RosBREED

Enabling marker-assisted breeding in Rosaceae

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

November 30, 2012

Volume 3 Issue 4

RosBREED Peach Breeder Training and Stakeholder Meeting

The RosBREED Marker-Assisted Breeding in Action peach workshop was held at the Madren Center of the James Martin Inn at Clemson University, South Carolina on October 16-17, 2012. The South Carolina Peach Council provided matching funds for the workshop, which was attended by peach breeders and supporting scientists from the U.S. as well as more than 60 growers from 16 different states. The workshop focused on the genetic tests (for further information, see page 7 of this issue) available to breeders to select parents and progeny with superior trait levels in their germplasm and to inform decisions on the best crosses to make in spring 2013. Genetic tests were presented and discussed for bacterial spot tolerance, skin blush levels, superior flavor, and large fruit size. These genetic tests are made available to breeders from the DNA information gathered in the RosBREED project. Participants in the workshop were able to see the benefits of using genetic tests in peach breeding programs by visiting the Clemson University peach breeding program led by Ksenija Gasic.

The workshop ended with interactive discussions on priority traits in peach cultivar development with peach industry representatives, particularly from the Southeast. Greg Reighard (Clemson University) from the RosBREED's Extension Team led discussions with participants from the peach industry. Breeders who attended the workshop left with new tools for making informed breeding decisions, and they were excited about the future of DNA-informed peach breeding. Peach growers, especially in the Southeast who are already benefiting from Ksenija's breeding program, left hopeful that DNA testing can enhance the efficiency of cultivar development with superior traits.



v.rosbreed.org

Ksenija Gasic, far left, explains to workshop attendees just how big the new peaches from her Clemson University breeding program are going to be



Greg Reighard, second from left, backs up Ksenija's story to growers

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USDA

United States Department of Agriculture National Institute of Food and Agriculture



RosBREED by the numbers

987

Number of samples sent (496 strawberry, 10 cherry, 91 apple) and will soon be sent (390 peach) to DNA diagnostic service providers. A comprehensive report and list of providers will be posted in the *Technology Portfolio* module of the Breeding Information Management System / Breeders' Toolbox.



Amy lezzoni preparing samples to ship to a DNA diagnostic service provider

17,703

Number of peach phenotypic data points for fruit appearance, flavor, texture and production traits in the *Reference Germplasm Database* module of the Breeding Information Management System, held in the <u>Breeders' Toolbox</u> of the Genome Database for Rosaceae. Data were compiled from the 2010-2012 growing seasons from cultivars, ancestors, and representative seedlings.

Sreeders looidox	
RosBREED Crop Reference Set available	Breeders Toolbox Tutorial
Choose Crop	
Set Crop	Peach 👻
Browse Database	
Browse Varieties	Browse Varieties by Datasets
Search Database	
Search Phenotyping Data	Search by Varieties
	Search by Traits
	Search by Parentage
Search Genotyping Data	Search by Varieties
	Search by Variety/Marker
	Search by Marker/Allele

937

Number of responses from market intermediaries to the Socio-Economics Team's survey sent out in 2011. Surveys were conducted by both fresh and processed fruit marketing sectors of the U.S. industry. Fresh crops included apple, peach, strawberry, and sweet cherry. Processed crops included apple, peach, strawberry, and tart cherry.



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MAB In Action! Part 2 - Further Crop Specific Breeder Workshops coming soon

Attention Rosaceae community breeders and industry leaders!!!

RosBREED recently held its first breeder workshop, on peach, focusing on the use of DNA information for planning exciting spring 2013 crosses (see page 1 for more details). We will soon be leading two additional breeder workshops, for apple and strawberry, in January 2013. All Rosaceae crop breeders and interested industry members are welcome to attend the upcoming workshops. You will be able to work together with RosBREED's Demonstration Breeders and MAB technical support crews to use the latest DNA information to increase the efficiency and success of your breeding program. The workshops will especially target the next season of crossing, helping to provide DNA information in support of crossing decisions.

If you are interested in attending one of these workshops, contact Audrey Sebolt (<u>grantzau@msu.edu</u>) no later than December 21, 2012.

