Integrated transcriptome and proteome analysis provides insights into leaf color differences between red-leaved poplar cultivars ('Quanhong' and 'Xuanhong') and 'Zhonglin 2025' (*Populus deltoides* cv. 'Zhonglin 2025')

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Abstract

Background

The red-leaved poplar cultivars 'Quanhong' and 'Xuanhong' are bud mutations of *Populus deltoides* cv. 'Zhonglin 2025'. These cultivars are valued for their beautiful shape, lack of flying catkins, and ornamental leaf colors. The molecular mechanism that leads to different leaf colors between these red-leaved poplars and 'Zhonglin 2025' remains unclear.

Results

In this study, we analyzed growth and physiological indicators in the 'Quanhong', 'Xuanhong', and 'Zhonglin 2025' poplar cultivars, and performed transcriptome and proteome analysis of their leaves. The results showed that plant height and ground diameter were significantly lower in both red-leaved poplars than in 'Zhonglin 2025', indicating that their growth and development were markedly inhibited. The ratio of anthocyanin to total chlorophyll and photosynthetic capacity of the leaves were higher and lower, respectively, in the red-leaved cultivars than in 'Zhonglin 2025'. At the transcript and protein levels, 6,792 differentially expressed genes (DEGs) and 2,786 differentially expressed proteins (DEPs) were screened in the 'Quanhong' cultivar, respectively, and 4,398 DEGs and 2,333 DEPs were screened in the 'Xuanhong' cultivar, respectively. We screened 769 DEGs/DEPs in 'Quanhong' and 399 DEGs/DEPs in 'Xuanhong' in an integrated transcriptomics/proteomics analysis. Based on the results of this integrated analysis, 15 and 11 genes/proteins involved in anthocyanin synthesis were further identified in 'Quanhong' and 'Xuanhong', respectively, including the CHS, F3H, and DFR genes. Among the 120 transcription factors, 3 (HY5, HYH, and TTG2), may be directly involved in the regulation of anthocyanin synthesis in both red-leaved poplars.

Conclusions

By comparing the proteomes and transcriptomes of red-leaved poplar cultivars and 'Zhonglin 2025', we identified the key genes and proteins related to red leaf coloration. The findings of this study provided insights that may aid further studies of the molecular mechanism of leaf red coloration in red-leaved poplars.

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Figures

Figure 1

Physiological parameters of 'Zhonglin 2025' (ZL2025), 'Quanhong' (QH) and 'Xuanhong' (XH). (A) real view of the three kinds of poplars; (B) comparison of the three poplar leaves; (C) height; (D) ground diameter; (E) anthocyanin content; (F) Chl a content; (G) Chl b content; (H) carotenoid content; (I) net photosynthetic; (J) stomatal conductance; (K) transpiration rate.

Figure 2

Analysis of differentially expressed genes (DEGs). (A) the statistics of DEGs of QH/ZL2025 and XH/ZL2025; (B) the venn diagram of the number between QH/ZL2025 and XH/ZL2025; (C) KEGG Pathway enrichment analysis of DEGs in QH/ZL2025; (D) KEGG Pathway enrichment analysis of DEGs in XH/ZL2025.

Figure 3

Analysis of differentially expressed proteins (DEGs). (A) volcano plot of differential expressed proteins in QH/ZL2025; (B) volcano plot of differential expressed proteins in XH/ZL2025; (C) KEGG Pathway enrichment analysis of DEPs in QH/ZL2025; (D) KEGG Pathway enrichment analysis of DEPs in XH/ZL2025.

Figure 4

Correlation analysis of transcriptome and proteome. (A) the venn diagram of the number of associations between transcriptome and proteome in QH/ZL2025; (B) the venn diagram of the number of associations between transcriptome and proteome in XH/ZL2025; (C) the venn diagram of the number between DEGs and DEPs in QH/ZL2025; (D) the venn diagram of the number between DEGs and DEPs in H/ZL2025.

Figure 5

Anthocyanin metabolism pathway and structural gene expression in the QH/ZL2025 and XH/ZL2025. PAL: Phenylalanine ammonia-lyase; C4H: Trans-cinnamate 4-monooxygenase; 4CL: 4-coumarate:CoA ligase; CHS: Chalcone synthase; CHI: Chalcone isomerase; F3H: Flavanone-3 β -hydroxylase; F3'H: Flavonoid-3'-hydroxylase; DFR: Dihydroflavonol reductase; ANS: Anthocyanin synthase; UFGT: UDP-glucose flavonoid 3-glucosyltransferase; GT/MT/AT: Glucosyltransferase/Methyltransferase/Acyltransferase; GST: Glutathione S-transferase.

Figure 6

qRT-PCR validation of differential gene expression. All data are presented as the mean $\pm$ SEM. (*, $P < 0.05$; **, $P < 0.01$).

Figure 7

Protein–protein interaction network constituted by differentially expressed transcription factors and structural genes controlling anthocyanin synthesis.

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