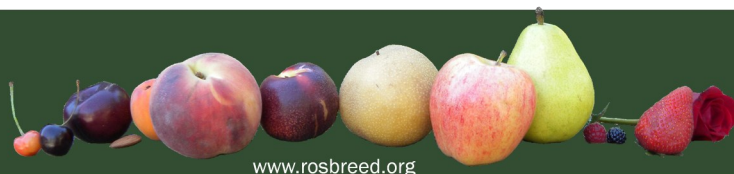# RosBREED

Enabling marker-assisted breeding in Rosaceae

www.rosbreed.org

Dedicated to the genetic improvement of U.S. rosaceous crops

RosBREED's Fourth Annual Project Meeting, East Lansing, Michigan, May 2013

Attendees of RosBREED's fourth annual meeting with project participants.

The final meeting of the RosBREED scientific teams focused on the project's many accomplishments over its four year duration and charted a course to achieve the goal of *enabling marker-assisted breeding in Rosaceae*, focusing on peach, apple, strawberry, sweet cherry, and tart cherry. Thirty-six participants gathered for three days in late May at the James B. Henry Center in East Lansing, MI to share exciting updates, discuss remaining challenges to solve jointly, and continue the networking that has made RosBREED such a unique, productive, and enjoyable endeavor.

In the morning session of the first day, after Project Co-Director Cameron Peace welcomed participants, Team Leaders gave brief updates on progress made to date during year 4 of the project. Highlights included the availability of more than 20 DNA tests validated, and some in routine use, for fruit quality and other traits. According to updated socio-economic survey results, traits and their levels targeted by these DNA tests cover many of those considered most valuable by breeders, growers, and market intermediaries (shippers and packers). With the results of the upcoming consumer surveys, we will further learn how valuable such traits are to our end user, the consumer. *Continued on next page….*

USDA

United States Department of Agriculture
National Institute of Food and Agriculture

NIFA

Each Team Leader explained the tasks that remain to ensure the project delivers its full impact. For example, Gennaro Fazio (Breeding Information Management [BIM] System Team Leader) said, "In the coming months, RosBREED will provide Rosaceae breeders with a set of online tools that will enable them to leverage trillions of data points for effective application of marker-assisted breeding". During the lunch break, project participants took their first opportunity to view and evaluate posters describing advances made in each RosBREED demonstration breeding program. Each poster was also carefully reviewed by Eric Van de Weg (Pedigree-Based Analysis Team Leader) for use in a session on day three devoted to discuss strengths and weaknesses of each poster – which was an excellent learning experience for all participants.

An afternoon presentation focused on RosBREED's impact to date. In addition to successes such as characterizing many valuable "jewels in the genome" and establishing and applying MAB in individual breeding programs, one of the greatest impacts RosBREED has achieved is the training of 18 future breeders for Rosaceae crops!

The Socio-Economics Team presented its most recent findings on relative trait values across the production and supply chain and described upcoming consumer surveys for peach, cherry, and strawberry. Crop-specific breakout groups then discussed remaining tasks and publication progress and plans. These breakout sessions were especially useful for the Peach group. After earlier hearing of MAB practices by the apple group, they had a conceptual breakthrough and realized that DNA information on newly discovered and validated regions in the peach genome can be used this summer to develop next year's crossing plans. With a handy trait loci guide in hand which describes each potential parent's alleles at trait loci, a breeder can formulate clever plans for the next generation of amazing offspring in the orchard, while viewing and tasting their fruit.

Continuing a tradition, day one concluded with a "Meet and Greet" session where the Demonstration breeders of the project discussed exciting fruit quality attributes being targeted and enhanced through marker-assisted breeding. Invited guests at this event included Regional Manager Kali Fox from Senator Debbie Stabenow's office, local RosBREED Advisory Panel members, MSU administration, and regional fruit industry leaders.

On day two of the meeting, Cameron Peace (MAB Pipeline Team Leader) described details behind many of the "jewels" (validated DNA tests) now available from project-wide efforts – "success stories". He gave advice on how participants, especially the graduate students, can efficiently mine RosBREED's unprecedentedly large and

Jim Hancock, John Clark, Chad Finn, Jim Luby, and Nahla Bassil enjoy each other's company and the fine hospitality of MSU's James B. Henry Business Center.

At the "Meet, Greet, *and Eat*", Chad Finn describes the difficulties of selecting superior strawberry seedlings for processing fruit traits in the field. The Pacific Northwest produces the bulk of U.S. processed strawberries and one of the many products is *Häagen-Dazs®* ice cream! Jim Hancock (right) told the story of how the remontancy (ever-bearing) trait was discovered in wild germplasm and incorporated into new cultivars via breeding to revolutionize the strawberry industry by essentially enabling year-round supply.


Kate Evans describes challenges faced when attempting to genotype large numbers of seedlings. For more information, please see her profile on page 5.

breeding-relevant datasets in these final months of the project to develop practical knowledge for breeding – "learning stories".

