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

Another major milestone accomplished for peach and cherry genetics

2010 was a breakthrough year for peach genetics with the release of the peach genome sequence. However, this DNA sequence was from just one variety. Therefore, RosBREED's task was to use this sequence information to identify the DNA differences that contribute to the wide diversity of peaches used in modern breeding programs. RosBREED scientists and their international partners did just that. They identified a set of 8144 genetic differences, called single nucleotide polymorphisms (SNP) spanning the eight peach chromosomes. Working with a commercial company, Illumina Inc., using state-of-the-art markers similar to those pioneered for human genetics, a "SNP chip" was developed that can examine 8144 SNP data points from an individual variety. A similar strategy was used in cherry, except 5696 SNP data points are on the cherry "SNP chip".

RosBREED purchased enough peach and cherry chips to genotype the full complement of plant material carefully selected for genetic analysis by the peach, sweet cherry, and tart cherry crop teams. This summer, with the help of the DNA genotyping lab headed by RosBREED Co-PD Dr. Dechun Wang, and with the technical expertise of Dr. Dan Zarka, the processing of the RosBREED peach and cherry chips was completed resulting in data files of more than 3.5 million data points for peach and 2 million data points for cherry. To put this in perspective, we now have DNA fingerprinting data of Redhaven peach (and 399 other commercial peach varieties) for 8144 data points; DNA fingerprinting of Bing and a number of other commercial sweet cherry varieties; and Montmorency tart cherry for 5696 DNA locations. Not all SNPs are going to result in usable data, but a significant milestone has been reached. We now have the genome-wide data we need to determine which chromosome regions contain genetic variation that controls the much sought-after traits that have been difficult to tease out in the past, such as firmness in cherry and flavor in peach. This winter will find many of us pouring over our computers hoping to identify new Jewels in the Genome.

The apple SNP chip of 8000 SNP genotyping points will be processed with our South African collaborator Dr. Jasper Rees this fall. Design of a strawberry SNP chip is being pilot tested (see page 7 for further details).

Left: Dan Zarka, Michigan State University. Right: an Illumina Infinium® SNP chip.

From left to right: José Antonio Campoy (INRA, France), Carolina Klagges (Andres Bello University, Chile), and from Michigan State University Umesh Rosyara, Travis Stegmeir, Amy Iezzoni, and Audrey Sebolt

José is a postdoc working with Elisabeth Dirlewanger and José Quero-Garcia. Carolina is a PhD student with Lee Meisel. José and Carolina traveled to Michigan State University this August and analyzed their respective sweet cherry data with the assistance of Umesh

Inside this Issue

Breeder profile: John Clark
By Audrey M. Sebolt, Project Assistant

John Clark, University of Arkansas

Box A: Traits that John Clark evaluates:

- ✦ Firmness at harvest
- ✦ Sweetness
- ✦ Acidity: normal and low
- ✦ Flesh texture: melting and non-melting flesh
- ✦ Fuzz and no fuzz (peach and nectarine)
- ✦ Fungal and disease resistance
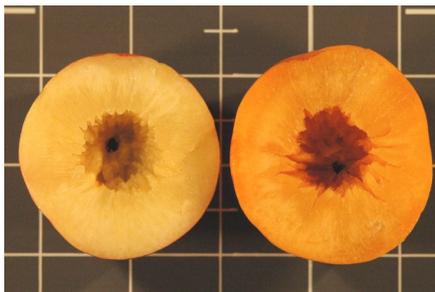
White (left) and yellow-fleshed (right)
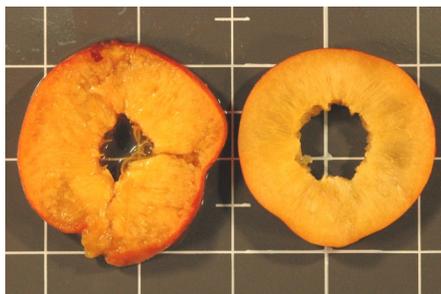
Melting (left) and non-melting flesh (right)

Freestone (left) and clingstone (right)

John Clark is one of the four RosBREED peach Demonstration Breeders and is a professor at the University of Arkansas. John started his career there in 1983 and in addition to peaches he also breeds nectarines, blueberries, blackberries, table grapes, and muscadine grapes. John considers his peach-breeding program to be a "mature program", where he breeds for improved cultivars using the germplasm that he inherited from his predecessor, James Moore. The program's aim is to develop high quality ripe fruit for consumers that are either melting or non-melting, clingstone or freestone, white- and yellow-fleshed peaches and nectarines for the fresh market. To achieve this goal, John aims to produce 4000-5000 first-generation peach seedlings every year and evaluates these seedlings for multiple traits (see Box A).

