

Genetic improvement of strawberry fruit quality with the RosBREED approach

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Strawberry is one of five fruit crops included in the USDA-funded multi-institutional and trans-disciplinary project, “RosBREED: Enabling Marker-Assisted Breeding in Rosaceae”. Crop reference sets that include cultivars and seedling populations representing the breadth of diversity and encompassing founders used in breeding the domestic strawberry were developed and are being propagated to plant in Oregon, Michigan, and California. Phenotypic traits were identified that will be used to comprehensively characterize this Crop Reference Set including fruit weight, firmness, skin toughness, soluble solids, titratable acidity, pH, external and internal color, flavor, shape, ease of capping, drip loss after freezing and thawing, and total anthocyanins for fruit quality attributes, together with remontancy, crop load, disease resistance and plant architecture. Genome-wide genotypic information will also be developed for each member of the Crop Reference Set using single nucleotide polymorphisms. Phenotypic and genotypic data will be integrated in the software FlexQTLTM to identify and validate QTLs for important fruit quality traits via Pedigree-Based Analysis. Economically valuable genetic tests will then be incorporated into breeding operations via an eight-stage Marker-Assisted Breeding Pipeline. This approach will provide powerful infrastructure for routine application of marker-assisted breeding in strawberry.

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, dedicated to genetic improvement of rosaceous crops by targeted application of genomics and socio-economics knowledge and tools to increase the efficiency of breeding programs, engage stakeholders, and train the next generation of plant breeders. The Rosaceae family provides vital contributions to human health and well-being and collectively constitutes the economic backbone of many U.S. rural communities. Rosaceae genomics resources are developing rapidly but have not been translated to routine practical application. The RosBREED project (www.rosbreed.org) is funded in 2009-2013 by the Specialty Crops Research Initiative of the United States Department of Agriculture’s National Institute of Food and Agriculture. Our goal is to sustainably integrate modern genomics tools with traditional breeding approaches. This goal is rooted in our vision that the common ancestral origin of diverse rosaceous genera can be harnessed to leverage knowledge and resources across commodity boundaries. SNP-based scans targeting fruit quality candidate genes will exploit homology among genomes of three fruit-bearing genera of Rosaceae: *Malus* (apple), *Prunus* (peach and cherry), and *Fragaria* (strawberry). RosBREED will establish standardized phenotyping across programs and institutions and use pedigree-linked reference germplasm sets to facilitate data pooling and enable powerful, robust analyses. We will employ Pedigree-Based Analysis to integrate genotypic and phenotypic information for identification and validation of marker-locus-trait associations directly in breeding germplasm. We are creating a breeding

information management system comprising a series of database-interfacing, analytical, and visualization software modules that allow breeders to obtain and direct genomics and socio-economics information to increase breeding efficiency. In any program willing to adopt this approach, routine marker-assisted breeding (MAB) will be enabled with the implementation of an eight-stage MAB Pipeline that identifies optimal selection targets and efficient selection strategies.

Breeding fruit crops in the USA Using Socioeconomic and DNA Information

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A wide array of fruits and fruit products has become more commonly available to the U.S. population in the past decade, yet per capita consumption remains static and does not come close to meeting recommended dietary intake. U.S. producers of crops in Rosaceae family (almond, apple, cherry, peach, pear, raspberry, and strawberry) also face economic challenges as costs and marketplace competition increase. A new coordinated research and extension project with a significant socioeconomic scientific component has been funded by the U.S. Department of Agriculture to translate genomics research into more efficient breeding of Rosaceae fruit crops and have real impact in the marketplace. This four-year project, called RosBREED: Enabling marker-assisted breeding in Rosaceae, has a number of similarities to ISAFRUIT and will

enhance rapid development and deployment of new cultivars with improved characteristics to meet dynamic industry and market needs and consumer preferences. Beginning in late 2009, the project has an overall budget of 14 million (\$US) and involves scientists from a range of disciplines and includes eleven U.S. organizations and six international partners. Its focus on socioeconomic factors underlying industry values and consumer preferences is intended to drive a genomics to the marketplace approach that more directly informs its twelve core breeding programs and engages the entire supply chain, including producers, market intermediaries, and commodity organizations. The concurrent establishment of a technical infrastructure for DNA-informed breeding will integrate breeding and genomics resources, exploit the shared ancestry of Rosaceae crops, help train the next generation of plant breeders, enlist allied scientists, and thoroughly engage industry stakeholders. We expect RosBREED will help increase the likelihood of new cultivar adoption, enlarge market potential, and increase consumption of rosaceous fruits. This presentation focuses on the project's socioeconomic and extension aspects.

A coordinated approach to peach SNP discovery in RosBREED

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In the USDA-funded multi-institutional and trans-disciplinary project, “RosBREED”, crop-specific SNP genome scan platforms are being developed for peach, apple, strawberry, and cherry at a resolution of at least one polymorphic SNP marker every 5 cM in any random cross, for use in Pedigree-Based Analysis. RosBREED focuses on fruit quality traits. The majority of genes targeted for SNP development will be those shared among crops, and specific cases of synteny will be exploited to leverage ancestral relatedness within the Rosaceae family. In peach, we are re-sequencing genomic DNA from about 60 peach accessions coordinated between the U.S. and the Italian Consortium for Peach Genome Sequencing (DRUPOMICS project). These accessions were chosen for worldwide use in peach breeding and for diversity of genetic background, geographical origin, and phenotype. The peach genomic libraries are being sequenced with the Illumina Genome Analyzer IIX (GAIIx) at 3X coverage using paired-end reads (2x80bp) and indexed adaptors. The resulting peach SNP platform will be a valuable resource available to the worldwide peach research community.

Marker-assisted breeding enabled by RosBREED

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Significant barriers limit application of marker-assisted breeding (MAB) in horticultural crops. Genomics knowledge must be translated into practical MAB tools and integrated into crop improvement programs. Breeding programs must receive training and access to MAB tools to permanently expand capacity. Socio-economic factors affecting cost, benefit, technology adoption, supply chain values, and consumer preferences must be considered. “RosBREED: Enabling marker-assisted breeding in Rosaceae” is funded (US\$14M) from 2009-2013 by the U.S. Department of Agriculture to address these barriers in three fruit-bearing genera: *Malus* (apple), *Prunus* (peach and cherry), and *Fragaria* (strawberry). Twelve U.S. breeding programs will serve as initial technology adopters. RosBREED focuses on fruit quality traits directly linked to consumer demand and stakeholder profitability. Socio-economic surveys and interview tools will establish supply chain trait preferences, integrate results into breeding programs, and examine adoption and non-adoption of MAB. An eight-stage MAB Pipeline will exploit genomic homology across commodity boundaries. Pipeline stages begin with economic weighting of available marker-locus-trait associations; continue through development of breeder-friendly genetic markers, crop-wide validation, and utility assessment within breeding program germplasm; and will be applied to crossing and seedling selection decisions. Infrastructure to integrate DNA information into routine breeding operations includes one-on-one training and the community resources of a genome-scanned, comprehensively phenotyped (for fruit quality) reference database on pedigree-linked breeding germplasm. The Pedigree-Based Analysis approach will functionally characterize alleles at detected QTLs and describe parental breeding value. Custom software will organize databases and decision-support analytical tools,

incorporating trait economic values, cost-efficiency calculation of seedling selection schemes, cross planning, and breeder-friendly interfacing to genomics information. Our extension platform seeks greater stakeholder involvement in local breeding programs. Successful technology transfer to additional Rosaceae breeders is critical to accelerate and increase the efficiency of rosaceous cultivar release and successful adoption.