RosBREED was a multi-state, multi-institution project dedicated to genetic improvement of U.S. rosaceous crops by targeted applications of genomics knowledge and tools to accelerate and increase the efficiency of breeding programs. This Coordinated Agricultural Project was funded through the USDA’s National Institute of Food and Agriculture - Specialty Crop Research Initiative by a combination of federal and matching funds, Grant 2009-51181-05808.
<table>
<thead>
<tr>
<th>Content Description</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>RosBREED Participants</td>
<td>3-4</td>
</tr>
<tr>
<td>Introduction to RosBREED</td>
<td>5</td>
</tr>
<tr>
<td>Impact statements</td>
<td>6-28</td>
</tr>
<tr>
<td>Overview</td>
<td>6</td>
</tr>
<tr>
<td>Bridging the chasm</td>
<td>7</td>
</tr>
<tr>
<td>Adoption of marker-assisted breeding</td>
<td>8</td>
</tr>
<tr>
<td>Demonstration Breeding programs map</td>
<td>9</td>
</tr>
<tr>
<td>Apple breeding overview</td>
<td>10</td>
</tr>
<tr>
<td>Apple breeding: University of Minnesota</td>
<td>11</td>
</tr>
<tr>
<td>Apple breeding: Washington State University</td>
<td>12</td>
</tr>
<tr>
<td>Apple breeding: Cornell University</td>
<td>13</td>
</tr>
<tr>
<td>Peach breeding overview</td>
<td>14</td>
</tr>
<tr>
<td>Peach breeding: Clemson University</td>
<td>15</td>
</tr>
<tr>
<td>Peach breeding: University of Arkansas</td>
<td>16</td>
</tr>
<tr>
<td>Peach breeding: University of California - Davis</td>
<td>17</td>
</tr>
<tr>
<td>Peach breeding: Texas A&amp;M</td>
<td>18</td>
</tr>
<tr>
<td>Cherry breeding overview</td>
<td>19</td>
</tr>
<tr>
<td>Cherry breeding: sweet cherry Washington State University</td>
<td>20</td>
</tr>
<tr>
<td>Cherry breeding: tart cherry Michigan State University</td>
<td>21</td>
</tr>
<tr>
<td>Strawberry breeding overview</td>
<td>22</td>
</tr>
<tr>
<td>Socio-Economics</td>
<td>23</td>
</tr>
<tr>
<td>Standardized phenotyping</td>
<td>24</td>
</tr>
<tr>
<td>Enabling genetic technologies</td>
<td>25</td>
</tr>
<tr>
<td>Enabling statistical tools</td>
<td>26</td>
</tr>
<tr>
<td>Breeding Information Management System software</td>
<td>27</td>
</tr>
<tr>
<td>Training future plant breeders</td>
<td>28</td>
</tr>
<tr>
<td>RosBREED partners and collaborators</td>
<td>29</td>
</tr>
<tr>
<td>RosBREED Industry Advisory Panel</td>
<td>30</td>
</tr>
<tr>
<td>RosBREED Extension Advisory Panel</td>
<td>31</td>
</tr>
<tr>
<td>RosBREED Scientific Advisory Panel</td>
<td>32</td>
</tr>
<tr>
<td>Logos of participant’s affiliations and funding agencies</td>
<td>33</td>
</tr>
</tbody>
</table>
# RosBREED Participants

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

www.rosbreed.org

## Team Leaders

<table>
<thead>
<tr>
<th>Role</th>
<th>Name</th>
<th>Institution</th>
<th>Contact Information</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Project Director</strong></td>
<td>Amy Iezzoni</td>
<td>Michigan State University</td>
<td><a href="mailto:iezzoni@msu.edu">iezzoni@msu.edu</a> 517.355.5191 x 1391</td>
</tr>
<tr>
<td><strong>Breeding</strong></td>
<td>James Luby</td>
<td>University of Minnesota</td>
<td><a href="mailto:lubyx001@umn.edu">lubyx001@umn.edu</a></td>
</tr>
<tr>
<td><strong>Socio-Economics</strong></td>
<td>Karina Gallardo</td>
<td>Washington State University</td>
<td><a href="mailto:karina_gallardo@wsu.edu">karina_gallardo@wsu.edu</a></td>
</tr>
<tr>
<td><strong>Marker-Assisted Breeding Pipeline</strong></td>
<td>Cameron Peace</td>
<td>Washington State University</td>
<td><a href="mailto:cpeace@wsu.edu">cpeace@wsu.edu</a></td>
</tr>
<tr>
<td><strong>Breeding Information Management System</strong></td>
<td>Gennaro Fazio</td>
<td>USDA-ARS Plant Genetic Resources Unit</td>
<td><a href="mailto:gf35@cornell.edu">gf35@cornell.edu</a></td>
</tr>
<tr>
<td><strong>Genomics</strong></td>
<td>Dorrie Main</td>
<td>Washington State University</td>
<td><a href="mailto:dorrie@wsu.edu">dorrie@wsu.edu</a></td>
</tr>
<tr>
<td><strong>Stakeholder</strong></td>
<td>Jim McFerson</td>
<td>Wash. Tree Fruit Research Commission</td>
<td><a href="mailto:mcferson@treefruitresearch.com">mcferson@treefruitresearch.com</a></td>
</tr>
<tr>
<td><strong>Pedigree-Based Analysis</strong></td>
<td>Eric van de Weg</td>
<td>Plant Research International, NL</td>
<td><a href="mailto:eric.vandeweg@wur.nl">eric.vandeweg@wur.nl</a></td>
</tr>
<tr>
<td><strong>Extension</strong></td>
<td>Cholani Weebadde</td>
<td>Michigan State University</td>
<td><a href="mailto:weebadde@msu.edu">weebadde@msu.edu</a></td>
</tr>
<tr>
<td><strong>Genotyping</strong></td>
<td>Nahla Bassil</td>
<td>USDA-ARS National Clonal Germplasm</td>
<td><a href="mailto:nahla.bassil@ars.usda.gov">nahla.bassil@ars.usda.gov</a></td>
</tr>
<tr>
<td><strong>Peach Breeding</strong></td>
<td>Ksenija Gasic</td>
<td>Clemson University</td>
<td><a href="mailto:kgasic@clemson.edu">kgasic@clemson.edu</a></td>
</tr>
<tr>
<td><strong>Evaluation</strong></td>
<td>Michael Coe</td>
<td>Cedar Lake Research Group, LLC</td>
<td><a href="mailto:michael@cedarlakeresearch.com">michael@cedarlakeresearch.com</a></td>
</tr>
</tbody>
</table>
the same gene that controls the presence of red pigment (skin and flesh) in apple controls the presence of red pigment in cherry.
U.S. Rosaceae crop industries face numerous limitations to profitability and sustainability. Overcoming these barriers requires rapid development and deployment of new cultivars with improved characteristics to meet dynamic industry and market needs and consumer preferences. This project identified breeding trait targets based on knowledge of what industry sectors and consumer’s value, and utilized genomics information to develop a sustainable technical platform to accelerate and increase the efficiency of cultivar development and adoption.

What need did RosBREED address?

RosBREED focused on fruit quality traits for four rosaceous crops: apple, peach, cherry and strawberry. Market-based information was used to objectively quantify the importance of fruit quality traits that were targeted for marker-assisted breeding.

What crops and traits were targeted in RosBREED?

This approach, usually shortened to MAB, uses genetic markers, usually DNA-based tests, to monitor the presence of desirable and undesirable genes in breeding plants. RosBREED’s focus was to enable breeders of apple, peach, cherry, and strawberry to make more informed selection of the best parents to combine and the best seedlings to advance in cultivar development. Selection for improved fruit quality traits including texture, size, and flavor was enabled prior to crossing and planting young trees or plants in evaluation orchards or field plots, and has set the stage for similar advances in other Rosaceae crops.

Marker-Assisted Breeding
RosBREED: Enabling marker-assisted breeding in Rosaceae crops

**ISSUE:** Almond, apple, caneberries, cherry, peach, pear, rose, and strawberry all belong to the same plant family, Rosaceae. Profitability and sustainability of U.S. rosaceous crop industries require an understanding of changing production, market, and consumer preferences, so breeders and supporting programs can develop and deploy new varieties addressing those preferences.

