

Editorial

# Molecular Regulation Mechanisms of Ripening, Senescence and Stress Resistance in Fruits and Vegetables

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Fruits and vegetables are two key daily sources of food for human beings. The development and ripening of both fruits and vegetables involve various biological changes, including changes in texture, color, volatile organic compounds, and other bioactive components [1,2]. The significant increase in the production of agricultural crops can be attributed to the development of scientific management strategies in the field, the breeding of crop varieties, and pre- and postharvest technologies. Multiple manipulating processes are involved in a series of regulations occurring at the physiological, biochemical, and molecular levels [3,4]. The development of both fruits and vegetables is widely reported to involve a network of hormones, transcription factors, epigenetic modifications, and modules, with different elements being regulated simultaneously. These regulations can help promote or stabilize the accumulation of nutrients and help plants adapt to stresses [5,6]. In addition, during their ripening, mature fruits and vegetables usually undergo postharvest senescence and incur stress damages such as browning, deteriorations, chilling injuries, pathogen invasions, etc. [7–9]. Numerous postharvest approaches, including physical and chemical treatments, have been developed to preserve the quality and extend the shelf life of fruits and vegetables. Many studies of the changes in the quality characteristics and stress response of both fruits and vegetables have been conducted to elucidate the regulation mechanisms at work at the physiological, biochemical, and molecular levels [4,10,11].

Although different advanced investigation methods and techniques have been combined to explore these quality changes and stress responses, the regulation mechanisms at work may differ depending on the variety of species, cultivars, and the organs present in various fruits and vegetables [12,13]. Additionally, the exploration of efficient approaches to improving their nutrient content during their development and maintaining their high quality during postharvest storage are still big challenges for fresh fruits and vegetables [10,14]. As a complication of fruit and vegetables' regulation networks, their transcriptomics, multi-omics, and physiological and molecular regulation mechanisms at the whole-genome level are still not fully understood. This Special Issue contains six papers featuring integrated knowledge on the physiological and molecular regulation mechanisms of fruits and vegetables, from their growth in the field to their postharvest shelf life. Brief introductions to each work are given below, and I hope that readers will be able grasp the key information presented easily.

The growth, development, and stress responses of fruit and vegetables are regulated by multiple genes. As a fresh, tender vegetable and edible oil crop, the growing of *Brassica napus* L. is largely affected by environmental factors. In Han et al.'s article, 21 *BnFAR1/FHY3* genes were identified and characterized, revealing their potential involvement in the response to shade and low-temperature stresses during the growth of *B. napus*. The authors predicted that there were cis-elements in the promoter regions of these *BnFAR1/FHY3* candidate genes which might be involved in the response to light and hormone signals. The shading treatment down-regulated the relative expression levels of *BnFAR1-10*, *BnFAR1-11*,



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and *BnFAR1-21*, while these genes were stimulated to increase their expression by low temperatures. *BnFAR1-4* exhibited as decrease trend with the shading stress, but maintained a steady expression level under low temperatures. In addition, the expression of these candidate genes showed spatial differences, with the lowest level in pollen and the highest in silique during the development of *B. napus*.

Li et al. analyzed the *MADS-box* candidate genes, which are involved in the flowering and fruit development of loquat, at the whole-genome level. Loquat is a fruit native to China which belongs to the Rosaceae family and has a unique flowering time. In total, 125 members were identified as *EjMADS-box* genes, with 49 type I genes, including  $M\alpha$  (25 genes),  $M\beta$  (10 genes), and  $M\gamma$  (14 genes), and 76 type II genes, including 70 MIKCC genes and 6 MIKC\* genes, in the loquat genome. Among these candidate genes, *EjMADS107* and *EjMADS109* are probably related to the differentiation of the flower bud, while *EjMADS24*, *EjMADS46*, *EjMADS49*, *EjMADS67*, *EjMADS55*, *EjMADS61*, *EjMADS77*, and *EjMADS86* might be involved in fruit development. In addition, the potential ABCDE model genes of the flowers were identified, which exhibited a conserved expression in loquat. It was concluded that these candidate genes may provide a foundation for investigations into the molecular regulations of *MADS-box* members in both the flower and fruit development of loquat.

