

RosBREED

Combining Disease Resistance with Horticultural Quality
in New Rosaceous Cultivars



V8/1 DEC 2017

In This Issue

Next generation: People, Problems, Places

Jim McFerson, Extension Team Leader, Washington State University



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Featured Team Member

Among the joys of participating in RosBREED have been the dynamic evolution of project participants, the emergence of new challenges, and the creation and application of new technologies, all enabled by the coming together of a worldwide research, extension, and stakeholder community with a common goal – developing superior new rosaceous crop cultivars.

elsewhere and place them into useful forms for the project's breeding programs. The Crop Postdocs are largely crop-specific, but also help develop strategies with implications for all Rosaceae, and beyond.



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Rosaceae Nemesis

In this newsletter, we feature examples across those areas, the next generation of people, problems, and practices that will contribute to the more efficient, effective, creative, and rapid breeding of new cultivars – cultivars that will exceed consumer expectations and help our industry stakeholders achieve a sustainable, prosperous future.

This newsletter's nemesis – Armillaria root rot – is not really a new one, because it is one of the 16 diseases originally targeted in RosBREED 2, but as authors Amy Iezzoni and Ksenija Gasic point out on p. 3, the rapidly-accelerating nature of the Armillaria threat to *Prunus* crops prompted our industry stakeholders to urge the project team to put aggressive effort into identifying novel sources of resistance to this ever more threatening pathogen. You will have to read the article to determine if we have been successful.



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Community Breeders' Page

Starting with the people, we feature a member of the Breeding Team, Bill Shane from Michigan State University (p. 2). Bill's growing participation in RosBREED fulfills a critical project intent – providing any breeder of rosaceous crops with the tools and knowledge base to conduct DNA-informed breeding. As he states: "I saw that RosBREED provided opportunities to interact with and learn from scientists knowledgeable about marker-assisted breeding. Involvement with RosBREED also opened up to me the use of technical services of RosBREED-allied laboratories for the analysis of markers."

Something else new pops up on p. 6, where project co-PD Cameron Peace suggests some new protocols for parent selection so breeders realize the full potential of their program's germplasm. Finally, while not in this issue, subsequent newsletters will be sharing some of the new careers that grad students from RosBREED 1 and 2 have followed (see bottom of p. 5). Along with superior new cultivars, it is a joy to see so many successful RosBREEDlings continue on to their exciting new careers, the next generation.



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Jewels in the Genome

Another group of new people is highlighted in our "Meet the Crop Postdoc Team" article (p. 5). The longest serving team member there is Lichun Cai, who began only in 2014, followed by Stijn Vanderzande in 2015, Jason Zurn in 2016, and Cassia Da Silva Linge in 2017. This talented group, distributed across the country, constitute the essential delivery vehicle to take upstream discoveries in RosBREED and

Along with the new, RosBREED offers something old in 2018 – returning to the lovely places where our annual get-togethers are held: San Diego and East Lansing, for our Advisory Panel and Project Participant meetings, respectively. Same old places, maybe, but with the likelihood of some new insights and the always wonderful opportunity to get together with rosaceous colleagues, solving problems new and old.



Fig. 1. Bill Shane in his propagation nursery, Benton Harbor, MI. Photo credit: Bill Shane

Featured Team Member

Bill Shane

Audrey Sebolt, Michigan State University

Michigan State University (MSU) is the proud home of what has been considered the gold standard of peach cultivars, ‘Redhaven’, which was bred by MSU pomologist Stanley Johnston and released in 1940. It was an instant success as it was the first red-skinned commercial peach cultivar. At the time Michigan primarily grew ‘Elberta’, considered to be rich in peach flavor; however, fruit are yellow-skinned, not very sweet, and difficult to handle when ripe – fruit need to be shipped green.

Despite the Michigan peach industry being considerably smaller than those of California and South Carolina, it produces 21.2 million pounds of peaches and is valued at more than \$9.2 million (NASS

2016). ‘Redhaven’ is still widely grown today in Michigan but new disease-resistant cultivars would be extremely beneficial for Michigan fruit growers and consumers.

Today the MSU peach breeding program is led by Bill Shane (Fig. 1). His predecessor was Amy Iezzoni, who stepped down from the program in order to devote more time to the tart cherry breeding program. As part of this “handoff”, Amy left behind a collection of elite selections to test further. Included was a seedling that matched a later season maturity window occupied by ‘Loring’, which has poor coloring. This elite seedling, released as ‘Beaumont™’ in 2007, ripens ~18 days after ‘Redhaven’ but has 60-90% red blush. It is currently grown on limited acreage in Michigan and other states.

