



RosBREED's Third Annual Meeting with Advisory Panel Members, San Diego, CA



RosBREED met in San Diego, California for the RosBREED III Advisory Panel Annual Meeting with its Industry, Scientific, and Extension Advisory Panel members on January 12, 2012. Forty-six RosBREED participants including 24 Advisory Panel (AP) members participated in the meeting, which focused on project outcomes, impacts, and challenges faced to date, as well as planned outcomes and impacts for our third year.

The afternoon session was devoted to break out group discussions of stakeholder opportunities, needs, and limitations, providing valuable feedback for future success. One of the Extension AP members, Dr. Peter Hirst, Associate Professor in Pomology at Purdue University (see page 11 in this issue), was especially excited about the degree of collaboration seen in RosBREED. He mentioned how the information generated by RosBREED about markers and genes that control fruit quality offer tremendous potential to pomologists like himself to advance understanding of the physiology of fruit development.

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United States Department of Agriculture
National Institute of Food and Agriculture



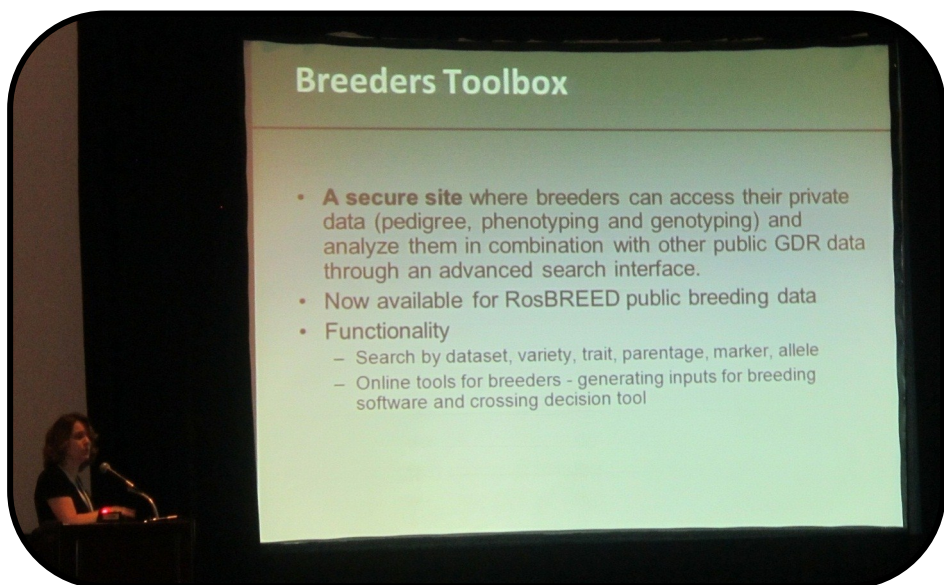
Early bird registration for
ASHS ends February 28th!

RosBREED by the numbers

3

Number of presentations led by RosBREED participants in the Fruit and Nut Crops Workshop held at the Plant & Animal Genome XX Conference.

Immediately following the RosBREED III Advisory Panel Annual meeting, several RosBREED project participants, and collaborators presented talks and posters at sessions in the Plant & Animal Genome Conference XX in San Diego, CA from January 14-18, 2012. The breadth of topics covered emphasized the excellent network, international collaborations, and far-reaching impacts and spillover effects that RosBREED has had with the Rosaceae community over the past two years. The talks and abstracts presented can be viewed at www.rosbreed.org/about/conferences.



Dorrie Main, Washington State University

8,392,540

Number of genotypic data points obtained for the RosBREED Apple Reference Germplasm. Genotypic data includes Single Nucleotide Polymorphisms and 4 markers for important trait loci.

Umesh Rosyara (top; Michigan State University) and Sujeet Verma (bottom; Washington State University) were responsible for compiling and quality-checking the huge data file. Data is being analyzed now and will be interpreted for breeding application at the March PBA Workshop!



MAB In Action Workshop

Save the date! On July 30th, 2012, RosBREED will host a one-day MAB In Action Workshop!

- ⇒ Who should attend this workshop? All U.S. Rosaceae breeders (public and private). Any other personnel associated with breeding programs and committed to their efficiency and success are invited to attend!
- ⇒ 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 develop new varieties. Folks - this is a *WORKSHOP*. This will not be death by PowerPoint!
- ⇒ Alright! I'm coming! What do I need to do to prepare? Simply register by e-mailing Cholani Weebadde (weebadde@msu.edu). If you can't wait until July to hear more, e-mail Cameron Peace, our fearless MAB Team Leader, for a private consultation (cpeace@wsu.edu)!

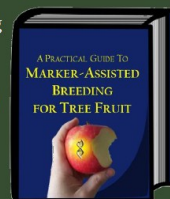


You are invited to a Participatory Workshop entitled
 “Marker-Assisted Breeding in Action”

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



Congratulations!