Apple Breeder Workshop The morning session will provide brief updates on MAB in action in Demonstration Breeding Programs and other resources available for facilitating MAB. The afternoon will focus on DNA tests available for apple, including those that are still going through the MAB Pipeline (and soon to be available to apple breeders!!!), as well as provide information on service providers who can conduct routine DNA testing for breeders. The afternoon session will also provide training for available software-based modules of the Breeding Information Management System. The workshop will be held a day after RosBREED's Advisory Panel meeting at the same venue, and will be followed by the nearby Plant & Animal Genome Conference.



We look forward to meeting with members of the national and international apple breeding community at this workshop.

Venue: DoubleTree Hotel, San Diego, California

Date: Friday, January 11, 2013

Strawberry Breeder Workshop The goal of this workshop is to give all strawberry breeders, regardless of their level of experience with MAB and genomics, an overview of new DNA-based tools and insights into integrating these tools in their programs using real world examples. The workshop will bring together RosBREED's strawberry Demonstration Breeders and Community Breeders across the U.S. with a focus on MAB for enhancing the efficiency of breeding superior strawberry cultivars. Among the topics discussed will be DNA tests to predict red stele resistance and to confirm trueness-to-type of strawberry cultivars across pedigrees and ploidy levels. Availability of



validated DNA tests, not-yet-validated marker-trait-locus-associations, analytical techniques for the challenging octoploid strawberry, as well as U.S. DNA diagnostics service providers available to assist breeders with DNA testing, will also be discussed. The workshop will conclude with a tour of Chad Finn's breeding program and the USDA-ARS strawberry collection.

Venue: USDA-ARS National Clonal Germplasm Repository, USDA-ARS Horticultural Crops Research Laboratory, and Oregon State University, Corvallis, Oregon

Date: Thursday, January 31, 2013

Consumer Taste Panels

By Karina Gallardo, Socio-Economics Team Leader

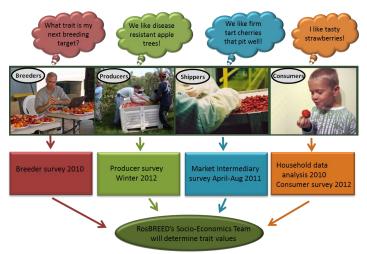
The Socio-Economics Team has conducted a study that included three rounds of experimental auctions and sensory taste tests of apples at Pullman, WA, Minneapolis-St. Paul, MN, and Portland, OR. The goal of this combined study is to elicit preferences and "nonhypothetical" willingness to pay for apple quality attributes, from a total of 384 consumers. The recruitment criteria was that panelists are fruit consumers and responsible for the grocery shopping in the household. For each city, eight sessions were conducted with 16 participants per session.

Apples were procured through the Washington Tree Fruit Research Commission. Gala and Honeycrisp apples were prescreened for appearance, texture and flavor traits so that samples with varying combinations of these traits could be experienced by consumer panelists according to a predetermined experimental design.

Panelists experienced apple samples and submitted three bids in each session. The first bid was based on the apples' external appearance, the second on the apples' taste (after the sensory tasting), and the third on the combined appearance and taste.

As of mid-November, the Socio-Economics Team had successfully conducted studies in Pullman, WA and Minneapolis-St. Paul, MN. This week, the study was conducted in Portland, OR. Stay tuned for the results!

Many thanks to Zachary Baumann, Nancy Buchanan, Claire Burrington, Lilian Carrillo, Jong Choi, Matt Clark, Emily Del Bel, Kate Evans, Ines Hanrahan, Christoph Krusse, Courtney Laskey, Huixin Li, Leontina Lipan, Jim Luby, Austin Miller, Karen Miller, Manoella Mendoza, Udel Mendoza, Brandon Mulvaney, Vicki McCracken, Jim McFerson, McKenzie Milton, Jordan Rasch, Johanna Nodop, Carolyn Ross, Alicia Rihn, Rand Santor, Cari Schmitz, Jenica Smith, Jack Tillman, Zata Vickers, Beata Vixie, Chengyan Yue, and Shuoli Zhao, who assisted with the WA and MN studies





Karina Gallardo (left) and Emily Del Bel (right) prepare apple samples for consumers.



