seemed to be decreased. While the ACS3, EIN2, EIN2A as well as CTR1-1, CTR1-2, and CTR1-4 genes were unchanged. 1-MCP treatment showed the opposite effect of ethylene, while reduced ETR1, CTRs and EIN2A. These results provide additional evidence that regulation of these genes expression is under the influence of ethylene. Analysis and identification of significant gene expression revealed that ethylene biosynthesis and perception during apple fruit ripening and senescence is associated with fruit ripening and responsive to treatment of ethylene or its action inhibitor. This study demonstrated the complexity and dynamic changes of transcriptional profiles of ethylene perception and biosynthesis. The understanding of significant changes of these genes and their functions may help to explore mechanisms controlling apple fruit ripening and their response to ethylene during ripening and senescence.

Sunday, September 25, 2011
2:00–4:00 pm **Kings 1**

Plant Biotechnology and Genomics

Moderator: Wagner Vendrame
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2:00–2:15 pm

The Genomic Sequencing of Diploid Blueberry (*Vaccinium corymbosum*)

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The ongoing blueberry (*Vaccinium* ssp. section *Cyanococcus*) genomic sequencing project has continued to generate high quality data, allowing us to refine our assembly and analysis techniques. DNA from a diploid *V. corymbosum* ('W8520') with a genome size of approximately 500 mb was used to construct libraries for both 454 and Illumina GAIIx. Long read structural scaffolds using paired end 454 libraries of different insert sizes (3 kb, 8 kb and 20 kb) are generated and gaps are filled with a high density of Illumina reads (36, 76, and 100 bp). To date, we have generated 8, 106, 330 sequences (or 2.7 billion bps) of raw data on the Roche 454 and 44.4 billion bps on the GA2x. This vast influx of data creates unique challenges for successfully manipulating, analyzing, and simulating assemblies. The Release of the genomic sequence is planned for late 2011 and the Genome Database for *Vaccinium* (GDV) (http://www.vaccinium.org) has been established to house the blueberry sequence and to incorporate genetic and breeding resources for blueberry, cranberry and other *Vaccinium* sp. Work is currently under way to integrate the genomic sequence to existing blueberry genetic linkage maps utilizing SSR markers identified from the largest 10% of the sequencing scaffolds. To date over 90% of existing ESTs have been identified and initial *ab inito* annotations have identified numerous homologous gene sequences to pathways of interest. The flavonoid pathway is provided as an example.

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2:15–2:30 pm

RosBREED Deploys Genome-wide Scans in Peach, Apple, and Cherry

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SNP-based genome scans are in development for peach, apple and cherry as public genomics resources for the international Rosaceae research community. The USDA-funded multi-institutional and trans-disciplinary project "RosBREED" is creating crop-specific SNP genome scan platforms at a targeted resolution of at least one polymorphic SNP marker every 5 cM in any random cross. Within RosBREED, these genome scans will be used with Pedigree-Based Analysis to identify and validate many marker-locus-trait associations for application in breeding. SNP detection, validation, and final content decisions were completed in 2010. For SNP detection, 27 founders of apple, cherry, and peach re-sequenced mostly with Illumina GA-IIx were chosen based on representation of worldwide breeding germplasm. Re-sequencing of apple genomic DNA was coordinated among the U.S., the Agricultural Research Council of South Africa, and New Zealand's Plant & Food Research. In peach, genomic DNA was re-sequenced from 58 accessions coordinated between the U.S., Europe's FruitBreedomics project, and the International Peach Genome Initiative. Sequences were also generated from 16 sweet and eight tart cherry accessions. A SOAP/SOAPSNP-based pipeline was developed to identify SNPs after alignment to the 'Golden Delicious' genome sequence for apple and the double haploid 'Lovell' peach genome sequence for peach and cherry. The GoldenGate assay was used to validate subsets of these SNPs and to investigate haplotypic diversity at the planned resolution of the final SNP arrays (one SNP per 70 Kb). These "fine-mapped regions" of the genome targeted particular loci responsible for important breeding traits. In apple, 20 of the 144 apple SNPs were located within a 1.4 Mb region at the *Malic acid* (*Ma*) locus on *Malus* linkage group (LG) 16. For cherry, a 0.86 Mb region spanning a fruit size locus on *Prunus* LG 2 was targeted with 24 SNPs, while for peach, 0.77 Mb around the *Freestone-Melting flesh* (*F-M*) locus was spanned with 14 SNPs. Considerable haplotypic diversity was detected in these regions. SNP filtering parameters were revised based on SNP conversion in the GoldenGate assay and resulted in ordering a 9K Infinium array for apple, a 9K Infinium array for peach, and a 6K Infinium array for cherry. Genome-wide scans using this high-throughput Infinium SNP technology are underway for 472 individuals representing important breeding parents for each of these crops. These genomics resources will enable new marker-locus-trait association discovery as well as validation of associations in breeding germplasm for major Rosaceae crops and across this economically important plant family.

2:30–2:45 pm

Novel Strawberry (*Fragaria* spp.) Gene Sequences That Affect Important Traits

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Genomic information has increased exponentially from valued crop plants, revealing orthologs of many genes with demonstrated functions in model systems. However, many genes defy convenient classification, as they lack conspicuous sequence homology or functional motifs that may imply function. One critical challenge for science is to connect the extensive suite of unknown, hypothetical or predicted genes to their biological functions. With a sequenced strawberry (*Fragaria vesca*) genome