Soon, Bill hopes to add additional new cultivars to the industry – he is on the cusp of releasing several new cultivars, both yellow and white melting flesh types, with the size, blush, firmness, bacterial spot resistance, and consistent yield needed for the wholesale peach market (Fig. 2).

The MSU peach breeding program is located at the South West Michigan Research and Education Center in Benton Harbor and is supported by the Michigan Peach Sponsors, a nonprofit organization supported through donations that funds research and the promotion of Michigan peaches.

The breeding program’s traits of interest include: harvest window timing, delayed bloom, winter hardiness, ability to withstand shipping, increased red blush (more than 70%), firm flesh, and low tendency to mealiness. Disease resistance to bacterial spot is also an increasingly critical trait. Peach bacterial spot is a serious leaf and fruit disease of peaches, nectarines, and apricots. It can be very difficult to manage on susceptible cultivars grown in sandy sites. Growers are on the lookout for improved bacterial spot resistant cultivars with all the desirable fruit and yield characteristics.

Therefore, Bill’s training in plant pathology is quite helpful towards developing disease resistant cultivars! Bill obtained a bachelor’s degree in botany and plant pathology from MSU, an MS in plant pathology from North Carolina State University, and a PhD in plant pathology from the University of Minnesota.

Advances in new technologies allow the development of new disease-resistant cultivars to be sped up through DNA testing, which allows more desirable seedlings to be moved forward. Currently, with the help of RosBREED scientists, several DNA tests are allowing peach breeders to be more efficient. RosBREED’s Clemson University group has developed a DNA test which confirms whether a plant is susceptible or resistant



Fig. 2. MSU peach breeding program elite selections. Photo credit: Bill Shane

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to bacterial spot. Bill has submitted many of his elite parents and elite selections for DNA testing within RosBREED and is, whenever feasible, using resistant elite parents for his crosses.

Unfortunately, the cost to conduct large-scale DNA tests is a prohibitive factor for the MSU peach breeding program and is the reason why Bill is not using DNA testing to screen the thousands of seedlings he generates.

Bill is one of five RosBREED peach breeders. Below are his thoughts about the project.

Why did you choose to be involved with RosBREED?

I saw that RosBREED provided opportunities to interact with and learn from scientists knowledgeable about marker-assisted breeding. Involvement with RosBREED also opened up to me the use of technical services of RosBREED-allied laboratories for analysis of markers.

What successes do you hope to see from RosBREED?

Better understanding of the genetics and techniques for the breeding and characterization of *Prunus* species. More efficient selection of parents and crosses to achieve the goal of developing improved varieties for the commercial peach industry.

Have you already benefited from RosBREED?

I have learned a great deal about marker-assisted breeding while participating in the yearly RosBREED Participant meetings. These meetings have been great way to meet and network with other scientists in this field.

My breeding program at Michigan State University has benefitted tremendously from the marker-assisted analyses (DNA tests) for peach bacterial spot resistance done initially by RosBREED cooperators at Washington State University and Clemson University. I have been able to make more informed choices of parents and elites with the bacterial spot resistance markers. We have saved much time and work, and made good progress in developing peach varieties with improved disease resistance for the peach industry.

What is one thing (or a few) your colleagues don't know about you?

I think it is great fun to walk in the Michigan upper peninsula woods and get semi-lost for the better part of a day. On one of these jaunts I found myself face to face with a rather large wolf.

Citation:

NASS. 2016. Noncitrus Fruits and Nuts 2016 Summary, <http://www.nass.usda.gov/>

Rosaceae Nemesis Finding a Solution to Armillaria Root Rot

Amy Iezzoni, Project Director, Michigan State University; Ksenija Gasic, Prunus Team Leader, Clemson University

Armillaria root rot fungus is prematurely killing stone fruit trees throughout many U.S. production regions. This Rosaceae nemesis has been particularly damaging in South Carolina and Georgia on peach, in Michigan on cherry, and in California on almonds (Figs. 3, 4). *Armillaria* is now a ubiquitous and rapidly-advancing threat in these regions and is the leading cause of premature tree decline and death in these stone fruit crops.

This soil-borne fungus enters the roots and grows through to the tree crown, damaging and clogging the host tissues, thereby reducing and ultimately eliminating the flow of water and nutrients to the tree (Fig. 5). Typically, infected trees collapse as they reach their maximum production capacity. Further, the orchard land is rendered unsuitable for subsequent stone fruit production as the fungus can live for years on root pieces in the soil, forcing prime orchard land out of production. Therefore, this disease was included in RosBREED with the goal of developing *Armillaria* resistant rootstocks. [See RosBREED Newsletter Mar 2016. Wilson et al. Rosaceae Nemesis: *Armillaria* Root Rot.]