Left: consumers were first asked to rate apples for visual appearance. Right: consumers rated apples for taste and aroma.



Washington State University researchers who conducted the WA consumer panels.



University of Minnesota researchers who conducted the MN consumer panels.

Volume 3 Issue 4 Breeder profile: Ksenija Gasic

By Audrey M. Sebolt, Project Assistant



Ksenija Gasic, Clemson University, showing off her wares



Resistance to brown rot (left) and bacterial spot (right) are key target traits that Ksenija Gasic emphasizes in her breeding program.



Red (left) and yellow (right) flesh colors are both breeding goals for Ksenija's program.



A research assistant in Ksenija's lab performs embryo rescue; the image on the right is of a rescued seed in tissue culture.

South Carolina's peach industry considers itself the "Tastier Peach State". Consumers wholeheartedly agree with this slogan and the numbers support this claim. South Carolina is ranked second (behind California) for fresh market peach production. In an average year, South Carolina produces 200 million pounds of peaches, valued at \$35 million. Consumers are able to enjoy a continuous supply of summer peaches, consisting of 30-40 cultivars that ripen from June to September. However, consumers increasingly demand excellent quality fruit and their taste preferences continue to change. South Carolina peach growers, in order to remain profitable, must meet consumer demands while dealing with numerous abiotic and biotic stresses that can affect production. In 2008, Clemson University hired Ksenija Gasic to revive a breeding program that had been dormat for 25 years and to breed new peach cultivars that meet the demands of the consumer yet provide the highest return on investment for growers.

Breeding for the perfect peach Ksenija's aim is to combine bacterial spot and brown rot tolerance (or preferably resistance) with large fruit that are of excellent quality. Fruit quality traits desired include round, large, firm fruit, melting flesh, freestone, and increased sugars and nutritional value. These traits are to be packaged in skin with a yellow ground color and an intense blush overcolor. Critical production traits include early and late maturing fruit (widening the ripening season), reliable cropping, optimal bloom density, scab resistance, drought tolerance, and freeze tolerance. Of these traits, the evaluation of early-maturing fruit is challenging and labor- and timeprohibitive because embryo-rescue must be performed. All of the seeds from Ksenija's crosses must be embryo-rescued after they are harvested because the fruit from early-ripening female parents ripen before the embryo has had a chance to fully develop.

Ksenija uses various pollen sources for her crosses from William Okie's (Byron, GA) breeding program, Dennis Werner's (North Carolina State University) advanced selections, Brazilian landraces courtesy of Maria Bassols Raseira, and Italian landraces courtesy of Tiziano Caruso and Daniella Giovanini. In a given year, Ksenija evaluates approximately 5000 seedlings, which are planted at Clemson University's Musser Research Farm, located in Seneca, SC.

Ksenija maintains a close working relationship with South Carolina's peach industry to ensure her breeding program goals align with the changing needs of growers and consumers. To facilitate this relationship, Titan Peach Farms, located in Ridge Spring, SC, serves as a second test site (Musser Research Farm is the first) for commercial cultivars. These cultivars are evaluated for ripening stage at commercial harvest time and fruit are packed on a packing line. In addition to commercial cultivars, fruit from RosBREED's Crop Reference Set are also evaluated for phytochemical components and their differences between years, locations, and harvesting times. Chalmers Carr III is Titan Peach Farms' President and CEO as well as a RosBREED Industry Advisory Panel member. For RosBREED, he represents the Southeast peach grower community and ensures that their concerns

Volume 3 Issue 4 Breeder profile cont.



Seedlings that have been embryo-rescued are grown in a greenhouse.



Seedlings planted at the Musser Fruit Research Farm, located in Seneca, South Carolina.

and needs are vocalized to the Rosaceae breeding and community of scientific support. In a previous interview with RosBREED, Chalmers stated that he felt that the peach industry is in need of great tasting, high-quality fruit that can be broadly grown on a consistent basis. Additionally, he is supportive of using new genetic knowledge to more efficiently and quickly meet these goals.

