

RosBREED

Combining Disease Resistance with Horticultural Quality in New Rosaceous Cultivars



VOLUME 5 | NO. 1

RosBREED v.2: You Asked, We Listened!

Amy Iezzoni, Project Director and Cameron Peace, Project Co-Director

Welcome to the new incarnation of the RosBREED project funded by the USDA-ARS Specialty Crop Research Initiative! RosBREED: Combining disease resistance with horticultural quality in new rosaceous cultivars, or “RosBREED 2” as we call it colloquially, is advancing new levels of support for U.S. Rosaceae breeding programs. What new levels? The levels that you asked for.

You asked for **disease resistance**. Fruit (and nut and flower) quality is the centerpiece of what makes Rosaceae crops special – it attracts, delights, and promotes the health of consumers. Exceptional quality creates market demand. When breeding enhances fruit quality, it provides genetic solutions to market risk. But production risks remain, and for most Rosaceae crops, industry stakeholders face a range of major disease threats, including apple scab, fire blight, and blue mold; peach bacterial spot and fruit brown rot; pear fire blight; Armillaria root rot of Prunus rootstocks; rose black spot; sweet cherry powdery

mildew; strawberry root and crown rots and bacterial angular leaf spot; and tart cherry leaf spot. Together, these diseases cause an estimated \$750 million in U.S. crop losses and control costs per year!

Rosaceous crop breeders have dedicated decades of effort breeding for disease resistance and have produced some resistant cultivars. But consider this remarkable fact: *Very few apple, peach, pear, sweet cherry, or tart cherry cultivars resistant to major diseases currently occupy any substantial U.S. market share!*

The perfect apple, cherry, peach, or strawberry – consistently exceeding consumer expectations with satisfying appearance, aroma, flavor, shelf life, and texture, and meeting industry needs for durable disease resistances – remains elusive.

We listened! Our new project title clearly articulates our commitment to enable breeders to combine disease resistance with horticultural quality. We believe that rosaceous

cultivars combining these two major components will no longer be elusive when we creatively apply advanced DNA-based knowledge and tools.

And we’re not talking just single-locus resistance. Our crop teams (breeders, plant pathologists, germplasm curators, and molecular geneticists) are identifying and assembling genetic factors (resistance alleles) into elite parents designed to provide durable resistance to the disease threats listed above.

These “multiple resistance allele donors” will contain resistance alleles to a disease from multiple original germplasm sources representing multiple resistance mechanisms to the target pathogen, as well as resistance alleles to other important diseases.

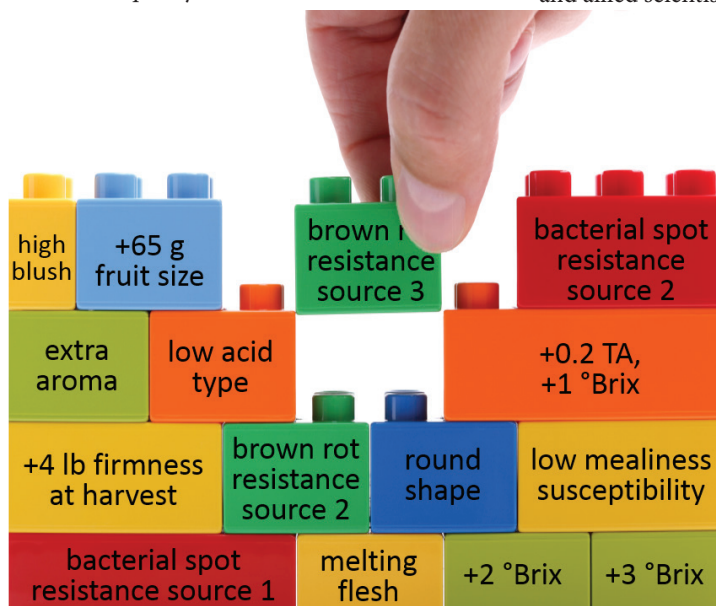
In other words, the genetic factors for disease resistance will be both “pyramided” and “stacked” in new cultivars. Similarly, alleles for exceptional fruit quality will continue to be pyramided, stacked, and combined with each other and with resistance alleles. Breeders and allied scientists won’t ignore other

desirable attributes either, such as outstanding yield, freeze tolerance, everbearing, and low-chill adaptation. The same tools and resources will be available for those phenotypes to incorporate genomics discoveries into new cultivars.