Even worse, *Armillaria* has a broad host range that includes many other tree fruit and forest species and sources of resistance are not readily available for any of them. For example, all peach and cherry selections tested to date have been highly susceptible.



Fig. 3. Tart cherry tree dying from *Armillaria* root rot. Photo credit: Erin Lizotte

The most promising *Armillaria* resistant rootstock for peach is an interspecific peach-plum hybrid 'MP-29' (Beckman et al. 2012). However, this rootstock is currently not widely accepted by growers because finished trees have been difficult to supply to the industry and being semi-dwarfing requires growers to transition their orchard operations to high density systems. In almond, the rootstock 'Krymsk® 86', which is also a peach-plum hybrid, appears to have



Fig. 4. Peach orchard afflicted with *Armillaria* in a replant site. Photo credit: Guido Schnabel

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some tolerance to *Armillaria*, but most of the orchards planted on this new rootstock are young. Unfortunately, this rootstock is susceptible to root knot nematode, limiting its use in California's San Joaquin Valley. For cherry, the ornamental species *P. maackii* exhibits *Armillaria* resistance in laboratory assays, although field resistance has not been confirmed.

Given the severity of the *Armillaria* threat and complete lack of proven rootstock options for growers, in 2016 stakeholders urged RosBREED scientists to accelerate their search for new sources of resistance. Amy Iezzoni and Ksenija Gasic quickly teamed up to seek new resistance sources for their rootstock breeding efforts on cherry at Michigan State University and peach at Clemson University, respectively. The majority of *Prunus* species are native to Europe and Asia and their focus turned to the *Prunus* germplasm collection maintained in the USDA-ARS National Clonal Germplasm Repository in Davis, CA. In spring 2017, Iezzoni and Gasic identified 91 *Prunus* accessions, representing 32 species, to screen for *Armillaria* resistance.

They immediately received enthusiastic support from the USDA-ARS *Prunus* curator, Carolyn Debus, who single-handedly collected 30 fruit from each of the 91 accessions (Fig. 6). The plant materials were shipped to Clemson University, where the Clemson team germinated seeds from each accession in vitro to provide plants for inoculation.

The search for new sources of resistance to *Armillaria* in previously uninvestigated *Prunus* species is one outcome of the increased effort to find a solution to the *Armillaria* problem. A strategy for further effort was hatched at the RosBREED Advisory Panel (AP) Meeting in January 2017, when industry AP members Chalmers Carr (peach: SC), Phil Korson (cherry: MI) and Bob Curtis (almond: CA), along with science AP member Dan Kluepfel (USDA-ARS: CA), floated the idea to hold an *Armillaria* Summit in summer 2017 to share expertise and coordinate activities across all *Prunus* crops. Thanks to Dan's leadership and support from the industry groups, the first U.S.-wide *Prunus* *Armillaria* Summit was held on UC-Davis campus August 10-11,



Fig. 6. Carolyn Debus, USDA-ARS *Prunus* curator, in the repository *Prunus* collection standing next to an accession of *P. hortulana*, a wild plum species, that is one of the species being screened for *Armillaria* resistance. Photo credit: Amy Iezzoni

2017. This Summit was attended by around 50 participants and included growers, tree fruit nursery representatives, and extension agents and researchers representing a vast array of expertise (horticulture, pathology, breeding, germplasm, genomics, tissue culture, and molecular biology).

Current knowledge and knowledge gaps, common challenges, and areas for future research were discussed. The outcomes: The group agreed on the adoption of a standard *Armillaria* screening protocol to make results for the host-pathogen interactions comparable across research groups and crops. There was an increased commitment to work with the Davis Clonal Repository to search for new sources of resistance and make crosses to incorporate resistance into graft compatible rootstock backgrounds. Additionally, the group committed to leverage strengths and expertise across states, crops, and institutions to undertake an aggressive research effort to search for solutions to this problem. The Clemson University team is taking the lead in formulating and submitting a USDA-SCRI planning grant to build momentum.

This outcome illustrates the synergistic role that national community-wide research projects like RosBREED can play in reacting quickly and successfully to emerging challenges such as *Armillaria* root rot. It stands as a superb example of the intent of the SCRI program, with direct benefits to industry stakeholders. Now that a core of RosBREED team members have mobilized and leveraged existing knowledge and ongoing professional relationships for this, the catastrophic impact of a disease as loathsome as *Armillaria* root rot might be lessened.

References

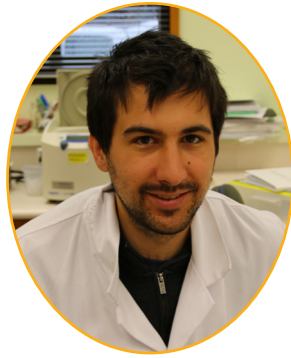
Beckman TG, Chaparro JX, and Sherman WB. 2012. 'MP-29', a clonal interspecific hybrid rootstock for peach. *HortScience* 47: 128-131.



