Genetics and Genomics of Grape Growth, Development, and Quality

ARS LOCATION:
Grape Genetics Resources Unit (PGRU)
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PRINCIPAL INVESTIGATORS:
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PROJECT OBJECTIVES:
1. Determine some of the key genetic factors controlling environmental adaptation and fruit quality differences among cultivated grapes and between cultivated and wild grapes.
2. Develop grape germplasm with novel phenotypes for fruit quality traits.

MAJOR ACCOMPLISHMENTS (2007–2010):
Localizing genes for cold hardiness in grape:
Grapevines grown in many regions of the eastern United States are poorly adapted to low-temperature and frequently are damaged by severe winters and fluctuating temperature during the spring and fall. There is tremendous variation among cultivated and wild grapes for tolerance to low-temperature stress, including some types that can survive -40 F. To understand the genetic control of freezing tolerance, the locations of genes controlling freezing-tolerance were identified in the grape genome based on the analysis of offspring of parents that differ dramatically in their cold hardiness. This experiment was conducted in a population of 190 individuals and utilized over 400 molecular markers to help identify regions of the genome that are important for freezing tolerance. The mapping of this trait is the first step in developing an assay that will improve the selection efficiency within grape breeding programs for this trait and generating improved cultivars of grape for cold climates.

Phenotyping Secondary Metabolites of USDA-ARS *Vitis* Germplasm:
Grape secondary metabolites (such as anthocyanins and other polyphenols) encompass a range of phytochemicals that are important to human nutrition and health. The distribution of these phytochemicals across a wide range of germplasm is poorly known, which limits the informed use of the germplasm for marker assisted, target oriented breeding. A collaborative project with several researchers of Cornell University was recently initiated to characterize key secondary metabolites, polyphenols in particular, of the USDA-ARS *Vitis* germplasm collections. Two years of data have been collected for 344 *V. vinifera* accessions from the Davis repository and 200 wild accessions of mainly native species from the Geneva repository. Tremendous variation of various polyphenolic compounds (anthocyanins, hedroxybenzoic acids, hydroxycinnamic acids, flavanols, and flavonols) was found in the collections. This

project will help develop a database of health and nutrition-related metabolites for USDA *Vitis* germplasm. It will also help develop future research models for integrating germplasm characterization with genetic and gene discovery research.

TECHNOLOGY TRANSFER/OUTREACH:

- Co-hosted 1-day GGRU and Grape Industry Workshop with National Grape Cooperative Association/Welch's in Dunkirk, NY, in December 2007.
- Hosted GGRU Focus Group meetings in May 2007 and October 2009 in Geneva, NY.
- Partnered with Cornell University in hosting various field tours, grape grower's meetings and other outreach activities.

EXTERNAL SUPPORT:

- Grape and Wine Genomics. Genome Canada. $3,440,481 (PI: Steve Lund, co-PIs: H. van Vuuren, C. Owens, J. Bohlmann, M. Howlett, D. Laycock, G. van der Merwe, V. Measdey) 2009-2012.
- WineGen-Genomics of Viticulture and Enology. GenomeBC. $5,035,588 (PI: Steve Lund, Co-PIs: C. Owens, R. Gardner, H. van Vuuren, J. Bohlmann, S. Murch, M. Trought, C. Winefield, V. Measdey, T. van Rooyen, M. Goddard) 2008-2009
- Viticulture Consortium East (2010): Improve Concord Grape Variety Through Mutation Discovery. $16,660

COLLABORATORS:

David Ramming, Angela Baldo, Peter Cousins, Lance Cadle-Davidson, Malli Aradhya, Ed Buckler, Doreen Ware, and Xiaohong Wang, ARS; Greg Loeb, Jan Nyrop, Bruce Reisch, Rick Dunst, Terry Bates, Lailiang Chen, and Sean Myles, Cornell University; Anne-Francoise Adam-Blondon and Patrice This, INRA; Jiang Lu, Florida A&M University; Anne Fennell, South Dakota State University; Jim Luby, University of Minnesota; and Steve Lund, University of British Columbia.

RECENT PUBLICATIONS:

- Myles S, Chia J-M, Hurwitz B, Simon C, Zhong GY, Buckler E, Ware D (2010) Rapid GenomicCharacterization of the Genus Vitis. PLoS ONE 5: e8219
- Owens, C.L., B.I. Reisch, H.R. Schwaninger, M. Aradhya, C. J. Simon, S. Manahil, R. Loughner, K. Wentworth, G. Loeb, J. Nyrop (2010). QTL analysis of predatory mite abundance and leaf morphology traits in a hybrid grape population. 10th international conference on grapevine breeding and genetics, Geneva, NY.
- Garris A, Clark L, Owens C, McKay S, Luby J, Mathiason K, and Fennell A (2009) Mapping of photoperiod induced growth cessation in the wild grape Vitis riparia, Journal of the American Society for Horticultural Science 123:261-272.
- Owens C.L. 2008 "Grapes". In *Breeding Temperate Fruit Crops: Germplasm to Genomics*, Hancock, J.F. (ed.). Springer.
- Zheng P, Allen W, Roesler K, Williams M, Zhang S, Li J, Glassman K, Ranch J, Nubel D,
- Solawetz W, Bhattramakki D, Llaca V, Deschamps S, Zhong GY, Tarczynski M, Shen B. (2008) A phenylalanine in DGAT is a key determinant of oil content and composition in maize. Nature Genetics 40:367-372.

- Mahanil, S., B.I. Reisch, C.L. Owens, P. Thipyapong and P. Laosuwan 2007. Resistance Gene Analogs (RGAs) from *Vitis cinerea*, *V. rupestris*, and *V.* hybrid 'Horizon'. American Journal of Enology and Viticulture. 58:484-493.
- This, P., T. Lacombe, M. Cadle-Davidson, and C.L. Owens. 2007. Wine grape color (*Vitis vinifera* L.) associates with allelic variation in the domestication gene *VvmybA1*. Theoretical and Applied Genetics 114:723-730.