You asked for **more crops**. In the first project, peach, apple, and strawberry, known to some as the three “pillars”

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of Rosaceae genomics, were the target crops for bridging the chasm between genomics research and breeding application. After all, their whole genome sequences were available from 2010. Distressingly, these and other major scientific advances in peach, apple, and strawberry genomics research had little impact on breeding up to that point. The first RosBREED project changed all that – now, more than half of all U.S. apple, peach, and strawberry breeding programs are routinely conducting marker-assisted breeding. But other crops in the Rosaceae family can and should also benefit from these advances.

We have already begun extending resources and knowledge from the three pillars to related crops. For example, in cherry, we have successfully relied on the peach genome as the stand-in for cherry, and marker-assisted breeding is routine for at least two pro-



grams. While this is amazing progress for a five-year project, equivalent benefits were not readily available to breeders in other rosaceous crops, crops that contribute substantially to many rural economies across the nation and have many production, handling, storage, processing, and marketing challenges too! Breeding can address these problems, and DNA information can expand breeding efficiency, accuracy, creativity, and pace in all Rosaceae crops.

We listened! Now we're going Rosaceae-wide. Breeders of pear, rose, blackberry, and Prunus rootstocks have been added to the project and will be directly supported to implement routine DNA-informed breeding. And, as in the first project, RosBREED's concepts and expertise in DNA-informed breeding are available for any member of the community of U.S. Rosaceae crop breeders. Furthermore, we'll be unveiling



Photos: (top left and bottom right), Fotolia Stock Images; top right, M. Olmstead; bottom left, Keith Fuller, USDA; bottom center, V. Whitaker.

“RosMAP,” an exciting new bioinformatics tool. RosMAP will leverage the shared ancestry of all rosaceous crops to efficiently reveal jewels in the genomes of any crop. Almond, apricot, blackberry, pear, plum, raspberry, and rootstocks are all poised to take advantage of the genomics era.

You asked for **superior new cultivars**. You don't just want an enhanced breeding process benefitting from genomics advances. You don't just want breeding advances that will take decades until industry impact. You want tangible outcomes of breeding, the sustained genetic solutions to industry challenges. You want the complete package: new cultivars which you are confident will carry excellent genetic potential for both disease resistance and horticultural quality. And you want them yesterday.

We listened! We have added another group of scientists to leverage genome scan information and cutting-edge statistical approaches to move selections from a breeding program through evaluation to commercialization more efficiently and effectively.

Breeding germplasm receiving RosBREED attention includes elite selections: potential stars of the commercial stage about to enter the spotlight. We will apply newly-developed tools to evaluate these candidate cultivars, already in replicated regional trials, to more accurately predict genetic potential under various management conditions in

various regions. In this way, the stability of performance over commercial environments, or suitability to particular conditions, will be ascertained for hundreds of important breeding selections. RosBREED scientists will investigate what impact the trade-offs between disease resistance and horticultural quality have on stakeholder decisions to adopt new cultivars. **adoption will be systematically investigated in case studies involving.** Outcomes will be used to refine how breeders target these trait groups.

Together, this research will enhance the critical interface between new cultivar development and adoption. Superior deliverables successfully delivered!

The stakes are raised. We are building on previous results and rapid scientific advances. Responding to the widespread needs of U.S. rosaceous crop industry stakeholders and supported by unprecedented federal funding, we are targeting more crops and have added an exciting new group of scientists to the team.

We are aiming high: superior new cultivars combining durable disease resistance with market-demanded horticultural quality across the diversity of U.S. rosaceous crops. You asked for it!

RosBREED By the Numbers

9+
Crops covered in
this project

**\$750
MILLION +**
Economic impact of
diseases covered

2192+
QTLs available in the
Genome Database for
Rosaceae (GDR)

31
Advisory Panel
members

34
Lead scientists in the
project

Featured Team Member – Jay Norelli

Audrey Sebolt, Project Manager, MSU

The long term goal of RosBREED is to develop new and improved cultivars that will combine disease resistance with improved fruit quality. Currently, the vast majority of apple, peach, strawberry, sweet cherry, and tart cherry cultivars grown today are susceptible to a wide range of diseases. Breeding towards the development of new disease-resistant cultivars is challenging and factors contributing to these challenges include:

1. Little knowledge of the nature and inheritance of disease resistance in fruit crops. Verifying the presence of resistant alleles is extremely difficult using traditional plant breeding methods.
2. Sources of resistance are often found in wild relatives, which are distantly related to commercial cultivars and are usually bitter tasting, small fruited, and of poor overall fruit quality.
3. Breeding for fruit quality traits can take 20 to 30 years. Disease resistance can add an additional 10+ years to the timetable for release.