John recognizes that his peach breeding must address the major limitations in peach production, which include achieving adequate fruit sizes, tolerating fungal diseases such as brown rot, and maintaining post-harvest durability for handling to enable delivery of high-quality fruit to consumers. The task is all the more daunting when he has to face mid-winter damage to tree buds, frost, hail, drought, and heat stress in different seasons of the year. Despite these challenges, John states that the genes for superior performance of these production traits are accessible in his program; however, the million-dollar question is: How should he package these production traits in a form that producers and consumers will accept?

For most fruit crops, it is generally understood that consumers have a wide preference range for aroma, acidity, and sweetness. When it comes to peaches, John often considers several questions while evaluating his seedlings for fruit quality and making selections: Will consumers accept the white-fleshed peaches or will they only prefer yellow-fleshed peaches? Will consumers buy a fresh-market clingstone peach? Are white peaches and nectarines important enough for eastern U.S. growers? How accepting are consumers of a range of fruit acidities and "light" flavors that some low-acid peaches and nectarines can provide? These are questions John ponders but he is hopeful that he will be able to narrow down these preferences after RosBREED's Socio-Economics Team surveys peach producers and consumers this winter and next year, respectively.

In the past, John Clark's program has used traditional plant breeding practices. When asked at the start of RosBREED if he would consider using marker-assisted breeding (MAB) in his program, John used this analogy: "I see the shiny new Lexus, I just need the keys to drive the car." One key for peach is the endoPG genetic test (for more information [click here](#)), which can readily distinguish melting versus non-melting flesh types and freestone versus clingstone. The RosBREED peach crop team has finished its second year of phenotyping and one of the many traits phenotyped was melting versus non-melting flesh. Phenotyping for this trait can be extremely challenging because the characterization of the trait can change as the fruit ripen, thus making it difficult to classify the flesh type with certainty. John is extremely excited that RosBREED will characterize some of his breeding germplasm for this trait at the molecular level using the endoPG genetic test. John will then know what alleles he has in his parents and seedlings and how those alleles were inherited. MAB can also be used in his program to select for larger fruit that have enhanced sweetness, optimal acidity, and desirable flesh color – in other words, he will soon be given the several keys to the "shiny new Lexus".

Breeder profile continued

John Clark feels that RosBREED is leading to many great things. RosBREED is providing innovation to Rosaceae breeding programs, which many of these breeding programs have not seen in the past. This innovation is being introduced through the development of RosBREED's Breeders' Toolbox and the use of DNA markers for MAB and the MAB Pipeline that Dr. Cameron Peace (Washington State University) has developed. RosBREED is also encouraging future breeders, "Breeding Trainees", to learn about and use these new innovations by supporting their degrees through assistantships and travel support so that they can attend scientific meetings and training workshops hosted by RosBREED. Breeding Trainee Paul Sandefur is currently working with John at Arkansas (for more information about Paul, read below).

RosBREED is developing a model for their Demonstration Breeding programs - the MAB Pipeline. Can this model be used for Rosaceae Community Breeders? John believes it can! He stated that he always hesitates when there is new technology, because it can sometimes be trendy but not useful. But, John feels that if a new technology, such as RosBREED's MAB Pipeline, has useful application and can show it has value to reduce costs, more precisely pinpoint genes and their phenotypes, while showing diversity for traits that we haven't been able to characterize in the past, this new technology can make a tremendous difference in breeding rosaceous crops!

