RosBREED
Enabling marker-assisted breeding in Rosaceae
www.rosbreed.org

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

November 19, 2010 Volume 1 Issue 4

International Horticultural Congress Conference, Portugal, August 2010

RosBREED's Co-Principle Directors (Co-PDs) participated in the 2010 International Horticultural Congress (IHC) Conference in Lisbon, Portugal from August 22-27. They presented talks and posters on RosBREED at several sessions of IHC (to view the posters and talks presented, please visit the weblink: www.rosbreed.org/resources/presentations/). In addition, at this meeting, our Co-PDs had the opportunity to discuss upcoming RosBREED events such as the SNP Summit, which was held in South Africa on November 13 and 14.

Top left: Ksenija Gasic (Clemson University; Peach Demonstration Breeder), Cameron Peace (Washington State University; MAB Pipeline Team Leader), and Nahla Bassil (USDA-ARS; Genotyping Team Leader) in front of Cameron's RosBREED poster.

Top middle and right: Jim McFerson (Washington Tree Fruit Research Commission; Industry Team Leader) presented "Breeding fruit crops in the USA using socio-economic and DNA information."
Photo credits: IHC Picasa Images (picasaweb.google.com/ihc2010congress)

Left: IHC attendees taking the opportunity to discuss RosBREED SNP genotyping. From left to right: Mark Davey (Collaborator; Centre for Fruit Culture, Belgium), Cameron Peace, Susan Gardiner (AP Member; Plant & Food Research, New Zealand), Michela Troggio (Collaborator; Plant and Food Research, New Zealand), David Chagné (Collaborator; Plant and Food Research, New Zealand), and Jasper Rees (Collaborator and Matching Partner; University of the Western Cape, South Africa). Photo taken by discussion organizer, Nahla Bassil.

Inside this Issue

NIFA
USDA
United States Department of Agriculture
National Institute of Food and Agriculture

RosBREED News

- **Advisory Panel Members:** If you are planning to attend **RosBREED II** on January 13, 2011 in San Diego, California, please **make your flight arrangements by December 5, 2010**. Please contact Audrey Sebolt (grantzau@msu.edu) if you have any questions.

- **Project Co-PDs and Project Associates:** **RosBREED II's** annual Meeting and Workshop will be held in East Lansing, Michigan March 8-9, 2011 followed by two and a half days of PBA Training (March 10-12). The **deadline to register is February 7, 2011**. Visit our website to view a draft agenda and download a registration form: www.rosbreed.org/about/project-management/meetings/rosbreed-ii-workshop/

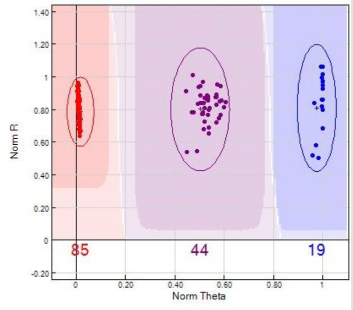
RosBREED by the numbers

28

Number of our Co-PDs who attended RosBREED's SNP Summit, held in Stellenbosch, South Africa on November 13th and 14th, immediately prior to the 5th International Rosaceae Genomics Conference held at the same location on November 14 - 17, 2010.

184,320

Number of potential data points generated for RosBREED's SNP Validation using the Illumina GoldenGate Assay. Three-hundred and eighty-four markers were multiplexed for 480 individuals of apple, peach, sweet cherry, and tart cherry. DNAs were from RosBREED Crop Teams as well as collaborators from Belgium, Spain, New Zealand, Italy, South Africa, and The Netherlands. The graph pictured at right was generated using Illumina software and depicts an apple SNP marker. The data points (dots) in each circle or cluster represent apple cultivars and selections that are homozygous (blue and red for each of the different alleles or forms) or heterozygous (in purple) for this SNP.