Fire blight is a potentially devastating bacterial disease that affects apple and pear (see *Rosaceae Nemesis* article, page 5). The severity of fire blight on apple has increased over the past half century due to the adoption of high-density planting systems and new commercial cultivars that are more



Dr. Jay Norelli, Pathology Team Leader, in his natural habitat.

susceptible to fire blight than older cultivars. Although host resistance has been recognized as an important component of fire blight management, its application has been limited by a lack of resistant parents with suitable commercial horticultural quality.

Jay Norelli is the Pathology Team Leader for RosBREED and is a member of the Pome Fruit Team as an apple Demonstration Breeder. His goal as Pathology Team Leader is to advance closer to his long term ambition of utilizing host resistance to effectively manage fruit diseases. Jay is excited to be involved with RosBREED because he feels RosBREED is a “great team of top-notch scientists working together to accomplish much more than they could working alone.”

Jay has always had an appreciation of plants; in his youth, he enjoyed spending summers in his grandparents’ small garden and trips to the New York Botanical Garden. However, when Jay began his undergraduate

studies at Cornell University, he had never heard of pathology. After meeting Dr. Jim Lorbeer, now Emeritus Professor at Cornell University, Jay was introduced to plant diseases, quickly became fascinated and subsequently spent his summers working for Dr. Lorbeer studying onion diseases. After his undergraduate studies, Jay served in the U.S. Peace Corp in the Philippines. Upon his return, Dr. Lorbeer introduced Jay to Dr. Steven Beer, a pathologist at Cornell University working with fire blight. Jay immediately became intrigued by this disease and remains so today.

Jay has been studying fire blight for 20+ years and currently works at the USDA-ARS Appalachian Fruit Research Station in Kearneysville, West Virginia. Jay’s research involves the discovery and characterization of new alleles for resistance to fire blight and blue mold. Jay is not a traditional breeder who develops new and improved cultivars. Rather, the crosses he conducts are aimed towards understanding the inheritance of disease resistance so that breeders can subsequently exploit “jewels in the genome.”

Although fire blight is Jay’s favorite disease to study, he also finds attractive quince rust on hawthorn or crab apple. Jay commented that fruits infected with this disease can be “covered with shocking pink horns that are chock full of light orange spores when they break.” Thankfully for fruit industries there are people like Jay in this world!

When Jay is not studying fire blight, he can be found in his garden, biking, or cooking. He also enjoys yoga.

Focus on: Breeding Teams

Mercy Olmstead, Extension Team Leader

Want that new variety with flavors and crispness alongside reduced pesticide applications? Chances are then that one of the breeders on this team will be involved. The center of the RosBREED project is the breeding team – and although some of the players are the same, we have added a few new faces to the group. Demonstration breeders will participate in lab and field activities to integrate existing genetic tools as well as those developed during the next five years.

Over the next five years, these breeders will help to phenotype and record various growth and fruit quality traits that will feed into our other teams for statistical genetics, marker development, economic studies, and outreach. Each member of the team has successful breeding programs, but with their participation in this project, we will advance breeding efforts and improve efficiencies more quickly.

Stone Fruit Breeding Team

Peach

- Ksenija Gasic (Clemson University)
- John Clark (University of Arkansas)
- David Byrne (Texas A&M University)
- Tom Gradziel (University of California)
- Bill Shane (Michigan State University)

Cherry

- Amy Iezzoni (Michigan State University)
- Nnadozie Oraguzie (Washington State University)

Rootstocks

- Amy Iezzoni (Michigan State University)

Pome Fruit Breeding Team

Apples

- Jim Luby (University of Minnesota)
- Kate Evans (Washington State University)
- Susan Brown (Cornell University)

Pear

- Richard Bell (USDA-ARS, Kearneysville, WV)

Berry & Rose Breeding Team

Blackberries

- Chad Finn (USDA-ARS, Corvallis, OR)
- John Clark (University of Arkansas)

Strawberries

- Tom Davis (University of New Hampshire)
- Jim Hancock (Michigan State University)
- Jim Luby (University of Minnesota)
- Vance Whitaker (University of Florida)
- Patrick Moore (Washington State University)

Ornamental Roses

- Stan Hokanson (University of Minnesota)
- David Byrne (Texas A&M)

Amy Iezzoni, MSU



Chad Finn, USDA-ARS



Tom Gradziel, UC-Davis



Jim Luby, UMN



David Byrne, Texas A&M



Nnadozie Oraguzie, WSU



John Clark, University of Arkansas



Susan Brown, Cornell University



Kate Evans, WSU



Ksenija Gasic, Clemson University



Bill Shane, MSU



Jim Hancock, MSU



Stan Hokanson, UMN



Vance Whitaker, UF



Richard Bell, USDA-ARS



Lise Mahoney and Tom Davis, UNH



Patrick Moore, WSU



Rosaceae Nemesis:

Apple Fire Blight

Jay Norelli, Pathology Team Leader

For apple and pear growers, the detection of fire blight in their orchards usually results in immediate concern, and for good reason. Its ability to kill young trees, the limited number of effective control measures available to control the disease and the explosive nature of fire blight epidemics make it a potentially devastating disease (Figs. 1, 2). Fire blight, which is caused by a bacteria named *Erwinia amylovora*, is native to the eastern half of North America and was first reported in 1780 on pear and quince in the Hudson Valley of New York. The name “fire blight” was the result of the rapid, almost firelike spread of blackened dead tissue in orchards. In the late 19th and early 20th century the disease made its way to the West Coast of North America and by the mid-20th century to England. It currently occurs throughout North America, in most of Europe, in the Middle East, northern Africa, Iran and New Zealand. It has not been reported in China, South America or South Africa, and was successfully eradicated from Australia in the late 20th century.

Pears are highly susceptible to fire blight and the disease has been the main factor limiting pear production in the eastern United States. Over the past 50 years the danger of fire blight in apple orchards has increased to unprecedented levels due to the adoption of high-density orchard systems and recent planting of susceptible cultivars and rootstocks (Fig. 1). A high-density apple orchard system depends upon the use of dwarfing rootstocks. The most commonly used dwarfing apple rootstocks, Malling (M.) 9 and M.26, are highly susceptible to fire blight (Fig. 2). Currently, there are no effective treatments available to protect rootstocks from infection.



Figure 1. A young orchard of ‘Cripps Pink’ apple near Pasco, WA devastated by fire blight. Photo: J. Norelli

Furthermore, many commercially successful apple cultivars, including ‘Braeburn’, ‘Fuji’, ‘Gala’, ‘Jonagold’, and ‘Cripps Pink’, are much more susceptible to fire blight than older cultivars.

Annual losses to fire blight and costs of control in the United States are estimated at over \$100 million (Norelli et al., 2003). Unlike many fungal diseases that reduce the market value of the current season’s fruit crop, losses from fire blight result mainly from diminished orchard productivity due to the loss of trees or their severe structural damage. These types of losses are compounded over several years, making

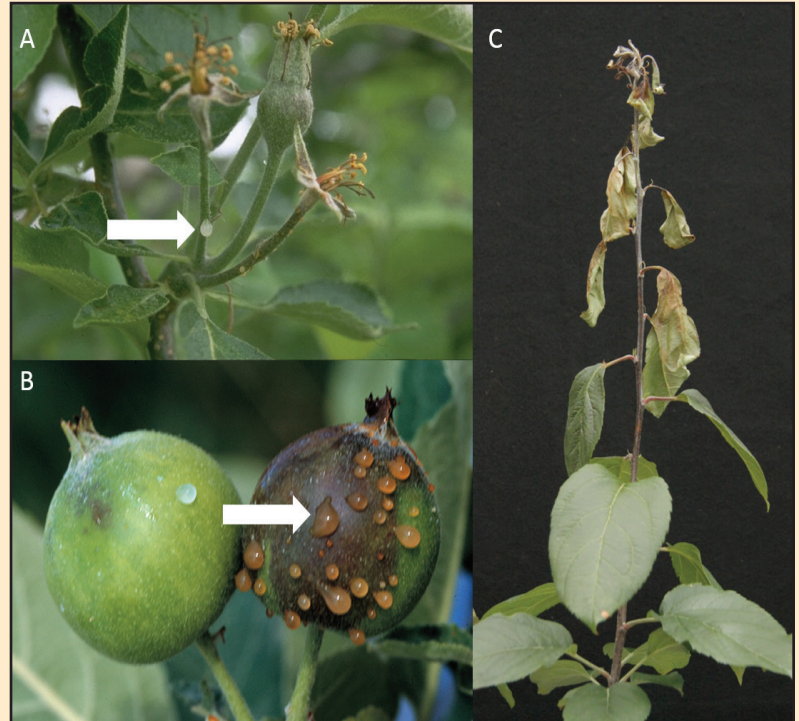


Figure 2. Fire blight infections of apple A) blossoms, B) fruit and C) shoot. The arrow points to bacterial ooze, a common symptom of fire blight infections. Photo: J. Norelli

them quite costly; however, compounded losses are more difficult to determine and often less apparent. For example, a 10% incidence of rootstock blight in a 4-year-old high-density planting can result in losses up to \$8,400 per hectare when the costs of tree replacement, lost investment in tree establishment and maintenance, and reduced yields over several years are considered (Norelli et al., 2003).

