glycoprotein levels such as AGPs and extensins resulting in pleiotropic effect in growth and development programs.

Keywords: Tomato, P4Hs, AGPs, fruit growth, abscission, RNAi

OS 3-6:

Characterization of the pollen-part modifier gene involved in self-incompatibility reaction in sweet cherry

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Self-incompatibility (SI) prevents self-fertilization and promotes outcrossing to generate genetic diversity within a plant species. However, SI can be an obstacle to production and breeding of cultivated plants. Amongst various SI systems in higher plants, three plant families, the Solanaceae, Plantaginaceae and Rosaceae, share theS-RNase-based gametophytic SI system. The Rosaceae includes Malus, Pyrus and Prunus genera, which contain commercially important fruit tree species. Although they commonly use S-RNase and F-box protein for self and non-self recognition, the underlying mechanism of SI recognition in Prunus is different from that of other species. Many self-compatible (SC) mutants were found and have been utilized extensively for commercial production. Analyses of these SC mutants have given us important clues to understand SI recognition mechanism. This study focused on a SC sweet cherry (Prunus avium) cv. Cristobalina, which is supposed to have a mutated pollen-part modifier gene located outside of the S locus. Several SI cultivars and ‘Cristobalina’ F1 populations segregating for SC and SI individuals were subjected to Illumina genome sequencing. Obtained reads were subdivided into 35-bp subsequences called k-mers. K-mers thus obtained were cataloged into SC and SI pools, and SC-specific k-mers were extracted. Then, the original reads containing the SC-specific k-mers were assembled into candidate contigs containing SC locus of ‘Cristobalina’. Analyzing the obtained SC-specific contig sequences, we found a transposon-like insertion in the promoter region of a gene that showed downregulated transcription in SC individuals. Although this gene is orthologous to ParMDO, which is a pollen-part modifier candidate in apricot (P. armeniaca), the mode of mutation in ‘Cristobalina’ appears to be different from that of SC apricot.

Functional characterization of the modifier gene will expand our understanding of the Prunus-specific SI recognition system.

Keywords: S-RNase, Modifier gene, Prunus, k-mer analysis

OS 3-7:

Abscisic acid-mediated transcriptional regulation of dormancy- associated MADS-box genes during peach bud dormancy

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Crop damages due to spring frosts may be devastating to peach producers in both cold and warm climates. Most frost events are usually preceded by unexpected warm weather in early spring that induces bud break in most deciduous trees. The co-occurrence of frost with the transition period from dormancy to growth has disastrous consequences on the emerging flowers. One of the mechanisms that has been suggested to avoid frost injury is to delay bloom date until the frost risk period passes. Flower phenology in peach and other deciduous trees is largely governed by bud dormancy. Dormancy- associated MADS-box genes (DAM), particularly DAM5 and DAM6, are strong candidate genes for the control of bud dormancy and bloom date in peach and other Prunus species. Transcript profiles of DAM genes during dormancy cycle show distinct patterns in early- versus late-bloom peach varieties. However, the transcriptional regulation of these genes by plant signaling molecules, e.g. plant hormones, have yet to be fully elucidated. Abscisic acid (ABA) is one of plant hormones that is known to control dormancy initiation, maintenance, and release in deciduous woody species. In the present research, we applied ABA (ProTone, from Valent BioSciences at 18 g/gal) and a surfactant (Regulaid, from KALO at 1.9 ml/gal) to an early-bloom peach cultivar (‘Century’ on Lovell rootstock) grown in Winchester, Virginia, the USA. Trees were sprayed twice a month from August to February (three trees per month; three branches per tree, and at least 50 buds on each branch). Each month, two sets of samples were collected from treated and untreated trees: One set for gene expression analyses and hormone profiling; and the other set to calculate chilling requirements and the percentage of bud break. Our results indicate that the timing of ABA application has differential effects on the induction kinetics of DAM genes and the bloom date in peach.

Keywords: DAM genes, peach, bloom date, Abscisic acid

OS 3-8:

Mechanism of male organ differentiation mechanism in the sex determination system of kiwifruit

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