RosBREED

Combining Disease Resistance with Horticultural Quality in New Rosaceous Cultivars

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Picking Peaches Possessing Perfect Postharvest Performance

Mercy Olmstead, Extension Team Leader, Ksenija Gasic, Stone Fruit Team Leader, Amy Iezzoni, PD, Cameron Peace, Co-PD, and Jim McFerson, Extension Team

Carlos Crisosto is happy. This world-renowned postharvest physiologist and member of RosBREED's Scientific Advisory Panel has spent his career investigating the factors that affect fresh peach eating quality and helping the peach industry worldwide improve its practices. While that is significant, Carlos now has the pleasure of seeing his research provide the essential foundation for application of DNA-informed selection in U.S. breeding programs.



Figure 1. Carlos Crisosto checks whether Ralph (Trey) Burrell, Clemson breeding technician, has given a semi-mealy peach a score of "3.5", not "3.0".

riod wreaks havoc on eating quality, since fruit flesh readily turns dry and mealy, brown, and develops off-flavors.

Peach breeders have long known they can improve postharvest quality genetically, but have lacked a protocol to evaluate postharvest performance of their germplasm rigorously and systematically – and thereby provide the basis for developing robust DNA tests to eventually bypass resource-intensive phenotyping.

We know when a consumer eats a peach fruit, it has usually traveled a long way from the orchard, spending days in refrigerated storage at the packing house, in transit, and at its final destination.

As Carlos has clearly demonstrated, this postharvest pemality since frui



Not any longer. This spring, Carlos began

a series of training sessions for postharvest

phenotyping, first at UC-Davis (Fig. 1) and

at Clemson University (overseen by Ksenija

Gasic) and the University of Arkansas (over-

During the Clemson visit, Carlos attended

in Ridge Spring, SC (owned by Chalmers

the opening of a packinghouse at Titan Farms

subsequently in peach breeding programs

seen by John Clark).



Figure 2. Carlos gives the hug of approval during the Titan Farms packingline tour. L to R: Greg Reighard, Clemson University, Carlos Crisosto, UC Davis, Ksenija Gasic, and Guido Schnabel, Clemson University.

(Cont. on page 4)

Featured Team: Statistical Genetics

Mercy Olmstead, Extension Team Leader, UF and Vance Whitaker, Statistical Genetics Team Leader, UF

Stats N DNA N Acronyms R Us. The Statistical Genetics Team is applying statistical approaches to solving complex genetics challenges in Rosaceae. These approaches were first developed and utilized in animal and agronomic systems and can now be adapted for use in Rosaceae crops.

Genome-Wide Selection (GWS), successfully demonstrated in corn (Bernardo and Yu, 2007) and in tree crops like pine (Resende et al., 2012) is showing promise for Rosaceae crops. How is GWS different than the marker-assisted breeding approaches that the RosBREED project has been applying during the last 5 years?

Traditional marker-assisted breeding has worked very well in cases where only one or a few loci (locations on the chromosomes) that control the trait each have a large genetic impact (which is manifested in a physical way in the form of improved fruit size, differing flesh color, or disease resistance). However, some traits are controlled by dozens or even hundreds of loci, each of which individually has a very small impact. These traits cannot be tracked by one or few markers. So, GWS utilizes thousands of markers spread throughout the entire genome combined with statistical models to predict the performance of an individual in the field or predict the value of an individual as a parent in a breeding population.

Preliminary testing of GWS in apple and strawberry has been positive. Now the Team is attempting to test the effectiveness of GWS approaches in real breeding populations and to extend GWS to peach and sweet cherry.

The Statistical Genetics Team's objectives are to model and improve performance prediction in Rosaceae breeding by: (1) quantifying the

impacts of individually small but cumulatively large "genetic background" effects (essentially, applying GWS); and (2) quantifying the impact of non-genetic effects such as testing location and random environmental factors (essentially, investigating genotype-by-environment-by-management interactions – $G \times E \times M$).

The connection between these two objectives is that both are predictive approaches. In GWS, performance can be predicted based on marker data that reflect genetic background effects in a training population. By modeling $G \times E \times M$ interactions, a combination of marker data and limited-replication trial data can allow predictions of performance for cultivar candidates in new environments where testing has not yet taken place.

