

## Session XII • FLOWERS, SEEDS AND FRUIT

Jim Giovannoni and Kimberly Rodriguez, Chairs

2:30 — 4:00 pm, Conference Center Ballroom

2:30 pm

### THE REGULATORY NETWORK CONTROLLING FRUIT RIPENING: A COMPLEX INTERACTION BETWEEN MULTI-HORMONAL SIGNALING AND DEVELOPMENTAL FACTORS

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While ethylene is the major phytohormone regulating climacteric fruit ripening, it is becoming clear that the ripening process is under multi-hormonal control in combination with the intervention of known developmental factors like RIN and NOR. However, how this complex regulatory mechanism operates

still remains quite elusive. Auxin has long been assigned a role in fleshy fruit ripening because treatment with this hormone results in delayed ripening. We recently showed that among all members of the *Auxin Response Factor (ARF)* gene family in the tomato, *SIARF2* displays the most prominent ripening-associated pattern of expression. Interestingly, *SIARF2* down-regulation results in strong ripening defects and conversely its over-expression accelerates ripening. ARF2 emerges therefore as a new component of the regulatory network controlling tomato ripening working along with known key regulators of fruit ripening, such as *RIN*, *CNR* and *NOR*. On the other hand, the regulatory mechanisms underlying ethylene action during climacteric fruit ripening are poorly understood, and in particular, the role of Ethylene Response Factors (ERFs) in mediating the ripening-associated ethylene responses still awaits clear demonstration. A small subset of *ERF* genes displaying consistent ripening-associated expression pattern were identified and showed to be linked to the mechanism underlying ethylene- and RIN/NOR-dependent ripening. In particular, sub-class E ERFs are shown to be the most active during ripening and considering their function as oxygen sensors, they might represent the missing link between the climacteric rise in respiration and the autocatalytic ethylene production. The data provide a new insight into the mechanisms underlying the control of fleshy fruit ripening, and open new avenues towards manipulating the ripening process through yet undescribed means.

2:55 pm

### ACCELERATION OF RIPENING-RELATED HOST CELL WALL DISASSEMBLY DURING *BOTRYTIS CINEREA* INFECTIONS OF UNRIPE TOMATO FRUIT

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The ripening of tomato fruit is an example of a developmental transition that coincides with increased susceptibility to necrotrophic pathogens, such as *Botrytis cinerea*. Ripening processes that promote susceptibility include softening-associated disassembly of the fruit host cell wall polysaccharide networks, modulation of the fruit's synthesis and perception of plant hormones, accumulation of organic acids and losses of preformed or induced defense responses.

As an opportunistic pathogen, *B. cinerea* modifies its infection strategy to take into account the ripening stage of the host. The diverse and versatile infection mechanisms that *B. cinerea* deploys on fruit help to define processes that the pathogen may use to hasten fruit susceptibility but also

demonstrate that *B. cinerea* takes advantage of opportune ripening events that render its host vulnerable to aggressive infections.

*B. cinerea* utilizes a large repertoire of enzymes that degrade multiple components of the cell walls of unripe tomato fruit. However, fruit susceptibility to *B. cinerea* not only depends on the array of enzymes secreted by the pathogen during infection, but also on modifications that alter the fruit cell wall as part of ripening. We have determined that *B. cinerea* induces the expression of tomato genes coding for cell wall degrading proteins that enhance the deconstruction and softening of the fruit tissues. Tomato and *B. cinerea* genes coding for pectin degrading enzymes are expressed more in infected unripe fruit than in infected ripe fruit. Glycome profiling of cell walls from *B. cinerea*-infected and healthy tomato fruit identified changes in the composition and structure of the wall caused by infections that are associated with fungal infections and the normal ripening process. Specific classes of cell wall polysaccharides that are depolymerized by *B. cinerea* during tomato fruit infections include the backbones and side-chains of homogalacturonan pectins. We detected significant correlations between the modifications in the fruit cell walls that occurred during *B. cinerea* infections of unripe fruit and those that occurred as a result of uninfected fruit ripening. Fruit susceptibility assays using *B. cinerea* knockout mutants of pectin degrading enzymes validated the role of particular enzymes during interactions between tomato fruit and *B. cinerea*.

**3:10 pm**

### **GENETICS AND MACROEVOLUTION OF FLOWER COLOR IN SOLANACEAE**

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Genetic and developmental studies in model species of Solanaceae have provided insights into the mechanisms underlying many ecologically important traits, such as fruit size, leaf shape and flower color. In the case of flower color, early work in the model system petunia elucidated the biochemistry and regulation of anthocyanin pigmentation, enabling parallel work in many other taxa. Building on this now rich body of literature, I will discuss how the genetic basis for different classes of flower color transitions relates to different macroevolutionary patterns. A priori, we might expect that colors that can arise from simple loss-of-function mutations would be common across the phylogeny while those that with a more complex genetic basis would be rare. Indeed, white flowers, which typically have a simple genetic basis, are extremely common in Solanaceae. Because these mutations are predominantly regulatory, lineages that have transitioned to white flowers are often able to regain floral pigmentation in the course of evolution. We observed a marked difference in phylogenetic distribution of red flower color, which appears to evolve through a combination of regulatory and structural mutations. Species with red flowers are exceptionally rare in Solanaceae (34 species or ca. 1% of the family), and we find no clear evidence of evolutionary reversals following transitions to red. These patterns suggest that understanding the genetic mechanisms responsible for different classes of transitions may help us to explain why some colors are common and others remain rare.

**3:22 pm**

### **REGULATORY VARIATION IN TOMATO: HARNESSING GENETIC DIVERSITY TO UNDERSTAND THE REGULATION OF FRUIT DEVELOPMENT**

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The wild relatives of tomato represent a rich reserve of phenotypic variation in fruit development traits