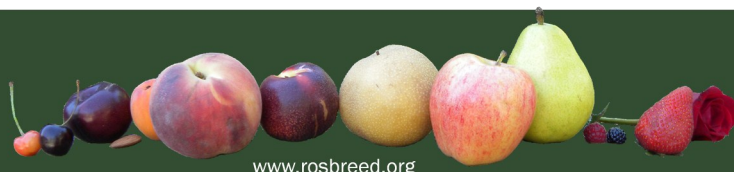


# RosBREED

Enabling marker-assisted breeding in Rosaceae



www.rosbreed.org

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

**May 31, 2012**

**Volume 3 Issue 2**

## **RosBREED's Third Annual Project Meeting, East Lansing, Michigan, March 2012**



RosBREED had its third annual meeting of its participants from March 12 - 15 at the James B. Henry Center in East Lansing, MI. The meeting was attended by 41 scientists.

On the first day of the meeting, Project Director Amy Iezzoni and the RosBREED Team Leaders gave brief updates on the progress made during the previous year. Each Team Leader also presented upcoming activities and breakthroughs, building on current momentum. Afternoon breakout sessions focused on discussions about upcoming activities, followed the day after by summaries of these breakout sessions. A "Meet and Greet" session highlighted the breeders and displayed fruit quality attributes that RosBREED is enhancing through marker-assisted breeding. Among the invited attendees of this session were Gloria Denning from Senator Debbie Stabenow's office (Democrat of Michigan), local RosBREED Advisory Panel members, MSU higher administration, and grower and fruit industry leaders in Michigan.

The project meeting was followed by a PBA Workshop led by Marco Bink and Eric van de Weg (Plant Research International, Netherlands) and assisted by Umesh Rosyara and Dechun Wang (Michigan State University). Over a three-day period, Demonstration Breeders and their Trainees worked within individual crops teams (cherry, peach, apple, and strawberry) to communally conduct QTL discovery and interpretation with their own data accumulated over the last two years. Participants left with a lot of momentum to discover many more QTLs and, critically, to polish them into genetic tests that each breeder can use routinely in their own program!



Phil Korson (Cherry Marketing Inst.), Gloria Denning (Senator Debbie Stabenow's office), and Jim McFerson (Washington Tree Fruit Research Commission).

### ***Inside this Issue***

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United States Department of Agriculture  
National Institute of Food and Agriculture

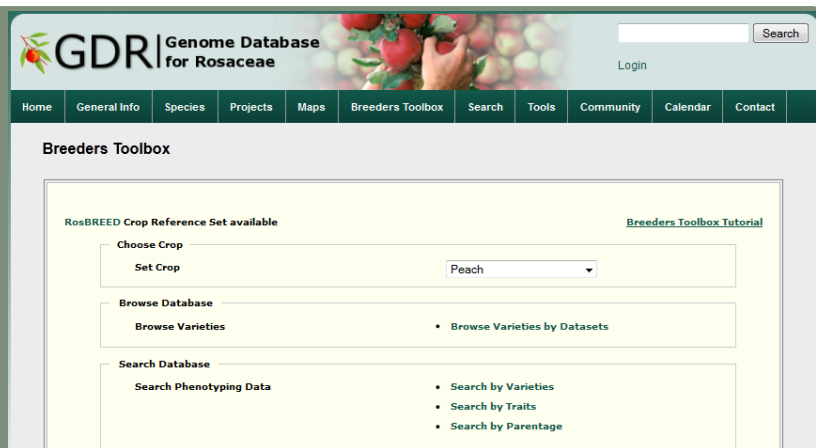


**Register for RosBREED's  
MAB In Action, to be held  
July 30!**

# RosBREED by the numbers

## 23,395

Number of phenotypic data points collected by Clemson University, Texas A&M, UC-Davis, and University of Arkansas peach breeding trainees from the 2010 and 2011 harvest that will be archived in the [Breeder's Toolbox](#).

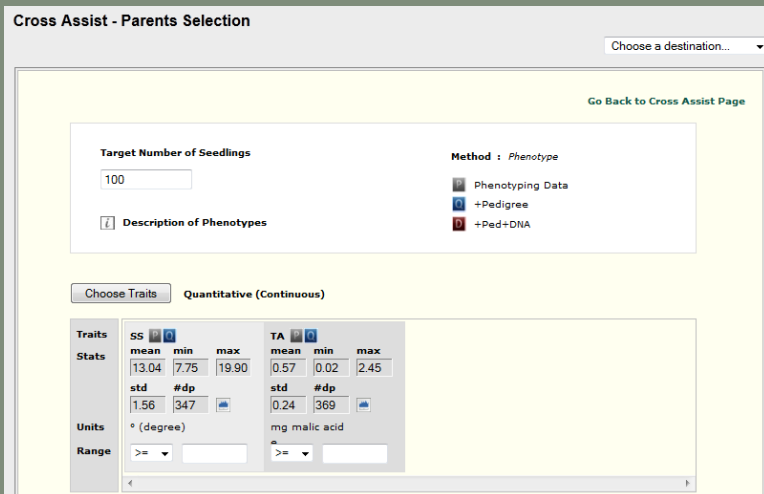


## 26

Number of apple crosses made by University of Minnesota breeding program in spring 2012 based on DNA and pedigree information facilitated by [RosBREED's Cross Assist](#).