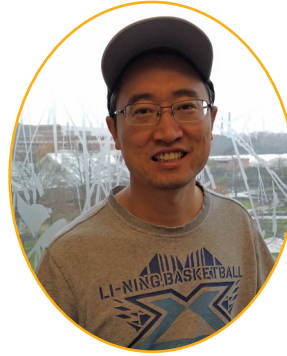
Fig. 5. *Armillaria* symptoms on lower trunk.. Photo credit: Erin Lizotte



Jason Zurn
USDA-ARS NCGR



Stijn Vanderzande
WSU



Lichun Cai
MSU



Cassia Da Silva Linge
Clemson

Meet our Crop Postdoc Team

Jason Zurn (USDA-ARS NCGR), Stijn Vanderzande (Washington State University); Lichun Cai (Michigan State University); and Cassia Da Silva Linge (Clemson University)

Creating positive breeding outcomes by leveraging DNA information is a key focus of RosBREED. Using DNA information to its full potential requires bridging the gap between molecular scientists and breeding programs. In RosBREED, a team of four crop postdocs are building this bridge by providing support for breeding programs to interpret and apply DNA information to improve horticultural quality and disease resistance.

The crop postdoc team comprises Cassia da Silva Linge, Jason Zurn, Stijn Vanderzande, and Lichun Cai. Each is responsible for a different set of crops and the specific needs of each breeding program. Cassia, who received her Ph.D. at the University of Milan, Italy is the most recent postdoc to join RosBREED, in spring 2017. She works on peaches and non-cherry *Prunus* crop species at Clemson University under the Stone Fruit Breeding Team leader Ksenija Gasic.

Jason obtained his Ph.D. at North Dakota State University and joined RosBREED in spring 2016. He works with Nahla Bassil at the USDA-ARS National Clonal Germplasm Repository in Corvallis, OR on strawberry, blackberry, rose, and pear. Stijn started working on RosBREED in the fall of 2015 after completing his PhD at the KU Leuven, Belgium. He works under the guidance of Cameron Peace at Washington State University, focusing on apple and cherry.

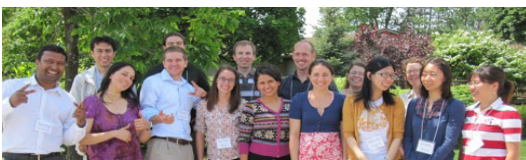
Lichun received his PhD from China Agricultural University in Beijing and was the first to join RosBREED, in Spring, 2014. He is developing new strategies to analyze data across all RosBREED crops, supervised by Amy Iezzoni at Michigan State University.

The team meets monthly via videoconference to update their activities and approaches for both common goals and crop-specific challenges. The common goals of the crop postdocs are to: 1) identify genetic factors associated with important traits; 2) develop diagnostic tests to facilitate more efficient breeding for these traits; and 3) run and interpret DNA tests to assist breeders in using DNA information in their programs. The postdocs are accomplishing these goals by using newly developed genotyping tools like SNP arrays, Genotyping-by-Sequencing, and Targeted Sequencing, along with the statistical analysis software FlexQTL™. They focus on populations that represent the germplasm developed by RosBREED demonstration breeders.

Some of the crop postdocs' recent accomplishments include discovering a new rose black spot resistance gene (Zurn); dissecting the genetic components of bloom time in tart cherry (Cai); developing an improved consensus map for peach to use as a reference for pedigree-based QTL analysis (Da Silva Linge); and detecting and developing 9,000 new SNP markers to be used in addition to the cherry 6K SNP array (Vanderzande).

A large part of the team's work currently revolves around ensuring that the large amounts of genotypic data generated by RosBREED have been properly curated. Each postdoc is working diligently to double-check allele scores and upload the data to the Genome Database for Rosaceae (www.rosaceae.org) for the use of other rosaceous scientists around the world.

All four crop postdocs work closely with breeders, other postdocs, and grad students to achieve the common goals of RosBREED. Additionally, they serve as liaisons between and among several RosBREED teams; DNA-Informed Breeding, Data Management, DNA Testing, and the several Crop Breeding teams to maximize data utilization for their target crops. To date, the postdocs' work has helped identify 27 trait loci and integrate 30 diagnostic tests into breeding programs – with many more to come!



Where are these former RosBREED grad students now? Check out the next Newsletter...

