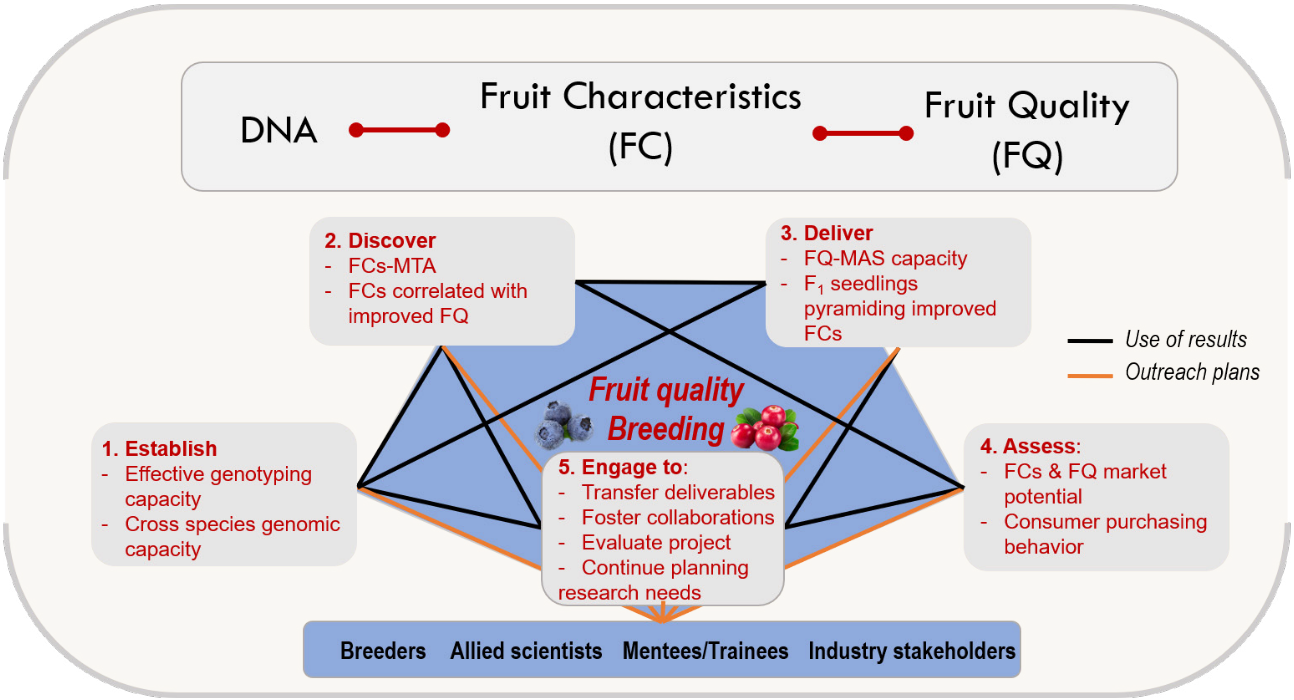
VacCAP
IMPROVING FRUIT QUALITY

Project Accomplishments Report

VacCAP Objectives

The Vaccinium Coordinated Agricultural Project (VacCAP) leveraged an interdisciplinary approach to advance development of blueberry and cranberry cultivars with improved fruit quality attributes.



DNA — Fruit Characteristics (FC) — Fruit Quality (FQ)

1. Establish
- Effective genotyping capacity
- Cross species genomic capacity

2. Discover
- FCs-MTA
- FCs correlated with improved FQ

3. Deliver
- FQ-MAS capacity
- F_1 seedlings pyramiding improved FCs

4. Assess:
- FCs & FQ market potential
- Consumer purchasing behavior

5. Engage to:
- Transfer deliverables
- Foster collaborations
- Evaluate project
- Continue planning research needs

Fruit quality Breeding

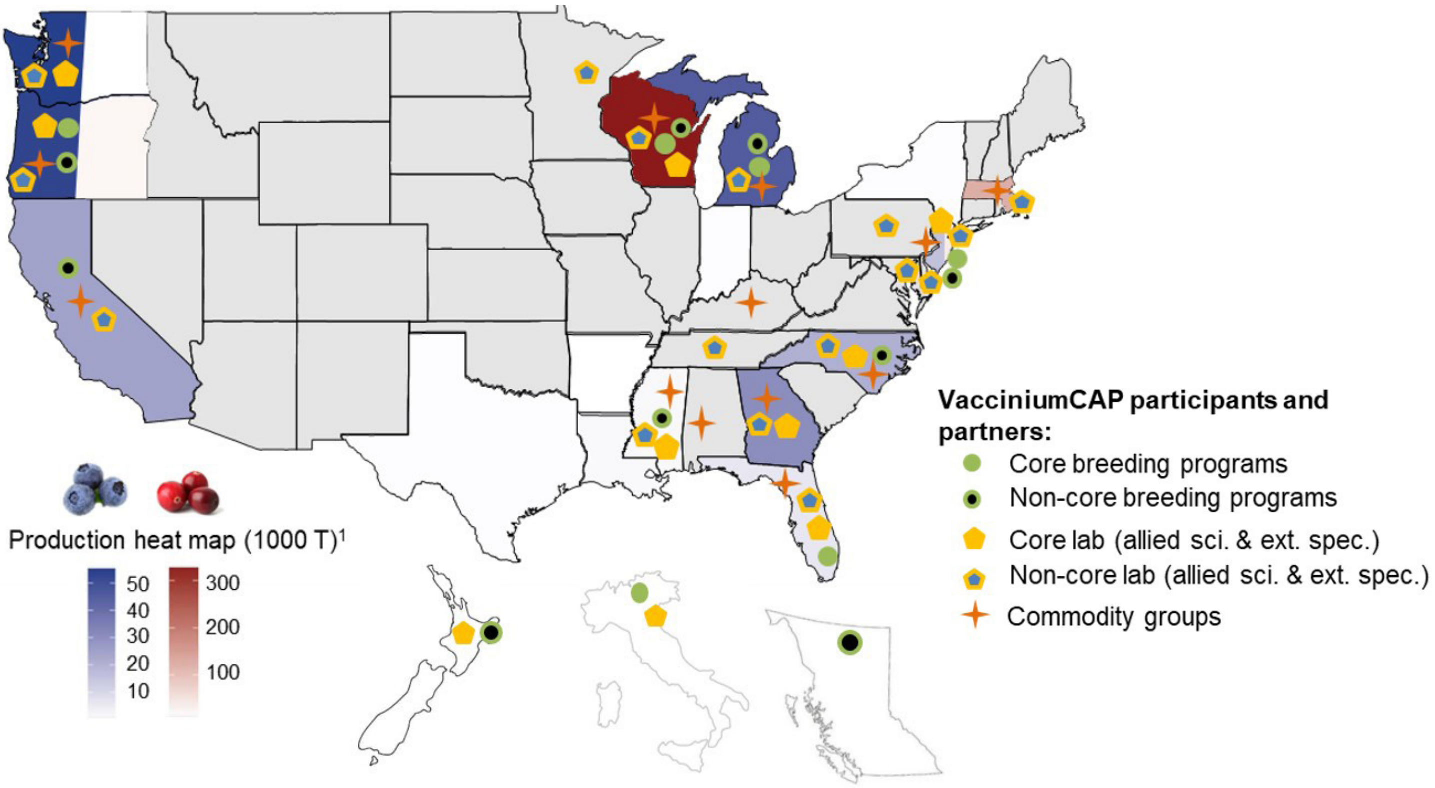
Use of results

Outreach plans

Breeders Allied scientists Mentees/Trainees Industry stakeholders

United States Department of Agriculture
National Institute of Food and Agriculture
Award #: 2019-51181-30015

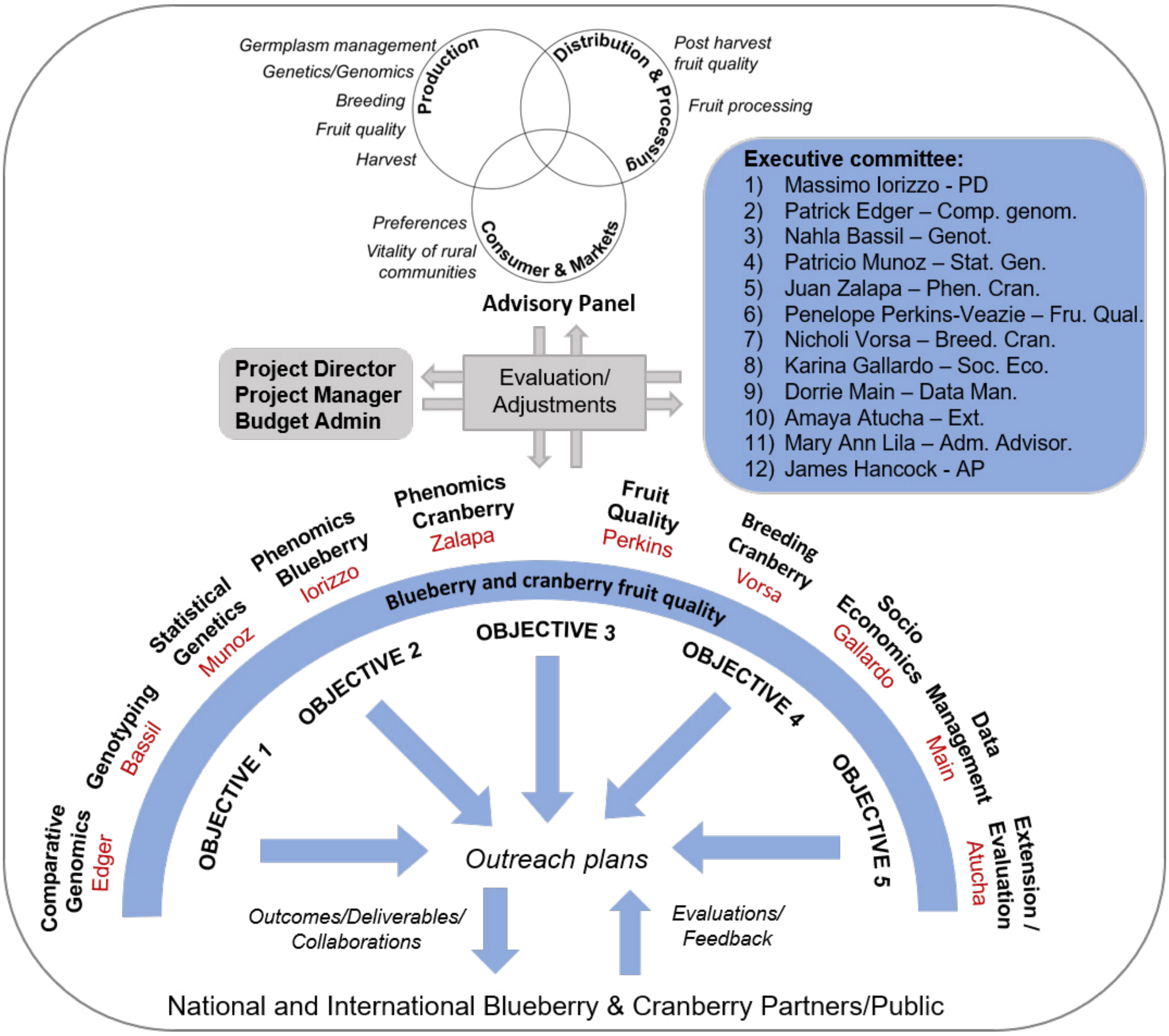
VacCAP PIs and Partners



- Massimo Iorizzo, Project Director, North Carolina State University
- Amaya Atucha, Co-PD, University of Wisconsin-Madison
- Nahla Bassil, Co-PD, USDA-ARS and NCGR
- Patrick Edger, Co-PD, Michigan State University
- Karina Gallardo, Co-PD, Washington State University
- Mary Ann Lila, Co-PD, North Carolina State University
- Dorrie Main, Co-PD, Washington State University
- Patricio Munoz, Co-PD, University of Florida
- Claire Luby, Co-PD, USDA-ARS and HCRL
- Penelope Perkins-Veazie, Co-PD, North Carolina State University
- Nicholi Vorsa, Co-PD, Rutgers University
- Juan Zalapa, Co-PD, University of Wisconsin-Madison
- Chad Finn, Co-PD, USDA-ARS and HCR
- Elizabeth Canales, Co-PI, Mississippi State University
- David Chagné, Co-PI, Plant and Food Research Ltd
- Lisa Wasko DeVetter, Co-PI, Washington State University
- Richard Espley, Co-PI, Plant and Food Research Ltd
- Lara Giongo, Co-PI, Fondazione Edmund Mach
- Changying Li, Co-PI, University of Georgia
- James Polashock, Co-PI, USDA-ARS and GIFVL
- Gina Sideli, Co-PI, Rutgers University
- Charles Sims, Co-PI, University of Florida
- Michael Coe, Key Personnel, Cedar Lake Research Group
- Jennifer Johnson-Cicalese, Co-PI, Rutgers University
- Jenyne Loarca, Co-PI, USDA-ARS
- Josie Russo, Communications Specialist

How VacCAP Was Managed

Our VacCAP team is listed below and organized by project objective. Nine project teams managed the project and worked collaboratively across project objectives.



Breeding Teams

- Team Leaders: Chad Finn (Blueberry), N. Vorsa (Cranberry)
- Team members: P. Munoz, P. Edger, N. Vorsa, L. Giongo, J. Zalapa, M. Iorizzo, C. Luby
- Tasks: Finalize the list and maintain the material to use in this project. Collect and distribute blueberry and cranberry materials to be used in this project. Develop blueberry/ cranberry F1 progenies to pyramid multiple superior fruit quality traits (Obj. 3). Coordinate the implementation of standardized phenotyping protocols for on-site fruit quality assessment in collaboration with the blueberry/cranberry Phenomic Teams (Obj. 2-3). Serve as a training group to use the data collection software (e.g. Field Book) and BIMS system in collaboration with the Data Management Team. Act as liaison between the Extension Team, the PD, and blueberry and cranberry industry organizations.

Comparative Genomics Team

- Team Leader: P. Edger
- Team members: N. Bassil, P. Munoz, J. Zalapa, N. Vorsa, J. Polashock, D. Chagné. R. Espley.
- Tasks: Coordinate the activities required to develop and characterize the *Vaccinium* pangenome (Obj. 1a) that will be used to develop the SNP catalog. Collaborate with Genotyping Team to establish the SNP catalog (Obj. 1b) and provide bioinformatic analysis needed to select the final set of SNPs used to validate the *Vaccinium* Genotyping Platform (Obj. 1c). Liaise with Breeding and Statistical Genetic Teams to finalize the list of blueberry and cranberry material needed for the comparative genomic analysis. Liaise with Data Management and Extension Teams to deliver genomic resources through the Genome Database for *Vaccinium* (GDV) and to provide content about the comparative genomic outcomes (Obj. 1a).

How VacCAP Was Managed

Genotyping Team

- Team Leader: N. Bassil
- Team members: P. Edger, P. Munoz, J. Zalapa, N. Vorsa, L. Giongo, D. Main, M. Iorizzo, J. Polashock, D. Chagné, J. Johnson-Cicalese
- Tasks: Coordinate activities to develop the SNP catalog, validate the SNP set, organize the *Vaccinium* Genotyping forum, and finalize selection and validation of the *Vaccinium* Genotyping Platform (Obj. 1b-c). Collaborate with the Breeding and Statistical Genetics Teams to finalize the list of blueberry and cranberry germplasm needed for the genotyping platform validation. Extract DNA and genotype the blueberry and cranberry samples for the genetic and validation studies (Obj. 2b, 3b). Will provide content for Extension efforts on outcomes.

Statistical Genetics Team

- Team Leader: P. Munoz
- Team members: J. Zalapa, M. Iorizzo, N. Vorsa, L. Giongo, N. Bassil, P. Edger, J. Polashock, J. Johnson-Cicalese
- Tasks: Coordinate activities required to perform marker-trait association analysis and QTL/marker validation (Obj. 2b, 3b). Will collaborate with Breeding Team to finalize the list of germplasm to be used in the project. Provide support for statistical analysis needs. Liaise with the Data Management Team to use the computational infrastructure to store and deliver markers/QTL data through the GDV (public and private partitions). Liaise with the Extension Team to provide content about the marker-trait association analysis and QTL/ marker validation outcomes (Obj. 2b, 3b).

Phenomic Teams

- Team Leaders: M. Iorizzo/L. Giongo (blueberry), J. Zalapa (cranberry)
- Team members: P. Munoz, P. Perkins-Veazie, M.A. Lila, D. Main, J. Polashock, N. Vorsa, J. Johnson-Cicalese
- Tasks: Coordinate activities required to implement phenotyping methods (Obj. 2a, 3a). Collaborate with the Statistical Genetics Team on marker trait association analysis (Obj. 2a) and QTL/ marker validation (Obj. 3b). Collaborate with the Fruit Quality and Socio-Economic (Blueberry) Teams to correlate fruit characteristics and their performance for shelf life, resistance to bruising, sensory panel (Obj. 2c) and potential economic value (willingness to pay) (Obj. 4a). Liaise with the Breeding and Statistical Genetics Teams to finalize the list of blueberry and cranberry germplasm needed for the phenotypic analysis (Obj. 2a-3a). Liaise with the Data Management Team to use the data management computational infrastructure to store and/or deliver phenotypic data through the GDV (public and private partitions). Liaise with the Extension Team to provide content about outcomes delivered through the phenotypic analysis (Obj. 5).

Fruit Quality Team

- Team Leader: P. Perkins-Veazie
- Team members: C. Li, C. Sims, M.A. Lila, L. Giongo, M. Iorizzo, P. Munoz
- Tasks: Coordinate activities required for the blueberry fruit quality studies, which includes the evaluation of shelf-life, sensory panel and bruising damage (Obj. 2c) in collaboration with the Phenomic and Breeding Teams. Will collaborate with the Socio Economic Team to plan and conduct a joint consumer panel analysis. Will liaise with the Extension Team to provide content regarding the outcomes delivered through the fruit quality studies (Obj. 2c) and the Extension outreach plans.

Socio-Economics Team

- Team Leader: K.R. Gallardo
- Team members: E. Canales, C. Sims
- Tasks: Coordinate activities required to perform the socio-economic studies (Obj. 4). Collaborate with the Breeding, Phenomic and Fruit Quality Teams to acquire blueberry plant material, phenotyping and sensory data. Work with Extension Team to provide content about the outcomes delivered through the socio-economic studies and to develop outreach activities planned by the Extension Team (Obj. 5).

Extension Team

- Team Leader: A. Atucha
- Team members: D. Main, L. De Vetter, M. Coe (External Evaluator)
- Tasks: Coordinate activities and provide content for the extension and outreach activities/resources (Obj. 5). Will collaborate with the Data Management Team to develop and populate the VacCAP extension platform and work with External Evaluator to collect and evaluate feedback

National and International Partners

Breeding and Molecular Geneticist Partners

- Hamid Ashrafi, Assistant Professor, North Carolina State University
- Mark K. Ehlenfeldt, Research Geneticist, USDA-ARS
- Stephen Stringer, Research Geneticist, USDA-ARS
- Lisa J. Rowland, Research Geneticist, USDA-ARS
- Jeff Neyhart, Research Geneticist, USDA-ARS
- Kalpalatha Melmaiee, Associate Professor, Delaware State University
- Ebrahiem Babiker, Research Geneticist, USDA-ARS
- Moira Sheehan, Director of Breeding Insight, Cornell University
- Jim Hancock, Breeder, Berry Blue, LLC
- Jim Olmstead, Global Breeding Director-Blueberry, Driscoll's, Inc.
- Mathew Kramer, Director of Product Development & Commercialization, Fall Creek Farm & Nursery, Inc.
- Bob Gabriel, President, Oregon Blueberry Farm and Nursery
- Edward Grygleski, Cranberry Breeder and Producer, Valley Corp.
- Rachel Itle, Assistant Research Scientist, University of Georgia
- Michael Hardigan, Research Geneticist, USDA-ARS

Fruit Quality Partners

- Anne Plotto, Research Plant Physiologist, USDA-ARS
- Randy Beaudry, Professor, Michigan State University
- Steve Sargent, Professor and Associate Chair, University of Florida
- Rod Serres, Manager Agricultural Science, Ocean Spray
- Andy Reitz, Director of Grower Relations, Mariani Co., Inc.
- Mike Mainland, Professor Emeritus, North Carolina State University
- Ann Colanna, Sensory Program Director, Food Innovation Center, Oregon State University

Bioinformatics and Biotechnology Partners

- Robert Reid, Assistant Professor Bioinformatics, University of North Carolina-Charlotte
- Margaret Staton, Associate Professor of Bioinformatics, University of Tennessee
- Guo-Qing Song, Associate Director Plant Biotechnology Resource & Outreach Center, Michigan State University

Extension Network

- Ali Sarkhosh, Assistant Professor, University of Florida
- Cassie Bouska, Assistant Professor, Oregon State University
- Carlos Garcia-Salazar, Extension Educator, Michigan State University
- Kim Patten, Director Pacific Co. and Extension Professor, Washington State University

Extension Network (Continued)

- Cesar Rodriguez-Saona, Extension Specialist, Rutgers
- Renee Allen, Extension Specialist, University of Georgia
- William O. Cline, Research and Extension Specialist, North Carolina State University
- Kathleen Demchak, Senior Extension Associate, Penn State University
- Ben Faber, Advisor, Cooperative Extension Ventura County
- Mary Rogers, Associate Professor, University of Minnesota
- Hilary A. Sandler, Director of UMass Cranberry Station and Extension Associate Professor, University of Massachusetts-Amherst
- Erick D. Smith, Assistant Professor, University of Georgia
- Eric Thomas Stafne, Extension/Research Professor, Mississippi State University
- Wei Qiang Yang, Associate Professor and District Berry Extension Agent, Oregon State University
- Mike Mainland, Professor Emeritus, North Carolina State University

Other Abiotic and Biotic Stresses Partners

- Christelle Guédot, Associate Professor, University of Wisconsin
- Jonathan Oliver, Assistant Professor-Fruit Pathologist, University of Georgia
- David Bryla, Research Horticulturist, USDA-ARS HCRU
- Scott Lukas, Assistant Professor, Oregon State University Hermiston Agricultural Research and Extension Center

International Partners

- Michael Dossett, Research Scientist at BC Berry Cultivar Development Inc., British Columbia
- Susan McCallum, Blueberry Researcher at James Hutton Institute, Scotland
- Luis Diaz Garcia, Instituto Nacional de Investigaciones Forestales y Agrícolas y Pecuarias, Aguascalientes, Mexico
- Paul Sandefur, Manager of Breeding Operations at Fall Creek Farm & Nursery Inc., Oregon, USA
- Simon Bonin, Director of Grower Relations and Agronomy at Fruit d'Or, Quebec, Canada
- Susan Thomson, Bioinformatician at Plant and Food Research Ltd, New Zealand
- Toshi Foster, Senior Scientist, Plant and Food Research Ltd, New Zealand

National and International Partners

Supporting Industry Partners

- British Columbia Blueberries
- Berry Blue, LLC
- California Blueberry Commission
- Cape Cod Cranberry Growers' Association
- The Cranberry Institute
- The Dole Food Company
- Driscoll's, Inc,
- Fall Creek Farm and Nursery, Inc.
- Florida Blueberry Grower's Association
- Georgia Blueberry Commission
- Kentucky Blueberry Growers Association
- Mariani Premium Dried Fruit
- New Jersey Blueberry Cranberry Research Council
- North American Blueberry Council
- North Carolina Blueberry Council, Inc.
- Ocean Spray Cranberries, Inc.
- Oregon Blueberry Commission
- Oregon Blueberry Farms and Nursery
- Oregon Cranberry Grower Association
- U.S. Highbush Blueberry Council
- Valley Corporation
- Washington Blueberry Commission
- Wayne County Blueberry Growers Association
- Wisconsin State Cranberry Growers Association

Advisory Panels

Stakeholder Panel

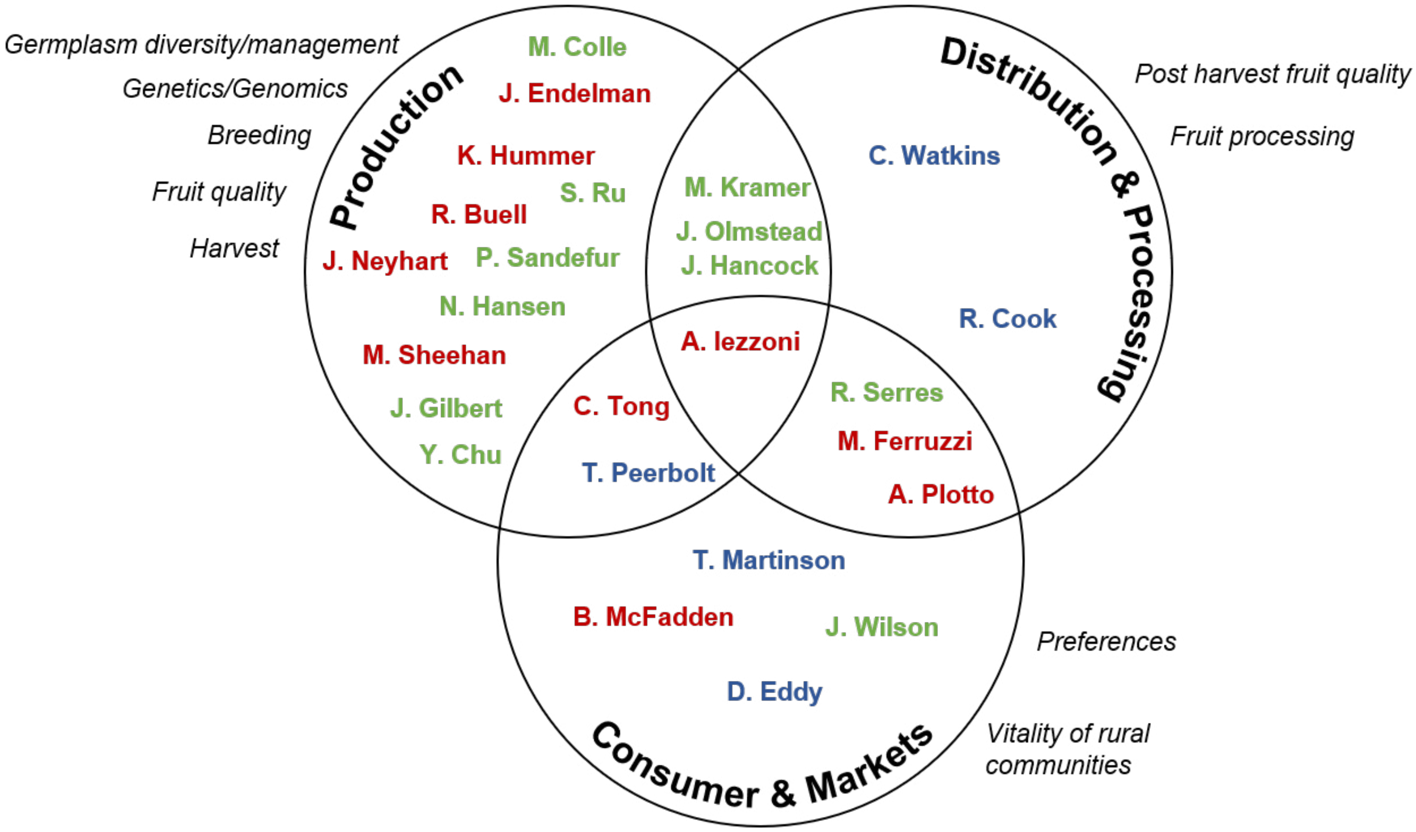
- James Hancock, Berry Blue LLC
- Nicole Hansen, Cranberry Grower
- Matt Kramer, Fall Creek Farm and Nursery
- James Olmstead, Driscoll's, Inc.
- Jessica Gilbert, Driscoll's, Inc.
- Mandie Driskill, Fall Creek Farm and Nursery
- Marivi Colle, Berry Blue LLC
- Rod Serres, Ocean Spray Cranberries, Inc.
- Paul Sandefur, Fall Creek Farm and Nursery
- William Frantz, The Cranberry Institute

Extension Panel

- Rodney Cook, Ag-View Consulting, Inc.
- David Eddy, Master Media Worldwide
- Tim Martinson, Cornell University
- Tom Peerbolt, The Northwest Berry Foundation
- Christopher Watkins, Cornell University

Scientific Panel

- Robin Buell, Michigan State University
- Jeffrey Endelman, University of Wisconsin-Madison
- Mario Ferruzzi, Arkansas Children's Nutrition Center (ACNC)
- Michael Dossett, BC Berry Cultivar Development Inc.
- Amy Iezzoni, Michigan State University
- Brandon McFadden, University of Delaware
- Anne Plotto, USDA-ARS (FL)
- Moira Sheehan, Cornell University
- Cindy Tong, University of Minnesota
- Jeannine Lisa Rowland, USDA-ARS
- Sushan Ru, Auburn University
- Ye Chu, The University of Georgia



US and Global Coordination Efforts for Improving Cranberry and Blueberry

Misson

Address major bottlenecks for growth of U.S. *Vaccinium* industry, by creating a nationwide coordinated transdisciplinary search approach to develop standard phenotyping methods and DNA assisted selection capacity in *Vaccinium* breeding programs, to enable breeders to select and pyramid fruit characteristics (FCs) that positively contribute to fruit quality and market value. In the long term this mission will increase production of fruit with improved characteristics that meet the ever changing industry, market demand, and consumer preferences.