Matt Clark, University of Minnesota, pollinating apples



## 59

Percent seedlings culled from Kate Evan's Washington State University Apple Breeding Program. 7452 seedlings were screened for the [apple texture \(\*Md-ACS1\*\)](#) and ["fresh sensation"](#) diagnostic markers. 4403 seedlings were culled as they did not contain favorable alleles for these traits.



96-well pot system used for ease of matching plants to a 96-well DNA plate. The high-throughput genetic screening was performed at the Pacific Northwest Tree Fruit Genotyping Lab, Pullman (Cameron Peace, Washington State University)



## Be sure to attend our ASHS Presentation Series: **Discoveries and Breeding Databases for the Fruit Research Community**

When: 8am - 10am, August 1, 2012

Location: Trade Room in the InterContinental Hotel, Miami, FL  
(attendees must register for ASHS)

### Talks include:

- ★ RosBREED mission - Jewels in the Genome: Amy lezzoni
- ★ RosBREED's breeding germplasm used for validation of promising trait loci: Jim Luby
- ★ Loci important for apple fruit quality: What is known about their functional alleles? Cameron Peace
- ★ Loci important for peach and cherry fruit size and quality: What Is known about their functional alleles? Ksenija Gasic
- ★ Data overload - Breeding decision-support software to the rescue! Sook Jung

RosBREED  
News

### Dr. Nahla Bassil Attends Biotech 2012 in New Zealand

As the Chair of the Molecular Markers Working Group of the International Society for Horticultural Sciences (ISHS), RosBREED Co-PD and Genotyping Team Leader Dr. Nahla Bassil was recently invited to the Second International Symposium on Biotechnology of Fruit Species (Biotechfruit 2012), held in Nelson, New Zealand March 25-29, 2012. She represented RosBREED at this meeting with three presentations titled: "RosBREED: Enabling marker-assisted breeding in Rosaceae"; "Phenotyping strawberry to further advance strawberry breeding"; and "Validating a marker for red stele (*Phytophthora fragariae*) resistance in *Fragaria*".

At this meeting, among others, Dr. Bassil met with collaborators from Plant and Food Research (New Zealand) to discuss ideas for enhancing RosBREED's future.



From left to right: Satish Kumar, David Chagné, Sue Gardiner from Plant and Food Research (New Zealand), Nahla Bassil (USDA-ARS, Oregon), and Emily Buck (Plant and Food Research, New Zealand)



## Breeder profile: Tom Davis and Lise Mahoney

By Audrey M. Sebolt, Project Assistant



Tom Davis, University of New Hampshire



Lise Mahoney, University of New Hampshire



An example of a showy red-flowered selection

Tom Davis is our third strawberry Demonstration Breeder, and the last to be interviewed. Tom is well known to the Rosaceae community: he is a member of the International Strawberry Genome Sequencing Consortium, the international strawberry SNP array development team, and a leading researcher in strawberry molecular evolution and genetics. Strawberry breeding has only recently become one of Tom's activities, spurred by his passion for the crop and the opportunities offered by RosBREED.

Tom has been with the University of New Hampshire since 1984. Since 1992, his primary interests have been to understand the evolutionary history of the strawberry genus, *Fragaria*, and to identify genes influencing traits of potential economic value including fruit quality, fruit color, flowering habit, and disease resistance. As part of these efforts, Tom has developed numerous germplasm and genomic resources for basic and applied strawberry research. Tom and his lab were the first researchers to publish a genetic linkage map for the ancestral diploid strawberry model species, *Fragaria vesca*, and are developing the first linkage map for a second ancestral diploid, *F. iinumae*. In 2004 he joined with Kim Hummer, Director of the National Clonal Germplasm Repository in Corvallis, OR, to collect *F. iinumae* and other fruit germplasm in Hokkaido, Japan. Tom was on the team that recently sequenced the diploid woodland strawberry (published December 2011 in [Nature Genetics](#)) and his knowledge of strawberry genetics and genomics has been instrumental to the ongoing process of developing RosBREED's strawberry genome scanning capability.

RosBREED, to date, has developed SNP arrays and used them to genome-scan reference germplasm sets for apple, peach, sweet cherry, and tart cherry. However, a SNP array for the octoploid cultivated strawberry is still in the development stage. The cultivated strawberry species, *F. × ananassa*, has eight sets of chromosomes, as compared to two sets for peach and apple, and two or four sets for cherry, thus making strawberry a particularly challenging subject for genetic research of any kind! Tom's expertise and knowledge of molecular diversity patterns in strawberry have been a tremendous resource for planning and developing the strawberry SNP array, which is advancing via an international collaboration coordinated by weekly conference calls that include several RosBREED participants and other partners ("[RosBREED leads effort to advance genetics for cultivated strawberry](#)"). To speed completion of the SNP array development process, a new Strawberry Bioinformatics Team has just been created at UNH under Tom's leadership. In close collaboration with other RosBREED scientists, their task will be to help provide octoploid strawberry a viable genome scan platform by the end of summer of 2012.