Community Breeders' Page

Which jewels are in your parents' genomes? – a Technology Interfacing article

Cameron Peace, DNA-Informed Breeding Team Leader, Washington State University

'Tis the season to know your parental germplasm. Consider it a Christmas present to yourself. Gift-wrapped inside prospective progenitors, valuable trait locus alleles – jewels in the genome – await their chance to fall far from the tree and fulfill their potential in the wide world. And (last cliché, I promise!) inherited alleles are the gift that keep on giving.

Determining which crosses to make is a far-reaching decision for a breeder. These decisions are helpfully informed with knowledge of which trait locus alleles are carried by each individual in the parent pool. Such alleles are those associated with statistically significant effects on traits of interest. Other valuable information at the DNA level is how related parents are, including which parts of their genomes are identical.

MTL alleles Self-fertility and cross-compatibility, fruit color type, columnar

vs. normal tree shape, peach vs. nectarine fruit type, and resistance/susceptibility to many diseases are examples of traits determined by phenotypic contrasts between huge-effect alleles, sitting at genomic regions we call Mendelian trait loci (MTLs). The MTL alleles each parent carries obviously has a major impact on the qualitative kinds of offspring possible. Not realizing that two crossed parents are each heterozygous at the G locus (peach vs. nectarine) will lead to unintended types for a sizeable chunk of the resulting family.

QTL alleles Many other traits of breeding interest have large-effect alleles segregating in breeding germplasm, but phenotypic contrasts among them only partially account for observed and breeding-relevant phenotypic variation. The genomic regions holding such quantitative-effect alleles are what we call quantitative trait loci (QTLs). With

knowledge of QTL alleles distributed among parents, you can avoid making undesirable allelic combinations in offspring. Or you can enrich new families with desirable alleles and thus increase the probability of eventual commercial success. Or you can create new allelic combinations to see what they conjure. And you'll be able to plan for which DNA tests should be run on the newly generated families for maximized selection efficiency and accuracy.

Not accounted for Unaccounted-for variation can be contained in other significant-effect QTLs, and/or in numerous tiny-effect trait loci individually non-significant but cumulatively explanatory (let's call them infinitesimal trait loci, ITLs), and/or micro-environmental factors variably experienced among individuals.

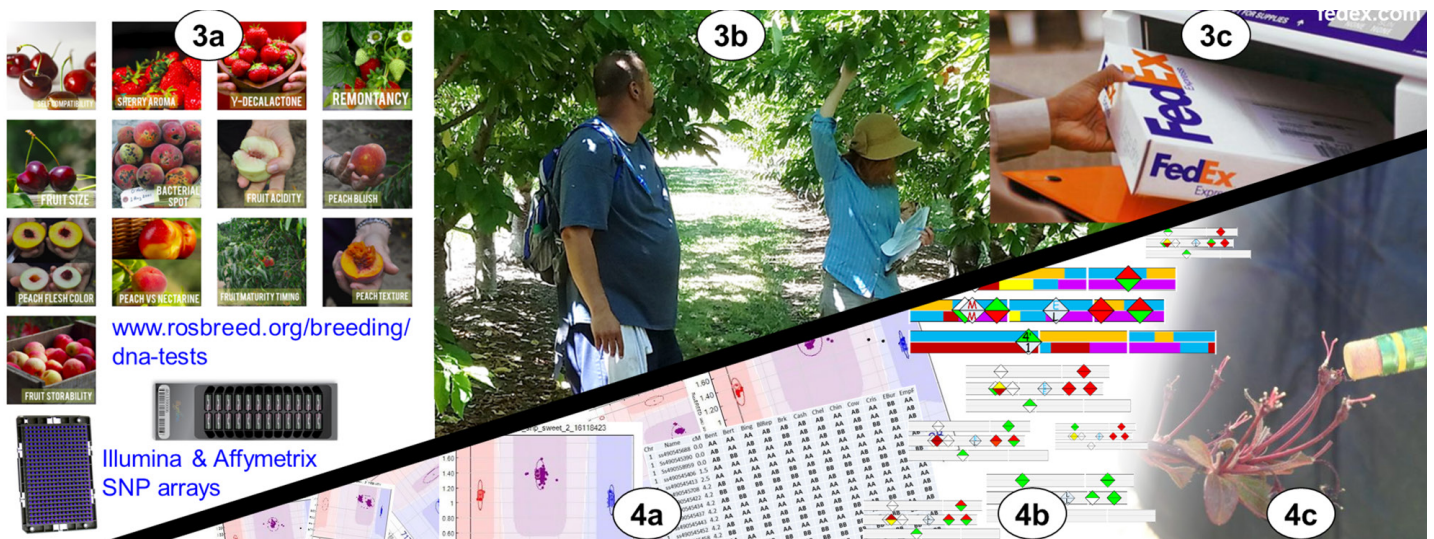
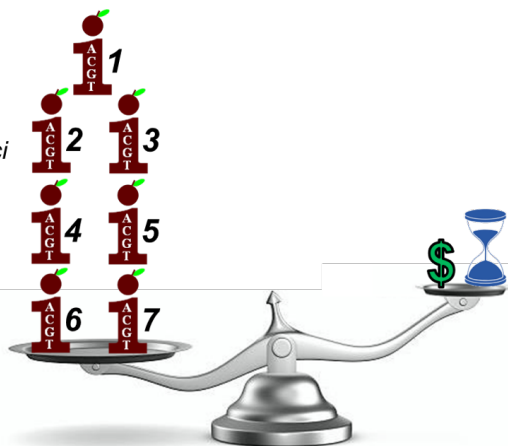