Specific software-based tools already developed as part of the BIM System were described by Gennaro Fazio. Gennaro and Cameron conducted a hands-on demonstration of the BIM System's online tools and how breeders can make use of the tools for arriving at informed breeding decisions using a combination of socio-economic, DNA, pedigree, and phenotypic information.

A one-and-a-half-day workshop on Pedigree-Based Analysis was held immediately after the main scientific meeting, as in previous years. This workshop was led by Eric van de Weg (Pedigree-Based Analysis Team Leader) and Marco Bink of Plant Research International, Netherlands and assisted by Umesh Rosyara (MSU) and Cameron Peace (WSU). The new and very user-friendly software VisualFlexQTL was unveiled and was met with awe and elation from the audience. Using an analogy from a wish expressed by one of the Demonstration Breeders during the previous year's meeting, this new software version enables users to jump in and drive without having to first know what's under the hood. Participants of the workshop left with the ability to convert the vast FlexQTL™ informational output into breeding-relevant knowledge. The workshop also provided an opportunity for understanding and advancing the results obtained to date by each of the crop teams.
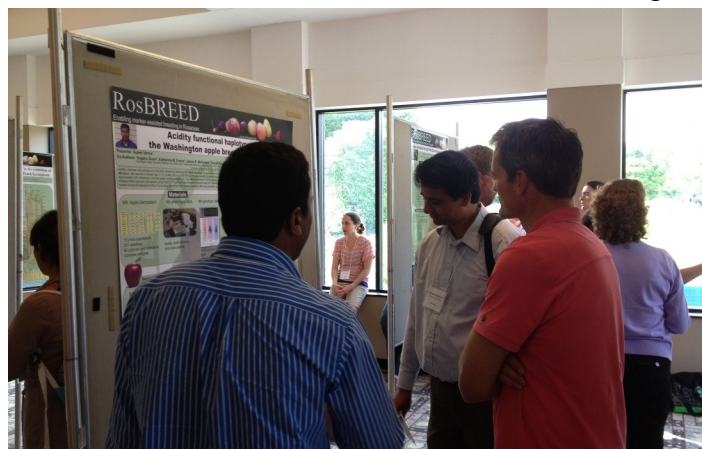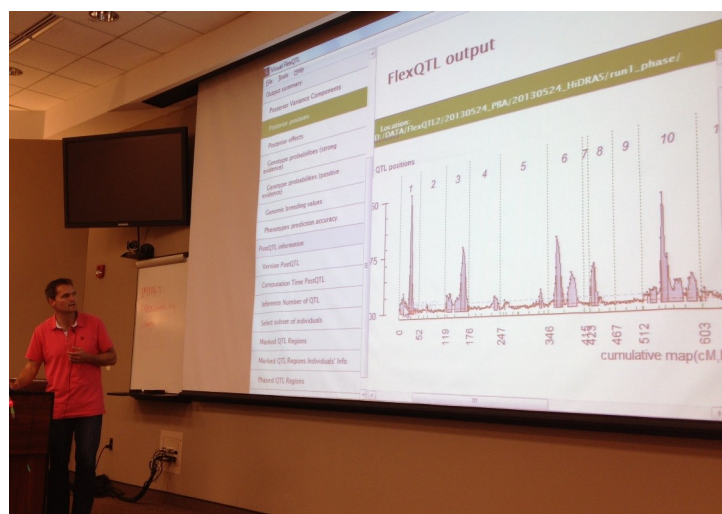

Sujeet Verma (left), one of the "RosBREEDlings" listens to valuable advice about research from Pedigree-Based Analysis Team members and statistics experts Marco Bink and Umesh Rosyara.
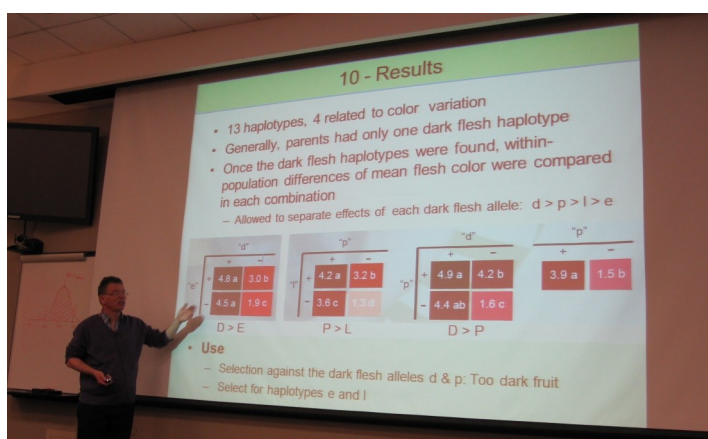
Eric van de Weg provides valuable feedback for each graduate student's poster.

Greg Reighard and Karina Gallardo discuss results of the Socio-Economic Team's surveys.

Marco Bink unveils the user-friendly VisualFlexQTL™.

FlexQTL™ is a statistical program that can perform QTL mapping, estimate identity by decent probabilities and breeding values in pedigreed populations.

VisualFlexQTL™ is a user friendly software program which provides a visualization interface for the FlexQTL™ output.