Until three years ago, Tom did not have a breeding program, although he does perform numerous crosses for the purposes of his genetics program. The resulting hybrids and segregating progeny populations serve the goals of creating genetic linkage maps, identifying markers and genes of interest, and understanding the ancestries of octoploid strawberry. However, Tom has recently undertaken a concerted effort to establish a strawberry breeding program at UNH, relying substantially upon the passionate enthusiasm and commitment of his RosBREED graduate student, Lise Mahoney. Upon starting her Ph.D. program in marker-assisted strawberry breeding three years ago, Lise Mahoney has become the driving force for establishing a strawberry breeding program for the University of New Hampshire as a natural extension of Tom's existing genetic research program and



**Breeder profile cont.**

RosBREED's support. The breeding program's aim will be to develop high quality, well adapted strawberry cultivars for local and regional fresh-market niches. Cultivars with flowering habits suitable for production of a strawberry crop during the autumn months are of particular interest as well as for the ornamental industry. Lise is utilizing wild strawberry germplasm in crosses aimed at incorporating valuable alleles from wild into cultivated genetic backgrounds. As one aspect of her thesis project, she is introducing showy red flowers and enhanced anthocyanin compositions into high quality cultivars. Last summer, Lise released the red-flowered, ornamental strawberry cultivar Red Runner. Lise hopes to release several more red-flowered cultivars with enhanced fruit qualities next summer.



Univ. of New Hampshire field plot where RosBREED's Crop Reference Set plants are grown

In a given year, Lise performs 100-150 crosses each spring and her target traits include enhanced anthocyanin composition, ever bearing, pleasing fruit shape, attractive flowers, and Verticillium wilt resistance. Lise also aims to develop and apply DNA markers that will allow her to genetically dissect and more efficiently breed for her traits of interest. She currently manages 2200 plants in the greenhouse, 1000 of which are diploid and are for genomic studies, 600 are germplasm, and 600 (33 families) are for the breeding program. In 2012, Lise is evaluating nine families (260 plants) that are grown in a cooperator's field and 14 families (290 plants) at the UNH Woodman Horticultural farm, which are closer to being released.

Tom and Lise are partnering in a mission to expand their strawberry breeding program, and both feel that the cultivars they release will be desired and well suited for their growing region because they are being bred locally. The expansion of their program is at a crucial stage because of the prospective availability of a strawberry SNP array that will become a powerful resource for marker-assisted breeding. They definitely intend to use marker-assisted breeding to increase the efficiency of their work, and by using markers and the SNP array developed by RosBREED, this promised efficiency can be realized. Lise aims to graduate in May 2013 and be able to continue as the program's breeder as a University employee or in some other capacity. Either way, she wants to continue to work with strawberries in New Hampshire!

**Meet Tom's Breeding Trainee: Lise Mahoney**

Lise Mahoney and Jim Hancock at a Michigan State Univ. strawberry research field, PBA Workshop 2010

**Why did you choose Tom Davis' program?** Because I love genetics and wanted to breed strawberries for anthocyanin composition in both flower and fruit. I had attended one of Tom's seminars and I was captivated by his presentation of his strawberry genetics research program. Tom's program had a prior and ongoing interest in anthocyanins for yellow versus red strawberry fruit and so my interest in the specific anthocyanins dovetailed perfectly.

**What is your thesis project?** Marker-Assisted-Breeding for Anthocyanin Composition in Strawberry. I became interested in strawberries, quite by accident. In researching for a paper on the health benefits of blueberries, I found a citing that wild strawberries contained equivalent levels of cyanidin and pelargonidin, while the cultivated strawberry contained only about 10% cyanidin and 90% pelargonidin. This could be important as cyanidin was reported to have about twice the antioxidant potential of pelargonidin. Was it really true that the cultivated strawberry (an octoploid) contained very little cyanidin and that some *F. vesca* (diploids) contained high levels of cyanidin? If the cultivated strawberry contained very little cyanidin, were there wild ancestral octoploid species that contained high cyanidin? And if so, could wild octoploid species be used to introgress the cyanidin trait into the cultivated strawberry? Could a strawberry with red flowers and delicious fruit be developed? And what are the genetic determinants for anthocyanin composition? The first two questions I was able to answer affirmatively in my master's thesis. The remaining questions are the focus of my doctoral thesis.

**What benefits have you seen by being part of RosBREED?** I feel so fortunate and grateful to be part of such an important project and have enjoyed meeting and interacting with renowned breeders and geneticists. We are in our second summer participating in the multi-location strawberry phenotyping project. Highlights include: participating in the RosBREED strawberry weekly SNP array design conference calls, the tour of Michigan State University strawberry (Jim Hancock's) and tart cherry (Amy Iezzoni) breeding programs during the 2010 PBA Workshop. I feel I have developed an understanding of marker-assisted-breeding and selection and I am working towards practical applications. I understand the bridge between Markers and Breeding; and how to build the bridge! I have really benefited from the instruction on the use and practical application of Pedimap and FlexQTL™. I was able to use FlexQTL™ to identify QTLs for anthocyanin composition in a diploid mapping population and presented these findings at PAG 2011 and I have been using Pedimap for my breeding populations. These tools are so powerful; I have only realized a fraction of their potential.

# Community Breeders' Page

By Cameron Peace and Sook Jung

You are invited to

## ***MAB in Action!***

### **Integrating DNA information into your breeding program**

A one-day workshop on 30 July 2012 preceding the ASHS conference

At the InterContinental Miami Hotel, Miami, Florida

Sponsored by RosBREED

Seats are limited. Register by emailing Cholani Weebadde (weebadde@msu.edu)



You are invited to a Participatory Workshop entitled  
“Marker-Assisted Breeding in Action”

---

Hosted by RosBREED researchers showcasing examples of Marker-Assisted Breeding currently used in apple, peach and cherry breeding programs

This Workshop will be held on 30 July 2012, one day prior to the ASHS annual conference. The Workshop and ASHS conference will be held at the InterContinental Miami Hotel in Miami, Florida.