Fig. 7. Finding out which are the jewels in your parents' genomes. First, peruse DNA testing and DNA profiling opportunities for your crop (3a). Then sample tissue for your parents (3b); at this time of year, forcing leaves is probably needed. Send samples to your service provider (3c). Look forward to the arrival of raw genotypic results (4a). These data can be converted to specific, desired genetic information (such as the haplotype mosaics shown here) – with your connection to RosBREED help or with your own in-house expertise (4b). Finally, you can use the knowledge gained to help make creative and effective crosses (4c).

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BENEFITS

1. Alleles carried at valuable trait loci
2. Value of "genetic background"
3. Identity
4. Parentage
5. Ancestry
6. Homozygous genomic segments
7. In common genomic segments



COSTS

- Time/cost to locate parent plants, collect leaf samples, label, keep samples cool & moist
- ~\$1200 per 24 samples
- Time/cost to ensure data is translated to useful genetic information
- Time and attention to use DNA info in breeding decisions optimally

DNA TESTING OR DNA PROFILING YOUR PARENT GERMPLOSM

Fig. 8. Using current tools to find out which jewels are carried by members of your parent pool has some further benefits you might not have thought of. Even gaining DNA information for the main purpose is well worth the costs in money and time.

Jewels to work with As long as... (1) the MTLs and QTLs have been located, (2) their alleles have been differentiated and effects assigned in germplasm representing your program, (3) genotypic assays have been performed on parents, and (4) you're in communication with a molecular genetics expert such as a RosBREED Crop Postdoc to help translate the results ...you'll know what jewels you have to work with.* The first two steps require upstream research by scientists allied to your program. The third and fourth steps are up to you (Fig. 7).

DNA testing and DNA profiling of your parents "DNA testing" (Box 1) is an efficient and rapid way to find out the trait locus alleles in each parent. Besides this evaluation of genetic potential for known genetic components of commercial performance, locus-specific assays can also be used to characterize germplasm in terms of identity or relatedness.

"DNA profiling" (Box 1) is an approach I recommend for elite material. Costs** are far outweighed by benefits (Fig. 8). DNA profiling is most powerful for both evaluation (of genetic potential for performance, encompassing MTLs, QTLs, and ITLs) and characterization (of identity/relatedness). The power comes from being genome-wide at high resolution. Service providers for DNA-based diagnostics in the U.S. (<https://www.rosbreed.org/breeding/dna-tests/testing>) are up to date on available DNA tests and DNA profiling assays. They are standing by to provide you transformative DNA information.

*And, you'll also have information from ITLs, as long as (1) training populations are assessed, (2) prediction algorithms relevant for your germplasm and target growing conditions are established (preferably on a regular basis), (3) genome scans have been performed on parents, and (4) an expert is available to translate the results ...you also have quantitative predictions of genetic potential.

**DNA profiling costs for RosBREED SNP arrays: ~\$50/individual for peach, apple, pear, cherry, strawberry; \$85 for rose. Includes tissue sample transport, DNA extraction, arrays, array reading, and automated genotype calling.

Box 1

DNA testing

= use of locus-specific assays that target trait loci

DNA profiling

= use of genome scans such as SNP arrays to reveal genome-wide patterns of allelic variation and recombination over generations

[\[https://www.rosbreed.org/sites/default/files/RB2_Newsletter_Oct_17.pdf\]](https://www.rosbreed.org/sites/default/files/RB2_Newsletter_Oct_17.pdf)

Community Events

RosBREED Advisory Panel Meeting

11 January 2018
San Diego CA

RosEXEC

14 January 2018
San Diego CA

RosBreed Project Participant Meeting

6-8 Mar 2018
East Lansing MI

Rosaceae Genomics Conference 9

26-30 June 2018
Nanjing Agricultural Univ
Nanjing, China
www.rgc9.org

ASHS

31 July-3 August 2018
Washington DC

Cultivar Corner

'Florida Beauty'

Inventor: Vance Whitaker, UF/IFAS, Gulf Coast REC, Wimauma, FL



Vance Whitaker (right) and Luis Osorio (left) are about to brave torrential Florida rains and walk their plots. Photo credit: Sujeet Verma.

