Grape genetic resources and research at the Davis California National Clonal Germplasm Repository

Ed. Stover[1], Malli Aradhya[1], Gerry Dangl[1], Bernard Prins[1], and Peter Cousins[2]
[1] USDA, ARS National Clonal Germplasm Repository, One Shields Ave., University of California, Davis, CA 95616, U.S.A. [2] USDA, ARS, Grape Genetics Research Unit, 630 W. North Street, Geneva, NY 14456

The U.S. National Plant Germplasm System is a component of the Agricultural Research Service of the United States Department of Agriculture (USDA). The National Clonal Germplasm Repository (NCGR) in Davis, California is one of 27 sites in the U.S. National Germplasm System, and is one of nine repositories which emphasize clonal materials. The NCGR houses most of the Mediterranean-adapted fruit and nut crop collections in the U.S., including grapes. Our missions are to acquire, preserve, characterize and distribute germplasm resources of our designated crops.

The Davis NCGR collection houses the world's largest grape species collection, including 46 *Vitis* species and totaling around 700 accessions. We also maintain a collection of over 1200 accessions of *V. vinifera*, about half of which are "wine grapes" and the other half "table grapes". In addition, we have over 900 designated hybrids, ranging from recognized "French hybrids" to *labrusca* types and breeders' selections. Our collection is further complimented by ~100 *V, rotundifolia* cultivars, wild collected material, and breeders' selections. Our *V. vinifera* collection includes cultivars from the following geographic areas: 167 accessions from France, 159 from Greece, 139 from Italy, 65 from Afghanistan, 61 from Germany, 46 from India/Pakistan, 24 from Hungary, and 16 from North Africa.

PUBLISHED PROJECTS ON GRAPE

Genetic structure and differentiation in *Vitis vinifera* L.: Eight Simple Sequence Repeat (SSR) loci, were used to fingerprint 222 cultivated *V. vinifera* and 22 wild *V. vinifera ssp*. *sylvestris* (1). Extensive genetic polymorphism and high levels of heterozygosity were observed among the accessions. All eight loci were polymorphic with the number of alleles per locus ranging from 5 to *19*. Multivariate relationships among accessions revealed sixteen genetic groups structured into three major clusters supporting the classical eco-geographic grouping of grape cultivars, *occidentalis, pontica*, and *orientalis* (6). French cultivars appeared to be distinct and showed close affinity to the wild progenitor, *V. v*. ssp. *sylvestris* from southwestern France (Pyrenees) and Tunisia. The gene diversity analysis revealed narrow divergence among groups and that most variation was found within groups (~85%).

Genetic diversity and classification within *V. vinifera* table grapes: Analysis of 40 seedless table grape cultivars using eleven highly polymorphic SSR loci confirmed several known synonyms, discovered a previously unknown synonym and disproved an alleged synonym in the literature (4). Cluster analysis grouped the cultivars loosely into three groups: a group of nine mostly Middle Eastern cultivars, a group of 22 accessions mostly from Russia and Afghanistan, which were morphologically similar to 'Thompson Seedless', and a third very loose group of 11 accessions consisting mostly of eastern European wine grape cultivars.

ONGOING PROJECTS ON GRAPE

Genetic variability and differentiation within and between European and Asian Grapes: In this study, 159 varieties representing the three eco-taxonomic groups, *pontica*, *occidentalis*, and *orientalis,* along with a fourth group comprising 58 varieties from Turkmenistan, were analyzed for genetic diversity and relationships using 17 polymorphic SSR markers (2). In the cluster analyses, the western European wine grapes, along with a few central European ones, formed three distinct groups. Several distinct groups contained both the West Asian and Turkmenistan grapes, with some subgroups exclusively containing Turkmenistan varieties. The FST, which is a measure of genetic differentiation among groups, accounted for nearly 84% of the total variability with only 18% residing within groups.

Transportability and phylogenetic utility of SSR markers in the genus *Vitis:* Transportability of SSR markers within and among cultivated and wild species of grapes was tested (3). Altogether, 304 accessions representing 44 taxa, including the cultivated *V. vinifera*, its putative progenitor, ssp. *sylvestris*, and three taxa of *Muscadinia*, were analyzed using 10 SSR markers known to be polymorphic

in *V. vinifera*. The cluster analyses revealed several affinities roughly corresponding to the seven taxonomic series recognized based on morphological criterion within the New World group (5). The distance Wagner tree, based on the Prevosti distance among different taxonomic series and Asian taxa with *Muscadinia* as outgroup, revealed two major affinities: (1) *Labruscae-Vulpinae-Precoces* affinity; (2) *Aestivales-Viniferae-Cinerascentes-Occidentales* affinity combined with the Asian group. Overall, the genetic structure suggests the existence of complex subdivisions within and between taxa and taxonomic series of the genus *Vitis*.

Utilization of markers in collection management: Since SSR marker analysis revealed that most variation in *V. vinifera* (~85%) is common to all the genetic groups, only minimal gains in variability are likely through extensive collection of varieties from diverse eco-geographic sources. Unique cultivated genotypes and wild *V. vinifera* (ssp*. sylvestris*) appear likely to be the sources of new alleles in cultivated *V. vinifera*, apart from the slow process of bud mutation. International adoption of a uniform set of six SSR markers (7) greatly enhances the ability to compare NCGR accessions with fingerprints from "type" collections around the world and verify accession identity. Trueness to type is being confirmed for French, Portuguese, and Spanish accessions in the NCGR collection by comparison with fingerprints from respective national collections. We welcome similar opportunities with other cultivars in the NCGR collection.

NEW ACQUISITIONS AND DISTRIBUTION FROM THE NCGR *VITIS* COLLECTION: We are committed to acquiring additional material and are very interested in learning of opportunities, with a special interest in protecting collections which may otherwise be lost. It is NPGS policy to distribute plant material, free of charge, to research interests around the world (see our website http://www.ars-grin.gov/dav/).

References

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