For further information, please contact Cholani Weebadde  
email: weebadde@msu.edu



*MAB in Action* is a full-day workshop prepared and delivered by RosBREED researchers, with the sole aim of facilitating MAB in Rosaceae breeding programs for maximized efficiency, precision, and creativity in new cultivar development. This workshop is therefore central to the RosBREED Mission and a major event on the project's four-year calendar. This one's for you.

*MAB in Action* will provide valuable how-to on the following breeding needs, with lots of discussion!

- ✓ staying abreast of available DNA information
- ✓ identifying valuable DNA information for your breeding program
- ✓ choosing a suitable genetic screening service provider
- ✓ adapting a genetic test to your breeding program
- ✓ validating the robustness of a promising genetic test
- ✓ determining the predictiveness of a genetic test for your conditions
- ✓ discovering the distribution of “jewels” in your germplasm
- ✓ using DNA information to enhance crossing decisions
- ✓ establishing routine DNA testing for seedlings

Here's what we expect you'll get out of it:

You will know where and how to *access useful RosBREED resources* (experts, tools, information, software, germplasm, collaborative networks) to enable your own MAB!

You will be *enabled to integrate DNA information* into your breeding program!

You will be *excited to use DNA information* in the near future in your breeding program!

**Now you know you've got to attend!**

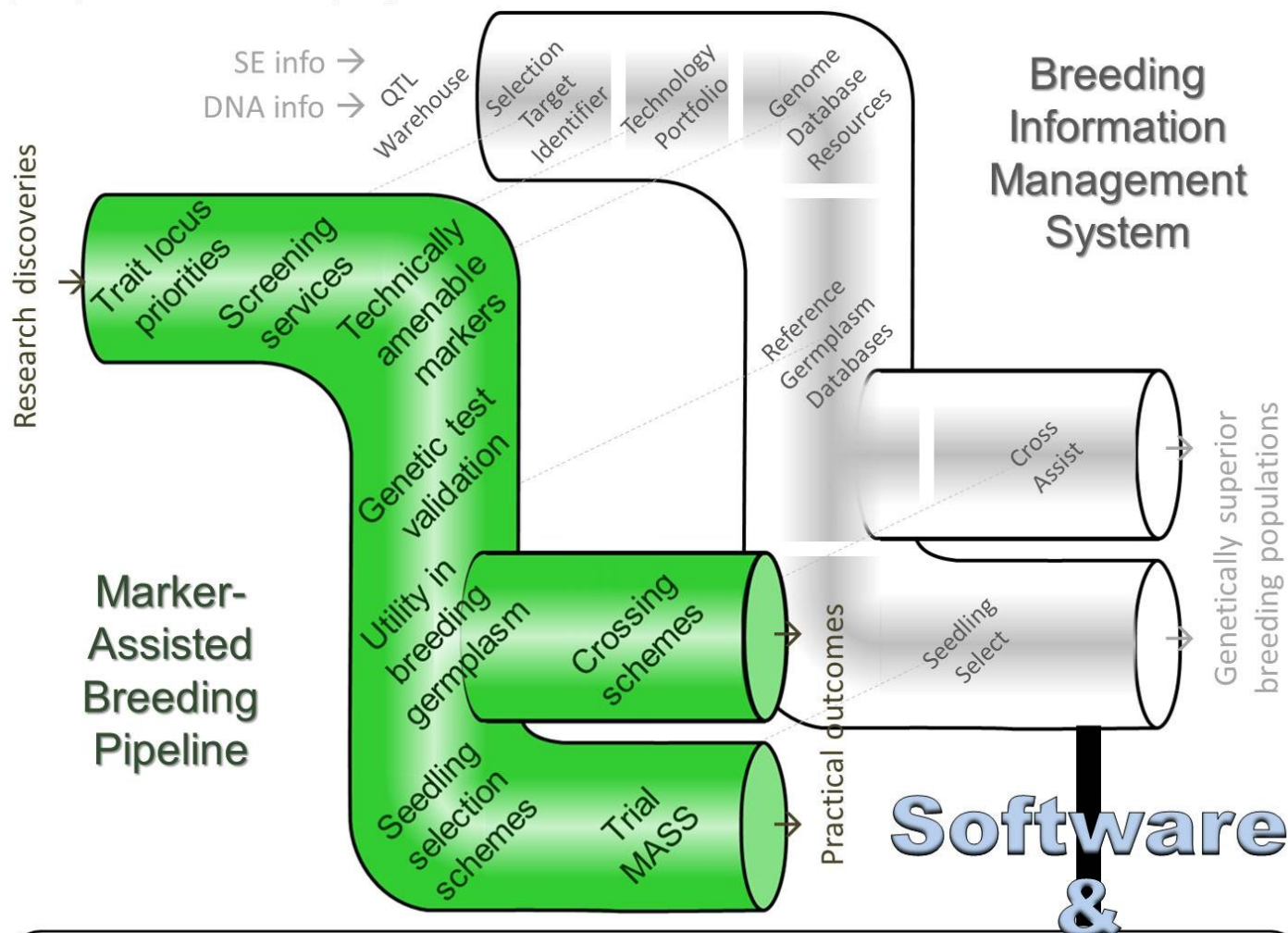


**Community Breeders' Page cont.****Special feature: MAB in Action workshop**

The *Marker-Assisted Breeding Pipeline* is RosBREED's systematic approach to translating genomics research discoveries into practical outcomes for breeders – introduced in the Nov 2010 Newsletter's Community Breeders' Page.