Thus far, the Team has assembled their data sets for apple, peach, sweet cherry, and strawberry breeding germplasm, with extensive SNP array marker genotypic and multi-trait phenotypic information from many locations under various management conditions. Analytical pipelines are under development to model $G \times E \times M$, especially where unreplicated trial data are available, such as apple test plots with only one or few trees per clone. GWS training populations are in various stages of development, field-testing, and SNP-genotyping. In Year 2, predictive capabilities of GWS will be empirically tested both to predict field performance of clones as well as parental performance.

References

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RosBREED By the Numbers

Number of peach

individuals evaluated

for postharvest

traits in 2015

15.1 Ibs

Average annual U.S. per-capita peach consumption (fresh, processed and frozen)

\$330M Economic losses due to peach diseases

annually

2,000+ Number of named peach cultivars

Featured Team Member: Carlos Crisosto

Audrey Sebolt, Project Manager, MSU

Everyone loves a juicy ripe flavorful peach, yet finding a fine quality peach in the grocery store is often extremely difficult. For some time, consumers have expressed frustration over poor eating quality. Criticisms included lack of taste, poor texture (due to mealiness), and flesh browning. To some degree, production methods contributed to the poor quality fruit as grower market incentives were solely based on fruit size and yield, but little was known about the effect of postharvest handling practices.

The research program of Dr. Carlos Crisosto at UC Davis has changed the situation completely. In his program, Carlos set out to develop a systematic postharvest protocol for growers to deliver consumers high quality freestone peaches. As an extension specialist and pomologist Carlos specializes in postharvest fruit quality of the rosaceous crops apricot, almond, cherry, nectarine, peach, and plum, as well as fig, kiwifruit, olive, pistachio, walnut, and persimmon. Carlos' passion for postharvest may have arisen as a young child growing up in the small port town of Talcahuano, Chile, where he would watch fruit and other produce leave the port for far off countries. In addition to those roles, Carlos is also the Director of UC Davis' Fruit & Nut Research & Information

Center and is the Associate Director of the Postharvest Technology Center.

California produces 74% of U.S. freestone peaches, and in 2012, the country exported peaches valued at \$173 million. Therefore, development of a protocol for growers to supply retailers with flavorful, excellent quality peaches was critical. For 20 years, Carlos led the efforts to develop this protocol. Now 80-90% of California freestone peach growers implement his "preconditioning/pre-ripening" protocol, resulting in increased consumer consumption. Fruit brought to retail markets using this protocol are labeled "Summeripe and Ready to Eat" and contain higher sugars, lack postharvest storage disorders, and are more flavorful, aromatic, and juicier than fruit grown and harvested traditionally. The preconditioning/preripening protocol requires that producers have access to high refrigeration capacity. The protocol is also cultivar-specific, and specific regimes have been developed for 11 peach cultivars to date. Here's a short video on the impact of this protocol: www. youtube.com/watch?v=gHMg-Zd9Rqg.

To ensure that cultivars of the future can genetically deliver excellent peach fruit quality to consumers, RosBREED is excited to have Carlos on the peach team. In recent months, Carlos has trained three of our peach Demonstration Breeders: Dave Byrne (Texas A&M), John Clark (University of Arkansas), and Ksenija Gasic (Clemson University). Their programs now use the standardized phenotyping protocol for postharvest fruit quality evaluation (see page 1 for more



27,852 Putative number of genes in the

peach genome

Carlos Crisoto

details). Each breeding program is now evaluating their seedlings (UC-Davis, ~200; Texas A&M n~280; University of Arkansas n~200; Clemson University n>200) and cultivars, selections, and ancestors that collectively compose the Advanced Peach Crop Reference Set. Postharvest traits measured include fruit external appearance (color and size), flavor (sugars and acidity), texture, and incidence of storage disorders (decay and chilling injury/internal breakdown symptoms of flesh mealiness, browning, and bleeding). Ksenija Gasic looks forward to seeing the results of this partnership as Carlos' protocol "clearly defines the problem we have with delivering high-quality peach fruit to consumers, because previously we lacked tools to predict which crosses and seedlings would have a better chance of giving us peach fruit with outstanding postharvest quality."

Carlos, why did you choose to be involved with RosBREED?

"I have spent almost 32 years working on fresh fruit quality with an emphasis on peach quality in the field and laboratory. Over the years, I created a new peach delivery system and established the concept of "peach consumer quality" as a novel approach to increase peach consumption. This was a big change from the "yield and size" as a perception of quality to "flavor and safe" (low pesticide use/disease resistance). A long time ago, I chose this path because I believed that flavor at consumption will increase sales and benefit consumers with a better diet to improve their health."