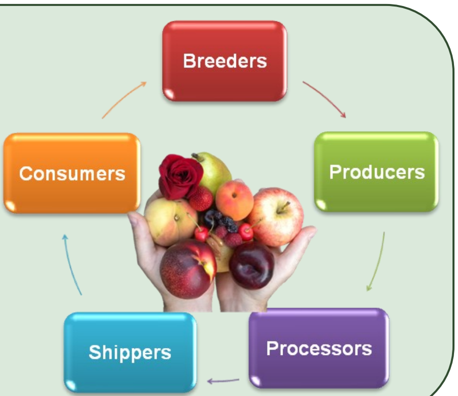
1,470

Number of firmness measurements Paul Sandefur, RosBREED Project Associate at the University of Arkansas, has generated for the Arkansas Breeding Pedigree Set (BP Set; see bottom of page 3 for definition). For accuracy, two readings were taken from each fruit, with five peaches from each cultivar or seedling being tested. All firmness readings were collected with a hand-held penetrometer. Please visit the following link for more details of how the Peach Team phenotyped their fruit - www.rosbreed.org/resources/fruit-evaluation/.

Paul Sandefur, Ksenija Gasic, and John Clark

1,000

Number of survey packets that will be mailed next month to Market Intermediaries (brokers, shippers, packers, and processors) that represent rosaceous crops. In addition to baseline questions (Market Intermediary type, volume of fruit purchased and from what sources in 2009, etc.), Market Intermediaries will be surveyed for fruit quality and horticultural trait preferences and the dollar values associated with their preferences. This market-based information will be used to objectively identify the most important industry traits for fruit quality so that breeding can be optimally targeted. To view the Socio-economics Team's brochure, which further describes their goals and activities, please visit http://www.rosbreed.org/socio-economics/.



Community Breeders' Page

The Marker-Assisted Breeding Pipeline: Channeling socio-economic and DNA information into routine breeding operations

By Cameron Peace, MAB Pipeline Team Leader

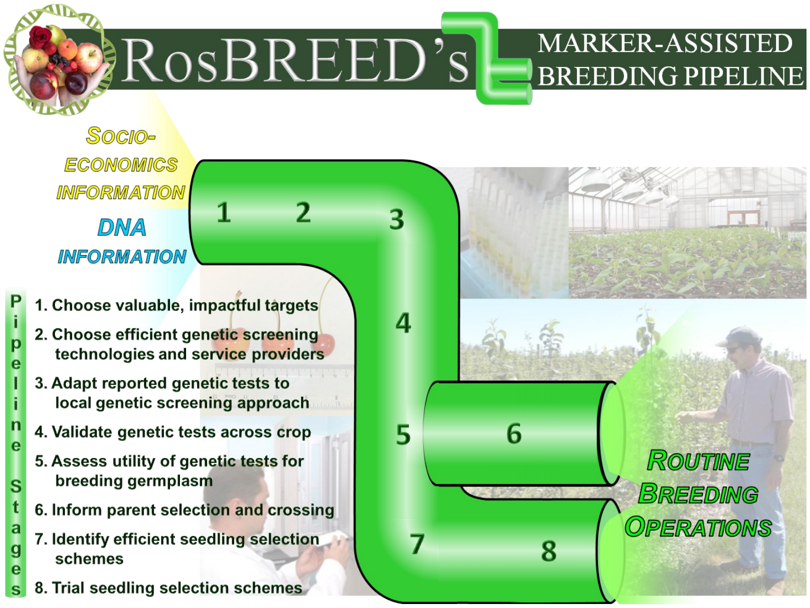
Marker-Assisted Breeding (MAB) is **decision-support** for breeders. Breeding involves many decisions such as choosing parents carrying desirable traits, crossing parents for efficient combinations, selecting the best-performing seedlings and commercially releasing the very best. RosBREED's approach is to integrate two types of information into breeding decisions: socio-economics information (trait values) and DNA information (molecular genetics & genomics describing the underlying genetic control of these traits). This information allows breeders to **objectively define selection targets** and **optimize selection strategies**. The catch, however, is translating the information into the language of breeding and channeling it into routine breeding operations.

Our MAB Pipeline brings focus and creates a sustained infrastructure, or pipeline, for the activities needed to make this happen – activities that have been typically overlooked or only addressed in an ad hoc manner previously. The MAB Pipeline will enable breeders to continuously apply new knowledge without the need for continued resource inputs. In fact, we believe that **successful MAB represents resource savings through improved breeding efficiency** rather than a cost to breeding programs as it is often perceived.

