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EDITORIAL Research Advances of Anthocyanin Accumulation in Plants Tissues

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The color of plants is mainly due to the rich content of chlorophylls, carotenoids, betalains, flavonoids, and other substances. Anthocyanins as an important group of flavonoids, have an important effect on the color of plant tissues, especially fruit color ^[1,2]. In the early 1900s, a summary of Mendelian studies on pea coloration was given by Weldon^[3]. Since then, the anthocyanin biosynthetic pathway has been continuously refined, until it was first summarized in plants in detail^[4]. Anthocyanins are important secondary metabolites in plants, and the metabolic starting material is phenylalanine produced from glucose breakdown. Finally, various anthocyanins resulting from glycosylation modifications, are furtherly modified by methylation accomplished by O-methyltransferases (OMTs) to produce final products such as malvidin, peonidin and petunidin^[5-7].

Generally, the anthocyanins formed in the cytoplasm

will be transferred to the cell vacuole for storage to avoid degradation and display multiple colors. Recent years, researchers also pay attention to the decisive effect of anthocyanin vacuolar transport on fruit anthocyanin accumulation. At present, the research on anthocyanin transport is mainly focused on the study of multidrug and toxic compound extrusion (MATE) and glutathione-S-transferase (GST) transporters. Previous report revealed the key role of MATE in the process of transferring anthocyanins from small vesicles to vacuoles in transgenic hairy roots of grapes ^[8]. The important effect of GST on anthocyanin transport was successively demonstrated on fruits such as apple, peach and so on ^[9,10].

The expression of plant anthocyanin biosynthetic genes is regulated by MYB-bHLH-WD40, called MBW complex, with a relatively conserved mechanism. The MBW complex is formed by specific interactions between

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MYB transcription factors, bHLH transcription factors and WD40 proteins, and its interaction was validated in apple fruit ^[11]. Studies on the regulatory mechanism of anthocyanin formation in Arabidopsis, have shown that MYB transcription factors such as AtMYB11/12/111 have an activating effect on the expression of the early genes of anthocyanin biosynthesis, AtCHS, AtCHI, AtF3H and AtF3'H, and the expression of the late synthesis genes, AtDFR, AtLDOX, and AtUFGT, is regulated by the MBW complex formed by AtMYB75/90/113/114 and so on ^[12,13]. It follows that MYB transcription factors play a crucial role in the regulation of anthocyanin biosynthetic genes. In addition, the stimulation of external environment can cause dramatic changes in anthocyanin accumulation in plant tissues. The effect of light exposure on anthocyanin accumulation is mainly determined by 2 factors, light intensity and wavelength ^[14]. Temperature can significantly affect the accumulation of anthocyanins and has an effect on its stability ^[15,16]. Drought stress, exogenous nitrogen and other treatments can also affect fruit coloration [17,18]. Furthermore, anthocyanin accumulation is also influenced by phytohormone signaling pathways such as ethylene (ETH), jasmonic acid (JA), abscisic acid (ABA), auxin and so on [19-22].

Conflict of Interest

There is no conflict of interest.

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