

FINAL PROJECT REPORT

Project Title: Sweet cherry breeding toolbox

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Cooperators: Kate Evans (Washington State University), Jim McFerson (Washington Tree Fruit Research Commission), Amy Iezzoni (Michigan State University)

Total Project Request: Year 1: \$5000 Year 2: \$5000

Other funding sources

Agency Name: NSF DIBBS

Amount awarded: \$1.485 M (Jan 2015 – Dec 2017)

Notes: “TriPal Gateway, a Platform for Next-Generation Data Analysis and Sharing.” PI: Ficklin (Horticulture). Co-PIs include Main and Jung.

Agency Name: USDA-NIFA NRSP

Amt. requested: \$1.99 M (Oct 2014- Sept 2019)

Notes: “Database Resources for Crop Genomics, Genetics and Breeding Research”. PI: Dorrie Main, writing team includes Sook Jung, Michael Kahn, Cameron Peace, and Jim McFerson.

Agency Name: USDA-NIFA Specialty Crop Research Initiative

Amount awarded: \$2.7 M (Sep 2014 – Aug 2019)

Notes: “Genome Database for Rosaceae: Empowering Specialty Crop Research through Big-Data Driven Discovery and Application in Breeding.” PI: Main. Co-PIs include Jung, Peace and Oraguzie.

Agency Name: USDA-NIFA Specialty Crop Research Initiative

Amount awarded: \$10 M (Sep 2014 – Aug 2019)

Notes: “RosBREED: Combining Disease Resistance with Horticultural Quality in New Rosaceous Cultivars.” PI: Iezzoni. Co-PIs include Peace, Oraguzie and Main.

Agency Name: USDA-NIFA Specialty Crop Research Initiative

Amount awarded: \$2.0 M (Sep 2009 – Aug 2014)

Notes: “Tree Fruit GDR: Translating genomics into advances in horticulture.” PI: Main. Co-PIs include Peace and Oraguzie.

Agency Name: WTFRC/OSCC

Amount requested: \$52,844 (2014–2015)

Notes: “New genomic regions controlling production and fruit disorder traits.” PI: Oraguzie. Co-PIs include Peace.

Agency Name: WTFRC/OSCC

Amount requested: \$13,000 (2014)

Notes: “Consulting for the sweet cherry breeding program.” PI: Iezzoni.

Agency Name: WTFRC/OSCC

Amount requested: \$7,500 (2014)

Notes: “Consulting for the NW cherry project.” PI: Bliss.

Agency Name: WTFRC/OSCC

Amount awarded: \$442,847 (2012–2014)

Notes: “PNW sweet cherry breeding and genetics program.” PI: Oraguzie. Co-PI: Peace.

Agency Name: USDA-NIFA Specialty Crop Research Initiative

Amount awarded: \$7.2 M (Sep 2009 – Aug 2014)

Notes: “RosBREED: Enabling marker-assisted breeding in Rosaceae.” PI: Iezzoni. Co-PIs include Peace and Oraguzie.

Agency Name: USDA-NIFA Specialty Crop Research Initiative

Amount awarded: \$2.0 M (Sep 2009 – Aug 2014)

Notes: “Tree Fruit GDR: Translating genomics into advances in horticulture.” PI: Main. Co-PIs include Peace and Oraguzie.

Budget 1**Organization Name:** WSU**Telephone:** 509 335-4564**Contract Administrator:** Carrie Johnston**Email address:** carriej@wsu.edu

Item	2014	2015
Salaries^a	3600	3600
Benefits^b	1200	1200
Wages		
Benefits		
Equipment		
Supplies		
Travel^c	200	200
Plot Fees	0	0
Miscellaneous		
Total	5000	5000

Footnotes: a and b = 5% of Dr. Sook Jungs salary and benefits (at a rate of 25%) for data curation; c = cost of once annual visit of Dr. Dorrie Main to provide face-to-face training on the toolbox to Dr. Oraguzies group in Prosser.
Originally requested \$29,893 in year 1 and \$30,928 in year 2.

OBJECTIVES

Overall goal: To maintain and expand the Pacific Northwest Sweet Cherry Breeding ToolBox and continue to enable efficient cherry breeding.

Specific objectives:

1. Enable efficient data management for the Pacific Northwest Sweet Cherry Breeding Program (*years 1 and 2*)
2. Enable selection comparisons through access to data mining tools that utilize up-to-date performance and genotypic data (*years 1 and 2*)
3. Enable efficient parental selection for desired cultivars through access to data analysis tools that utilize up-to-date performance and genotypic data (*more toward start of year 2*)
4. Ensure optimal utilization of the Sweet Cherry Breeding ToolBox through hands-on training to the PNSWBP team (*years 1 and 2*)

Through support provided by other newly funded federal projects (USDA SCRI and NRSP) we will have the resources needed to complete all these objectives, so they remain unchanged.

SIGNIFICANT FINDINGS

1. Curation of publicly useful Prunus trait and marker data in GDR, accessible through the Sweet Cherry Breeding Toolbox of the Pacific North West Sweet Cherry Breeding program (PNWSCBP)

New data extracted in Year 2 (final year) from the public literature includes 5 genetic maps and 2425 marker loci from 2 publications. We are in the process of checking the curated data from 18 additional publications which will be online by the end of the project end in December 2015.

Other relevant data includes Peach Genome v2.0.a1 is available along with the IRSC 9K SNPs anchored to the new assembly.