To efficiently and more rapidly deliver superior, commercially successful new varieties, breeding efforts can benefit greatly from new technologies and personnel trained in these appropriate technologies. Marker-Assisted Breeding (MAB) using DNA diagnostic information is one such technology that is particularly effective to select for desirable fruit quality traits such as size, color, flavor, and texture.

DNA diagnostic information helps breeders make creative parent combinations and select for desirable traits at the seedling stage, before plants even flower. This early screening reduces expenditures for planting, maintaining, and testing full-grown plants. While this approach can enhance all rosaceous crop breeding programs, it is especially helpful in perennial rosaceous crops such as fruit trees, because it can take more than 25 years to develop and commercialize a new variety. Tools, knowledge, and training in this area were needed for Rosaceae breeding to capitalize on decades of upstream scientific advances.

**WHAT HAS BEEN DONE:** The RosBREED project has developed and, for the first time, enabled the application of DNA diagnostic information to assist fruit breeding decisions on four rosaceous crops: apple, cherry, peach, and strawberry. United States breeding programs can now efficiently identify superior parents for making crosses and reduce expenses required to grow seedlings of unknown quality to maturity for field selection. The technologies are applicable for all Rosaceae crops.

RosBREED has created an advanced set of broadly accessible software tools and online resources so breeders can readily use MAB technologies. Socio-economists surveyed Rosaceae breeders, growers, market intermediaries, and consumers so that project resources for genetic test development were directed to better understand which traits would best be improved via MAB. A cohort of new graduate students was trained in modern breeding techniques.

**IMPACT:** Using RosBREED’s socio-economic and DNA diagnostic information and tools, breeders can now make exciting crosses by selecting parents that provide the highest proportion of desired offspring types for valuable fruit quality traits. DNA information then allows breeders to efficiently eliminate offspring unlikely to have desired fruit qualities preferred by industry sectors and consumers. Newly-trained professionals are now available to conduct MAB for efficient, accurate, and creative development of superior new cultivars addressing consumer and industry needs.

For example, the apple breeding program at the University of Minnesota used DNA tests to select parents most likely to produce the highest number of desirable offspring with superior crispness and juiciness, long fruit storability, disease resistance, and attractive skin color. Combining this information with flowering time, tree availability, and pollen quality, the team made many exciting crosses in 2012. Because only some of the resulting offspring will bear the desired trait combinations, MAB was further used to eliminate undesirable seedlings and reduce costs of field testing.

Project Director: Amy Iezzoni, Michigan State University
Bridging the Chasm – Collaborations between breeders and genomicists

ISSUE: Until the RosBREED project, genomics research had not been translated into routine practical application in breeding Rosaceae fruit crops (almond, apple, caneberries, cherry, peach, pear, strawberry, and others). There was a disconnect between crop genomicists and plant breeders. Genomicists had been generating information they believed would be valuable to plant breeders without asking them what they needed. Plant breeders were largely ignoring the efforts of genomicists, who they felt were unconcerned about ‘real world’ breeding problems.

WHAT HAS BEEN DONE: RosBREED provided a vehicle to facilitate discussion between genomicists and plant breeders working on apple, peach, strawberry, sweet cherry, and tart cherry crops. Genomicists, geneticists, and plant breeders met two to three times a year as crop-focused teams to facilitate communication and technology transfer. Geneticists used scientific advances made by genomicists to develop tests to identify individuals carrying valuable genetic factors contributing to desirable attributes prioritized by breeders of each crop. A stepwise process equipped breeders and their students to implement new genetic tests and statistical tools in their programs. Genomics advances were thereby leveraged to improve breeding efficiency, accuracy, and creativity by the technique of marker-assisted breeding (MAB).

IMPACT: Programs in targeted crops now use genomic information to enhance breeding efforts. None of them were using these tools before RosBREED. Participating programs now routinely use genetic testing to verify parentage. For example, the tart cherry breeding program at Michigan State University (MSU) discarded 30% of its seedlings in one breeding population because DNA markers indicated they derived from unintended parentage. Similarly, the MSU and USDA-Corvallis strawberry breeding programs discarded 42 individuals from 13 populations when DNA test results showed them to be of unintended parentage. Genetic tests were used to correct the pedigrees for 200 selections in the peach breeding program at UC-Davis.

Parents are now selected using genetic tests in all RosBREED breeding programs:
1) Programs at Cornell University, University of Minnesota (UM), UC-Davis, and Washington State University (WSU) use genetic tests for fruit texture and storability.
2) Peach breeding programs at Clemson University, University of Arkansas, Rutgers, and Texas A&M use genetic tests for flesh type, bacterial leaf spot resistance, acidity, blush, and soluble solids concentration.
3) The sweet cherry breeding program at WSU uses genetic tests for self-fruitfulness, ripening season, and fruit firmness and size.
4) The tart cherry breeding program at MSU uses genetic tests for fruit color and cherry leaf spot resistance.
5) The strawberry breeding programs at MSU and USDA-Corvallis use genetic tests for red stele root rot resistance and the everbearing fruiting characteristic.

Three RosBREED programs now use genetic tests to cull seedlings and the rest are poised to follow. Nearly 15,000 seedlings in the apple breeding programs at WSU and UM were discarded prior to planting over the last three years, based on the prediction they would have inferior fruit quality traits or disease susceptibility. Nearly 4000 sweet cherry seedlings at WSU were discarded prior to planting, based on the prediction their flowers would be self-sterile and the fruit small and soft. These applications of MAB saved resources totaling $250,000 that would have otherwise been spent on seedlings likely to have inferior characteristics.
Adoption of Marker-Assisted Breeding

ISSUE: To safeguard sustainability of the rosaceous fruit industry in a highly competitive business environment, Rosaceae crop breeding programs need to develop and commercialize new varieties that are productive and appealing to stakeholders, including producers, processors, shippers and packers, retailers, and consumers. However, many rosaceous crops are long-generation tree crops. Development and commercialization of new varieties can take more than 25 years. To serve the needs of a wide range of stakeholders, breeders face challenges in allocating appropriate attention and resources to the many possible traits. Breeders also have limited tools for efficiently and accurately improving “complex” traits that are influenced by many genetic factors acting in concert.

WHAT HAS BEEN DONE: Demonstration breeders are now routinely using and benefiting from the DNA diagnostic tools developed by RosBREED to assist breeding decisions on five rosaceous crops: apple, peach, sweet cherry, tart cherry, and strawberry. During several workshops, the wider community of U.S. Rosaceae breeders was trained in the core concepts of marker-assisted breeding (MAB) and provided with resources to enable their adoption of efficient MAB approaches.

IMPACT: RosBREED genomics and genetics researchers eliminated the need for individual breeders to develop DNA diagnostic tests. Because the new DNA diagnostic information was developed using germplasm from U.S. breeding programs, the new tools are directly applicable in these programs. The workshops helped breeders overcome various concerns. Breeders are now better prepared to use MAB to make their programs more effective.

A baseline survey conducted in 2009 established the level of MAB adoption among U.S. Rosaceae breeders and allied scientists at that time. Both groups reported moderately positive attitudes toward the future importance of MAB but low levels of actual use of genetic tests in their work. A follow-up survey in December 2013 will allow us to quantify change in adoption over these years.

