



Bioinformatic and expression analysis of the *OMT* gene family in *Pyrus bretschneideri* cv. Dangshan Su

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ABSTRACT. With high nutritional value in its fruits, Dangshan Su pear has been widely cultivated in China. The stone cell content in fruits is a key factor affecting fruit quality in pear, and the formation of stone cells has been associated with lignin biosynthesis. O-Methyltransferase (OMT) is a key enzyme involved in lignin metabolism within the phenylpropanoid pathway. Here, we screened 26 *OMT* genes from the *Pyrus bretschneideri* cv. Dangshan Su genome using the DNATOOLS software. To characterize the *OMT* gene family in pear, gene structure, chromosomal localization, and conserved motifs of *PbOMTs* were analyzed. *PbOMTs* were divided into two categories, type I (designated *PbCCOMTs*) and type II (designated *PbCOMTs*), indicating the differentiation of function during evolution. Based on the analysis of multiple sequence alignment, cis-element prediction, and phylogenetic relationships, two candidate genes, *PbCCOMT1* and *PbCCOMT3*, were selected for the analysis of temporal and spatial gene expression

in pear. The promoter regions of both *PbCCOMT1* and *PbCCOMT3* contain regulatory motifs for lignin synthesis. Moreover, the two genes show high similarity and close phylogenetic relationships with *CCOMTs* in other species. Expression analysis showed that transcript levels of two *PbCCOMTs* were positively associated with the contents of both stone cells and lignin during the development of pear fruit. These results suggest that *PbCCOMT1* and *PbCCOMT3* are closely associated with lignin biosynthesis. These findings will help clarify the function of *PbOMTs* in lignin metabolism and to elucidate the mechanisms underlying stone cell formation in pear.

Key words: *OMT* gene family; *Pyrus*; Lignin synthesis; *PbCCOMTs*; Phylogenetic analysis