# RosBREED: Enabling marker-assisted breeding in Rosaceae

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"RosBREED" is a large-scale initiative of the U.S. Rosaceae genomics, genetics, and breeding community with strong international involvement. This project is dedicated to genetic improvement of rosaceous crops by targeted application of genomics and socio-economics knowledge and tools to increase breeding efficiency, engage stakeholders, and train the next generation of plant breeders. Our goal is to sustainably integrate modern genomics tools with traditional breeding approaches.

Ten teams carry out the RosBREED mission. The Socio-Economics Team has dissected current breeding priorities of U.S. Rosaceae breeders through a comprehensive survey. The Industry Team has initiated enhanced engagement of industry sectors in regional breeding efforts. The Breeding Team has cooperated across 12 breeding programs to establish reference germplasm sets representing their crops and programs and develop standardized phenotyping protocols with the first season of performance evaluation undertaken in 2010. The Pedigree-Based Analysis (PBA) Team has trained breeders in the use of Pedimap software for visualizing breeding pedigrees, including the portrayal of traits and genotypes over generations. Advanced training in FlexQTL™ software enables participating RosBREED breeders and their breeder-in-training graduate students to identify or validate QTLs with local relevance using routine breeding data from multiple variable-sized and pedigree-linked populations. The Breeders' Toolbox Team has developed prototype calculation and visualization tools, query interfaces, and databases for managing breeding information that, over time, will increasingly include DNA-based knowledge. The MAB Pipeline Team, aiming for early impact, has helped translate several available marker-locus-trait associations into ready-to-use information for supporting breeding decisions. The Genotyping Team conducted genetic screening for two high priority trait loci each for peach, cherry, and apple. In addition to current use in supporting crossing decisions, these marker data identified a significant proportion of incorrect parentage in breeding records. The Genomics Team led international development of 6K and 9K genome-scanning SNP arrays for peach, cherry, and apple. With so many inter-Team activities to coordinate, events to arrange, and news to announce, the Extension Team has filled a critical role that extends beyond traditional extension responsibilities. The Administration Team has ensured smooth running of this huge project through timely management of reports and budgets with an eye for detail. RosBREED is removing the barriers, dispelling myths, accumulating experience, identifying pitfalls to avoid, and developing MAB success stories for efficiently developing superior new cultivars of the Rosaceae family bearing delicious and nutritious fruit.

## RosBREED facilitates peach genetic improvement via marker-assisted breeding

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New cultivar development for peach in the U.S. can be divided into two types according to usage of fruit: fresh market and processing market. Objectives common to all peach breeding programs include improving and maintaining fruit quality (flavor, firmness, and appearance), productivity, size, and season extension. These trait targets are complemented with emphases on ease of processing, disease and pest resistance, a greater diversity of fruit types, and adaptation to low-chill zones in individual programs. Genetic markers associated with some of these traits are available and useful for informing crossing decisions and seedling selection decisions. Despite being one of the best characterized *Rosaceae* crops with genomic resources including a whole genome sequence, a reference genetic map, EST libraries, and a growing list of marker-locus-trait associations, application of these resources in peach breeding efforts is still limited. The RosBREED project (www.rosbreed.org) aims to bridge this chasm by providing markers and simplified technologies to enable marker-assisted breeding for fruit quality and other critical traits. The four public peach breeding programs in California, Texas, South Carolina, and Arkansas representing a range of breeding objectives, are integral to this project. The peach breeders have established a comprehensive crop reference germplasm set of important breeding parents represented by about 500 popular cultivars, ancestors, breeding selections, and breeding populations. This material is connected through many pedigree linkages, which is characteristic of peach breeding germplasm and can be exploited via the statistical approach of Pedigree-Based Analysis. Pedimap software was used to visualize these pedigree connections, revealing unrealized fractions of shared genomes. Large-scale phenotyping and genotyping of this reference germplasm is underway. Standardized phenotyping protocols for peach fruit quality evaluation were initiated during the 2010 season. High-resolution SNP-based genome scans with a 6K array are providing an unprecedented view of cultivated peach genetic diversity, and, through association with phenotypic performance, functional variation for breeding program-specific predictive marker development. Genetic tests for promising trait targets were recently fast-tracked through RosBREED's "MAB Pipeline". Useful outcomes include designation of fruit type (melting and non-softening for fresh market and non-melting for canning; freestone vs. clingstone) for breeding selection decisions.