During the project period, RosBREED provided three in-depth workshops for the dozen RosBREED “demonstration” breeders and five workshops for the wider community of U.S Rosaceae breeders. On average, more than 80 percent of workshop participants “strongly” or “moderately” agreed that they gained new knowledge which they intended to apply in their work. In interviews with a random sample of breeders in winter 2011-12, almost three quarters reported using markers for plant identification and about one quarter were using markers for more advanced applications.
RosBREED’s Demonstration Breeding Programs

RosBREED crop teams include demonstration breeding programs and breeder advisory panelists in five rosaceous fruit crops. They evaluated germplasm for fruit quality traits and other critical traits in multiple US production regions:

**Strawberry** - California, Florida, Michigan, New Hampshire, Oregon

**Peach** – Arkansas, California, South Carolina, Texas

**Apple** – Minnesota, New York, Washington

**Sweet Cherry** – Washington

**Tart cherry** - Michigan
Apple Breeding

ISSUE: New apple varieties with improved fruit quality will lead to increased consumer consumption, enjoyment, and health, and will contribute to the profitability and sustainability of the U.S. apple industry. However, breeding a new apple variety is a slow and inefficient process that can take 15 to 25 years. Predicting which individuals will serve as the best parents is difficult. From the seedlings produced after crossing, thousands must be grown and tested in evaluation orchards to identify the few with commercial potential.

WHAT HAS BEEN DONE: Apple breeders in Washington, New York, and Minnesota evaluated many important breeding parents, their ancestors, and their offspring for fruit quality traits and other critical attributes like disease resistance. Evaluating these individuals across different sites added to our understanding of key traits and their interrelationships, making it possible to more efficiently improve them genetically.

DNA tests were developed to predict apple skin color, fruit firmness, crispness, juiciness, acidity, storability, and storage disorders. These new genetic tests enable apple breeders to select parents with the greatest likelihood of transmitting favorable traits. The tests also identify the best seedlings for advanced testing, reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

Using this strategy, called Marker-Assisted Breeding, apple breeders can now more efficiently, accurately, and creatively develop superior new apple varieties that meet the needs and desires of consumers and producers.

IMPACT: As a result of genetic testing in the apple breeding programs:

- New crosses designed since 2011 and earlier have incorporated expanded genetic knowledge of each parent’s potential to transmit desirable traits to their offspring, resulting in greater genetic gain in the next generation.

- More than 14,000 seedlings were discarded in 2011 to 2013, prior to field planting, after DNA screening predicted that they would have inferior fruit quality or disease susceptibility, thus avoiding resource expenses totaling nearly $200,000.

University of Minnesota apple breeder: James Luby
Washington State University apple breeder: Kate Evans
Cornell University apple breeder: Susan Brown
Apple Breeding:
University of Minnesota

ISSUE: New apple varieties with improved fruit quality will lead to increased consumer enjoyment and consumption and will contribute to the profitability and sustainability of the U.S. apple industry. However, breeding new apple varieties is inefficient and slow, taking 15 to 25 years from the initial cross to variety release. Predicting which individuals will be the best parents is difficult. Thousands of progeny individuals must be grown and evaluated in the orchard to identify the few with commercial potential.

WHAT HAS BEEN DONE: DNA tests were developed to predict apple fruit skin color, firmness, crispness, juiciness, acidity, and storability. These new genetic tests enable apple breeders to select the best parents to combine and the best seedlings to advance, reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

Using this strategy, called Marker-Assisted Breeding, apple breeders can more efficiently, accurately, and creatively develop superior apple varieties that meet the needs and desires of consumers and producers.

IMPACT: As a result of genetic testing in the University of Minnesota apple breeding program:

- A set of parents chosen for crossing (out of 150 prospective parents), partly based on the results of DNA diagnostic tests, have increased potential to transmit red skin color, bitter pit resistance, desirable levels of acidity, exceptional crispness, long storage potential related to ethylene production, and resistance to apple scab disease.

- The power of marker-assisted parent selection is apparent in the following example: Crosses planned in 2012 using only DNA test results on parents for skin color saved the University of Minnesota apple breeding program approximately $20,000 in future costs of caring for seedlings in the breeding orchard that have no commercial potential due to undesirable skin color.

- Between May and July 2013 about 1600 seedlings were DNA tested for crispness, skin color, storage potential, and apple scab disease at a cost of $5000. Approximately 900 seedlings were culled based on the results of the genetic tests. Our cost for carrying a seedling to fruiting is about $20; therefore, this DNA testing yielded a net savings of about $13,000.

University of Minnesota apple breeder: James Luby
Apple Breeding:  
Washington State University

ISSUE: New apple varieties with improved fruit quality will lead to increased consumer enjoyment and consumption and will contribute to the profitability and sustainability of the U.S. apple industry. However, breeding a new apple variety is slow and inefficient, taking 15 to 25 years. Predicting which selections will be the best parents is difficult. Thousands of progeny individuals must be grown and evaluated in the orchard to identify the few with commercial potential.

WHAT HAS BEEN DONE: DNA tests were developed to predict apple fruit skin color, firmness, crispness, juiciness, acidity, and storability. These new genetic tests enable apple breeders to determine the best parents to combine and the best seedlings to advance, reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

Using this strategy, called Marker-Assisted Breeding (MAB), apple breeders can more efficiently, accurately, and creatively develop superior apple varieties that meet the needs and desires of consumers and producers.

IMPACT: As a result of genetic testing in the Washington State University apple breeding program:

- Parents are chosen partly based on the genetic potential to transmit key attributes of excellent texture and long storability, using new DNA information about the family pedigree and trait characteristics of WSU apple selections and new varieties.
- Twenty-three crosses were designed based on the increased potential for transmitting desirable attributes to their progeny according to results of parent DNA testing.
- More than 7000 seedlings were discarded prior to field planting in 2011 and 2012 based on the prediction that they would have inferior texture and storability. The estimated total resource saving from this seedling culling was $98,000.
- In 2013, 9000 seedlings were DNA-tested, resulting in a third eliminated.
- A seedling planting system was designed and implemented to streamline the application of MAB. This new system ensures that the genetic test results are reliably matched with each of the thousands individual seedlings that are sampled – vital for confidently making culling decisions on so many seedlings.

Washington State University apple breeder: Kate Evans

Washington State University

United States Department of Agriculture
National Institute of Food and Agriculture

Washington Tree Fruit Research Commission
Apple Breeding:
Cornell University

ISSUE: New apple varieties with improved fruit quality can help increase consumption of a very popular fruit and add to healthy choices in battling child and adult obesity. New varieties will also contribute to industry profitability and sustainability, especially new varieties suited to the expanding fresh-cut market.

WHAT HAS BEEN DONE: DNA tests were developed to predict apple fruit skin color amount, firmness, crispness, juiciness, acidity, and storability. These new genetic tests enable apple breeders to select parents with the greatest likelihood of transmitting favorable traits to their offspring, reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

This strategy, Marker-Assisted-Breeding, and the genetic analyses based on phenotyping across sites, is adding to our understanding of key traits and their interrelationships.

IMPACT: As a result of genetic testing in the Cornell apple breeding program:

- Crosses were designed beginning in 2011, based on genetic knowledge of each parent’s potential to transmit desirable traits to their offspring. Seedling screening, to begin in 2013 for several progenies, is also now enabled.

- Knowledge of key traits and their inheritance have changed our choices in parent selection. We expect that our use of this knowledge to date and into the future will be reflected in fewer undesirable seedlings and greater genetic gain. These enhancements should result in high quality advanced selections – tomorrow’s future varieties.

- Understanding genomic regions influencing multiple traits, such as the one discovered for beneficial phenolic compounds, crispness, juiciness, acidity, bitter pit incidence, fruit size, and harvest maturity, is helping us make more efficient increases in genetic gain.

Cornell University apple breeder: Susan Brown
Peach Breeding

ISSUE: New peach varieties with improved fruit quality will lead to increased consumer consumption, enjoyment, and health, and will contribute to the profitability and sustainability of the U.S. peach industry. However, breeding a new peach variety is a slow and inefficient process that can take 15 to 20 years. Predicting which selections will be the best parents is difficult. Thousands of seedlings produced after crossing must be grown and evaluated in the orchard to identify the few that have commercial potential.

WHAT HAS BEEN DONE: Peach breeders in California, South Carolina, Texas, and Arkansas evaluated almost 1000 individual trees, including important breeding parents, their ancestors, and their offspring, for fruit quality and other critical traits such as disease resistance. Evaluating these individuals across different sites added to our understanding of key traits and their interrelationships, making it possible to more efficiently improve them genetically.