The goal of RosBREED's MAB Pipeline Team is to establish and successfully implement the MAB Pipeline in Rosaceae breeding programs. This involves coordinating with other RosBREED Teams to connect all the dots. The Breeding Team is the most involved, because breeders – both Demonstration and Community Breeders – are the immediate beneficiaries of RosBREED's outputs. While our Demonstration Breeders jump in the deep end, we encourage Community Breeders to at least get their feet wet.

So, what is the MAB Pipeline? It is a series of eight stages (see right and below) to systematically consider, adjust, test, and apply available knowledge regarding Rosaceae crop traits. Many of these activities actually do not require DNA information, but rather compile and mobilize genetic, physiological, and physical data on breeding individuals and practices. DNA information simply enhances this underlying knowledge base, but this enhancement can literally transform current breeding programs.

In upcoming Newsletters, this column will discuss examples of RosBREED's use of the MAB Pipeline in supporting Rosaceae breeding decisions and highlight the role of other RosBREED Teams in this coordinated interplay.



The MAB Pipeline's Eight Stages:

1. **Prioritization** of reported marker-locus-trait associations is essential to sift through the volumes of available genomics information. Not all genomics discoveries are created equal, and their impact on crop improvement varies by socio-economic (value of a trait to breeding, industry, and consumers) and genetic (the strength of association and effect on performance of the tagged controlling genes) factors. Marker-locus-trait associations are specific genetic markers with a known position (locus) in the genome that tag a specific trait of interest.

2. **Genetic Screening Efficiency** is identified by locating and testing high-throughput genetic screening methodologies (sampling, DNA extraction, genotyping, and timely provision of data to the breeder) that are logistically feasible and suit the idiosyncratic routine operations of individual breeding programs.

3. **Improved Markers** are developed by converting markers from their originally reported format to ensure technical robustness and amenability to use in high-throughput platforms needed for genetic screening of thousands of seedlings, as well as screening potential parents.

4. **Validation** of robust marker-locus-trait associations is performed in the wider germplasm pool of the crop – beyond the experimental material in which associations are usually first discovered, using the new marker type they have been converted to.

5. **Utility** assessment of improved validated markers is conducted to determine their potential application specifically within a breeding program, detecting the maintenance of marker-locus-trait associations in breeding program germplasm and describing functional marker variants (favorable or not) present in and inherited from each potential breeding parent.

6. **MAPS (marker-assisted parent selection) Decisions** are enabled, where the information gained from the previous stage is used to guide crossing decisions with a better understanding of genotype-based breeding value.

7. **MASS (marker-assisted seedling selection) Cost Efficiency and Logistics** calculations and considerations are made to identify optimal seedling selection schemes that integrate available robust, validated, utile genetic tests for some traits into routine breeding operations with phenotypic selection for other traits or for other aspects of the same trait.

8. **MASS Trial Use** is conducted in a high-throughput manner on a subset of breeding program seedlings to gain experience with genotype-based seedling culling, comparing theory with practice to optimize MASS implementation.

RosBREED definition

BREEDING PEDIGREE SET (BP Set): is a Pedigree-linked reference germplasm set of a crop representing alleles across the genomes of important breeding parents. This may include 100-300 extra plants for each breeding program; <u>together with the Crop Reference Sets</u>, this allows full representation of important parents in the program.

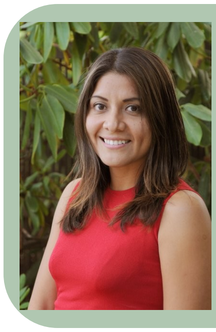
Who's Who in the Socio-economics Team?

Team Leader: Chengyan Yue

University of Minnesota

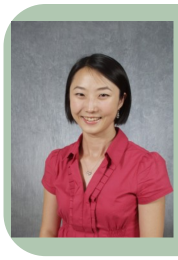
Role: to ensure that the Team's goals and deliverables are reached. This includes generating, disseminating, and evaluating surveys for breeders, market intermediaries, consumers, and producers.

Washington State University



Karina Gallardo

Role: to provide input in the decisions the team makes with respect to the directions of the research. For example, decisions on the type of questions and format to use in surveys (breeders, market intermediaries), facilitate input from industry representatives, choose appropriate economic analysis tools, and interpret results obtained.



Nan Yang

Role: to perform data analysis and model building to obtain economic values of fruit traits. Nan is a postdoctoral researcher at the University of Minnesota.