Be sure to attend our ASHS Presentation Series:
RosBREED Fruit Quality QTLs:
from Publications to Applications

When: 11:30am—1:30pm, Thursday, July 25th, 2013
Location: Springs Salon A/B, JW Marriott Desert Springs Resort, Palm Dessert, CA
*(attendees must register for ASHS)*

Talks include:

✸ Discovering a QTL: A major milestone or a stepping-stone into practical marker-assisted breeding? Cholani Weebadde

✸ You've just identified a QTL for a major trait of interest—what now?
 ⇒ QTL and QTL allele validation in cherry—Amy Iezzoni
 ⇒ QTL and QTL allele validation in apple—Sujeet Verma
 ⇒ QTL and QTL allele validation in peach—Ksenija Gasic

✸ Marker-assisted breeding for apple at the University of Minnesota and Washington State University—Jim Luby

✸ Discussion

For more information, access this link: ashs.confex.com/ashs/2013/webprogram/Session5713.html
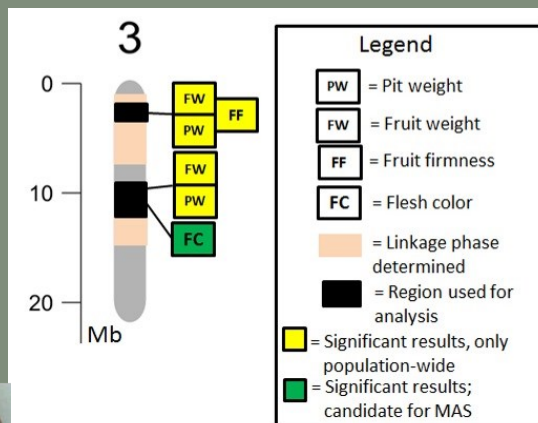
RosBREED by the numbers

4639

Number of datapoints collected in spring 2013 on seedlings for the University of Minnesota's apple breeding program. This was the program's first foray into routine marker-assisted seedling selection and the data was generated by Cameron Peace's Washington Tree Fruit Genotyping Lab at Washington State University, Pullman, WA. A combined total of 1693 seedlings from three families were screened for DNA tests for skin color, acidity, crispness, bitter pit susceptibility, and apple scab resistance.
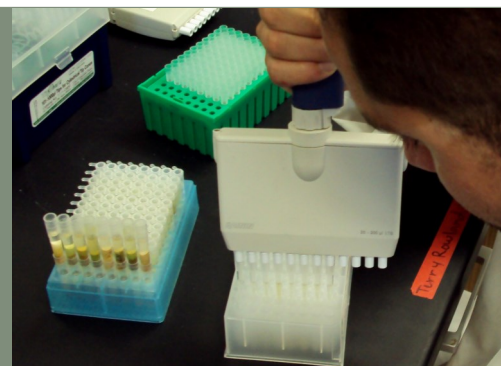
Terry Rowland conducts high-throughput DNA analysis of Minnesota apple seedlings.

471

Number of DNA markers painstakingly phased for eight polyploid tart cherry chromosome segments throughout the genome. DNA markers were phased for 328 tart cherry cultivars, ancestors, and representative seedlings. These regions are associated with fruit firmness, color, size, acidity, and phenological traits of bloom and maturity date.

Legend
PW = Pit weight
FW = Fruit weight
FF = Fruit firmness
FC = Flesh color
= Linkage phase determined
= Region used for analysis
= Significant results, only population-wide
= Significant results; candidate for MAS

Marker-assisted breeding in strawberry: Win-win public, private, and international partnerships for collaborative research

By Cholani Weebadde

Strawberry is one of the focus crops in RosBREED for enabling marker-assisted breeding (MAB) in Rosaceae despite notoriously difficult genetics with its 56 chromosomes and octoploid genome! For this challenge, collaborative research is and will continue to be the key to enabling MAB.

RosBREED's collaborations for MAB in strawberry started when the project took an ambitious step toward collecting important parent germplasm to represent major strawberry breeding programs in the U.S. and the world. This representative germplasm (referred to as the "Crop Reference Set" – CR Set) uniquely included the four most important mapping populations from Europe, in addition to their breeding parents. RosBREED's collaborators made it all possible! The four strawberry breeding populations were generously provided by RosBREED's European partners: INRA, France; PRI, The Netherlands; EMR, UK; and IFAPA-Centro de Churriana, Spain. RosBREED's first industry partner, Driscoll Strawberry Associates, substantially contributed by processing and multiplying the plant materials from Europe through their propagation facility in Watsonville, CA. What excited strawberry breeders was that this assembled germplasm exemplified how the different breeding programs were interconnected despite each having their own trait foci. In practical terms, DNA tests developed for strawberry using this germplasm could benefit any strawberry breeder worldwide!

Excellent collaborations between public and industry partners in the U.S. continued for evaluating performance of the entire CR Set in multiple locations in multiple seasons, using standardized phenotyping protocols (developed by RosBREED; Mathey et al., 2013) for traits of value. Work started with all partners being provided with germplasm, subsequently propagated and then phenotyped in five U.S. locations where three Demonstration Breeders (Jim Hancock, Michigan State University; Chad Finn, USDA-ARS-Corvallis; and Tom Davis, University of New Hampshire) and the two Associate Demonstration

Strawberry CRS Phenotyping Locations

Fig. 1. Locations in the U.S. where strawberry phenotyping occurred.