When was 'Florida Beauty' released?

2017

What makes 'Florida Beauty' special?

'Florida Beauty' is the first day-neutral (perpetual flowering) variety released from the University of Florida. Its unique combination of day-neutrality, low chill requirement and compact plant habit make it ideal for the early planting period in Florida, approximately Sept 20 to Oct 1. When planted during this period, fruit harvest will begin in mid-November and continue steadily thereafter until the end of the season.

What is the pedigree?

Queensland Australia selection 2010-119 (female parent) by 'Florida Radiance'

When was the cross made?

2012

What is the size of the family from which 'Florida Beauty' was selected? Do any siblings from this cross have commercial potential?

'Florida Beauty' arose from a cross from which only 30 seedlings were tested. Two other full-siblings were selected for testing in the next year, but only 'Florida Beauty' ultimately demonstrated commercial potential.

How has this cultivar been used in RosBREED?

A DNA test for day-neutrality was validated in several UF breeding selections, including 'Florida Beauty', which has the diagnostic allele associated with the attribute. It also possesses resistance to *Phytophthora cactorum* conferred

by the *FaR_{Pc}2* locus, for which DNA tests have been developed in RosBREED.

Any other interesting notes about 'Florida Beauty'?

Because of its excellent fruit quality, 'Florida Beauty' will qualify for retail marketing under the SWEET SENSATION® brand. It is distinguished from 'Florida127' by its smaller size and superior rain tolerance. The fruit also have an excellent conical shape and an even medium-red color.

Why should growers plant 'Florida Beauty'?

When planted early in Central Florida, it will begin flowering more quickly and have a better yield distribution than current cultivars, not to mention excellent fruit quality. It probably does not have sufficient fruit size or total season yield to be commercially grown in the day-neutral production areas of



'Florida Beauty' Photo credit: Vance Whitaker, Univ Florida IFAS

the central coast of California, but it would be interesting to see it tested in more northern, temperate locations where day-neutral varieties are cultivated in the summer months.

References:

Seijo, T., J. Mertely, V. M. Whitaker, and N. Peres. 2013. Evaluation of strawberry cultivars and advanced selections for resistance to anthracnose and Botrytis fruit rots, 2012–13. Plant Dis. Mgmt. Rep. 8:SMF029. Online publication. doi:10.1094/PDMR05.

Jewels in the Genome

Powdery Mildew Resistance in Sweet Cherry

Amy Iezzoni, Project Director, Michigan State University; Cameron Peace, Co-Project Director, DNA-Informed Breeding Team Leader, and interim sweet cherry breeder, Washington State University

Powdery mildew of sweet cherry, caused by *Podosphaera clandestina*, is a major disease affecting sweet cherry production in low-humidity regions such as the Pacific Northwest. In susceptible cultivars, infected leaves and fruit become covered with a white fungal growth, reducing vegetative growth and rendering the fruit unmarketable. Fungicides are used to control the disease, but this comes at a high financial cost and the risk that the fungus will develop fungicide resistance. Season-long disease control is required initially to manage foliar infection and subsequently to prevent fruit infection. Managing powdery mildew is especially challenging for late-season cultivars, as they may require fungicide protection for as long as three months. Therefore, developing cultivars with reduced susceptibility to powdery mildew (or, dare we hope, resistance) is a high priority for the breeding programs in low-humidity production areas.

Fortunately, there is genetic variation in susceptibility for this disease within sweet cherry germplasm available in the U.S. A genetic study led by the RosBREED sweet cherry team at Washington State University (WSU) verified the presence of a locus named *Pmr1*, located near the top of sweet cherry chromosome 5, that acts as a Mendelian trait locus for both

foliar and fruit response to the powdery mildew infection. The dominant allele at this locus that conferred resistance to both foliar and fruit infection was derived from the resistant cultivar Moreau and the small-fruited Mildew Immune Mazzards which are available from the *Prunus* collection at the USDA-ARS National Clonal Repository, Davis, CA. Any sweet cherry individual with one or two resistance alleles for *Pmr1* exhibited no foliar and fruit infection, even when surrounded by infected individuals with no resistance alleles (Fig. 9).

A DNA test for routine screening for alleles at *Pmr1* conferring fruit and foliar resistance to powdery mildew has been developed and is currently in use in the sweet cherry breeding program at WSU. Therefore, because knowledge of this genetic region will lead to the more effective breeding of sweet cherry cultivars for fruit and foliar powdery mildew resistance, it is featured as a RosBREED “Jewel in the Genome”.