Box B: Cultivars John Clark has released (all have bacterial spot resistance):

Fresh Market peaches (all are white-fleshed)

- White Diamond: low-acid and medium-sized freestone peach that has a sweet, distinct flavor often associated with white flesh
- White Cloud: non-melting cling peach, standard acidity and a distinct flavor often associated with white flesh
- White County: exceptional low-acid peach with large size
- White River: first fresh-market, white free peach to be released from Clark's program. The tree is very productive and produces large fruit that are high quality and ripen mid-late season
- White Rock: very productive tree. Fruit ripen mid-early season, low-acid, and have a flavor and firmness exceeding anything achieved in previous Arkansas breeding

Nectarines

- Westbrook: yellow, cling nectarine with excellent flavor for the very early season
- Arrington: yellow, non-melting cling nectarine, early season, very firm at maturity
- Bradley: yellow, non-melting cling nectarine with large size

Processing peaches (for baby food and canned peaches)

- AllGold
- Goldilocks
- GoldJim
- Roygold
- Goldnine

Meet John's Breeding Trainee: Paul Sandefur

Paul Sandefur, University of Arkansas

Why did you choose John Clark's program? During the final semester of my undergraduate horticulture studies, I completed a special project course under the advisement of Dr. John Clark. While working on my project, I realized that I had finally found my calling. Fruit breeding became my passion and I knew Dr. Clark would be the perfect mentor to provide me with the knowledge and experience needed. Dr. Clark's relentless drive yet relaxed attitude make even the hottest Arkansas summer days enjoyable.

What is your thesis project? For my thesis project, I am evaluating the flesh type and storage performance of Arkansas peach and nectarine genotypes. My first goal is to develop a peach and nectarine storage protocol for evaluating selections and other genotypes within the program, with the goal of this protocol being incorporated into yearly evaluations. Second, I am assessing the accuracy and functionality of endoPG molecular markers in predicting flesh type differences in peaches and nectarines through the first application of marker-assisted breeding in the Arkansas program.

What benefits have you seen by being part of RosBREED? Above all, RosBREED has provided me with a broad view of the diverse and complex world of fruit breeding. Thanks to RosBREED, I have had the opportunity to get to know many of the 'all-stars' within the breeding community. I now know that the professionals who have published groundbreaking and truly inspiring research are real people! RosBREED has also been a valuable resource for information regarding genetics and genomics, greatly expanding my knowledge and experience. Although the last RosBREED meeting left me excited for the future, I left on a sad note knowing it would be my last. After two years and three meetings I have made many new friends, am excited to be a part of the breeding community, and am very thankful for having the opportunity to be a part of the RosBREED team.

Community Breeders' Page

Fast-tracked MAB pipelining in peach: the *endoPG* genetic test for fruit texture type
By Cameron Peace, MAB Pipeline Team Leader

A genetic test exists for predicting whether peach and nectarine fruit will have the texture of freestone melting flesh, clingstone melting flesh, clingstone non-melting flesh, or clingstone non-softening flesh, as described in the "Jewel in the Genome" of August 2010. The genetic test is based on *endoPG* genes present at the *Freestone-Melting flesh* (*F-M*) locus. RosBREED is translating the promise of this Jewel into specific tools and information for peach breeders to use in their ongoing breeding decisions. At the risk of mixing metaphors… Using Demonstration Breeder John Clark's analogy of "keys" to his "shiny new Lexus" (see this issue's Breeder profile), the *endoPG* genetic test is a key to start the breeding engine for a high-tech drive to superior new cultivars!

How can the endoPG key be used?
How is RosBREED cutting the keys for each peach demonstration breeder?
How can other stone fruit breeders get their keys?

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

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.

Extension - Media

BRIAN SPARKS
Editor, American/Western Fruit Grower (published by Meister Media Worldwide),
BDSparks@meistermedia.com

<u>What work do you do?</u> As editor of *American/Western Fruit Grower* magazine, I work with our editorial and publishing team in developing print and digital content for our audience. *American/Western Fruit Grower* is circulated to more than 30,000 commercial tree fruit, grape, nut, and berry growers across the country and also has an online presence at GrowingProduce.com, which is the home of information for our entire fruit and vegetable audience. This website features daily news updates, educational and event-based videos, webinars, and a variety of market resources.