Genetic tests were developed to predict peach maturity date and fruit quality traits including fruit texture, flavor, size, and skin color. These new genetic tests enable peach breeders to select parents with the greatest likelihood of transmitting favorable traits. The tests also identify the best seedlings for advanced field testing, reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

Using this strategy, called Marker-Assisted Breeding, peach breeders can now more efficiently, accurately, and creatively develop superior peach varieties that meet the needs and desires of consumers and producers.

IMPACT: As a result of genetic testing in the peach breeding programs:

- New crosses designed since 2012 have included expanded genetic knowledge of each parent’s potential to transmit desirable traits to their offspring, resulting in greater genetic gain in the next generation.
- Corrected pedigrees of parents, selections, and seedlings enabled breeders to make well informed crossing, culling, and advancement decisions rather than partially informed guesses.
- Previously unexplained inheritance patterns for some interspecific breeding materials were deciphered.
- MAB increased the efficiency of peach breeding programs by focusing resources on seedlings that have the greatest potential for commercial success.

Clemson University peach breeder: Ksenija Gasic
University of Arkansas peach breeder: John R. Clark
Texas A&M peach breeder: David Byrne
University of California – Davis peach breeder: Thomas Gradziel
Peach Breeding:
Clemson University

ISSUE: New peach varieties with improved fruit quality will lead to increased consumer enjoyment and consumption and will contribute to the profitability and sustainability of the U.S. peach industry. However, breeding new peach varieties is slow and inefficient. Predicting which selections will be the best parents is difficult. Thousands of seedlings must be grown and evaluated in the orchard to identify the few with commercial potential.

WHAT HAS BEEN DONE: Genetic tests were developed that predict peach maturity date and fruit quality traits including fruit texture, flavor, size, and skin color. These new genetic tests enable us to determine the best parents to combine and the best seedlings to advance, thereby reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

Using this strategy, called Marker-Assisted Breeding (MAB), we are now more efficiently, accurately, and creatively developing superior peach varieties that meet the needs and desires of consumers and producers.

IMPACT: As a result of genetic testing of 310 peach selections in the Clemson peach breeding program:

- Twenty-four selections were chosen to enter the breeding program’s parent pool based on their genetic potential to transmit freestone, melting, or non-softening flesh types, high skin blush levels, and/or resistance to bacterial spot.
- Seventy crosses designed since 2012, combining parents in various combinations, included DNA information on their efficiency to transmit freestone, melting flesh, and high blush levels to their progeny, resulting in a greater proportion of seedlings with target fruit types in the next generation.
- Twenty of the above crosses also combined parents for efficient transmittance of bacterial spot tolerance.

The overall impact of MAB is an increased efficiency to identify peach seedlings that have bacterial spot resistance and desired fruit quality attributes. DNA-informed parent selection and cross combination generates a greater proportion of superior seedlings and an increased overall efficiency of the Clemson peach breeding program.

Clemson University peach breeder: Ksenija Gasic
Peach Breeding:
University of Arkansas

ISSUE: New peach varieties with improved fruit quality will lead to increased consumer enjoyment and consumption and will contribute to the profitability and sustainability of the U.S. peach industry. However, breeding new peach varieties is slow and inefficient. Predicting which selections will be the best parents is difficult. Thousands of seedlings must be grown and tested in the orchard to identify the few with commercial potential. Prior to RosBREED, our breeding program relied solely on traditional breeding methods.

WHAT HAS BEEN DONE: Genetic tests were developed that predict peach maturity date and fruit quality traits including fruit texture, flavor, size, and skin color. These new genetic tests enable us to determine the best parents to use in future crosses and the best seedlings to advance, reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

Using this strategy, called Marker-Assisted Breeding (MAB), we can now more efficiently, accurately, and creatively develop superior new peach varieties that meet the needs and desires of consumers and producers.

IMPACT: As a result of genetic testing in the Arkansas peach breeding program:

- We selected four varieties and advanced 16 selections and 136 seedlings for field-testing. MAB has increased our efficiency by focusing resources on seedlings that have the greatest potential for commercial success.
- We discovered new peach flesh types in our genepool, one of which, “non-softening” flesh, maintains its firmness and quality for three or more weeks in postharvest storage and the fruit is more resistant to mechanical damage. Another discovery, the “slow-melting” type, also maintains its firmness for a longer period, then, upon full ripeness, melts and reaches the same texture as that of melting types. Both these new flesh types may provide a wider range of fruit quality options for the consumer.
- We are confident now in moving beyond traditional breeding to using MAB to improve peach traits such as texture, size, flavor, skin color, bacterial spot resistance, bloom date, and fruit maturity date.

University of Arkansas peach breeder: John R. Clark
Peach Breeding:
University of California – Davis

ISSUE: New processing peach varieties with improved fruit quality will lead to increased consumer enjoyment and consumption and will contribute to the profitability and sustainability of the U.S. peach industry. However, breeding improved processing peach cultivars is slow and inefficient. Related species, such as almond, offer sources of valuable new traits but this approach is particularly challenging genetically.

WHAT HAS BEEN DONE: Genetic tests were developed that predict peach maturity date and fruit quality traits including fruit texture, flavor, size, and skin color. These genetic tests enable us to identify the best parents to use in future crosses. When related species are used in breeding, the chosen parents have the desirable characteristics, while avoiding the undesirable ones. Genetic tests also help us avoid planting in the orchard many seedlings predicted to be undesirable.

Using this strategy, called Marker-Assisted Breeding (MAB), we are now more efficiently, accurately, and creatively develop superior processing peach varieties that meet the needs and desires of consumers and producers.

IMPACT: As a result of genetic testing of 409 peach selections in the UC Davis Processing Peach Breeding Program:

- The pedigrees for 200 selections were corrected. Accurate pedigrees are desired for the official documenting and release of new cultivars.
- Groups of genetically similar plant materials that were detected enabled us to adjust and improve the crossing schemes. Parents were identified that had an increased likelihood of transmitting the desired fruit weight and diameter.
- We also identified previously unknown genetic complications in some advanced interspecific breeding materials that explained unexpected inheritance patterns.

The impact of MAB is an improved understanding of the genetic relationships among current breeding lines and an increased efficiency in identifying peach traits that are controlled by a relatively few number of genetic factors.

University of California – Davis peach breeder: Tom Gradziel
Peach Breeding:
Texas A&M

ISSUE: New peach varieties with improved fruit quality will lead to increased consumer enjoyment and consumption and will contribute to the profitability and sustainability of the U.S. peach industry. However, breeding new peach varieties is slow and inefficient. Predicting which selections will be the best parents is difficult. Thousands of seedlings must be grown and tested in the orchard to identify the few that have commercial potential.

WHAT HAS BEEN DONE: Genetic tests were developed to predict peach maturity date and fruit quality traits including fruit texture, flavor, size, and skin color. These new genetic tests enable us to combine the best parents and to advance the best seedlings, reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

Using this strategy, called Marker-Assisted Breeding (MAB) superior peach varieties that meet the needs and desires of consumers and producers can be bred more efficiently, accurately, and creatively.

IMPACT: As a result of genetic tests in the Texas A&M peach breeding program:

- We discovered that our program’s breeding genepool only carries the genetic factors providing “melting flesh” texture. To widen the range of fruit types, we designed crosses to incorporate the genetics for non-melting flesh combined with adaptation to the warm winters of Texas.
- Genetic testing of 100 important selections and varieties for flesh types, resistance to bacterial leaf spot, acidity, blush, and soluble solids concentration was combined with performance information to select parents for crossing in 2014.
- We genetically tested an entire population of 350 seedlings to improve our knowledge on traits related to adaptation (bloom dates, flower density, and fruit density).

The collective impact of MAB is enhanced ability to identify peaches superior in climatic adaptation, fruit texture, size, flavor, skin color, bacterial spot resistance, bloom date, and maturity date. The Texas A&M University peach breeding program will save resources and increase its efficiency, accuracy, and creativity using these new genetic tools.
**Sweet and Tart Cherry Breeding**

**ISSUE:** New sweet cherry varieties with improved fruit quality and new disease resistant tart cherry varieties will lead to increased consumer enjoyment and consumption and will contribute to the profitability and sustainability of the U.S. cherry industries. However, breeding new cherry varieties is slow and inefficient, taking 15 to 25 years from the initial cross to variety release. Predicting which selections will be the best parents is difficult. Thousands of seedlings must be grown and evaluated in the orchard to identify the few with commercial potential.

