NCCC-212 Annual Report for 2020: Small Fruit
USDA ARS National Clonal Germplasm Repository
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List of projects

Objective 1 - Develop improved small fruit germplasm through cooperative breeding and evaluation programs.

Blackberry and Raspberry:

1. *Using synteny and candidate genes to identify loci controlling fruit sweetness in blackberry.* Jason Zurn, Mandie Driskill, Nahla Bassil, USDA ARS NCGR-Corvallis, OR; Margaret Worthington, John Clark, University of Arkansas, Fayetteville, AR; Chad Finn, USDA ARS HCRU-Corvallis, OR; Dorrie Main, Sook Jung, Washington State University, Pullman, WA; Lailiang Cheng, Cornell University, Ithaca, NY.
2. *Developing two fingerprinting sets in red raspberry.* Jason Zurn, Mandie Driskill, Kim Hummer, Nahla Bassil, USDA ARS NCGR-Corvallis; Chad Finn, Jana Lee, USDA ARS HCRU-Corvallis, OR; Michael Dossett, BC Berry Cultivar Development Inc. (in partnership with Agriculture and Agri-Food Canada), Agassiz, Canada.
3. *Fine mapping black raspberry aphid resistance to the North American large raspberry aphid.* Christina Mulch, Kelly Vining, Oregon State University, Corvallis, OR; Nahla Bassil, Jill Bushakra, USDA ARS NCGR-Corvallis, OR; Chad Finn, Jana Lee, USDA ARS HCRU-Corvallis, OR; Michael Dossett, BC Berry Cultivar Development Inc. (in partnership with Agriculture and Agri-Food Canada), Agassiz, Canada.
4. *Blackberry fingerprinting set to confirm parentage in new cultivars and identity in the NCPN collection.* Nahla Bassil, USDA ARS NCGR-Corvallis, OR., April Nyberg,

USDA ARS NCGR-Corvallis, OR; Chad Finn, Bob Martin, Amanda Lake, USDA ARS HCRU-Corvallis, OR.

5. *GWAS study by phenotyping diverse Rubus species and cultivars.* Jill Bushakra, Nahla Bassil, and Kim Hummer, USDA ARS NCGR-Corvallis OR; Pairwise Plants, Durham, NC, Plant Sciences, Inc., Watsonville, CA; Courtney Weber, Cornell University, Ithaca, NY; Gina Fernandez, North Carolina State University, Raleigh, NC; Margaret Worthington, University of Arkansas, Fayetteville, AR; Michael Dossett, BC Berry Cultivar Development Inc. (in partnership with Agriculture and Agri-Food Canada), Agassiz, Canada.

Blueberry:

1. *Confirming identity of blueberry cultivars by DNA Fingerprinting.* Nahla Bassil, Kim Hummer, April Nyberg, USDA ARS NCGR-Corvallis, OR; Ozgecan Yalcin, Oregon State University, Department of Horticulture, Corvallis, OR
2. *Determining ploidy using leaves and pollen grains of diverse Vaccinium species.* Sunny Green, Kim Hummer USDA ARS NCGR-Corvallis, OR; Ryan Contreras, Oregon State University, Department of Horticulture, Corvallis, OR
3. *Evaluating Vaccinium germplasm for heat tolerance, drought tolerance, and cold tolerance.* Todd Anderson, Nahla Bassil, Kim Hummer USDA ARS NCGR-Corvallis, OR; Scott Orr, Dave Bryla, USDA ARS HCRU, Corvallis, OR
4. *Developed a genetic framework to improve the efficiency of bioactive delivery from blueberry.* Nahla Bassil, Kim Hummer, USDA ARS NCGR-Corvallis, OR; Molla F. Mengist, Haley Burtch, Hawi Debelo, Marti Pottorff, Hamed Bostan, Candace Nunn, Sydney Corbin, Colin D. Kay, Mary Ann Lila, Mario G. Ferruzzi, Massimo Iorizzo, Plants for Human Health Institute, North Carolina State University, Kannapolis, NC
5. *Phenotyping blueberry for fruit quality traits.* Nahla Bassil, Kim Hummer, USDA ARS NCGR-Corvallis, OR; Marti Pottorff, Massimo Iorizzo, Penelope Perkins-Veazie, Mary Ann Lila, Plants for Human Health Institute, North Carolina State University, Kannapolis, NC; Ted Mackey, USDA-ARS-HCRU, Corvallis, OR
6. *Developing a high throughput genotyping platform for blueberry and cranberry.* Nahla Bassil, Mandie Driskill, USDA ARS NCGR-Corvallis, OR; Massimo Iorizzo, Plants for Human Health Institute, North Carolina State University, Kannapolis, NC; Patrick Edger, Michigan State University, Department of Horticulture, E. Lansing, MI; Patricio Munoz, University of Florida, Horticultural Science Department, Gainesville, FL; David Chagne, Plant & Food Research Limited, Palmerston North, New Zealand
7. *Assisting Breeding Insight (BI) in enabling genomic selection in blueberry.* Nahla Bassil, USDA ARS NCGR-Corvallis, OR; Dongyan Zhao, Moira Sheehan, Cornell University, Department of Plant Biology; Amanda Hulse-Kemp, USDA-ARS; Jodi Humann, Dorrie Main, Washington State University, Department of Horticulture, Pullman, WA
8. *Testing Allegro Targeted Genotyping for blueberry genome wide association.* Nahla Bassil, USDA ARS NCGR-Corvallis, OR; Amanda Hulse-Kemp, USDA-ARS-GBRU; Lauren Redpath, Rishi Aryal, and Hamid Ashrafi, North Carolina State University, Horticultural Science Department, Raleigh, NC

Strawberry:

1. *Assessing genetic diversity in the cultivated strawberry (Fragaria ×ananassa) collection at the National Clonal Germplasm Repository.* Jason Zurn, Nahla Bassil, Kim Hummer, USDA ARS NCGR-Corvallis, OR; Steve Knapp, Michael Hardigan, UC Davis, CA.
2. *Evaluating genotype x environment interactions for predicting SSC in strawberry*. Jason Zurn, Nahla Bassil, USDA ARS NCGR-Corvallis, OR; Mulusew Ali, Craig Hardner University of Queensland, St. Lucia, QLD, Australia; Vance Whitaker, University of Florida, Wimauma, FL; Chad Finn, USDA ARS HCRU-Corvallis, OR; Jim Hancock, Michigan State University, E. Lansing, MI; Iraida Amaya, IFAPA, Malaga, Spain; Helen Cockerton, Richard Harrison, NIAB-EMR, East Malling, United Kingdom; Lise Mahoney, Tom Davis, University of New Hampshire, Durham, NH; Jodi Neal, Queensland Department of Agriculture and Fisheries, Nambour, Australia.
3. *Phenotyping diverse strawberry cultivars in Corvallis, Oregon.* Kim Hummer, Nahla Bassil, and Jason Zurn, USDA ARS NCGR-Corvallis, OR

Other small fruit crops:

1. *Developing a Ribes fingerprinting set for germplasm management.* Nahla Bassil, Jill Bushakra, Kim Hummer, USDA-ARS NCGR-Corvallis, OR

Objective 2 - Develop practices for small fruit production tailored for climatic and market needs of growers.

Objective 3 - Explore the association between fruit constituents and human health impacts.

Impact statements

Objective 1 - Develop improved small fruit germplasm through cooperative breeding and evaluation programs.

Blackberry and Raspberry:

Using synteny and candidate genes to identify loci controlling fruit sweetness in blackberry: Increased sugar content is one of the most important traits desired by blackberry consumers. A synteny-based approach was used to identify candidate genes responsible for sugar production in blackberry (*Rubus* L.). Three sugar quantitative trait loci (QTL) were identified from the GDR QTL database that are conserved among apple, peach, and alpine diploid strawberry. The physical regions for these QTLs were identified in the *F. vesca* v1.1 assembly and 26 genes with functions associated with sugar production were extracted. Additionally, 789 sugar-associated genes were extracted from the *M. domestica* v3.0.a1 assembly. The strawberry and apple genes were used to conduct a BLAST search in the GDR *Rubus* reference transcriptome. Of 279 *Rubus* candidate transcripts identified, predicted exons were used to design 9,355 Hyb-Seq baits. The baits covered 99.6% of the targeted regions. These baits were used in conjunction with PacBio sequencing to genotype 40 cultivars with high and low sugar content from the University of Arkansas and USDA blackberry breeding programs. A total of 430,167 high quality circular consensus sequences (CCS) were generated. Alignment to the 'Hillquist' blackberry and *Rubus occidentalis* genomes, followed by variant identification, resulted in 929,430 and 1,324,854 markers, respectively. Welch's t-test and a Benjamini-Hochberg correction identified 467 and 312 significant loci from the 'Hillquist' and the *R. occidentalis* genotype tables, respectively. Population structure modeling identified a total of 173 loci that were significantly ($\alpha = 0.05$) associated with sugar production regardless of population structure. A set of 111 KASP markers were developed and validated on 192 blackberries from the USDA-ARS HCRU and University of Arkansas breeding programs and 48 markers distributed across 16 genomic regions were found to be significantly associated with soluble solids content. A region on chromosome 1, known as qSSC-Ruh-ch1.1, was stable across three growing environments and was responsible for a 1.5 °Brix increase in soluble solids. The regions identified represent the first sweetness related QTLs in blackberry and the new markers will be used to develop sweeter cultivars.

Developing two fingerprinting sets in red raspberry:
DNA sequence data from the public domain and that we have previously generated was mined for structural variants and long core repeat simple sequence repeats after alignment to the black raspberry genome. At this time, we are identifying single copy polymorphic loci to compile a list of genome-wide single copy SSRs and structural variants. Once identified we plan to develop 1,000 RhAMPSeq markers to use in genotyping our red raspberry collection. A subset of the polymorphic SSRs will also be developed into a fingerprinting set and used to genotype these same individuals.

Fine mapping black raspberry aphid resistance to the North American large raspberry aphid:
Market expansion of black raspberry is currently hindered by aphid-vectored viruses, such as Black Raspberry Necrosis virus. Natural, genetic resistance to aphids exists and has been identified from three geographic sources: Maine, Michigan, and Ontario, Canada. These sources are being used by Chad Finn to breed cultivars with durable aphid resistance. We have developed three new populations (ORUS 5291, ORUS 5296, and ORUS 5306), that are expected to segregate for each of these three sources, to fine map this trait. Segregation of resistance in each of these populations was phenotypically evaluated by aphid inoculation resulting in segregation ratios of 1:1 resistant (R) to susceptible (S) by Chi-squared analysis. Differential expression in 10 R and 10 S seedlings is being assessed with IsoSeq (Full-Length Isoform Sequencing) for one source (ORUS 5306). In addition, Illumina Sequencing for 5 R and 5 S seedlings from each population before and after aphid inoculation is being evaluated. We plan on performing fine mapping of QTL (quantitative trait loci) for aphid resistance in each of these populations using previously developed microsatellite markers and new markers identified using IsoSeq. Our goals are to use these resources to develop useful genetic markers for each source of resistance, and to allow pyramiding of these resistance loci in new breeding populations.

Blackberry fingerprinting set to confirm parentage in new cultivars and identity in the NCPN collection:
An 8-SSR fingerprinting set has already been developed to fingerprint and validate parentage in blackberries. We used this fingerprinting set to confirm parentage of three new releases from Chad Finn's breeding program, 'Eclipse', 'Galaxy', and 'Twilight'. Genotyping and parentage

analyses are under way for 38 of the selections and parents from the USDA-ARS-HCRL Blackberry Breeding Program. Parentage analysis is in progress to identify the genotype that could have resulted from the reported cross.

GWAS study by phenotyping diverse Rubus *species and cultivars.*
Provided 647 accessions from the USDA-ARS-NCGR *Rubus* collection for genotyping and phenotyping. The accessions were propagated by Pairwise Plants to generate at least 10 plants of each genotype and are being grown in pots under protection in Watsonville, CA. The accessions will be evaluated for 79 traits in Watsonville, CA. Traits include plant architecture, cane characteristics, flower characteristics, fruit characteristics, fruit quality, and seed characteristics. A selection of six standard genotypes are being grown and evaluated at USDA-ARS, Corvallis, OR, Cornell, Ithaca, NY, NCSU, Raleigh, NC, and Agassiz, Canada for 10 traits.

