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Editorial

Genetics and Breeding of Fruit Trees

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"Genetics and Breeding of Fruit Trees", published in *Horticulturae*, is a collection of 11 manuscripts focusing on commercially important fruit crops, such as apple, peach, pear, kiwi, persimmon, blueberry, and red bayberry.

Fruit trees have great economic value and, as long-living crops, pose a significant challenge for efforts aiming to produce considerable changes in many of their traits (for example, the color, shape, aroma, taste, tree structure, and environmental adaptation), particularly in comparison to their wild ancestors, over prolonged periods of rigorous cultivation and breeding practices. Fruit tree breeding research has mostly focused on the discovery of new economically valuable varieties to fulfill different consumer and industrial demands, improving the fruit tree's tolerance to environmental challenges, increasing its postharvest life, and developing cost-effective cultural approaches. The breeding of woody fruit trees is restricted by a variety of drawbacks, including long breeding cycles from the seed to fruit-bearing stage, long developmental stages that increase the costs of growing individuals to maturity in the field, and, frequently, severe heterozygosity impeding theoretical breeding methods. The expansion of biotechnology and the increasing prevalence of genomics have created new prospects to counter these limitations in the breeding of major fruit species, including the use of rapid sequencing techniques, the selection of molecular markers, whole-genome sequencing, genome-wide studies, transcriptomics, metabolomics, proteomics, etc. Because of their biological characteristics and, for some species, rigidity to plant evolution and/or rejuvenation, woody species frequently present a challenge for detailed functional analyses. These challenges severely restrict the application of conventional genetic and biotechnological techniques to functional genomic studies or plant breeding. In the past decade, the sequencing of many genomes, combined with rapid improvements in bioinformatics, has offered critical tools for in-depth molecular studies on agricultural crops, in addition to the traditional model species. The provision of sequencing data is simply a beginning, since bioinformatic techniques are insufficient for the establishment of gene roles. For this information to be useful, it is essential that we understand how thousands of genes interact with one another to establish a plant's architecture and how the metabolic pathways in which they take part affect plant growth and environmental adaptation.

The fruit sugar content is regulated by photosynthesis, but it is also influenced by the transport and accumulation of assimilates, with sugar transporter genes playing a crucial role in this process. The aim of Xiaoli Wang's [1] work was to provide insights into dwarfing rootstocks for pears (*Pyrus* spp.). 'Yunnan' quince (*Cydonia oblonga* Mill.) positively controlled the fruit sugar contents by controlling the flow of PbSWEET6-related assimilates in the scion. Breeders may use this knowledge to select pear rootstocks with the highest possible fruit sugar contents.

Sugar is a crucial component affecting the fruit's flavor quality. Fruit metabolism and sugar storage are major variables influencing fruit quality. To a considerable extent, the types and quantities of sugars impact the quality of the fruit. The aim of Junjie Tao's [2] work was to provide insights into the dynamic changes in the fruit quality, soluble sugar

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contents, sucrose-metabolism-related enzyme activities, and sucrose-metabolism-related gene expressions during the growth and development of *Actinidia eriantha* 'Ganlv 1'.

During the ripening period, peaches experience textural modifications that result in tissue firmness. The importance of the role of auxin in peach post-ripening is widely accepted. The aim of Jiahui Wang's [3] work was to provide insights into the role of small auxin-up RNA (SAUR) genes in fruit post-ripening and softening. This work reported 72 SAUR family members in the peach genome. The functions of *PpSAUR43* in peaches were then established using transient overexpression. *PpSAUR43* acts as a repressor in the process of the post-ripening of peaches by inhibiting the function of the PpCMB1 protein. This study's findings will aid in the development of technologies aiming to precisely manage peach post-ripening and improve the fruit's shelf life.

The prompt and simple maturation of apples is of major interest for the determination of the harvest time and post-harvest storage conditions. The aim of Mengsheng Zhang's [4] work was to establish that quality changes result in major spectral changes during the ripening process of apples, and these changes can be monitored using low-resolution multispectral sensors. As a tool for the rapid and simple detection of the apple's maturity, cost-effective multispectral sensors could be used to identify the best harvest time and post-harvest processing approach.