What Success Would Look Like

Discovery. VacCAP project outputs will increase the knowledge of:

- Cranberry and blueberry genome structure and evolution
- Genetic mechanisms and genes controlling economically important traits including fruit characteristics
- The relationships between fruit characteristics and fruit quality (shelf life, texture, bruising and sensory traits)
- Consumer behavior and interests regarding blueberry fruit quality and cranberry products
- New *Vaccinium* stakeholder priorities for the sustainability and profitability of the industry

Delivery. VacCAP project will deliver:

- New genomes and genetic maps
- Cost effective genotyping platforms for marker trait association studies
- Standardized phenotyping methods to evaluate texture, appearance and chemical composition
- DNA markers and QTL regions associated with FCs
- DNA assays to use for marker assisted selection
- FCs benchmarks to select for improved quality
- Online platforms and communication material/activities to transfer project deliverables and outcomes

Engagement. VacCAP deliverables and outcomes will be utilized by the *Vaccinium* community for the following goals:

- VacCAP DNA tools and phenotyping methods will be utilized by VacCAP PIs and the *Vaccinium* community worldwide to advance breeding and/or research programs
- VacCAP outcomes will be used by growers, processors and distributors to plan production and distribution strategies
- Funding of new off-shoot projects from VacCAP developed tools and deliverables with new collaborative alliances established

Education. The VacCAP team influences the next generation of breeders and scientists, increasing knowledge through collaborations:

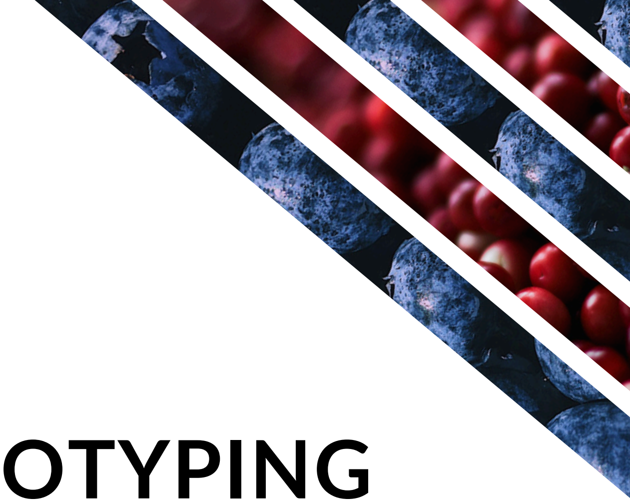
- MS/PhD students and post-docs are trained in plant breeding, genetics, fruit phenotyping, postharvest physiology, socio-economics, sensory analysis and extension practices, to become the next generation of breeders, scientists, and agriculture liaisons

Long-Term Impact

- Increased ability of the *Vaccinium* growers, processors and distributors to market a higher percentage of premium fruit through the use of improved varieties without increased production costs
- Increased consumption of blueberry and cranberry products in the US and worldwide due to improved fruit quality
- Increased efficiency of *Vaccinium* breeding programs for selection and improvement of fruit quality traits important to the consumer and industry
- Increased profitability, competitiveness, and sustainability of *Vaccinium* industries

VacCAP

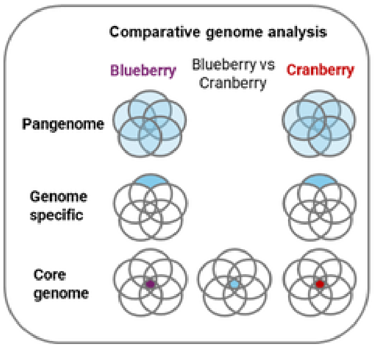
IMPROVING FRUIT QUALITY



»» OBJECTIVE 1

GENOMICS AND GENOTYPING

VacCAP Objective 1 aimed to establish genomic resources to enable effective association mapping studies in blueberry and cranberry



Develop *Vaccinium* pangenome

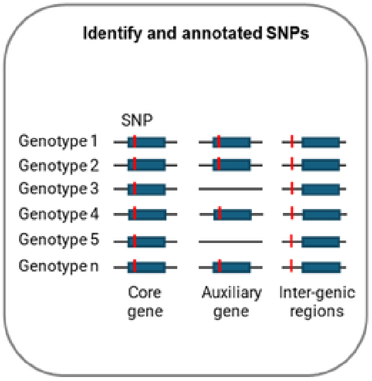
»» Comparative Genomic Team

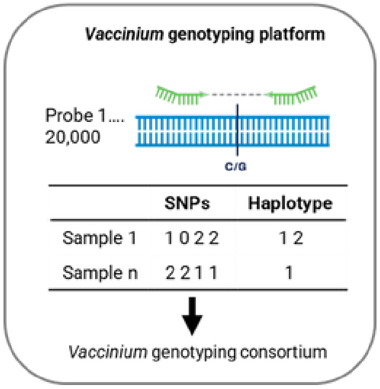
Assemble new blueberry and cranberry genomes for comparative analysis and to construct the Vaccinium pangenome. Identify the core and auxiliary genes. Core gene are conserved across genomes, auxiliary genes are not-conserved and present only in some genomes.

Develop a SNP catalog that combines de-novo with existing SNP sets (within linkage maps or representing QTLs). Annotate the SNPs catalog with SNP location within genes, core or auxiliary genes. This approach will ensure the identification of highly informative SNPs.

Compile a SNP catalog

»» Genotyping Team





Develop the *Vaccinium* Genotyping Platform

»» Genotyping Team

Select DNA regions surrounding SNPs to design a genotyping platform. Criteria for SNP selection aim to maximize the representation of core genes, SNPs associated with QTLs and even distribution. Engage *Vaccinium* breeders and geneticist to establish a genotyping consortium that will help to lower the genotyping costs per sample, while ensuring use of the platforms.

»» ACCOMPLISHMENTS IN GENOMICS AND GENOTYPING

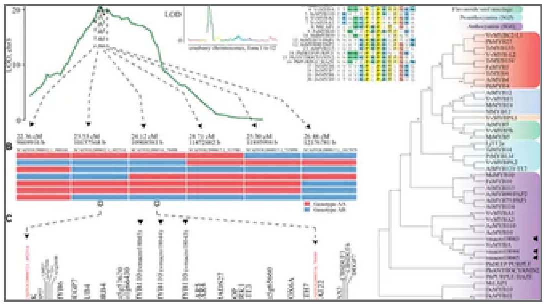
OUTCOMES ARE

- Released **5** linkages maps, **6** genomes and the *Vaccinium* pangenome
- Developed **2** genotyping platforms, established and coordinated the *Vaccinium* Genotyping Consortium
- New genomic resources were made available to the *Vaccinium* and broader research community through The Genome Database for *Vaccinium* (GDV)

EXPANDING GENOMIC RESOURCES

*Reference genomes for two blueberry wild species (*Vaccinium myrtillus *and* V. caesariense*), two cultivated cranberry cultivars ('Stevens' and 'Ben Lear') and two cranberry wild species (*V. microcarpum *and* V. oxycoccos*) were assembled and annotated. In addition, a blueberry and cranberry pangenome was developed.*

These reference genomes were assembled using long read sequencing technology which improved the quality of genomic resources available for the *Vaccinium* community. To build the blueberry and cranberry pangenomes, **20** blueberry and **10** cranberry genomes representing the Northern Highbush (NHB), Southern Highbush (SHB) and cranberry cultivars were resequenced at high coverage and used to build the Vaccinium pangenome. Comparative genome analysis identified the core and auxiliary genes. Core genes are conserved across genomes, auxiliary genes are not-conserved and present only in some genomes. Highlights from these studies are reported below.



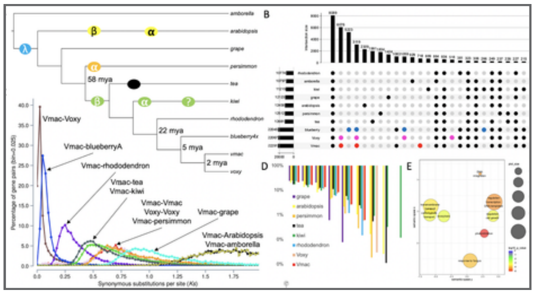
Chromosome-Level Genome Assembly of the American cranberry (*Vaccinium macrocarpon ait.*) and Its Wild Relative *Vaccinium microcarpum*

LINK TO PAPER

In this study Dr. Zalapa's team developed the first chromosome-scale genome assembly of cranberry, cultivar Stevens, and a draft genome of its close wild relative species *Vaccinium microcarpum*. More than 92% of the estimated cranberry genome size (492 Mb) was assembled into 12 chromosomes, which enabled gene model prediction and chromosome-level comparative genomics. Comparative genome analysis revealed two polyploidization events, the ancient γ-triplication, and a more recent whole genome duplication that occurred approximately 61 Mya.

Furthermore, comparative genomics within the *Vaccinium* genus suggested cranberry-*V. microcarpum* divergence occurred 4.5 Mya, following their divergence from blueberry 10.4 Mya. Finally, a cluster of subgroup-6 R2R3 MYB transcription factors were identified within a genomic region spanning a large QTL for anthocyanin variation in cranberry fruit. Phylogenetic analysis suggested these genes likely act as anthocyanin biosynthesis regulators in cranberry. These new cranberry genomic resources facilitate the dissection of the genetic mechanisms governing agronomic traits and further breeding efforts at the molecular level.

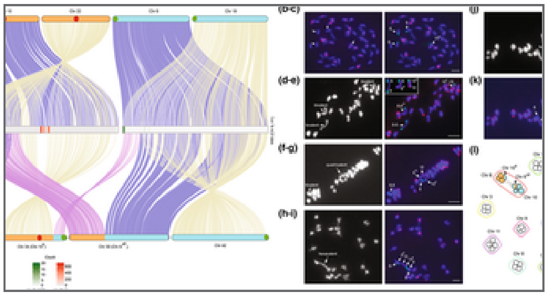
Contrasting a reference cranberry genome to a crop wild relative provides insights into adaptation, domestication, and breeding



LINK TO PAPER

In this study Dr. Polashock's and Dr. Michael's teams presented an updated, chromosome-resolved *V. macrocarpon cv* 'Ben Lear' reference genome and the draft genome of the wild cranberry *V. oxycoccos*. The 'Ben Lear' genome assembly improved contiguity of the assembly at contig level. The study confirmed that the Ericaceae has undergone two whole genome duplications that are shared with blueberry and rhododendron. Leveraging resequencing data for 'Ben Lear' inbred lines, as well as several wild and elite selections, common regions that are targets of improvement were identified. These same syntenic regions in *V. oxycoccos*, harbored genes involved in environmental response and plant architecture. The study provided insight into early genomic selection in the domestication of a native North American berry crop.

Autopolyploid inheritance and a heterozygous reciprocal translocation shape chromosome genetic behavior in tetraploid blueberry (*Vaccinium corymbosum*)

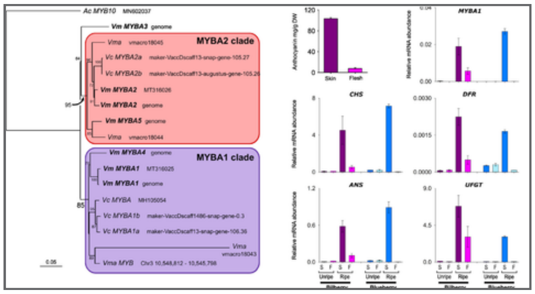


LINK TO PAPER

In this study the Iorizzo, Edger and Iovene teams, described a new high-quality, phased, chromosome-scale genome of a diploid blueberry, clone W85. The genome was integrated with cytogenetics and high-density, genetic maps representing six tetraploid blueberry cultivars, harboring different levels of wild genome admixture, to uncover recombination behavior and structural genome divergence across tetraploid and wild diploid species. Analysis of chromosome inheritance and pairing demonstrated that tetraploid blueberry behaves as an autotetraploid with tetrasomic inheritance. Comparative analysis demonstrated the presence of a reciprocal, heterozygous translocation spanning one homolog of chr-6 and one of chr-10 in the cultivar Draper. The translocation affects pairing and recombination of chromosomes 6 and 10. Besides the translocation detected in Draper, no other structural genomic divergences were detected across tetraploid cultivars and highly inter-crossable wild diploid species.

These findings and resources will facilitate new genetic and comparative genomic studies in *Vaccinium* and the development of genomic assisted selection strategy for this crop.

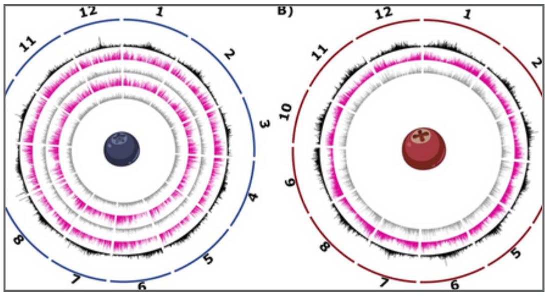
A chromosome-scale assembly of the bilberry genome identifies a complex locus controlling berry anthocyanin composition



LINK TO PAPER

In this study the Chagne and Espley teams presented the first bilberry (*Vaccinium myrtillus* L.) chromosome scale genome assembly. Comparative analysis with other blueberry genomes indicated a high conservation of synteny. A total of 36,404 genes were annotated after nearly 48% of the assembly was masked to remove repeats. The genome unveiled a complex MYBA locus, and identified the key regulating MYB genes that determine anthocyanin production. The new bilberry genome builds on the genomic resources and knowledge of Vaccinium species, to help understand the genetics underpinning some of the quality attributes that breeding programs aspire to improve. The high conservation of synteny between bilberry and blueberry genomes indicates that comparative genome mapping can be applied to transfer knowledge about marker-trait association between these two species, as the loci involved in key characters are orthologous.

Blueberry and cranberry pangenomes as a resource for future genetic studies and breeding efforts



LINK TO PAPER

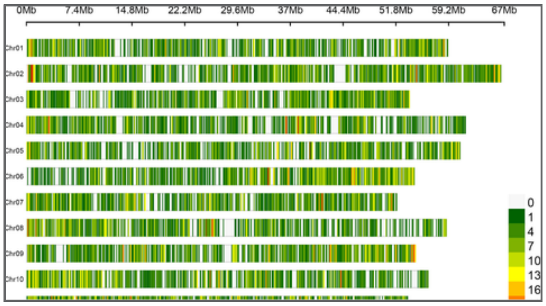
In this study Dr. Edger's team described the construction and analysis of the first pangenome for both blueberry and cranberry. The analysis of these pangenomes revealed both crops exhibit great genetic diversity, including the presence–absence variation of 48.4% genes in highbush blueberry and 47.0% genes in cranberry. Auxiliary genes, those not shared by all cultivars, are significantly enriched with molecular functions associated with disease resistance and the biosynthesis of specialized metabolites, including compounds previously associated with improving fruit quality traits. The discovery of thousands of genes, not present in the previous reference genomes for blueberry and cranberry, will serve as the basis of future research and as potential targets for future breeding efforts.

The pangenome, as a multiple-sequence alignment, as well as individual annotated genomes, are publicly available for analysis on the Genome Database for *Vaccinium*—a curated and integrated web-based relational database. Lastly, the core-gene predictions from the pangenomes will be useful to develop a community genotyping platform to guide future molecular breeding efforts across the family.

EXPANDING GENOTYPING CAPACITY

The new genomes and the pangenome were used to develop a genotyping platform for blueberry and cranberry that is optimized for performing genome wide association studies (GWAS) and work across the blueberry and cranberry germplasm.

The platforms were made available to the Vaccinium community by forming a consortium that enabled us to lower the costs for genotyping. The *Vaccinium* Genotyping Consortium includes **15** members representing public and private breeding programs, from U.S., France, New Zealand, Canada, and Italy and has genotyped **14,137** samples. The platform has been already used for **23** projects by **24** studies/experiments.



Development of a targeted genotyping platform for reproducible results within tetraploid and hexaploid blueberry

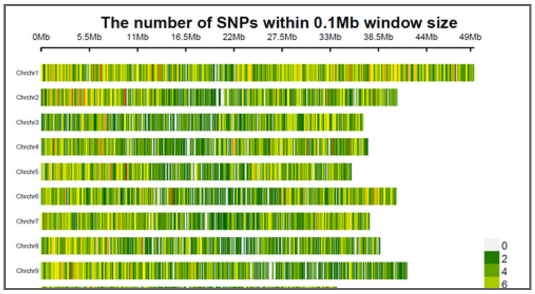
LINK TO PAPER

The development of a standardized genotyping platform that targets a specific set of polymorphic loci can unify the scientific and breeding community toward blueberry improvement. In this study ths Bassil team developed and evaluated a targeted genotyping platform for cultivated blueberries that is affordable, reproducible, and sufficiently high density to warrant large-scale adoption for genomic studies. The Flex-Seq platform was developed in a two-step procedure that resulted in 22,000 loci that yielded 194,365 single nucleotide polymorphisms when assessed in a diversity set of 192 samples including cultivated and other related wild *Vaccinium* species. Locus recovery averaged 89.4% in the cultivated polyploid blueberry (NHB, SHB, and rabbiteye [RE]) and on average 88.8% were polymorphic. While recovery of these loci was lower in the other *Vaccinium* species assayed, recovery remained high and ranged between 60.8% and 70.4% depending on the taxonomic distance to the cultivated blueberry targeted. NHB had the highest mean number of variants per locus at 9.7, followed by RE with 9.1, SHB with 8.5, and a range between 7.7 and 8.5 in other species. As expected, the total number of unique-in-state haplotypes exceeded the total number of variants in the domesticated blueberries. Phylogenetic analysis using a subset of the SNPs and haplotypes mostly conformed to known relationships.

The platform also offers flexibility about the number of loci, depth of sequencing for accurate dosage calling, loci and haplotype reconstruction from increased fragment length. This genotyping platform will accelerate the development and improvement of blueberry cultivars through genomic-assisted breeding tools.

Development of a targeted genotyping platform for cranberry

LINK TO PAPER



The Flex-Seq platform has also been used to develop a standardized genotyping platform for cranberry. The study led by Dr. Nahla Bassil is currently ongoing and the manuscript is in preparation. The cranberry platform aims to replicate the success of the blueberry platform with 17,500 loci distributed evenly across the cranberry genome, and it was designed to be affordable, reproducible, and sufficiently high density for widespread adoption. The platform is being evaluated on 192 cranberry samples that are predominately American cranberry and yielded approximately 60,000 single nucleotide polymorphisms. The mean number of variants per locus is approximately five with unique-in-state haplotypes currently being assessed. The platform will offer similar benefits to the blueberry Flex-Seq platform to accelerate the development and improvement of cranberry cultivars.

ONGOING RESEARCH

- Annotating and mining genes associated with quality characteristics
- Completing annotation of a new tetraploid genome
- Continue coordinating the *Vaccinium* genotyping consortium

IMPACT

Outcomes of Objective 1 enabled optimization of genetic studies, provided access to genes for genetic studies and functional characterization and have significantly expanded use of DNA tools in the Vaccinium *community.*

To take advantage of the new genotyping platforms, breeding programs are developing genetic stocks (mapping populations and diversity panels) that best fit genetic studies design. As a result, research in *Vaccinium* crops is focusing more on understanding the genetic architecture of important traits and gene identification. This new scenario expands capacity for making new genetic discoveries for application in blueberry and cranberry breeding. Also, the VacCAP project fostered active collaboration among *Vaccinium* research groups. This new dynamic contributed to reducing duplication of work and turning research projects to be complementary to each other. This outcome is a critical step to accelerate genetic advances within the large and expanding *Vaccinium* community.

Testimonials From the Lab

Dr. Sujeet Verma
Genomics and Molecular Diagnostics Manager
Fall Creek Farm and Nursery, Inc.

What impact has the genotyping platform had for your breeding program?

The impact of Flex Seq 22K (FS22) genotyping platform (GP) on the Fall Creek (FC) blueberry breeding program is huge because now we have a high-throughput high-density genotyping tool that will give us clarity on genetic architecture of traits. The most valuable impact is the application of genomic selection (GS) and enhanced trait selection. Apart from that, accurate parentage verification and estimation of genetic diversity are other impactful utilities of FS22.

With FS22 application, breeders and geneticists can pinpoint genomic locations of loci controlling traits and differentiate monogenic versus polygenic traits. Blueberry being autotetraploid, the FS22 can help understand the segregation of alleles and their dosage effects better and facilitate the development of molecular markers.

Overall, the implementation of the FS22 genotyping platform will help enhance breeding efficiency and selection at Fall Creek Farm and Nursery, ultimately leading to the development of superior blueberry varieties that meet both grower and consumer needs.

Have you changed anything in your program as a result of using the platform?

We have started implementing genomics selection and parentage verification using the FS22. Moving forward we will make breeding selections based on genomic predictions that will help speed-up the breeding cycle. This will also help inform crossing decisions.

Would you recommend it to other breeding programs?

Yes, I would recommend the FS22 genotyping platform to other breeding programs.

How do you think having this new tool will help your program in the future?

This new tool will help in the development of the marker-assisted breeding program at Fall Creek. It will enhance precision in breeding decisions, greater flexibility in adapting to climate change, sustained genetic diversity, innovative breeding techniques, better collaboration and data sharing, advanced disease management, and future-proofing the breeding program.

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Overall, the FS22 genotyping platform will provide a robust foundation for the continuous improvement and innovation of blueberry breeding program, ensuring its success and relevance in the future.

Do you have any other comments?

The FS22 genotyping platform provides an opportunity to establish a stronger collaboration between industry and academia. Having said that, the price per sample genotyping with FS22 is limiting at the moment, and for high throughout genotyping, the price per sample needs to be more affordable! In addition, mid-density and low-density SNP panels should be rolled out for high throughput applications.

Testimonials From the Lab

Dr. Jeffrey Neyhart, Research Geneticist, USDA-ARS
Genetic Improvement for Fruits and Vegetables Laboratory
Rutgers P.E. Marucci Center for Blueberry and Cranberry
Research and Extension

What impact has the genotyping platform had for your breeding program?

The high-quality cranberry reference genomes and annotations directly enabled us to identify genomic regions potentially associated with local climate adaptation and abiotic stress tolerance in diverse germplasm. These resources also greatly expedited the development of small- and medium-sized genotyping platforms for rapidly adopting marker-based selection.

Have you changed anything in your program as a result of using the platform?

Our pre-breeding program is very new, which means we can design the program with these genomics resources in mind. For example, we are considering alternative parent and mate selection strategies that use genomic information.

Would you recommend it to other breeding programs?

Based on our experience, I would encourage other programs to consider using these resources.

How do you think having this new tool will help your program in the future?

The goal of our cranberry pre-breeding program is to identify favorable or novel productivity, quality, and abiotic/biotic stress tolerance traits in wild or under-improved germplasm. By using and expanding upon the genomic resources currently available through VacCAP, along with other resources, we hope to catalog the unique haplotypes or alleles that are present in this germplasm and determine which may contribute favorable traits.

Additionally, we think the genotyping platforms developed from the genomic resources will have a profound effect on the resource efficiency of our program. Dealing with wild and underimproved germplasm is genetically “messy,” with many unfavorable traits present alongside those that are favorable. By using markers to predict and select the best individuals from our crosses, we hope to reduce the impact of linkage drag and allocate more resources to those with the greatest potential to be outstanding parents

Do you have any other comments?

We are excited to continue to utilize the genomic resources developed through the VacCAP.

Partner Project

Dr. Moira Sheehan
Senior Research Associate & Director, Breeding Insight
Member of the VacCAP Advisory Panel

How did the VacCAP team collaborate with Breeding Insight?

Breeding Insight (BI) developed a mid-density genotyping platforms (3,000 SNPs) for blueberry and cranberry that are tailored for routine genotyping in structured breeding populations (including GS populations and QTL populations), MAS introgression, parental or variety verification. These platforms complement the high density platforms that VacCAP team developed. The BI and VacCAP genotyping teams have been collaborating on developing these platforms by sharing sequences and target SNPs.

For blueberry, BI used skim sequencing of 31 parents and available GBS data from USDA-ARS and NCSU to develop a SNP database. This database was ultimately used to identify 10,000 SNP loci from which a final, high-quality set of 3,000 loci were selected for DArTag assay production. These 3,000 loci were also shared back with VacCAP and all were included in the blueberry FlexSeq panel produced by the VacCAP team.

For cranberry, BI used skim sequencing of 53 and available GBS data from USDA-ARS to develop a SNP database. Given that the cranberry FlexSeq panel was already created or in progress, when BI selected a set of 3,000 SNPs to target on DArTag, we maximized the overlap of markers with those in the FlexSeq panel. In other words, BI targeted 3,000 genomic regions where we'd like a marker, and if the VacCAP FlexSeq panel already had a nearby marker, we used that same marker rather than a different one.

Development of these two platforms provides the *Vaccinium* community with options that they can choose depending on their application needs. Shared SNP across the platforms facilitate comparison across studies.

Where do BI and VacCAP collaborate in the future?

BI and VacCAP are in a very unique position in the plant breeding community. Both are examples of how genomic technologies from major crops have been adopted in a clonal propagated perennial fruit crop with success. One place VacCAP and BI could push ahead of the major crops is by using multi-allelic data in genomic analysis. All modern SNP analyses require the data to be bi-allelic, which works well in diploids but fails to produce good results in polyploids. The capture, databasing, and utilization of multi-allelic genomic data in polyploids by BI and VacCAP for blueberry and cranberry could be the first of its kind.

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Already, BI has evidence that using microhaplotypes in polyploids allows genomic analyses to achieve higher significance (with lower error) for marker-trait associations, due to the greater information content contained in microhaplotypes. BI is already planning the architecture for a new community resource: one microhaplotype database for the blueberry 3K panel and one for the cranberry 3K DArTag panel. These databases will hold all the observed microhaplotypes with fix-allele identifications and associated sample metadata.

BI and VacCAP can work together on what breeders want to see in these databases as well as how they can use them to find new alleles that might be missing in their germplasm stocks.

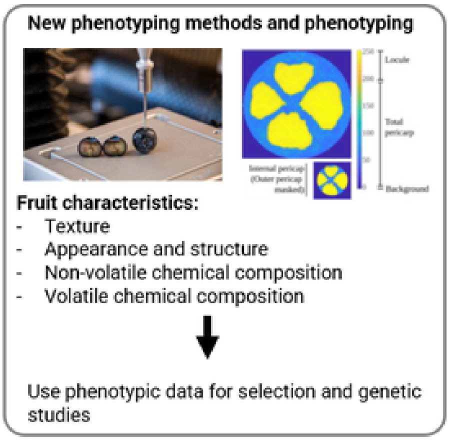
VacCAP

IMPROVING FRUIT QUALITY

>>> OBJECTIVES 2 & 3 | BLUEBERRY

BLUEBERRY PHENOTYPING, GENETICS, DNA MARKERS, AND FRUIT QUALITY

VacCAP Objectives 2 and 3 aimed to establish phenomics and DNA based strategies to select for improved fruit quality.



Phenotyping Fruit Characteristics

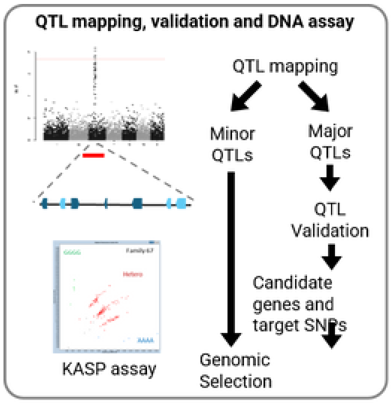
>>> Phenotyping Team

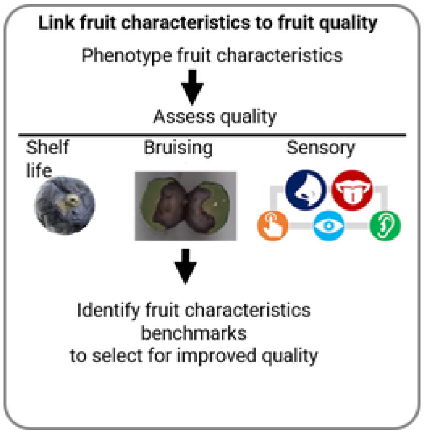
Develop new and more accurate phenotyping methods to evaluate fruit characteristics, including texture, non-volatile chemical composition, volatile chemical composition and appearance. Use phenotyping data to perform genetic studies, and select breeding lines with improved characteristics.

Perform marker traits association analysis to understand the genetic mechanisms controlling fruit characteristics. Based on results of genetic studies, initiate efforts to develop DNA assay and genomic prediction models .

Genetics and DNA Markers for Fruit Characteristics

>>> Statistical Genetics Team





Associate Fruit Characteristics to Fruit Quality

>>> Fruit Quality Team

Identify fruit characteristics (e.g. texture parameters) that contribute to quality attributes such as shelf-life, bruising and consumer purchasing behavior. Use these fruit characteristics to select breeding lines with improved quality attributes.

>>> ACCOMPLISHMENTS IN GENETIC DISCOVERY AND PHENOTYPING

OUTCOMES ARE

- Developed accurate phenotyping methods to evaluate fruit characteristics
- Elucidated the genetic mechanisms controlling several fruit characteristics
- Developed a DNA marker for marker-assisted selection
- Identified fruit characteristics parameters that contribute to improve fruit quality
- Advance selection of blueberry breeding lines with improved quality

ADVANCING PHENOTYPING FOR FRUIT CHARACTERISTICS

- *Developed accurate and/or high-throughput phenotyping methods to evaluate blueberry fruit, assessing:*
  - *chemical composition (Brix, titratable acidity, pH, sugars, amino acids, flavonoids and anthocyanin)*
  - *fruit appearance (size and internal bruising)*
  - *texture and associated shelf-life indicators including wrinkling and weight loss*

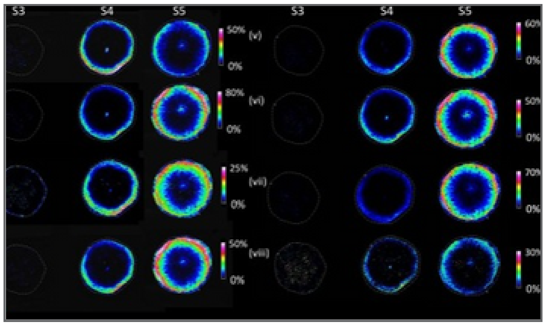
- *Created a QR barcode system to manage samples across core labs.*

- *Developed trait ontologies for blueberry to standardize phenotypic analyses across studies.*

- *Made methods available to the Vaccinium community, with some already implemented or in the early stages of implementation by stakeholders.*

CHEMICAL COMPOSITION

We have established cost effective and accurate methods for evaluating Brix, acidity, anthocyanins, flavonoids, and other primary metabolites like sugars and amino acids. These traits are important quality characteristics in blueberries because they influence their taste, flavor perception, and potential health benefits.