Two RosBREED Trainees Graduate



Paul Sandefur, University of Arkansas, received his Masters in Science December, 2011. His major professor was John Clark.

I will be hanging around the University of Arkansas for one more season to apply my post-harvest evaluation protocol to program selections and continue some ongoing molecular work. I would also like to spend some time with blackberries and grapes to broaden my knowledge of fruit breeding to species other than *P. persica*. Before long I plan on applying to PhD programs to continue down the fruit breeder path.

It has been a pleasure to get to know all of the RosBREEDers!



Sonali Mookerjee, Michigan State University, received her PhD in Science, January, 2012. Her major professor was Jim Hancock.

I joined the Technology Pipeline Solutions team in Monsanto (St Louis, MO) and will work with the Information Technology team to develop software solutions for the breeders.

I would like to thank everyone in the RosBREED group for giving me the opportunity to be a part of this unique effort. I enjoyed working in field-based and marker-assisted breeding with Dr. Jim Hancock and the strawberry team. The extensive training workshops were extremely useful for learning how to collect good (=useful) data and use it to answer our research questions.

SNP Summit II

RosBREED's Genotyping and Genomics Teams and International Partners Update the Rosaceae Genomics, Genetics, and Breeding Community with Huge Advances Made in 2011

By: Chalani Weebadde, Amy Iezzoni, Dorrie Main, Cameron Peace, and Nahla Bassil

With the availability of apple, peach, and strawberry genome sequences along with the large number of Expressed Sequence Tags and affordable DNA sequencing costs, the Rosaceae community entered a new era of genotyping with genome-wide Single Nucleotide Polymorphism (SNP) markers. Previously, SNPs could only be mined from GenBank using just one or a few cultivars for each crop and only at random genomic positions. In 2009, RosBREED and its international partners took the challenge of developing SNP arrays for apple, peach, cherry, and strawberry using a wide range of breeding-relevant founders and for a greater depth of genome coverage. These arrays are intended for use in Pedigree-Based Analyses to help bridge the gap between genomics research and plant breeding efforts.

RosBREED's Genomics and Genotyping Teams have since worked tirelessly to reach this goal. With the help of RosBREED's Breeding Team, a wide range of breeding-relevant germplasm was collected, sequenced, and the SNPs among them identified. Next, the Genomics and Genotyping Teams met with international partners for each crop, formed an Illumina SNP Consortium for Rosaceae, and determined how to optimize parameters for choosing these genome-wide SNPs for the high-throughput Infinium genotyping platform. The task was especially difficult for the notorious octoploid strawberry genome with its 56 chromosomes and was the "talk of the day" at the RosBREED-sponsored SNP Summit held in Stellenbosch, South Africa, in November 2010, immediately prior to the 5th International Rosaceae Genomics Conference. The SNP Summit was attended by 28 of RosBREED's co-PDs and international collaborators. The SNP Summit further extended RosBREED's collaborative network as it brought together the international Rosaceae genomics community with a single objective, making the partnerships more meaningful and ensuring the resulting SNP arrays are a Rosaceae-wide public resource.

A little over a year after the SNP Summit, the Genomics and Genotyping Teams and key international partners from Italy and New Zealand reported their progress to the Rosaceae research community with a public session dubbed "SNP Summit II", sponsored by RosBREED and held on January 13, 2012 in San Diego, CA, immediately prior to the Plant & Animal Genome Conference. At SNP Summit II, the progress made in developing the rosaceous SNP arrays and preliminary findings of the resulting genotypic data for apple, peach, and cherry were discussed. Also, an emerging strategy for developing a genome scan capability for strawberry was presented. Weekly conference calls among strawberry researchers worldwide, hosted by Illumina®, are moving us closer to a novel strategy that can be applied to plants of higher ploidy like strawberry. This effort has led to unprecedented collaborations among strawberry scientists world-wide. Our ranks were recently joined by Dr. Iraida Amaya (IFAPA, Spain) and Dr. Amparo Monfort (IRTA, Spain).

SNP Summit II was attended by more than 60 RosBREED participants and collaborators. Noteworthy was Illumina®'s one-year extension (until December 31, 2012) for the commercial availability of the rosaceous Infinium SNP arrays to the international research community.

As a community, we recognize how very fortunate we are to have colleagues worldwide who continue to work together so effectively to develop the resources needed to enable marker-assisted breeding in Rosaceae crops.



Nahla Bassil, USDA-ARS; RosBREED Genotyping Team Leader, led the morning discussions



The afternoon session featured a public reporting session by the RosBREED crops; apple, peach, cherry, and strawberry

More Power to the Breeder!

