitis* species. Grapes (*Vitis vinifera* spp. *vinifera*) have been a source of food and wine since their domestication from their wild progenitor (*Vitis vinifera* ssp. *sylvestris*) around 8,000 years ago, and they are now the world's most valuable horticultural crop. In addition to being economically important, *V. vinifera* is also a model organism for the study of perennial fruit crops for two reasons: Firstly, its ability to be transformed and micropropagated via somatic embryogenesis, and secondly its relatively small genome size of 500 Mb. The economic importance of grapes made *V. vinifera* an obvious early candidate for genomic sequencing, and accordingly, two draft genomes were reported in 2007. Remarkably, these were the first genomes of any fruiting crop to be sequenced and only the fourth for flowering plants. Although riddled with gaps and potentially omitting large regions of repetitive sequences, the two genomes have provided valuable insights into grape genomes. Cited in over 2,000 articles, the genome has served as a reference in more than 3,000 genome-wide transcriptional analyses.

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