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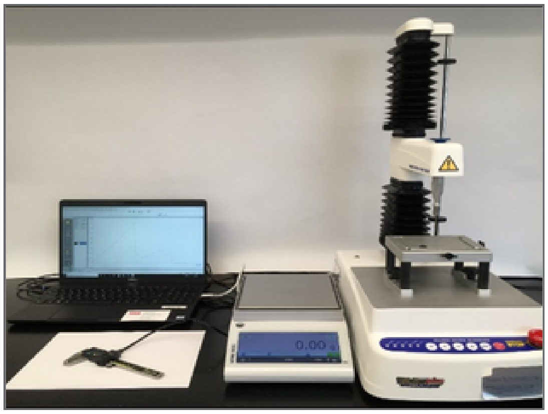
For sugar evaluation, we used Near-Infrared Spectroscopy (NIRS), which has proven to be a reliable and rapid method for predicting sucrose, glucose, fructose, and total soluble sugar levels in blueberry fruits (Perkins-Veazie et al., 2023). Our analysis across various blueberry germplasm samples revealed that fructose and glucose are predominant sugars, while sucrose is present in a very limited amount. We also developed rapid tests using handheld meters to evaluate acidity and Brix as proxies of organic acids and sugars, respectively. A comparison of the rapid tests with more accurate methods (HPLC) showed that soluble solids content (SSC or Brix) does not always correlate with sugar content, while titratable acidity (TA) is the best proxy for organic acids. Fruit pH, on the other hand, has a low correlation with organic acids.

Mass spectrometry imaging was used to quantify anthocyanin, flavonoids, and primary metabolites (e.g. sugars and amino acids) in blueberry fruits (Dare et al., 2022). Our spatial segmentation analysis suggests that ripening progresses from the skin into the flesh of the fruit. Overall, these new methods provide a deeper understanding of blueberry chemical composition and ripening, while offering more accurate and efficient strategies to phenotype germplasm in breeding programs with the overall aim of improving fruit quality for consumers.



TEXTURE, SIZE, AND SHELF LIFE INDICATORS

We established an integrated system to evaluate mechanical texture, fruit size, and correlate them with quality attributes like shelf life and sensorial texture.

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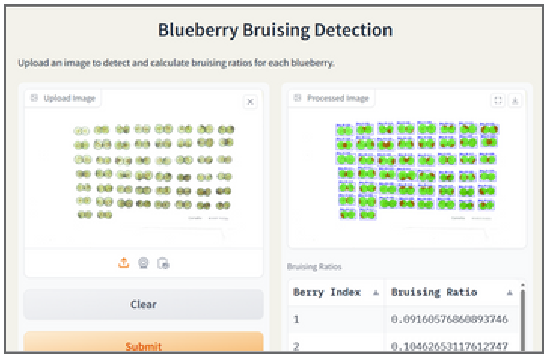
Texture analysis was performed using the TA.XTPlus Texture Analyzer (Stable Micro Systems, Hamilton, MA, USA) and was integrated with a high-precision scale, digital caliper, and programmed to input visual phenotypic data to assess shelf-life indicators. This integrated system measures 17 texture parameters, fruit weight and diameter (a proxy for size), scar diameter, and two shelf-life indicators (presence of mold and rate of wrinkle/shrivel) (Oh et al., 2024). This methodology has been used in four studies to understand the link with fruit quality and identify parameters that can be used in breeding programs (see page 10).

A macro developed for this system is available for use by breeding programs and it has already been transferred to several programs for implementation. Handheld tools were also tested, and some parameters were highly correlated with those measured by the texture analyzer (Giongo et al., 2022). For more information about the texture analysis system, see this VacCAP How to video, and webinars 1, 2.

INTERNAL BRUISING

We established a rapid method to quantify internal bruising in blueberries. Dr. Tan leveraged image analysis and deep learning models to assess internal bruising (Ni et al., 2022; Tan et al., 2025).

The method achieved moderate-to-high accuracy, and with over three years of data, it was able to clearly differentiate cultivars with low bruising ratios from those with moderate-to-high bruising ratios. Cultivars within the lowest bruising ratios included those with crisp texture, like 'Indigocrisp' and 'Keecrisp'.



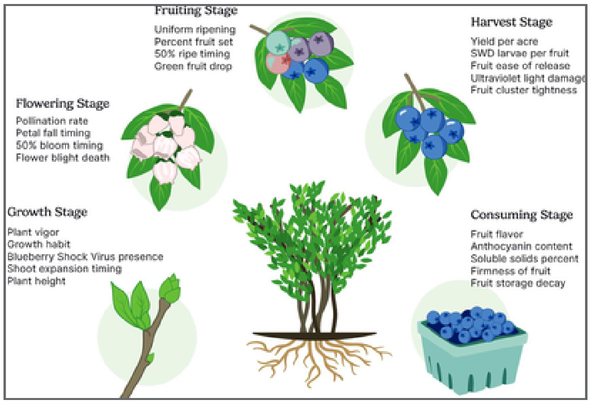
Blueberry Bruising Detection

Upload an image to detect and calculate bruising ratios for each blueberry.

Berry Index	Bruising Ratio
1	0.09160576860893746
2	0.10462653117612747

Blueberry bruising detection web app.

The method is integrated into a user-friendly computer interface that is accessible to potential users here. For more information about this work see this VacCAP webinar.



CROP ONTOLOGY

In collaboration with Breeding Insight, the project contributed to developing a blueberry Crop Ontology to standardize phenotyping for breeding and research programs (Hislop et al., 2024).

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A total of 83 traits were classified into nine categorical groups. This ontology has been integrated into the Genome Database for *Vaccinium* species platform and Breeding Management System. To facilitate comparison of data across locations, programs, and years, we encourage adopting the trait ontology and contributing to its development.

The blueberry crop ontology can be searched using the Trait Descriptor Search.

If researchers would like to request that traits be added or adjusted in the ontology, they can submit their requests through here.

SAMPLE MANAGEMENT

A QR barcode system was developed to manage samples across core labs.

This system enables tracking of fruit and leaf samples from harvest through processing, including downstream assays such as DNA extraction, genotyping, and fruit quality evaluation. For more information about the QR code system see this VacCAP How to video.

ADVANCING GENETIC DISCOVERY AND MOLECULAR BREEDING FOR FRUIT CHARACTERISTICS

- *Completed seven genetic studies for fruit characteristics, identified over 1,500 QTLs and SNPs associated with target traits. Key findings include:*
    - *Major and stable (highly heritable) QTLs control pH, titratable acidity, organic acid, anthocyanin, chlorogenic acid, and volatile content.*
    - *At least 24 of these QTLs were validated across different genetic stocks, making them suitable targets for designing DNA assays for marker-assisted selection strategies.*
    - *Fruit size, sugar content, and texture showed moderate-to-high heritability with complex genetic control, suggesting genomic and phenomic selection are the best strategies for selecting these traits.*

- *Found that organic acid content data, rather than pH and titratable acidity data, were more effective at detecting QTL associated with acidity.*

- *Integrated QTL data with new high-quality genomes to identify candidate genes for anthocyanin and volatiles traits. Verified the function of genes involved in anthocyanin acylation.*

- *Developed the first DNA assay for eucalyptol, a volatile compound associated with consumer dislike of blueberries.*

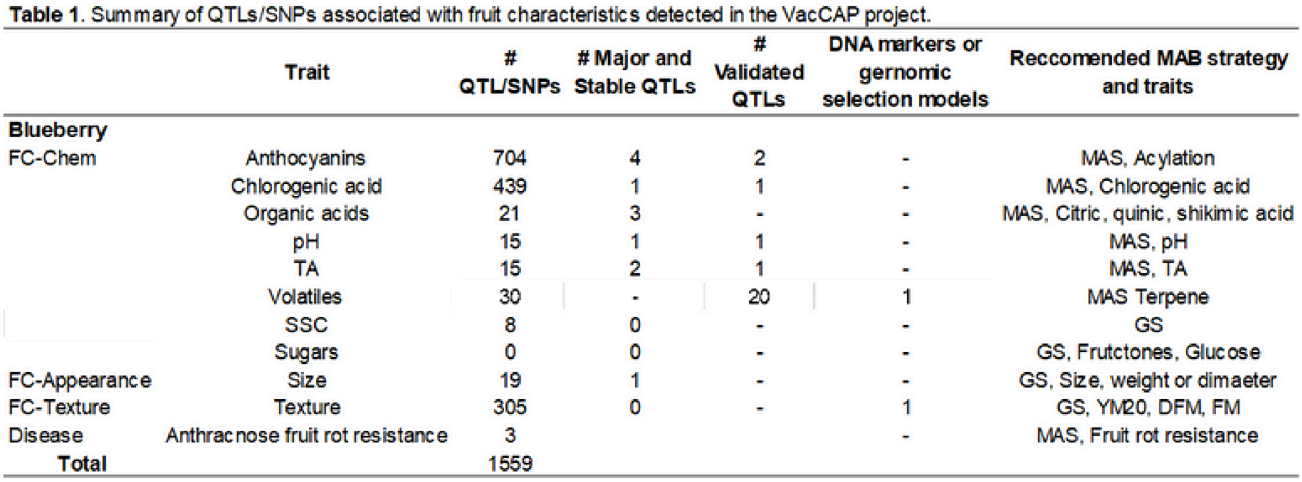


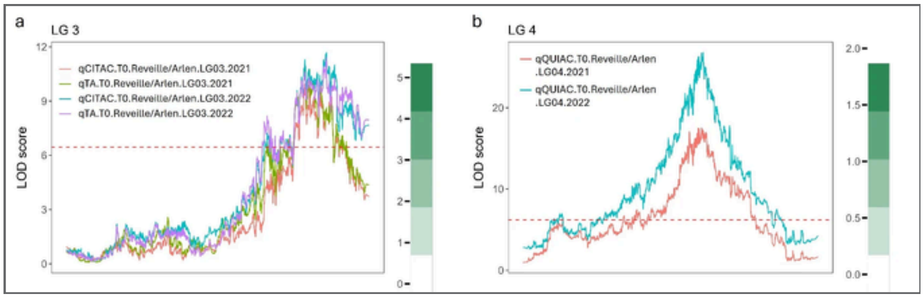
Table 1. Summary of QTLs/SNPs associated with fruit characteristics detected in the VacCAP project.

	Trait	# QTL/SNPs	# Major and Stable QTLs	# Validated QTLs	DNA markers or gernomic selection models	Reccomended MAB strategy and traits
Blueberry						
FC-Chem	Anthocyanins	704	4	2	-	MAS, Acylation
	Chlorogenic acid	439	1	1	-	MAS, Chlorogenic acid
	Organic acids	21	3	-	-	MAS, Citric, quinic, shikimic acid
	pH	15	1	1	-	MAS, pH
	TA	15	2	1	-	MAS, TA
	Volatiles	30	-	20	1	MAS Terpene
	SSC	8	0	-	-	GS
	Sugars	0	0	-	-	GS, Frutctones, Glucose
FC-Appearance	Size	19	1	-	-	GS, Size, weight or dimaeter
FC-Texture	Texture	305	0	-	1	GS, YM20, DFM, FM
Disease	Anthracnose fruit rot resistance	3			-	MAS, Fruit rot resistance
Total		1559				

ORGANIC ACIDS AND SUGARS

Organic acids and sugars determine the perception of sourness and sweetness in blueberry fruits, which are the most important attributes for consumer preference.

Two genetic studies on organic acids and sugars revealed that the variation in organic acids is much higher than that for sugars in blueberry fruits, with total organic acid content being the primary driver of the sugar-to-acid ratio (Mengist et al., 2021, Oh et al., 2025). Organic acids are controlled by major and stable QTLs, which can be targeted for identifying candidate genes and developing DNA assays for marker-assisted selection. In contrast, sugar content exhibits more quantitative genetic control, suggesting phenomic or genomic selection would be better strategies for selecting for these traits.



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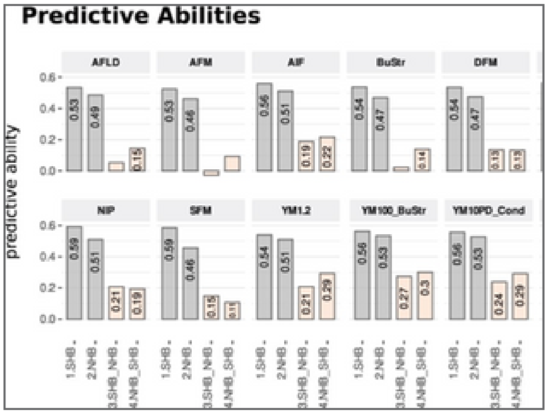

SIZE AND TEXTURE

Size and texture are important attributes that contribute to consumer preferences in blueberries. Early work on fruit size showed that blueberry fruit volume, surface area, and weight are highly correlated and can serve as proxies of fruit size (Mengist et al., 2020).

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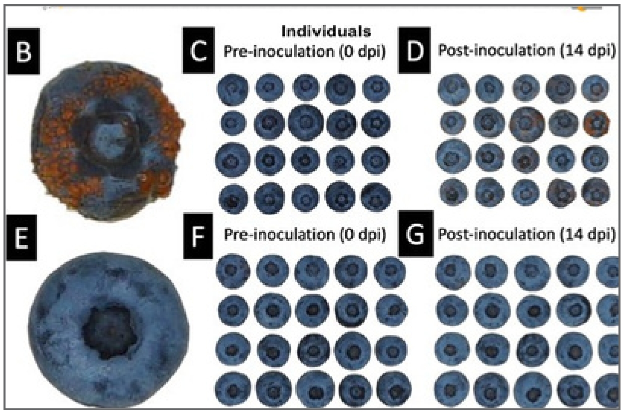
Two studies evaluated the inheritance and genetic mechanisms controlling fruit size (Mengist et al., 2021, Oh et al., 2025). The trait exhibits a relatively high level of heritability (0.6-0.74), however it appears to be under complex genetic control. One study identified a minor, stable QTL on chromosome 4, while a second study found no QTL. Similarly, texture exhibited moderate-to-high heritability and complex genetic control across two studies (Oh et al., 2025, Ferrao et al., 2024). These findings suggest that genomic or phenomic selection would be more effective strategies to select for these traits. Preliminary work on genomic selection for texture showed a moderate level of predictability but indicated that predictability across different populations (e.g., southern highbush vs northern highbush) is very low.

HEALTH-RELATED BIOACTIVE COMPOUNDS

We uncovered the genetic mechanisms and genes controlling accumulation of health-related metabolites, such as anthocyanin and chlorogenic acids, in blueberry fruit.

A locus located on blueberry chromosome 8, conserved across *Vaccinium* species, harbors multiple transcription factors (TFs) that control anthocyanin accumulation (Karppinen et al., 2021, Wu et al., 2021, Lafferty et al., 2021, Lafferty et al., 2022, Albert et al., 2023). Comparative analysis revealed that a complex pattern of duplications differentiates these TFs, explaining tissue-specific expression differences of anthocyanin in *Vaccinium* species. Other genes, such as ANS and UFGT2, are highly conserved and modulate anthocyanin production in *Vaccinium* species (Nguyen et al., 2023). Four genetic studies identified five regions of the blueberry genome controlling the accumulation of anthocyanin and chlorogenic acid in blueberry fruit. QTLs for chlorogenic acids and anthocyanin acylation on chromosome 2, and anthocyanin glycosylation on chromosome 4, were validated across populations (Montanari et al., 2022, Herniter et al., 2023, Mengist et al., 2022). Two acyltransferase genes responsible for anthocyanin acylation were identified (Mengist et al., 2025, Dare et al, 2024). This work identifies target regions and genes that can be used to develop DNA assays for marker-assisted selection. Acylation of anthocyanin pigments could increase the absorption of these health-related bioactive compounds, hence potentially enhancing the nutritional value of blueberry as a superfood.



ANTHRACNOSE RESISTANCE

Anthracnose fruit rot (AFR), caused by the fungal pathogen Colletotrichum fioriniae, is one of the most destructive and widespread fruit diseases in blueberries, affecting both yield and overall fruit quality.

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Blueberry cultivars exhibit highly variable resistance against AFR. The first genetic study for AFR identified three QTLs and candidate genes controlling resistance traits (Jacobs et al., 2023). The study also highlighted a possible interaction between secondary metabolites (e.g., anthocyanins) and pathogen resistance. Overall, the findings from these studies present an opportunity to develop DNA assay for selecting blueberries with resistance or low susceptibility to AFR.

DNA MARKERS

Efforts were initiated to develop a workflow for marker-assisted selection (MAS). This involved the development of a rapid DNA extraction protocol, testing different in-lab genotyping assays and addressing other logistics (Fig 1).

The rapid DNA extraction method was developed by modifying the protocol from Keb-Llanes et al. (2002) and adapted it for a 96-well plate extraction system (Keb-Llanes et al., 2002). The target trait for developing the first DNA assay was eucalyptol, a volatile compound associated with consumers' disliking of blueberries (Ferrao et al., 2022). The DNA assay targets a single SNP located on chromosome 2, which is associated with eucalyptol content. We tested 63 KASP markers across 374 genotypes and found that selecting homozygous dominant alleles for the target SNP resulted in a 45% cutoff for high eucalyptol individuals and selection gain of 58.3 units.

After testing both high-resolution melting curve (HRM) and KASP genotyping approaches, the KASP assay resulted in the most cost-effective and reliable method for DNA assay design (Fig 2). The KASP assay is capable of distinguishing allele dosages for the target SNP, enabling the distinction of homozygous dominant, recessive, and intermediate alleles (Fig 3).

In the University of Florida Blueberry breeding and Genomics Program, over 12,000 germinated seedlings were screened using the single marker. Based on the marker results, about 50% of the seedlings were selected and transplanted in the field for future validation and breeding. With the implementation of MAS in the breeding program, breeders expect to make selection more efficiently and effectively at an earlier stage, while developing more significant markers for important traits.

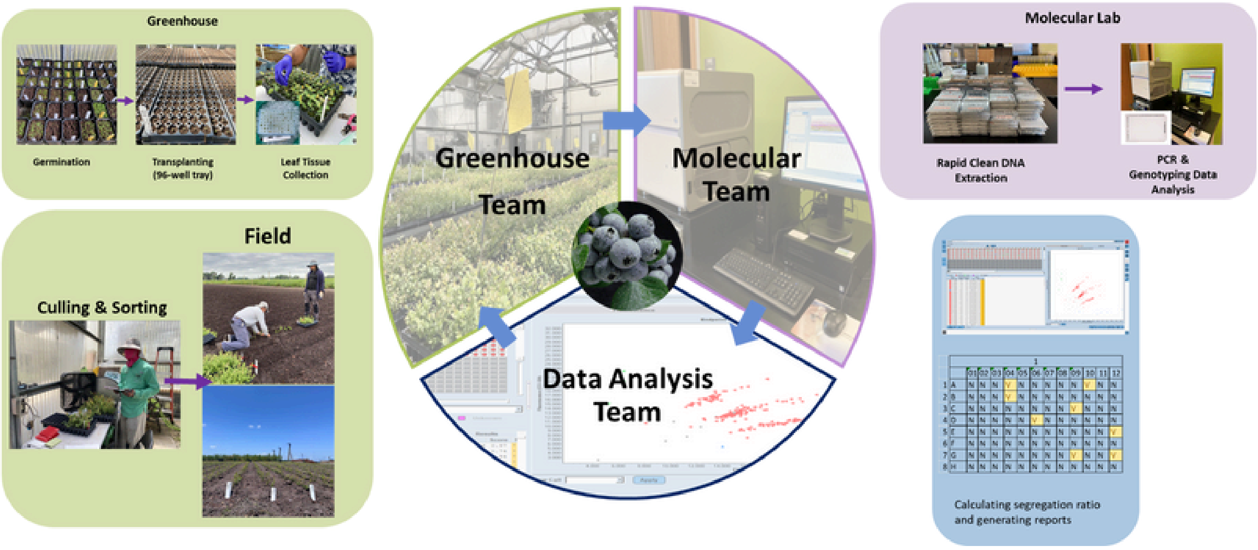


Figure1. Logistics of marker-assisted selection in the University of Florida Blueberry Breeding and Genomics program.

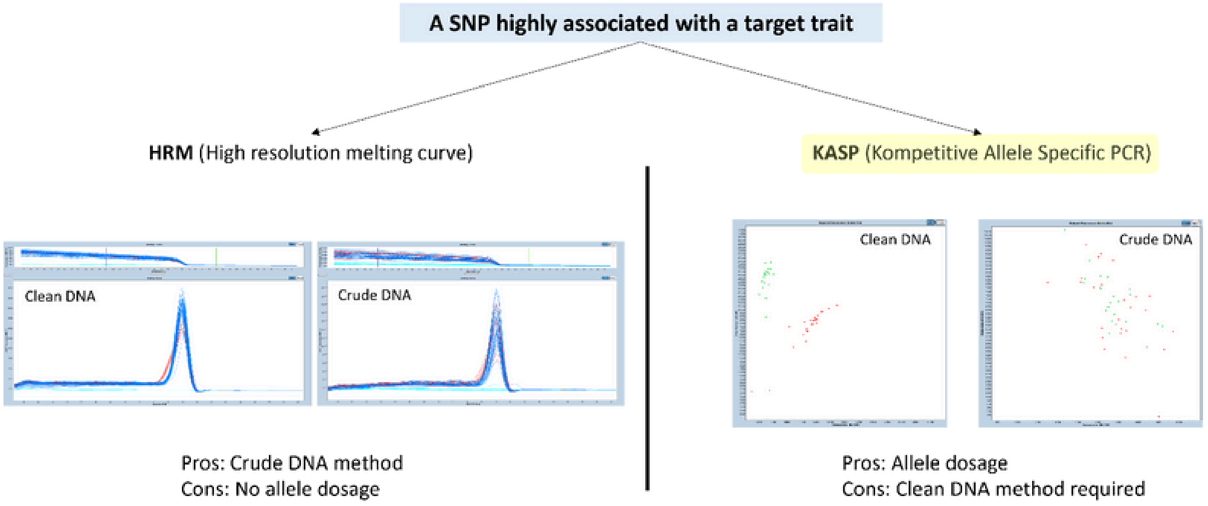


Figure 2. Testing results of two DNA assay methods for MAS implementation.

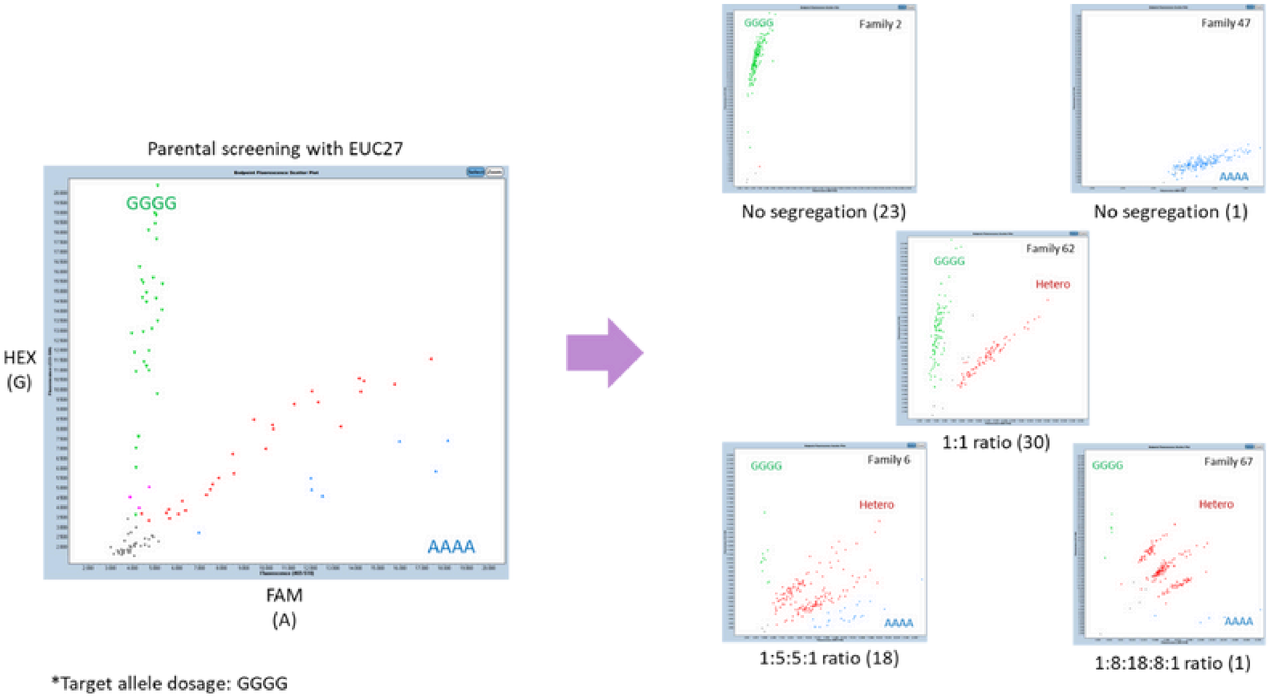
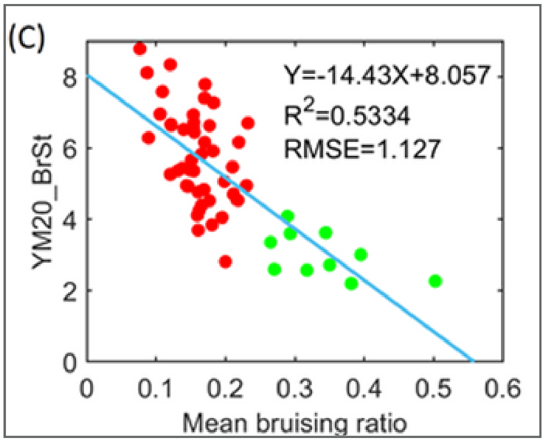


Figure 3. Images of parent and seedling screening results using a single SNP marker for eucalyptol traits.

ADVANCING UNDERSTANDING OF FRUIT QUALITY IN BLUEBERRY

- *Identified fruit characteristics associated with fruit quality in terms of shelf-life, sensorial texture, and internal bruising. Identified a set of parameters that breeders can use to select for improved quality.*
- *Advanced understanding of the cell wall composition in pulp and peel of crisp, firm, and soft blueberry cultivars at harvest.*



PREDICTING SENSORIAL TEXTURE, SHELFLIFE, AND INTERNAL BRUISING

Completed four studies to associate fruit characteristics with sensorial texture, shelf life, and bruising (Oh et al., 2024a, Oh et al., 2024b, Mengist et al., 2024, Tan 2024).

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Highlight of these studies were:
1. Multiple components contribute to mechanical texture in blueberry
2. Fruit size and chemical composition (pH, TA, sugars, organic acids) have no significant contribution to texture
3. Texture at harvest is the driver of texture after storage
4. Larger berries are correlated with lower weight loss and appearance of wrinkle/shrivel
5. Mechanical texture parameters can predict texture after storage, texture changes, weight loss, and wrinkle/shrivel with low-to-moderate accuracy, sensorial hardiness/springiness/crispness and juiciness with moderate-to-high accuracy and internal bruising with moderate accuracy.

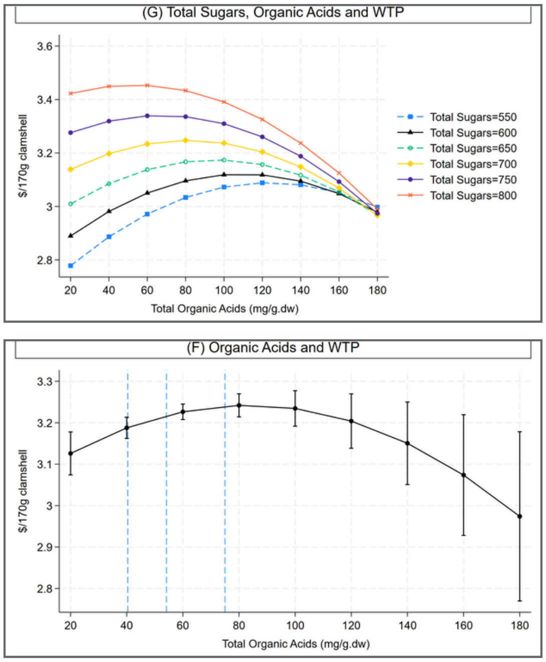
Overall, the following parameters can be used in breeding programs to select for improved fruit quality: high value for “Young’s modulus” (YM_ 20% Burst Strain), “distance to maximum force” (DFM), “Maximum Force” (FM), and large diameter. These parameters contribute towards selection for improved sensorial texture, extended shelf life, and reduced bruising, which are also likely important in machine harvesting for fresh market scenarios.

INSTRUMENTAL BENCHMARKS TO SELECT FOR IMPROVED QUALITY

Used data from a consumer study and instrumental measurements for sugars and acids to identify benchmarks to select for higher quality (Canalese et al., 2024).

Fruit pH values between 3 - 3.5 and a total sugar-to-organic acids ratio between 25 - 30 increased consumer willingness to pay. A total organic acid content higher than 80 mg/g dw reduced consumer willingness to pay while organic acid content <80 mg/g dw and higher total sugar content increased consumer willingness to pay. Fruit larger than 17 mm diameter had a positive effect of willingness to pay.

Fruits with higher "Maximum Force" (FM) and "Young's modulus" (YM_ 20% Burst Strain) had a higher willingness to pay



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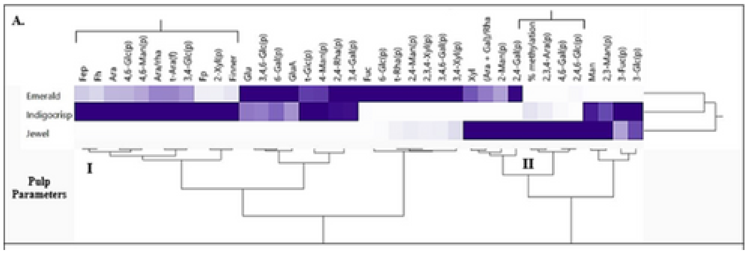
UNDERSTANDING BLUEBERRY CELL WALL COMPOSITION AND TEXTURE

Completed two studies to assess cell wall composition in crisp, firm, and soft cultivars and its changes during storage (Trandel-Hayse et al., 2023).