<u>Why are you interested in RosBREED?</u> Our magazine's audience is interested not only in what is happening on their own farm, but also in research labs. The work being done by the RosBREED team will have several long-term benefits for the fruit growing industry, from better variety development to improved insect and disease resistance packages.

<u>How do you feel you can contribute to RosBREED?</u> With a direct connection to a wide grower audience, we can assist in disseminating RosBREED's information. In addition, we have strong relationships with several of RosBREED's team leaders, members, and advisors, and can work with them to inform growers about the most important developments they need to know about. We can also assist in anything from audience surveys to educational videos. We currently assist in editing RosBREED's e-newsletter.

Industry

BRUCE GRIM
Executive Director, Washington State Horticultural Association (WSHA), Wenatchee, Washington,
bruce@wahort.org

<u>What work do you do?</u> As the Executive Director of the WSHA, my goal is to advance Washington's tree fruit industry by educating and training growers to meet the changing needs of the tree fruit industry and assist in developing public policy by closely working with the Office of the Governor, the legislature and state and federal agencies.

<u>Why are you interested in RosBREED?</u> RosBREED brings together some of the best research minds connected with an impressive array of research universities to work on critically important genetics/genomics plant breeding issues.

<u>How do you feel you can contribute to RosBREED?</u> I would be bringing a non-science background to the RosBREED project; it may be helpful to 'ground truth' the team's efforts from the perspective of growers, marketers and consumers.

Scientific

SUSAN GARDINER
Principal Scientist, Team Leader Mapping & Markers, The New Zealand Institute for Plant & Food Research Limited (PFR), Sue.Gardiner@plantandfood.co.nz

<u>What work do you do?</u> For the past 20 years I have led the PFR team that specializes in using genomics tools for genetic map construction and mapping of traits in specialty fruit crops as well as development of high throughput marker screening systems utilizing SNPs for marker-assisted selection in our fruit breeding programs. I began identifying major loci in apple for pest and disease resistance, for pyramiding resistances in breeding parents and since have expanded into identifying the genetic control of more complex traits, such as tree architecture, colour, flavour and texture in apple.

<u>Why are you interested in RosBREED?</u> RosBREED's vision of integrating modern genomics tools with traditional breeding approaches to transform crop improvement and enhance the profitability of US rosaceous crop industries fits with my vision for my team in New Zealand. I enjoy working with international partners and the RosBREED collaboration has strengthened research of all my partners; a good example being the development of the Illumina apple SNP chip that required different contributions globally, for its successful production.

<u>How do you feel you can contribute to RosBREED?</u> I have received much assistance from US partners in the past and want to reciprocate. I gladly welcome RosBREED researchers to my laboratory to utilize our technologies for transferable marker identification, SNP validation and genetic mapping, to advance RosBREED's goals. The breeding tools being developed in RosBREED are of great significance to all rosaceous researchers, including breeders, genomicists, pomologists and physiologists. It is an exciting program!

RosBREED leads an unprecedented effort to advance genetics for the cultivated strawberry

By: Amy Iezzoni, Megan Mathey, Chad Finn, Nahla Bassil, Tom Davis, Jim Hancock, and Eric van de Weg

Strawberry genetics has been considered by many scientists as too tough to tackle. This difficulty is due to the large number of chromosomes in the inter-specific hybrid strawberry of commerce (56 chromosomes compared with 16 chromosomes for peach and sweet cherry, and 34 chromosomes for apple) and the redundancy of genetic information on these chromosomes. In partic-ular, this redundancy makes it extremely difficult to identify unique genome-wide markers that can be used for linkage map construction. Despite this daunting task and realizing that at the time of proposal submission, our path-way to unraveling strawberry genetics was still unclear, we "held the family together" and included strawberry in the RosBREED project. Inclusion of strawberry was due to two factors: (1) the huge impact advanced genetics could bring to strawberry breeding; and (2) recent evidence that the straw-berry and peach genomes have very similar gene order, suggesting that lev-eraging information across Rosaceae genera could lead to big payoffs (see "Jewel in the Genome" page 8).