What successes do you hope to see from RosBREED?

"RosBREED1 created the environment for all Rosaceae breeders, molecular biologists, and physiologists to work together with the final goal to improve fruit consumer quality. It was proven that selecting important key quality components (size, color, texture, flavor, storage potential quality, etc.) will assist the breeding programs to meet this common goal. RosBREED2 will deliver these tools to breeders and we will soon hear testimonies on the impact of using these markers in our cultivar development."

How have you already benefited from RosBREED?

"I am very happy to see my peers sharing my vision by introducing storage-chilling injury quality parameters such as susceptibility to chilling injury disorders and flavor into their current active and successful breeding programs. Directly, I am benefiting by interacting with the great group of peers and graduate students. The genomic resources such as genotyping, sequences, etc. are helping my studies on biological mechanisms that control the expression of genes related to key quality components during storage."

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

"My wife, Gayle Crisosto, is the person in charge of the sensorypostharvest quality protocols. My oldest daughter, Nicole, is getting her PhD in Physics in a joint project between University of Washington, Seattle and University of Florida, Gainesville. My youngest daughter, Michelle, is working in an art promotion company in Los Angeles and getting ready for a year in Italy to learn more Italian and art. What genetic segregation — marker-assisted tools could not have predicted this outcome!"

Welcome RosBREED Students & Postdocs!

A vital part of RosBREED is training the next generation of Rosaceae plant breeding scientists. Many RosBREED senior personnel have partial funding to train students in their areas.

Welcome to our new Ph.D. students:

• Liz Blissett, recently graduated from the University of Illinois and now supervised by Rex Bernardo (University of Minnesota), has joined the Statistical Genetics Team and will help Rosaceae breedersbenefit from Genome-Wide Selection.

- Seth Wannemuehler, recently graduated from Purdue University and now supervised by Chengyan Yue (University of Minnesota), has joined the Socio-Economics Team to elucidate the economic tradeoffs between disease resistance and fruit quality in new cultivar candidates.
- Jennifer Lewter started a project in June on peach mealiness phenotyping and genotyping at the University of Arkansas, supervised by John Clark (RosBREED demonstration breeder).

Also, welcome to our new M.S. student:

 Melinda Yin began a project in May on blackberry phenotyping and genotyping as part of RosBREED at the University of Arkansas, supervised by John Clark (RosBREED demonstration breeder).

Picking Peaches



(Continued from page 1)

The new after-storage fruit quality evaluations challenged the capacity of each program, with technicians and seasonal staff working hard to handle the increased sampling activities. Not only were each program's elite selections being evaluated, but also a wildly diverse set of hundreds of seedlings and parents composing the Advanced Peach Crop Reference Set.

Was Carlos' protocol a

useful innovation, or just

more work?! Too soon to

tell. However, RosBREED

researchers will be grinding

though the data and gearing

Figure 3. Terrence Frett not looking too Frett-ful over his peach postharvest data at Clemson.

up for 2016 (Fig. 3), with new DNA tests optimized to efficiently and accurately identify excellent postharvest storage characteristics. These tests can then be routinely used to evaluate parents and seedlings for their potential to avoid postharvest disorders, informing breeders about which parental combinations to avoid and which seedlings to eliminate at the greenhouse stage so they can be discarded prior to field planting.

This is what RosBREED is meant to do, systematically building on the creativity of Carlos Crisosto's research, the skilled application within RosBREED breeding programs, and other RosBREED Teams' development of new tools to craft new cultivars with superior eating quality. And all this already in Year 1 of RosBREED. We'll be back with an update of what peach postharvest "jewels" we find in the genome in the next four years!

Rosaceae Nemesis: Cherry Leaf Spot

Mercy Olmstead, Extension Team Leader, UF with Amy Iezzoni, Kristen Andersen, and Audrey Sebolt, MSU

For tart cherry (*Prunus cerasus* L.), the number one disease nemesis in humid growing regions is cherry leaf spot (CLS), caused by the fungal pathogen *Blumeriella jaapii*. This disease can be devastating for tart cherry growers, defoliating the entire tree early in the growing season. If defoliation is severe before harvest, fruit will have poor quality characterized by insufficient fruit color, reduced soluble solid concentration, and sunscald. If defoliation continues after harvest (Fig. 1), the trees will have reduced carbohydrates stored, resulting in a loss of coldhardiness that can lead to tree decline and death.