Ray Jussaume

Role: to provide input into survey design and implementation from the perspective of sociology.

Vicki McCracken

Role: to work with the other members of the Socio-economic Team on all aspects of the RosBREED project, in order to provide broad-based economic direction to the project. Vicki has been involved in the design and quantitative analysis of the breeder survey; designing the market intermediary survey; and early planning of the grower survey. Vicki was also involved in analyzing the national Nielson scanner panel data to characterize household apple variety demand. She will also be actively involved in all other RosBREED consumer-level research.

Mykel Taylor

Role: to analyze apple variety choice data based on national household-level data.

University of Minnesota

Jim Luby

Role: to serve on the SE Team as a liaison with the rosaceous breeding community. Jim is an apple breeder and the Breeding Team leader.

Lan Liu

Role: to assist in survey and experimental design and data analysis.

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 Rosaceae. 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

MERCY OLMSTEAD

Stone Fruit Extension Specialist, University of Florida-IFAS, mercy1@ufl.edu

What work do you do? As a stone fruit extension specialist, I help growers produce high-quality, low-chill subtropical stone fruit varieties through both outreach and research activities. I run a statewide extension program designed to help extension educators provide pertinent information to their growers on the latest disease and insect management techniques, optimum production techniques to achieve excellent fruit quality, and variety selection. My current research focuses on: 1) nitrogen rate management and effects on tree growth and fruit quality, 2) the peach root-knot nematode, *Meloidogyne floridensis* and its resistance mechanisms in peach rootstocks, and 3) economic analyses of establishment and production of low-chill stone fruit in Florida.

Why you are interested in RosBREED? As a trained plant physiologist, I see where the discipline has evolved to include molecular tools and an understanding of the importance of genetics. Being married to a plant breeder, I had many nights when I "tuned" out the G-C, A-T language until I could no longer deny how these genetic tools helped me ask interesting questions about plant physiology. I am embarking on a career shift to include molecular markers as tools to aid in exploring the inheritance of disease mechanisms and help in the breeding of new subtropical peach rootstocks, and it is exciting! RosBREED will help both scion and rootstock breeders significantly streamline the breeding process and help build the bridge between the plant processes and genetics.

How you feel you can contribute to RosBREED? I am very excited to be part of the Extension Advisory Panel – I am always the person with the "So what?" question. As people explain the technical aspects of this project, I can see where outreach tools can be developed for both the primary focus of the outreach – allied scientists, and further outreach to consumers – education about Rosaceae crops. With my 6+ years as an extension specialist in Washington State and here in Florida, I want to be able to help develop outreach material for this and future RosBREED programs.

Industry

HENRY BIERLINK

Executive Director – Washington Red Raspberry Commission (WRRC). henry@red-raspberry.org

What work you do? Administer the current programs of the WRRC including research, promotion, government affairs. Anticipate future needs of the industry and develop partnerships that will help us address them.

Why you are interested in RosBREED? Issues surrounding effective plant breeding and the intellectual property rights surrounding these programs are fundamental building blocks for long term success of our national raspberry industry.

How you feel you can contribute to RosBREED? Support the raspberry members of the Technical Team. Help facilitate the flow of information both from and to the RosBREED team.

Scientific

FRED BLISS

Professor Emeritus, Department of Plant Sciences, University of California Davis. fbliss@dcn.org

What work do you do? I retired in January, 2010 from Seminis Vegetable Division of Monsanto where I worked for a decade in several roles including Director of worldwide breeding, of research technology support and of special projects. Prior to that I retired from UC Davis where as a faculty member of the Pomology (currently Plant Sciences) Dept. I was involved in fruit crops breeding, genetics and teaching. I now am Prof. Emeritus at UC Davis and also consult on several national and international projects involving some facets of plant breeding research and education.

Why you are interested in RosBREED? I have continuing interest in crop improvement in general, more specifically in horticultural crops and especially fruit crops. Prior to the availability of DNA-based technology, most fruit crop breeding was of long duration and very resource intensive. The opportunity to enhance fruit breeding efficiency by combining breeding, genetics and genomics is exciting and I am fortunate to be able to see the very promising outcomes of this collaborative project.