RosBREED's effort towards marker-assisted breeding Ksenija is the team leader for the RosBREED Peach Breeding Team. The RosBREED Demonstration Peach Breeding programs include Clemson University, Texas A&M (Dave Byrne), UC Davis (Tom Gradziel), and the University of Arkansas (John Clark). As team leader, Ksenija coordinated the efforts of prioritizing and constructing the Crop Reference (CR) and Breeding Pedigree (BP) Sets that were phenotyped and genotyped. The CR and BP Sets for peach consist of 953 peach cultivars, ancestors, and representative seedlings from all four peach Demonstration Breeding Programs. The CR and BP Sets were phenotyped during the 2010, 2011, and 2012 seasons under standardized protocols, which focused on fruit quality. This data is now available in the RosBREED Breeders' Toolbox. Traits and methods for generating this data have recently been published. Terrence Frett, Ksenija's past graduate student, is the lead author of this manuscript, titled, "Standardized phenotyping for fruit quality in peach [Prunus persica (L.) Batsch]" for which he won the U.P. Hedrick award from the American Pomological Society. Co-authors include John Clark, Dave Byrne, Tom Gradziel, and Carlos Crisosto.

Towards genotypic data, SNP arrays have been developed as a collaborative effort and a manuscript describing the development and validation of the peach SNP arrays was published this past <u>April</u> (2012) in <u>PLoS One</u> with Ksenija as a co-author. The RosBREED peach team generated 7,761,232 peach SNP data points for the 953 CR and BP Set individuals and Ksenija and Terrence Frett compiled

and quality-checked much of this data. Ksenija and Terrence have also led the efforts in QTL discovery.

This past October, Ksenija and Greg Reighard hosted a successful Peach Breeder Workshop (see page 1). One of the presentation series, titled "Jewels You Can Use", showcased a peach "Jewel" for maturity date. This jewel was <u>first described in our August 2012 newsletter</u>. Maturity date is a critical trait because peach breeders aim to target cultivar development for specific maturity dates to fill gaps held by less desirable cultivars. At the Peach Breeder Workshop, Ksenija described the functional haplotypes that have been defined for this trait and how DNA diagnostic markers can be used to more efficiently breed for maturity date.

During the workshop, Ksenija also defined haplotypes for bacterial spot. Bacterial spot is a serious disease of peach because it can severely defoliate a tree, which can then reduce yield and blemish the fruit, making it unmarketable. Ksenija's lab has discovered 14 QTLs associated with bacterial spot. For five of the major QTLs, haplotype information is available. Haplotypes from resistant parents clearly contribute to the higher fruit tolerance/resistance of bacterial spot in peach.

The Peach Team are currently working towards converting the trait locus SNPs into markers that can be routinely run (i.e. the 2x 24-SNP mini-arrays). The team will soon be submitting leaf tissue from 390 cultivars, ancestors, and representative seedlings to a DNA diagnostic service provider, who will analyze a set of converted SNP markers which are associated with bacterial spot, maturity date, acidity, fruit size, and sweetness, and softening characteristics including slow melting flesh, blush, and flesh browning. For further details, see Cameron's article on the next page.

This coming spring, Ksenija will use RosBREED's Cross Assist tool to maximize her crossing efficiency. <u>Cross Assist</u> will inform her about which peach selections are the best crossing parents based on her traits of interest.

Frett T, Gasic K, Clark J, Byrne D, Gradiel T, Crisosto C. 2012. Standardized phenotyping for fruit quality in peach [*Prunus persica* (L.) Batsch]. Journal of the American Pomological Society 66(4):214-219.

Routine DNA Testing

By Cameron Peace and Nahla Bassil, MAB Pipeline and Genotyping Team Leaders

Routine DNA testing. It's done once you've MAB Pipelined promising QTLs within your own breeding program and thereby established the performance-predictive power of each DNA test for your germplasm under your conditions. By then you are ready to screen your parent pool and/or various seedling families to gain insights into genetic potential that help with your crossing and selection decisions.