Differences in cell wall composition in the pulp and peel could explain differences in mechanical texture profiling. Greater abundances of arabinan and type II arabinogalactan in the pulp of the firm and crisp cultivars might contribute to the texture characteristics of these phenotypes. The storage study indicated that epidermal firmness is related to the degradation of pectin in the pulp and cellulose content in the pulp decreases with storage and is related to softening. For more information about cell wall composition analysis in blueberry, see this VacCAP webinar.



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ADVANCING BREEDING FOR FRUIT QUALITY TRAITS

- *Phenotypic data collected during the project enabled blueberry breeders to advance selections into replicated trials and to make new crosses aimed at combining multiple FQ traits. A few examples of selections from two breeding programs are illustrated below.*


USDA-OR 1739-2.
Crisp/firm, exceptional flavor


USDA-OR 1633-3.
Firm, good flavor


USDA-OR
Firm, good flavor.


USDA-OR 1735-4.
Good flavor


USDA-OR 1720-3.
Crunchy


USDA-OR 264-1.
Large size, dry scar, firm/crunchy with good shelf life.


USDA-OR 1637-8.
Firm, good flavor long shelf life.


USDA-OR 1642-6.
Firm, good flavor, long shelf life.


USDA-OR 1617-30.
Firm, large size


Advanced selections propagated in the field and in vitro at USDA-OR breeding program

USDA-OR Loarca

Pictures by Dr. Nahla Bassil, Chad Finn and Marti Pottorff

FEM A *Firm, large size, early, high sugars and good flavor.*

FEM B. *Firm, large size, uniform bloom, high sugars and yield*

FEM C. *Firm and crisp, uniform bloom, large size, high yield*

FEM D. *Firm, large size, early season, double cropping.*

FEM E. *Firm, large size, concentrated harvest, very good shelf life.*

FEM F. *Firm, uniform, late, good flavor, good shelf life.*

FEM – Italy Giongo

Pictures by Dr. Lara Giongo

IMPACT

Outcomes from Objectives 2–3 resulted in new phenotyping tools and target benchmarks to support selection for improved fruit quality in blueberry breeding programs. This information is also valuable for growers and packers aiming to enhance fruit quality in their operations. Several stakeholders have already engaged with and begun adopting these methods. The genetic studies clarified the mechanisms underlying key fruit quality traits, laying the groundwork for molecular breeding strategies. For traits such as volatiles and texture, the use of DNA markers for marker-assisted selection (MAS) and genomic selection was tested, providing direct proof of concept. As a result, research in *Vaccinium* crops is increasingly focused on identifying and characterizing genes that control fruit quality and on implementing molecular breeding approaches.

Molecular and phenotypic data have also been used to advance the selection of breeding lines with improved quality traits, representing potential new cultivar releases. In addition, the VacCAP project fostered strong collaboration among *Vaccinium* research groups, reducing redundancy and promoting complementary efforts. Collectively, these outcomes represent a critical step forward in advancing research and breeding across the growing *Vaccinium* community.

ONGOING RESEARCH

- Completing testing of an acoustic method to evaluate texture in blueberry
- Completing additional studies to understand the genetic mechanical controlling volatile, sugars and organic acid accumulation in blueberry
- Continuing development of DNA assays and genomic selection models for fruit quality traits
- Developing the next phase of the VacCAP project (VacCAP 2.0)

Testimonials From the Lab

Dr. Sushan Ru
Assistant Professor of Small Fruit Breeding and Genetics
Auburn University

How do you see the parameters associated with improved blueberry quality from VacCAP benefiting your breeding program? Do you think these parameters will help in selecting for better fruit quality?

The VacCAP project identified key traits and their optimal ranges to enhance blueberry quality, including fruit pH, organic acid content, sugar-to-organic acids ratio, and texture. Understanding consumer preferences related to these quality traits is essential for guiding future breeding efforts to improve marker acceptance for blueberries. The findings from VacCAP will help blueberry breeding programs like ours to refine and optimize breeding targets, ensuring better fruit quality and increased consumer satisfaction.

Based on what we've learned about the genetics of multiple fruit characteristics, do you think the insights gained from VacCAP will advance molecular breeding efforts for blueberry? In what ways?

VacCAP identified stable QTL associated with traits such as pH, titratable acidity, organic acid, anthocyanin and volatile content. Based on these findings, future development of DNA tests can facilitate marker-assisted selection, significantly reducing selection costs and potentially shortening breeding cycles. For traits with complex genetic architectures, such as fruit size, sugar content and texture, genomic and phenomic selection are recommended approaches. Together, these insights and tools developed by VacCAP provide valuable resources for blueberry breeding, enabling the application of appropriate molecular techniques to improve fruit quality traits more efficiently.

VacCAP has integrated more accurate phenotyping, new genotyping tools, and enhanced genomic resources. As a result, research is shifting towards identifying and characterizing candidate genes. Do you think this can benefit your breeding program? Why is this shift important for the future of breeding in blueberry?

The phenotyping tools developed by VacCAP, covering traits related to fruit chemical composition (e.g., Brix, acidity), fruit appearance (size and internal bruising), and texture and shelf life, are critical to improve the efficiency of blueberry evaluation.

continued on next page

Many of these recommended phenotyping protocols have been adopted by the small fruit breeding program at Auburn University and other institutions. Standardized and optimized phenotyping protocols lay the foundation for accurate assessment of key traits, leading to a deeper understanding of the genetic architecture of these traits and allow the discovery of candidate genes or associated DNA markers.

Additionally, the genotyping platforms provided by VacCAP offer the community reliable, affordable, and standardized genetic information, accelerating gene discovery and speeding up cultivar development through marker-assisted breeding.

Has VacCAP provided new tools or opportunities that you plan to incorporate into your breeding program? How do you foresee using the data or resources generated from this project in your future breeding efforts?

We have incorporated several phenotyping and genotyping platforms from VacCAP into the small fruit breeding program at Auburn University. Looking ahead, we plan to adopt additional high-throughput phenotyping tools, such as those for measuring total sugar content and bruising. The data and resources generated by VacCAP offer valuable insights into the genetic architecture of fruit quality traits, which will guide our breeding strategies, including crossing design and the optimization of selection methods, to accelerate the development of superior blueberry cultivars.

Do you think VacCAP opened opportunities for you to collaborate with the community? Do you see any potential collaborations or partnerships that could emerge from the research and resources developed through VacCAP? How might these collaborations benefit your breeding program?

VacCAP has effectively brought together blueberry and cranberry breeders through project meetings, presentations at scientific conferences, grower meetings, and various outreach initiatives. This community building has enabled breeders to share knowledge, foster collaboration, and explore new opportunities for future projects. Notably, breeders across both crops have benefitted from exchanging insights on high-throughput phenotyping and other research advances, helping to accelerate technological progress. As a new member of this community, I have greatly benefited from these interactions by learning from fellow breeders and exchanging research ideas and breeding materials, strengthening our collective efforts toward cultivar improvement.

Testimonials From the Lab

Dr. Ye (Juliet) Chu
Assistant Professor, Blueberry Breeding
University of Georgia

How do you see the parameters associated with improved blueberry quality from VacCAP benefiting your breeding program? Do you think these parameters will help in selecting for better fruit quality?

The methodology for fruit quality measurement developed by the VacCAP project is very useful for selecting blueberries with better fruit quality. I would like to implement some of the parameters and methods in my breeding program.

Based on what we've learned about the genetics of multiple fruit characteristics, do you think the insights gained from VacCAP will advance molecular breeding efforts for blueberry? In what ways?

It is possible to use genetic markers to accelerate blueberry breeding. However, before that happen, marker validation across genetic materials will need to be performed and the genotyping platform that are breeder-friendly and cost-effective needs be established.

VacCAP has integrated more accurate phenotyping, new genotyping tools, and enhanced genomic resources. As a result, research is shifting towards identifying and characterizing candidate genes. Do you think this can benefit your breeding program? Why is this shift important for the future of breeding in blueberry?

Discovering genes controlling fruit quality traits is very important. If markers within the genes can be discovered and utilized for molecular breeding, it will greatly improve the accuracy of genotype selection in my program.

Has VacCAP provided new tools or opportunities that you plan to incorporate into your breeding program? How do you foresee using the data or resources generated from this project in your future breeding efforts?

We are already using the whole genome sequence data developed by the VacCAP project to assemble genomes and develop markers from our breeding materials.

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Do you think VacCAP opened opportunities for you to collaborate with the community? Do you see any potential collaborations or partnerships that could emerge from the research and resources developed through VacCAP? How might these collaborations benefit your breeding program?

Yes, the VacCAP research community is highly collaborative, and I am glad to be a new member and work with everyone. New collaborations will allow blueberry genetic material and technology transfer among breeding programs and minimizing redundant research efforts.

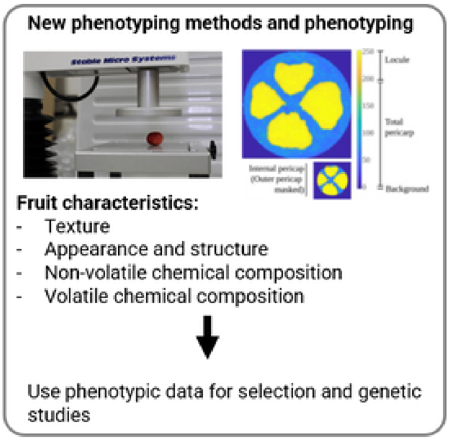
VacCAP

IMPROVING FRUIT QUALITY

OBJECTIVES 2 & 3 | CRANBERRY

CRANBERRY PHENOTYPING, GENETICS, DNA MARKERS AND BREEDING

VacCAP Objective 2-3 aimed to establish phenomics and DNA-based strategies to select for improved fruit quality and yield in cranberry



New phenotyping methods and phenotyping

Fruit characteristics:

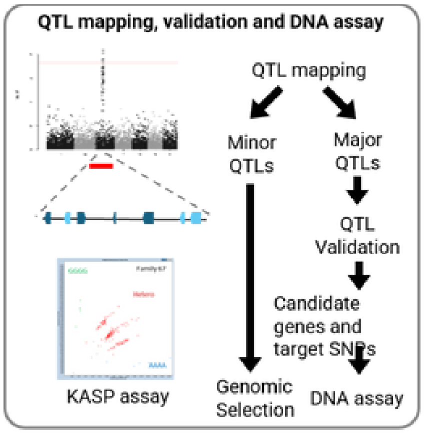
- Texture
- Appearance and structure
- Non-volatile chemical composition
- Volatile chemical composition

Use phenotypic data for selection and genetic studies

Phenotyping Fruit Characteristics

Phenotyping Team

Develop new and more accurate phenotyping methods with improved accuracy and efficiency to evaluate fruit characteristics (FC) and yield- related traits. Use phenotyping data to perform genetic studies and select breeding lines with improved FC.



QTL mapping, validation and DNA assay

Genetics and DNA Markers for Fruit Characteristics

Statistical Genetics Team

Perform marker-trait association analysis to understand the genetic mechanisms controlling fruit characteristics. Based on results of genetic studies, initiate efforts to develop DNA assays.

ACCOMPLISHMENTS IN GENETIC DISCOVERY AND PHENOTYPING

- Developed quantitative, multi-trait phenotyping methods to evaluate fruit characteristics efficiently and accurately.
- Elucidated the genetic architecture underlying key fruit characteristics and yield.
- Advanced selection of cranberry breeding lines with improved fruit quality and yield.

ADVANCING PHENOTYPING FOR FRUIT CHARACTERISTICS

- *Developed accurate, high-throughput phenotyping methods for cranberry fruit, covering external appearance (color, size, shape, uniformity) and texture.*
- *Shared these methods with the cranberry community; some are already in use or being piloted by public- and private-sector stakeholders.*

TEXTURE

Cranberry texture is a critical component for the production of sweetened dried cranberries (SDCs), the most profitable product in the cranberry industry. However, texture is difficult to measure accurately, and previously implemented techniques have given inconsistent results.

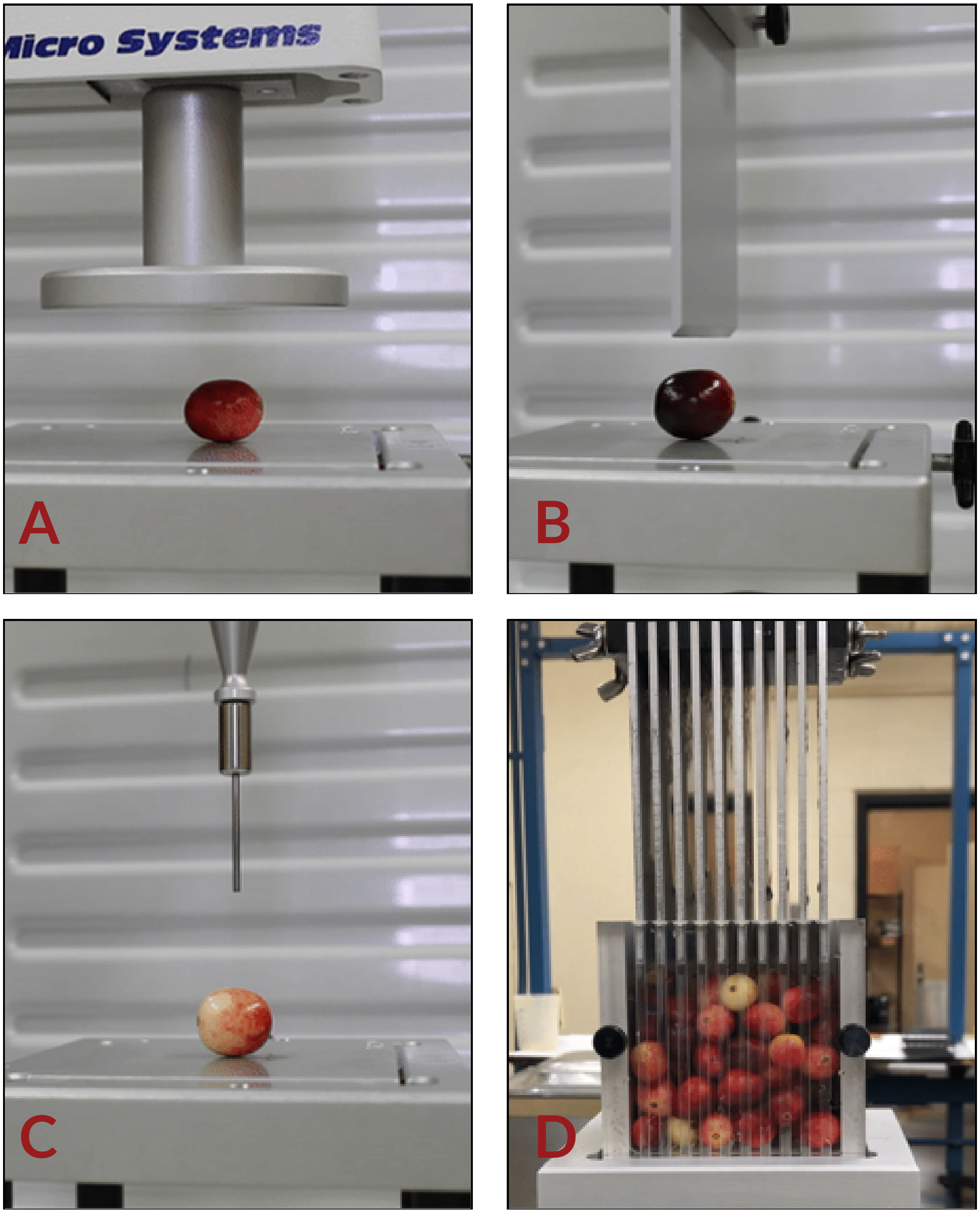
A standardized method for evaluating cranberry texture was developed to help breeders obtain consistent results in marker-trait association analyses, enabling selection of lines with superior texture for release to market. This in turn, will help farmers grow higher-quality fruit and maximize profits, while providing processors with a more consistent product. Optimal conditions for texture testing were determined, and we compared methods and traits at fresh harvest and postharvest.

We utilized five methods - double compression, single compression, puncture, shearing, and Kramer shear cell - resulting in 47 textural features related to cranberry fruit flesh, structure, and skin (Lopez-Moreno et al.,2023; 2024). At least 25-30 fruit per genotype constitutes an optimal sample size across methods and traits. Firmness measurements were stable during the first 30 days of cold storage. The greatest changes in texture were observed after 30 days indicating that firmness analysis should be conducted within the first month if fruit is destined for the fresh market. We also found that certain conventional measurements (e.g., maximum force) were highly biased by fruit size and shape, whereas other measurements (e.g., apparent modulus of elasticity, maximum contact pressure) were less biased.

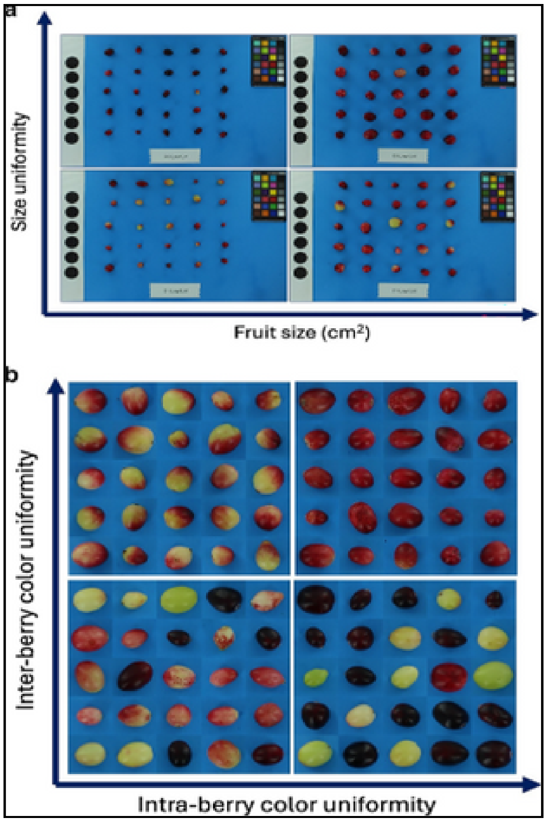
The puncture and double compression methods were identified most effective for texture analysis in cranberry, as they differentiated cultivars at harvest, after refrigeration storage, and after defrosting. The following tests were selected and fine-tuned for cranberries: single compression test (10% strain); C_h1, C_MCP, C_AMOE, and P_R1 and puncture test; P_W, P_DR.

Overall, a multi-trait approach was developed to characterize cranberry texture using the most descriptive methods and traits for both fresh and postharvest conditions. The complementary use of methodologies enables efficient, reliable texture evaluation in breeding programs and industry settings. These methods have been shared at meetings, workshops, and webinars with growers, processors and scientists.

All three public cranberry breeding programs in the country have implemented the methodology for selecting superior cultivars for SDC production. Additionally, the methods were presented and made available to cranberry fruit processors, including Mariani Packing Company (Wisconsin), Graceland Fruit Inc. (Wisconsin), and Ocean Spray (U.S. and Canada).



Cranberry fruit evaluated with double compression probe (A), chisel probe, puncture probe (C), and shearing probe (D).



EXTERNAL APPEARANCE

Measuring external cranberry fruit characteristics is critical for the production of sweetened dried cranberries (SDCs), a key product for the industry.

We developed a high-throughput image analysis software, BerryPortraits, which rapidly detects and segments berries to extract morphometric data on fruit quality traits such as color, size, shape, and uniformity (Loarca et al., 2024). BerryPortraits has potential applications for other specialty crops, such as blueberry, lingonberry, caneberry, grape, and more.

LINK TO IMAGE PAPER

As an open-source phenotyping tool based on widely-used Python libraries, BerryPortraits allows users to modify, optimize, and integrate it into other image analysis pipelines. The software was developed to be user-friendly and implemented through a partnership with VacCAP scientists and Breeding Insight. Based on this work, the cranberry industry commissioned the development of a large-scale imaging data collection system specific to cranberries that is now deployed across the major cranberry handlers. This method increased the accuracy and efficiency of color evaluation. Also, a different research group leveraged these imaging techniques to develop an app that allows growers to measure fruit color and harvest their fruit at peak color.

Finally, phenotyping and data collection efficiency and accuracy are the biggest challenges in a breeding program. BerryPortraits has opened up the opportunity to easily measure cranberry external appearance and is now being implemented by all cranberry public breeding programs for genetic mapping. These advances allow researchers to take measurements of thousands of berries more expediently.

ADVANCING GENETIC DISCOVERY AND BREEDING FOR FRUIT CHARACTERISTICS

- *Completed 10 genetic studies on fruit characteristics (FC), fruit rot resistance (FRR), yield, and vegetative yield-related traits. Key findings include:*
    - *Yield traits were positively correlated with vegetative upright traits. FRR was not correlated with yield or FC, suggesting that improvement in FRR can be made without compromising other traits*
    - *Yield data collected at plot level, rather than on individual number of upright per plant, were predictive and could be more amenable to high-throughput phenotyping (e.g. by imaging)*
    - *QTLs were identified for berry shape/size, yield, anthocyanins (TAcy), titratable acidity (TA), Brix, flavonols, texture, proanthocyanidins-PAC, epicuticular wax, FRR, and vegetative upright traits*
    - *At least 25 QTLs were validated across different populations, making them stable targets for designing DNA assays for marker-assisted selection strategies*
    - *Yield, FRR, texture, fruit size and fruit shape showed moderate-to-high heritability with complex genetic control, suggesting that genomic and phenomic selection are the best strategies for selection.*
    - *Stronger-effect QTLs were identified for anthocyanin accumulation/color, organic acids and, flavanols, which are more promising targets for marker assisted selection.*

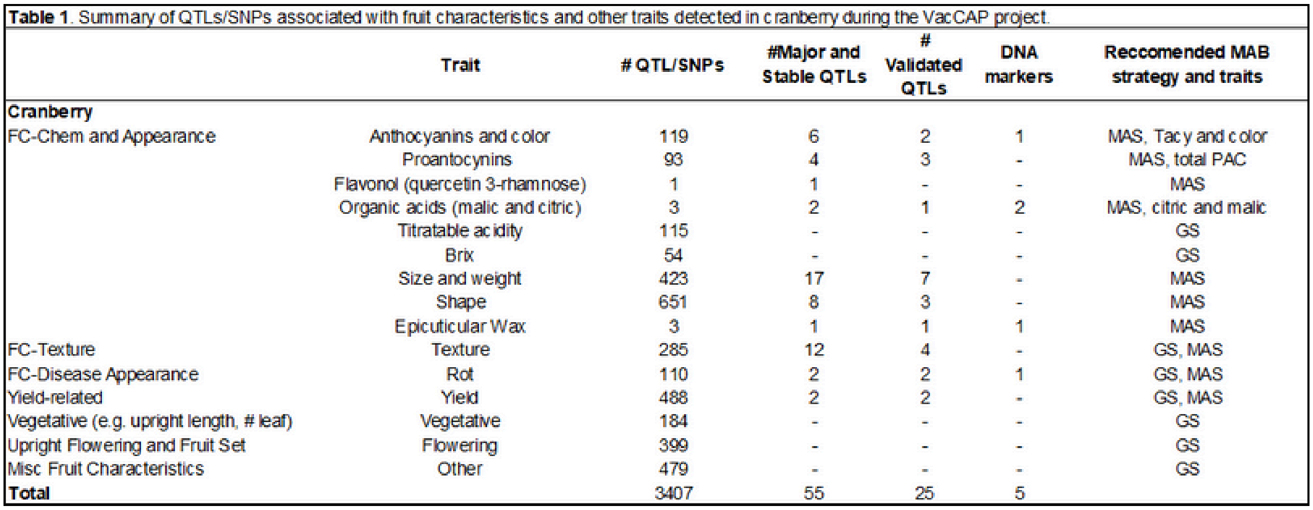


Table 1. Summary of QTLs/SNPs associated with fruit characteristics and other traits detected in cranberry during the VacCAP project.

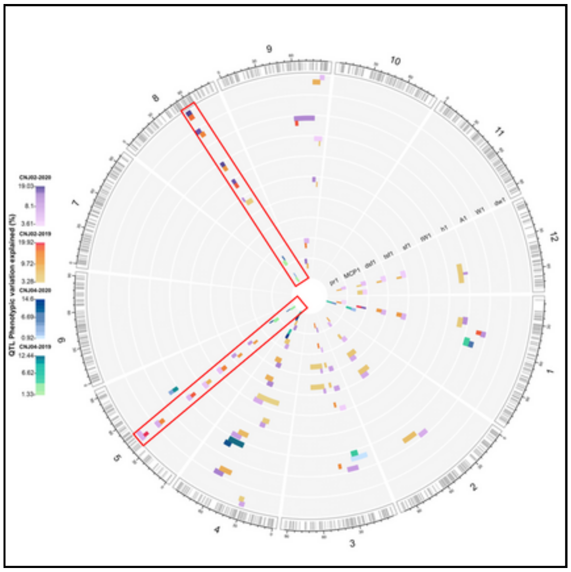
	Trait	# QTL/SNPs	#Major and Stable QTLs	# Validated QTLs	DNA markers	Reccomended MAB strategy and traits
Cranberry						
FC-Chem and Appearance	Anthocyanins and color	119	6	2	1	MAS, Tacy and color
	Proantocynins	93	4	3	-	MAS, total PAC
	Flavonol (quercetin 3-rhamnose)	1	1	-	-	MAS
	Organic acids (malic and citric)	3	2	1	2	MAS, citric and malic
	Titratable acidity	115	-	-	-	GS
	Brix	54	-	-	-	GS
	Size and weight	423	17	7	-	MAS
	Shape	651	8	3	-	MAS
	Epicuticular Wax	3	1	1	1	MAS
FC-Texture	Texture	285	12	4	-	GS, MAS
FC-Disease Appearance	Rot	110	2	2	1	GS, MAS
Yield-related	Yield	488	2	2	-	GS, MAS
Vegetative (e.g. upright length, # leaf)	Vegetative	184	-	-	-	GS
Upright Flowering and Fruit Set	Flowering	399	-	-	-	GS
Misc Fruit Characteristics	Other	479	-	-	-	GS
Total		3407	55	25	5	

ADVANCING GENETIC DISCOVERY AND BREEDING FOR FRUIT CHARACTERISTICS

- *Found that specific organic acid profiles, rather than juice pH and TA measurements, were more effective at detecting QTLs associated with fruit acidity*
- *Integrated QTL data with new, high-quality reference genomes to identify genetic loci contributing to variation in fruit organic acids, anthocyanins, flavonols, epicuticular wax, fruit rot resistance, and textur*
- *Developed the first set of DNA markers for FRR, fruit color, organic acids and epicuticular wax. These markers were tested in mapping populations and are currently being tested across a wider set of cranberry germplasm*

TEXTURE

We used 10 texture measurements that allowed us to assess the firmness and elasticity of cranberry fruit flesh in two biparental breeding populations [CNJ02 (n=168) and CNJ04 (n=67)], derived from crosses among three cranberry cultivars (Stevens, Mullica Queen, and Crimson Queen).



Red boxes (right) highlight example of stable QTLs identified for texture in two cranberry mapping populations.

We used the data to conduct the first genetic study implementing a compression method to elucidate the genetic basis of cranberry texture (Lopez Moreno, 2025). Some of the traits were strongly related to each other and showed similar phenotypic and genetic patterns. We found that siblings from the two different crosses had a wider array of firmness levels from softer to firmer than their parents.

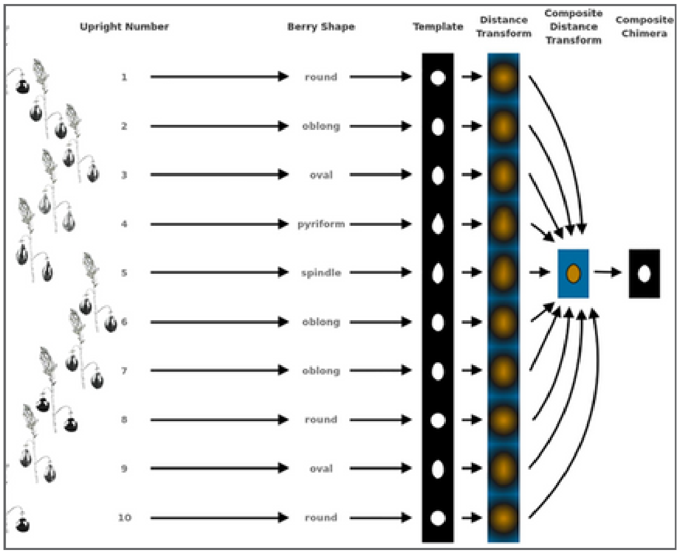
Textural traits that were adjusted for fruit size and shape stood out and proved more reliable from year to year and across different populations. Thus, adjusting for size and shape made the measurements more consistent and less affected by other factors and resulted and better genetic signal detection. Genetic mapping revealed polygenic architecture of this trait. Twelve QTLs located on chromosomes 1,2,3,4,5,8,9, and 12 were stable and/or of major effect.

These genomic regions explained, on average, 5.8-13.6% of the phenotypic variance in CNJ02 and 3.2-10.6% in CNJ04. Four QTLs were validated across the two populations.

Overall, the study indicates that although some QTLs were stable across years and populations, they explain limited amounts of phenotypic variation, suggesting that a combination of genomic selection and marker-assisted selection (MAS) may be the best approach for texture traits. These findings provide insights into the genetic architecture of texture in cranberry, informing breeders about the best DNA-based strategy to select for this important trait. Furthermore, we anticipate that these results will guide future studies aimed at optimizing postharvest fruit handling and management practices.

FRUIT SIZE, SHAPE, AND WEIGHT

Berry size and shape are important for the processing industry because large and round berries are preferred for producing sweetened dried cranberries (SDCs).



Example showing the methodology for generating representative genotype shape, or berry chimera, from 10 upright samples.