Disease Symptoms and Control

B. jaapii primarily affects the leaves of tart cherry trees, and the first evidence of infection is small, dark colored spots on young leaves. In a susceptible host, these spots will eventually coalesce and turn brown (Figure 2), often with a yellow halo with white sporulation on the underside of the leaf. The lesions and yellow-

ing will eventually

infected leaves will

fall from the tree.

When CLS pressure is severe, fruit pedicels can also become infected. CLS is currently controlled by as many as 8-10 fungicide applications throughout the growing season. However, in many years, achieving good spray coverage in a timely

manner can be

very challenging,

spread over the

entire leaf, and



Figure 2. A tart cherry leaf infected by cherry leaf spot.

especially because 'Montmorency', the major tart cherry cultivar grown in the U.S., is highly susceptible to this fungus.



Figure 1. Cherry leaf spot can defoliate tart cherry orchards during the growing season. This photo of the tart cherry cultivar Montmorency was taken July 29, 2015, after fruit harvest.

Breeding for Disease Resistance

Resistance and tolerance to CLS in new cultivars is a major goal of the Michigan State University (MSU) tart cherry breeding program. Sources of tolerance (Fig. 3) include the tart cherry cultivar 'North Star', sweet cherry cultivars, and some accessions of the wild cherry species P. maackii. In these tolerant sources, the fungus can infect the leaves but disease progression is significantly slower than in a susceptible host, and leaf yellowing and defoliation is delayed. Another wild cherry species, P. canescens, is being used as a source of CLS resistance. In some accessions of this species, the fungus does not establish well in the host and leaf vellowing and abscission does not occur (Figure 4 A-C).

Advances in RosBREED

To date, a major locus underlying the *P. canescens*-derived CLS resistance has been identified and is being routinely used in the breeding program. A DNA test recently developed for this locus identifies resistant seedlings when they are still in the greenhouse, and seedlings predicted to be susceptible are happily discarded prior to field planting. Additional loci influencing CLS tolerance and resistance from other sources are being uncovered. The MSU breeding program expects to be able to develop new-CLS resistant cultivars that have multiple resistance alleles.



Figure 3. Cherry leaf spot tolerant tree (left) with good leaf retention compared to a susceptible cultivar, Montmorency (right), in an orchard that had not been controlled for CLS during the growing season. Photo taken July 29, 2015.

Deliverables to industry? Superior new cultivars with excellent horticultural quality and durable CLS resistance!



Figure 4. (A) Cherry leaf spot (CLS) susceptible cultivar Montmorency (left) and a resistant MSU selection (right) in an orchard that had not been sprayed to control CLS during the growing season. Photo was taken July 29, 2015. (B) 'Montmorency' (left) and resistant MSU selection (right). (C) Microscope images of leaves infected with B. jaapii. The image on the left is of the susceptible cultivar Montmorency infected with the CLS fungus. The image on the right is a resistant MSU selection in which the fungus does not establish in the host due to a hypersensitive type host defense response.

Jewels in the Genome

Amy Iezzoni, Project Director, Michigan State University

Sweetness is an important component of apple flavor, and when balanced with acidity (or tartness) is associated with overall apple eating quality. In apple fruit, sweetness is determined by levels of individual sugars, including fructose, glucose, sucrose, and sorbitol. Of these sugars, fructose is typically perceived as sweeter than the other sugars, particularly sucrose (Hanover and White, 1993).

The degree of genetic control of sweetness is typically lower than for other breeding targets with a broad-sense heritability of only about 0.2-0.3.

A large-effect trait locus for fruit fructose concentration was identified on apple linkage group (chromosome) 1 and named LG1Fru (Guan et al. 2015). LG1Fru was consistently associated with fructose differences across years and from harvest through storage and explained almost all of the genetic variance in fructose concentration across a large set of breeding germplasm from the Washington State University apple breeding program.

This locus also explained a smaller but significant amount of variance for the individual sugars of glucose, sucrose, and sorbitol, but interestingly was not associated with soluble solids content (SSC), the commonly used instrumental measure of sweetness (for better or worse). Because of the complexity of the SSC measurement, it is not surprising that not one single region of the genome was found to be consistently associated with apple fruit SSC.

Apple breeders already have access to DNA tests to select for many other components of apple fruit quality, including apple texture (Md-ACS1 = Jewel 1) crispness, juiciness, acidity (Ma locus = Jewel 6), and firmness (Md-PG1 = Jewel 9). With genetic knowledge of which apple seedlings will most likely have high fructose content (along with the other components of apple fruit quality), breeders can plan crosses to maximize the probability of obtaining selections with excellent fruit quality.