What is a DNA test? A DNA test is one or more predictive DNA markers that must be run together to provide a sensible prediction about the genetic potential of any individual screened. For example, predicting apple fruit storability by targeting the Md-ACS1 gene is currently a DNA test that uses just a single marker. The DNA test for sweet cherry fruit size prediction relies on simultaneous genotyping with two markers flanking a valuable QTL. marker 1 Prediction: marker 2 Prediction: large fruit Prediction: small fruit

But how are DNA tests run routinely? And what's all the fuss about SNPs? Genotyping costs are dropping to the point where the multi-locus approach of SNP mini-array genotyping is becoming attractive, especially if breeders coordinate their needs...

To find out the answers to these questions visit the full article at www.rosbreed.org/breeding/community-breeders.

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FruitBreedomics

By: Francois Laurens, FruitBreedomics Project Coordinator

FruitBreedomics is a European-funded project which started in March 2011 and will end in September 2015. Fruit-Breedomics' strategic goal is to improve the efficiency of (European) fruit breeding by bridging the gap between scientific genetics research and application in breeding.

This consortium is composed of 26 partners: 20 research institutes among which some are from Israel, New Zealand and China; five enterprises; and <u>INRA Trans-</u> <u>fert</u>, which manages FruitBreedomics.

FruitBreedomics takes a multidisciplinary approach, including genetics, genomics, ecophysiology, and bioinformatics, to improve the efficiency of apple and peach breeding programs by: 1) developing new and adapted tools, 2) studying a wide range of traits to enlarge the coverage of selection criteria, 3) analyzing and exploiting the wide genetic diversity available, 4) making the research outputs (valuable traits, genetic markers and genes, innovative tools and methodologies, new plant material) directly applicable for the breeders, and 5) establishing a breeder stakeholder network.

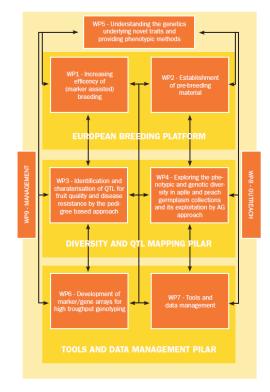
The project is focused primarily on apple and peach, but many tools and much knowledge gained will also benefit other species of the Rosaceae family via the strong ancestral relatedness among these species.

FruitBreedomics' aims, like those of RosBREED, especially concern the development of Marker-Assisted Breeding and Pedigree-Based Analysis. For these two tasks, the two projects are working collaboratively by developing and using the same genotyping tools and regularly discussing joint strategies. We also have

PROJECT STRUCTURE

The project is structured in 9 Workpackages. WP1 will develop a validated pipeline for Mar ker Assisted Breeding and it will implement this major breeding tool in ongoing commercial breeding programs. WP2 will prepare for and make available to the consortium selected pre-breeding material. It will also evaluate a way to reduce the introgression time of new traits from wild species to pre-breeding material with advanced fruit quality by inducing early flowering thanks to fast-breeding technology. The research efforts will be directed to improve our understanding of the genetics of some major horticultural traits and develop innovative research tools to efficiently find marker trait associations in breeding populations and genebank germplasm. To overcome the main issues of the past genetic studies on fruit trees (narrow genetic diversity, low mapping density, single environment), FruitBreedomics will focus on two innovative and complementary genetic mapping approaches based on a wider genetic diversity: i) pedigree-based analysis (PBA) (WP3) and ii) Linkage disequilibrium (LD) mapping over the whole genome, i.e. genome-wide association (GWA) mapping (WP4). WP5 will help to understand the genetics and developing high throughput phenotyping on novel and important traits (Monilia/ peach; texture/apple and abiotic stresses/ peach). WP6 will develop marker and gene ar rays for highthroughput genotyping and WP7 will develop software and data management tools with interface for breeder usage. Fina-Ily, WP8 will take care of dissemination and communication tasks while WP9 will manage the project.







FruitBreedomics participants at their first annual meeting, which was held in Prague, Czech Republic, on February 7-10, 2012

to thank very much the <u>Genome Database for Rosaceae</u> for the help provided in establishing the FruitBreedomics' database.