Previous studies have identified QTLs for size and shape, but the data had not been integrated. A new study was conducted to identify and integrate QTLs for size, weight and shape across three populations (Maule et al., 2024). All data were collected using high-throughput and accurate phenotyping methods. In total, 151, 266, and 651 SNPs were associated with size, weight, and shape, respectively. Across these analyses, 25 QTLs were stable across years and 10 were validated across studies. For example, multiple meta-QTL associated with round, spherical berries, berry length:width ratio, and shape eccentricity were identified on chromosomes 2, 11, and 12. The QTLs can be targeted to narrow regions of interest for these traits and to develop DNA markers for MAS.

YIELD

Yield is the most important characteristic for cranberry production. Cranberry yield traits, including total fruit mass and number, have traditionally been measured on a per-upright basis. However, given the substantial cost and time required to accurately phenotype these traits, yield evaluation is now done at the plot-level (or per-unit-area) basis.

A study was conducted to evaluate the relationship between upright yield-related traits and plot-based yield (Maule et al., 2024). The genetic mechanisms controlling these traits were also evaluated. The results indicated that several plot yield traits are correlated with upright yield-related traits. For example, plot-level mean fruit mass (MFM) was strongly correlated with upright mean fruit mass (UMFM). Total yield measured at the plot level correlated moderately with upright berry width, upright berry mass, upright mean fruit mass, and upright number of mature berries. In total, 488 markers were associated with yield-related traits. Multiple QTLs for upright and plot-level yield traits colocalized, further supporting their relationships. A region of chromosome 11 harbored several QTLs for plot-level total yield and multiple upright yield traits.

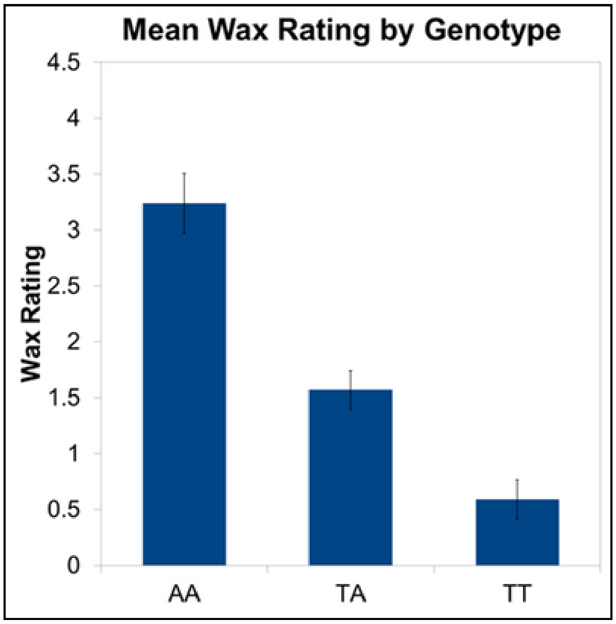
Overall, results indicated that evaluating yield at the plot level is accurate and could be more amenable to future high-throughput phenotyping (e.g., imaging). Although promising QTLs were detected for yield, given the complexity of the traits, future work will focus on testing genomic selection and assessing the integration of associated markers into the models.

Example of plot level phenotyping. This method is accurate and more amenable to high-troughput phenotyping than uprights based phenotyping. The upright based phenotyping is the traditional method of evaluation in blueberry and require the breeder to randomly collect fruits from 10 uprights.

EPICUTICULAR WAX

A study was conducted to understand the effect of epicuticular wax (ECW) on light and heat tolerance and evaluate the genetic mechanisms controlling ECW (Erndwein et al., 2023).

Intense solar radiation causes fruit sunscald across cranberry growing regions, reducing yield. The study indicated that genotypes with more ECW had lower berry mass percent loss (i.e., less water loss) and maintained cooler berry surface temperatures relative to genotypes with less ECW. QTL mapping identified a QTL on chromosome 1 that explained over 36% of the phenotypic variation.



Segregation of cranberry ECX at QTL loci. Allele AA has significantly higher wax than allele TA or TT. ***LINK TO IMAGE PAPER***

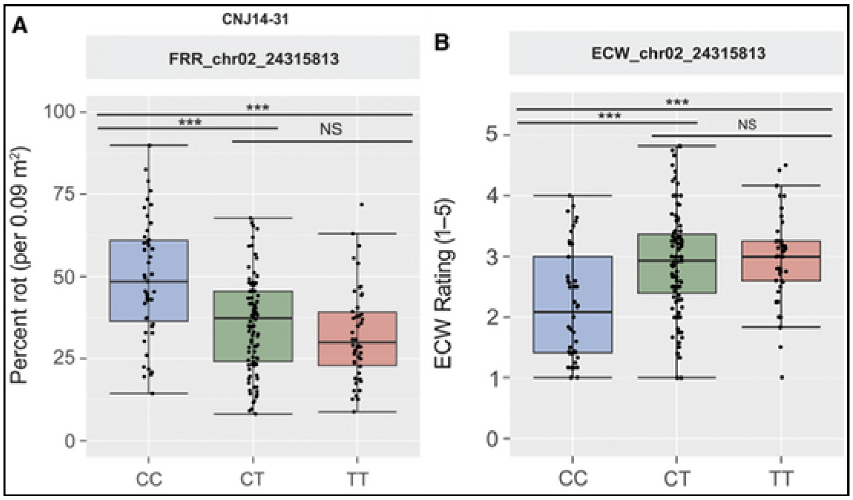
A second QTL study in a different mapping population identified two QTLs for ECW and further validated the QTL on chromosome 1 (Kawash et al., 2024). Within the chromosome 1 QTL interval, 11 potential gene sites were identified. Within this region a SNP at position 38,782,094 bp (chr01_ 38,782,094; using the 'Ben Lear' reference genome) was used to develop a PACE genotyping assay. The assay was used to genotype 34 individuals chosen for high, medium, and low ECW phenotypes. Genotyping results demonstrated that for this marker, there were significant differences in wax ratings among genotypes. The results suggest that while this marker can be used to reliably predict high or low ECW phenotypes among cranberry seedlings (i.e. homozygous CC vs. homozygous TT), phenotypic predictions for individuals that are heterozygous TC are less reliable. Future work should narrow the region associated with ECW and validate the marker across the cranberry germplasm collection.

FRUIT ROT RESISTANCE

Two studies evaluated the genetic mechanisms controlling fruit rot resistance (FRR). Fruit rot is a fungal disease complex that threatens cranberry yields in North American growing regions. Control methods heavily rely on fungicide applications, a practice tht may be increasingly restricted in the long term. Breeding for FRR is essential for sustainable production.

The first study evaluated the genetic mechanisms controlling FFR and its relationship to ECW (Kawash et al., 2024). Correlation analysis between ECW and FRR indicated a significant negative relationship between these two traits, suggesting that individuals with higher ECW tend to exhibit lower fruit rot. Significant QTLs for FRR were located on chromosomes 2, 3, 10, and 11. The combined QTLs accounted for 43.67% of the FRR variance. Interestingly, a QTL on chromosome 2 associated with FRR was found to overlap with one associated with fruit ECW. A PACE genotyping assay was designed for the QTL marker identified on chromosome 2, position 24,315,813 bp ('Ben Lear' reference genome) and used to genotype cranberry accessions with varying levels of FRR and ECW. Genotyping results demonstrated that, for marker FRR_chr02_24315813, there were significant differences in percent fruit rot among genotypes and ECW classes. The DNA assay successfully identified accessions that exhibit the desired phenotypes (i.e., lower rot and higher ECW), thus making it a useful tool for marker-assisted selection. Possible functional genes were identified in associated genomic regions that may contribute to FRR and ECW.

A second study integrated multiple available QTL studies for FRR evaluated as field fruit rot (Maule et al., 2024). The study identified 108 SNPs associated with field fruit rot, and one QTL located on chromosome 12 ('Stevens' reference genome) was validated across studies. Future work will evaluate the marker across the cranberry germplasm collection and assess interactions between markers developed for ECW and FRR, and explore the region identified on chromosome 12 for additional DNA assay development. We will also evaluate genomic prediction models will be evaluated. This work will expedite breeding for improved cranberry fruit quality.

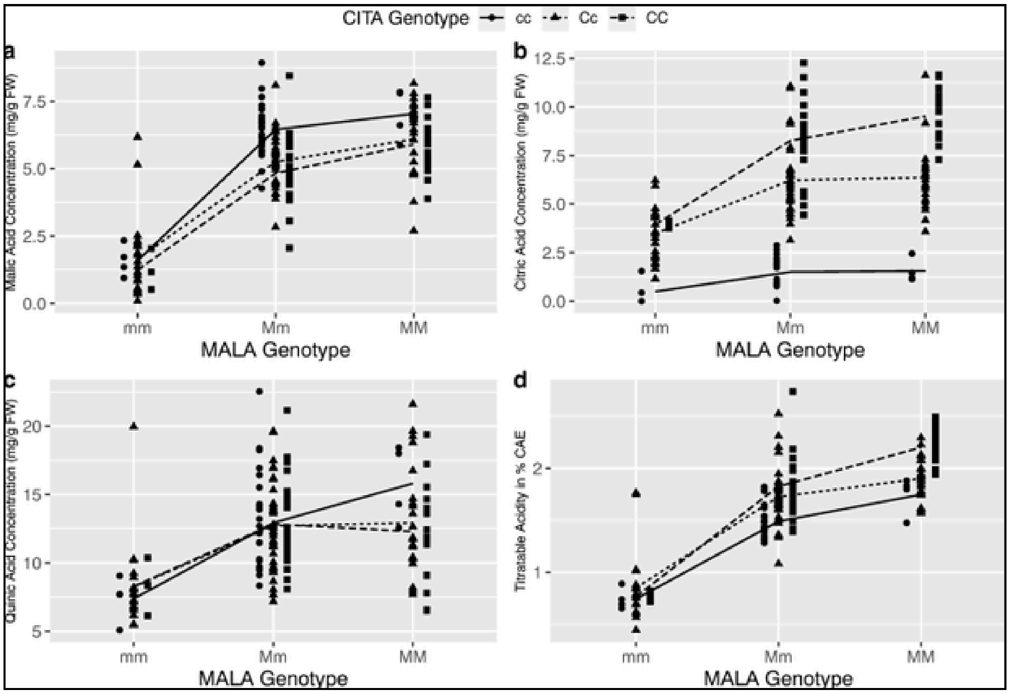


PCR allele competitive extension (PACE) genotyping assays for FRR and ECW.

LINK TO IMAGE PAPER

ORGANIC ACIDS AND SUGARS

Cranberry fruits contain very high level of organic acids relative to sugars, about five times that of other fruits, which contribute to high titratable acidity (TA)–the tartness of cranberries.



The effect of mala *and* cita *on organic acid concentration and titratable acidity. Non dwarf lines that are* Mm *and* cc *in panel d can reach TA value as low as 1.1-1.3.* ***LINK TO IMAGE PAPER***

To offset the tartness for consumers, higher amounts of sugar is added to cranberry products, such as sweetened dried cranberries (SDCs) and juices. As a result, consumers have a negative perception of cranberry products (see Obj. 4 newsletter) despite the health benefits of cranberries. Reducing cranberry acidity would allow less sugar to be added to cranberry products. Previous work evaluated Brix, TA, and organic acids in the Rutgers cranberry germplasm collection. Brix is traditionally used as a proxy of sugar content while TA is used as a proxy of organic acids. Results indicated that variation for Brix is limited in the cranberry germplasm while higher variation exists for TA. Lines with lower organic acids and TA were identified.

During the VacCAP project, these materials were characterized, genetic studies were conducted, and the low acid lines were used to develop new cranberry selections. Genetic studies indicated that two major QTLs control low acidity in the low acid lines (Fong et al. 2020; Fong et al. 2021). The two QTLs named cita and mala, control the level of citric and malic acids, respectively. Ongoing work in a diversity panel and biparental populations validated the QTL for citric acid.

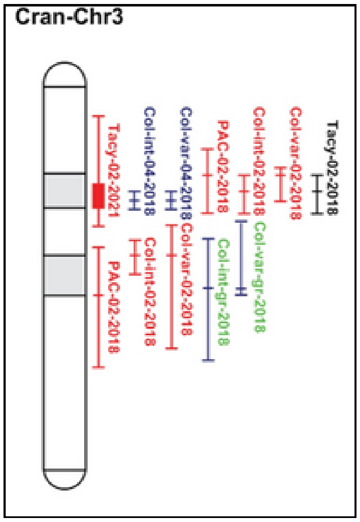
The low citric acid QTL can reduce TA to 1.6%. The low malic QTL can decrease TA to below 1%, which is within the range of fruits that are consumed fresh. However plants with very low acidity have a dwarf-like growth habit which is likely not commercially viable. Interaction analysis between the cita and mala loci indicated genotypes heterozygous for mala and homozygote recessive for the cita locus that are non-dwarf (commercially viable) and can bring the TA value down to 1.5, which is significantly lower than the normal TA value in current cranberry cultivars (>2). These studies demonstrated that lowering acidity in cranberry cultivars is possible and the DNA markers developed can help accelerate this process. This has allowed the cranberry breeding program at Rutgers University to select lines with lower acidity before field evaluation. This material will be used to assess SDCs production and reduce the amount of added sugars. Ongoing work focuses on developing high-throughput SNP markers for the cita and mala loci.

HEALTH RELATED BIOACTIVE COMPOUNDS

Four studies evaluated the genetic mechanisms controlling the accumulation of anthocyanin, proanthocyanidins and flavonols in cranberries (Maule et al., 2024, Diaz Garcia et al., 2021, Albert et al., 2023, Jiménez et al., 2025).

These bioactives are associated with health benefits and fruit color in cranberries. Anthocyanin and proanthocyanidins were evaluated using spectrophotometric and color intensity measurements, while flavonols were evaluated using high-performance liquid chromatography.

A major and stable QTL for quercetin-3-rhamnoside was identified in chromosome 3 (‘Ben Lear’ reference genome). This locus is a potential target for candidate gene discovery and DNA marker development. Ten stable QTLs were identified for anthocyanins and proanthocyanidins. Three QTLs for proanthocyanidins overlapped with QTLs for anthocyanins and measurements of total anthocyanins (TAcy), suggesting interaction between these metabolites.

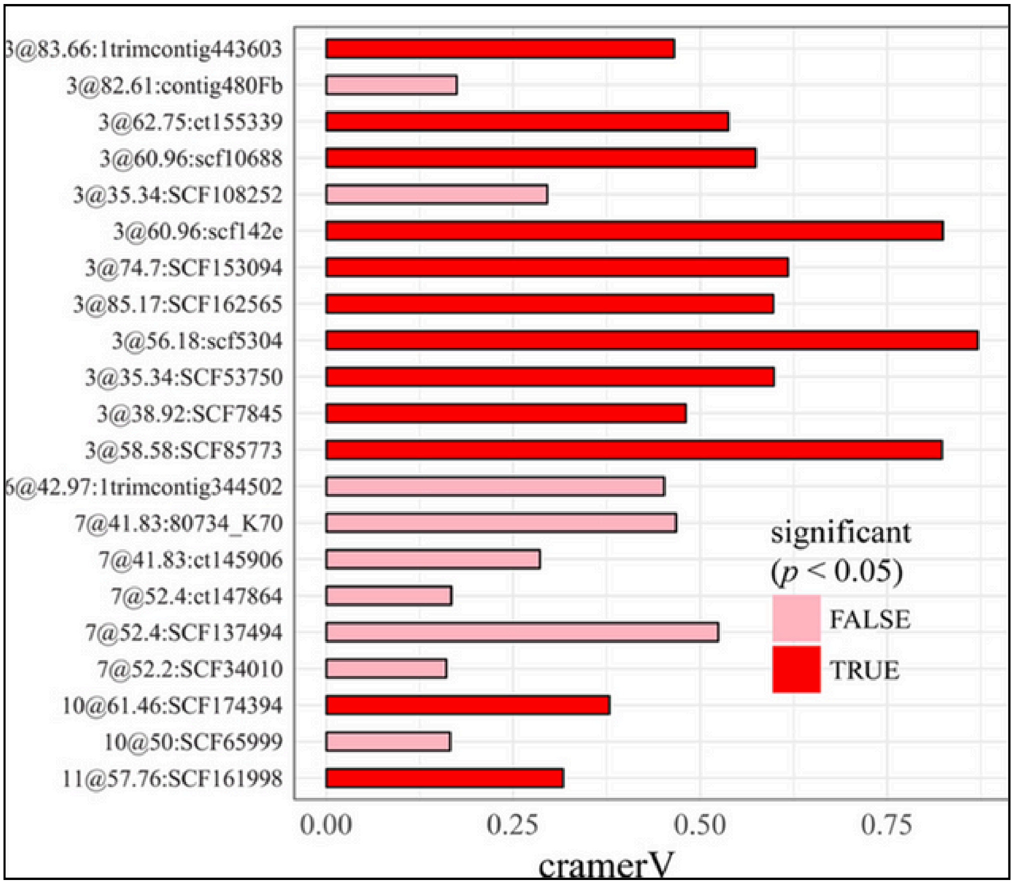


Two QTLs for anthocyanins and three QTL for proanthocyanidins were validated across studies. Two QTLs for color and anthocyanin content (presence vs. absence of red color) mapped to two regions on chromosome 3, including the most significant QTL that was evaluated for candidate genes. A transcription factor controlling anthocyanin accumulation was identified in this region. This QTL region was used as a target to develop a SSR marker for fruit color.

Validated and stable QTLs for anthocyanin and color detected in cranberry chromosome 3. ***LINK TO IMAGE PAPER***

During the VacCAP project, the SSR markers were tested by the USDA-ARS cranberry breeding program at UW-Madison and used to select cranberry lines that lack anthocyanin accumulation in fruit skin (yellow skin color).

This work was done in collaboration with Valley Corporation, a fourth-generation private cranberry breeding company in Tomah, Wisconsin. The selected line was named ‘Lemon Drop’ (see page 14) and is expected to be released as a cultivar by Valley Corporation. Future work will focus on developing SNP-based markers for the presence/absence of red color and detecting QTLs for color intensity.



Strength of association between SSR markers at a major TAcy/color QTL in chromosome 3 and fruit color phenotype (red vs yellow). ***LINK TO IMAGE PAPER***

ADVANCING BREEDING FOR FRUIT QUALITY TRAITS

- *Phenotypic data collected during the project enabled cranberry breeders to advance selections into replicated trials and to make new crosses aimed at combining multiple fruit quality traits. A few examples of selections from two breeding programs are illustrated below.*

USDA-24-64. Very large size, firm, early, low rot.

Possible name **'Lemon Drop.'** Valley Corporation Inc. (Ed Grygleski). First yellow variety; rich in proanthocyanidin.

USDA-24-29. High yield, low fruit rot

USDA-24-100. Large size, firm, round, high yield, low fruit rot

USDA-WI Zalapa

Pictures by Dr. Juan Zalapa

CNJ12-092-073

A low acid selection. Titratable acidity = 1.8, Yield at 186 barrels/acre, Brix = 9.1, Fruit weight 1.5 g

CNJ12-092-075

A low acid selection. Titratable acidity = 2.0, Yield at 221 barrels/acre, Brix = 9.1, Fruit weight 1.4g . Well liked at a 12.5% sugar reduction in a consumer panel (n=63).

NJ93-117-004

A high flavonol selection. High in quercetin 3-rhamnoside and heat stress responsiveness. A wild selection collected in Cape Henlopen, Delaware.

CNJ14-031-142

A fruit rot resistant selection. Yield at ~255 barrels/acre with two in-bloom sprays and less than 20% rot. Titratable acidity = 2.08, Brix = 8.64, Fruit weight = 1.27g

Rutgers University Sideli

Pictures by Dr. Gina Sideli

IMPACT

The outcomes of Objectives 2-3 provided new phenotyping tools and DNA markers, which will benefit cranberry breeding programs in their development of cultivars with improved fruit quality. Growers and processors seeking to maximize fruit quality within their operations will also benefit from these advances. A number of stakeholders are already starting to adopt these methods.

The genetic studies elucidated the mechanisms controlling several fruit quality traits, laying the foundation to advance the development of molecular breeding strategies for these traits. For some traits, like fruit color, organic acids, and epicuticular wax, it also tested the use of DNA markers for marker assisted selection, providing direct proof of concepts. As a result, research in cranberry is now focusing more on identification and functional characterization of genes controlling fruit quality traits and testing implementation of molecular breeding. Molecular and phenotypic data were also used to advance selections of cranberry breeding lines with improved quality characteristics, which represent new potential cultivar releases.

Further, the VacCAP project fostered active collaboration among *Vaccinium* research groups. This new dynamic contributed to reducing duplicative work, leveraged the unique expertise of all participants, and tuned research projects to be complementary to each other.

Overall, these outcomes represent a transformative step to advance research and breeding within the large and expanding *Vaccinium* community.

ONGOING RESEARCH

- Additional studies to understand the genetic mechanisms controlling organic acid, flavonoids and texture in cranberry
- Continued development of targeted DNA assays
- Developing the next phase of the VacCAP project (VacCAP 2.0)

Testimonials From the Field

Dr. Jeff Neyhart
Research Geneticist, USDA-ARS
Genetic Improvement for Fruits and Vegetables Laboratory

Based on what we've learned about the genetics of multiple fruit characteristics, do you think the insights gained from VacCAP will advance molecular breeding efforts for both blueberry and cranberry? In what ways?

Certainly, yes. The genetic studies of fruit quality in cranberry and blueberry from the VacCAP project indicate that many of these traits are not simply inherited (that is, more than a handful of genes are influencing these traits) and that environment plays an important role. This is the case for fruit yield and cranberry fruit rot, but size, shape, color, and texture. With such traits, molecular breeding can switch to utilizing a whole-genome approach, like genome-wide selection, instead of focusing on only a few markers. In other crops, this has led to faster breeding progress, and it could be the same for cranberries and blueberries.

VacCAP has integrated more accurate phenotyping, new genotyping tools, and enhanced genomic resources. As a result of this, research is shifting towards identifying and characterizing candidate genes. Do you think this can benefit your breeding program? Why is this shift important for the future of breeding in blueberry and cranberry?

Identifying candidate genes is a nice form of validation that helps us confirm whether a signal from a genetic mapping study may be biologically real. In that case, a marker tagging that gene can be expected to reliably predict the phenotype of new offspring carrying that marker.This works very well for those traits that are controlled by a few genetic loci with large effects, such as some fruit quality traits or disease resistance that follow a simple gene-for-gene model in pathogen recognition. Characterizing the function of these genes allows us to reliably predict how they will behave in potential new cultivars. In the case of more complex traits like yield, quantitative disease resistance, or abiotic stress tolerance, the genes influencing these traits are likely to be so numerous that characterizing candidates will produce only marginal returns on the investment of time.

So, we need to strike a balance betweencharacterizing genes for "low-hanging fruit"and high-impact simple traits (pun most definitely intended) and improving traditional breeding and selection with phenotyping and genotyping tools for more complex traits.

Has VacCAP provided new tools or opportunities that you plan to incorporate into your breeding program? How do you foresee using the data or resources generated from this project in your future breeding efforts?

Yes, definitely! We are alreadyexploiting the 3K marker arrayfrom Breeding Insight(developed using the 17K array from VacCAP) to predict phenotypes and make selections of seedlings before they enter field trials, and wewill continue using this tool for routine genotyping of new offspring from theprogram. We also plan to expand on our collaborative work in image-based phenotyping of fruit quality; we assisted in the development of the “BerryPortraits” software with Dr. Jenyne Loarca of the VacCAP and Breeding Insight, and we are deploying similar software in our custom-made “BerryBox” fruit imaging platform, which allows us to measure fruit size, shape, color, uniformity, and percentage of rotten fruit using only color images and an AI model. Finally, the genomic data in the GenomeDatabase for Vacciniumhas already been immensely usefulfor our pre-breeding work. We have used this data to identify candidate genes for cold tolerance, flowering time, and disease resistance.

In the future, we will take advantage and expand upon genomic resources, including the cranberry pangenome, to more fully inventorythe haplotypes (groupsof genes that are inheritedtogether) present in cranberry germplasm. This will have two direct benefits: first, we can target unadapted germplasm (such as wild or landrace clones) with novel alleles that may confer favorable quality, disease resistance, or stress tolerance traits; second, we can use this haplotype inventory to impute from the high-density pangenome data down to the low-density 3K or 17K marker data. In thisway, we can obtain whole-genome coverage of new offspring for the very modest price of a few thousand markers.

Do you think VacCAP opened opportunities for you to collaborate with the community? Do you see any potential collaborations or partnerships that could emerge from the research and resources developed through VacCAP? How might these collaborations benefit your breeding program?

Absolutely. My first task after starting in my position was to reach out to the community to start establishing collaborations, and VacCAP was a great mechanism to facility those connections. We already have good collaborations with the other cranberry breeders to facilitate joint testing of new populations, alongwith others to investigate diseaseresistance, fruit quality,phenology, and stress tolerance traits. Breeders must wear many hats, but we obviouslycannot do everything alone; these collaborations are critical to provide 1) direct, actionable information to guide the selection program, or 2) inform how we design new evaluation schemes to measure important traits on the large populations needed to sustainbreeding progress.

I have been impressed by how we have been able to quickly use genomic and phenomic tools developed through VacCAP in the breedingprogram. My graduateand postdoc researchwere in small grains (barley and oats), and that community has very impressive genomic resources. I think VacCAP has helped rapidly close the resource gap between the blueberry and cranberry community and those of crops with a longer history of research investment.

Testimonials From the Field

Dr. Gina Sideli
Assistant Professor
Rutgers University, Department of Plant Biology

Based on what we've learned about the genetics of multiple fruit characteristics, do you think the insights gained from VacCAP will advance molecular breeding efforts for both blueberry and cranberry? In what ways?

Yes, I believe the *Vaccinium* community has gained substantial insights into fruit traits during the VacCAP project period, which will significantly advance molecular breeding efforts in both blueberry and cranberry. Most importantly, we now have comprehensive genomic resources available, including sequenced genomes, pangenomes, and high-throughput genotyping platforms—all of which provide the foundational infrastructure necessary for advanced genomic studies.

Regarding specific traits, the project has delivered improved phenotyping methods for texture, color, and fruit chemistry, enabling breeding programs to implement both marker-assisted selection and genomic prediction modeling for more effective cultivar development. These combined advances create a comprehensive toolkit that moves breeding programs from traditional phenotypic selection toward precision genomics-based approaches.

VacCAPhas integrated more accurate phenotyping, new genotyping tools, and enhanced genomic resources. As a result of this, research is shifting towards identifying and characterizing candidate genes. Do you think this can benefit your breeding program? Why is this shift important for the future of breeding in blueberry and cranberry?

Absolutely! The transition from broad genetic associations to specific candidate genes allows us to identify the actual genes controlling trait expression, enabling the development of precise molecular markers that remain reliable across diverse genetic backgrounds—unlike broader associations that can fail in different breeding populations. This knowledge also creates opportunities for gene editing applications, particularly for fine-tuning fruit chemistry such as sugar-acid balance to meet specific market requirements.

As both consumer expectations and environmental conditions continue to shift, there's increasing demand for varieties that deliver targeted flavor profiles and nutritional attributes while maintaining performance under climate stress. Understanding the underlying genetic mechanisms of fruit development provides breeding programs with the precision needed to address these complex, interconnected demands

Has VacCAP provided new tools or opportunities that you plan to incorporate into your breeding program? How do you foresee using the data or resources generated from this project in your future breeding efforts?

Yes, we have now genotyped numerous breeding populations and germplasm collections in both my blueberry and cranberry programs, which enables marker validation and implementation as well as genomic prediction modeling. I view this as an opportunity to implement genomic tools that improve selection decisions before field planting, allowing us to make more informed choices about which seedlings merit the investment of field space and evaluation resources.

Do you think VacCAP opened opportunities for you to collaborate with the community? Do you see any potential collaborations or partnerships that could emerge from the research and resources developed through VacCAP? How might these collaborations benefit your breeding program?

Definitely! I really value this collaborative network that promotes open exchange of ideas and resources. It allows me to collaborate with scientists who specialize in domains beyond breeding and genetics, complementing my work and deepening our understanding of the traits I focus on. In turn, these collaborations help expand the range of traits I can evaluate, ultimately leading to better products for the industry. For example, in blueberry, I'm currently collaborating with southern highbush blueberry breeders to obtain, test, and integrate germplasm into my breeding program, introducing genetic variation that we currently lack in our northern materials.

Are there any additional comments or thoughts you'd like to share regarding the value of the VacCAP project's outcomes for your breeding work?

VacCAP consists of a solid group of dedicated researchers. These collaborations have enabled us to advance much further than any single lab could achieve independently, which is tremendously valuable. Regarding practical outcomes, the extension and outreach component has been particularly helpful in disseminating research findings and facilitating meaningful dialogue with growers about implementing these advances.

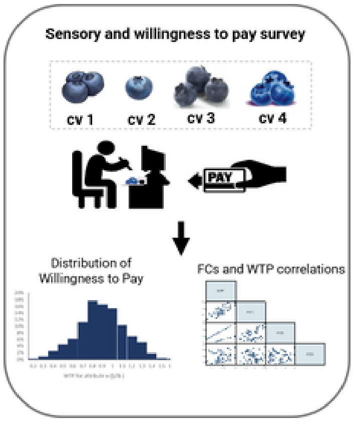
VacCAP

IMPROVING FRUIT QUALITY

>>> OBJECTIVE 4

CONSUMER PREFERENCE AND BEHAVIOR

VacCAP Objective 4 assessed the potential socio-economic impact of blueberry and cranberry fruit quality improvements on market demand



Understanding Consumer Preferences for Fresh Blueberries

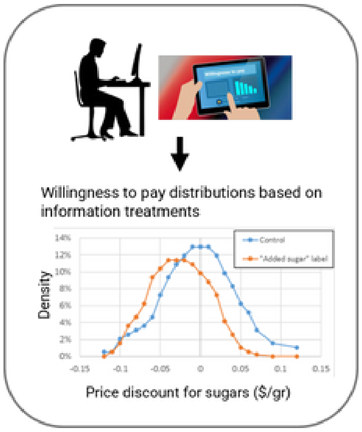
>>> Socio-Economic Team

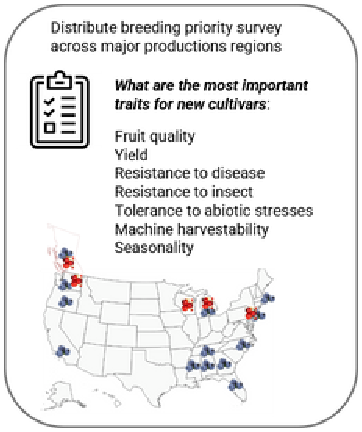
Conducted an online survey and a consumer panel to asses how consumer and fruit characteristics, along with sensorial attributes, affect willingness to pay for fresh blueberries and to identify factors affecting purchasing behavior.