Therefore, because knowledge of this genetic region will lead to more efficient breeding of apple cultivars, it is chosen as one of RosBREED's "Jewels in the Genome."

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Hanover, L.M. and J.S. White. 1993. Manufacturing, composition, and applications of fructose. Am. J. Clin. Nutr. 58:724S-732S.



Cultivar Corner

Mercy Olmstead, Extension Team Leader, UF

COLUMBIA STAR

INVENTOR: CHAD FINN, USDA-ARS CORVALLIS

COLLABORATORS: Bernadine Strik, Oregon State University (OSU) Department of Horticulture; Brian Yorgey, OSU Department of Food Science; Mary Peterson, USDA-ARS Corvallis; Jungmin Lee, USDA-ARS Parma; Robert Martin, USDA-ARS Corvallis; and Harvey Hall, Plant and Food Research, New Zealand



What makes 'Columbia Star' special?

It is the first machine-harvestable, thornless cultivar that has fruit quality that, based on blind panel assessment, was rated equal to or better than 'Marion', the current industry standard. Besides having thornless canes, it is high yielding and is the first thornless blackberry cultivar using the 'Lincoln Logan' source of thornlessness.

When was the cross made?

2005

What is the pedigree of 'Columbia Star'?

NZ 9629-1 and ORUS 1350-2 ('Black Butte' × ORUS 828-43). See below for some history behind these selections!

What is the size of the family from which 'Columbia Star' was chosen?

55, a moderate size. Tried for 100.

Are there other siblings that have commercial potential?

Yes. Another sibling, ORUS 3447-2 will be released in the upcoming year.

Will this cultivar be used in RosBREED and how?

'Columbia Star' is the parent of crosses that will be phenotyped and genotyped with the goal of identifying loci controlling fruit sweetness.



Other interesting tidbits...

'Columbia Star' is a true story of great germplasm, collaboration, and serendipity.

- One parent has a long history in our program. The NZ 9629-1 parent was a selection we made out of a population Harvey Hall sent to us from New Zealand (Plant & Food Research). That gave us the 'Lincoln Logan' source of thornlessness.
- The OSU Food Science Department did blind trials of it the first year we had it in a replicated trial, which identified it as outstanding.
- Grower collaborators in Lynden (Wash.) showed it was coldhardy enough and would machine-harvest well.
- One Oregon grower took a couple of leftover gallons of puree after a field day sampling and sent it to a major manufacturer who gave it their "seal of approval" as equal to 'Marion.'
- A grower with one of the largest blackberry acreages in Oregon happened to visit the station the day we were going over our plots with a machine harvester. He saw the fruit coming off and was really excited. Two months later he told the growers who sell to him that he would back them on planting 'Columbia Star' and take their fruit.

This combination of people, germplasm, efforts, and events meant that 'Columbia Star' went from a selection to hundreds of thousands of plants being planted in less than 10 years from the time the cross was made!



Meet Our Advisory Panel Members

Our advisory panel members are a critical part of our success in RosBREED, as they verify from their experience the impact of our research and guide our priorities. They dedicate not only a day (plus two for travel) to our advisory panel meetings in January, but they also are called upon during the year to provide feedback to questions that our project members have.

Joe Arvai Scientific Advisory Panel What is your job description? How do you serve the Rosaceae community?



I am the Max McGraw Professor of Sustainable Enterprise, and the incoming Director, for the Frederick A. and Barbara M. Erb Institute for Global

Sustainable Enterprise within the School of Natural Resources & Environment, and the Ross School of Business, at the University of Michigan. I am a decision scientist, who studies consumer behavior, as well as decision-making by a variety of pubic and expert groups more broadly. I am helping the Rosaceae community as a member of the Scientific Advisory Panel.

Why are you interested in RosBREED?

I'm interested in how people make choices instinctively, and based on these findings, what we can do to help people improve their decision-making capabilities in situations when it matters. I hope that I can offer something to RosBREED as they work with growers trying to make decisions that may improve the quality of their products.

How do you feel that you can contribute to RosBREED?

I've got many years of experience doing this kind of work, so if there's an opportunity to help, I'd like to give it a try. That said, there are great natural and social scientists working with the RosBREED group; they're big thinkers, and I know they can do just fine on their own. But, when called upon to provide some ideas, I think what I have to offer may be of some value.



