

Use of Genomics for Blueberry Improvement

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The U.S. is the world's leading blueberry producer. Commercial production of blueberry utilizes multiple species in the section *Cyanococcus* of the genus *Vaccinium*. About 2/3 of blueberry production is from improved cultivars of highbush blueberry (*V. corymbosum*), and to a lesser extent rabbiteye blueberry (*V. virgatum*). The other 1/3 of blueberry production is from wild, managed stands of lowbush blueberry (*V. angustifolium*). Environmental stresses, such as low temperature extremes, reduce blueberry yields and impact the profitability and competitiveness of U.S. producers. Enhanced cold tolerance, including tolerance to winter freezing and spring frosts, is needed for genetic improvement of current highbush blueberry cultivars. Our laboratory has been using a genomic approach to increase our understanding of the genetic control of cold hardiness in blueberry to ultimately use this information to develop more cold hardy cultivars. Specifically, EST libraries, cDNA microarrays, and subtractive hybridizations have been used to identify many genes that are differentially expressed during cold acclimation in blueberry under field and cold room conditions, and to compare expression of these genes in cold sensitive and cold tolerant genotypes. An important transcription factor in the cold-response pathway, called CBF, was identified in our subtracted libraries, cloned and sequenced, and expressed in *Arabidopsis* to examine its effect on cold tolerance. A recently funded Specialty Crop Research Initiative grant entitled "Generating Genomic Tools for Blueberry Improvement" is currently allowing us to perform deeper sequencing of the blueberry transcriptome using "next generation" 454 sequencing technology, develop SSR and EST-PCR markers from the ESTs, and use these markers to further saturate our genetic linkage maps and identify quantitative trait loci associated with cold hardiness, chilling requirement, and fruit quality traits. Markers are also being used in studies of genetic diversity, spatial genetic structure, and gene flow in the wild lowbush blueberry and to construct a phylogenetic tree of *Vaccinium* species in the section *Cyanococcus*. To date, over one million transcriptome sequences have been generated from fruit at different stages of development, flower buds at different stages of cold acclimation, and leaves by 454 sequencing. Over 600,000 sequences have been assembled into approximately 15,000 contigs. Availability of these genomic tools will allow future advances such as the development of a larger blueberry microarray and the use of marker-assisted breeding.