How you feel you can contribute to RosBREED? I have experience in academic settings at the University of Wisconsin-Madison and UC Davis along with work in the private sector in the U.S. and internationally. This helps me provide broad perspectives on targeted research and applied plant breeding. I can offer insight into research project management and integration of DNA-based technology with applied breeding.

Breeder profile: Amy Iezzoni

By Audrey M. Sebolt, Project Assistant

Breeding new and improved plant cultivars requires the availability of and access to a diverse germplasm collection. Such a collection is used to make crosses between divergent parents in hopes of recombining traits of interest to result in a superior cultivar. A diverse germplasm collection can be comprised of old landrace varieties collected from different growing areas around the world, as well as representatives from wild species relatives.

Tart cherry is a species that is in itself genetically diverse because it originated from hybridizations between two very different species. It is believed that multiple natural hybridizations between *Prunus fruticosa* (ground cherry) and *P. avium* (sweet cherry) occurred (see Box A) thousands of years ago in Central and Eastern Europe, giving rise to a new species, tart cherry, which exhibits a wide range of tree archetypes and fruit quality characteristics. Trees can range from small and bushy with willowy limbs to tall and upright with limbs that have wide branch angles. Fruit also exhibit a wide range in sugar content, acid and anthocyanin profiles, and size and shape (see Box B). Bloom and ripening time also vary widely among different selections (see Box C).

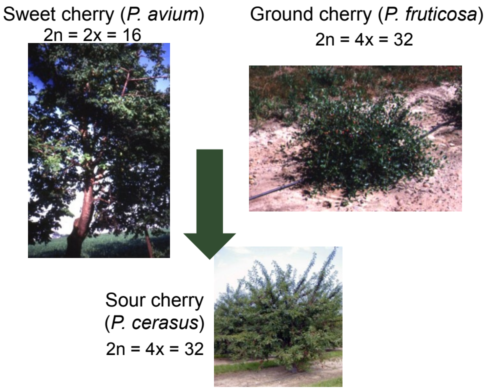
Amy Iezzoni is the only tart cherry breeder in the United States (both private and public). Amy was hired in 1981 by Michigan State University and her first tasks as the tart cherry breeder were to access the available germplasm and determine the industry needs for tart cherry.

The tart cherry industry: Virtually all tart cherries are processed. Processed tart cherry products include jams, dried cherries, individually quick frozen (IQF), juice, with the largest portion for pie filling. Michigan produces approximately 75% of the tart cherries grown in the U.S. The tart cherry industry is a monoculture and consists of essentially only one cultivar, 'Montmorency', which is a 400-year-old cultivar from France. Why is tart cherry production in the U.S essentially a monoculture of this one variety? Two major reasons that contribute to its dominance. First, most of the cherry germplasm and excellent varieties that would have provided alternatives to 'Montmorency' evolved or were bred in Eastern Europe, but prior to the Cold War they were essentially unavailable to the U.S. Secondly, 'Montmorency' is extremely productive. The trees flourish in the sandy soils of Western Michigan; they can withstand its harsh winters and set very heavy crops, even with up to 60% blossom freeze damage. 'Montmorency' requires very little horticultural management and can withstand trunk damage inflicted by mechanical harvesting. Fruit produced from this cultivar are generally uniform in size and have clear flesh and bright red skin, characteristics which have become the standard for "American cherry pie" (see Box B).

However, there are limitations to 'Montmorency' – the fruit can be soft and the trees are highly susceptible to cherry leaf spot (*Blumeriella jaapii*), which is a major financial cost for tart cherry producers. A grower, in the months of May through July, may have to spray as many as 14 times. Also, when an industry relies on only one cultivar to supply fruit to its various market sectors, the industry can be paralyzed if a freeze occurs during a critical bloom stage. This scenario unfortunately did occur – in 2002, the combination of an early bloom and a hard freeze resulted in a crop loss of over 95%. In an average year, Michigan produces approximately 180 million pounds of tart cherries valued at ~ $39 million. In 2002, production estimates were around 3 million pounds and valued at $7.2 million (Kleweno and Matthews, 2003)! The financial impact of the 2002 freeze was devastating to the industry and associated communities.