By: Gennaro Fazio, Dorrie Main, and Cameron Peace

Much has been mentioned in our Newsletters about increasingly sophisticated consumers and their desires for products from improved fruit varieties – which can be provided by new cultivars from the sustainable process of breeding. Fruit breeders routinely use several methods to accomplish two critical tasks in the breeding process, 1) selecting parents for new crosses that will increase the probability of creating superior progeny, and 2) culling inferior progeny early in the breeding process while identifying superior material. These two tasks usually require coordination of the breeder’s experience and vast amounts of knowledge stored in many places and formats (notebooks, spreadsheets, publications, etc.). As you will be well aware, RosBREED aims to integrate Marker-Assisted Breeding into these tasks. As such, the project is generating vast amounts of data of many different types; which need to be organized and managed to support robust decisions. Being able to distill the vast amounts of information into valuable drops of elixir is what the Breeding Information Management System (BIMS) Team is all about. As the name implies, this team creates (software-based) systems and online breeder-friendly tools that help manage and utilize breeding information to optimize the creation of desirable fruit for the marketplace.

The public online portal, through which all of the breeding information available in the RosBREED project is being distilled, is the Genome Database for Rosaceae (www.rosaceae.org/breeders_toolbox). This ToolBox will be a web-based, one-stop-shop for breeders’ needs regarding the application of marker-assisted breeding (MAB) in their own programs. It currently features interfaces through which users are able to browse, query, and download performance data on RosBREED crops.

By the end of the four-year RosBREED project, the Toolbox will be expanded to include:

- 1) Marker-Locus-Trait Warehouse where genomic regions associated with traits of interest will be stockpiled;
- 2) Selection Target Identifier which will compare targets for MAB based on industry and consumer values;
- 3) Technology Portfolio which will allow breeding programs to choose commercial genetic screening service providers based on customized needs;
- 4) Genome Database Resources leveraging genomic tools to allow the creation of specific genetic tests usable by a breeding program;
- 5) Reference Germplasm Databases to enable systematic validation and utility assessment of each genetic test for a breeder, via Pedigree-based Analysis;
- 6) Cross Assist tool that will allow breeders to leverage the knowledge arising from the previous module on genotype-based breeding values to select efficient crosses to achieve specific trait goals for new cultivars;
- 7) Seedling Select tool that will examine breeding operations to identify efficient seedling selection schemes incorporating available genetic tests

Cross-Assist

What


Database and Capabilities

For


Breeders

Impact


Ability to plan crosses with CrossAssist and other MAB applications



Which parents have the jewels?



Which combinations to create?



Which seedlings have the jewels?

Method : Phenotype [?] Description of Phenotyps

Target Number of Seedlings Display Calculations

Maximum Co-parentage

Select Traits Select Quantitative Phenotypes

Traits	SS			TA			Weight		
	mean	min	max	mean	min	max	mean	min	max
Stats	13.038	7.7500	19.900	0.5669	0.0210	2.4475	182.87	17.400	574.24
	std	#dp		std	#dp		std	#dp	
	1.5574	347		0.2397	369		68.235	374	
Unit	n/a			n/a			n/a		
Range	>= <input type="text" value="12"/>			>= <input type="text" value="0.4"/>			>= <input type="text" value="180"/>		

Selection of desired traits and number of seedlings with those traits

Go Back to Parents Selection Page

Parent Selection Criteria

Parental Sources APPLE CRS

Target # of Seedlings 100

Max Co-parentage 0.25

of parents 49

of pairs of parents 1176

Method Phenotype

Quantitative	SS	: >= 12
	TA	: >= 0.4
	Weight	: >= 180
Qualitative	Crisp	3

# of Seedlings ▲	Parent	Parent	Inbreeding Coefficient
376	Pinova	Enterprise	IC formula
397	Pinova	Goldrush	IC formula

Identification of optimal parent combinations to generate a target number of seedlings with desired trait levels.

More Power to the Breeder! cont.

Representative data on which the Breeding Information Management System will operate are being collected by several RosBREED Teams. Such data represent that which individual breeding programs already have (such as performance data on cultivars, selections, and seedlings), may have (such as genetics of traits of interest), or need to most effectively implement MAB (such as functional allele effects and distribution in germplasm, genetic screening service costs and logistics, and socio-economic trait values). MAB in Demonstration Breeding programs will demonstrate use of the data management system, especially through the primary interfaces of "Cross Assist" and "Seedling Select". For example, our crop teams are gathering phenotypic data for fruit quality and some other traits on reference germplasm sets with previously characterized pedigree connections, and the Genotyping Team is gathering genotypic data on this same germplasm. Ongoing community efforts are expected to continue to load the underlying databases with increasing volumes of data during and beyond the RosBREED project.

Data browsing, searching, and downloading for subjective consideration of cultivar, selection, and seedling performance is already a useful feature. Breeders will likely be even more interested in the calculation, visualization, and directly decision-supporting functionalities currently in development. For example, "Cross Assist" and "Seedling Select". will permit a breeder to more accurately and efficiently make critical breeding decisions. "Cross Assist" is designed to help a breeder more precisely select efficient parental combinations that will provide a high proportion of seedlings with desired performance levels. "Seedling Select" is designed to help a breeder more accurately and efficiently cull seedlings that do not contain the desired performance levels and retain the ones that do. Both of these abilities will help a breeder to pack more "good material" into their available greenhouse and land space, rather than carrying large amounts of "poor material" along for many years. Both of these abilities will rely on pedigree and DNA information in addition to performance data, with the light of socio-economic value shining down.