In RosBREED's Year 1, the first task of each crop team was to come up with a set of germplasm, called a Crop Reference Set, that would represent the genetic diversity and important breeding parents used in breeding. These Sets provide lineages and populations that would allow for elucidation of the genetic control of trait diversity. In strawberry, this discussion was held among RosBREED breeders/geneticists (Nahla Bassil, Tom Davis, Chad Finn, Jim Hancock, and Eric van de Weg) and international cooperators (Dan Sargent, Beatrice Denoyes-Rothan, Iraida Amaya, and José F. Sánchez Sevilla). In an unprecedented collaboration, the group agreed to a Crop Reference Set of germplasm that represents not only the relevant di-versity used internationally in breeding strawberry, but also includes four ex-tremely valuable genetic populations generously provided by European insti-tutions (INRA, France; PRI, The Netherlands; EMR, UK; IFAPA-Centro de Churriana, Spain). By this time, the word was out. This was shaping up to be the biggest international collaborative project in strawberry breeding and ge-netics since strawberry breeding began roughly 300 years ago! As a result, big U.S. players, Dr. Phil Stewart (Driscoll Strawberry Associates) and Dr. Vance Whitaker (University of Florida), representing breeding for vast acre-ages in California and Florida, joined the RosBREED-led effort. This addition increased the number of RosBREED strawberry performance evaluation sites from three (Michigan, Oregon, New Hampshire) to five (with Florida and California).

Nahla Bassil (USDA-ARS; Genotyping Team Leader), and Eric van de Weg (PRI, Netherlands; PBA Team Leader) enjoying a sunny break dur-ing the SNP Summit in South Africa, November 2010

Dan Sargent (East Malling, UK, and recently the Instituto Agraraio San Michele, Trento, Italy) sharing his progress in strawberry at the SNP Summit in South Africa, November 2010

This led to the next challenge, how to propagate all this plant material and get identical sets to all these U.S. planting and evaluation sites. Once again, everyone rolled up their sleeves and pitched in. The three providers of the U.S.-based germplasm propagated at their respective locations. This material included breeding selections provided by Jim Hancock and Chad Finn and founders maintained at the USDA-ARS National Clonal Germplasm Repository in Corvallis. Each in-ternational partner also propagated their plant material. However, Driscoll Strawberry Associates helped put it all togeth-er by their offer to have all the European-derived strawberry propagules brought into the U.S. through their quarantine site in Watsonville, CA. This importation included 57 individuals from France, 50 from the Netherlands, 51 from the Unit-ed Kingdom, and 50 from Spain.

So where are these plants now? Approxi-mately 687 strawberry genotypes were planted in the Michigan and Oregon loca-tions in August 2010 (North American propa-gations) and 127 genotypes representing three European mapping populations (France, The Netherlands, and the UK) in July 2011 (European propagations). In Octo-ber 2010, 212 genotypes were planted at the New Hampshire location, and over 600 gen-otypes were planted in California (646) and

University of New Hampshire strawberry Crop Reference Set, planted October 2010. Photo courtesy of Lise Mahoney, RosBREED Breeding Trainee.

Florida (608). A mapping population from Spain is currently in quarantine and will hopefully be planted at several locations this fall or next spring.

With the plant material now in place and phenotyping underway, the attention shifted back to genotyping, specifically the dilemma posed by the 56 strawberry chromosomes. The breakthrough occurred at the RosBREED-led SNP Summit held in November 2010 in conjunction with the 5th International Rosaceae Genomics Conference hosted by Dr. Jasper Rees in Stellenbosch, South Africa. At this meeting, Dan Sargent committed to moving ahead to explore for strawberry, the potential of a high-throughput genotyping platform using state-of-the-art single nucleotide polymorphism (SNP) markers. These markers and platforms have since been developed for the genetically simpler Rosaceae crops of apple, peach, and cherry. Spurred by Dan's commitment and enthusiasm, the ever-energetic geneticist Nahla Bassil, working with Cindy Lawley and Mark Hansen from Illumina Inc. (the company interested in adapting this technology to octoploid strawberry), began weekly conference calls to plan the way forward. Listening to the top strawberry geneticists in action is amazing as Dan Sargent, Eric van de Weg, Tom Davis, and Jasper Rees came up with idea after idea supported by complicated explanations and diagrams. As a result, a pilot study is being undertaken to create synthetic octoploids of known genotypic composition to test the capabilities of the Illumina Infinium® SNP platform and its software to correctly identify the genotypic composition of octoploid strawberry individuals. If this works, we will have a solid strategy to get the genetic information needed to move strawberry forward.