Fire blight is host-specific to the apple tribe (Maleae) of the rose family, and in addition to apples and pears its other hosts include fruit crops such as quince and loquat, and several woody ornamentals, including mountain ash (*Sorbus*), hawthorn, firethorn (*Pyracantha*), Photinia, Cotoneaster, shadbush (*Amelanchier*), crab apple and ornamental pear (Van der Zwet et al., 2012). Fire blight bacteria are able to infect most plant parts including blossoms, fruits, vegetative shoots, woody branches and rootstock crowns, through either wounds or natural opening in the plant (Figs. 2 and 3). The disease is usually spread to fire blight-free regions by non-symptomatic nursery stock containing the bacteria. Within the orchard, the bacteria are spread by wind-driven rain and insects. Honey bees play an important role in spreading the disease during bloom. Within

the plant, the disease spreads systemically, resulting in the death of woody tissues (Fig. 3).

The management of fire blight requires an integrated approach of cultural practices, such as pruning out cankers from previous infections, spray treatments to prevent infection, and the planting of resistant cultivars (Norelli et al., 2003). Several models based on climatic and phenological data have been developed to predict the occurrence of fire blight infection periods during bloom, thus improving our ability to control this phase of the disease by the



Figure 3. Fire blight infection of a rootstock crown. Photo: J. Norelli

timely application of antibiotic sprays. However, the fire blight bacteria has developed resistance to streptomycin, traditionally the most effective antibiotic for fire blight control, in most production regions. Although blossom blight control has relied heavily on the use of antibiotic sprays to prevent infection, progress has also been made in the biological control of blossom infection, and some biological control products are

now commercially available. Although increasing host resistance has been recognized as an important component of fire blight management, its application has been limited by a lack of resistant varieties suited to commercial needs.

There are many known sources and defined quantitative trait loci (QTL) for fire blight resistance, but most of these are found in wild species with poor fruit quality. Because the quality of their fruit is irrelevant to the performance of rootstocks, fire blight-resistant apple rootstocks have been developed by conventional breeding much more quickly than have apple scion cultivars and several fire blight-resistant rootstocks are beginning to be commercially available. The development of donor parents for scion breeding containing multiple QTL for fire blight resistance and the development of new apple cultivars with durable resistance to fire blight are both goals of the current RosBREED project.

Further information:

Norelli JL, Jones AL, Aldwinckle, HS. 2003. Fire blight management in the twenty-first century: using new technologies that enhance host resistance in apple. *Plant Disease* 87(7):756-765.

Van der Zwet T., Orolaza-Halbrendt N, Zeller W. 2012. *Fire Blight History, Biology and Management*. The American Phytopathological Society, St. Paul, Minn.

Vanneste JL (ed). 2000. *Fire Blight: the Disease, and Its Causative Agent, Erwinia amylovora*. CABI Publishing, NY, NY and Oxon, UK.

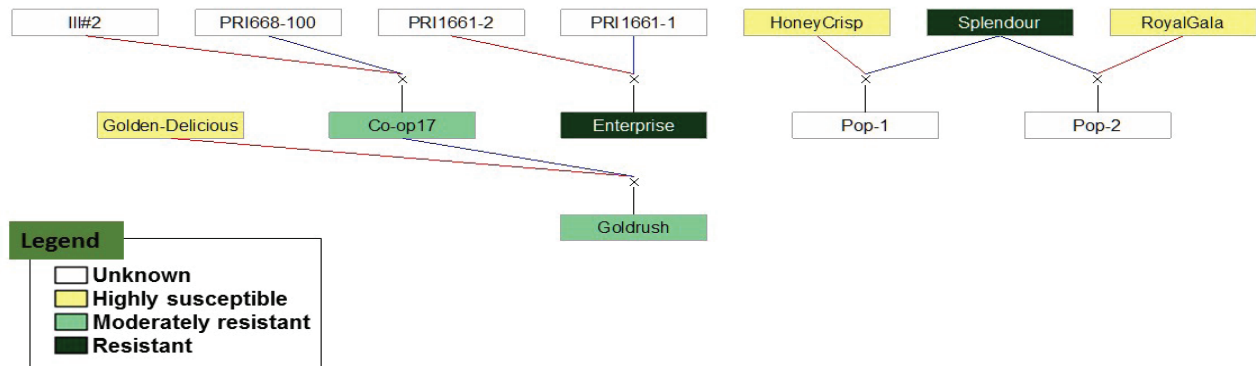


Figure 4. Pedigrees of some of the various sources of fire blight resistance that RosBREED will attempt to exploit. This subset of founding parents, cultivars, and populations will be mined for resistance alleles with the goal of developing multiple resistance allele donors. Pop-1 and Pop-2 are segregating for fire blight resistance.