Tart cherry germplasm collection at Michigan State University: After reviewing the industry's needs, Amy evaluated the germplasm that was available to her. Unfortunately, all that was available was a small collection of 'Montmorency' sports and varieties from Western Europe. So during the Cold War, Amy sought permission to visit Eastern Europe, the center of diversity for tart cherry, to collect cherry accessions to enhance her germplasm base. Through the support of the USDA and bilateral agreements with the authorities in these former communist countries, Amy made multiple trips to Central and Eastern Europe, first to bring

Box A. Origins of Tart Cherry



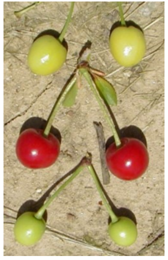
Box B. Amerello versus morello tart cherries

Amerello cherries (pictured left; Montmorency) have pigmented skin, yellow to pink flesh, and generally clear juice. Morello cherries (pictured right; Balaton™) have pigmented skin and flesh and generally pigmented juice.

Box C. Variation in flower bloom and fruit ripening exhibited in tart cherry.

Picture taken May 5, 2010: Tamaris tart cherry flowers (left) and Red Delicious apple flowers (right).

Emperor Francis sweet cherry (top), MSU tart cherry seedling (middle), and Montmorency tart cherry (bottom).



Breeder profile cont.

pollen to the U.S. for making crosses, and then eventually to obtain budwood. Over a 15-year period, Amy scheduled her trips to coincide with bloom and fruit ripening in the countries she visited, including Bulgaria, Germany, Hungary, Poland, the former nation of Yugoslavia, Russia, Serbia, and Ukraine. The results of these efforts led to the establishment of the world's largest germplasm collection, which is located at Michigan State University's Clarksville Horticultural Research Station, as well as lifelong collaborations and friendships with many of the breeders from these countries. One such collaboration resulted in the joint release in the U.S. of three cultivars that Dr. Maliga Pál, from the Újfehértó Fruit Station in Hungary, developed. The three cultivars released in the U.S. are (listed with the U.S. trademarked name followed by the Hungarian name): Balaton™ (Újfehértói Fürtös), Danube® (Erdi Botermo), and Jubileum® (Erdi Jubileum).

Amy traveled specifically to Russia because Russian scientists had previously identified sources of resistance to cherry leaf spot in the wild small-fruited tetraploid cherry species, *P. maackii.* Scientists in Russia had made crosses with *P. maackii* in attempts to introgress cherry leaf spot resistance into domesticated tart cherry. The seedlings from these crosses were brought back to Amy's germplasm collection, to observe whether or not the resistant gene/s are dominant (highly heritable), characterize the resistance mechanism in the plant, and to make further crosses. Screening progeny derived from *P. maackii* and another wild species *P. canescens*, confirmed that these small-fruited species contained valuable genes for resistance to cherry leaf spot. Microscopic analysis of the infection sites revealed that in the resistant seedlings, the fungus enters the stomata but is not able to establish itself in the plant. Instead the plant "responds" by killing the infected cell and the leaf spot fungus along with it (Box D; Wharton et al, 2003)! To increase the efficiency of transferring this disease resistance into new tart cherry cultivars, Amy and her group, including Drs. Dechun Wang and Esther van der Knaap, embarked on a project to identify the major genes controlling fruit size in cherry. Amy reasoned that if they knew the controlling genes, that this would ultimately result in fewer generations required to combine the disease resistance with large fruited types. With USDA Plant Genome funding, Amy and her group were successful in identifying the location of a major gene for fruit size, which was a previously featured Jewel in the Genome (RosBREED Jewel in the Genome - Sweetcherry.pdf).

Amy began making crosses with the imported germplasm but soon encountered problems with fruit set that severely limited productivity. One of the culprits contributing to low fruit set turned out to be genetically controlled self-incompatibility, which was very prevalent in the hybrid seedlings (see page 8 - Jewel in the Genome for more details). Thanks to funding from the USDA-Plant Genome Program, Amy and her Team, which included Dr. Ryutaro Tao's group in Japan, were able to elucidate the genetic control of self-incompatibility and self-compatibility in tart cherry. Most importantly, the results can be used to plan crosses that do not result in any self-incompatible progeny. However, even with self-incompatibility solved, breeding for high yield continues to be challenging. One of Amy's motivations for involvement in RosBREED is to harness all of the available genetic knowledge to overcome this critical yield hurdle.