Qiu et al. evaluated the regulations present in 'SJH' fruits with on-tree black packages and a bio-organic fermentation fertilizer treatment compared to 'SBY' fruits with a chemical fertilizer treatment and without packages, using olecranon honey peaches. The 'SJH' fruits exhibited a larger fruit weight, length, diameter, hardness, and TSS than the control 'SBY' fruits at their mature stage. RNA sequencing and qRT-PCR revealed that the larger fruit size and higher hardness in 'SJH' might be related to the up-regulation of xyloglucan endotransglucosylase/hydrolase protein B (*XTHB*) and cellulose synthase-like protein D (*CS-LPD*) genes as part of their cell wall biogenesis metabolism during their development. Consistent with the increase in sugar content in 'SJH' fruits during development, the sugar-metabolism-related genes sucrose-phosphate synthase (*SPS*), sucrose synthase (*SUS*), and raffinose synthase (*RAFS*) were expressed at higher levels than in the 'SBY' fruits. These reported genes could be potentially selected as biomarkers to guide the optimization of planting strategies for the improvement of fruit quality during fruit development.

Pathogens severely affect the yield and quality of fruit and vegetables. Jiang et al. tried to quantify the nucleotide-binding site leucine-rich repeat (*NBS-LRR*) genes involved in the response to bacteria in eggplant using a whole-genome analysis. As a result, 269 members, categorized into three subgroups containing 231 CNLs (CC-NBS-LRR), 36 TNLs (TIR-NBS-LRR), and 2 RNLs (RPW8-NBS-LRR), were found to be *SmNBSs* in the eggplant genome. It is notable that the member *EGP05874.1* exhibits an obvious up-regulation in response to the infection of eggplant with *R. solanacearum*. This study provides us with the insight to identify the potential key genes involved in pathogen resistance across the whole genome, taking eggplant as an example.

The article contributed by Yin et al. analyzed non-coding RNA members (ncRNAs) and tried to find the potential members involved in the response to downy blight (*Peronophythora litchi*). Through a whole-transcriptome analysis, there were found to be 2627 lncRNAs, 4682 circRNAs, and 525 miRNAs in litchi. After an inoculation of *P. litchi*, three mRNAs (TCHI008759.m1, LITCHI018040.m1, and LITCHI027850), two lncRNAs (MSTRG.15825.1 and MSTRG.29637.2), and one circRNA (Chr15:6362006|6368000) were differentially expressed in fruit or leaf tissues. This is the first time ncRNAs have been taken into consideration as regulators involved in the response to the pathogen causing downy blight infections in litchi.

Postharvest treatments are usually applied to prolong the shelf life of both fruit and vegetables. In the study conducted by Liu et al., broccoli flowers were treated with 2 ppm selenite solution (Se), which could inhibit their rapid browning, the accumulation of hydrogen peroxide, and the increase in MDA seen after their harvest. Concomitantly, the Se treatment was demonstrated to obviously modify the enzyme activity of CAT, SOD,

POD, and APX, as well as that of their corresponding genes, *BoCAT*, *BoSOD*, *BoCAT*, and *BoCAT*, during storage. The expression level of the respiratory burst oxidase homolog (RBOH) members *BoRBOHf* and *BoRBOHd* was retarded, inhibiting the production of reactive oxygen species (ROS) after the treatment. In addition, the expression of WRKY transcription factors such as *BoWRKY33*, *BoWRKY6*, *BoWRKY25-1/2*, and *BoWRKY15*, which are involved in ROS metabolism, were down-regulated by the Se in broccoli. These results indicate the potential of a Se treatment to extend the storage life of broccoli by inhibiting ROS metabolism through the modification of the corresponding enzymes, genes, transcription factors of RBOH and WRKY.

These studies provide new insights into the basic molecular responses to biotic and abiotic external stresses in both fruit and vegetables, combining transcriptomic and whole-genome analyses to do so. However, the physiological, biochemical, and molecular regulations involved in the development and postharvest changes in fruits and vegetables are intricate and require elucidation. Therefore, many more studies on molecular regulation mechanisms that integrate different methods and techniques should be conducted.

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#### List of Contributions

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