Contact: francois.laurens@angers.inra.fr Website: <u>www.fruitbreedomics.com</u>

Advisory Panel Member Profile Page

The success of RosBREED will be determined in large part by the people behind it. Because of this, we wanted to give you some insight into these individuals — whether they represent university extension, the scientific community, or industry — who are at the core of our efforts. Panel members were asked about their background and what they want to accomplish as part of the RosBREED project. Here is what they had to say.

Industry



KEVIN MOFFITT

Manager of the Federal Marketing Order Fresh Pear Committee and President & CEO of the Pear Bureau Northwest, kmoffitt@usapears.com

<u>What work do you do?</u> We provide the industry with crop reports, estimates and statistics while conducting and distributing consumer and nutrition research. The Bureau is also very involved in helping increase consumer awareness and consumption of fresh pears through marketing, public relations, and social media tactics. The Fresh Pear Committee also funds and oversees pre- and postharvest pear research.

<u>Why are you interested in RosBREED?</u> To stay competitive in today's worldwide marketplace requires investment in research. Collaboration is extremely important in order to be as efficient and effective as possible. RosBREED is dedicated to cutting-edge forward-looking research with a collaborative approach.

How do you feel you can contribute to RosBREED? Serving on and contributing to our Fresh Pear research subcommittee I have a good feel for the priorities of the fresh pear industry in the Northwest. As an advisor to RosBREED, I can bring these priorities to the forefront while providing insights from the perspective of the retail and end-user.

Industry



TOM STOKES

CEO, Tree Top, Inc., Selah, WA, tom.stokes@treetop.com

What work do you do? Oversee the activities of Tree Top, Inc., a fruit processor located in Selah, Washington

<u>Why are you interested in RosBREED?</u> As the CEO of the largest apple processor in the United States, which is a grower-owned cooperative, it is imperative that I and the organization participate/assist in efforts to insure the long-term viability of the industry as a whole. RosBREED is one of those efforts that has the potential to make very positive advances for the long-term.

<u>How do you feel you can contribute to RosBREED?</u> My primary contribution should be in providing input on the basic business aspects of the desired outcomes of the research direction. In addition, my thoughts on the consumer/market reaction will hopefully be of value.

Scientific



KIM HUMMER

Research Leader and Small Fruit Curator, USDA-ARS, National Clonal Germplasm Repository, Corvallis, OR, kim.hummer@ars.usda.gov

<u>What work do you do?</u> I study genetics and germplasm of temperate fruit and nuts and minor crops, and include studies of botanical and horticultural systematics and plant physiology. Specialty research interest concerns the characterization and evaluation of *Fragaria*, *Ribes*, *Rubus*, and *Vaccinium* species and cultivars for morphological, phenological and disease traits.

<u>Why are you interested in RosBREED?</u> As curator for the *Fragaria* and *Rubus* collections, I am very interested in the RosBREED project. It is imperative that RosBREED and the NCGR-Corvallis genebank cooperate. RosBREED has requested more than 200 samples of strawberries from the NCGR-Collection for study. The genotypic and phenotypic coordination of information on these genotypes will need to be compiled and recorded for long-term use in our Germplasm Resources Information Network (GRIN and GRIN-Global) the publicly accessible gene bank information system. This information will be very useful to me to manage the collections. It will assist with correct taxonomic identification of the accessions in

the collection and will help evaluate qualities of each genotype for further use by everyone.

<u>How do you feel you can contribute to RosBREED?</u> I and my facility have provided living plant materials and information for RosBREED. Once further information is generated and confirmed in the genotyping-phenotyping study, I would like to discuss the results with the RosBREED scientists so that the information can be applied to manage our genebank. Other evaluation information that our unit may generate could be added to the information base that RosBREED uses.

Jewels in the Genome

By Amy lezzoni, Project Director

What is a "Jewel in the Genome?"

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

The pattern of apple skin color differs widely among commercial cultivars and unique patterns are associated with major market cultivars. For example, the cultivars Granny Smith and Golden Delicious have no red overcolor on the skin in contrast to other cultivars that have a medium or high proportion of overcolor. The popular cultivar Honeycrisp exhibits some red overcolor whereas Empire and Jonathan often have complete cover. The pattern of red overcolor on the fruit can also vary. Fruit of cultivars such as Pink Lady have a red blush that is seamlessly blended with a yellow ground color. In comparison, other cultivars such as strains of Red Delicious, have red pigment "painted" in a striped pattern on the fruit. Furthermore, the color of the blush or stripes can be orange to pink to red to almost purple, depending on the cultivar.