For genetic challenges, strategy developed through weekly conference calls....

Fig. 2. Locations of those who participated in weekly conference calls.

Breeders (Vance Whitaker, University of Florida and Phil Stewart, Driscoll Strawberry Associates) were located (Fig. 1). This propagation was a massive undertaking, as the CR Set consisted of more than 900 genetically unique individuals, and phenotyped for ten development and fruit characteristics for two seasons.

While phenotyping work was underway through public and private collaborations, RosBREED's Genotyping Team was busy forming public-private partnerships for developing genome-scanning capability. The team worked closely with geneticists in the U.S. and internationally for more than a year to decide upon a strategy to develop a reliable strawberry SNP-based array. RosBREED's European collaborators (Fig. 2) worked tirelessly with U.S. scientists (in particular, RosBREED Genotyping Team leader Nahla Bassil and Demonstration breeder Tom Davis), Pedigree-Based Analysis Team Leader Eric van de Weg, and Affymetrix, to devise strategies to develop the strawberry SNP array. RosBREED especially appreciates the efforts of our industry collaborator on this venture, Affymetrix, for taking up the challenge of developing a strawberry SNP array as a pilot project to test their platform for octoploids.

With these efforts, RosBREED is proud to say that we are currently in possession of a brand new strawberry SNP array, IStraw90® (for International Strawberry 90 K). The team is now working on analyzing the SNP data obtained with the array and implementing filtering criteria to identify SNPs with robust genotypes. Thanks to the collaborative efforts and judging by the experiences of developing arrays for the other focus crops of RosBREED, soon strawberry breeders will be able to increase the efficiency of breeding through MAB! How exciting – all resulting from great public-private international partnerships!!!

Mathey, M., Finn, C., Mookerjee, S., Gündüz, K., Hancock, J., Iezzoni, A., Mahoney, L., Davis, T., Bassil, N., Hummer, K., Stewart, P., Whitaker, V., Sargent, D., Denoyes, B., Amaya, I., and van de Weg, E. Large-scale standardized phenotyping of strawberry in RosBREED. Journal of the American Pomological Society (Accepted).
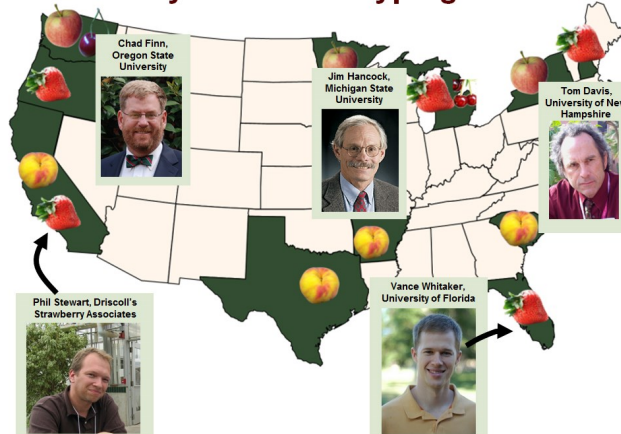
Breeder profile: Kate Evans
By Audrey M. Sebolt, Project Assistant

Fig. 1. Kate Evans, Wash. State University.
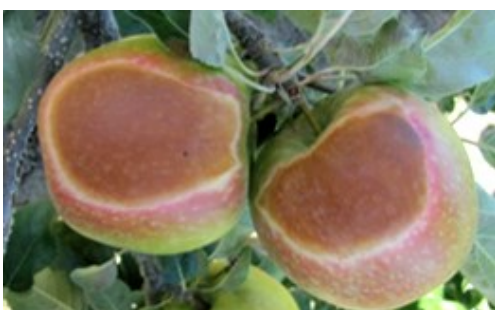

Fig. 2. Bitter pit.

Fig. 3. Sunburn on apples.

Fig. 4. WA 38 on display at the Fourth Annual RosBREED Advisory Meeting, January 2013.

Washington Apple Industry: Washington state produces 60-70% of the U.S. fresh consumption apples – this represents 44% of the total U.S. apple production (fresh consumption and processing) and supplies consumers both nationally and internationally with 'Golden Delicious', 'Gala', 'Fuji', 'Granny Smith', 'Braeburn', 'Honeycrisp', 'Cripps Pink', and 'Cameo®'. These cultivars were developed by the University of Minnesota, Australia, Japan, and New Zealand. Roughly 30% of the apples produced are 'Red Delicious'. Washington has successfully produced and marketed this cultivar because it is generally able to produce market-preferred larger sizes with a deep red skin color and successfully supply fruit throughout the year.