In March 2012 there will be two years of phenotypic data for peach, apple, and cherry, and one year for strawberry, to browse, search, and download. A functioning "Cross Assist" for apple and tart cherry will also be available at this time, with other crops following soon after. The release of "Cross Assist" v2.0, currently slated for mid 2012, will provide tools and data to Community Breeders while soliciting feedback. We will solicit feedback from users of this beta version and design and implement subsequent software improvements. Further features listed earlier will also be added and refined, until the public release of v3.0 of the full System by mid 2013. We are still seeking a suitable name for the complete package, and are accepting suggestions!

Please visit the Breeder's Toolbox page at www.rosaceae.org/breeders_toolbox.

Who's Who in the Breeding Information Management System Team?**Team Leader: Gennaro Fazio**

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Breeder profile: Dave Byrne

By Audrey M. Sebolt, Project Assistant



Dave Byrne, Texas A&M

Peaches are considered to be the leading deciduous fruit crop grown in Texas, which on average grows 16 million pounds of fresh peaches and in 2010 produced 26 million pounds. In Texas, fresh peaches are sold locally and many orchards are pick-your-own operations. In 2010, the season-average price received by growers was ranked second in the United States (Fruit and Nuts Outlook, USDA).

The Texas A&M peach breeding program was started in 1939 and in 1983, Dave Byrne, RosBREED Peach Demonstration breeder, was hired to lead the fresh peach breeding program. In addition to peaches, Dave was also given the responsibility to breed other rosaceous fruit crops; nectarines, peentaos (flat peaches), and plums. In the early 1990's Dave began working on a project to develop disease-resistant and heat tolerant landscape roses, and he now holds the Basye Endowed Chair in Rose Genetics.

The goal of the Texas A&M peach breeding program is to deliver superior new cultivars that are low- to medium-chill (see figure 1) and early ripening (late April through June). In the spring, Dave makes 100 to 200 combinations of peach crosses. His main objective is to develop new peach and nectarine cultivars adapted to mild winter conditions. Dave conducts crosses beginning in mid-January in Mexico to target the development of new low-chill cultivars and in early to mid-February in California to target low- to medium-chill cultivars. Once seeds from the crosses are harvested, many need to be embryo rescued because the fruit from early ripening female parents ripen before the embryo has had a chance to fully develop. In a normal year, he rescues approximately 5000 embryos. Dave currently works with commercial partners in California, Mexico, Brazil, South Africa, Spain and Egypt and with various public breeding programs in China, Thailand, and Brazil among others. In the coming year, Dave will release a series of varieties of nectarines and white- and yellow-fleshed peaches.

In addition to several fruit quality and production traits, Dave is interested in examining the health benefits of peaches and plums. Anthocyanins and antioxidants are believed to promote good health and reduce the risk of various diseases. Dave and his research team measured the antioxidant content and activity in a wide range of peaches, nectarines, and plums. This work has shown that plums rival blueberries in their antioxidant content. Consistent with previous research, Dave and his collaborators found the total phenolics content to be well correlated with antioxidant activity. Stone fruit phenolics have been found to inhibit LDL oxidation, the proliferation of breast cancer in vitro, reduce inflammation, and reduce weight gain in obese rats that have been fed a high fat diet. The challenge now is to figure out how to efficiently select for these health-promoting traits in peaches and plums.

Over the last 15 years, Dave has worked with Dr. Unaroj Boonprakob, from Kasetsart University, on a Stone Fruit Breeding Program in Northern Thailand that is funded by the Royal Project. The objective of this program is to develop alternative, high value horticultural crops to replace opium

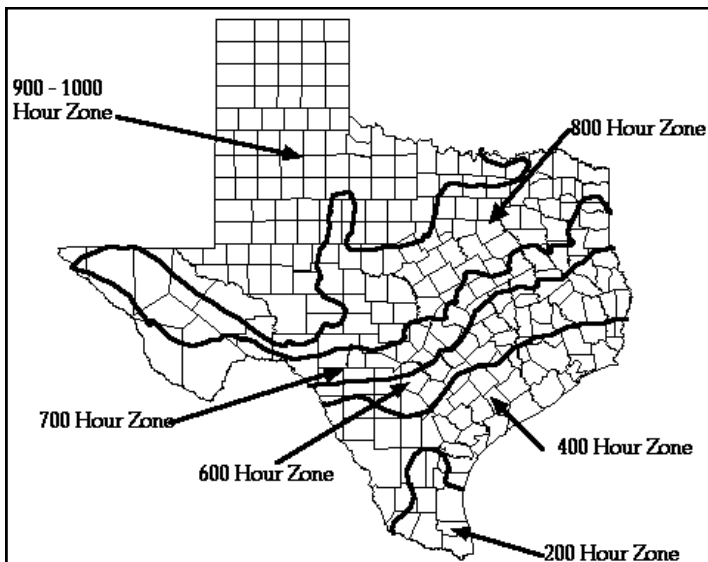


Figure 1: Chilling requirements for Texas (image borrowed from <http://aggie-horticulture.tamu.edu/extension/peach/fig1.html>)