Blueberry:

Confirming identity of blueberry cultivars by DNA Fingerprinting:
The genotypic identity of the blueberry cultivars in the NCGR collections is critical to genebank management and operations. We had previously developed a 5-SSR and a 10-SSR fingerprinting set. Genotyping 367 samples with one or both of these SSR sets and parentage analysis, where possible, detected 96 plants representing 54 cultivars that were true-to-type (TTT) cultivars, 13 sets of homonyms and ten groups of synonyms. Parentage analysis identified five of the TTT cultivars among the homonyms ('Bluecrop', FL 4B, 'Nelson' and 'Clara') and 'Elizabeth' among the synonym sets. Identity challenges were detected in 50 plants representing 23 cultivars. We have obtained leaf samples of parents and cultivars that had genotypes that were inconsistent with the reported parentage from up to seven different sources and are in the process of genotyping them to resolve these identity challenges. Confirmed blueberry genotypes will benefit the germplasm community for use in continued breeding and genetic studies.

Developed a genetic framework to improve the efficiency of bioactive delivery from blueberry:
In collaboration with Massimo Iorizzo and his team at NCSU, we applied a novel high-throughput *in vitro* gastrointestinal digestion model to phenotype bioaccessibility of phenolic acids in 66 diverse blueberry accessions from the NCGR collection in 2017-2019. Results revealed significant ($P<0.05$) differences between accessions, years, and accession by year interaction for relative and absolute bioaccessibility of flavonoids and phenolic acids. Broad sense heritability estimates revealed low to moderate inheritances of relative and absolute bioaccessibility, suggesting that besides environmental variables, genetics factors could control bioaccessibility of phenolics. Acylated anthocyanins had significantly higher relative bioaccessibility than non-acylated anthocyanins. Correlation analysis indicated that relative bioaccessibility did not show significant association with fruit quality or raw concentration of metabolites. The study also identified accessions that have high relative and absolute bioaccessibility values. Overall, combining the bioaccessibility of phenolics with genetic and genomic approaches will enable the identification of genotypes and genetic factors influencing these traits in blueberry. Data from this study will be uploaded to GRIN-Global.

Phenotyping blueberry for fruit quality traits:
In the spring and summer of 2020, we harvested ripe blueberry fruit from 196 seedlings for the 'Draper' x 'Jewel' population, 200 accessions from the NCGR Field collection, and 960 northern

highbush blueberry accessions (GenStudy) from the 2016 and 2017 USDA-ARS-HCRL breeding program as part of the VacCAP project. We use the Texture Analyzer to simultaneously evaluate blueberry texture (Tx), stem scar diameter (ScD), scar tear (ScT), fruit weight (Wg) and shelf life indicators such as wrinkle/shrivel (Wr/Shr), mold, leakage (Lk) at harvest time and six weeks post-harvest (stored at 4 °C). Preliminary analyses indicated a wide range of variation for most of the traits and parameters. Fruits for non-volatile chemistry analysis were frozen and shipped to Co-PIs Perkins-Veazie and Lila.

Developing a high throughput genotyping platform for blueberry and cranberry:
We lead the Genotyping Team for the VacCAP with the objective to develop a high-throughput genotyping platform for blueberry and cranberry. We surveyed 18 core and non-core *Vaccinium* groups to identify their needs for a high-throughput platform that can be of use to the *Vaccinium* research community. We began compiling a SNP catalog by obtaining 47,025 SNPs of interest from linkage maps and QTL studies. We obtained sequence data from collaborators and NCBI and cleaned them up and stored them to use for SNP detection once the pangenome is ready. We also identified four high-throughput data providers that could meet our needs, organized webinars from these companies to provide an overview of their services to the *Vaccinium* community, and are in the process of evaluating their offers.