New Cultivar Corner

Mercy Olmstead and Cameron Peace, Extension Team

A focus of the RosBREED efforts over the past five years has been to make the breeding process more efficient so that breeders are more responsive to industry challenges and incorporate traits that make consumers want to buy Rosaceae fruit.

Although the tools developed in the first RosBREED are just being integrated into breeding programs around the country, new varieties are being released with interesting traits that were derived from “jewels in the genome”! Each quarter we will highlight two or three new cultivars that have unique traits that will make consumers come back for more!



'Florida127' fruit size is large. Photo: V. Whitaker

SWEET SENSATION™ 'FLORIDA127'

Inventor: Dr. Vance Whitaker, University of Florida

This strawberry was recently released from the University of Florida (2013), and in an interview with Dr. Whitaker, he listed some unique features of this variety.

What are the unique features of Florida127?

Its combination of early yield (grower demanded) and sugar content (consumer demanded) along with fruit size (wholesale buyer demanded) make it desirable for multiple levels of the market chain.

How long did it take to develop this variety (when was the original cross made)?

The original cross was made during the 2008-09 season and the seedling was selected in spring 2009.

To have made a cross during the winter season of 2008-09, and then to have chosen the seedling in 2009 – what was it that caught your eye about it? It's a fast turnaround!

We only have one season at the seedling selection stage due to the nature of our annual production system. But you are right, this one caught our eye particularly early on. It was actually randomly selected for inclusion in a genetic study, which used a mating design and progeny testing to estimate genetic parameters. When we took a look at the clonal values of the various seedlings for an index of traits, one seedling came out on top, mainly due to its unusual combination of high yield and high soluble solids. In the very next year of testing it again impressed and was, thus, moved to our advanced trials at an unusually early stage.

What is the pedigree of 'Florida127'?

It is a cross between WinterStar™, a 2011 release known for its fruit firmness and high early yield, and FL 02-58 as the pollen parent, a selection with high fruit firmness, excellent flavor and open plant habit.

What was the size of the family among the other seedlings that 'Florida127' was chosen?

Approximately 100 seedlings

Were there other seedlings in that family that were advanced to the next stage of selection?

Multiple selections from the family were advanced to the second stage of evaluation, but only this selection made the cut for advanced trials.

How will 'Florida127' be used for the RosBREED project?

It is a parent in several populations used for QTL discovery and validation for important fruit quality traits including yield, fruit size, soluble solids content, and angular leaf spot resistance.



'Florida127' in field production. Photo: V. Whitaker

Jewel in the Genome: Update

Amy Iezzoni, Project Director, and Cameron Peace, Project Co-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”.

DNA-informed breeding is now a reality for the majority of apple, peach, strawberry, and cherry breeding programs in the U.S., resulting in increased ability to achieve the combination of desired characteristics demanded by producers and consumers. The major breakthrough that fueled the application of DNA-based diagnostics was the development of DNA tests for significant loci that influence these phenotypes. Many of these significant loci, i.e., “Jewels”, were reported in this Newsletter column and then published in eXtension (<http://tinyurl.com/kup2oej>). These available DNA tests and their targeted loci are illustrated here.

Over the previous year, since the last Jewel was reported, RosBREED scientists and international collaborators have revealed and polished many new Jewels! Soon to be described are DNA tests for: apple skin color, fruit size, and fruit sugar content; peach maturity time, amount of skin blush, and soluble solids content; cherry maturity time and fruit and skin color; and strawberry berry size. The process of DNA test development will be accelerated in the new 2014–2019 RosBREED project with dedicated attention by multiple postdocs. As these new DNA tests become available and are put in application, they will be reported in this column. Just a heads-up: there appear to be locations within each crop genome where many significant loci for valuable traits co-locate. Therefore, when we report the Jewels, often we will be reporting on the “Necklace” – the relative linkage of Jewels along the chromosomes. Stay tuned!