Lise Mahoney, University of New Hampshire, Breeding Trainee

To recognize this expanded effort within RosBREED for strawberry genetics and genomics, Dr. Kim Hummer generously agreed to join RosBREED's Scientific Advisory Panel earlier this year. Dr. Hummer is the Supervisory Research Horticulturist and Research Leader for the USDA-ARS National Clonal Germplasm Repository (NCGR) in Corvallis, Oregon. Her research expertise includes plant exploration and conservation of specialty crop genetic resources. Her present research passion involves the study of ploidy in strawberry species. She contributed her expertise in strawberry to choosing the germplasm to include in the RosBREED strawberry Crop Reference Set and provided 6-8 runners from more than 200 strawberry accessions only available at the NCGR.

Kim Hummer, USDA-ARS and newly appointed RosBREED Scientific Advisory Panel Member

Megan Mathey, Oregon State University, Breeding Trainee

Who are we?
RosBREED Strawberry Breeders/Geneticists
Dr. Nahla Bassil & technicians Elisabeth Alperin and April Nyberg, USDA-ARS National Clonal Germplasm Repository
Dr. Tom Davis & breeding trainee Lise Mahoney, University of New Hampshire
Dr. Jim Hancock & breeding trainee Sonali Mookerjee, Michigan State University
Dr. Chad Finn & breeding trainee Megan Mathey, USDA-ARS Corvallis, Oregon
Dr. Eric van de Weg, Plant Research International, The Netherlands

U.S. Partners
Dr. Phil Stewart, Driscoll Strawberry Associates
Dr. Vance Whitaker, University of Florida

International Collaborators
Dr. Dan Sargent, East Malling Research, East Malling, UK, and now the Istituto Agrario San Michele All'adige, Trento, Italy
Dr. Béatrice Denoyes-Rothan, INRA, Bordeaux, France
Dr. Iraida Amaya and Dr. José F. Sánchez Sevilla, IFAPA-Centro de Churriana, Spain
Dr. Andrew Jamieson, Agriculture and Agri-Foods Canada, Kentville, Nova Scotia

Other Contributors on the Weekly Strawberry Conference Calls
Dr. Jasper Rees, Agricultural Research Council, South Africa
Drs. Cindy Lawley, Mark Hansen, and Jill Orwick, Illumina Inc., CA
Dr. Hailong Zhang, University of New Hampshire
Drs. Dorrie Main, Cameron Peace, and Stephen Ficklin, Washington State University

Sonali Mookerjee, Michigan State University, Breeding Trainee

Jewels in the Genome
By Amy Iezzoni, Project Director

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

Strawberry flavor is influenced by fruit acidity in combination with sugars and aroma compounds. Improving strawberry flavor is a high priority for breeding programs; however, obtaining the optimum combination of these desirable taste attributes has been challenging as little was known about their inheritance. Recently, a locus that affects acidity in octoploid strawberry fruits was identified near the top of linkage group V (Zorrilla-Fontanesi et al. 2011). Phenotypic measurements of titratable acidity and pH were used to identify this acidity locus, named *TaV-M.2*. This trait locus is of particular interest as it was identified in all three years of evaluation and it clusters with genes controlling variation for fruit color. Interestingly, the orthologous region in peach, i.e. the top of *Prunus* linkage group 5, also contains a major trait locus (*D*) that controls acidity in peach fruit (Boudehri et al. 2009).

TaV-M.2 was identified in progeny from a cross between two diverse octoploid strawberry selections; therefore, the task still remains to identify the functional variations of this locus in strawberry breeding germplasm. The RosBREED strawberry crop team, including its international partners, is preparing to do this experiment using Pedigree-Based Analysis of genotypic and phenotypic data collected on the strawberry Crop Reference Set (see pictures right).

