

Advances in Fruit Tree Physiology and Molecular Biology

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1. Introduction

As an important branch of agricultural science, fruit tree physiology and molecular biology have in recent years been driven by the intensification of global climate change and the upgrading of consumer demands towards high-quality and diversified products. The research focus has gradually shifted to four core issues: adaptation to extreme environments, efficient resource utilization, precise quality improvement, and variety innovation. By leveraging multi-omics technologies (genomics, transcriptomics, metabolomics, etc.) and gene editing methods (CRISPR/Cas9, single-base editing, etc.), breakthroughs have been made in areas such as stress response mechanisms, nutrient regulatory networks, quality formation pathways, and molecular breeding applications, providing key theoretical support and technical paths for improving the quality and efficiency of the fruit tree industry and promoting stress-resistant breeding.

In the research on adaptation to extreme environments, Asharf et al. [1] systematically expounded how fruit trees precisely regulate the plasticity adaptation of lateral organs (such as adventitious roots, aerated tissues, and stem elongation) through hormone interaction networks during hypoxia and reoxygenation processes, in response to abiotic stresses like high temperature, waterlogging, and saline–alkali conditions. This provided a new theoretical framework and strategic direction for the waterlogging resistance breeding and cultivation management of fruit trees. By integrating single-cell omics to locate key response cell types, core regulatory factors such as ERF-VIIs and PIN proteins were identified, providing precise targets for the breeding of stress-resistant varieties.

The field of efficient resource utilization focuses on nutrients such as nitrogen, phosphorus, boron, and manganese. Wang et al. [2] identified a transcription factor *MhNAC1* that was highly correlated with the nitrogen absorption efficiency of apples. Interfering with the expression of *MhNAC1* would promote nitrogen absorption and citric acid secretion in the root system and enhance the tolerance of apple rootstocks to low-nitrogen stress. Further research demonstrated that under low-nitrogen stress, *MhNAC1* directly bound to and inhibited the activity of the nitrate transporter *MhNRT2.4* and the citric acid transporter *MhMATE* promoter. Xiao et al. [3] cloned a gene related to nitrogen assimilation in peaches. This gene actively responded to low-nitrogen signals, promoted lateral root development and nitrogen absorption and utilization in peaches, and effectively enhanced the nitrogen use efficiency of transgenic plants, providing genetic resources for high nitrogen use efficiency breeding in peach trees. It can solve the current situation of excessive use of nitrogen fertilizer due to low nitrogen utilization efficiency in peach tree production.

Quality improvement research focuses on key traits such as flavor, color, and storability. Liang et al. found [4] that the α subunit of peach SNF kinase 1 (PpSnRK1 α) could respond to nitrogen regulation, and its transcriptional level was strongly induced by nitrogen. Through the functional analysis of overexpressed/silenced peach fruit materials, it was



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found that PpSnRK1 α inhibited the biosynthesis of γ -decanolactone. Further analysis confirmed that PpSnRK1 α could directly interact with PpNAC6/PpNAC36 and phosphorylate PpNAC36, thereby regulating the biosynthesis of γ -decanolactone. This study proposed the regulatory pathway of PpSnRK1 α –PpNAC6/PpNAC36–peach aroma biosynthesis, revealing the mystery of nitrogen signaling regulating peach aroma biosynthesis. It provided a key theoretical basis for improving the flavor quality of peach fruits through molecular breeding and promoting precise nitrogen fertilizer management. Cao et al. [5] found that PpNAC1 could directly bind to the promoter of *PpDML1* and activate its expression, thereby affecting the DNA methylation levels of its own and downstream ripening-related genes. Transcription factor PpNAC1 and DNA demethylase PpDML1 synergistically regulated the ripening of peach fruits and the formation of flavor quality. Cao et al. [6] found that the interaction among PbHB.G7.2, PbHB.G1, and PbHB.G2.1 affected the expression of the ethylene synthesis gene *PbACS1b* and the ethylene yield in pear fruits, thereby regulating the ripening of pear fruits and revealing the molecular mechanism by which HB family proteins interact to regulate ethylene synthesis during the ripening process of pear fruits.

