Title: Genome-Wide Analysis of Aluminum-Activated Malate Transporter Family Genes in Six Rosaceae Species, and Expression Analysis and Functional Characterization on Malate Accumulation in Chinese White Pear

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Genome-Wide Analysis of Aluminum-Activated Malate Transporter Family Genes in Six Rosaceae Species, and Expression Analysis and Functional Characterization on Malate Accumulation in Chinese White Pear

Short title: Identification of Aluminum-Acitivated Malate Transporters in Chinese White Pear

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Highlights

- We are the first to identify Aluminum-Activated Malate Transporter （ALMT）gene family in six Rosaceae species, and a total of 113 ALMT homologous genes were identified.
- We are the first to carry out a Genome-Wide analysis of these ALMT family genes.
- Based on the results of transcriptome data, the malate content and qRT-PCR, we firstly screened out a candidate gene associated with the malate accumulation in Chinese white pear.
- We characterized the function of the candidate gene by transgenic assay.

Abstract

Aluminum-activated malate transporters (ALMTs) exhibit a variety of physiological roles in plants to regulate fruit quality, but the evolutionary history of the ALMT family in the Rosaceae species remains unknown. In this study, a total of 113 *ALMT* homologous genes were identified from six Rosaceae species (*Pyrus bretschneideri, Malus × domestica, Prunus persica, Fragaria vesca, Prunus mume, and Pyrus communis*), and 27 of these sequences came from Chinese white pear, designated *PbrALMT*. Based on the phylogenetic analysis, we divided these *ALMT* genes into three main clusters (A, B, and C). Conserved domain analysis indicated that all