With genetic knowledge of performance-enhancing *TaV-M.2* variants in their plant material, strawberry breeders will begin to predict fruit taste, resulting in more efficient parental selections. Therefore, because knowledge of the *TaV-M.2* region will lead to more efficient breeding of strawberries with desirable eating quality, it is chosen as our seventh featured "Jewel in the Genome."

Figure 1. Fruit color variation in octoploid strawberry
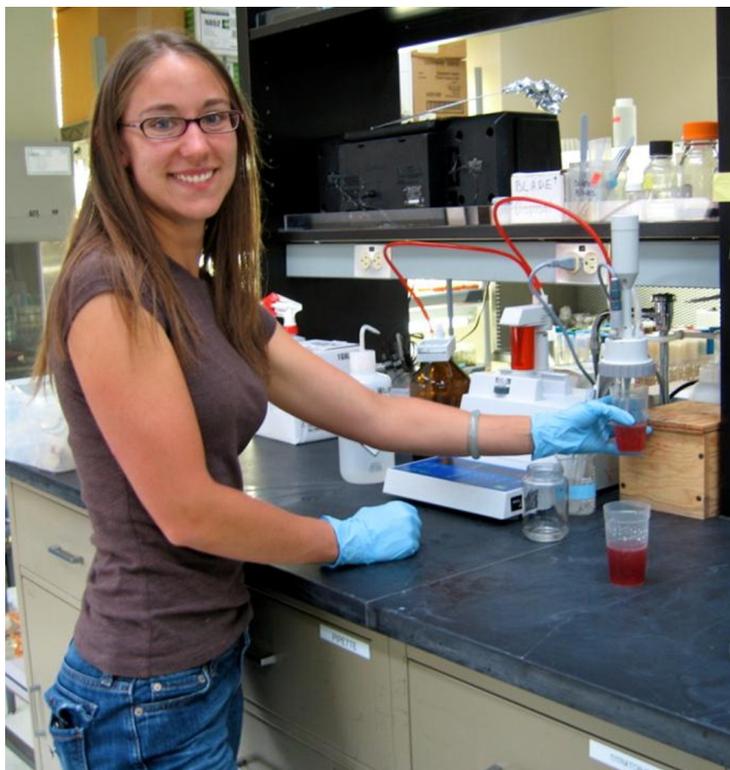
Figure 2. Megan Mathey, Oregon State University, measuring titratable acidity in strawberry

Boudehri K, Bendahmane A, Cardinet G, Troadec C, Moing A, Dirlewanger E. 2009. Phenotypic and fine genetic characterization of the *D* locus controlling fruit acidity in peach. BMC Plant Biol 9:59

Zorrilla-Fontanesi Y, Cabeza A, Dominguez P, Medina JJ, Valpuesta V, Denoyes-Rothan B, Sanchez-Sevilla JF, and Amaya I. 2011. Quantitative trait loci and underlying candidate genes controlling agronomical and fruit quality traits in octoploid strawberry (*Fragaria × ananassa*). Theor Appl Genet DOI 10.1007/s00122-011-1624-6

RosBREED: Enabling marker-assisted breeding in Rosaceae

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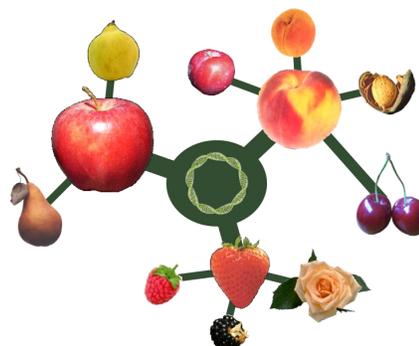
Visit us at
www.rosbreed.org

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    Amy Iezzoni (Michigan State University)
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Name	Team	Organization
Nahla Bassil	Genotyping	USDA-ARS, Corvallis
Gennaro Fazio	Breeding information management system	USDA-ARS, Cornell 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
Chengyan Yue	Socio-economics	University of Minnesota

Calendar of events

- **September 25-28, 2011: American Society for Horticultural Sciences will meet in Hawaii. For more details, please visit ASHS.**

- **January 12, 2012: Annual RosBREED Advisory Panel Member meeting. San Diego, CA**

- **March 12-15, 2012: Annual RosBREED Project Planning meeting for project participants. East Lansing, MI**