**WHAT HAS BEEN DONE:** Genetic tests were developed to predict cherry fruit color, fruit size, fruit firmness, self-fruitfulness, and resistance to leaf spot in tart cherry. These genetic tests enable cherry breeders to determine the best parents to combine and the best seedlings to advance, thereby reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

Using this strategy, called Marker-Assisted Breeding (MAB), cherry breeders can more efficiently, accurately, and creatively develop superior cherry varieties that meet the needs and desires of consumers and producers.

**IMPACT:** In the Washington State University sweet cherry and Michigan State University tart cherry breeding programs:

Genetic testing of sweet cherry seedlings, selections and varieties resulted in:

- Forty-two individuals chosen as parents and 146 crosses designed, based on their genetic potential to transmit self-fruitfulness and firm and large fruit.
- 3735 seedlings were discarded prior to orchard planting because they were predicted to be genetically inferior for the above traits.

Genetic testing of tart cherry seedlings, selections, and varieties resulted in:

- Twenty-five crosses designed based on their potential to transmit bright red fruit color to their progeny.
- About 30 percent of seedlings, predicted to be inferior, discarded prior to orchard planting.
- Seedlings predicted to be disease resistant propagated on a rootstock to induce early flowering. This leap-frog action should decrease the number of years to release of a disease resistant variety.

The collective impact of MAB is increased efficiency in identifying superior cherry varieties. Resources can therefore be spent on individuals with a greater chance of having desired trait attributes. For example, without MAB, approximately 3.5 acres of sweet cherry seedlings, with little commercial potential, would have been planted, maintained, and evaluated for years – a very resource-intensive process. A projected cost to the Washington State University program of $75,000 was avoided.

Michigan State University tart cherry breeder: Amy Iezzoni
Washington State University sweet cherry breeder: Nnadozie Oraguzie
Sweet Cherry Breeding:
Washington State University

ISSUE: New sweet cherry varieties with improved fruit quality will lead to increased consumer enjoyment and consumption and will contribute to the profitability and sustainability of the U.S. sweet cherry industry. However, breeding new sweet cherry varieties is slow and inefficient and can take 15 to 25 years from the initial cross to variety release. Predicting which selections will be the best parents is difficult. Thousands of seedlings must be grown and evaluated in the orchard to identify the few that have commercial potential.

WHAT HAS BEEN DONE: Genetic tests were developed to predict cherry fruit color, fruit size, fruit firmness, and self-fruitfulness. These genetic tests enable sweet cherry breeders to determine the best parents to combine and the best seedlings to advance, reducing the need to grow out and sort through thousands of seedlings with unacceptable fruit quality.

Using this strategy, called Marker-Assisted Breeding (MAB), cherry breeders can more efficiently, accurately, and creatively develop superior cherry varieties that meet the needs and desires of consumers and producers.

IMPACT: As a result of genetic testing of 7000 seedlings, selections, and varieties in the Washington State University sweet cherry breeding program:

- Forty-two selections were chosen as parents based on their genetic potential to transmit self-fruitfulness and firm and large fruit.
- 146 crosses were designed based on their efficient paired ability to generate self-fruitfulness, large fruit, and good firmness in the next generation.
- Sixteen advanced selections were characterized for their genetic potential for key traits to increase confidence in their adoption as potential new varieties
- 3735 seedlings were discarded prior to field planting based on the prediction that the flowers will be self-sterile and the fruit will be small and soft.

The collective impact of MAB is increased efficiency of identifying sweet cherries that are large, firm, and self-fruitful with potential to extend the marketing window and increase profitability. Without MAB, approximately 3.5 acres of sweet cherry seedlings with little commercial potential would have been planted and evaluated. Therefore, a projected cost of $75,000 to the Washington State University program was avoided.
Tart Cherry Breeding:  
Michigan State University

ISSUE: New disease resistant tart cherry varieties with improved fruit quality will lead to increased consumer enjoyment and consumption and will contribute to the profitability and sustainability of the U.S. tart cherry industry. However, breeding a new tart cherry variety is slow and inefficient. Predicting which selections will be the best parents is difficult. Hundreds of progeny individuals must be grown and tested in the orchard to identify the few with commercial potential.

WHAT HAS BEEN DONE: DNA tests were developed to predict cherry fruit and pit size, cherry skin and flesh color, self-fruitfulness, and resistance to cherry leaf spot fungus. These genetic tests enable tart cherry breeders to determine the best parents to combine and the best seedlings to advance, reducing the need to grow out and sort through hundreds of seedlings with unacceptable fruit quality or disease susceptibility.

Using this strategy, called Marker-Assisted Breeding (MAB), cherry breeders can more efficiently, accurately, and creatively develop superior tart cherry varieties that meet the needs and desires of consumers and producers.

IMPACT: As a result of genetic testing in the Michigan State University tart cherry breeding program:

- About 30 percent of seedlings from one cross were discarded prior to orchard planting because DNA tests identified them as derived from unintended parentage.
- Twenty-five crosses were designed based on their increased potential for transmitting the desired red skin and light red juice color to their offspring.
- Seedlings predicted to be resistant to cherry leaf spot were propagated on a rootstock that induces early flowering. This new activity will reduce by two years the time required to breed disease resistant varieties.
- In 2014, seedlings from 10 crosses will be DNA tested to discard those seedlings that are predicted to have undesirable fruit color, thus avoiding future expenses for growing and evaluating these seedlings.

The collective impact of MAB is increased efficiency of identifying new tart cherry varieties. Resources needed to grow seedlings to maturity can be targeted to those individuals with a greater chance of having the desired trait attributes.

Michigan State University tart cherry breeder: Amy Iezzoni
Strawberry Breeding

ISSUE: New strawberry varieties with improved fruit quality will lead to increased consumer enjoyment and consumption, and will contribute to the profitability and sustainability of the U.S. strawberry industry. To meet this challenge, new strawberry varieties are needed that are high yielding due to continuous flowering and that are resistant to soil pathogens that cause serious diseases like root rot. However, breeding new strawberry varieties is slow and inefficient. Predicting which selections will be the best parents is difficult. Thousands of seedlings must be grown and tested in the field to identify the few with commercial potential.

WHAT HAS BEEN DONE: Strawberry breeders in California, Florida, Michigan, New Hampshire, and Oregon evaluated more than 900 individuals including old and new varieties, wild plants from North and South America, elite breeding parents, and experimental crosses from the Netherlands, United Kingdom, Spain, France, and the United States. This data was used to enable the development of genetic tests that strawberry breeders can use to verify plant identity and determine the best parents to combine, giving them the best seedlings to advance. A genetic test was developed to predict resistance to one of the sources of root rot resistance. This genetic test enables breeders to identify seedlings that have this source of resistance without the need to carry out expensive, time-consuming disease inoculation tests.

IMPACT: As a result of genetic testing of strawberry selections in the USDA-ARS Corvallis, Oregon and Michigan State University breeding programs and extensive performance evaluations of these strawberries:

- Forty-two individuals from 13 crosses were discarded because DNA tests identified them as derived from unintended parentage.
- For several important varieties used as parents, plants from multiple sources were found to be different genetically and therefore somehow mislabeled during cultivation and breeding use.
- Fourteen strawberry selections were identified as having new sources of root rot resistance.
- Two interspecific hybrids of wild strawberries were found which are strongly continuously flowering in multiple environments (California, Michigan, and Oregon). These individuals will provide breeders with a unique genetic source of repeat flowering.