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Assisting Breeding Insight (BI) in enabling genomic selection in blueberry:
We identified 384 diverse blueberry accessions and collected them from the NCGR and the blueberry community to test the genotyping platform selected (DArTag), once it is ready. We provided leaf tissue for ~600 samples for two companies to test their blueberry DNA extraction protocols. We worked with Ted Mackey and Michael Hardigan on identifying traits to phenotype ~2,700 seedlings from the 2017 USDA-ARS-HCRL seedling field. In collaboration with Amanda Hulse-Kemp (USDA-ARS) and Jodi Humann (GDR, WSU), we compiled a comprehensive list of all traits being used to phenotype blueberry, and phenotyping method from the blueberry research and breeding community (ARS, university, and private companies) and converted the information into the BI template that is interoperable with BreedBase.

Testing Allegro Targeted Genotyping for blueberry genome wide association:
In collaboration with Hamid Ashrafi and his team at NCSU, 1.7 million SNPs were selected, and the flanking sequences were extracted. Single primer enrichment technology (SPET) was used to specifically target SNPs of interest in a diversity panel of 252 individuals that included 77 accessions from the NCGR. Phenotypic data for phenological traits were collected in 2019 and 2020 from the 77 accessions at the NCGR and ripe fruit were shipped to NCSU for fruit quality trait and anthocyanin analyses. The pooled paired-end libraries of 184 and 96 individuals of two diversity panels were used to generate 308 GB of data with an average of 900 MB per genotype. Two bioinformatics pipelines were used for SNP identification. Data analysis is in process. Through association of these SNPs to measured phenotypic traits of the diversity panels, candidate genes for fruit size, weight, and color, as well as soluble solid content, titratable acidity, pH, and different anthocyanins, will be investigated. Further, comparative analysis of resequencing data of native diploid, tetraploid, and hexaploid *Vaccinium* species will be used to ascertain the origin of introgressed SNPs.

Strawberry:

Assessing genetic diversity in the cultivated strawberry (Fragaria ×ananassa) collection at the NCGR:
The USDA-ARS national collection includes 560 diverse *Fragaria ×ananassa* accessions of modern and historical U.S. and foreign cultivars and breeding selections. An initial core subset of 447 *Fragaria* cultivars (304) and world species (143) was identified in the 1980s by the curator and the Small Fruit Crop Germplasm committee members to represent maximum genetic diversity. Very little has been done to characterize these accessions genotypically. Pedigrees are unknown for many. Since the original core designation, an additional 160 cultivated strawberry cultivars were received by NCGR. The objectives of this study is to genotype the entire *F. ×ananassa* collection, assess genetic structure and diversity, confirm pedigrees within the collection, and identify a core collection based on genetic data. The Knapp group has already genotyped 211 of these accessions with the IStraw35 Axiom strawberry array. We submitted DNA from the remaining 332 accessions for genotyping with a new strawberry array that contains 6,000 markers in common with the IStraw35 Axiom array. Population structure analysis of the *F. ×ananassa* collections revealed eight sub-populations associated with geographical regions or major breeding programs. F_{st} values were very low confirming the narrow genetic diversity within cultivated strawberry germplasm and may also be related to the germplasm sharing by 1950's era breeding programs. Two 100 individual core collections were developed that maximize diversity within the collection and have a uniform distribution of alleles. These core collections will help breeding programs streamline characterization of the collection for useful traits. Pedigree confirmation is underway.

Evaluating genotype x environment interactions for predicting SSC in strawberry:
Strawberry fruit flavor is due to a complex mix of sugars, acids, and aromatic compounds. Consumers tend to prefer sweeter strawberry cultivars. Therefore, sweetness has been an important target trait for breeders. The majority of strawberry soluble solids are sugars, and soluble solid content (SSC) is used as a proxy to determine sweetness. A strong genotype × environment (G × E) interaction has been observed for SSC, causing difficulties when studying the genetics underlying SSC in individual environments. A meta-analysis of multiple environments may provide new insights toward unraveling the genetics underlying SSC. Genotypic and phenotypic data were collected for 3,407 total individuals from seven breeding programs (four in the United States, and one each from Spain, the United Kingdom, and Australia). Subsets of the individuals were evaluated for SSC in 19 environments. Genotypic information from the 90K and 35K Axiom arrays was reduced to 12,951 high quality single nucleotide polymorphism markers shared by all accessions. Missing data was imputed, linkage disequilibrium was calculated, and a relationship matrix was constructed for all samples. Using this information, multiple G × E models were evaluated for their predictive ability among environments. Results are being analyzed to identify genomic models that can be used to predict strawberry SSC in new environments.