Over the last few years, consumers' preferences have expanded to include a broader range of fruit quality attributes. Washington growers recognized this change and grew concerned because the majority of the apples they produced fit essentially one similar taste profile; sweet and mild flavor with low acidity. This profile describes 'Red Delicious' as well as 'Fuji' and 'Cameo', offsprings of 'Red Delicious'. Growers partnered with Washington State University (WSU) to initiate a new apple breeding program. In 1994, Bruce Barritt, originally a strawberry and raspberry breeder, initiated the program in Wenatchee. In 2008, Bruce retired and Kate Evans (Fig. 1) took over the program.

Kate Evans' WSU Breeding Program: The Washington apple breeding program (WABP) aims to release new and improved cultivars that are specifically suited for the growing conditions of central Washington. Fruit quality, which comprises excellent eating quality, appearance, and storability, is the primary focus of the WABP. Kate is assisted by three graduate students, Yingzhu Guan, Julia Harshman, and Marco Galli, by scientific assistant Lisa Brutcher, and by research technician Bonnie Konishi.

Traits that are routinely evaluated in the WABP include flavor attributes, which are acidity, sweetness, and aroma, texture attributes of crispness, juiciness, and firmness, and incidence of storage disorders [especially bitter pit (Fig. 2), water core, soft scald, internal browning, and superficial scald]. Further traits are listed in RosBREED's apple phenotyping protocol.

One trait that has become increasingly critical in recent years is reduced susceptibility to apple sunburn. This disorder, caused by heat and light stress, causes economic losses of millions of dollars annually. Light-skinned apples, such as 'Granny Smith', are extremely sensitive to sunburn (Fig. 3) and new tree production systems which have trended towards high density plantings with smaller trees, have led to increased sunburn incidence. Disease pressure is very low in the major apple production regions in Washington, consequently, disease resistance is of much lower priority than in other production areas.

Currently, several elite selections have been planted in commercial grower trials in central Washington. The WABP program has released three cultivars over the last three years. 'WA 2', was the first to be released, in December 2009, and took 15 years to develop. 'WA 2' is very productive, has an appealing appearance, and excellent eating quality, storability, and shelf life. 'WA 5' was released in 2010 and took 16 years to develop. This apple has a good sugar/acid balance and is very juicy and crisp. 'WA 38' was released in early 2012 and is a large dark red apple with a remarkably firm, crisp, and juicy texture and excellent suitability for storage. This cultivar was sampled at RosBREED's Advisory Panel meeting in San Diego, January 2013, in a mock second-price auction (Fig. 4)!

High-throughput Marker-Assisted Seedling Selection (MASS): In 2010, a high-throughput system of DNA diagnostic screening of large seedling popu-

Fig. 5. Washington State University apple breeding program's 96-pot planting grid for streamlined DNA testing of large seedling populations.

lations for key traits of interest was first implemented in Kate's program. DNA tests for valuable traits are developed by Cameron Peace's program (WSU Pullman).

In 2013, the largest number of seedlings yet, 9000, were put through the DNA testing gauntlet. Newly germinated seedlings are grown in tubes in an 8x12 gridded tray. This grid mirrors a DNA sampling plate of tubes filled with desiccating silica gel (Fig. 5) into which collected leaf tissue is dropped. Following this relatively painless sample collection, plates are sent to the Washington Tree Fruit Genotyping Lab, established by Cameron Peace on WSU's main campus. Once the leaf tissue arrives to the genotyping lab, DNA is extracted and relevant DNA tests are performed. Currently, seedlings from specific progenies are screened for storability and firmness, crispness and juiciness, and acidity. The new harmonized 8x12 seedling pot and DNA tube format greatly reduces potential errors that can creep into any large-scale sampling project, improving the likelihood that data points match seedlings, so that Kate can be more confident about which seedling to cull. Screening seedlings prior to field planting is estimated to have saved the program $160K in field and labor costs in 2010-2012, although recent recalculations of conventional seedling selection costs indicate that the savings from MASS for this program may be several times more than $160k.

Thanks to the development and deployment of the International RosBREED SNP Consortium apple 8K SNP array v1, all of the WABP's founders have been genotyped genome-wide at high density. Careful analysis of this data with performance data has revealed much information about the jewels carried by each potential parent. Marker-assisted parent selection has been completed — crossing plans for spring 2013 utilized new DNA information with the aim of Kate and her crew to produce 20,000 seedlings enriched for superior genetics. DNA diagnostic markers have also confirmed the parentage of elite selections. One elite selection was thought to be 'Hatsuaki' × 'Cripps Pink,' but DNA markers determined this parentage to be incorrect. Fortunately, one parent has been successfully identified as 'Honeycrisp' (www.rosbreed.org/breeding/deliverables).

In the future, Kate would like to see the efficient development of robust diagnostic marker information by use of approaches and new technologies for combining several tests into one. With a breeding program on the cutting edge that already incorporates MAB and other new technologies, Kate is always thinking of new ways to streamline routine operations, improving her efficiency and delivering better outcomes faster. With Washington's huge apple industry behind the WABP's products, the rest of us as consumers have a delicious and healthy future to look forward to!