## RosBREED enables marker-assisted breeding for apple

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U.S. apple breeders primarily target consumer-preferred traits of excellent texture, flavor, and appearance. The ability to retain superior fruit quality after storage, so that a year-round domestic supply of nutritious apples is available to the public, is a particular focus. Also considered are traits valued by industry sectors, especially suitability to local production environments. DNA information, if gathered, validated, deployed, and routinely used in breeding decision-making, offers the opportunity for apple genetic improvement to become more efficient and precise in delivering long-term solutions to industry challenges and consumer demands. The multi-institutional RosBREED project (www.rosbreed.org) is enabling such marker-assisted breeding (MAB) for apple. Major public apple breeding programs in Washington, Minnesota, and New York have united in this project to establish a comprehensive crop reference germplasm set of important breeding parents represented by about 500 popular cultivars, ancestors, breeding selections, and breeding populations. This material is connected through many pedigree linkages, which is characteristic of apple breeding germplasm and can be exploited via the statistical

approach of Pedigree-Based Analysis. Pedimap software was used to visualize these pedigree connections, revealing unrealized fractions of shared genomes. Large-scale phenotyping and genotyping of this reference germplasm is underway. Standardized phenotyping protocols for apple fruit quality evaluation were conducted since the 2010 season. High-resolution SNP-based genome scans with an 8K array are providing an unprecedented view of cultivated apple genetic diversity, and, through association with phenotypic performance, functional variation for breeding program-specific predictive marker development. Genetic tests for promising trait targets were fast-tracked through RosBREED's "MAB Pipeline". Useful outcomes include verification of pedigrees and identification of some incorrect records, with deduction of likely pedigrees in some cases. Markers for fruit storability are assisting seedling selection in the Washington apple breeding program since 2010 to cull inferior seedlings prior to expensive field maintenance and evaluation. Most powerfully, DNA information is informing crossing decisions of U.S. apple breeders, bringing to bear available information to efficiently enrich the next generations of apples with the genetics for superior fruit quality.

## RosBREED provides DNA-informed opportunities for cherry breeding

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Fruit size, firmness, flavor, self-fertility, and yield are valuable targets for cherry genetic improvement. DNA markers for some of these traits have been previously reported but require validation in breeding germplasm under commercial conditions, beyond the experimental populations in which the marker-locus-trait associations were first discovered. Each genetic test must also be adjusted to the specific needs, capabilities, and logistics of individual breeding programs. The RosBREED project (www.rosbreed.org) is enabling cherry breeding programs to integrate DNA information into breeding decisions for more precise and efficient delivery of long-term solutions to industry challenges and consumer demands. State University breeding programs in Washington (sweet cherry) and Michigan (tart cherry) serving the major U.S. cherry growing regions follow standardized phenotyping protocols for performance evaluation and have established a reference cherry germplasm set for advancing cherry genetics knowledge. Pedigree-linked cultivar, ancestors, selections, and seedling populations represent important breeding parents. SNP-based genome-scanning capability was recently developed with a 6K cherry array. Determination of genotypically based breeding values to guide breeding decisions will be achieved with adaptation of the Pedigree-Based Analysis approach to breeding germplasm. Marker-assisted parent selection using a genetic test for cross-compatibility and self-fertility has been conducted for several years. Since 2010, marker-assisted seedling selection at a high-throughput scale for fruit size and firmness has also improved breeding efficiency.