In apple (and many other fruits), members of an anthocyaninactivating group of genes called MYB transcription factors control this variation for red color. Rosaceae-wide MYB gene was selected as our 5th Jewel in the Genome because of its importance in controlling apple and cherry fruit and skin color. In apple, the morphological locus is known as Red fruit, with the partially dominant Rf allele conditioning the high skin overcolor proportion and cultivars like Granny Smith and Golden Delicious being homozygous for the rf allele. Genotypes at the Rf locus can therefore be used to predict the proportion of overcolor on apple skin in cultivars, selections, seedlings, and arising from cross combinations. Variations of the two primary alleles, detected as unique SNP haplotypes, were recently detected in RosBREED investigations. These secondary alleles appear to be associated with subtle differences in skin color attributes and other traits such as sunburn incidence (presented at the 2012 6th Rosaceae Genomics Conference, Mezzocorona, Italy).

However, the *Rf* locus does not act alone. Additional loci are being detected from Pedigree-Based Analysis of RosBREED datasets. For example, another locus on chromosome 2, nick-named the "blush" locus (*Bl*), influences how this overcolor is "painted" on the apple fruit surface. Those apple selections with two dominant *Bl* alleles are more likely to have a red (or orange or pink) blush blended across the fruit surface, while those selections that have two recessive *bl* alleles are more likely to have the overcolor appear as stripes.

" PercOvrClr" = "% red / overcolor color of skin" Rt rfrf Golden Delicious, Granny Smith, Aurora Golden Gala Rfrf Honeycrisp, Gala, Zestar, Pacific Rose, Braeburn, Pinova, McIntosh, Cripps Pink, Splendour, Cameo, Red Delicious RfRf Jonathan, Jonamac, Empire, Scired OSBKEED no. **Rf Predictions for Sunburn** 200 150 RfRf All rfif 100 50 rf1rf2 rf2rf4 25 rf1rf1 18% rf2rf2 Probability 10% 10 of no 5 9% sunburn none slight medium severe KOSBKEE. Rf – Has a Friend Another locus, on LG2, is nicknamed the "blush" locus (BI) because on its own it is associated with degree of blushiness vs. stripiness blbl BIBI is more often is more often like this like this But the "BI" locus also interacts with Rf to influence apple skin blush amount (PercOvrClr) - blbl less blush than BIBI .osBREED

Rf – Functional Genotypes

Genetic knowledge of alleles at the *Rf* and *Bl* loci will allow apple breeders to design crosses and select seedlings that are more likely to have desired skin color amounts and patterns, perhaps including new appearances not seen in common cultivars. Therefore, the *Rf* and *Bl* loci are selected as one of RosBREED's "Jewels in the Genome" because it will lead to more efficient breeding of apples with desirable appearance.

RosBREED: Enabling marker-assisted breeding in Rosaceae

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Visit us at www.rosbreed.org

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1				
1	Name	Team	Organization	
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	Gennaro Fazio	Breeding information management system	USDA-ARS, Cornell University	
	Karina Gallardo	Socio-Economics	Washington State University	
	James Luby	Breeding	University of Minnesota	
	Jim McFerson	Industry	Washington Tree Fruit Research Commission	
	Dorrie Main	Genomics	Washington State University	
	Cameron Peace	Marker-assisted breeding pipeline	Washington State University	
	Eric van de Weg	Pedigree-based analysis	Plant Research International, The Netherlands	
	Cholani Weebadde	Extension	Michigan State University	

Calendar of events

- January 10, 2013. Annual RosBREED Advisory Panel Member Meeting, San Diego, CA.
- January 11, 2013. RosBREED Apple Breeder Workshop, San Diego, CA.
- January 30-31, 2013. RosBREED Strawberry Breeder Workshop, Corvallis, OR.