Meet Kate's Breeding Trainees: Yingzhu Guan and Julia Harshman
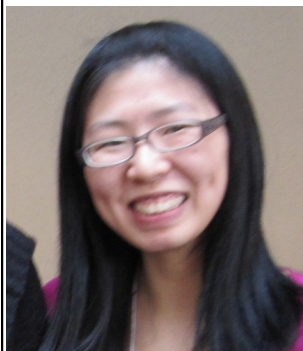
Yingzhu Guan

Yingzhu Guan, why did you choose Kate's program? I became interested in Kate's program after she was a guest lecturer in Cameron Peace's class. I was impressed with her more than 20-year breeding experience and her program sounded very interesting and promising.

What is your thesis project? My thesis is about identification of QTLs and marker development for sweetness in apple.

What benefits have you seen by being part of RosBREED? First, RosBREED is multi-national project, which connects the scientists from different fields together. It is a valuable experience. Second, RosBREED is also a great chance for a graduate student to meet other graduate students working in similar fields to know each other's projects, discuss the problems that we have, and help each other out! Third, RosBREED also supports graduate students by encouraging them to attend conference meetings in order to communicate with other scientists. So I feel so lucky to be part of RosBREED and appreciate the opportunity to work with so many great scientists.

Julia Harshman

Julia Harshman, why did you choose Kate's program? I chose Kate's program because I knew that I wanted to be a fruit breeder after my PhD. Her program was attractive to me because of its size, her experiences here and at East Malling Research, that she was working on both apples and pears, and that she was so adoptive of new technologies. As someone who will be hopefully entering the plant breeding community several years from now, it behooves me to learn how these new technologies could fit into a program. Kate is a wonderful professional and a great role model for how a plant breeder can successfully interface with many different research projects, other academics, and the industry.

What is your thesis project? My thesis project hasn't yet been determined.

What benefits have you seen by being part of RosBREED? One of the benefits for me, as someone who came in near the end and helped phenotype for the last season, is that I have access to the entire apple data set. While I pursue other projects that require hands-on time, such as harvesting, phenotyping, and storage, I will still be able to analyze this data and extract further information. It's an amazing opportunity to get to explore this data without having had to do all of the phenotyping.

Community Breeders' Page

Deliverables of the RosBREED project for U.S Rosaceae breeders: Part two
By Cameron Peace

In the last Community Breeders' Page, we began to describe the deliverables for breeders coming out of the RosBREED project. Deliverables were defined as "A tangible or intangible object produced as a result of a project that is intended to be delivered to a customer." You, breeders of Rosaceae (and perhaps other) specialty crops are the "customer." RosBREED's "objects produced" and made available to breeding programs like yours are in three categories: *Knowledge*, *Tools*, and *Germplasm*. For your convenience, a summary of the types of deliverables in each category is included at the end of this article.

Many deliverables are streaming out of RosBREED! Given the track record of molecular genetics of the last couple of decades, you'd be forgiven to assume that these represent knowledge only a molecular biologist could understand, tools only a DNA lab could decipher and use, and germplasm fit only for another round of genetic mapping research. But your assumptions would be wrong.

These are *breeding* deliverables. These are tangible and intangible objects improving the efficiency, accuracy, and creativity of U.S. Rosaceae breeding programs. See the examples below. Be amazed. Be inspired. Go to www.rosbreed.org/breeding/deliverables for a longer and growing list of Deliverables – evidence of the sea change in Rosaceae breeding.

Here's a taste:

"...this knowledge will be used... to target diversified acidity levels..."

"...a peach postharvest cold-storage evaluation protocol was developed and incorporated for standardized assessment of postharvest performance..."

"...knowledge of their genotypes was used in the 2011-13 crossing seasons to enable decisions about smarter ways to use them in crosses..."

"...we upgraded the DNA test, adapting it to high-throughput running..."

"...alleles associated with bacterial spot resistance... have been uncovered..."

"...alleles contributing to early and mid-season maturity were identified..."

"...successfully fathered thousands of breeding seedlings, infusing valuable alleles..."

"...this crossing strategy will be particularly useful for delivering potentially new early ripening cultivars that are large and firm..."

"...RosBREED was essential for the incorporation of molecular techniques into this conventional program..."

"...thus enriching the germplasm for large fruit size..."

Deliverable #25: Knowledge – evolution of the Arkansas peach and nectarine breeding program

To Whom: John R. Clark, peach, grape, and small fruit breeder, University of Arkansas

Story: The University of Arkansas peach breeding program began in the 1960s and since then has developed several peach and nectarine cultivars. The first peaches released were clingstone, non-melting with yellow flesh and destined for baby food. In recent years the objectives of the program have changed to focus on fresh-market cultivar development. To date, the program has released nine peach cultivars, five nectarine cultivars, advanced more than 800 selections, and generated more than 100,000 seedlings using controlled crosses. Individuals are evaluated in the field by scoring of various traits. This evaluation method has been a successful and simple way to characterize the germplasm. Recently, the program has incorporated new techniques to more accurately evaluate commercially important traits such as sugar content, acidity, flesh firmness, flesh color, and skin color. These techniques along with the implementation of DNA-based tools are increasing the efficiency and efficacy of breeding decisions within the program.
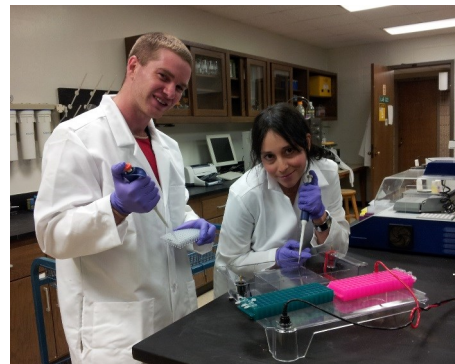
Terrence Frett and Alejandra Salgado

Community Breeders' Page cont.