In the field of genomic research, Sun et al. [7] used the representative varieties of Asian and Western pears, ‘Dangshan Su Pear’ and ‘Hongba Pear’, as test materials to construct a high-quality, gap-free haplotype typing genome. By systematically integrating high-quality genomes, multi-omics data, and population and quantitative genetic analyses, they were the first to systematically explore the genetic differences between Asian pears and Western pears at the haplotype level, revealing that long-term differentiation and independent domestication were important reasons for the significant differences in quality and adaptability between Asian and Western pears. The structural variations and key functional genes closely related to important agronomic traits such as self-incompatibility, fruit quality, and yield of pears were precisely located using methods such as SV-GWAS and SV-gene expression association, providing rich genetic information resources for the mining of key genes and the development of molecular markers for superior traits of pears. It also provided a theoretical foundation and technical support for accelerating the molecular design breeding of pears and the aggregation of superior traits. Based on 30 high-quality genomes of *Malus* plants, Li et al. [8] systematically analyzed the evolution of the genus *Malus* over tens of millions of years and constructed the first graphical pan-genome of the genus *Malus*, releasing a panoramic view of genetic diversity of the genus *Malus*. Li et al. [9] successfully identified the key genes causing dwarfing in apples, deciphered the genetic code of dwarfing in apple rootstocks, and lifted the veil of mystery surrounding apple dwarfing. This laid a solid foundation for initiating molecular design breeding of dwarfing rootstocks in the field of woody economic fruits such as apples, accelerating the realization of the “green revolution”. Cai et al. [10] found that the short-branch trait existed in multiple branches of the ‘Fuji’ lineage, indicating that short-branch varieties may have different origins. The main short-branch varieties had a 167 bp heterozygous sequence deletion in the upstream promoter region of the *MdTCP11* gene, which overlapped with the MITE transpose element and was modified by methylation. The methylation level of short-branch varieties in this region was relatively low, while the expression of *MdTCP11* significantly increased. The deletion of MITE sequences could enhance the gene expression activity. Overexpression of *MdTCP11* led to a decrease in apple plant height, indicating that *MdTCP11* played an important role in the internode development of short-branch varieties.

Although biotechnology has not been applied in practice in the innovation and breeding of fruit tree varieties, its research on other crops provides a reference for its application in fruit trees. Scientists have targeted the modification of Rubisco enzyme through gene editing to enhance the efficiency of photosynthetic carbon assimilation, laying the foundation for the breeding of high-quality varieties [11]. Innovations in molecular breeding

techniques, such as the combination of CRISPR/Cas9-targeted editing and whole-genome selection, have significantly shortened the breeding cycle, accelerated the industrial application of stress-resistant and high-quality varieties [12], and promoted the upgrading of the fruit tree industry towards “strong climate resilience, high resource efficiency, and excellent product quality”.

2. Overview of Published Articles

Huang et al. [13] compared gene expression differences between mature leaves of continuous-flowering and once-flowering longan by transcriptome sequencing. The high levels of transcription factor (TF) expression and the high number of gibberellic acid (GA)-signaling-pathway-specific genes expressed at high levels in continuous-flowering longan were shown. Floral-induction-gene expression levels in continuous-flowering longan, such as levels of GA-signaling-related and FT genes, were always high. Wang et al. [14] detected the components and contents of polyphenols in the peel and pulp of the red flesh *Malus* plant ‘Hongxun 2’ (*Malus neidzwetzkyana* (Dieck) Langenf.) and green flesh *Malus* plant ‘Xinye 13-11’ (*Malus sieversii* (Led.) Roem.) during the development period, and the dynamic changes and differences in the polyphenols between the two kinds of fruit were discussed. The accumulation of major polyphenol components in the peel and flesh of ‘Hongxun 2’ and ‘Xinye 13-11’ apples was significant in the period before and after 65 days after flowering, and the contents of procyanidin B1 and procyanidin C1 were the highest in this period. The results supported the viewpoint that *Malus neidzwetzkyana* (Dieck) Langenf was a separate species to *Malus sieversii* (Led.) Roem. Wang et al. [15] collected tissues from pear trees infected with ring rot from orchards located in Liaoning, Hebei, Shandong, and other regions throughout China. A total of 21 strains belonging to the *Botryosphaeria* spp. were utilized to evaluate the resistance levels of various pear varieties against ring rot disease. The resistance was assessed by inoculating different isolates onto distinct pear varieties; it established the criteria for evaluating resistance while minimizing identification errors stemming from the variable responses exhibited by certain varieties towards individual strains, and provided a theoretical foundation for effective prevention and treatment strategies against pear ring rot. Zhao et al. [16] used ‘Zaosu pear’ as a test material, and five different tree shapes—Y, trunk, single-arm, double-arm, and spindle shapes—were studied regarding three aspects, branching and leafing parameters, light radiation parameters, and root distribution. The single-arm and double-arm shapes had the highest fruit weight per fruit values. The trees mainly had short fruiting branches when they entered the fruiting stage, and the double-arm shape had the highest number of short fruiting branches, which was significantly higher than those of the other tree shapes. It provided a theoretical basis for the selection of pear tree shapes in arid areas. Liang et al. [17] investigated the effects of varying durations of aerated irrigation, administered at a consistent frequency, on the growth of greenhouse grape seedlings and the structure of the rhizosphere soil microbial community. It was found that 20 min aeration duration could effectively promote grape seedling growth, enhance the diversity of rhizosphere soil microbial communities, increase beneficial aerobic microorganisms, and reduce harmful ones. The study provided a theoretical basis for optimizing aerated irrigation practices in facility grape cultivation. Mou et al. [18] carried out research on 156 crisp pear fruit germplasm samples to analyze the diversity level of texture traits. It showed that puncture parameters were significantly different between crisp pear cultivars, and the analysis of the influencing factors of flesh texture showed that fruit maturity and shelf life had significant effects on flesh quality. It provided an important reference for the standardization, evaluation, and utilization of crisp pear variety resources. Li et al. [19] collected leaf images of 33 pear varieties against natural backgrounds to introduce