Most fruit species have what is known as a chilling requirement. More specifically, each fruit variety has a certain number of hours of temperatures between 32-45 °F that they must experience in order to break dormancy and induce normal bloom and vegetative growth. If a variety that has a high-chill requirement is planted in a low-chill area, the variety will most likely bloom early and will therefore be more susceptible to frost injury. If a low-chill variety is planted in a high-chill area, the variety may slowly break bud dormancy and therefore abort its fruit. Growers must ensure that they purchase varieties that are suited for their chilling zone. Dave focuses his attention on developing peach varieties adapted for several of the different chilling zones experienced in Texas.

Breeder profile cont.

Box A: Traits that Dave selects for according to type and genetic test availability.

Current M-L-T	Future M-L-Ts	Additional Traits
Increased sugars	High fruit quality	Bacterial leaf spot resistance
Low acid	Targeted chilling requirement	Range of types of varieties a grower can produce
Yellow- and white-flesh	Targeted ripening date	Adapted to Texas growing conditions
		Increased antioxidants and phenolics




Figure 2: Red-fleshed selections that Dave is evaluating.

rose genetics and did not strive to release commercial roses. This changed with the donation by Ralph Moore (Moore's Miniature Roses, CA), who was known as the "Father of the Miniature Rose", of his large collection of rose germplasm to Texas A&M University. Traits that are critical to the rose industry include ever-blooming bushes that are heat tolerant, resistant to multiple races of black spot fungus, look appealing, and produce a range of flower colors and sizes.

Given the synteny between rosaceous crops, Dave is excited about the new findings coming out of the RosBREED project that may provide insights for understanding rose germplasm using new tools and technologies. Dave's peach and rose breeding programs currently use DNA diagnostics to fingerprint and understand the germplasm diversity in his collections. Dave looks forward to using Pedigree-Based Analysis software to discover and validate QTLs and convert them into predictive tests to enhance both his peach and rose breeding.

poppy production in Thailand. This work has resulted in the release of a series of four low-chill yellow-fleshed peach cultivars for this region, which have been named the Thai Tiger peach series. These four peach cultivars ripen to provide a continuous supply of peaches over a six-week period. Other low-chill releases include a yellow-fleshed peach variety 'TropicPrince' and most recently the 'TexFirst' peach variety, which ripens in late April in the medium-chill zone of Texas.

In addition to stone fruit, Dave also conducts a breeding program, which began in the early 1990's, for landscape roses. Dr. Robert Bayse, a retired mathematician from Texas A&M University and a rose enthusiast and backyard breeder, approached the Department of Horticultural Sciences and offered to endow a chair if the University would establish a rose breeding program. This program developed as a research program in



Meet Dave's Breeding Trainee: Tim Hartmann

Why did you choose Dave Byrne's program? My experience with plant breeding began late in my undergraduate career as a Horticulture student at Texas A&M. I started working as a part-time student-worker for the TAMU Stone Fruit Breeding Program toward the end of my junior year, when I quickly developed an interest in pomology and applied breeding. Wanting to learn more about fruit breeding, I approached Dr. David Byrne about graduate school and working in his lab. I was given a position as a graduate research assistant and teaching assistant in August of 2009. At the time I really wasn't completely set on plant breeding, but knew that I wanted to do something related to fruits, and the genetics aspect was intriguing.

What is your thesis project? My thesis project entails working with nine F₁ families resulting from wide crosses with respect to the sugar content of eight parents (relatively high x low soluble solids content). These resulting seedlings (~400) and their parents were cloned by budding onto a common rootstock to generate four replicates that will be evaluated in Fresno, CA and College Station, TX. Data will be collected for two seasons from both locations for ~ 25 fruit quality traits. The phenotypic data will be used along with the RosBREED SNP marker data and pedigree information for detection of QTLs. I am also working on an applied breeding project; studying heritability and combining abilities for several fruit quality traits in peach. Of these traits, soluble solids will receive the most attention. From this data, variance components will be partitioned to estimate heritability in the narrow-sense as well as combining abilities crosses between individuals and families. Having been hampered by weather-related problems, I am hoping to be able to collect meaningful data for the first season this year from the Texas plot, and for the second from the California plot. I am planning to defend my thesis by the spring of 2013.

What benefits have you seen by being part of RosBREED? Being a more traditional, "hands-on" student in plant breeding, the training conferences have truly opened my eyes to a whole new aspect of tools for better understanding the genomics of my crop that can also be used in applied breeding programs. In addition to the obvious benefits related to funding for my project and the massive amount of knowledge gained from the training conferences, I have also had the unique opportunity to learn about other diverse breeding programs that work with different related crops in different parts of the country. This type of collaboration has provided me with the valuable experience of working with others toward a common and worthy goal. I have been able to make contacts and network with talented people from many institutions, with whom I hope to have the opportunity to collaborate some day.