Deliverable #13: <u>Tool – a DNA test for cherry leaf spot resistance for parent selection</u>

To Whom: Amy Iezzoni, tart cherry breeder, Michigan State University

Story: Cherry leaf spot is the most important disease affecting tart cherry in the major U.S. production regions, with multiple fungicide applications required to maintain healthy leaves on the trees. Leaf spot resistance is being bred into tart cherry from the wild species, *Prunus canescens*. Breeding Trainee Travis Stegmeir developed an SSR-based DNA test targeting a chromosome 4 region that can predict whether a cherry seedling will be resistant to cherry leaf spot. Those seedlings with the resistance-associated SSR allele can be used as parents to transfer the resistance more quickly to the next generation. All resistant tart cherry individuals must carry this *P. canescens*-derived SSR allele; however, a second as-yet unidentified locus is also needed to confer resistance.

Travis Stegmeir

Deliverable #8: <u>Knowledge – Honeycrisp haplotypes at key loci for flesh texture and apple scab</u>

To Whom: David Bedford and Jim Luby, apple breeders, University of Minnesota

Story: UMN breeders used knowledge, developed by Breeding Trainees Cari Schmitz and Matthew Clark, of the expected breeding values of UMN selections derived from 'Honeycrisp' for flesh texture and apple scab resistance to help decide which MN selections to use in 2013 crossing and how they should be matched with other parents.

Cari Schmitz, Jim Luby, and Matt Clark

Deliverable #24: <u>Germplasm – access to new genepools and potential cultivar-generating progenies with novel sources of self-fertility and early season ripening</u>

To Whom: Nnadozie Oraguzie, stone fruit breeder, Washington State University

Story: Two newly flowering seedlings of the cross 'Rainier' x 'Cristobalina' were used as parents in spring 2013. These seedlings were determined to carry the right alleles for a new source of self-fertility and large-size fruit by DNA tests and probably also carry alleles for early season ripening judging by their extreme phenotype. By making crosses with these two individuals, the valuable alleles were imparted to the next generation, synergistically combining with alleles for other traits from other parents. This next generation, grandchildren of the Spanish landrace 'Cristobalina', may result in exciting new cultivars to support the sweet cherry industry of the Pacific Northwest. The timely use of DNA information to identify the most suitable introgression lines to feed into crossing decisions is a model approach for introgression of valuable traits from many other exotic germplasm sources used in WSU's sweet cherry breeding program.

Nnadozie Oraguzie

Community Breeders' Page cont.

Deliverable #32: Tool – a DNA test for red stele resistance

To Whom: Chad Finn, strawberry and other small fruit breeder, USDA-ARS-HCRL, Corvallis, OR, and James Hancock, strawberry and blueberry breeder, Michigan State University

Story: Red stele is an important root rot disease affecting strawberry in U.S. production regions, where a combination of cultural and chemical control and use of disease-free planting stocks are required to maintain healthy plants. Strawberry cultivars have been bred for red stele resistance since the 1930s and resistance to one or a few races of the pathogen was established by controlled screening, a time-consuming process requiring maintenance of isolates of well-defined differential races of this pathogen. It is currently limited to a single program in North America, that of Andrew Jamieson in Agriculture and Agri-Food Canada, in Nova Scotia, Canada. Cultivars that are resistant to one or a few of the pathogen races can be suitable for some growing regions but are not resistant to the disease overall. However, as not all races occur in the same regions, resistance can be bred for certain target regions. An SSR-based DNA test targeting one of the resistance loci, *Rpf1*, was proven to predict whether a strawberry seedling will be resistant to a specific set of races of the pathogen. Those seedlings with the resistance-associated SSR allele can be used as parents to transfer the resistance more quickly to the next generation and can be crossed with cultivars that are resistant to other races to develop new cultivars with multiple sources of resistance to this disease.

Red stele infected roots; notice the brown roots. Photo by Andrew Jamieson.

Read the rest at www.rosbreed.org/breeding/deliverables. Bookmark this webpage and keep checking back in.

If you are touched by this project and have your own deliverables to describe, please send them to me at cpeace@wsu.edu for inclusion in this expanding list.

Types of RosBREED Deliverables

Knowledge: expanded **professional networks**, understanding of useful **concepts** and removal of action-limiting misconceptions, new breeding **strategies**, new **protocols**, information on **plant identity**, **socio-economic information** about the value of traits, information on **trait genetics**, **pedigree** information, information on **genetic potential** of breeding germplasm, and **experience** using DNA markers in breeding programs.

