Marker-assisted breeding enabled by RosBREED

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Enabling marker-assisted breeding in Rosaceae

www.rosbreed.org

Overview

• Significant barriers limit application of marker-assisted breeding (MAB) in horticultural crops.
• Genomics knowledge is being translated into practical MAB tools and integrated into crop improvement programs.
• Breeding programs are receiving training and access to MAB tools to permanently expand capacity.
• Socio-economic factors affecting cost, benefit, technology adoption, supply chain values, and consumer preferences are being considered.
• RosBREED focuses on fruit quality traits directly linked to consumer demand and stakeholder profitability.

Twelve U.S. breeding programs - demonstration breeding programs, serve as initial technology adopters (Fig. 1). Other Rosaceae breeding programs are active participants (e.g. Crop Reference Set selection) and beneficiaries of RosBREED deliverables.

MAB Pipeline

• An eight-stage MAB Pipeline will exploit genomic homology across commodity boundaries (Fig. 2).
• 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.

Strategy for Constructing reference Germplasm Sets

• The Pedigree-Based Analysis approach will functionally characterize alleles at detected QTLs and describe parental breeding value.
• Pedigree-linked reference germplasm sets represent alleles across the genomes of Important Breeding Parents (Fig. 3).
• Each relative represents an Important Breeding Parent; goal was

>12.5 representation units (e.g. 25 F1s) for statistical power
– Offspring represent alleles of these Parents (Fig. 4)
– Other relatives can also represent Parent alleles through shared ancestors (because a proportion of alleles will be Identical By Descent)
– F1, offspring, full-sibs, and parents provide best genome coverage

Traits and Standardized Phenotyping protocols

• Identify critical fruit quality traits and other important traits
• Develop standardized phenotyping protocols to enable data pooling across locations/institutions
• Protocols available at: www.rosbreed.org/resources/fruit-evaluation

Crop Reference Sets (CRSets)

• ~480 individuals (cultivars, ancestors, founders, breeding lines, selections, and seedlings) that are fruiting in 2010-2012 (Fig. 3)
• Enable efficient validation and utility assessment of marker-locus-trait associations
• Genotyped genome-wide with SNP markers and phenotyped for fruit quality traits and other high-impact traits

Breeding Pedigree Sets (BP Sets)

• ~100-300 extra plants for each breeding program that, together with the CR Set for that crop, allow full representation of important parents in that program
• Information may remain proprietary with each breeding program; data-sharing improves power

Figure 1. RosBREED demonstration breeding programs and evaluation sites

Figure 2. The Marker-Assisted Breeding Pipeline

Figure 3. Sweet Cherry Crop Reference Set, visualized by Pedimap software (www.plantbreeding.wur.nl/UK/software_pedimap.html)

Figure 4. Representation by offspring in Crop Reference Set

Figure 5. Sweet Cherry Crop Reference Set, visualized by Pedimap software (www.plantbreeding.wur.nl/UK/software_pedimap.html)