To ease and streamline such translation, a series of software and database modules supports the Pipeline. Together, these modules encompass the *Breeding Information Management System* – introduced in the Feb 2012 Newsletter ("More Power to the Breeder!").

Both the MAB Pipeline approach and the software and database support will be described during the workshop – putting the tools and knowledge in your hands!



*Data → Information → Knowledge → Wisdom*

...your **Breeding Information Management System**

Breeding programs generate large performance, pedigree, and geographical datasets. Information extracted from these data must be integrated to gain valuable knowledge about efficient and accurate breeding operations. Knowledge applied over time provides breeding experience. Wisdom is the accumulated knowledge to consistently make robust decisions such as which parents to cross, which offspring to cull, and which selections to advance. Efficient, accurate, and robust breeding opens the door to creativity.

RosBREED is adding volume and complexity to conventional breeding data. Socio-economics (SE) information describes trait values. DNA information describes locations and effects of "jewels in the genome" – genes controlling valuable traits.

RosBREED's software and database support is beginning to enable integration of a range of information sources to provide knowledge to use in wise decisions. Computer power is key: the vast underlying datasets are more than the human mind can process! Previously available software had insufficient scope and functionality.

**Database Support**



# FAQs

## ❖ What is the MAB in Action Workshop?

*A Workshop to facilitate marker-assisted breeding in Rosaceae. At this workshop, we will highlight success stories in RosBREED's demonstration breeding programs then dissect the practical steps to explain how all U.S. breeders can be similarly routinely DNA-informed.*

## ❖ Where and when will it take place?

*One day prior to the ASHS annual conference at the InterContinental Miami Hotel (same venue as the ASHS conference itself) in Miami, FL. The workshop, held in the Junior Ballroom, starts (registration) at 8:00 am and finishes at 5:30 pm. Come earlier and join us for a free continental breakfast! Lunch, drinks, and snacks throughout the day are also provided.*

## ❖ Is there a registration fee?

*No, all of the day's activities, food, and refreshments are provided free for you.*

## ❖ Who is this workshop for?

- All U.S. Rosaceae breeders (public and private).
- Any other professionals associated with Rosaceae breeding programs and committed to their efficiency and success.
- Breeders and allied scientists of similar specialty crops and other countries are also welcome.

## ❖ What topics will be covered?

*See the Agenda on page 10.*

## ❖ Why should I attend this workshop?

*You will get to use first-hand the tools, technologies, and techniques that RosBREED is developing for breeders to enable you to more efficiently, accurately, and creatively develop new cultivars.*

## ❖ What do I need to know before attending the workshop?

*Breeding – why it's done and how it's done. In other words, what you already know. It will help if you have been keeping up with RosBREED's quarterly Newsletters or have recently read over past ones.*

# Software & Database Support

continued...

The *Toolbox* is our colloquial name for the online portal to marker-assisted breeding software and database support. The Genome Database for Rosaceae hosts the Toolbox.



**GDR** | Genome Database  
for Rosaceae

Currently available features of the Toolbox include:

- Browsing and searching varieties with specific trait levels and genotypes
- Downloading genotypic and phenotypic data of user-chosen varieties
- Generating input files to use in breeding software
- *Cross Assist*, a tool allowing breeders to identify efficient crosses to achieve desired performance targets in seedling populations. This tool leverages knowledge on DNA-based breeding values

## Cross Assist

Cross Assist, RosBREED's software and database support for crossing decisions, was first released to Rosaceae breeders at the project's annual scientific meeting in mid March 2012 at East Lansing, MI.

Some new functionalities have since been added.

Grad student Sushan Ru (Washington State University) is particularly focused on developing this module as far as she can go, for maximum utility by Rosaceae breeders.

Programmer Taein Lee (Washington State University) converts ideas into software reality, for Cross Assist and other Toolbox modules.

*You can choose the traits and their levels that you want to achieve in the next generation*

Choose Traits      Quantitative (Continuous)

Traits	SS	P	Q	TA	P	Q	Weight	P	Q
Stats	mean	min	max	mean	min	max	mean	min	max
	13.04	7.75	19.90	0.57	0.02	2.45	182.88	17.40	574.25
	std	#dp		std	#dp		std	#dp	
	1.56	347		0.24	369		68.24	374	
Units	° (degree)			mg malic acid e..			grams		
Range	>= <input type="text" value="12"/>			>= <input type="text" value="0.4"/>			>= <input type="text" value="180"/>		



# FAQs

continued...

## ❖ What should I bring to the workshop ?

Your inquisitiveness (there will be lots of discussion), your skepticism (lots of myths and mindsets will be confronted), and your needs (lots of resources will be provided and/or their means of accessibility explained). Breeders, bring your colleagues and support staff if you want to share the understanding and most rapidly integrate the many facets of MAB you'll learn about. Bring your laptop if you want to try using some of the helpful software modules (but not for checking emails, please...). If you do not have a laptop, we can partner you with a member of the RosBREED organization team. Pens and writing paper will be provided for you.

## ❖ What will be the structure of the workshop?

A mix of discussions, quizzes (!), explanatory slides, and computer-based and pen-and-paper exercises.