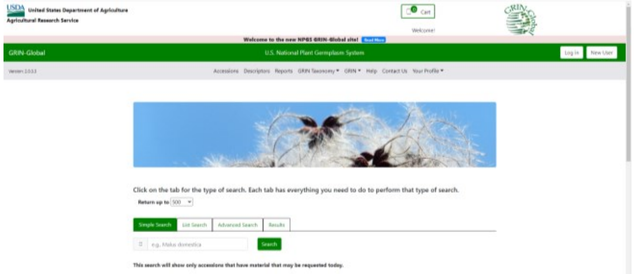
Other Small Fruit Crops

Developing a Ribes fingerprinting set for germplasm management:
We identified 13 high core repeat SSRs from the literature that appeared to be polymorphic in different species. We evaluated them in a testing panel of 12 accessions representing *R. aureum, R. nigrum, R. uva-crispa*, *R. spicatum*, *R. petraeum*, and *R.* × *nidigrolaria*. We identified 7 SSRs that appear polymorphic across these species and optimized this 7-SSR *Ribes* fingerprinting set and will be testing it for ability to identify 51 accessions in the NCGR collection.

Objective 2 - Develop practices for small fruit production tailored for climatic and market needs of growers.
Objective 3 - Explore the association between fruit constituents and human health impacts.
Data, germplasm/cultivar descriptions, research results, for discussion at the meeting. Note that this data is preliminary and not for public dissemination

Genus	Accessions	Field locations	SH /GH locations	Total plant locations	Total seed accessions
Fragaria (Strawberry)	**2,013**	**900**	**1,726**	**2626**	**652**
Ribes (Currant, Gooseberry)	**1,299**	**651**	**65**	**716**	**672**
Rubus (Blackberry, Raspberry)	**2,221**	**-**	**948**	**948**	**1819**
Sambucus (Elderberry)	**201**	**47**	**1**	**48**	**170**
Vaccinium (Blueberry, Cranberry)	**1,852**	**311**	**686**	**1,001**	**1072**

Berry collections summary for the National Clonal Germplasm Repository.
GRIN-Global searches for particular accessions can be obtained by searching:
https://npgsweb.ars-grin.gov/gringlobal/search



Click on the tab for the type of search. Each tab has everything you need to do to perform that type of search.

This search will show only accessions that have material that may be requested today.

4. Publications

Bassil, N.V., Bidani, A., Nyberg, A.M., Hummer, K.E., Rowland, L.J. 2020. Microsatellite markers confirm identity of blueberry plants in the USDA-ARS National Clonal Germplasm Repository collection. Genetic Resources and Crop Evolution. 67:393-409. https://doi.org/10.1007/s10722-019-00873-8.

Bassil, N.V., Zurn, J.D., Hummer, K.E., Hardigan, M.A., Knapp, S.J., Montanari, S.,Postman, J.D., Worthington, M., Clark, J.R., Ashrafi, H., Aryal, R., Dossett, M., Finn,C.E., Driskill, M.J., Mulch, C., Vining, K.J., Rapp, R., Ochsenfeld, C., Zhang, X., Poorten, T., Pham, G. 2020. Molecular characterization of caneberries, strawberries, pear, mint and hops at the Corvallis genebank. Abstract for American Society for Horticultural Science Conference, August 9-13, 2020, Orlando, FL

Bradish, C., Bushakra, J.M., Robbins, L., Karaaoac, E., Sabrina, T., Willard, J.L., Perkins-Veazie, P., Lee, J., Scheerens, J., Weber, C., Dossett, M., Bassil, N.V., Finn, C.E., Fernandez, G. 2020. Standardized phenotyping in black raspberry. Journal of American Pomological Society. 74(1):2-17.