Michigan State University strawberry breeder: James Hancock
USDA-ARS, Corvallis, Oregon strawberry breeder: Chad Finn
University of New Hampshire strawberry breeder: Thomas Davis
Driscoll’s Strawberry Associates strawberry breeder: Philip Stewart
University of Florida strawberry breeder: Vance Whitaker
ISSUE: The development of new crop varieties of the Rosaceae plant family with improved horticultural performance and market potential can be accelerated with use of DNA information in breeding, benefiting all supply chain members through more efficient, accurate, and creative breeding for desirable crop traits. However, DNA-informed breeding requires extensive genetic knowledge, trained personnel, and sufficient financial resources. Therefore, it is crucial for breeders to focus their efforts and resources on valuable crop attributes throughout the whole supply chain and of value to consumers.

However, systematically identifying these valuable attributes is challenging. Very few studies of crop plants have evaluated the importance of attributes across the supply chain members and consumers. Breeders have therefore had to focus their breeding programs on specific targets with little systematic knowledge of the relative value of incremental improvements in those traits for producers, market intermediaries, and consumers.

PROGRESS: The relative importance to different stakeholders (breeders, growers, market intermediaries, and consumers) of trait levels for apple, peach, strawberry, sweet cherry, and tart cherry were investigated. In addition, economic values of achieving particular fruit quality trait thresholds (added dollar value per pound) for growers and marketing intermediaries were estimated in these crops. Marginal values for consumers of achieving fruit quality trait thresholds in fresh market apples were also estimated.

IMPACT: Project resources for genetic test development were directed to those genomics discoveries having the highest relative value of importance across stakeholders. Information about the economic values of specific crop trait levels is now available to inform the ongoing work of geneticists and breeders as they develop new genetic tests and direct those to efficiently, accurately, and creatively developing superior new crop varieties of value to stakeholders.

Examples of high value trait levels for which genetic tests have been developed include: apple exceptional crispness, juiciness, tartness, and freedom from bitter pit blemishes, various peach fruit types (normal/low acid, yellow/white flesh, peach/nectarine, melting/non-melting, and freestone/clingstone) that can be targeted across the fruiting season, strawberry sufficient acidity, sweet cherry large size and firmness, and tart cherry red fruit color.
Standardized Phenotyping

ISSUE: Learning how crop traits are related to specific DNA markers requires measuring many individual plants for many valuable characteristics – known as “phenotyping”. These traits must be evaluated and recorded in a consistent, standardized manner regardless of the location, personnel, or time. With this high quality phenotypic data, links between specific DNA sequences and important fruit and plant traits can be accurately determined because confounding “noise” is greatly reduced. Furthermore, when several breeders use standardized phenotyping protocols they can pool the data. The resulting large data sets give incredible power to identifying and characterizing genomic regions influencing important traits. Prior to RosBREED, phenotypic data was collected in small, isolated studies, limiting the size of data sets and limiting the extent to which results could be extended.

WHAT HAS BEEN DONE: Each RosBREED crop team (apple, peach, strawberry, sweet cherry, and tart cherry) chose a reference set of several hundred individual plants (including ancestral and modern varieties, breeding selections, and seedlings) that represent the pedigrees of current important parents in U.S. breeding programs. Participating breeders agreed on the traits to be evaluated and then developed and documented standardized protocols to collect measurements of these plant and fruit characteristics. They compiled extensive databases for fruit quality and other critical traits, with measurements were made over multiple years and locations.

IMPACT: A database of trait measurements on approximately 500 hundred individuals in each apple, peach, strawberry, sweet cherry, and tart cherry is now documented and publicly accessible. Breeders and allied scientists now use the database to discover specific genomic regions that are associated with important crop traits. The resulting genetic tests enable efficient marker-assisted breeding for more than 150 critical fruit quality and production traits in rosaceous fruit crops.

- Apple: 43 fruit traits evaluated at harvest and after cold storage of fruit, and five production traits
- Peach: 29 fruit traits and seven production traits
- Strawberry: 30 fruit traits, six disease resistance traits, and 13 plant architecture and production traits
- Sweet Cherry: 19 fruit traits
- Tart Cherry: 23 fruit traits, 12 production traits, and nine disease resistance traits

The standardized phenotyping protocols are available at www.rosbreed.org. By using these protocols in future work to measure more individual plants, the public database can be expanded, and private datasets can be developed that are compatible and lead to even more powerful analyses and thereby more accurate genetic tests.

Breeding Team Leader: James Luby, University of Minnesota
All contributors are identified by authorship on the following publications:
Enabling Genetic Technologies

ISSUE: Prior to this project, genetic tests for traits of interest in Rosaceae crops either had not yet been developed or they were expensive and cumbersome to use. Genome-scanning DNA markers were small in number which did not allow the efficient identification of chromosome regions influencing important traits. Moreover, most of these markers were laborious to use and relatively expensive, therefore limiting their applications in genetic discovery and breeding.

PROGRESS: Cost-effective, high throughput marker technologies were developed, commercialized, and made available to the U.S. and worldwide scientific community. Thousands of single nucleotide polymorphism (SNP) markers were developed for apple, peach, cherry, and cultivated strawberry in international RosBREED-led efforts. The genome scan platforms developed were the 9K (9000 genetic points testable across the crop’s chromosomes) peach, 8K apple, and 6K peach SNP marker Infinium® II arrays partnering with the commercial genomics technology company, Illumina Inc., and the 90K SNP marker (IStraw90™) Axiom® genotyping array, partnering with Affymetrix Inc.

IMPACT: Rosaceous breeders and geneticists can now efficiently generate and analyze thousands of well-performing genetic markers at low cost. These genetic marker tools are being used by numerous U.S. breeding programs to better understand the genetic control of high-value traits and make more informed crosses.

IStraw90™ is the first genome-wide scan ever developed for an octoploid crop (which is an organism like strawberry that has eight rather than two sets of chromosomes). This enabling genetic technology paves the way for further advances in genomics and breeding for other important polyploid crops (organisms with more than two sets of chromosomes).

As a result of developing and using these genome-wide scans:

- Arrays to process 20,000 samples at a value exceeding 1.3 million dollars were purchased from Illumina Inc., by ten groups in ten countries.
- Fourteen scientific articles were published to date describing the use of these tools to identify genomic regions influencing important traits, to characterize the genetic architecture of complex traits in apple, peach, and cherry, and other genetics and breeding applications like confirming or deducing pedigrees.
- IStraw90™, the first high-resolution genome-wide scan ever developed for an octoploid crop, is now available for use by breeders and researchers.

Genomics Team Leader: Dorrie Main, Washington State University
Genotyping Team Leader: Nahla Bassil, USDA-ARS National Clonal Germplasm Repository
All contributors are identified by authorship on the following publications:
Enabling Statistical Tools

ISSUE: The first step in the development of genetic tests for use in Marker-Assisted Breeding is the discovery of genomic regions influencing traits of interest. The second step is to determine whether these discoveries are relevant for breeding germplasm. In the past, discoveries for rosaceous crops were conducted in dedicated experimental families for which the underlying genetic models were simple and the statistical tools well developed. The discoveries were rarely and inconsistently validated in breeding families, because such families are genetically complicated due to great diversity and unbalanced pedigree structures.

WHAT HAS BEEN DONE: Advanced statistical methods and software tools were developed to help genetic researchers manage and analyze data directly using breeding genepools. The statistical software developed were also adapted to efficiently process the large and unprecedented amount of genetic data available from genome scans. The first applications of these new software tools were performed on RosBREED data.

IMPACT: An efficient pipeline from genetic discovery to breeding application is now available. U.S. rosaceous crop breeders and geneticists can now efficiently analyze thousands of well performing DNA markers across each crop’s entire genome. Finding genomic regions influencing important traits for breeding is now commonplace.