Community Breeders' Page

Can You Afford Not to be a DNA-Informed Breeder?

By Cameron Peace, MAB Pipeline Team Leader

Marker-assisted breeding (MAB), in any and all of its myriad forms, is the future of rosaceous crop breeding. That forecast was obvious from the recent FruitBreedomics first annual meeting in Prague, Czech Republic.

The air outside might have been frigid, but communication was warm and topics were hot as 90 interested invited breeders and project participants gathered to discuss progress and plans at the Czech University of Life Sciences in Prague on 6-10 Feb 2012. The FruitBreedomics project (fruitbreedomics.com) is now in the twelfth month of a 4.5-year effort that closely parallels RosBREED. The project is equivalent in its goal ("bridging the gap between genomics and fruit breeding"), scope (€10M including in-kind support), approach (e.g. Pedigree-Based Analysis is integral), and even has a breeder as its Coordinator (Francois Laurens, apple breeder at INRA, Angers, France) who is committed to translating the promise of genomics and molecular genetics breakthroughs into a revolution in new cultivar development for rosaceous crops. I was invited to attend the meeting, as RosBREED's emissary to this sister initiative and part of the Advisory Board, to strengthen our synergies and expand the potential impact of both projects.

Did you know that ~1/3 of apple breeders on the other side of the Atlantic are already using DNA information routinely in their breeding decisions?



Drs. Marco Bink and Eric van de Weg share Pedigree-Based Analysis expertise with European breeders at the first annual Fruit Breedomics meeting in Prague, 6-10 Feb

European fruit breeders were the stars of the "Stakeholder Platform Day" held on Tue 7 Feb! Did you know that perhaps a third of apple breeders on the other side of the Atlantic are already using DNA information routinely in their breeding decisions? That result from a breeder survey conducted during 2011 with 31 respondents surprised even the project leaders. Current applications of genetic markers in Europe run the whole gamut, from identifying exotic sources of novel attributes, through understanding genetic relationships in breeding germplasm, choosing optimal cross combinations, confirming or identifying parentage, pre-selection of superior seedlings, variety identification, and for IP protection. I think I also detected some genetic marker evaluation for performance potential of advanced selections and new releases. Several breeders gave inspiring presentations on the

objectives and scope of their programs, and their MAB experiences and expectations. The mood was positive and several breeders explained how they are already using markers to support breeding decisions. Ramping up of MAB was a common theme, especially if FruitBreedomics delivers.

Costs and benefits of routine genetic screening Are Rosaceae crop breeders willing to pay the cost of DNA-testing their material? Both FruitBreedomics and RosBREED are giving attention to enabling routine genetic screening for Rosaceae breeders at large. Genetic screening involves the four steps of tissue sampling, DNA extraction, genotyping, and timely provision of results to the breeder. These services are each associated with a cost. Recent investigations by our Genotyping Team of the costs of genetic screening services provided by most commercial companies indicates that for each individual screened with just a few markers, a breeder will rarely get change from \$10 per for the full service. But large orders drop the price, my own experiences attest that services without profit are a small fraction of this cost, and technological advances will continue to drive down prices.

To be conducted routinely, such costs obviously need to be less than the benefit gained by a breeder. So what are the benefits? Here are four:

- 1) Staying ahead of the competition
- 2) Knowledge of efficient crosses
- 3) Knowledge of inferior seedlings
- 4) Knowledge of genetic potential and uniqueness of advanced selections





Staying ahead of the competition An interesting discussion on this topic ensued at the Prague meeting. Consider this: Breeding for short-generation field and row crops in the private sector now routinely involves MAB. Because MAB is now the norm, breeders who aren't DNA-informed will quickly fall behind their competition. In this scenario, breeders will be willing to genetically screen their material for predictive markers even if it represents a cost to their program because of the benefits of more rapidly releasing more superior new cultivars than without MAB. For breeders of long-generation rosaceous crops, the current average "competition" is still conducting conventional breeding rather than MAB, and the pay-offs for MAB can seem many years away. However, judging from the proportion of European breeders that are getting on board, some U.S. breeders may soon be left behind. And current breeding for shorter-generation crops like strawberry seems held back not by cost concerns but by a lack of predictive markers.

Community Breeders' Page cont.