Used an online survey to assess consumer perception for added sugar labeling in cranberry processed products and for genetic approaches to lower added sugar content.

Understanding Consumer Preferences for Cranberry Products

>>> Socio-Economic Team





Reassessing cranberry and blueberry breeding

>>> Extension & Socio-Economic Teams

Surveyed growers, distributors, breeders and scientists to reassess blueberry and cranberry breeding priorities.

ACCOMPLISHMENTS IN SOCIO-ECONOMIC STUDIES

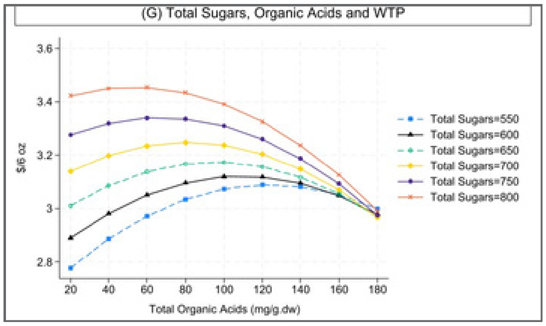
OUTCOMES ARE

- Generated new insight into consumer preferences for blueberry quality attributes and their impact on purchasing behavior
- Advanced knowledge about consumer reactions to added sugar labeling and the use of gene editing technology for cultivar development in cranberry products
- Identified stakeholders breeding priorities

UNDERSTANDING CONSUMER PREFERENCES FOR FRESH BLUEBERRIES: THE IMPACT OF SENSORY AND FRUIT QUALITY TRAITS

Blueberries have become one of the most economically significant berries in the United States, with per capita consumption soaring by 879% between 2000 and 2021.

As the blueberry market becomes increasingly selective and quality-driven, it is important for the industry and breeders to focus on fruit quality traits that enhance consumer demand. While current selection efforts prioritize agronomic traits like yield and storage performance, consumers tend to value attributes like flavor, texture, appearance, and fruit size. Despite this, research connecting blueberry sensory and quality attributes to increased consumption remains limited. The two studies featured in this newsletter aim to bridge this gap by exploring consumer preferences for quality attributes and their impact on purchasing behavior. By understanding these preferences and the role of quality descriptors, the industry can better meet consumer expectations, drive higher consumption, and implement targeted marketing strategies.



Willingness to Pay for Blueberries: Sensory Attributes, Fruit Quality Traits, and Consumers' Characteristics

LINK TO PAPER

This study investigates how sensory attributes and fruit quality traits influence consumers' willingness to pay (WTP) for fresh blueberries. Using a combination of consumer sensory tests and a double-bounded contingent valuation method, the study assessed consumer preferences for various northern and southern highbush blueberry cultivars across Oregon and Florida over two years.

Sensory attributes and WTP: This study assessed how various sensory attributes—such as flavor, sweetness, and firmness sensory liking and intensity scores— influence how much consumers are WTP for fresh blueberries. Flavor emerged as the most important factor in determining consumer acceptance and WTP. Blueberries with higher flavor liking scores were associated with higher WTP. Consumers generally preferred blueberries with a sweeter taste and lower sourness intensity.

Instrumental quality measurements and WTP: The study also examined the relationship between instrumental measures of fruit quality—such as soluble solids, titratable acidity, sugars, organic acids, and firmness—and WTP.

The findings revealed that higher sugar content increases WTP, while higher organic acid content enhances flavor but can reduce WTP if the concentration is too high. The balance between sweetness and acidity seems to be key to consumer satisfaction.

Firmness also positively correlates with WTP, except at extreme values. Consumers generally preferred firmer blueberries, but extremely firm blueberries saw a decrease in WTP, suggesting that there is an optimal level of firmness that consumers find most desirable. Larger fruit size (over 17mm) also contributed to higher WTP.

Consumer characteristics and WTP: WTP varied among different consumer groups, with younger individuals, females, and frequent blueberry consumers showing a greater WTP.

This research offers insights for blueberry breeders and producers, highlighting the importance of selecting for specific fruit quality traits. By aligning production with consumer preferences, the industry can enhance market demand and ensure the continued growth of the blueberry industry.

Quality-Related Descriptors to Increase Fresh Blueberries Purchase—Evidence from a Basket-Based Choice Experiment

LINK TO PAPER

With growing interest in the health benefits of blueberries, this research sought to identify marketing strategies that can drive increased consumption. The study investigated how quality-related descriptors on blueberry packaging affect consumer purchasing decisions, particularly their likelihood of buying blueberries and their sensitivity to price changes.

The study used a Basket-Based Choice Experiment (BBCE), simulating a real shopping experience by allowing participants to select a combination of fruits from a virtual basket. Conducted via an online survey, the study included 3,208 U.S. participants. Respondents were asked to choose from various baskets containing 14 types of fresh fruits, including blueberries labeled with descriptors like "Crunchy," "Stay Fresh," and "Sweety," at different price points. We use these words to refer to the attributes: crispiness, extended shelf-life, and sweetness.

Key insights revealed that price, short shelf-life, and freshness concerns are the primary reasons for infrequent blueberry consumption, with 55% of respondents citing price as the main deterrent. The profile of consumers most likely to purchase blueberries includes male, older individuals who are employed, hold college degrees, have higher fresh fruit budgets, reside in the Northeast, and prioritize health.

Impact of quality descriptors on purchasing behavior: The study found that blueberries labeled with “Stay fresh”, which indicates a longer shelf life, increased the likelihood of blueberry purchases. In contrast, the “Sweety” and “Crunchy” descriptors did not effectively boost purchase intent.

Blueberries labeled with “Stay Fresh” or “Sweety” showed lower price elasticity compared to unlabeled blueberries, indicating that consumers were less likely to reduce their purchases in response to price increases. Notably, the “Stay Fresh” label had the strongest impact on reducing price sensitivity, aligning with the finding, also in this study, that consumers prioritize freshness as a key quality attribute.

This research highlights that while sensory and hedonic descriptors on blueberry packaging can influence consumer behavior, not all descriptors are equally effective in driving purchases or reducing price sensitivity. For instance, the “Stay Fresh” label enhanced consumer appeal more than the “Crunchy” label, which did not significantly impact purchase intent. These findings can help guide blueberry marketers and producers in crafting strategies to boost sales.

UNDERSTANDING CONSUMER PREFERENCES FOR CRANBERRY PRODUCTS: THE IMPACT OF ADDED SUGARS LABELS AND CRISPR TECHNOLOGY

Two studies were conducted, the first one explored consumer reactions to added sugar labeling in cranberry products. It found that disclosing added sugars reduced willingness to pay (WTP) for sweet and dried cranberries and cranberry juice.

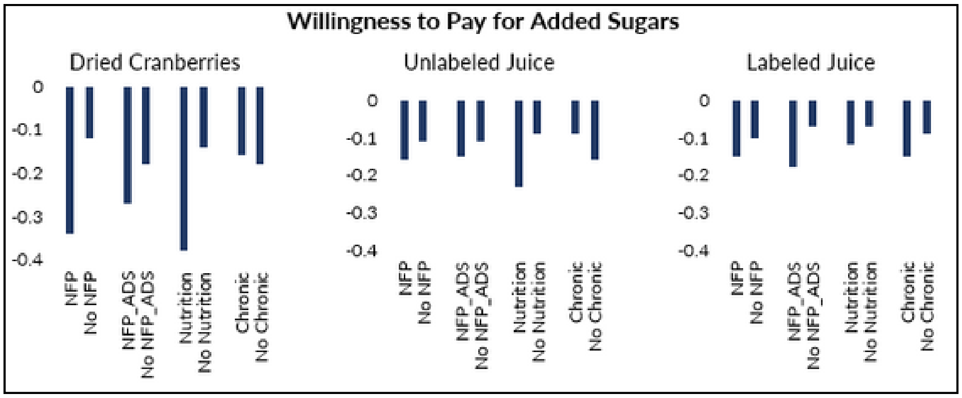
Health benefits and sugar intake recommendations did not increase WTP, suggesting strong negative consumer perception of added sugars despite product health benefits. The second study examines consumer attitudes towards CRISPR-edited cranberries versus conventionally bred and genetically modified (GM) crops. Findings show consumers are generally less willing to pay for CRISPR-edited products unless they offer clear benefits like reduced sugar. Effective communication about CRISPR's advantages and distinctions from GMOs could enhance acceptance and market appeal.

Consumer Response to “Added Sugar” Labeling in Cranberry Processed Products

LINK TO PAPER

This study examines the impact of disclosing added sugars in packaged cranberry products on consumer choices. We first determined the willingness to pay (WTP) for added sugars in sweet and dried cranberries (SDCs) and cranberry juice. Willingness to pay is the amount of money an individual is willing to give up obtaining a product with the levels of attributes (added sugar content, different sweetening methods) described in the survey. Then, we assessed how providing information about cranberry health benefits and recommended sugar intake influences WTP estimates, aiming to understand if health claims can offset the negative impact of the added sugar information on the label of cranberry products.

Additionally, we analyzed how various consumer groups reacted to the added sugar information. This research shed light on how labeling policies affect consumer behavior and the efficacy of health information on decision-making. The study collected data through a survey conducted by Qualtrics Research Services, comprising 2,000 respondents.



Heterogeneous WTP across different cranberry survey sub-samples of respondents.

NFP means: Respondents for whom the information in the Nutrition Facts Panel (NFP) is important. NFP_ADS means: Respondents for whom added sugars are the main piece of information in the NFP. Nutrition means: Respondents who are nutrition conscious. Chronic means: Respondents who have been diagnosed with diet-related chronic diseases.

SDC: Findings revealed that each additional gram of added sugar decreased respondents' WTP for dried cranberries by $0.20/6-oz bag. For example, if a 6-oz bag is priced at $3.99, and the label indicates it contains 12 grams of added sugars, individuals would only be willing to pay $1.79 for the same bag if the label indicates it contains 23 grams of added sugars. Respondents showed no preference between SDC sweetened with fruit juice plus regular sugar versus regular sugar alone. Information on cranberry health benefits didn't increase respondents' WTP, but information on recommendations to limit sugar intake lowered respondents' WTP (i.e., consumers were willing to pay even less for the cranberry products with added sugar). Combining both (i.e., cranberry health benefits and recommendation to limit sugar intake) reduced respondents' WTP.

Unlabeled cranberry juice: Respondents' willingness to pay decreased by $0.13/64-oz bottle for each gram of added sugar. For example, if a 64-oz bottle is priced at $3.49 and indicates it contains 12 grams of added sugars, individuals would only be willing to pay $2.06 for the same bottle if it indicates it contains 23 grams of added sugars. Considering other findings, respondents preferred cranberry juice sweetened with a combination of fruit juices and regular sugar over regular sugar alone. Information on cranberry health benefits or sugar intake recommendations did not increase the estimated WTP for added sugar.

Labeled cranberry juice: Respondents' willingness to pay decreased by $0.11/64-oz bottle for added sugar increases. Therefore, if a juice labeled as 100% juice is priced at $3.49 for 0 grams of added sugars, then individuals would be only willing to pay $2.17 for the same bottle, if it indicates it contains 12 grams of added sugars. Respondents showed no preference between juice sweetened with fruit concentrate plus regular sugar versus regular sugar only. Information on cranberry health benefits or sugar intake recommendations didn't raise WTP. However, presenting both sets of information lowered WTP.

Subsample analyses: We analyzed WTP variations across consumer segments. Not surprisingly, those prioritizing Nutrition Facts Panel information (NFP), added sugars on NFP, and health-conscious individuals expressed significantly lower WTP due to added sugars. Differences were observed based on demographics and health status, suggesting varied impacts across consumer groups.

Conclusions: Our study confirmed the concerns of the U.S. cranberry industry about FDA regulations that require the labeling of added sugars. People are willing to pay less for cranberry products with added sugars and prefer those sweetened with fruit juices instead. Even when health benefits are highlighted, the negative perception of added sugar remains strong. These labeling policies particularly influence health-conscious shoppers, but their overall impact depends on how much consumers pay attention to nutrition labels. Although cranberries have health benefits, the presence of added sugar can overshadow these positives. Future research should explore ways to minimize bias in studies, possibly using virtual reality and experimental auctions, along with actual sales data from stores.

Consumers’ Perceptions of Using Gene-Editing in Cranberries

LINK TO PAPER

We conducted a study to understand consumer opinions on gene-edited cranberries, using CRISPR technology, to see if these opinions differed from those about genetically modified (GM) crops. Gene editing offers a potential way to enhance the taste of cranberries without adding sugar, addressing the issue of cranberries’ naturally low sugar content, which requires added sugar to improve their palatability. This is particularly relevant following the new FDA regulations that require the separate listing of "Added Sugars" on nutrition labels, potentially discouraging consumers from choosing cranberry products.

Note that current regulations in the U.S. do not automatically consider products developed with CRISPR technology to be GM products. Also, no gene edited cranberry cultivar exists on the market and no efforts are supported by this project (VacCAP) to develop CRISPR based cranberry cultivars. This study simply sought to understand consumer perceptions about CRISPR based products. This information could be useful in the future in case the industry would need to promptly adopt CRISPR to address production/demand challenges.

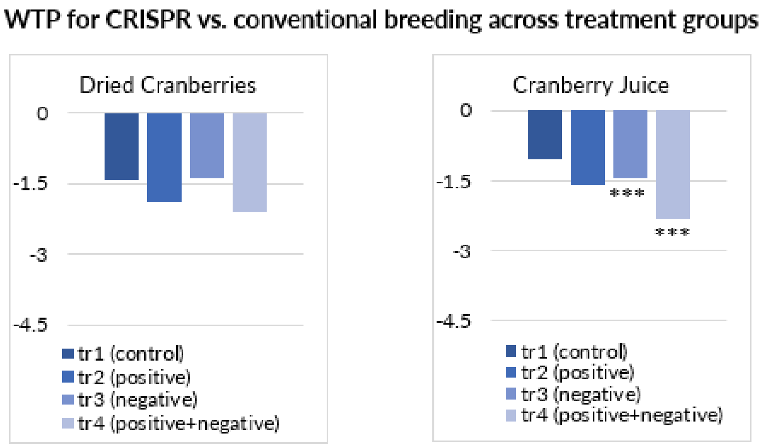
This study has three main objectives:

1. To understand if consumers are willing to pay more for gene-edited (specifically CRISPR) compared to conventionally bred cranberries.
2. To investigate how information about cranberry health benefits and recommendations to limit sugar consumption affect consumer preferences for CRISPR cranberries.
3. To evaluate if different groups of consumers have varying preferences for cranberry product attributes.

Willingness to pay for total sugar content and information effects: Respondents were willing to pay less for regular/standard compared to reduced sugar content for both SDC and cranberry juice. The effect of information varied across products.

- For SDC, information about the health benefits of cranberries didn't affect participants' willingness to pay. When participants were informed about dietary recommendations to limit sugar intake (alone or in combination with information about cranberry health benefits), they were willing to pay less for the product compared to the scenario when participants received no information.
- For cranberry juice, only when receiving both sets of information, respondents were willing to pay less compared to a scenario with no information.

Willingness to pay for CRISPR and information effects: Participants were willing to pay less for both dried cranberries and juice produced using CRISPR compared to conventional breeding. Information on the dietary recommendation to limit sugar intake alone and combined with cranberry health benefits information significantly reduced the willingness to pay.


WTP for CRISPR vs. conventional breeding across treatment groups

WTP across different information treatment groups of respondents.

Single, double, and triple asterisks (, **, ***) indicate the statistical significance of the pairwise t-tests at the 10%, 5%, and 1% levels. The pairwise t-tests were based on the following hypotheses:*

- *H01: WTPtreatment1WTPtreatment2*
- *H02: WTPtreatment1WTPtreatment3*
- *H03: WTPtreatment1=WTPtreatment4.*

The t-test uses WTP values that were bootstrapped from the normal distribution based on estimates from the GMNL–II model.

Differences in willingness to pay across respondents' segments: Not all respondents were willing to pay less for CRISPR compared to conventional breeding.

- For SDC, 35% of the respondents (out of N=250) were willing to pay more for CRISPR. Note that this group believed that CRISPR could help reduce the need for adding sugar, however they didn't understand the difference between total sugar and added sugar on nutrition labels and didn't pay much attention to total sugar content.
- When it came to cranberry juice, 24% of respondents (out of N=250) strongly rejected CRISPR, 56% mildly rejected it, and 19% did not have a strong opinion. The group with mild rejection of CRISPR was more willing to buy CRISPR-made cranberry products if it meant less added sugars during processing.

Our findings suggest that consumers are more receptive to gene-editing technologies like CRISPR when it leads to tangible benefits, such as reduced sugar content. This has significant implications for growers, processors, and marketers: Emphasizing the health benefits and sugar reduction potential of CRISPR cranberries can improve consumer acceptance. Clear communication about the differences between CRISPR and GMOs can help mitigate negative perceptions. These insights can guide the development and marketing strategies for new cranberry products, making them more appealing to health-conscious consumers and potentially increasing market acceptance of gene-edited foods.

Reassessing Cranberry and Blueberry Breeding Priorities

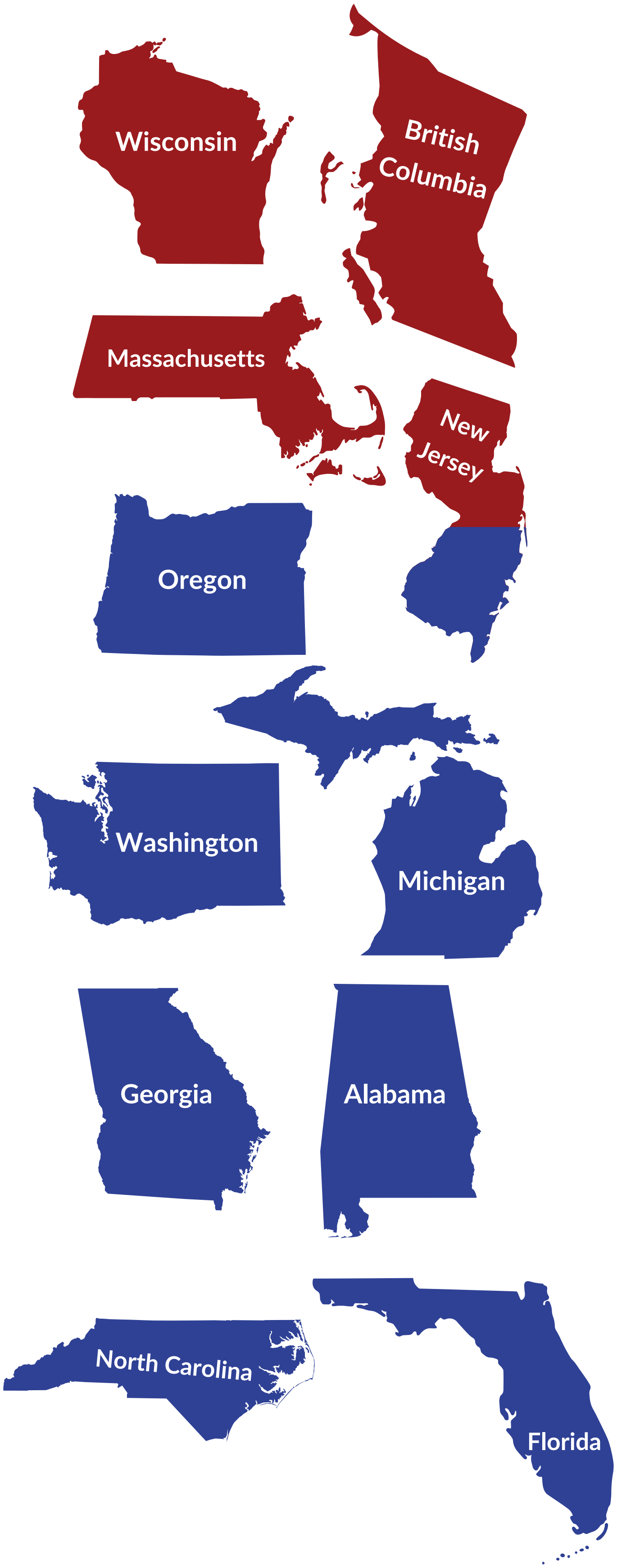
Assessing stakeholder breeding priority traits for new cranberry and blueberry cultivars is crucial to align breeding programs with industry needs and market demands.

By understanding which traits—such as fruit quality, disease resistance, and stress tolerance—are most valued by producers, packers, and processors, breeders can focus on developing cultivars that improve production efficiency and profitability.

Reassessing these priorities on a regular basis is critical to incorporate new traits that may have become relevant due to shifts in consumer preferences or the rapid effects of climate change, which can introduce new pests and increase plant stress. This ensures that breeding programs remain responsive and adaptive to evolving industry challenges, ultimately supporting the long-term sustainability of the sector.

With this in mind, the VacCAP team conducted two surveys in 2023 to reassess the breeding priorities of the blueberry and cranberry industries.

Survey distributed to ***cranberry*** *and* ***blueberry*** *stakeholders in:*



CRANBERRY BREEDING PRIORITY SURVEY RESULTS

In 2023, the VacCAP team developed and distributed a survey to reassess cranberry stakeholder's preferences for fruit and plant quality traits. The survey was distributed to cranberry stakeholders in Wisconsin (WI), Massachusetts (MA), New Jersey (NJ), and British Columbia (BC), which are the most important regions for this crop.

The survey asked the participants to rank which group of characteristics for a new cultivar were most and least important, and those included: Disease resistance, Yield/Productivity, Insect Pest Resistance, Plant Stress Tolerance (frost, heat stress, etc.), and Fruit Quality (Table 1) . A second set of questions focused on each one of the above mentioned groups and asked participants to rank specific traits related to the individual groups (Table 2).

Results from the survey indicated that Yield/Productivity is the top priority, and fruit quality, disease resistance and tolerance to stress had similar level of importance depending on the regions. Stakeholders in NJ identified Diseases Resistance as their most important group characteristic, while MA, WI, and BC ranked Yield/Productivity as their top one, while Fruit Quality and Tolerance to Plant Stress ranked second and third in different regions.

Regarding the most important fruit quality traits, respondents in MA, WI, and NJ identified fruit size and firmness as the top 2 traits, while respondents in BC identified fruit size and shelf life as their top priority. Across all growing regions, Field Fruit Rot was identified as the top priority in the disease resistance group characteristic. Regarding top priorities in the Plant Stress Tolerance group characteristics, there was consensus among cranberry stakeholder in all growing regions that Heat Stress was within the top 2 most important stress tolerance traits for new cultivars, however WI and BC regions listed cold hardiness as their top trait. There was significant variability across all regions regarding the top priority in the Insect Pest Resistance group characteristic which was expected given the distinctive climatic conditions among growing regions that impact insect populations.

Table 1: Cranberry priority traits determined from industry surveys in MA, WI, NJ, and BC, 2023, ranked 1 (most important) through 5 (least important)

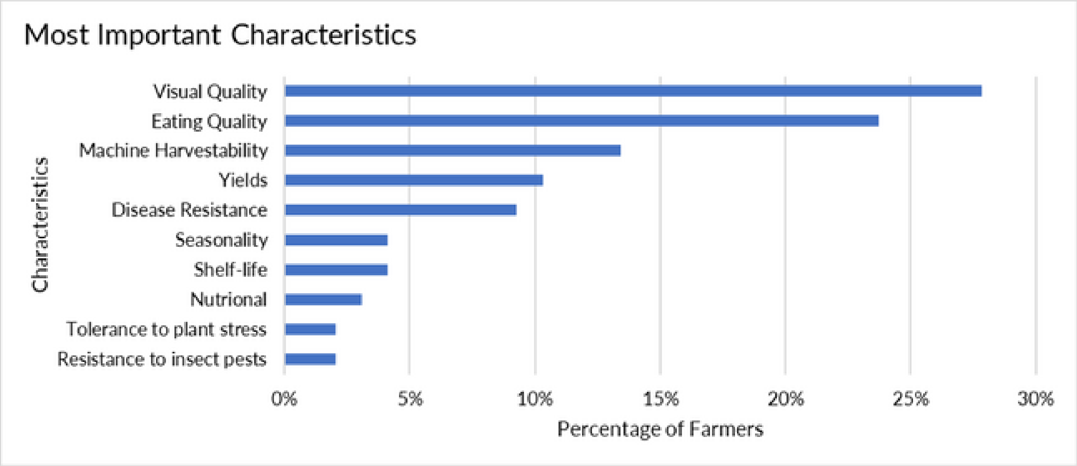
Importance	MA	WI	NJ	BC
1	Yield/Productivity	Yield/Productivity	Disease Resistance	Yield/Productivity
2	Disease Resistance	Fruit Quality Traits	Yield/Productivity	Fruit Quality Traits
3	Plant Stress Tolerance	Plant Stress Tolerance	Fruit Quality Traits	Disease Resistance
4	Insect Pest Resistance	Disease Resistance	Plant Stress Tolerance/Insect Pest Resistance	Insect Pest Resistance
5	Fruit Quality Traits	Insect Pest Resistance	-	Plant Stress Tolerance

STATE	MOST IMPORTANT FRUIT QUALITY TRAIT	MOST IMPORTANT DISEASE RESISTANCE TRAIT	MOST IMPORTANT INSECT PEST RESISTANCE TRAIT	MOST IMPORTANT STRESS TOLERANCE TRAIT
MA	1. Fruit Size 2. Firmness 3. Anthocyanin content (TAcy)	1. Field Fruit Rot 2. Early Rot and Phyllosticta leaf drop 3. Phytophthora	1. Cranberry weevil 2. Sparganothis fruitworm 3. Cranberry fruitworm	1. Drought Resistance 2. Heat Stress 3. Cold Hardiness 4. Flower Stress
WI	1. Fruit Size 2. Firmness 3. Anthocyanin content (TAcy)	1. Field Fruit Rot 2. Early Rot and Phyllosticta leaf drop 3. False Blossom	1. Cranberry fruit worm 2. Blackheaded fireworm 3. Flea beetle	1. Cold Hardiness 2. Drought Resistance 3. Heat Stress 4. Flower Stress
NJ	1. Fruit Size 2. Firmness 3. Flavor	1. Field Fruit Rot 2. Fairy Ring 3. Early Rot and Phyllosticta leaf drop/False Blossom	1. Blunt-nosed Leafhoppers 2. Sparganothis fruitworm 3. Spotted fireworm	1. Heat Stress 2. Drought Resistance 3. Flower Stress 4. Cold Hardiness
BC	1. Fruit Size 2. Shelf Life 3. Firmness	1. Field Fruit Rot 2. Storage Rot 3. Cottonball and Early Rot/Phyllosticta leaf drop	1. Blackheaded Fireworm 2. Cranberry Tipworm 3. Cranberry Fruit Worm	1. Cold Hardiness 2. Heat Stress 3. Drought Resistance 4. Flower Stress

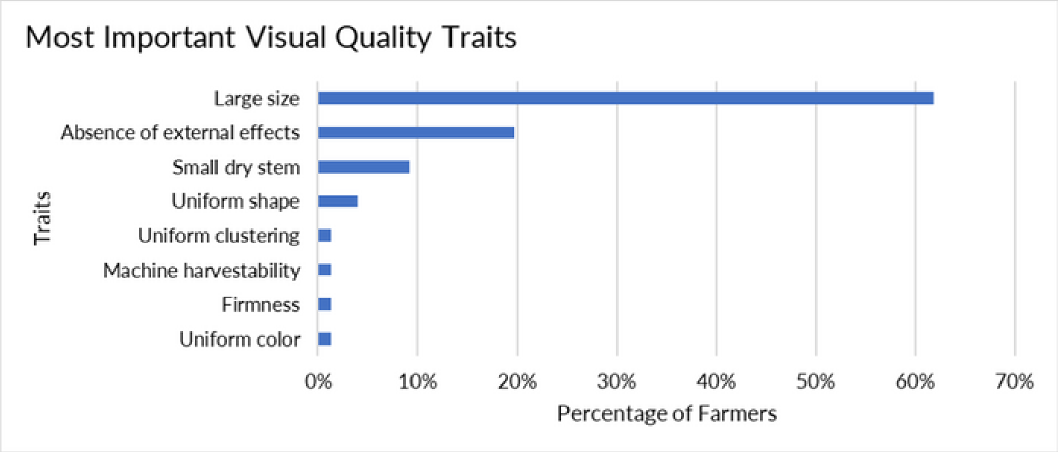
BLUEBERRY SURVEY RESULTS

The survey was distributed to blueberry stakeholders in Washington (26% of total responses were from this state), North Carolina (18%), Florida (16%), Oregon (16%), New Jersey (8%), Georgia (5%), Michigan (4%), and Alabama (2%)

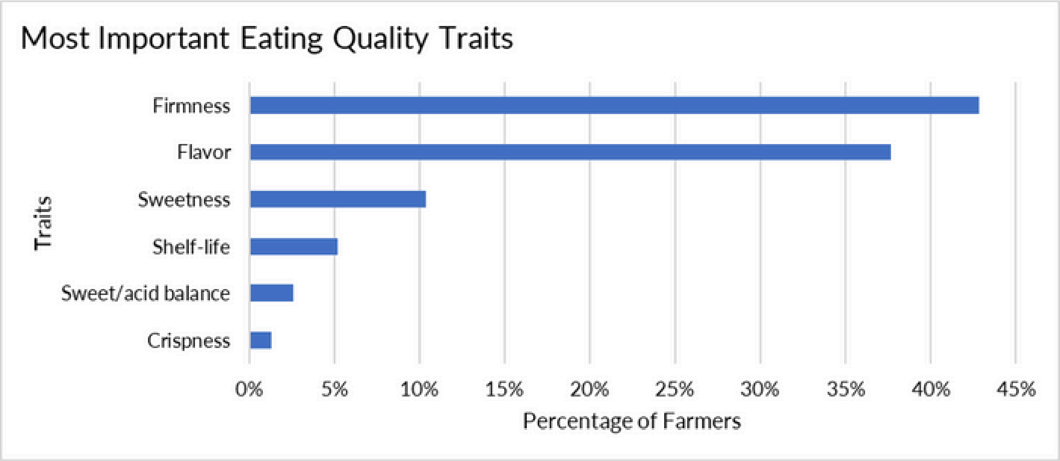
The survey on cultivar characteristic preferences revealed priorities among respondents. Visual quality was the top priority for 28% of respondents, followed closely by eating quality at 24%, and machine harvestability at 13%. These findings highlight the importance of prioritizing sensory attributes such as visual and eating quality to enhance market competitiveness. Additionally, considerations for machine harvestability reflect growers' focus on efficiency-driven practices.