Fruit storability
Md-ACS1



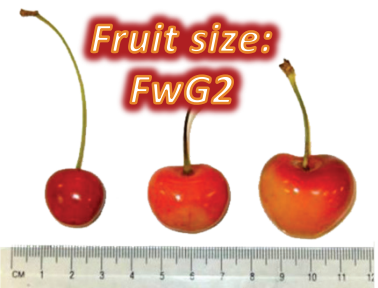
Self-fertility: S



Ever-bearing: FaPFRU



Acidity: Ma



Fruit size:
FwG2



Fruit skin coloration: Rf



“Fresh sensation”
(crispness, tartness,
juiciness) : Ma



Freestone vs. clingstone: F-M

Melting vs. non-melting flesh

Community Breeder's Page

Your Guide into the Unknown

Cameron Peace, DNA-Informed Breeding Team Leader

Welcome to the future! Whether you're charging in with open arms, simply enjoying the ride, or being dragged along kicking and screaming, the art of Rosaceae crop breeding is changing. It's becoming more scientific. More objective, planned, efficient, accurate, creative, exciting, transformative!

Large genetic gains are still possible in a single generation, and opportunities abound for unusual and valuable crossing outcomes. Because relatively few generations separate our crops from their wild ancestors, alleles providing large, commercially relevant phenotypic contrasts for most target traits still segregate in breeding germplasm. So a chance cross can still result in an industry-changer.

Recent advances in the technology known as DNA-informed breeding are providing breeders with an unprecedented window on and access to the genetic factors and combinations underlying commercial success and environmental sustainability. Desired outcomes can be more efficiently, accurately, and creatively targeted than ever before.

How can each Rosaceae breeder take advantage of scientific advances in the genetics of their crop? By keeping up to date with the latest knowledge, tools, and concepts. This regular RosBREED Newsletter column, and its associated webpage (<http://www.rosbreed.org/breeding/community-breeders>), is intended as a reference resource to keep the community of rosaceous crop breeders in touch with upstream research approaches, technology interfacing, new DNA information, and events.

Upstream Research Approaches

RosBREED is investigating many interesting research approaches to gain insights into the genetics of rosaceous crops. These investigations are "upstream" of breeding because they are not directly for breeding application. Instead, the insights gained will be used to develop tools and knowledge for subsequent breeding application.

For example, the SNP array-based genome scanning developed in the first project is an upstream research approach. Use of the SNP arrays in well-planned experiments provided us with unprecedented genomic resolution on relatedness and functional allelic diversity

for U.S. breeding germplasm of peach, apple, strawberry, and cherry. The SNP arrays were not meant for direct breeding use, as the raw results obtained from genome-wide SNP genotyping – just a huge file of As and Bs – do not immediately reveal anything of breeding utility. Even now, as geneticists have interpreted what many of those binary bits mean, we do not yet recommend breeders scanning the genomes of their important breeding parents and elite selections. Only a few demonstration breeders of the first project with postdocs or advanced graduate students ready to spend months to years analyzing the SNP datasets are daring to use the arrays. We're not yet at the interpretive stage of human genome-scanning companies like 23andMe! But we're aiming for it during the next five years of this project.

While geneticists supporting breeding programs will be the most likely to find utility in these topics, breeders should find it useful remaining abreast of the latest scientific approaches being trialed and refined for their crops.

Technology Interfacing

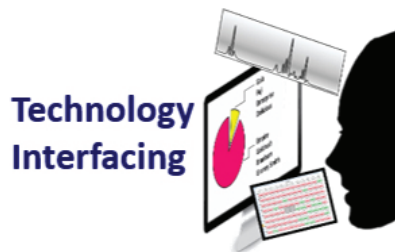
The outputs of successful upstream research become new technologies that Rosaceae breeders can use to enhance their endeavors. But how do they work conceptually? Where can they be accessed? How can they be best integrated with ongoing breeding operations?

In this category of Community Breeders' Page article, answers to these questions will be provided for available technological innovations in DNA-based diagnostics. An example research outcome is a valuable trait-predictive DNA test. Articles will extend to advice on what features about a DNA test that a breeder should ask for, strategies for using a little to a lot of DNA information in various breeding operations, what to expect and how to find service providers for DNA-based diagnostics, available decision-support software, and so on. And to ensure we're all on the same planes of communication and understanding, now and then there will be updates on terminology in the DNA-informed breeding arena. Starting below:

DNA-informed breeding: The use of DNA-based information, obtained via direct assays of an organism's DNA, to directly support breeding decisions.

In this definition, the word "information" implies data interpreted for its breeding utility, not raw data from the assays of DNA marker genotyping or DNA sequencing. DNA-informed breeding is often successfully used synonymously with "marker-assisted breeding" (MAB). Both include use of DNA marker information for phenotype

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predictions as well as relatedness/identity. However, MAB is not a term to be thrown around in polite (non-geneticist) company, as you'll find yourself back-tracking to painfully explain what a "marker" is. DNA-informed breeding provides a much less jargoned term that anyone can appreciate.

