

CORRECTION

Correction: Comprehensive genome-wide analysis of the pear (*Pyrus bretschneideri*) laccase gene (*PbLAC*) family and functional identification of *PbLAC1* involved in lignin biosynthesis

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In [Fig 12](#), incorrect images are shown for panels A and B. The authors have provided a corrected version here.



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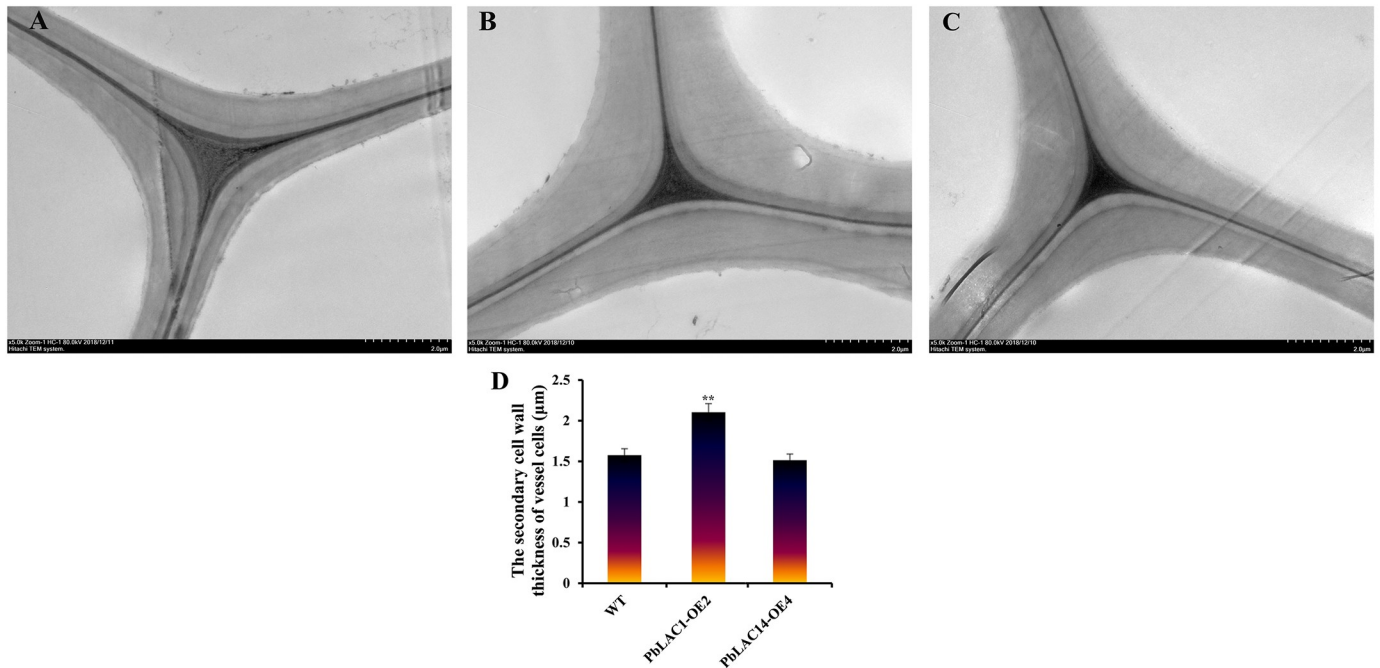


Fig 12. Ultramicroscopic observation of cell walls in the inflorescence stems of WT and transgenic lines. TEM images of the ultrastructure of the cell wall. (A) WT plants; (B) *PbLAC1*-overexpressing transgenic plants; (C) *PbLAC14*-overexpressing transgenic plants; (D) Statistical analysis of the secondary cell wall thickness of vessel cells in WT and transgenic plants. ** Significant difference between the secondary cell wall thickness of the WT and transgenic plants ($P < 0.01$).

<https://doi.org/10.1371/journal.pone.0228183.g001>

Reference

1. Cheng X, Li G, Ma C, Abdullah M, Zhang J, Zhao H, et al. (2019) Comprehensive genome-wide analysis of the pear (*Pyrus bretschneideri*) laccase gene (*PbLAC*) family and functional identification of *PbLAC1* involved in lignin biosynthesis. PLoS ONE 14(2): e0210892. <https://doi.org/10.1371/journal.pone.0210892> PMID: 30753186