David Eddy

Stakeholder Advisory Panel What is your job description? How do you help the Rosaceae community?

I am editor of American/Western Fruit Grower magazines; the two are quite similar, with those subscribers East of the Rocky Mountains receiving American Fruit Grower[™], while those to the West get Western Fruit Grower[®]. The key difference between the two is in the crops covered. Almonds, for instance, are largely only grown in California, at least in the U.S., so coverage on them might appear only in Western Fruit Grower. I help the Rosaceae community by editing the community's newsletters.

Why are you interested in RosBREED?

We're dedicated to helping U.S. fruit growers. The RosBREED effort goes to the heart of what the great majority of growers want: better fruit to grow.

How do you feel that you can contribute to RosBREED?

Along with my fellow editors Richard Jones and Christina Herrick, we're trying to spread the good news about the RosBREED project in our magazines, website, eNewsletters, and social media to not only U.S. fruit growers, but the fruit industry at large. We thank you for this opportunity.

RosBREED Personnel Updates

Masterfully Succeeded!

Congratulations to Natalia Salinas, who successfully defended her M.S. thesis at Oregon State University. Nahla Bassil, DNA Testing Team Leader, USDA-ARS NCGR Corvallis, and Chad Finn, RosBREED Berry Team Leader, USDA-ARS Corvallis, were her major professors. Her thesis was titled: "Molecular Markers Associated with Perpetual Flowering (PF) and Soluble Solids Content (SSC) in Strawberry". Congratulations, Natalia!



L to R: Chad Finn, Victor Salinas, Natalia Salinas, Rosa Salinas, Nahla Bassil, and Shawn Mehlenbacher, collectively testing the supporting capacity of Nahla's home's deck.

Jack Roach, University of Florida successfully defended his M.S. thesis and graduated on August 8, 2015. Congratulations, Jack!

The topic of his thesis was "Introgression and Genetic Mapping of Resistance to *Xanthomonas fragariae* in Octoploid Strawberry". This research was partially funded by RosBREED to conduct SNP genotyping and resulted in the identification and verification of a locus related to *X. fragariae* resistance.

Jack is planning on taking a semester off to bike and hike in Scotland and then plans to

pursue a Ph.D. in plant breeding/genetics.

Community Breeders' Page

Where is RosBREED? - an Events article

Chris Johnson, DNA-Informed Breeding Team Member, WSU, and Cameron Peace, DNA-Informed Breeding Team Leader, WSU

Someone asked me recently, "Where is RosBREED?" At the time I couldn't give a satisfactory answer, but the question stuck in my mind...

Three emissaries gathered in Davis, California. A glossy brochure was unfolded in a cozy restaurant. Tall, colorful cards were passed around a crowded corner table.

All parties agreed: the information was clear, the illustrations meaningful, and the message inspiring. RosBREED had something tangible to deliver, especially to peach breeders.

This past July, the trio drove up and down the San Joaquin valley, home to the largest and most productive stone fruit-growing region in the country for three days. Breeders and nursery folk, both public and private, were met on their home turf – the third time in five years by RosBREED delegates (Fig. 1). We shook hands, shared advances in new cultivars and helpful new technologies, and sampled

the delicious bounty of the season. "DNA test cards," passed around conference tables and orchards alike, met with nods of understanding and glances of intrigue. Time and time again, the question we had been hoping for was asked: "When can we get started?" A simple question, with a simpler answer: "Right now".



asked: "When can we get started?" A simple question, with a simpler answer: "Right now". Figure 1. Greg Reighard, Clemson University, testing new stone fruit varieties from Terry Bacon's program at Sun World during the recent California stone fruit breeders' tour by RosBREED.

Getting started on

DNA-informed breeding is as easy as having dinner at a restaurant. But the real achievement is not the hard work of the chef or the wait staff. It's the serving of a well-prepared meal with great ingredients, and making it look easy.

Reflecting on those three days, I found my answer to that question of "Where is RosBREED?" RosBREED fills the space between the possible and the actual, between academic speculation and commercial viability. RosBREED is in the space between publications and new cultivars, but is also much more than that. RosBREED is our community, and its fruits are the opportunities made by filling the space between the possible and the actual – bridging the chasm.



Coming up in the next issue:

- Meet new members of the Advisory Panel
- Jewels in the Genome focus on more Rosaceae crops
- New DNA Test Cards
- Meet project members of the DNA-Informed Breeding Team
- What will be the next Rosaceae Nemesis? Read next quarter's Newsletter to find out!

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