Knowledge of efficient crosses Genetically screening the parental gene pool is a wise investment. As few individuals are involved, the cost is low. Information gained includes identifying the presence of favorable alleles with excellent combining potential, as well as defining relatedness among possible parents to help avoid unwanted inbreeding, maximize crossing among unrelated individuals for transgressive segregation via complementarity of favorable alleles, and avoid incompatible crosses. The value of this DNA information is multiplied because screened parents are considered and used over and over. Furthermore, where DNA information identifies more efficient cross combinations than those indicated by phenotype, pedigree records, or past experience, the value is greatly amplified because it affects many individuals of the next generation. For example, screening 50 parents with a single genetic test to identify several that are homozygous for a favorable major-effect allele and then crossing among them is much more cost efficient than crossing parents of unknown zygosity, then genetically screening hundreds to thousands of seedlings to cull inferior genotypes.

Knowledge of inferior seedlings Marker-assisted seedling selection (MASS) is one extreme of MAB for cost considerations, yet also affordable for any breeder with even a single genetic test of interest. Information gained on each individual is used once and the seedling then either discarded or kept. For MASS to be cost-effective, the cost of genetic screening must be below the average cost of raising and evaluating an inferior seedling. For both Washington State University's apple and sweet cherry breeding programs, this latter cost is much more than \$10, and thus MASS is cost-effective even with a commercial service provider. (However, my own Pacific Northwest Tree Fruit Genotyping Lab in Pullman,

MAB use is not a cost but a resource savings

AVAILABLE TESTS	NOT A COST	A RESOURCE SAVINGS	
 <p>fruit size self-fertility</p>			 <p>All likely large fruit & self-fertile</p>
<p>Genetic tests providing sufficient predictability for a breeder are used. These tests may be for a small fraction of breeding targets – even one test is helpful and quite affordable (example tests here for sweet cherry)</p>	<p>In a breeding program with positive cash flow and a multi-year outlook, low upfront costs of DNA testing (50c+ per plant) are greatly offset by avoiding subsequent rearing and evaluation of inferior plants</p>	<p>Seedlings with undesirable genetic attributes are not created or fewer are created (thanks to MAPS) and/or are culled prior to expensive planting, maintenance, and evaluation operations (thanks to MASS)</p>	<p>Remaining seedlings are evaluated for other breeding targets Resources are reallocated for more efficient goal achievement – one or more of these compared to conventional breeding: - evaluate more seedlings - evaluate in more detail - raise the performance bar → release more cultivars → release better cultivars Or achieve same output as before with less resources</p>

which routinely screens thousands of seedlings annually for these two breeding programs, conducts the service without profit for well under 10% of the cost of phenotypic selection*.) If you do the sums for conventional breeding in your own program, you'll find that high-throughput genetic screening of thousands of seedlings is worthwhile even with just a single predictive marker, and even if you had to go through the most expensive quartile of commercial service providers. My breeding-assistance program has developed a spreadsheet tool that makes doing these sums much easier, which I'm happy to share; RosBREED is converting this spreadsheet into software for eventual release as one of the eight modules of the Breeding Information Management System (see pages 5 and 6 of this issue). Use of this tool will change your perspective: MASS is a resource savings strategy, not a cost.

* Sorry, this service is not available to the rest of you, only the advice from our practical experiences on the front line of MAB!

Knowledge of genetic potential and uniqueness of advanced selections Genetic screening your advanced selections brings the impact of DNA technologies to your program now rather than a generation from now. Advanced selections are limited in number and therefore genetic screening costs are relatively small. Yet the benefits can be enormous. First, newly available or previously unused performance-predictive markers can be used to cull inferior selections from advancing any further in the program. All Rosaceae breeders can take advantage of this opportunity now and increasingly in the future – because there are already some available jewels for most crops, RosBREED is currently polishing many more, and into the foreseeable future researchers will continue to fill the public treasury. Second, predictive markers can be used to describe but not cull selections. Most genetic tests currently available are for attributes that are not superior or inferior in all production situations – for example, genetic tests for level of skin blush of apple, or for non-melting vs. non-softening flesh of peach. Describing advanced selections with such markers can help direct a new cultivar release to its optimal production environment, guide management decisions, or at least help inform growers of what to expect. For what it's worth, DNA-verified parentage is becoming the norm in Rosaceae crops for which cultivar recognition in the industry is important, for all but the shortest generation crops. Cherry breeders cannot afford to release cultivars without DNA information of S-genotypes. DNA information is already finding its way into nursery descriptions of cultivars and may expand in the future as we refine the predictive power of genetic tests. In some cases, genetic tests will reveal information of genetic flaws, perhaps unwanted – but perhaps it's better to know that as early as possible and manage the release of such information than to leave it up to someone else to soon find out.

**So, can you afford to become a DNA-informed breeder? Yes!
Can you afford not to?**

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



PETER HIRST

Associate Professor, Department of Horticulture, Purdue University, hirst@purdue.edu

What work do you do? Extension, research, and teaching of pomology. Primary research interests are flowering and fruit development of apple.

Why are you interested in RosBREED? Integrating genetics, genomics, and physiology offers incredible scope for advancing our understanding. Closer communication between those of us with different interests and expertise can be very thought-provoking and enjoyable.