## ❖ Who will conduct this workshop?

RosBREED's MAB Pipeline Team Leader (Cameron Peace), Extension Team Leader (Cholani Weebadde), and Genotyping Team Leader (Nahla Bassil). Also featuring RosBREED's Project Director (Amy Iezzoni) and various Demonstration Breeders.

## ❖ What will I know and be able to do after the workshop?

You'll be able to get your marker-assisted breeding underway. Your arms will be loaded up with available genetic tests, reference germplasm data, websites, and contact details. Your new skill set will include the ability to critically evaluate how ready any genetic test really is for your program, how to polish them up for maximum decision support using systematic software and logic, and how to apply them routinely for crossing and performance prediction. You'll know who and where to go to obtain further tools and information as needed and as they become available. And a little bonus is planned so you can hit the ground running!

## ❖ Will this workshop be offered again?

There are no plans to hold this workshop again within the current RosBREED project.

# Software & Database Support

## Cross Assist continued...

### Choices Made

Parental Dataset	APPLE_CRS
Target # of Seedlings	100
# of Parents	48
# of Pairs of Parents	1128
Method	+Ped+DNA

You can choose the target number of seedlings that you would want to achieve with your specified trait levels—within which you can then select for other traits

In this example, 48 apple parents are available which could be potentially combined pairwise in 1128 ways. To examine the efficiency of each combination in achieving targets, the calculation will rely on phenotypic data plus (in this example, and always recommended for MAB!) pedigree and DNA information

### Filter Results

#### Data Completeness

☒ ☐ ☐

● Both parents have data for all chosen traits  
● One parent has no data for at least one trait

#### Number of Seedlings

#### Mother

#### Father




Calculation results can be filtered according to data completeness, required number of seedlings, and parentage

### Cross List

# of Seedlings Required ▲	Mother	Father	Formula
137	MN1914	Goldrush	$f_x$
139	Fiesta	Goldrush	$f_x$

The filtered results can be viewed, sorted, and downloaded. In this example, showing just the top of a very long table, a cross of 'Fiesta' and 'Goldrush' is expected to require a family size of only 139 seedlings to provide 100 seedlings that have fruit with a soluble solids (SS) concentration of  $\geq 12^\circ\text{Brix}$ , titratable acidity (TA) of  $\geq 0.4$  meq/L, and weight of  $\geq 180$  g. Quite an efficient cross for this purpose, according to the underlying dataset

Cross Assist can be accessed at:

[www.rosaceae.org/bt\\_cross\\_planning\\_tool/ca\\_front\\_page](http://www.rosaceae.org/bt_cross_planning_tool/ca_front_page)

A detailed tutorial on Cross Assist and other Toolbox modules can be found at:

[www.rosaceae.org/sites/www.rosaceae.org/modules/breeders\\_toolbox/bt\\_document/docs/breeders\\_toolbox\\_tutorial.pdf](http://www.rosaceae.org/sites/www.rosaceae.org/modules/breeders_toolbox/bt_document/docs/breeders_toolbox_tutorial.pdf)



Community Breeders' Page cont.

Special feature: MAB in Action workshop

# FAQs

continued...

- ❖ If I can't come, where else can I get the information to remain MAB-empowered?

*Because of its interactive nature, this workshop will focus on serving attendees. The workshop content will not be available in one place in its entirety. Some parts will appear on the Community Breeders' Page and feature in future Newsletters. Your primary MAB information portal remains as [www.rosbreed.org](http://www.rosbreed.org). You can also schedule a private consultation with Cameron Peace ([cpeace@wsu.edu](mailto:cpeace@wsu.edu)).*

- ❖ What do you mean by "MAB in action"?

*This refers to actual use of genetic tests in breeding – as opposed to the development of those genetic tests or the promise of the value of MAB. This was a term first used in last year's ASHS RosBREED posters on peach, apple, and cherry MAB. We have success stories of MAB in demonstration breeding programs and want to share the how-to with you! Come get active!*

- ❖ How do I sign up?

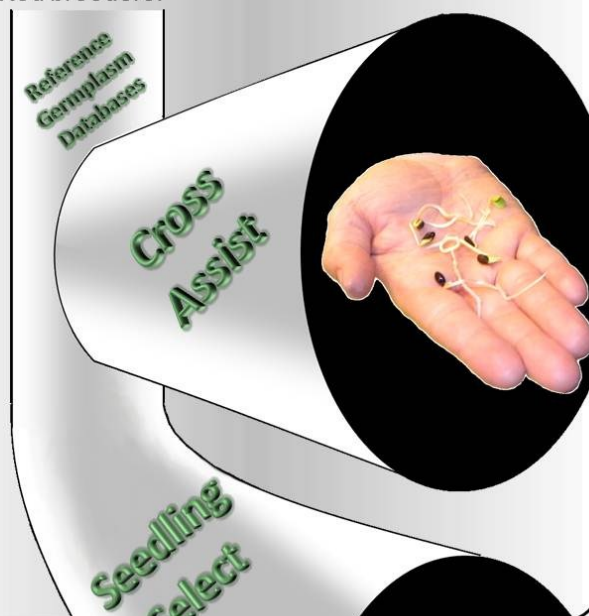
*Seats are limited but still available. Register by emailing Chalani Weebadde ([weebadde@msu.edu](mailto:weebadde@msu.edu)), RosBREED's Extension Team Leader.*

# Software & Database Support

continued...