References

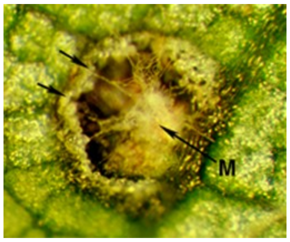
Iezzoni A. 2005. Acquiring cherry germplasm from Central and Eastern Europe. HortScience 40: 304-308.

Kleweno, D. D. and V. Matthews. 2003. Michigan agricultural statistics, 2002-2003. Michigan Agricultural Statistics Service, Lansing, MI. 2002 Annual Report.

Wharton, P., Iezzoni, A., and Jones, A. 2003. Screening cherry germplasm for resistance to leaf spot. Plant Disease 87: 471-477.

Box D. Susceptible and resistant infection of cherry leaf spot in tart cherry.

Susceptible lesion showing large spore mass (S) in the center of the lesion.



Resistant lesion showing stunted mycelia (M) surrounded by an abscission zone (arrows).

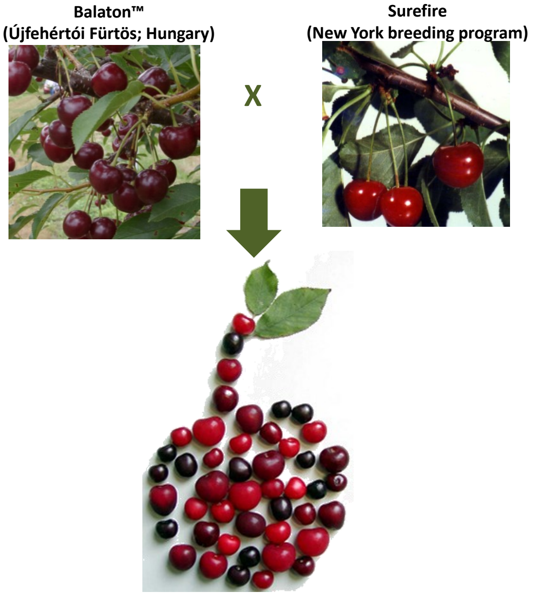
P. Wharton and A. F. Iezzoni.

Traits that are the focus of the Michigan State University's Tart Cherry Breeding Program:

- Increased firmness
- Pit size and shape: most tart cherries are pitted and processed, therefore pits can not be too long (which could result in an increase in chip fragments found in the final product) and the pit weight to fruit weight ratio are key. If a new cultivar that has a long sharp pit and/or a large pit were to be released, it would not be accepted by the industry.
- Late bloom time
- Decreased pesticide use due to disease resistance
- Processing savings due to less use of colorants and/or sugar
- Freestone or "airfree", see picture to right.
- High yielding

An airfree seedling from Michigan State University's breeding program.

Example of the variation of fruit shapes and sizes found in progeny from a tart cherry cross:



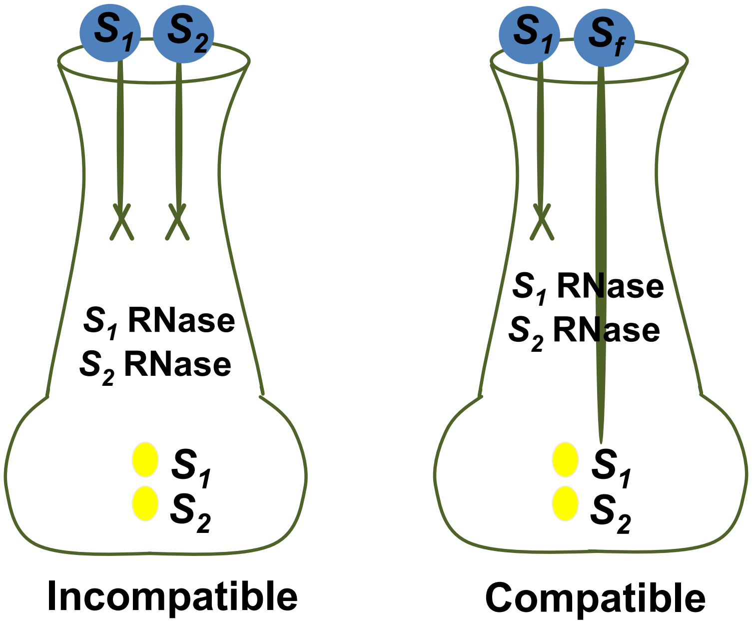
Jewels in the genome

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."*

<u>Incompatible versus compatible pollination:</u> If the *S*-allele in the pollen matches the *S*-allele in the style, that pollen's growth will be arrested in the style. When all the pollen is incompatible, fertilization will not occur and the fruit will not develop. However, when the *S*-allele in the pollen has a mutation that causes it to be self-fertile (S_f), it grows the length of the style, fertilization is successful, and fruit development follows.