For what it's worth, the term is also free of GMO connotations. In two ways, "DNA-informed breeding" is not quite the same as MAB: (1) it does not encompass the MAB strategy of using morphological markers in breeding selection, such as apple seedling leaf color to predict flesh color (red leaves = red flesh); but (2) it does include genome-wide selection, also known as genomic selection, which uses performance predictions based on genome-wide markers designed to capture both large-effect and small-effect loci segregating in breeding families. Thus, DNA-informed breeding is not restricted to using information only about significant QTLs.

New DNA Information

The successful application of new technologies on publicly available germplasm by publicly funded researchers leads to new DNA information that can be shared in this category of article. Information that breeders should find valuable are new insights into trait genetics, relatedness, and functional genotypes at trait-predictive loci for specific breeding germplasm individuals.

Did you hear about the discovery by Rosyara and co-workers (2014) that the sweet cherry industry standard 'Bing' was fathered by the old French 'Napoleon'? This pedigree connection significantly increases the known inbreeding coefficients among numerous North American cultivars. Which publicly available important breeding parents are heterozygous for dominance-effect Mendelian trait loci, such as peach flesh color (Y locus), acidity (D locus), and peach vs. nectarine (G locus)? Find out in upcoming Community Breeders' Page articles.

Events

Over the coming years, RosBREED will host numerous in-person information delivery and DNA-informed breeding training events for U.S. Rosaceae breeders. Other momentous and interesting events are on the international stage. The plans and outcomes of these events will be described here.

If you have a request for a Community Breeders' Page topic in one of the above categories, please email me at cpeace@wsu.edu.

Community Breeders' Web-Page: <http://www.rosbreed.org/breeding/community-breeders>

Reference cited

Rosyara U, Sebolt A, Peace C, Iezzoni A. 2014. Identification of the paternal parent of 'Bing' sweet cherry and confirmation of descendants using Single Nucleotide Polymorphism markers. *J. Amer. Soc. Hort. Sci.* 139:148-156.

Community Events

ASHS Symposium

New Orleans, LA

From Wild Germplasm to Molecular Tools for Applied Breeding: Black Raspberry as a Case Study

3 August 2015, 9 am - 4:30 pm

Come learn about our experience with black raspberry from collecting and evaluating wild germplasm, to developing molecular tools, to applied breeding.

Michael Dossett – Informing phenotypic selection of wild germplasm with genotype information: black raspberry as a case study. Michael will describe using both phenotypic and genotypic methods to evaluate wild germplasm for genetic diversity, population structure, and to compare wild to cultivated germplasm to select the most interesting plants.

Jill Bushakra – Molecular marker development, genotyping and linkage map construction. Jill will lead an interactive session on using the genotype information for genetic mapping using JoinMap software, and show how the genetic linkage map can be used for quantitative trait analysis.

Paul Sandefur – DNA test development and deployment in tree fruit breeding programs: what can be gleaned to enable marker-assisted black raspberry breeding? Paul will provide examples on how to design, develop and use DNA tests for genetic analysis, and what is needed to use these tools in applied breeding.

The afternoon will be dedicated to answering questions and for practicing what was presented in the morning session.

Ten scholarships are available to cover early conference registration (before 1 April 2015), ASHS Student membership, and up to 6 nights of lodging at the Sheraton New Orleans. Applications are available online.

Contact: Jill Bushakra (Jill.Bushakra@ars.usda.gov) or Nahla Bassil (Nahla.Bassil@ars.usda.gov) with any questions.

11th International Rubus and Ribes Symposium

Asheville, NC

21-24 June 2015

North Carolina State University, the Plants for Human Health Institute, the Rubus and Ribes Working Group and the Vine and Berry Fruits Section of the International Society for Horticultural Science (ISHS), are proud to host the XIth International Rubus and Ribes Symposium. The Symposium will be held June 21-24, 2015 in Asheville, NC. A pre-symposium tour will take place June 18-20, 2015 in the Charlotte, NC area.

This ISHS Symposium attracts researchers from around the world who work in aspects of Rubus and Ribes research, teaching, extension, business, and public services. The attendees of this symposium have a reputation of being a convivial group and this event in

Coming up in the next issue:

- Meet new members of the Advisory Panel
- Introduction of a new column, "Industry Perspectives"
- Meet project members: Extension Team
- What will be the next Rosaceae Nemesis? Read next quarter's Newsletter to find out!

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