Tools: **DNA tests** and **software**.

Germplasm: access to new **genepools**, new **parents**, new **progenies**, promising **selections**, and **cultivar releases**.

RosBREED

www.rosbreed.org

Jewels in the Genome
By Amy Iezzoni, Project Director

What is a "Jewel in the Genome?"
- *An individual's genome is the full complement of genetic information that it inherited from its parents. Within this vast repertoire of genetic information, individual genes are being discovered that control critical production and fruit quality traits. As these valuable rosaceous gene discoveries are made and put into breeding applications, we will describe them in this column as "Jewels in the Genome."*

Maturity date differences for fresh-market sweet cherry cultivars allow growers to choose cultivars that will help them to capitalize on high prices at the start or end of the fresh-market season. Having a range of maturity dates also benefits consumers seeking a continuous summer supply of sweet cherries. Sweet cherry breeders therefore target cultivar development for specific maturity dates to fill gaps held by less desirable cultivars. In contrast, new tart cherry cultivars are preferred that ripen later in the season so the harvest does not overlap with that of sweet cherry, as most tart cherry growers also grow sweet cherries. As tart cherries are primarily processed for use in pies, jams and juices, for example, having a range of maturity dates for consumer fresh consumption is not an important criterion.

Having genetic knowledge of what crosses will yield a higher percentage of seedlings predicted to be in the targeted maturity date classes would help breeders more efficiently reach their maturity date goals. In peach, an important maturity date locus has been identified on chromosome 4 at ~44 cM (based on the *Prunus* T×E reference map) and a putative candidate gene has been identified at ~10.5 Mbp based on v.1 of the peach genome sequence (Dirlewanger et al. 2012). The same region has been shown in sweet cherry to contribute to the early ripening of 'Cristobalina' and 'Early Burlat' and the late ripening of 'Sweetheart' and 'Ambrunes'. In tart cherry, one allele at this locus contributing to early ripening was also found in the tart cherries 'Montmorency' and 'Ujfehertoi Furtos'.

With genetic knowledge of what cherry seedlings will ripen at specific maturity dates, breeders can plan crosses to maximize the probability of obtaining cultivars that target these maturity dates. Such an approach helps redirect resources to be spent on other critically important consumer-related traits such as the wonderful fruit flavors. Therefore, because knowledge of this genetic region will lead to the more efficient breeding of sweet and tart cherry varieties, it is chosen as one of RosBREED's "Jewels in the Genome."

Dirlewanger E, Quero-Garcia J, Le Dantec L, Lambert P, Ruiz D, Dondini L, Illa E, Quilot-Turion B. 2012. Comparison of the genetic determinism of two key phenological traits, flowering and maturity dates in three *Prunus* species: peach, apricot and sweet cherry. Heredity 109: 280-292.
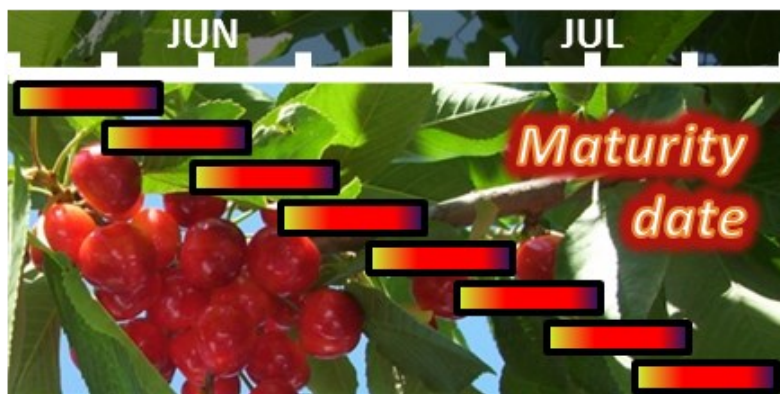

Nnadozie Oraguzie harvesting sweet cherries from a promising new selection with large firm fruit – unusually excellent attributes for so early in the season.

RosBREED: Enabling marker-assisted breeding in Rosaceae

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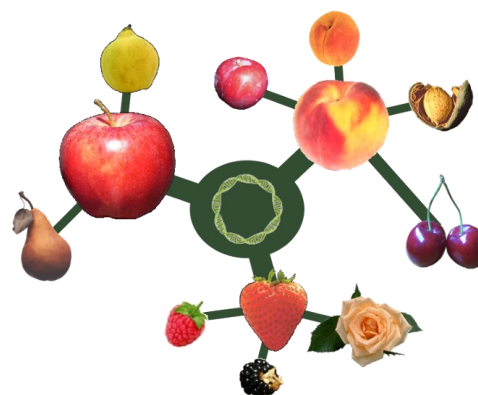
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Calendar of events

- July 22-25, 2013. American Society for Horticultural Science Conference, Palm Desert, CA.

- July 25, 2013. RosBREED workshop at ASHS on "RosBREED Fruit Quality QTLs: From Publications to Applications", Palm Desert, CA.