Self-fertility, the ability to set fruit following self-pollination, is an important trait in many *Prunus* species that contributes to higher, more consistent yields. For example, in self-incompatible almond, sweet cherry, tart cherry, plum and apricot cultivars, pollen borne in a flower is unable to grow the length of its pistil and therefore fruit set does not occur. However, in self-fertile selections, the pollen borne in a flower is able to pollinate that flower and successfully grow down the style, resulting in fruit set. Therefore with a self-fertile variety it is not necessary to take up orchard space planting a "pollinator" variety. Additionally, self-fertile varieties characteristically have higher yields than self-incompatible varieties as compatible ("self") pollen is always available at the perfect time.

For many *Prunus* species such as almond, sweet cherry, tart cherry, apricot and plum, we know the two major genes that control self-fertility! These two genes reside at the *S*-locus on stone fruit chromosome #6. One gene is expressed in the style and encodes a cytotoxic ribonuclease called the *S-RNase*. The second gene, expressed in the pollen, encodes an F-box protein named SFB that interacts with the S-RNase in an allele specific manner. All the self-fertile alleles described to date in these *Prunus* species disrupt either the S-RNase function in the style or the SFB function in the pollen, leading to self-fertility.

Knowledge of the genetic changes in the *S-RNase* and *SFB* that lead to self-fertility has resulted in the development of simple diagnostic tests to screen progeny for self-fertility early in a breeding program. For example, the *S*-allele in the self-fertile sweet cherry varieties 'Lapins' and 'Sweetheart' is called S4'. This allele has a four base pair deletion in the S4 SFB gene that results in the production of a shortened non-functional SFB protein, e.g. S4'. Pollen containing this shortened non-functional protein is self-fertile and compatible on styles of all other cherry varieties. The DNA diagnostic test for self-fertility simply involves differentiating between the S4 and the S4' by resolving the four base pair difference.

Utilizing DNA tests to determine if young seedlings are self-fertile or self-incompatible prior to field planting dramatically increases the efficiency of breeding for self-fertile varieties. Genetic knowledge of which breeding parents contain the self-fertile variants also enables the breeder to select parental combinations that maximize their chances of obtaining self-fertile offspring. Therefore, because knowledge of the self-fertile variants of the *S*-locus will lead to the more efficient breeding of self-fertile varieties of cherry, almond, apricot and plum, it is selected as our fourth featured "Jewel in the Genome."

RosBREED: Enabling marker-assisted breeding in Rosaceae

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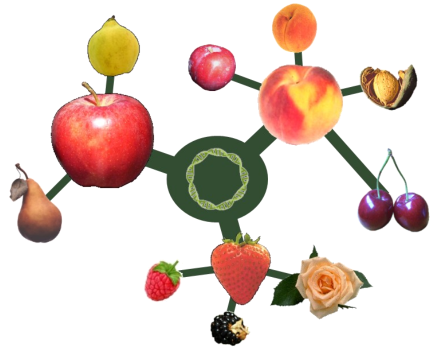

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Eric van de Weg	Pedigree-based analysis	Plant Research International, The Netherlands
Cholani Weebadde	Extension	Michigan State University
Chengyan Yue	Socio-economics	University of Minnesota

Calendar of events

- **January 13, 2011: RosBREED Advisory Panel Member Meeting, San Diego, CA. For further details and a draft agenda, please visit www.rosbreed.org/about/project-management/meetings/rosbreed-ii-san-diego/**

- **March 8-12, 2011: RosBREED General Meeting and Workshop, East Lansing, MI. Registration deadline is February 7, 2011. For more details, see the workshop website at www.rosbreed.org/about/project-management/meetings/rosbreed-ii-workshop/**