Contributions of the *Vitis*Gen2 project to grapevine breeding and genetics

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Abstract

The *Vitis*Gen projects (2011-2022) have improved the tools available for breeding new cultivars with regional adaptation, high quality and disease resistance. *Vitis*Gen2 (the second project in the series) is a multi-state collaboration (USDA-Geneva, New York; University of California, Davis; USDA-Parlier, California; Cornell University; Missouri State University; University of Minnesota; South Dakota State University; Washington State University; North Dakota State University; and E&J Gallo, California) to develop improved genetic mapping technology; to identify useful DNA marker-trait associations; and to incorporate marker-assisted selection (MAS) into breeding programs. A novel genetic mapping platform (rhAmpSeq) now provides 2000+ markers that are transferable across the *Vitis* genus. rhAmpSeq has been used in California, New York, Missouri, and South Dakota to identify new QTL for powdery and downy mildew resistance. In addition, fruit/flower traits that would normally take years to phenotype have been associated with predictive markers accessible from seedling DNA (e.g. malate metabolism, anthocyanin acylation, mono:diglucoside ratio, bloom phenology and flower sex). Over the past ten years, the project has used MAS to screen thousands of grape seedlings from public breeding programs in the United States, and and has produced "RenStack" public breeding lines to enable simultaneous access to 4 or 6 powdery mildew resistance loci from single source genotypes. High-throughput phenotyping for powdery and downy mildew resistance has been revolutionized with the Blackbird automated-imaging system powered by artificial intelligence for image analysis. Affordable DNA sequencing along with phenotyping innovations are transforming grapevine breeding.

Keywords: *Vitis*, breeding, marker-assisted selection, QTL, disease resistance, phenotyping, molecular markers