

## **RosBREED: Enabling marker-assisted breeding in Rosaceae**

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The Rosaceae family (including apple, peach, sweet and tart cherries, and strawberry) provides vital contributions to human health and well-being, and collectively constitutes the economic backbone of many U.S. rural communities. These 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 industry and market needs and consumers preferences. Rosaceae genetics and genomics are developing rapidly but have not been translated to routine practical application. RosBREED ([www.rosbreed.org](http://www.rosbreed.org)) is bridging this gap by using genomics information and knowledge of what industry sectors and consumers value to accelerate and increase the efficiency of cultivar development and adoption. Specific objectives are to: (1) enhance the likelihood of new cultivar adoption, enlarge market potential, and increase consumption of rosaceous fruits by using socio-economic knowledge of stakeholder values and consumer preferences to inform breeding; (2) establish sustainable technical infrastructure for an efficient MAB Pipeline in Rosaceae, including crop-specific SNP genome scan platforms for breeding-relevant germplasm exploiting the shared ancestry of Rosaceae crops; (3) integrate breeding and genomics resources by establishing a user-friendly U.S.-wide standardized statistical framework and breeding information management system; (4) implement MAB in the RosBREED demonstration breeding programs with a common focus on fruit quality traits; and (5) enhance sustainability of cultivar development by transferring MAB technologies to the public and private community of U.S. Rosaceae breeders through training current and future breeders as well as engaging the production, processing, and marketing sectors, allied scientists, and consumers. RosBREED funding is provided from the USDA-SCRI, award number 2009-51181-05808.

### **Germplasm sets and standardized phenotyping protocols for fruit quality traits in RosBREED**

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The prevalent Rosaceae crop breeding approach utilizes a common set of ancestors within breeding programs, resulting in relatedness among individuals and extensive linkage disequilibrium. Pedigree-Based Analysis (PBA) using FlexQTL™ software exploits these genetic considerations to identify and validate QTL using genotype and phenotype information. RosBREED involves 12 demonstration breeding programs in five rosaceous fruit crops (apple, peach, strawberry, and tart and sweet cherries). Key roles for breeders in utilizing PBA to establish and exploit marker-trait associations are 1) identifying founder germplasm sets for single nucleotide polymorphism (SNP) detection, and Crop Reference (CR) and Breeding Pedigree (BP) sets for genotyping and phenotyping, and 2) choosing important fruit quality traits and developing standardized phenotyping protocols to assess them. Breeders used PediMap

software to visualize relationships and ancestry in their germplasm. SNP Detection Panels were assembled by including important founders that provide maximum likelihood of polymorphism detection based on pedigree position and presumed diversity. CR and BP sets were assembled to include important contemporary parents and offspring in breeding programs, as well as available ancestors. CR sets contain pedigree-linked germplasm that represents the diversity in current and anticipated future breeding stock. CR sets will be genotyped genome-wide with SNP markers and phenotyped for fruit quality traits and other high-impact traits. Breeders in each crop developed standardized phenotyping protocols for each trait, allowing data pooling across programs and more powerful PBA outcomes. Phenotyping protocols and PBA results for CR sets will be archived and made publicly available for reference at [www.rosbreed.org](http://www.rosbreed.org) hosted on the Genome Database for Rosaceae. Breeders may add their own germplasm and phenotyping interests to the CR set data by collecting data and performing PBA on their proprietary BP sets combined with CR set data, to verify pedigrees and determine utility of marker-locus-trait associations for their own program.

### **Using socio-economic values to help set objective breeding targets**

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Breeders tend to subjectively decide their breeding targets based on a production orientation using interactions between their viewpoints, industry input, and market forces. Breeders, growers, and processors can benefit greatly by including in their breeding target-setting, cultivar adoption, and produce quality acceptance decisions the values and preferences of market chain participants, such as consumers' purchasing motives, attitudes, beliefs, concerns, and constraints, and willingness to pay. With use of such information, new cultivars would have targeted appeal to both large- and small-scale niche market segments, be more quickly accepted, and have enhanced commercial impact. To broaden the decision-making process, we will investigate market-based information on the impact of several traits on the entire supply chain. This information must acknowledge and involve various key stakeholders at early breeding decision-making stages. As a means of providing this information to breeders, RosBREED's socio-economics activities will estimate social values and economic weights of fruit traits of five rosaceous crops (apple, peach, strawberry, tart cherry, and sweet cherry) currently valued by the key market chain members including breeders, growers, market intermediaries, and consumers. We will gather information using multiple approaches including one-on-one interviews and telephone surveys. We will develop and compare relative economic weights of various fruit quality and production traits posed by different groups on the five targeted RosBREED crops. Relative economic weights for a trait will be calculated as a weighted average of marginal values that the three key audiences (consumer, market intermediary and producer/processor) place on a trait, resulting in objectively quantified values for breeding priority setting.

