

“Development of disease resistant grapes for cold climates and the integration of traditional with molecular approaches”

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Since 1885, Cornell University and the New York State Agricultural Experiment Station have continuously operated a program in grapevine breeding. The current emphasis is on quality wine grape variety development among interspecific hybrids, which combine cold tolerance with fungal disease resistance. The traditional program (based on hybridization of elite parental lines and field/lab selection protocols) has produced new cultivars with a significant economic impact upon the wine grape industry in the eastern United States. To aid this process, Lance Cadle-Davidson and Bruce Reisch are now leading a national effort (25 investigators), funded by a competitive grant from the USDA-National Institute of Food and Agriculture, to use the tools of next-generation sequencing to find up to 100 new marker-trait associations, and to apply this information for both parent and seedling selection. This project, called “*VitisGen*”, has been underway for nearly two years. Maps based on SNPs acquired through “genotyping-by-sequencing” (GBS) in 18 populations are under development with a goal of 50,000 markers per map. Our current approach to the analysis of GBS marker data results in the mapping of up to 20,000 genetic markers per population, including alleles not present in the *V. vinifera* reference genome. In addition to the cutting-edge GBS markers, traditional SSR marker analyses contributed to marker-assisted breeding (MAB) efforts in the first year, as the project works to develop direct MAB decisions from GBS/SNP data. More information about the *VitisGen* project can be found at <[www.vitisgen.org](http://www.vitisgen.org)>.