We will show you how to access and use Cross Assist and other tools during the workshop. Such Toolbox modules are to help you conduct or establish routine MAB.

BIMS v2.0, which is the interconnected series of Toolbox modules to enable MAB, is expected to be released just prior to or at this workshop – for use and beta-testing by interested breeders.



## WORKSHOP AGENDA 30 July 2012, Junior Ballroom, InterContinental Miami Hotel, Miami, FL

7:30 am Continental breakfast

8:00 am Registration

### MORNING: CONCEPTS & RESOURCES

8:15 am 1. Welcome & Introductions

8:30 am 2. What is DNA-informed breeding?

9:30 am 3. What does it take to conduct MAB in your program?

9:45 am Break 30 min

10:15 am 4. What does it take... cont.

11:00 am 5. Systematically integrating DNA information into breeding: The MAB Pipeline

11:45 am 6. Available QTLs for you

12:00 noon Lunch

### AFTERNOON: HOW TO POLISH & APPLY YOUR GENETIC TESTS

1:00 pm 7. Which reported QTLs are worth your while? Prioritizing available marker-locus-trait associations

1:25 pm 8. Who is going to run these tests? Finding service providers for genetic screening

1:45 pm 9. How can the genetic test be made more user-friendly? Adapting a genetic test to the local service provider

2:00 pm 10. Is it really predictive? Validating promising genetic tests

2:45 pm 11. How cool is your genepool? Determining functional allele distributions in your germplasm

3:15 pm Break 30 min

3:45 pm 12. What are some clever crosses? Conducting marker-assisted parent selection

4:45 pm 13. What are the opportunities to cull inferior seedlings? Conducting marker-assisted seedling selection

5:00 pm 14. Wrap-up  
5:30 pm End of workshop



# 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



**CHRIS WATKINS**

Professor, Department of Horticulture, Cornell University, Ithaca, New York, cbw3@cornell.edu

What work do you do? I have a postharvest science research program on quality of fruits and vegetables, but my primary focus is apples. My research and extension includes work on the storage quality of new apple cultivars, the effects of postharvest techniques on the nutritional quality of fruit, and investigation into the underlying mechanisms of fruit responses to storage conditions such as temperature, atmosphere, the inhibitor of ethylene perception, 1-methylcyclopropene (1-MCP), and the interaction of these factors with the development of storage disorders.

Why are you interested in RosBREED? My career started with research on the traditional storage problems of bitter pit and superficial scald. Along with new cultivars came the new storage problems to focus on. While postharvest performance could be included in the breeder's selection process, evaluation is difficult because it is often a 'numbers game'. Fruit numbers and growing regions are limited by cost and logistics. RosBREED is a step in the right direction as ultimately there is hope that genetic markers will be developed that provide additional tools in the breeders' arsenals. I am also intensely interested in RosBREED be-

cause of my involvement in another SCRI project where we are trying to identify 'omic tools that can be used to predict susceptibility of apple cultivars to physiological storage disorders.

How do you feel you can contribute to RosBREED? My role in RosBREED is as extension advisor, and in that role I hope that I add useful input into the discussions. As an administrator in Cornell Cooperative Extension, I am well aware of the difficulties in carrying out genuine extension rather than outreach. RosBREED is doing a great job with commitment of the outstanding scientists involved in the project in meeting these challenges.

## Industry



**RICK HARRISON**

Vice President of Global Variety Development, Driscoll's, rick.harrison@driscolls.com

What work do you do? My role is to manage the four global breeding programs for Driscoll's in blackberry, blueberry, raspberry, and strawberry. I help develop Driscoll's long-term strategy and work with the breeders and their programs to stay coordinated on all aspects of breeding.

Why are you interested in RosBREED? Driscoll's has used markers here and there for many years. However, as the costs to genotype drop we feel the time is right to consider further investments in marker-assisted breeding. RosBREED provides an excellent opportunity for us to stay connected with some of the finest scientists in this area of research.

How do you feel you can contribute to RosBREED? I can provide the perspective of private breeding of rosaceous crops. I have a little experience in many areas such as breeding, program management, strategic planning and even molecular biology. Hopefully my broad perspective can highlight some interesting opportunities and perhaps help the group avoid a few "pot holes" along the way.

## Scientific



**PHIL SIMON**

Research Geneticist, USDA-ARS and Professor, Dept. of Horticulture, Univ. of Wisconsin-Madison, philipp.simon@ars.usda.gov

What work do you do? Carrot breeding and genetics.

Why are you interested in RosBREED? RosBREED is establishing a foundation for developing genomic tools for horticultural crops, and this foundation provides a great model for directions we might go in crops I work with.

How do you feel you can contribute to RosBREED? Provide a perspective from the vantage point of a vegetable crop breeder that might be constructive to developments in RosBREED.