Genetic discoveries leading to new genetic tests include:

- **Peach**: Fruit texture, flesh type, flavor, size, skin color, maturity date, and bacterial spot tolerance
- **Apple**: Fruit firmness, crispness, juiciness, sweetness, acidity, skin color, bitter pit incidence, and storability
- **Sweet cherry**: Fruit size, firmness, skin and flesh color, sweetness, acidity, and maturity date
- **Tart cherry**: Fruit and pit size, cherry skin and flesh color, ability to self-pollinate, and resistance to cherry leaf spot fungus
- **Strawberry**: Red stele resistance, continuous flowering

Pedigree-Based Analysis Team Leader: Eric van de Weg, Plant Research International, The Netherlands
Software Developers: Marco Bink, Roeland Voorrips and Hans Jansen, Plant Research International, Wageningen, The Netherlands
Breeding Information Management System Software

ISSUE: Marker-assisted breeding of crops in the Rosaceae family requires massive amounts of data, including:

- measurements of observed characteristics (phenotypes),
- genetic variation in the form of DNA sequences and their variants (genotypes),
- pedigrees connecting breeding germplasm individuals,
- DNA information describing associations between phenotypes and genotypes, and
- DNA information describing what form of each trait-influencing genomic region is carried by each breeding individual.

Managing all these data types and making them accessible to inform breeding and associated research decisions is a daunting task. Online tools that leverage the trillions of data points generated are needed. By performing both simple and complicated calculations and visualizations, users can efficiently and strategically manage the information for genetic improvement of rosaceous crops.

WHAT HAS BEEN DONE: Online, searchable data repositories and associated calculation and visualization tools to assist apple, cherry, peach, and strawberry breeding were developed and made available for public use on the Genome Database for Rosaceae portal (www.rosaceae.org).

IMPACT: U.S. rosaceous crop breeders and allied scientists can now efficiently upload, browse, search, and download genetic data and observed traits of crop varieties for apple, peach, cherry, and strawberry; generate input files to use in breeding pedigree software; visualize all of these data types from any web portal (even on smartphones); receive decision support for identifying efficient crosses and seedling selection schemes; and develop and validate their own genetic tests using the best available genomic knowledge about each crop. These breeding decision-support tools are increasing the efficiency, accuracy, and creativity and capability of breeding programs. These tools are:

1) **Trait Locus Warehouse** – where all known genetic discoveries to date across each crop’s genome are compiled, visualized, and chosen for further consideration.
2) **Selection Target Identifier** – where the most promising genetic discoveries are determined by associating socio-economic values to the trait level increase promised by each “trait locus”.
3) **Technology Portfolio** – where regularly updated details about commercial service providers for genetic testing are made available to all breeding programs.
4) **Marker Converter** – where breeders or supporting researchers use DNA sequences and other genomics data to design new genetic tests for valuable discoveries that are appropriate for a breeder’s genetic testing service provider.
5) **QTL Validator** – where tools reside for characterizing the predictiveness of each new DNA for a specific breeder’s parents and families.
6) **Cross Assist** – where breeders use all available genetic information to determine efficient cross combinations among their parent pool for target performance outcomes in the next generation.
7) **Seedling Select** – where breeders model the costs and logistics of evaluating the genetic potential of thousands of young seedlings to identify when and how much to best integrate available genetic tests to save resources.

Breeding Information Management Team Leader: Gennaro Fazio, USDA-ARS Plant Genetic Resources Unit
Training Future Plant Breeders

ISSUE: Plant breeders who can utilize DNA information will be more efficient in developing superior new varieties with improved fruit quality and greater productivity. Preparing future plant breeders who can integrate DNA-based knowledge and technology into their breeding programs, a process called Marker-Assisted Breeding (MAB), assures an exciting future for new cultivar development. Training of the next generation in appropriate application of state-of-the-art technologies leverages public and private investments in advanced genetics and genomics research for sustained breeding outcomes. Breeder education programs that include MAB will help meet industry needs for new breeders, in turn serving producers, packers, shippers, and sellers who will have new fruit varieties that meet their various needs and the preferences of consumers.

WHAT HAS BEEN DONE: RosBREED’s “demonstration” apple, cherry, peach, and strawberry breeders are each training one or more graduate students. These Breeding Trainees have gained knowledge, experience, and skills in setting breeding targets, accurately measuring fruit and plant characteristics, determining trait inheritance, designing and implementing genetic tests, evaluating alternative selection strategies, and managing breeding program logistics, personnel, budgets, and timelines. A coordinated team approach is used to provide a multi-disciplinary learning experience for these students.

IMPACT: As a result of RosBREED’s investment in the next generation of plant breeders:

- Four doctoral students have graduated and an additional two doctoral students will graduate in the next two years with skills, knowledge, and experience in MAB that would not have been provided without RosBREED funding, training opportunities, and collaborative networks among breeding programs and educational institutions.

- Four Master’s students have graduated and an additional one Master’s student will graduate in the next year with similar added skills, knowledge, and experience.

- These 11 students represent a doubling in the number of students trained in these programs in the last decade. Many of their graduate education opportunities would not have existed without RosBREED support, and all of their educational experiences were greatly enriched by learning opportunities in MAB provided through the RosBREED project.

- These students are prepared for the breeding jobs of the future. They have learned how to use new genetic tests to determine the best parents to combine in new crosses and to determine the best seedlings to advance through their programs. These applications reduce the costly and time-consuming need to plant, maintain for years, and thoroughly field test thousands of seedlings that are likely to have unacceptable fruit quality or growth characteristics. By using genetic tests to avoid the least promising parents and eliminate inferior seedlings early in this multi-year process, these students have learned how to focus breeding program resources where they are most likely to succeed.
Collaborators and Nature of Collaboration

Pedigree-Based Analysis
- Hans Jansen - Plant Research International, Wageningen-UR, NL
- Chris Maliepaard - Plant Breeding, Wageningen-UR, NL
- Roeland Voorrips - Plant Research International, Wageningen-UR, NL

Strawberry Breeders
- Phil Stewart - Driscoll’s Strawberry Associates, Watsonville, CA
- Vance Whitaker - University of Florida IFAS, Gulf Coast Research and Education Center, Wimauma, FL

Bioinformatics
- Todd Mockler - Donald Danforth Plant Science Center, St Louis, MO
- Hailong Zhang - Tom Davis’s Team, University of New Hampshire, Durham, NH
- Kirstin Bett - Plant Sciences, University of Saskatchewan, Canada

Sequencing/Molecular Groups
- Cindy Lawley & Mark Hansen, Illumina Inc, Haywood, CA
- Mike Mittman, LuAnn Glaser & Affymetrix Genotyping Team, Affymetrix Inc., Santa Clara, CA
- Amit Dhingra - Dept of Hort. & Landscape Arch., Washington State Univ., Pullman, WA
- Bryon Sosinski - Dept. of Hort Sci North Carolina State University, Raleigh, NC

International Partners and Nature of Partnership

Sequencing/Molecular Groups
- David Chagné - Plant & Food Research, Palmerston North, 4474, New Zealand
- Lee Meisel - Center of Plant Biotechnology, Ecology & Natural Resources. Andres Bello Univ Santiago, Chile
- Jasper Rees – Agricultural Research Council, South Africa
- Dan Sargent - Biology Department Istituto Agrario San Michele, Trento, Italy
- Herman Silva - Center of Plant Biotechnology, Ecology & Natural Resources. Andres Bello Univ Santiago, Chile
- Ignazio Verde - Centro di Ricerca per la Frutticoltura, Rome, Italy
- Riccardo Velasco - Biology Department Istituto Agraro San Michele, Trento, Italy

INRA – Breeding & Genetics teams
- Beatrice Denoyes-Rothan, Elisabeth Dirlewanger, and Jose Quero Garcia - Unité de Recherche des Espèces Fruitières (UREF), INRA CR Bordeaux.Villenave d’Ornon, France
- Francois Laurens and Charles-Eric Durel - Unité de Génétique et Horticulture (GENHORT), INRA CR Angers, Beaucouze, France
- Benedicte Quilot-Turion, Patrick Lambert, and Thierry Pascal - Unité de Génétique et Amélioration des Fruits et Légumes (UGAFL), INRA CR Avignon, France

INRA – Breeding & Genetics teams
- Beatrice Denoyes-Rothan, Elisabeth Dirlewanger, and Jose Quero Garcia - Unité de Recherche des Espèces Fruitières (UREF), INRA CR Bordeaux.Villenave d’Ornon, France
- Francois Laurens and Charles-Eric Durel - Unité de Génétique et Horticulture (GENHORT), INRA CR Angers, Beaucouze, France
- Benedicte Quilot-Turion, Patrick Lambert, and Thierry Pascal - Unité de Génétique et Amélioration des Fruits et Légumes (UGAFL), INRA CR Avignon, France
RosBREED had three Advisory Panels, representing industry, scientific, and extension interests. Panel members broadly represented the diversity of Rosaceae by crop, region, and professional expertise.