New data previously extracted and curated from the public literature in year 1 includes 4 genetic maps, 1 high-resolution mapping of MTL in the peach genome, 1675 marker loci, 108 QTLs/MTLs for 9 traits from 4 publications. It also includes sweet cherry molecular diversity data for self-compatibility from two cultivars and two populations using 3 markers. In total, new data from year 1 have been added for the following traits:

2. Breeding Data: All phenotype and genotype data for the WTFRC PNWSCBP provided by Dr. Nnadozie and Dr. Peace is being extracted and curated into database templates for upload to the GDR private Sweet Cherry Breeding Toolbox. These complete data for the PNWSCBP will be made available through the secure Toolbox to assigned personnel as decided by the WTFRC and WSU.
3. Editing and uploading capability for the GDR Breeders toolbox is being implemented for the current version of the Cherry Breeders Toolbox. We are upgrading GDR to Drupal 7 and converting the GDR toolboxes to Tripal. To this end we held a Breeders Needs Assessment Workshop immediately after the National Association of Plant Breeders Annual Meeting in July in

Pullman. As part of that meeting, which involved Drs. Iezzoni, Peace, Evans and McFerson, we introduced breeders to Field Book App, an application for use on handheld devices which was designed by Jesse Poland's group at Kansas State University, to enable more efficient collection and upload of wheat field data. We provided breeders with the app, preinstalled on a Samsung handheld device, for them to test in their programs. The breeders are providing us with their recommendations for new or improved functionality as needed for collection of tree fruit and we will work with the developers to provide this to our tree fruit breeders.

Also as part of this Breeders Needs Assessment Workshop we identified more functionality breeders would like in the Breeders Toolbox to provide a more comprehensive solution to managing all aspects of tree fruit breeding. With our other sources of funding we will develop a generic solution, customizable for each breeding program, which we will make available to personnel in the PNWSCBP.

4. As it becomes available we will provide hands-on and audio visual training tutorials for PNWSCBP personnel.

METHODS

1. **Enable efficient data management for the Pacific Northwest Sweet Cherry Breeding Program:** We will curate new germplasm, phenotype and genotype data generated from the PNWSCBP. We will also curate the relevant cherry genomics, genetics and breeding data for inclusion in the GDR. This data will be submitted by other *Prunus* researchers and extracted from publications. The collection and curation of data in one integrated database will allow building an efficient system not only for keeping track of the large volume of PNWSCBP breeding data, but also for enabling direct utilization of genomics and genetics data worldwide for marker assisted breeding.
2. **Enable selection comparisons through access to data mining tools that utilize up-to-date performance and genotypic data:** We will upload and integrate the PNWSCBP data to the GDR so that the current data mining tools can be continuously used for newly updated breeding data. The data mining tools include breeding data search tools by dataset, germplasm names, trait values, alleles and parentage. Breeders can download genotypic and phenotypic data of germplasm that meet the various categories and thresholds that users specified.
3. **Enable efficient parental selection for desired cultivars through access to data analysis tools that utilize up-to-date performance and genotypic data:** In addition to the genotypic and phenotype data, we will integrate the breeding values and DNA-based functional genotype data from available parent pools in PNWSCBP. This will allow PNWSCBP to use the parental selection tool in GDR. The tool is designed to predict the efficient parent combinations that can produce a target number of seedlings with specific traits thresholds specified by users.
4. **Ensure optimal utilization of the Sweet Cherry Breeding ToolBox through hands-on training to the PNWSCBP team:** We will conduct hands-on in-person training on data template completion and use of the toolbox and hold quarterly conference calls to ensure toolbox is kept current with

data and functionality.

RESULTS AND DISCUSSION

Publicly available trait and marker data that is relevant to the PNWSCBP continues to be added to GDR and the performance and genotypic data specific to the breeding program will be completed over the next couple of months. We will continue to offer this facility to personnel associated with the PNWSCBP as needed, through the use of easy to use interfaces and tools for the breeding program personnel to be able to upload, edit, browse and compare these data across years and locations. This up to date breeding management system for the PNWSCBP that will help facilitate marker-assisted breeding and more efficient development of new cultivars for PNW sweet cherry growers.

EXECUTIVE SUMMARY

Tree fruit breeding programs generate copious amounts of data. Utilizing this data requires proper management plans and interrogation tools to enable breeders to efficiently mine their data and extract what they need to enable more efficient breeding. Concordant with this is the need to also access all relevant public information such as what's known about traits, markers for these traits, germplasm containing useful traits in the same and related crops. Within the Rosaceae community database, GDR (www.rosaceae.org), a private breeding database for the PNWSCBP exists, connecting the programs private breeding data with all publicly available, quality checked, genomic, genetics and breeding data for Prunus crops. Searchable interfaces allow the data to be searched by trait, trait levels, location, marker, pedigree, germplasm, year, etc and tools enable download of data for upload to analysis programs. The Cross-Assist tool takes this concept one step further. Using component data from the breeding program it outputs the optimal parents to cross and numbers of seedlings needed to generate the desired offspring and eventually new cultivar(s) which meet producer and consumer needs.

The Cherry Toolbox in GDR will continue to be updated with the PNWSCBP breeding data and other public data following the end of this WTFRC award. Funds from this WTFRC project were leveraged to support federal crop database proposals that have generated over \$5M in new funds over the next 4 years. Tools to allow direct upload of the data are developed, which enable breeders to be responsible for managing their own data. The Field Book App currently being evaluated for this purpose is looking very promising for this purpose and we are working with its developers to optimize for tree fruit breeding. We will continue to develop the GDR breeding tools into a comprehensive breeding management system that provides secure, one stop access to all the data management and analysis tools that Rosaceae breeders and allied scientists need to more efficiently develop new cultivars.