a novel approach to classifying pear varieties. YOLOv10 based on the PyTorch 1.11.0 framework was applied to train the leaf dataset, and constructed a pear leaf identification and classification model. The results showed that the model precision could reach 99.71%, and that it provided a reference for the conservation, utilization, and classification research of pear resources, as well as for the identification of other crops. Shi et al. [20] utilized PMAT to assemble the mitogenomes of six *Rubus* species according to long-read HiFi reads, and annotated them through homologous alignment. A large number of gene transfers were detected between organellar genomes of six *Rubus* species. It clarified the mitogenome characteristics of *Rubus* and provided valuable insights into the evolution of the genus. Song et al. [21] revealed cultivar-specific linalool accumulation patterns among the three aroma-distinct cultivars. It revealed that cytochrome P450 CYP76F14 mediated the conversion of its substrate linalool in table grape berries, especially of Muscat-type grapes, and proposed the CYP76F14 polymorphic variants as molecular markers for aroma-type breeding. Zavala et al. [22] addressed the relevance of endocarp lignification and *PavSPLs* expression for the transition to ripening. *PavSPL2* and *PavSPL9* were targeted by mtr-miR156a and gma-miR156f. Both *PavSPLs* and miRNAs were expressed in fruits and seeds at the yellow stage, an advanced point in the transition to ripening in sweet cherry. Shi et al. [23] comprehensively characterized the *CDPK* gene family in the apple cultivar 'Hanfu' at the genome-wide level, and 38 *MdCDPKs* were identified. *MdCDPK24* played a positive role in apple bitter rot resistance through *MdCDPK24*-overexpressing calli. Chen et al. [24] analyzed the physiological, transcriptomic, and metabolomics of two yellow passion fruit cultivars, including heat-tolerant and heat-sensitive cultivars. It showed that transcription factors (e.g., MYB, HSF, WRKY) played pivotal roles in heat adaptation, and knockdown of *PeGDA* and *PeXDH* markedly altered the heat tolerance of heat-tolerant cultivar. It offered new insights into the molecular mechanisms of heat tolerance and potential targets for breeding climate-resilient passion fruit varieties. Li et al. [25] found that Mn deficiency exacerbated B-deficiency-induced corky split vein not only by intensifying photosynthetic dysfunction and carbohydrate accumulation but also by promoting lignin biosynthesis in citrus. The findings highlighted the synergistic nature of B and Mn deficiencies in impairing leaf function and structure, providing new insights into the physiological and molecular mechanisms underlying corky split vein development.

3. Conclusions and Prospects

Studies on fruit tree physiology and molecular biology focus on the core mechanisms of fruit tree growth and development, stress adaptation, and quality formation, providing important theoretical support for improving the quality and efficiency of the industry. In this Special Issue, researchers have focused on aspects such as the identification and evaluation of germplasm resources, the determination of resistance to biological and abiotic stresses, the formation of fruit quality, soil nutrition, and cultivation techniques. The physiology and molecular biology of fruit trees such as apples, pears, grapes, longans, cherries, raspberries, passion fruits, and citrus fruits were studied using techniques such as model construction, physiological index determination, transcriptome and metabolome, and genome assembly. Despite having achieved many breakthrough results, there are still many problems that need to be urgently solved. Future research needs to further strengthen the verification of the correlation between molecular mechanisms and physiological phenotypes, and deepen the application of multi-omics joint analysis in the analysis of complex traits. In terms of breeding direction, efforts should be focused on target traits such as continuous flowering, stress resistance, and quality, and the transformation and application of molecular marker-assisted breeding and gene editing technologies should be accelerated. At the same time, it is necessary to enhance the coupled research on cultivation techniques

and environmental adaptability, and improve the intelligent identification and precise management technology system. In addition, in response to industrial pain points such as nutritional imbalance and disease prevention and control, research on multi-factor interaction mechanisms is carried out to provide more comprehensive theoretical and technical support for the high-quality and sustainable development of the fruit tree industry.

Conflicts of Interest: The authors declare no conflicts of interest.

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