Bushakra, J.M., Alice, L., Carter, K., Dossett, M., Lee, J.C., Liston, A., Meiers, R., Mulch, C., Nyberg, A.M., Peterson, M.E., Clark, M.C., Vining, K., Worthington, M., Yin, M., Sutherland, B., Zurn, J.D., Clark, J., Finn, C.E., Bassil, N.V., Hummer, K.E. 2020. Status of *Rubus* germplasm at the US National Clonal Germplasm Repository in Corvallis,Oregon. Acta Horticulturae. 1277:121-128. https://doi.org/10.17660/ActaHortic.2020.1277.17..

Finn, C.E., Strik, B., Yorgey, B.M., Peterson, M.E., Jones, P.A., Lee, J., Bassil, N.V., Martin, R.R. 2020. 'Twilight' thornless semi-erect blackberry. HortScience. 55(7):1148-1152. https://doi.org/10.21273/HORTSCI14992-20.

Finn, C.E., Strik, B.C., Yorgey, B.M., Peterson, M.E., Jones, P.A., Buller, G., Serce, S., Lee, J., Bassil, N.V., Martin, R.R. 2020. ‘Eclipse’ thornless semi-erect blackberry. HortScience. 55(5):749-754. https://doi.org/10.21273/HORTSCI14891-20.

Finn, C.E., Strik, B., Yorgey, B.M., Peterson, M.E., Jones, P.A., Buller, G., Lee, J., Bassil, N.V., Martin, R.R. 2020. ‘Galaxy’ thornless semierect blackberry. HortScience. 55(6):967-971. https://doi.org/10.21273/HORTSCI14985-20.

Hummer, K.E., Bushakra, J.M. 2020. Recent acquisitions of *Rubus* L. at the USDA National Clonal Germplasm Repository, Corvallis, Oregon: profiles of four species. Acta Horticulturae. 1277:33-38. https://doi.org/10.17660/ActaHortic.2020.1277.5.

Hummer, K.E., Postman, J. 2020. Guardians of the germplasm: hazelnuts, berries, pears, hops, and mint. Journal of American Pomological Society. 74(2):104-110.

Mengist, M.F., Grace, M.H., Xiong, J., Kay, C.D., Bassil, N.V., Hummer, K.E., Ferruzzi, M.G., Lila, M., 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. Frontiers in Plant Science. 5. https://doi.org/10.3389/fpls.2020.00370.

Whitaker, V.M., Knapp, S.J., Hardigan, M.A., Edger, P.P., Slovin, J.P., Bassil, N.V., Hytonen, T., Mackenzie, K.K. 2020. A roadmap for research in octoploid strawberry. Horticulture Research. https://doi.org/10.1038/s41438-020-0252-1.

Willman, M., Bushakra, J.M., Bassil, N.V., Finn, C.E., Dossett, M., Fernandez, G., Weber, C., Scheerens, J., Dunlap, L., Fresnedo-Ramirez, J. 2020. Genetic analysis of drupelet count in black raspberry (*Rubus occidentalis).* Acta Horticulturae. 1277:65-72. https://doi.org/10.17660/ActaHortic.2020.1277.9.

Worthington, M.I., Aryal, R., Bassil, N.V., Mead, D., Fernandez, G.E., Clark, J.R., Fernandez-Fernandez, F., Finn, C.E., Hummer, K.E., Ashrafi, H. 2020. Development of new genomic resources and tools for molecular breeding in blackberry. Acta Horticulturae. 1277:39-46. https://doi.org/10.17660/ActaHortic.2020.1277.6.

Zurn, J.D., Ivors, K.L., Cole, G.S., Knapp, S.J., Hummer, K.E., Hancock, J.F., Finn, C.E., Bassil, N.V. 2020. Assessing cultivated strawberries and the *Fragaria* Supercore for resistance to soilborne pathogens. Journal of American Pomological Society. 74(1):18-23.

Zurn, J.D., Meiers, R.C., Ward, J., Finn, C.E., Dossett, M., Bassil, N.V. 2020. Identifying variation in red raspberry MLO genes thought to provide resistance to powdery mildew. Acta Horticulturae. 1277:25-32. https://doi.org/10.17660/ActaHortic.2020.1277.4.