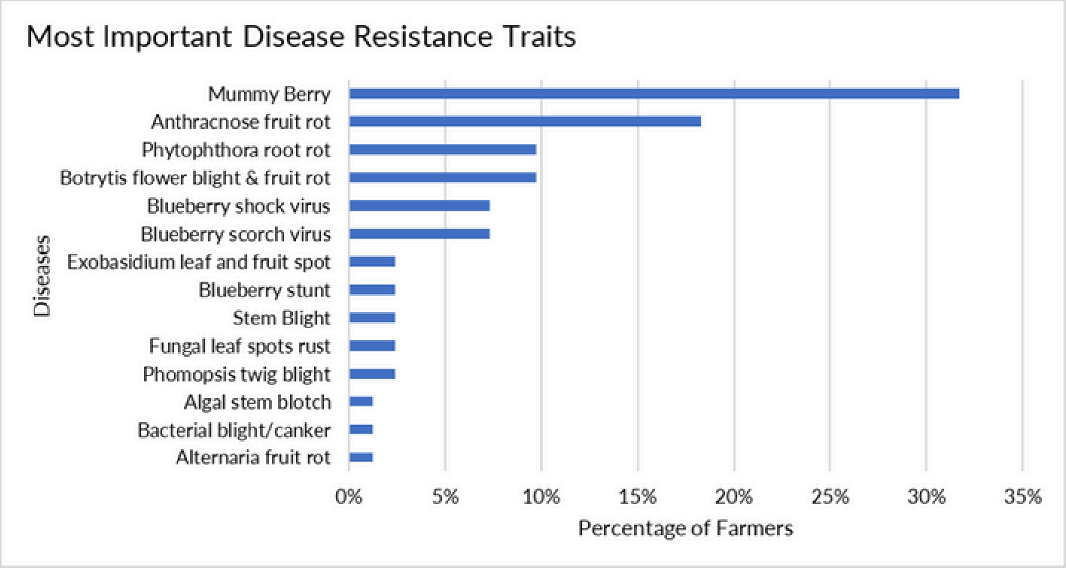
The survey on visual quality traits within blueberry operations revealed key insights into growers' priorities. The overwhelming preference for large size, shown by 62% of respondents, reflects consumer perceptions of value and taste. Additionally, the emphasis on the absence of external effects, shown by 20% of respondents, reveals the importance of fruit integrity in maintaining market competitiveness. By prioritizing these traits, growers can strategically select and breed cultivars that meet consumer expectations, enhancing their position in the blueberry market.



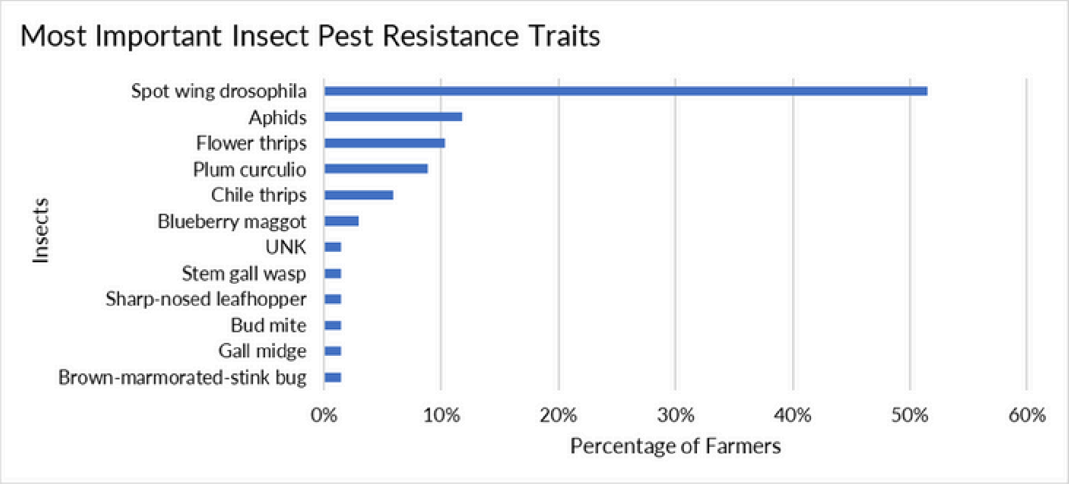
The examination of eating quality traits provided valuable insights into growers' focal points. Among the various attributes assessed, firmness emerged as the top priority, with 43% of respondents highlighting its significance. This preference reflects consumers' expectations for a satisfying texture and prolonged shelf life. Additionally, flavor was emphasized by 38% of respondents, underscoring its pivotal role in driving consumer satisfaction and repeat purchases. These findings show the critical importance of eating quality traits in shaping consumer preferences and market competitiveness within the blueberry industry.



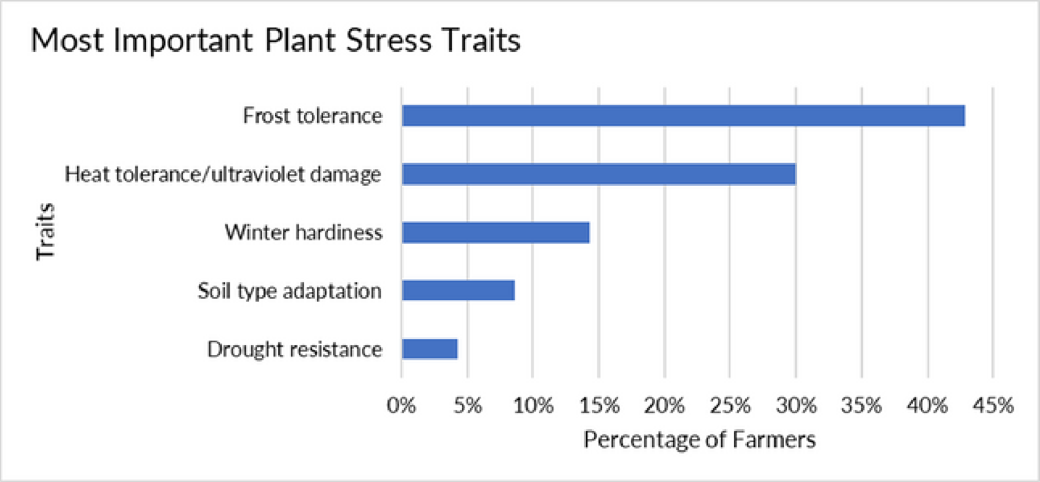
The exploration of disease resistant traits unveiled crucial insights into growers' concerns. Among the various disease resistant traits surveyed, mummy berry emerged as the most important, with 32% of respondents highlighting its significance. This preference reflects growers' recognition of the devastating impact mummy berry disease can have on blueberry crops if left unchecked. Additionally, anthracnose fruit rot was noted by 18% of respondents. These findings underscore the critical importance of disease resistance traits in safeguarding crop health and productivity. By prioritizing cultivars with robust resistance to mummy berry and anthracnose fruit rot, growers can mitigate risks and ensure sustainable yields, thereby securing their position in the competitive blueberry market.



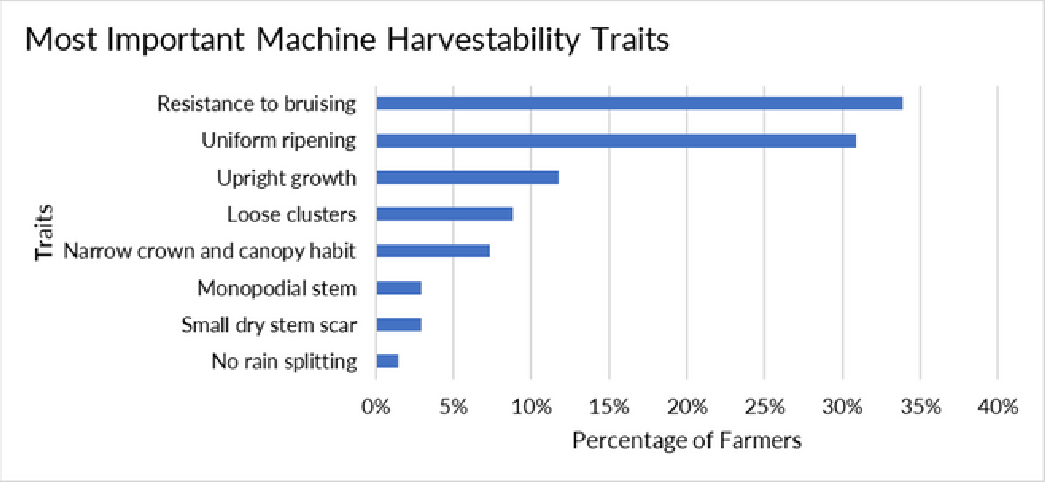
The exploration into the most important insect pest resistance traits within blueberry operations showed insights into grower's primary concerns. Spot wing drosophila (SWD) emerged as the predominant focus, with a staggering 51% of respondents highlighting its significance. This overwhelming response underscores the significant threat posed by SWD to blueberry crops and the urgent need for effective pest management strategies. While aphids and flower thrips were also noted by 12% and 10% of respondents, respectively, their relatively lower mentions suggests that the attention is primarily directed towards mitigating the impact of SWD infestations. These findings emphasize the critical importance of prioritizing insect pest resistance traits, particularly against SWD, in safeguarding crop health and ensuring sustainable yields within the blueberry industry.



The examination of plant stress traits revealed crucial insights into growers' concerns. Frost tolerance emerged as the top priority, cited by 43% of respondents, reflecting awareness of its impact on crop health, particularly in colder climates. Additionally, 30% of respondents emphasized the importance of heat tolerance and protection against ultraviolet damage, showing the need to mitigate the effects of extreme temperatures and environmental stressors. These findings highlight the critical role of plant stress traits in ensuring crop resilience and yield stability in blueberry cultivation.



The exploration of the most important machine harvestability trait within the survey unveiled crucial insights into growers' priorities. Resistance to bruising emerged as the top concern, cited by 34% of respondents, reflecting their emphasis on minimizing post-harvest damage. Additionally, 31% of respondents highlighted the importance of uniform ripening, showing the need for consistency in fruit maturity to optimize mechanical harvesting efficiency. These findings show the critical role of machine harvestability traits in ensuring efficient and damage-free harvesting processes within the blueberry industry.



OVERALL SURVEY RESULTS

Overall, compared with a previous breeding priority survey distributed in 2016, the results of this survey indicated that fruit quality continues to be the most important priority for the blueberry and cranberry industries.

However, traits associated with mechanical harvestability and resistance to biotic and abiotic stresses are becoming more important. These results reflect some of the challenges that the industry is facing. Blueberry cultivars that produce fruit with inconsistent texture and sensory profile (e.g., firmness, crispness, sweetness) often do not meet consumer expectations which limit consumption growth. Also, most of the cultivars that are currently grown are not well-adapted to mechanical harvest and not resistant to major diseases. These challenges, combined with increasing labor costs for hand harvest, for inputs to manage disease, increasing competition due to rapid and significant increasing production from other countries, are limiting profitability of this industry in the U.S.

In cranberry, the market shift from juice to higher value products such as sweetened dried cranberry (SDC), requires fruits with stricter quality parameters (e.g., larger size, uniform color, and firm berries). As a result, a large portion of the production is sold into the juice concentrate market which depresses the price for juice concentrate and limit the expansion of the higher value SDC market. In addition, increasing disease pressure and more frequent extreme weather events (heat wave, early or late frost) are increasing the risk of production losses. On the consumer side, the new FDA regulation that requires the declaration of added sugars on the Nutrion Fact Panel of packaged foods and beverages is creating a negative perception by consumers for cranberry juice and SDC.

Given these challenges, the economic sustainability of the blueberry and cranberry industries is dependent on finding solutions that allow for increasing availability and adoption of cultivars that produce fruit that consistently meet consumer expectations and processing needs while can reduce production costs and risk of crop loss. Also, developing strategies that can increase and sustain blueberry and cranberry consumption are critical for continued success.

Testimonials From the Marsh

Nicole Hansen
Plant Health and Operations Manager
Cranberry Creek Cranberries, Inc

Why is it important for the cranberry industry to understand consumer reactions to added sugar information on the labels of processed cranberry products?

It's important for the industry to understand consumer reactions, because consumer reaction drives buying decisions. Cranberries are an extremely healthy product, but we have to add sugar to make them palatable. Depending on how that is portrayed and how the consumer interprets it, it can be extremely important to whether you're going to be able to continue to sell a product that's healthy versus sell a product that consumers might think is unhealthy due to influences. It is extremely important to understand the reactions, because it's going to drive your knowledge of how to educate the consumer and market.

Do you think that knowing the reactions of the consumer has any implication of push for new products, changing what you're doing, for innovation in the kind of products that that are being produced by the by the industry?

The difficulty with new products is the time that it takes to make a change like that, and by the time you make a change, the consumer's reactions have changed. Somehow, we have to understand from an industry standpoint, and a consumer standpoint, how to balance that. Where the product can be healthy, but palatable and something that consumers are willing to include in their diet. Some of it is changing products for the consumer, but some of it is educating the consumer, because you just can't make quick changes on some things.

How can insights into consumer reactions to sugar content information on cranberry product labels inform the industry's labeling and marketing strategies?

I believe it's going to be really important to actually repeat these surveys. Just like we do research and we have replicated data, I'd like to replicate this and see if consumer reactions stay the same. Because what we saw during Covid, when you're in a health scare, consumers look for functional foods that are healthy, so, all of a sudden, the consumption of cranberry juice increased tremendously. That data shows for itself, without doing surveys, the consumer realizes cranberries are healthy and the added sugar is acceptable as long as that's what is the healthiest.

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Do you think [this study] is something the industry would take and say "Okay, we need to do something about the labeling,"? Who would take this information and say something needs to be done if we want to continue having increasing the consumption of cranberry products?

From a processor standpoint, the best one to work through it would be Ocean Spray Cranberries and other cranberry marketers, because they do the majority of the marketing. They're already working on analyzing product labels. Cranberry Institute could be involved to support processor and grower needs.

Unfortunately, navigating a health claim on a product is difficult. So, the environment to add sugar to a healthy product to make it palatable, is not conducive to supporting the cranberry. Especially in the current atmosphere where we have labeling requirements that advertise added sugar. There needs to be dialogue with FDA working through, 'What is the proper way to label if we do have a healthy product.'

Even natural added sugars to the cranberry require to be labeled as added sugar. This can be misleading to the consumer based on their understanding of what the labeling is trying to accomplish. In comparison, the total sugar content of cranberries can be lower than the natural sugar in products like raisins. When you're computing it up against something that's comparable, all of a sudden, you're giving cranberries a black eye, even though they have less sugar. That's the challenge.

I think that this study's information will be helpful to show the industry that added sugar does have an impact to consumer decisions. I think they know that already, this just confirms it.

How can the cranberry industry balance the need for added sugar labeling with the goal of maintaining product appeal across different consumer segments?

I believe the industry needs to continue to work toward finding other product categories that the cranberry can be beneficial in. The industry can continue to work on products with added sugar that consumers approve of.This is a wide basket, depending on the consumer.

Do you think there will be a push to develop products are no added sugar or things that have artificial sweeteners?

That's been happening for years; These products do have a dedicated customer base that is important. The bigger question is why these products don't pull in the entire consumers base in a large manner. What variables are limiting consumption on these products that should be meeting a larger consumers preference? Is it price point, or what other variables? Is it, how do you get the product out so the consumer buys it, is it distribution, is it customer follow through?

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How might the studies' findings inform policy makers, processors, and producers about the potential impact of sugar labeling on the cranberry industry?

I think that's the key with this research and the studies' findings, is that it tells us that consumers say they aren't going to buy the product, even though it's healthy, because it shows added sugar, and so I think that it gives the industry the data to actually put in front of policymakers to help conversation. Advocate for changing what they're requiring on the label and come to a balanced approach to promote a healthy product that needs some added sugar depending on the preference of consumption.

How has your knowledge regarding consumer reactions to added sugar information on cranberry products changed. How do you plan to use this information?

This data provides background for the industry to have the conversations, to drive leadership, to either take action or make decisions.

We did one study that looks at the consumer attitude towards CRISPR edited cranberries. The consumers are more willing to accept the product and consume them, and we actually didn't expect that that was going to be the case. So we'll be willing to accept those products if there's no sugar added?

I think that that information is extremely important. My first reaction was "Well, this is great," because that tells me that we should be using CRISPR. We should be working on developing a cranberry and that has higher sugar content, that would be more palatable, and have the health benefits as well. We're trying to do that now through traditional breeding, but it is going to take so long that the CRISPR could actually help us. The cranberry industry is a niche industry, and it's not a staple food, and so they've always been concerned that they don't want to touch the GMO side of things. The hope was that, because CRISPR was not considered GMO, that this would be an avenue for us to actually do some work with CRISPR and get a cranberry that has higher sugar content naturally. The industry will have to decide how to move forward.

What did you think about the results of the CRISPR? Were you surprised that they that the consumer is actually willing to accept CRISPR, as long as you can clearly show them that there's a health benefit?

I was surprised that they were willing pay less for CRISPR edited product. I figured that they would either respect the cranberry for it's health benefits and flavor or not like it. They're still willing to buy it, but they are going to pay less. That was surprising to me.

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Given VacCAP's generation of information regarding consumer preferences, what new information could VacCAP generate to help the industry and expand consumption of cranberries? What are new things we could do?

The biggest key is educating the consumer. But also to understand the changing customer preference over time and study if the consumer preference on surveys actually follows through to actual buying.

What is deterring them from consuming more cranberry products, and what are the kind of products that we could develop to try to target that new generation to also be a cranberry consumer?

That question is best suited for the processors with all the analytics they have on consumer preference. Personally, I would think that a product that would appeal to the grab and go market of convenience stores, coffee shops, and smoothie shops would have new generation appeal.

What about the supplements? Do you think that that is something that that should be studied more like? Do we have enough data about the potential like cranberries as a supplement.

We need more data on the total chemical composition of the cranberry. What does a cranberry actually have in it? The supplement/powder side of cranberry would be considered one of the product categories.

Testimonials From the Field

Dr. Paul Sandefur
Blueberry Breeding Manager, Fall Creek Farm and Nursery

Based on the results of our studies, do you think the industry will consider including quality descriptors in their fresh blueberry packaging?

There are already examples of quality descriptors on fresh fruit packaging (e.g., Driscoll's Sweetest Batch) and I would expect this to increase as more data emerges showing an increased likelihood of purchase when such descriptors are used on packaging. Now we just have to make sure that our "crunchy" labeled blueberries are truly crunchy and "sweet" labeled blueberries are exceptionally sweet.

Do you think information about consumer preferences for certain quality attributes will impact future breeding efforts?

Yes. Clear information on consumer preferences can provide guidance for specific trait level selection thresholds in breeding programs. Any breeding program that uses a multi-trait selection model would be amiss to not factor in consumer preference weights.

Price and freshness or shelf-life was found to be a barrier to frequent blueberry consumption. Is this information useful to you? If so, how do you plan to use it?

In our breeding program we have been specifically selecting genotypes that maintain exceptional quality (firmness, flavor, and lack of breakdown) over long-term storage periods (60+ days). The finding that poor shelf-life was a barrier to frequent consumption was valuable to see as it validates our focus on these traits and dedication of the substantial resources it takes to evaluate. New blueberry varieties with improved shelf-life have the potential to help the entire industry via reduced fruit waste in grower fields and warehouses, and increased consumption at retail.

What new information could VacCAP generate to help the industry and expand consumption?

To continue to grow the industry we need to increase consumption globally, not just in the mature markets. Information on consumer preferences across more regions would be helpful in increasing our breeding efforts to target traits preferred by different and emerging consumer groups. It has been my experience that “one size fits all” is not true for blueberries. Although the recent findings show that as a whole consumers prefer specific trait levels (e.g., sweet), the more granular we can get on the preferences of different consumer groups the better. With this type of information, we can develop different blueberry varieties targeting specific consumers, thereby giving growers and retailers more customer tailored variety options and driving up global consumption.

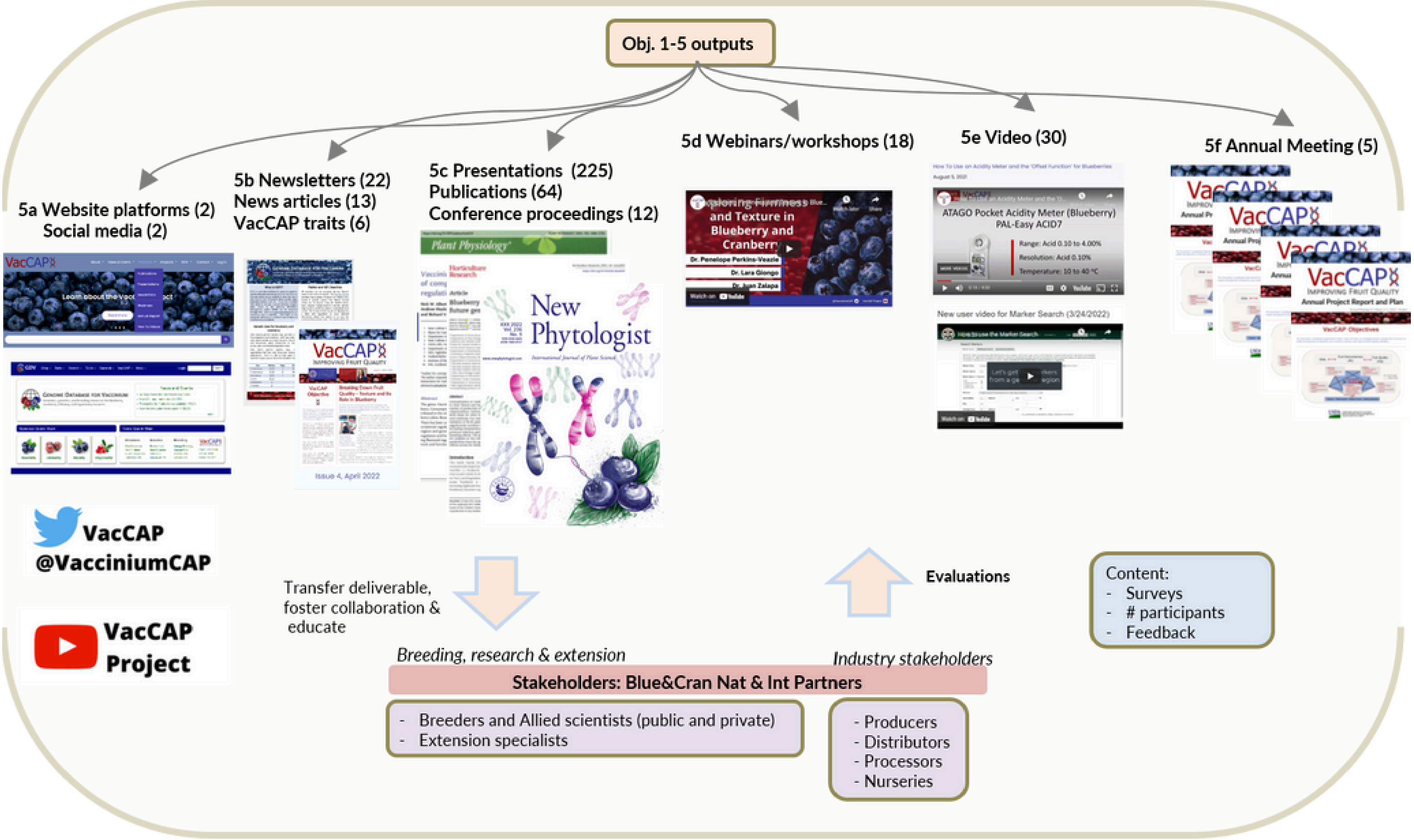
VacCAP

IMPROVING FRUIT QUALITY

OBJECTIVE 5

ENGAGING STAKEHOLDERS & BREEDERS

VacCAP Objective 5 engaged U.S. Vaccinium *breeders and stakeholder groups to transfer advanced phenomics and genomics tools to build a more coordinated and efficient cultivar development system.*



Obj. 1-5 outputs

5a Website platforms (2)
Social media (2)

5b Newsletters (22)
News articles (13)
VacCAP traits (6)

5c Presentations (225)
Publications (64)
Conference proceedings (12)

5d Webinars/workshops (18)

5e Video (30)

5f Annual Meeting (5)

VacCAP
@VacciniumCAP

VacCAP
Project

Transfer deliverable,
foster collaboration &
educate

Evaluations

Content:
- Surveys
- # participants
- Feedback

Breeding, research & extension

Industry stakeholders

Stakeholders: Blue&Cran Nat & Int Partners

- Breeders and Allied scientists (public and private)
- Extension specialists

- Producers
- Distributors
- Processors
- Nurseries

New Genomic Resources Shared Through the Genome Database for *Vaccinium* (GDV)

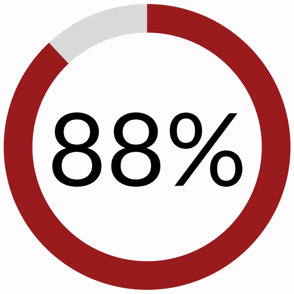
GDV houses and integrates genomic, genetic and breeding data for blueberry, cranberry and other Vaccinium *species.*

According to the GDV team, genome data had a very large increase in 2022 thanks to VacCAP additions. The Pangenome Project contributed **22** blueberry and **10** cranberry genomes. VacCAP also provided **4** other cranberry genomes, and new blueberry and bilberry genomes.

- Chromosome-Level Genome Assembly of the American Cranberry (*Vaccinium macrocarpon* Ait.) and Its Wild Relative *Vaccinium microcarpum*
- Contrasting a Reference Cranberry Genome to a Crop Wild Relative Provides Insights Into Adaptation, Domestication, and Breeding
- A Chromosome-Scale Assembly of the Bilberry Genome Identifies a Complex Locus Controlling Berry Anthocyanin Composition

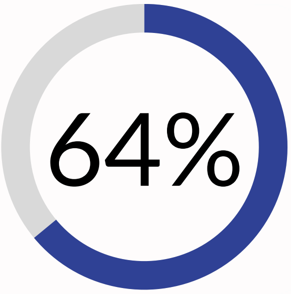
Genomes

VacCAP contributed **37** out of **42** genomes to the GDV



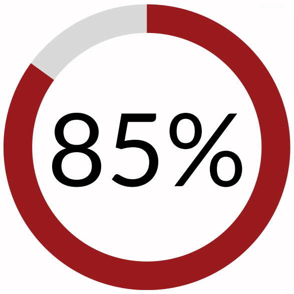
Genetic Markers

VacCAP provided **183,342** out of **287,025** genetic markers available on the GDV



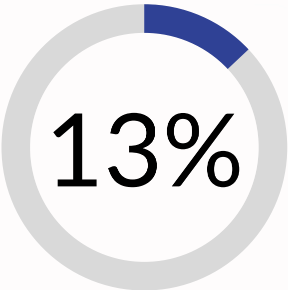
QTL

3,692 out of **4,328** quantitative trait loci (QTL) were identified by VacCAP



Genetic Maps

5 of the **39** genetic maps on the GDV were mapped by VacCAP



Genetic Marker and QTL Data Was Entered Into GDV From These Publications:

High-Density Linkage Map Construction and Identification of Loci Regulating Fruit Quality Traits in Blueberry

17,433 markers | 40 QTL | 1 map

18,195 markers | 163 QTL | 1 map

High-Density Linkage Map Construction in an Autotetraploid Blueberry Population and Detection of Quantitative Trait Loci for Anthocyanin Content

Autopolyploid Inheritance and a Heterozygous Reciprocal Translocation Shape Chromosome Genetic Behavior in Tetraploid Blueberry (*Vaccinium Corymbosum*)

108,153 markers | 3 maps

5 markers

A Low Malic Acid Trait in Cranberry Fruit: Genetics, Molecular Mapping, and Interaction With a Citric Acid Locus

Quantitative Trait Loci Analysis and Marker Development for Fruit Rot Resistance in Cranberry Shows Potential Genetic Association with Epicuticular Wax

6 markers | 3 QTL

22,047 markers | 194 QTL

Development of a Targeted Genotyping Platform for Reproducible Results Within Tetraploid and Hexaploid Blueberry

Genetic Marker and QTL Data Was Entered Into GDV From These Publications:

Of Buds and Bits: A Meta-Qtl Study Identifies Stable Qtl for Berry Quality and Yield Traits in Cranberry Mapping Populations (*Vaccinium macrocarpon* Ait.)

3,117 QTL

1 marker | 175 QTL

Unraveling the Genetic Architecture of Blueberry Fruit Quality Traits: Major Loci Control Organic Acid Content While More Complex Genetic Mechanisms Control Texture and Sugar Content

A High-Recovery, High-Density Targeted Genotyping Platform for Cranberry

17,502 markers

Total GDV Data By Year

YEAR	GENOMES	GENES	mRNA	MAPS	MARKERS	QTL	GWAS
2025	46	3309929	3426198	39	287025	4328	320
2024	45	3288063	3404332	39	269522	4153	320
2023	42	3193094	3235659	39	247457	836	308
2022	42	3193094	3235659	38	245127	816	-
2021	8	466354	476613	34	136212	465	-
2020	4	245382	253280	31	89951	403	-

Primary citations refer to manuscripts that cite GDV directly. Secondary citations are the number of times the primary citations were cited. Citations increased since the VacCAP project started in 2019. 2025 is partial data.

