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

Cameron Peace(1)

Nahla Bassil(2)

Michael Coe(3)

Gennaro Fazio(4)

Jim Luby(5)

Dorrie Main(1)

Jim McFerson(6)

Cholani Weebadde(7)

Eric van de Weg(8)

Chengyan Yue(5)

Amy Iezzoni(7)

(1)Washington State University, Pullman, WA, USA

(2)USDA-ARS, National Clonal Germplasm Repository, Corvallis, OR, USA

(3)Cedar Lake Research Group, Portland, OR, USA

(4)USDA-ARS Cornell University, Geneva, NY, USA

(5)University of Minnesota, St. Paul, MN, USA

(6)Washington Tree Fruit Research Commission, Wenatchee, WA, USA

(7)Michigan State University, East Lansing, MI, USA

(8)Plant Research International, Wageningen, Netherlands

RosBREED is a large-scale community initiative dedicated to genetic improvement of rosaceous crops, focusing on fruit quality. Our goal is to sustainably integrate modern genomics tools with traditional breeding approaches by enabling marker-assisted breeding (MAB) in peach, apple, strawberry, cherry, and related rosaceous crops. Socio-economic surveys of breeders, growers, and marketing intermediaries have uncovered knowledge on trait values to help direct research and breeding efforts toward highest priority traits. Genome-scanning SNP arrays developed for peach (9K), apple (8K), and cherry (6K) are being used to characterize genomes in large germplasm sets representing U.S. breeding stock. The same germplasm is undergoing three years of comprehensive, standardized fruit quality evaluation across 14 breeding programs. Participating breeders are using Pedigree-Based Analysis (PBA) software of Pedimap and FlexQTL™. We have already achieved MAB successes, with routine marker-assisted parent and seedling selection underway in apple and sweet cherry. This MAB targets QTLs to enrich future generations with superior alleles. 2012 is set to be a landmark year for U.S. fruit MAB. First, several previously reported QTLs have progressed through our systematic Marker-Assisted Breeding Pipeline for translation into ready-to-use information for supporting breeding decisions. Second, translation of PBA results from genome scans integrated with standardized phenotypic data is expected to fill a treasure chest of jewels in the Rosaceae genome. RosBREED’s powerful advances are due to a very collaborative international Rosaceae genomics, genetics, and breeding community that vigorously shares expertise, resources, knowledge, and ideas.