

Session 7: Big Data

Keynote lecture

Genomes as research tools: from loci to candidate genes

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Abstract

Advances in sequencing technologies and assembly algorithms have led to astounding improvements in the quality of grape genome assemblies. Further development of scaffolding tools, like HaploSync, allow generating fully phased diploid and chromosome-anchored genomes. HaploSync (<https://github.com/andreaminio/HaploSync>) scaffolds sequences from a draft diploid assembly into phased pseudomolecules guided by a genetic map and/or the genome of a closely related species; it leverages the relationship between haplotypes to increase the assembly contiguity, improve completeness by filling gaps, correct scaffolding, and phase highly heterozygous, complex regions. Phased assemblies of grape genomes have revealed genomic complexities that were inaccessible in previous haploid representations, such as haplotype-specific structural variation events, trait-associated alleles, and allele-specific gene expression and methylation. The availability of wild and cultivated grape diploid genome references containing the genes and alleles underlying traits of interest has been instrumental in dissecting the genetic basis of disease resistance, flower sex determination, aroma, and flavor. Online services that provide public and timely access to these new genomic resources have also been developed. User-friendly web platforms, like www.grapegenomics.com and www.grapedia.org, aim to rapidly and broadly share genomic datasets and tools, and foster multidisciplinary collaborations and progress in grape research.