How do you feel you can contribute to RosBREED? My perspective and experience is in conducting applied research to not only address current industry concerns, but also issues likely to be constraints in the future. To combine this perspective with the activities of RosBREED is synergistic and benefits the project as well as those of us who are allied scientists.

Industry



CHALMERS CARR III

Owner/operator of Titan Peach Farms, Inc., Ridge Spring, SC; Treasurer, South Carolina Peach Council; President USA Farmers, chalmers@titanfarms.com

What work do you do? I grow, pack and ship freestone peaches. I also grow bell peppers and broccoli and am a H-2A employer.

Why are you interested in RosBREED? I believe genetic marker-assisted breeding is the future of fruit breeding. The peach community is in need of great tasting, high-quality fruit that can be grown in many different locations on a consistent basis. The RosBREED effort can help deliver this in a shorter time frame and will be less expensive than conventional breeding.

How do you feel you can contribute to RosBREED? By representing the growers' community to ensure that our concerns and needs are vocalized to the breeding community. To observe that funds and efforts stay on track to the original goal of the RosBREED grant. And lastly, I want to make sure that grower terminology and the research vocabulary mesh together so that information is not lost in translation.

Scientific



CAROLYN ROSS

Associate Professor in the School of Food Science, Washington State University, cfross@wsu.edu

What work do you do? I am a food scientist, with a specialization in analytical chemistry and sensory evaluation. I've worked in many different foods and wine, but have much experience in horticultural products, specifically cherries and apples.

Why are you interested in RosBREED? I'm interested in this project from the food science perspective. I'm interested in how the properties of the crops can be modified by breeding, and how the modifications induced by breeding impact the resulting sensory and chemical properties.

How do you feel you can contribute to RosBREED? I feel that I can contribute with quality and sensory assessments of the different crops, providing a practical examination of the Rosaceae plant materials.

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.”

Crisp, firm apples are highly desired by consumers as they have the much sought-after crunch when bitten into. However, making sure that consumers can enjoy these attributes is particularly challenging given the storage and transport required for most apples. Recently, genetic variation was discovered that helps differentiate whether apples will tend to be firm and crunchy or otherwise. The finding that this jewel is located on apple chromosome 10 led to the identification of a major gene that encodes the causal enzyme polygalacturonase. Polygalacturonase degrades fruit cell walls during ripening – resulting in apple softening and loss of the much sought-after crunchiness. This particular gene, *Md-PG1* (for *Malus × domestica* polygalacturonase), exhibits two variants in apple germplasm (Costa et al. 2010; Longhi et al. 2012). If an apple variety has one of the *Md-PG1* variants, common in older cultivars, the fruit tends to have accelerated loss of firmness after harvest compared to apple varieties that have the other *Md-PG1* variant. Breeding efficiency for apple eating quality can be increased by selecting for the desirable *Md-PG1* variant. Therefore, because *Md-PG1* will lead to the more efficient breeding of crunchy apples, it is chosen as one of RosBREED’s “Jewels in the Genome.”

However, selecting for *Md-PG1* should not be done without knowledge of some other apple loci that influence apple eating quality. These include [Md-ACS1, a major gene controlling apple texture](#), [Md-ACO1](#), and [Ma, a major gene influencing crispness](#). Therefore, *Md-PG1* represents the third jewel for the necklace of genes that impact apple texture and eating quality.

Costa F, Peace C, Stella S, Serra S, Musacchi S, Bazzani M, Sansavini S, van de Weg E. 2010. QTL dynamics for fruit firmness and softening around an ethylene-dependent polygalacturonase gene in apple (*Malus × domestica* Borkh.). *J Exp Bot* 61: 3029-3039.

Longhi S, Moretto M, Viola R, Velasco R, Costa F. 2012. Comprehensive QTL mapping survey dissects the complex fruit texture physiology in apple (*Malus × domestica* Borkh.). *J Exp Bot* 63:1107-1121.



Photo credit: David Hansen, University of Minnesota



Penetrometer measures firmness of apple flesh (Photo credit: David Hansen, University of Minnesota)

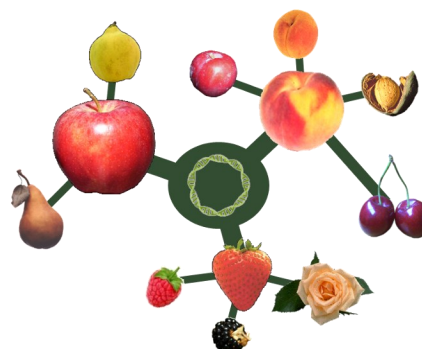


A consumer sensory panel evaluates the firmness and crispness of apples from the University of Minnesota breeding program (Photo credit: University of Minnesota).

RosBREED: Enabling marker-assisted breeding in Rosaceae

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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

- **March 12-15, 2012: Annual RosBREED Project Planning meeting for project participants. East Lansing, MI**
- **July 30, 2012: Rosaceae Community Breeder Participatory Workshop in conjunction with the ASHS annual conference, Miami, FL**