## 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.”

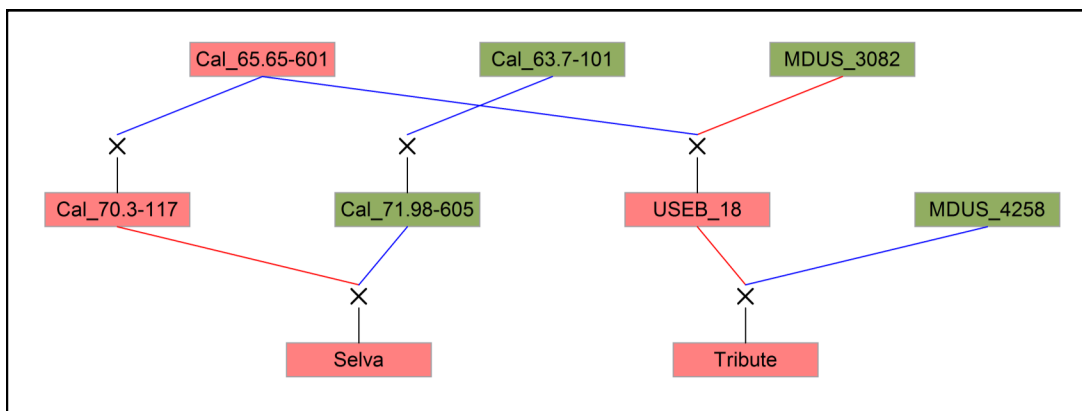
**Floral initiation** in strawberries is directly related to crop productivity. Most older strawberry varieties only initiate flowers during short days and therefore produce just one crop, in the spring. However, other strawberry varieties have been bred that initiate flowers irrespective of photoperiod, providing several cycles of flowering and fruiting during one growing season. Therefore, the genetics are available for multiple strawberry fruit crops a year on the same plants. The term used to describe the everbearing strawberries is “remontant”.

In California, short day varieties are grown from January to April and remontant types are grown from April to October. Remontant varieties are also highly desirable for summer production in other U.S. production areas. However, breeding remontant cultivars for the midwestern and eastern U.S. has proved challenging as additional cycles of flower initiation can be inhibited by hot summer temperatures. In addition, determining which seedlings are remontant is extremely difficult as environmental conditions greatly affect this trait.

Using a remontant variety, ‘Tribute’, which inherited its remontancy from Californian ancestors, Dr. Jim Hancock and his RosBREED Breeding Trainee, Sonali Mookerjee, discovered several genetic markers that are associated with the remontant trait in this lineage (Mookerjee 2012). One of the most robust simple sequence repeat markers, EMFn117, is on strawberry chromosome 7 (Sargent et al, 2006). The functional allele, present as a single copy in ‘Tribute’-derived progeny, is predictive of remontancy even during the challenging hot summers. However, not all remontant varieties have this functional allele – there are other sources too. Nevertheless, the EMFn117 marker will likely provide a predictive genetic test when using remontant germplasm derived directly from ‘Tribute’ or from ‘Tribute’s Californian ancestors. Nahla Bassil and her group at the National Clonal Germplasm Repository are currently evaluating several segregating families to verify this association.

With genetic knowledge of what strawberry seedlings will be remontant, breeders can select for remontancy in the greenhouse without spending the time and resources on large field plots and without the concern of imprecision from environmental factors. This knowledge increases resources that can be allocated to critically important consumer-related traits such as the wonderful fruit flavors and aromas present in strawberry germplasm. Therefore, because the EMFn117 genetic test for remontancy will lead to the more efficient breeding of productive strawberry varieties, it is selected as one of RosBREED’s “Jewels in the Genome.”

Figure 1. Tribute used the same California selection (Cal\_65.65-601) that is in the background of all the UC-Davis remontant types. Here Selva is shown as a representative. Selections in red are remontant and green are non-remontant. Figure is illustrated by Pedimap.



Mookerjee, S. 2012. Genetics of remontancy in octoploid strawberry (*Fragaria × ananassa*). Ph.D. Dissertation, Michigan State Univ., 191 pp.

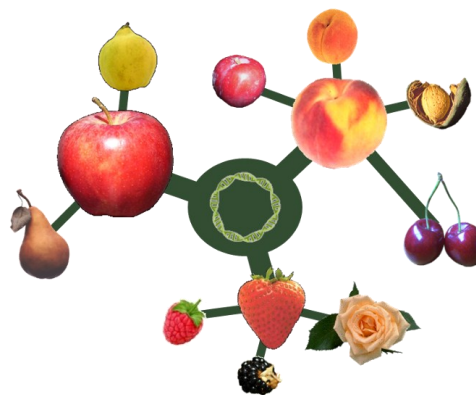
Sargent, D.J., J. Clarke, D.W. Simpson, K.R. Tobutt, P. Arús, A. Monfort, S. Vilanova, B. Denoyes-Rotham, M. Rousseau, K.M. Folta, N.V. Bassil, and N.H. Battey. 2006. An enhanced microsatellite map of *Fragaria*. Theor. Appl. Genet. 112, 1349-1359.



## RosBREED: Enabling marker-assisted breeding in Rosaceae

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James Luby	Breeding	University of Minnesota
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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

SAVE THE DATE: Click on our [Events Calendar](#) to see when we will be holding our Regional and AP Member meetings!

- July 30, 2012: RosBREED Workshop: "[MAB In Action! Integrating DNA Information Into Your Breeding Program](#)", one day prior to the ASHS annual conference, Miami, FL
- July 31, 2012: U.S. Rosaceae Genomics, Genetics, and Breeding Executive Committee meeting, ASHS annual conference, Miami, FL
- August 1, 2012: [RosBREED Presentation Series](#): "Discoveries and Breeding Databases for the Fruit Research Community", ASHS annual conference, Miami, FL
- August 2, 2012: ASHS Colloquia: "[Breeding in a Genomics Era: State of the Art and New Opportunities](#)", ASHS annual conference, Miami, FL.