GDV Usage by Year

YEAR	SESSIONS	PAGEVIEWS	USERS	COUNTRIES
2025	9,435	259,304	4,608	81
2024	13,540	301,228	5,917	129
2023	13,292	334,692	5,660	117
2022	11,235	95,163	6,136	90
2021	10,922	101,998	5,643	94
2020	9,110	66,694	5,465	88
2019	6,832	39,904	4,746	92
2018	4,723	30,437	3,006	88
2017	3,549	21,781	2,267	91
2016	2,054	6,393	1,560	83
2015	1,669	6,875	1,221	71
2014	1,708	5,271	1,320	86
2013	1,735	5,834	1,329	84
2012	1,651	5,898	1,120	84
2011	1,463	8,810	835	75

Sessions indicate the number of times users visit the site, and pageviews refers to the number of pages they view. Use of GDV as a platform to download and mine genomic and genetic data for Vaccinium species has increased since VacCAP started. 2025 is partial data.

GDV Peer-Reviewed Citations by Year

YEAR	PRIMARY CITATIONS	SECONDARY CITATIONS
2023	14	38
2022	23	172
2021	22	216
2020	6	73
2011-2019	22	817
TOTAL	**87**	**1,316**

Primary citations refer to manuscripts that cite GDV directly. Secondary citations are the number of times the primary citations were cited. Citations increased since the VacCAP project started in 2019.

PROJECT IMPACT

- Expanded use of DNA tools in the blueberry and cranberry breeding and genetic programs, resulting in the development of genetic stocks tailored for genetic studies and accelerating research on the genetic architecture of key traits.
- Increased the capacity to discover and characterize genes, leading to new insights into gene function and enabling targeted breeding strategies.
- Supported the adoption of DNA markers and advanced phenotyping methods in breeding programs, improving the efficiency and accuracy of selecting new cultivars with superior fruit quality.
- Advanced the development of new cultivars with improved fruit quality, bringing breeding programs closer to releasing higher-value varieties for growers.
- Established a strong interdisciplinary framework connecting fruit characteristics, fruit quality, and socio-economic research, ensuring that breeding goals align with market demands and consumer preferences.
- Fostered collaboration across the Vaccinium research community, reducing duplication of efforts and increasing the collective research output, ultimately benefiting growers and the industry.

VacCAP Team Publications

Journal Article

- Ni X, Li C, Jiang H, and Takeda, F. (2020). Deep learning image segmentation and extraction of blueberry fruit traits associated with harvestability and yield. Horticulture Research, 7(1), 1-14. https://doi.org/10.1038/s41438-020-0323-3
- Farneti B, Emanuelli F, Giongo L, Toivonen P, Iorizzo M, Folta KM and Finn CE. 2020. Editorial: Interdisciplinary approaches to improve quality of soft fruit berries. Frontiers in Plant Science, section Crop and Product Physiology, 11:592222. https://doi.org/10.3389/fpls.2020.592222 .
- Mengist MF, Grace MH, Xiong J, Kay CD, Bassil N, Hummer K, Ferruzzi MG, Lila MA and Iorizzo M. 2020. Diversity in metabolites and fruit quality traits in blueberry enables ploidy and species differentiation and establishes a strategy for future genetic studies. Frontier in Plant Science, 11:370. https://doi.org/10.3389/fpls.2020.00370.
- Diaz-Garcia L, Rodriguez-Bonilla L, Phillips M, Lopez-Hernandez A, Grygleski E, Atucha A and Zalapa J. 2019. Comprehensive analysis of the internal structure and firmness in American cranberry (Vaccinium macrocarpon L.) fruit. PlosOne, 14(9): e0222451. https://doi.org/10.1371/journal.pone.0222451.
- Kay Fong S, Kawash J, Wang Y, Johnson-Cicalese J, Polaschock J and Vorsa N. 2020. A low citric trait in cranberry: genetic and molecular mapping of a locus impacting fruit acidity. Tree Genetics & Genomes, 16:42. https://doi.org/10.1007/s11295-020-01432-4.
- Günther CS, Dare AP, McGhie TK, Deng C, Lafferty DJ, Plunkett BJ, Grierson ERP, Turner J L, Jaakola L, Albert NW and Espley RV. 2020. Spatiotemporal modulation of flavonoid metabolism in blueberries. Frontiers in Plant Science, 11.545. https://doi:10.3389/fpls.2020.00545
- Vorsa N. and Zalapa J. 2019. Domestication, Genetics, and Genomics of the American Cranberry. Plant Breeding Reviews, Volume 43:279-310
- Diaz-Garcia L, Garcia-Ortega LF, Rodríguez MG, Delaye L, Iorizzo M and Zalapa J. 2021. Chromosome-level genome assembly of the American cranberry (Vaccinium macrocarpon Ait.) and its wild relative Vaccinium microcarpum. Frontiers in Plant Science, 12:633310. https://doi.org/10.3389/fpls.2021.633310
- Diaz-Garcia L, Covarrubias-Pazaran G, Johnson-Cicalese J, Vorsa N, Zalapa J. 2020. Genotyping-by-sequencing identifies historical breeding stages of the recently domesticated American cranberry. Frontiers in Plant Science, 11:607770. https://doi.org/10.3389/fpls.2020.607770
- Diaz JT, Foegeding EA, Stapleton L, Kay C, Ferruzzi MG, Iorrizo M, and Lila MA. 2021. Foaming and sensory characteristics of protein-polyphenol particles in a food matrix. Food Hydrocolloids, 123, 107148. https://doi.org/10.1016/j.foodhyd.2021.107148
- Fong SK, Kawash J, Wang Y et al. 2021. A low malic acid trait in cranberry fruit: genetics, molecular mapping, and interaction with a citric acid locus. Tree Genetics & Genomes 17, 4. https://doi.org/10.1007/s11295-020-01482-8
- Giongo L, Matteo A, Pottorff M, Mainland M, Perkins-Veazie P and Iorizzo M. 2021. Comparative multi-parameters approach to dissect texture subcomponents of blueberry at harvest and postharvest. Postharvest Biology and Technology, Volume 183, 111696. https://doi.org/10.1016/j.postharvbio.2021.111696
- Jung S, Lee T, Gasic K, Campbell BT, Yu J, Humann J, Ru S, Edge-Garza D, Hough H and Main D. 2021. The Breeding Information Management System (BIM): an online resource for crop breeding. Database, Volume 2021, 2021, baab054. https://doi.org/10.1093/database/baab054
- Jung S, Cheng CH, Buble K, Lee T, Humann J, Yu J, Crabb J, Hough H and Main D. 2021. Tripal MegaSearch: a tool for interactive and customizable query and download of big data. Database,Volume 2021, 2021, baab023. https://doi.org/10.1093/database/baab023
- Karppinen K, Lafferty DJ, Albert NW, Mikkola N, McGhie T, Allan AC, Afzal BM, Häggman H, Espley RV and Jaakola L. 2021. MYBA and MYBPA transcription factors co-regulate anthocyanin biosynthesis in blue-coloured berries. New Phytologist. https://doi.org/10.1111/nph.17669
- Mengist MF, Bostan H, Young E, Kay K, Ashrafi H, Gillitt N, Ballington J, Ferruzzi MG, M.A. Lila MA and Iorizzo M. 2021. High density linkage map construction and identification of loci regulating fruit quality traits in blueberry. Horticulture Research, 8, 169.
- Samkumar A, Jones D, Karppinen K, Dare AP, Sipari N, Espley RV, Martinussen I and Jaakola L. 2021. Red and blue light treatments of ripening bilberry fruits reveal differences in signalling through abscisic acid-regulated anthocyanin biosynthesis. Plant, Cell &

VacCAP Team Publications

Environment, 1–19. https://doi.org/10.1111/pce.14158

- Staton M, Cannon E, Sanderson LA, Wegrzyn J, Anderson T, Buehler S, Cobo-Simón I, Faaberg K, Grau E, Guignon V and Gunoskey J. 2021. Tripal, a community update after 10 years of supporting open source, standards-based genetic, genomic and breeding databases. Briefings in Bioinformatics, bbab238. https://doi.org/10.1093/bib/bbab238
- Wu C, Deng C, Hilario E, Albert N, Lafferty W, Grierson D, Plunkett BJ, Elborough C, Saei A, Günther CS, Ireland H, Yocca A, Edger PP, Jaakola L, Karppinen K, Grande A, Kylli R, Lehtola VP, Allan AC, et al. Chagné D. 2021. A chromosome-scale assembly of the bilberry genome identifies a complex locus controlling berry anthocyanin composition. Molecular Ecology Resources, 00, 1–6. https://doi.org/10.1111/1755-0998.13467
- Xueping N, Changying L, Huanyun J and Takeda F. 2021. Three-dimensional photogrammetric reconstruction and deep learning instance segmentation to extract berry fruit harvestability traits. ISPRS Journal of Photogrammetry and Remote Sensing. 171: 293-309. https://doi.org/10.1016/j.isprsjprs.2020.11.010
- Yocca, AE, Edger, PP. 2021. Machine learning approaches to identify core and dispensable genes in pangenomes. Plant Genome, e20135. https://doi.org/10.1002/tpg2.20135
- Kawash J, Colt K, Hartwick NT, Abramson BW, Vorsa N, Polashock JJ, et al. 2022. Contrasting a reference cranberry genome to a crop wild relative provides insights into adaptation, domestication, and breeding. PLoS ONE 17(3): e0264966. https://doi.org/10.1371/journal.pone.0264966
- Dare AP, Günther CS, Grey AC, Guo G, Demarais NJ, Cordiner S, McGhie TK, Boldingh H, Hunt M, Deng C, Karppinen K, Jaakola L and Espley RV. 2022. Resolving the developmental distribution patterns of polyphenols and related primary metabolites in bilberry (Vaccinium myrtillus) fruit. Food Chemistry 374, 131703. https://doi.org/10.1016/j.foodchem.2021.131703
- Lafferty DJ, Espley RV, Deng CH, Günther CS, Plunkett B, Turner JL, Jaakola L, Karppinen K, Allan AC and Albert NW. 2022. Hierarchical regulation of MYBPA1 by anthocyanin- and proanthocyanidin-related MYB proteins is conserved in Vaccinium species. Journal of Experimental Botany. 73, 1344-1356. https://doi.org/10.1093/jxb/erab460
- Lafferty DJ, Espley RV, Deng CH, Dare AP, Günther CS, Jaakola L, Karppinen K, Boase MR, Wang L, Luo H, Allan AC and Albert NW. 2022. The coordinated action of MYB activators and repressors controls proanthocyanidin and anthocyanin biosynthesis in Vaccinium. Frontiers in Plant Science. 13:910155. https://doi.org/10.3389/fpls.2022.910155
- Samkumar A, Karppinen K, McGhie TK, Espley RV, Martinussen I, Jaakola L. 2022. Flavonoid biosynthesis is differentially altered in detached and attached ripening bilberries in response to spectral light quality. Frontiers in Plant Science. 2529. https://doi.org/10.3389/fpls.2022.969934
- Günther CS, Plunkett BJ, Cooney J, Jensen D, Trower T, Elborough C, Nguyen HM, Deng C, Lafferty DJ, Albert NW, Dare AP and Espley RV. 2022. Biotic stress-induced and ripening-related anthocyanin biosynthesis are regulated by alternate phytohormone signals in blueberries. Environmental and Experimental Botany, 203, 105065. https://doi.org/10.1016/j.envexpbot.2022.105065
- Edger PP, Iorizzo M, Bassil NV, Benevenuto J, Ferrão LFV, Giongo L, Hummer K, Lawas LMF, Leisner CP, Li C, Munoz PR, Ashrafi H, Atucha A, Babiker EM, Canales E, Chagné D, DeVetter L, Ehlenfeldt M, Espley RV, Gallardo K, Günther CS, Hardigan M, Hulse-Kemp AM, Jacobs M, Lila MA, Luby C, Main D, Mengist MF, Owens GL, Perkins-Veazie P, Polashock J, Pottorff M, Rowland LJ, Sims CA, Song G, Spencer J, Vorsa N, Yocca AE and Zalapa J. 2022. There and back again; historical perspective and future directions for Vaccinium breeding and research studies. Horticulture Research 9, 10.1093/hr/uhac083. https://doi.org/10.1093/hr/uhac083
- Ni X, Takeda F, Jiang H, Yang WQ, Saito S and Li C. 2022. A deep learning-based web application for segmentation and quantification of blueberry internal bruising. Computers and Electronics in Agriculture. 201:107200. https://doi.org/10.1016/j.compag.2022.107200
- Alan E, Yocca, Patrick P. Edger PP. 2022. Current status and future perspectives on the evolution of cis-regulatory elements in plants. Current Opinion in Plant Biology. 65: 102139. https://doi.org/10.1016/j.pbi.2021.102139
- Teresi SJ, Teresi MB and Edger PP. 2022. TE Density: a tool to investigate the biology of transposable elements. Mobile DNA. 13, 11. https://doi.org/10.1186/s13100-022-00264-4
- Mengist MF, Bostan H, De Paola D, Teresi SJ, Platts AE, Cremona G, Xinpeng Q, Mackey T, Bassil NV, Ashrafi H, Giongo L, Jibran R, Chagné D, Bianco L, Lila MA, Rowland LJ, Iovene M, Edger PP and Iorizzo M. 2022. Autopolyploid inheritance and a heterozygous reciprocal translocation shape chromosome genetic behavior in tetraploid blueberry (Vaccinium corymbosum). New Phytologist, 237: 1024-1039. https://doi.org/10.1111/nph.18428

VacCAP Team Publications

- Montanari S, Thomson S, Cordiner S, Günther CS, Miller P, Deng CH, McGhie T, Knäbel M, Foster T, Turner J, Chagné D and Espley R. 2022. High-density linkage map construction in an autotetraploid blueberry population and detection of quantitative trait loci for anthocyanin content. Frontiers in Plant Science. 13:965397. https://doi.org/10.3389/fpls.2022.965397
- Mengist MF, MH Grace, T Mackey, B Munoz, B Pucker, NV Bassil, C Luby, M Ferruzzi, MA Lila and M Iorizzo. 2022. Dissecting the genetic basis of bioactive metabolites and fruit quality traits in blueberries (Vaccinium corymbosum L). Frontier in Plant Science, 13:964656. https://doi.org/10.3389/fpls.2022.964656
- Herniter IA, Kim Y, Wang Y, Havill JS, Johnson-Cicalese J, Muehlbauer GJ, Iorizzo M and Vorsa N. 2023. Trait mapping of phenolic acids in interspecific (Vaccinium corymbosum var. caesariense x V. darrowii) diploid blueberry population. Plants, 12:1346. https://doi.org/10.3390/plants12061346
- Trandel M., S. Johanningsmeier, H. Oh, M. Iorizzo and P. Perkins-Veazie. 2023. Blueberry cell wall polysaccharide composition of three distinct fruit firmness phenotypes. Food Science & Technology, 3, 11, 1920-1930. https://doi.org/10.1021/acsfoodscitech.3c00284
- Farneti B., L. Giongo1, F. Emanuelli, P. Toivonen, K. Folta, M. Iorizzo. 2023. Editorial: Interdisciplinary Approaches to Improve Quality of Soft Fruit Berries II. Frontier in Plant Science, 14:1341519. https://doi.org/10.3389/fpls.2023.1341519
- Alan E. Yocca, A. Platts, E. Alger, S. Teresi, M.F. Mengist, L.F.V. Ferrão, J. Benevenuto, M. Jacobs, M. Babinski, P. Bayer, A. Golicz, J.L. Humann, D. Main, R.V. Espley, D. Chagné, N.W. Albert, S. Montanari, N. Vorsa, J. Polashock, L. Díaz, J. Zalapa, N.V. Bassil, P.R. Munoz, M. Iorizzo, and P.P. Edger. Blueberry and cranberry pangenomes as a resource for future genetic studies and breeding efforts. Hort Research, Volume 10, Issue 11, November 2023, uhad202. https://doi.org/10.1093/hr/uhad202
- Erndwein L, Kawash J, Knowles S, Vorsa N and Polashock J. 2023. Cranberry fruit epicuticular wax benefits and identification of a wax-associated molecular marker. BMC Plant Biol. 23(1):181. https://doi.org/10.1186/s12870-023-04207-w
- Albert NW, Iorizzo M, Mengist MF, Montanari S, Zalapa J, Maule A, Edger PP, Yocca AE, Platts AE, Pucker B and Espley RV. 2023. Vaccinium as a comparative system for understanding of complex flavonoid accumulation profiles and regulation in fruit. Plant Physiology, 192(3), 1696–1710. https://doi.org/10.1093/plphys/kiad250
- Nguyen HM, Putterill J, Dare AP, Plunkett BJ, Cooney J, Peng Y, Souleyre EJF, Albert NW, Espley RV and Günther CS. 2023. Two genes, ANS and UFGT2, from Vaccinium spp. are key steps for modulating anthocyanin production. Frontiers in Plant Science, 14 (2023): 1082246. https://doi.org/10.3389/fpls.2023.1082246
- Jacobs M, Thompson S, Platts AE, Body MJA, Kelsey A, Saad A, Abeli P, Teresi, A Schilmiller SJ, Beaudry R, Feldmann MJ, Knapp SJ, Song G, Miles T and Edger PP. 2023. Uncovering genetic and metabolite markers associated with resistance against anthracnose fruit rot in northern highbush blueberry, Horticulture Research, uhad169. https://doi.org/10.1093/hr/uhad169
- Lopez-Moreno H, Phillips M, Diaz-Garcia L, Torres-Meraz MA, de La Torre F, Berro I, Loarca J, Mura J, Ikeda S, Atucha A, Giongo L, Iorizzo M and Zalapa J. 2023. A Survey of Key Methods, Traits, Parameters, and Conditions for Measuring Texture in Cranberry (Vaccinium macrocarpon Ait.). Horticulturae. Apr 11; 9(4):479. https://doi.org/10.3390/horticulturae9040479
- Espley RV and Jaakola L. 2023. The role of environmental stress in fruit pigmentation. Plant, Cell & Environment, 46, 3663–3679. https://doi.org/10.1111/pce.14684
- Canales E, Gallardo RK, Iorizzo M, Muñoz P, Ferrao F, Luby C, Bassil N, Pottorff M, Perkins-Veazie P, Sandefur P, Colonna A and Sims C. 2024. Willingness to Pay for Blueberries: Sensory Attributes, Fruit Quality Traits, and Consumers' Characteristics. HortScience 59(8): 1207-1218. https://doi.org/10.21273/HORTSCI17947-24
- Ma X, Gallardo RK, Canales E, Atucha A, Zalapa J and Iorizzo M. 2024. Consumers' Discount for Added Sugars: An Application to Cranberry Products Under Different Nutrition-Related Information Treatments. Journal of the Agricultural and Applied Economics Association, 1-20. https://doi.org/10.1002/jaa2.121.
- Ma X, Gallardo RK, Canales E and Iorizzo M. 2024. Quality-Related Descriptors to Increase Fresh Blueberries Purchase - Evidence from a Basket-Based Choice Experiment. Journal of the Agricultural and Applied Economics Association, 1-20. https://doi.org/10.1002/jaa2.118
- Ma X, Gallardo RK, Canales E, Atucha A, Zalapa J and Iorizzo . 2024. Would Consumers Accept CRISPR Fruit Crops if the Benefit Has Health Implications? An Application to Cranberry Products. Agricultural and Resource Economics Review. 1-23. https://doi:10.1017/age.2023.38.

VacCAP Team Publications

- Mengist MF, Pottorff M, Mackey T, Ferrao F, Casorzo G, Lila MA, Luby C, Giongo L, Perkins-Veazie P, Bassil N, Munoz P and Iorizzo M. 2024. Assessing predictability of post-storage texture and appearance characteristics in blueberry at breeding population level. Postharvest Biology and Technology, 214, p.112964. https://doi.org/10.1016/j.postharvbio.2024.112964
- Oh H, Pottorff M, Giongo L, Mainland CM, Iorizzo M and Perkins-Veazie P. 2024. Exploring shelf-life predictability of appearance traits and fruit texture in blueberry. Postharvest Biology and Technology, 208, p.112643. https://doi.org/10.1016/j.postharvbio.2023.112643
- Oh H, Stapleton L, Giongo L, Johanningsmeier S, Mollinari M, Mainland CM, Perkins-Veazie P and Iorizzo M. 2024. Predicting of Bsensory texture attributes by integrating multiple instrumental measurements. Postharvest Biology and Technology, 218, p.113160. https://doi.org/10.1016/j.postharvbio.2024.113160
- Lopez-Moreno H, Phillips M, Diaz-Garcia L, Torres-Meraz M, Jarquin D, Loarca J, Ikeda S, Giongo L, Grygleski E, Iorizzo M and Zalapa J. 2024. Multiparametric Cranberry (Vaccinium macrocarpon Ait.) Fruit Textural Trait Development for Harvest and Postharvest Evaluation in Representative Cultivars. J Texture Stud, 55: e12866. https://doi.org/10.1111/jtxs.12866
- Maule AF, Diaz Garcia L, Loarca J, Lopez-Moreno H, Johnson-Cicalese J, Vorsa N, Iorizzo M, Neyhart J and Zalapa J. 2024. Of Buds and Bits: A QTL study on traditional upright traits and modern plot phenotyping in cranberry (Vaccinium macrocarpon Ait.). Frontier in Plant Science, 15:1294570. https://doi.org/10.3389/fpls.2024.1294570
- Clare SJ, Driskill M, Millar TR, Chagne D, Montanari S, Thomson S, Espley RV, Munoz PR, Benevenuto , Zhao D, Sheehan M, Mengist MF, Rowland LJ, Ashrafi H, Melmaiee K, Kulkarni KP, Babiker EM, Main D, Olmstead J, Gilbert J, Havlak , Hung H, Kniskern J, Percival D, Edger P, Iorizzo M and Bassil NV. 2024. Development of a targeted genotyping platform for reproducible results within tetraploid and hexaploid blueberry. Frontiers in Horticulture, 2:1339310. https://doi.org/10.3389/fhort.2023.1339310
- Kawash J, Erndwein L, Johnson-Cicalese J, Knowles S, Vorsa N and Polashock J. 2024. QTL analysis and marker development for fruit rot resistance in cranberry shows potential genetic association with epicuticular wax. Phytopathology 114:6, 1366-1372. https://doi.org/10.1094/PHYTO-12-23-0477-R
- Dare PA, Wu C, Carvajal JI, Nguyen HM, Günther CS, Hamiaux C, Bailey S, Deng C, Mengist MF, Iorizzo M, Foster TM, Chagné D, Montanari S and Espley RV. 2024. Haplotyped genome mapping and functional characterisation of a blueberry anthocyanin acetyltransferase (AAT) controlling the accumulation of acylated anthocyanins. Journal of Experimental Botany, 2024;, erae489. https://doi.org/10.1093/jxb/erae489
- Loarca J, Wiesner-Hanks T, Lopez-Moreno H, Maule A, Liou M, Torres-Meraz MA, Diaz-Garcia LA, Johnson-Cicalese J, Neyhart J, Polashock J, Sideli G, Strock CF, Beil CT, Sheehan MJ, Iorizzo M, Atucha A and Zalapa JE. 2024. BerryPortraits: Software for phenotyping of ripening traits with rapid automated imaging tools in cranberry (Vaccinium macrocarpon Ait.). Plant Methods, 20, 172 (2024). https://doi.org/10.1186/s13007-024-01285-1
- Ferrão LF, Luby C, Pottorff M, Casorzo G, Mengist MF, Mackey T, Lila MA, Giongo L, Bassil N, Perkins-Veazie P, Iorizzo M and Munoz P. 2024. Inference of the genetic basis of fruit texture in Northern and Southern highbush blueberries using genome-wide association analysis. Horticulture Research 11 (10): uhae233. https://doi.org/10.1093/hr/uhae233
- Hislop LM, Loarca J, Humann J, Hummer KE, Bassil N, Zhao D, Sheehan M, Casa AM, Billings GT, Echeverria D, Ashrafi H, Babiker E, Edger P, Ehlenfeldt MK, Hancoock J, Finn C, Iorizzo M, Mackey T, Olmstead J, Rowland LJ, Sandefur P, Spencer J, Stringer S, Vorsa N, Wagner A and Hulse-Kemp AM. 2024. A Blueberry (Vaccinium L.) Crop Ontology to Enable Standardized Phenotyping for Blueberry Breeding and Research. HortScience, 59(10), 1433-1442. https://doi.org/10.21273/HORTSCI17676-23
- Oh H, Mengist MF, Ma G et al. 2025. Unraveling the genetic architecture of blueberry fruit quality traits: major loci control organic acid content while more complex genetic mechanisms control texture and sugar content. BMC Plant Biol 25, 36 (2025). https://doi.org/10.1186/s12870-025-06061-4
- Mengist MF, Muhammad Ali Abid, Grace MH, Seth R, Bassil N, Kay CD, Dare AP, Chagné D, Espley RV, Neilson A, Lila MA, Ferruzzi M, Iorizzo M. 2025. Identification and functional characterization of genes associated with anthocyanin acylation in blueberry, Horticulture Research, 2025;, uhaf041, https://doi.org/10.1093/hr/uhaf041
- Tan C, Li C, Perkins-Veazie P, Oh H, Xu R and Iorizzo M. 2025. High throughput assessment of blueberry fruit internal bruising using deep learning models. Frontier in Plant Science, 16:1575038. https://doi.org/10.3389/fpls.2025.1575038
- Jiménez NP, Fong S, Neyhart JL, Johnson-Cicalese J, Vorsa N and Sideli GM. 2025. Leveraging genetic resources and genomic prediction to enhance flavonol content in cranberry fruit. The Plant Genome, 18, e70074. https://doi.org/10.1002/tpg2.70074

VacCAP Team Publications

- Clare SJ, Zheng P, Driskill M, Kawash J, Neyhart J, Millar TR, Main D, Polashock J, Edger P, Vorsa N, Johnson-Cicalese J, Maule AF, Zalapa J, Sideli GM, Iorizzo M and Bassil N. A high-recovery, high-density targeted genotyping platform for cranberry. Under review.
- Lopez-Moreno H, Phillips M, Kawash J, Torres Meraz MA, Rojas-Barros P, Maule AF, Atucha A, Neyhart JL, Sideli GM, Polashock J, Iorizzo M and Zalapa J. Genetic mapping of fruit texture traits uncovers cell wall modifying genes in American cranberry. Under review.

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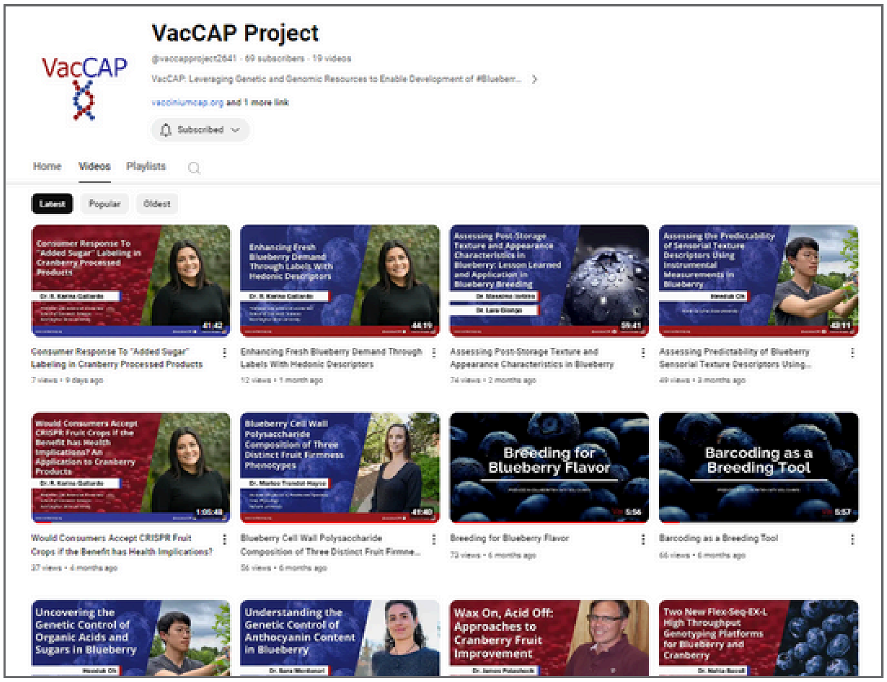
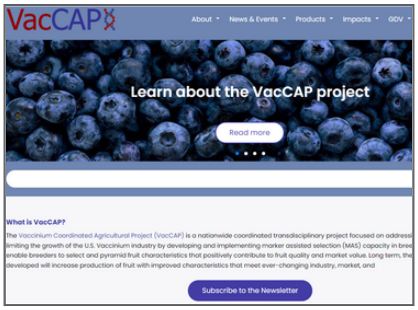
MORE RESOURCES

Recordings of all project webinars are available on the VacCAP Project YouTube Channel. Visit www.vacciniumcap.org or follow us @VacciniumCAP on X (Twitter) to stay updated on the latest VacCAP news. A list of presentations to conferences and industry meetings are available on the VacCAP website. All of our annual reports are also available on the website.



VacCAP: Leveraging Genetic and Genomic Resources to Enable Development of #Blueberr...

VacCAP: Leveraging Genetic and Genomic Resources to Enable Development of #Blueberry and #Cranberry Cultivars with Improved Fruit Quality Attributes



What is VacCAP?

The Vaccinium Coordinated Agricultural Project (VacCAP) is a nationwide coordinated transdisciplinary project focused on addressi
limiting the growth of the U.S. Vaccinium industry by developing and implementing marker assisted selection (MAS) capacity in bree
enable breeders to select and pyramid fruit characteristics that positively contribute to fruit quality and market value. Long term, the
developed will increase production of fruit with improved characteristics that meet ever-changing industry, market, and

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