RosBREED Industry Advisory Panel

- **Jim Allen**: President
  New York Apple Association, Fishers, NY (www.nyapplecountry.com)
  Board of Trustees, US Apple Association (www.usapple.org)
- **Phil Baugher**: Co-owner
  Adams County Nursery, Aspers, PA (www.acnursery.com)
  Chair, US Apple Association Research Committee
- **Henry Bierlink**: Director
  Washington Red Raspberry Commission, Lynden, WA (www.red-raspberry.org)
  National Berry Crops Initiative (www.nationalberrycrops.org/)
- **Chalmers Carr III**: CEO
  Titan Peach Farms, Inc., Ridge Spring, SC (www.titanfarms.com/default.asp)
  Board of Directors, South Carolina Peach Council (www.scpeach.com/about.htm)
- **Fred Cook**: National Research Department Manager
  Driscoll’s Strawberry Associates, Watsonville, CA (www.driscolls.com)
- **Robert Curtis**: Associate Director, Agricultural Affairs
  Almond Board of California, Modesto, CA (www.AlmondBoard.com)
- **Bill Dodd**: President
  Ohio Fruit Growers Marketing Association, Newcomerstown, OH
  (www.ohioapples.com/ohio_apples_fgma.htm)
  Board of Trustees, US Apple Association
- **Bruce Grim**: Director
  Washington Marketing Associations, Wenatchee, WA (www.themarketingassociations.org)
  Executive Director, Washington State Horticultural Association (www.wahort.org)
  President, Board of Trustees, US Apple Association
- **Rick Harrison**: VP – Global Variety Development
  Driscoll Strawberry Associates, Watsonville, CA (www.driscolls.com)
- **Philip Korson**: President
  Cherry Marketing Inst., Inc., Lansing, MI (www.choosecherries.com)
- **John Lott**: President
  Bear Mountain Orchards, Inc., Aspers, PA (www.bearmountainorchards.com)
- **Kevin Moffitt**: President
  Pear Bureau Northwest, Portland, OR (www.usapears.com)
- **Tom Stokes**: CEO
  Tree Top Inc, Selah, WA (www.treetop.com)
  Board of Trustees, US Apple Association
- **Gary van Sickle**: President
  California Plum Marketing Board
• **Jessica Goldberger:** Asst. Professor, Dept. of Crop and Soil Sciences, Washington State Univ.
  Professional interests: agricultural knowledge, science, and technology
  (www.crs.wsu.edu/facstaff/goldberger/goldberger.html)

• **Peter Hirst:** Assoc. Professor, Dept. of Horticulture, Purdue Univ.
  Professional interests: tree fruit production systems and physiology, physiological genetics of
  flowering and fruit development in Rosaceae; state Extension specialist; undergraduate and
  graduate education
  (www.hort.purdue.edu/hort/people/faculty/hirst.shtml)

• **David Karp:** Associate, Agricultural Experiment Station, UC Riverside
  Professional interests: freelance food journalist and photographer

• **Mercy Olmstead:** Asst. Professor, Department of Horticultural Sciences, University of Florida-IFAS,
  Professional interests: Stone Fruit Extension Specialist (http://hos.ufl.edu/stonefruit)

• **Ron Perry:** Professor, Dept. of Horticulture, Michigan State Univ.
  Professional interests: extension and research in cherry and apple orchard systems
  (www.hort.msu.edu/faculty/perry.htm)

• **Clark Seavert:** Professor & Director of the NW Agribusiness Executive Seminar Department
  of Agricultural & Resource Economics, Oregon State Univ.
  Professional interests: assessment and advancement of technologies that increase
  profitability and feasibility in commercial agriculture, with the aim of aligning business model
  innovation strategies to existing and future technologies.
  (http://arec.oregonstate.edu/seavert)

• **Jamie Sherman:** Asst. Professor, Dept. of Plant Sciences and Plant Pathology, Montana State Univ.
  Professional interests: wheat genetics and Outreach Coordinator for USDA-NRI WheatCAP
  (http://plantsciences.montana.edu/facultyorstaff/faculty/sherman/sherman.html)

• **Brian Sparks:** Group Editor, American/Western Fruit Grower:
  Willoughby, OH
  Professional interests: trade and web-based publication covering U.S fruit production
  (www.growingproduce.com/americanfruitgrower)

• **Chris Watkins:** Professor, Dept. of Horticulture, Cornell Univ.,
  Assoc. Director for Cornell Cooperative Extension
  Professional interests: postharvest physiology and management of apple, pear, peach, and
  cherry; state-wide agricultural extension activities
  (http://hort.cals.cornell.edu/people/faculty.cfm?netId=cbw3)
• **Albert Abbott**: Professor, Dept of Biological Sciences, Clemson Univ.
  Research areas: structural genomics of *Prunus*, sequencing of peach genome
  (www.clemson.edu/cafls/departments/genbiochem/people/aabbott.html)

• **Pere Arús**: Head, Plant Genetics Dept., Institut de Recerca i Tecnologia
  Agroalimentàries (IRTA), Cabrils, Spain
  Research areas: molecular tools for plant genetics; comparative genomics and
  application of molecular markers in Rosaceae breeding. co-PD: European Integrated
  Research Project ISAFRUIT
  (www.isafruit.org/Portal/about.php)

• **Joe Arvai**: Svare Chair in Applied Decision Research, Haskayne School of Business
  and Institute for Sustainable Energy, Environment, & Economy, University of Calgary
  Research areas: Behavioral decision research and decision support systems

• **Frederick Bliss**: Professor Emeritus, Univ. of California, Davis and Sr. Director, R&D
  Special Projects, Seminis Vegetable Seeds, Woodland, CA
  Research areas: genomics, genetics, and breeding of fruit and vegetable crops;
  research administrator in public and private sectors; commercialization of breeding
  products

• **Robin Buell**: Professor, Dept. of Plant Biology, Michigan State Univ.
  Research areas: genomic aspects of plant biology and plant pathogens; high throughput
  sequencing, functional genomics, comparative genomics, and bioinformatics
  (www.plantbiology.msu.edu/faculty/faculty-research/robin-buell/)

• **Lailiang Cheng**: Assoc. Professor, Dept. of Horticulture, Cornell Univ., Ithaca, NY
  Research areas: plant nutrition, fruit physiology, molecular, cellular, and whole plant
  response to abiotic stress in apple, cherry, grape; undergraduate and graduate
  education
  (hort.cals.cornell.edu/cals/hort/people/faculty.cfm?netId=lc89)

• **Susan Gardiner**: Principal Scientist, The Horticultural and Food Research Inst. of New
  Zealand (Plant & Food Research [PFR])
  Research areas: leads Gene Mapping Team integrated with PFR breeders in several
  Rosaceae crops, including, apple, apple rootstock, pear, peach/nectarine and apricot

• **Kim Hummer**: Supervisory Research Horticulturist, National Clonal Germplasm
  Repository (Corvallis, OR)
  Research areas: conservation of fruit, nut, and specialty crop genetic resources; ploidy
  in strawberry species. She also actively studies genetics of a wide range of crops.

• **Carolyn Ross**: Assoc. Professor, Dept. of Food Science, Washington State Univ.
  Research areas: sensory analysis and consumer preferences of fruit and fruit products,
  including fresh and processed apple, pear, and cherry and wine
  (sfs.wsu.edu/facultystaff/Ross.html)

• **Phil Simon**: Research Geneticist, USDA-ARS and Professor, Dept. of Horticulture, Univ.
  of Wisconsin-Madison
  Research: vegetable breeding and genetics; biochemistry of culinary and nutritive
  factors, terpenoids, and sugars in carrots and garlic.
  (www.horticulture.wisc.edu/faculty/facultylist.php)