### **RosBREED's marker-assisted breeding pipeline**

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Translation of DNA information arising from genomics research into application in breeding is presently a bottleneck. RosBREED is a large-scale initiative seeking to bridge the chasm between genomics research and breeding programs, centered on breeders and ensuring they can capitalize on genomics discoveries and accelerating technological innovation.

RosBREED's translational approach is the establishment and implementation of a marker-assisted breeding (MAB) "pipeline" consisting of a series of connected stages. At one end, any available marker-locus-trait (M-L-T) associations are objectively prioritized for each breeding program using socio-economically derived relative economic weights. In the next stages, markers are adjusted to match available genetic screening services. Then, each marker is assessed for relevance to breeding germplasm using the Pedigree-Based Analysis approach, determining the distribution of functional alleles in potential parents. Information is used to inform crossing decisions, improving proportions of genetically superior seedlings. Cost-efficient and logistically feasible marker-assisted seedling selection schemes are identified and trialed on several thousand seedlings to cull those predicted to have poor performance potential. Finally, robust genetic tests are routinely integrated into breeding operations, while newly reported M-L-T associations enter the pipeline.

In 2010, in addition to the establishment of infrastructure components to powerfully enable each pipeline stage in future years, two major activities are taking place. The first is that twelve demonstration breeders will each fast-track the pipelining of several already reported M-L-T associations, up to the stage involving marker-assisted parent selection decisions. Second is the choice of reference germplasm sets across programs representing U.S. breeding stock, the beginning of its standardized phenotyping for high-impact traits, and its genotyping with genome-wide SNP markers targeting fruit quality candidate genes. The database of this comprehensive phenotypic and genotypic information on key germplasm will serve as the reference resource for future genetic discovery and validation and will exploit homology among genomes of three fruit-bearing genera of Rosaceae: *Malus* (apple), *Prunus* (peach and cherry), and *Fragaria* (strawberry). The archived database is expected to stock the shelf with hundreds of promising predictive M-L-T associations for entry into the MAB pipelines of many Rosaceae breeding programs. Successful demonstration of the RosBREED approach will lead to technology transfer to the wider community of U.S. Rosaceae breeders and international partners, so that, ultimately, new cultivars with superior fruit quality will be efficiently delivered by a powerful breeding network mobilizing modern technologies and exploiting the full extent of Rosaceae's genetic diversity.

### **Use of PediMap in RosBREED for visualizing genetic and phenotypic data across pedigrees in rosaceous crops**

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RosBREED is a multistate, multi-institution project dedicated to genetic improvement of U.S. rosaceous crops and will be using applications of genomics knowledge and tools to accelerate and increase the efficiency of breeding programs. This project focuses on fruit quality traits in apple, peach, sweet cherry, tart cherry, and strawberry to demonstrate marker-assisted breeding. DNA markers that are genetically linked to fruit quality traits can play a critical role in identifying desirable parents for crossing.

Breeders can efficiently make informed crossing decisions with DNA marker information when relevant data is displayed in a format that is easily visualized. PediMap is a software designed to graphically present genetic information in pedigrees and can be used to present information such as phenotypic data, observed marker alleles, identity by descent probabilities, and QTL functional allele probabilities, thus allowing breeders to visualize the distribution of desirable alleles for important breeding traits across their germplasm. The freely available PediMap software is currently being used by 12 RosBREED demonstration breeders. These breeders have collaborated to develop Crop Reference sets representing U.S.-wide breeding germplasm and Breeding Pedigree sets to further represent their own individual programs, and are already using PediMap to visualize pedigree relationships. Demonstration breeders have found PediMap to be a valuable tool even before the integration of DNA information. As an outcome of RosBREED outreach, we would like to extend the training and use of PediMap to the U.S. community of Rosaceae breeders building on experiences and successes of the demonstration breeders.