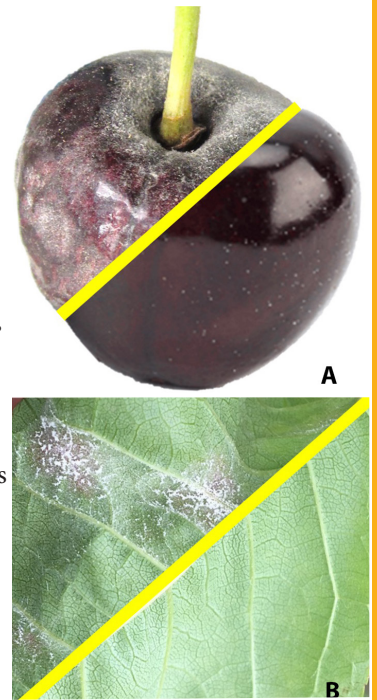


Fig. 9. Susceptible vs. resistant: A. sweet cherry fruit, B. sweet cherry

RosBREED by the Numbers

2730

Number of *Prunus* seeds* sent from the USDA-ARS Davis genebank to undergo Armillaria resistance screening this winter/spring.



47

Number of *Prunus* seedlings* and cultivars planted this fall to expedite the development of Armillaria resistance screening protocols.



2624

Number of strawberry seeds produced from crosses between parents screened for resistance to *Macrophomina*, *Fusarium*, and *Verticillium* wilt.**

* Peach, sweet cherry, and tart cherry

**Populations expected to segregate for resistance to these diseases will be grown, phenotyped, genotyped, and analyzed for QTLs

Meet our Advisory Panel Members

Our Advisory Panel (AP) members are a critical part of RosBREED, as they provide constructive feedback and guide our priorities. They dedicate not only a day (plus two for travel) to our AP meetings in January, but they also are called upon during the year to provide feedback to questions our project members have.

Thanks so much to all our AP members—see you in January!



Peter Hirst
Extension Advisory
Panel Member

What is your job description?

I am a professor in the Department of Horticulture and Landscape Architecture at Purdue University. I have statewide extension responsibilities for tree fruit, conduct research on apples, and teach horticultural production and plant physiology. My research focuses on flowering and fruit development and also on sensing and automation.

Why are you interested in RosBREED?

The genetics and genomics toolbox now has tools that have wide application for understanding fruit development at a level that has previously not been possible. Understanding flowering and fruit development at such a level offers the potential to fine tune crop management practices as well as providing more fundamental knowledge of tree physiology.

How do you feel you can contribute to RosBREED?

I provide knowledge of pomology and a conduit for tools developed by RosBREED to the pomology research community. I also provide a linkage to industry through my extension role.



Phil Simon
Science Advisory
Panel Member

What is your job description?

I am a USDA-ARS Research Geneticist and Professor of Horticulture at the University of Wisconsin, Madison. My research in vegetable genetics and breeding has focused on fresh market carrot improvement, targeting improved flavor and nutritional quality, nematode, disease and abiotic stress resistance, and genetic mapping of these and other traits.

Why are you involved with RosBREED?

I was asked to serve on the RosBREED Advisory Panel, and I am glad to do so. RosBREED has demonstrated the value of bringing public sector horticultural crop researchers closer together with the crop production industry to accelerate the development and transfer breeding technologies for crop improvement to users of those technologies in the field. So being on the RosBREED Advisory Panel provides me with the opportunity to not only share my ideas with RosBREED breeders, but also for me to learn about new ideas I may be able to apply in improving the crops I work with.

How do you feel you can contribute to RosBREED?

I have background experience in horticultural crop breeding, genetics, and molecular marker development with research in crop quality, production traits and germplasm development that may be pertinent to improving rosaceous crops.



Bill Dodd
Industry Advisory
Panel Member

What is your job description?

My family owns Hillcrest Orchards in Amherst, OH, an 85-acre farm that is mostly a seasonal agritainment operation. I am also the President of the Midwest Apple Improvement Association (MAIA), a grass roots, grower owned apple breeding program. MAIA has patented and released seven new selections, including 'EverCrisp'.

Why are you involved with RosBREED?

The apple industry needs to increase per capita consumption of apples. I believe that RosBREED is developing tools to help breeders and the apple industry accomplish that goal.

How do you feel you can contribute to RosBREED?

As a pick-your-own and retail marketer and grower, I am able to interact with customers one on one and hear first-hand what types of apples excite them.

In the next issue

- Meet more members of our Advisory Panel
- Progress and updates from key teams from the first third of the year
- Where did all the RosBREEDlings go?
- What will be the next Rosaceae Jewel and Nemesis + solution?

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