The evolution of sex differentiation is a fascinating subject, because it is crucial for outbreeding strategies and the mitigation of inbreeding depression and is a major source of genetic diversity. The aim of Huimin Jia's [5] study was to identify the molecular mechanism underlying sex development and differentiation in the red bayberry (*Morella rubra*) through next-generation transcriptome sequencing and comparative analyses in order to identify differentially expressed genes in the male and female flower buds. Furthermore, ethylene is the primary hormone that interacts with other hormones and transcription factors to control sex differentiation.

Persimmon (*Diospyros kaki*) anthracnose is a fatal disease that is primarily caused by the *Colletotrichum horii* pathogen and results in fruit rotting, shoot wilting, and, sometimes, whole plant death in persimmons. The aim of Changfei Guan's [6] study was to identify a new source of resistance to anthracnose among persimmon germplasms. In total, 142 varieties were used to study anthracnose disease resistance. Eight of these highly resistant or resistant accessions exhibited the required agronomic traits. The expansion of genetic diversity and the creation of novel resistant varieties could benefit from the application of these resistance sources in the breeding of persimmons.

Endodormancy is a phase during which perennial plants prepare for the next seasonal cycle, as well as an adaptation that allows the plants to survive harsh winters. The aim of Yongqiang Li's [7] study was to comprehend the underlying molecular mechanisms of bud dormancy release in blueberries (*Vaccinium* spp.). The transcriptomes of the flower buds were examined at seven dormancy stages. RNA transport, circadian rhythm, plant hormone signal transduction, etc., are all pathways possibly related to the dormancy release process.

Kiwifruit black spot disease has increased in prevalence in many 'CuiXiang' kiwifruit planting regions. Yaming Yang's [8] study focused on the pathogenic micro-organisms of black spots using high-throughput internal transcribed spacer (ITS) sequencing to analyze the black spot disease microbial community. Seven pathogens were isolated from the infected kiwifruit. The authors predicted that the candidate pathogenic fungi, such as *Cladosporium cladosporioides*, *Diaporthe phaseolorum*, *Alternaria alternata*, and *Trichothecium roseum*, may cause black spots. The study presented a preliminary assessment of kiwifruit black spots that can be used as a foundation for future research.

Auxin response factors (ARFs) are a family of transcription factors that control the expression of auxin phase-responsive genes. Yu Zong's [9] study focused on the genome-wide identification of *ARF* genes in the tetraploid blueberry (*Vaccinium corymbosum* cv. 'Draper'). In total, 70 blueberry *ARF* genes were identified in the genome, which could be further divided into six subfamilies. *ARF* genes are crucial for the ripening of blueberry fruit, and *VcARF3*, *VcARF4*, *VcARF14*, and *VcARF52* are also important. Future studies should illuminate their function in defining the differences in firmness between the soft and firm flesh cultivars.

In the sand pear (*Pyrus pyrifolia* Nakai), ethylene production has a negative correlation with the storage life, primarily at the time of fruit harvest. The rate-limiting enzyme in the ethylene biosynthesis process, 1-aminocyclopropane-1-carboxylic acid synthase (ACS), is considered to be crucial for the fruit storage life. Jing-Guo Zhang's [10] study identified 13 *ACS* genes in the genome of the sand pear. The sand pear genome sequencing data revealed a total of 13 *ACS* genes, 9 of which were novel members. Seven of these genes seemed to be involved in the process of fruit ripening, whereas four were found to be engaged in system 1 ethylene biosynthesis, suggesting that they may play a variety of roles in ethylene biosynthesis systems.

The formation of adventitious roots (ARs) is necessary for the asexual reproduction of commercially valuable horticultural crops, such as apples. Vegetative propagation is widely used in breeding programs due to its short life cycle, high efficiency, and true-to-typeness. The inability of stem segments to generate AR limits fragment survival. Therefore, understanding the AR regulation mechanisms is critical for the long-term and appropriate use of biological resources. The aim of Muhammad Mobeen Tahir's [11] review was to present the current state of knowledge of AR formation from the physiological and molecular perspectives and highlight recent advances in research aiming to discover the underlying mechanisms involved in adventitious rooting. Although there has been progress in recent years, several questions regarding excision-induced AR creation remain unanswered. These concern the specific activities and interactions of a variety of hormonal, molecular, and metabolic components, as well as the entire structure of the stem cutting in a challenging environment.

There is no doubt that this Special Issue will provide significant knowledge to its readers and will be useful for further studies aiming to improve fruit crops.

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