

Genome-wide investigation and expression profiling of polyphenol oxidase (PPO) family genes uncover likely functions in organ development and stress responses in *populus trichocarpa*

Fang He (✉ hefang1231@qq.com)

Sichuan Agricultural University

Yu-Jie Shi

Sichuan Agricultural University

Qian Zhao

Sichuan Agricultural University

Kuang-Ji Zhao

Sichuan Agricultural University

Xing-Lei Cui

Sichuan Agricultural University

Liang-Hua Chen

Sichuan Agricultural University

Han-Bo Yang

Sichuan Agricultural University

Fan Zhang

Sichuan Agricultural University

Jia-Xuan Mi

Sichuan Agricultural University

Jin-Liang Huang

Sichuan Agricultural University

Xue-Qin Wan

Sichuan Agricultural University

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Abstract

Background: Trees such as *Populus* are planted extensively for reforestation and afforestation. However, their successful establishment greatly depends upon ambient environmental conditions and their relative resistance to abiotic as well as biotic stress. Polyphenol oxidase (PPO) is a ubiquitous metalloproteinase in plants, which plays crucial roles in plant resistance against biotic and abiotic stresses. Although the whole genome sequence of *populus trichocarpa* has long been published, little is known about the PPO genes in *Populus*, especially those related to drought stress, mechanical damage, insect feeding and hormone response at the whole genome level.

Results: In the recent research, a genome-wide analysis of the Poplar PPOs family was finished and 18 PtrPPOs gene were identified. Then, bioinformatics and qRT-PCR were applied to analyze the gene structure, phylogeny, chromosomal localization, gene replication, Cis-elements, expression patterns of PtrPPOs. Sequence analysis revealed that 2/3 of the PtrPPO genes not contained introns. Phylogenetic analysis revealed that all PPOs gene were split into 11 subfamilies, and woody plants differentiated a large number of PPO genes. 18 PtrPPOs gene were disproportionally apportioned on 19 chromosomes, and the number of three pairs of segmented replication genes and four tandem repeat genomes were detected in poplars. Cis-acting element analysis identified a large number elements of growth and development, secondary metabolism process, and stress-related elements on the promoters of different PPO members. Furthermore, PtrPPO genes were expressed preferably in young plant tissues and fruits. In addition, some PtrPPOs could be significantly induced by PEG, ABA and JA, thus revealing their potential role in regulating stress response.

Conclusions: Comprehensive analysis is helpful to select candidate PPO genes for the follow-up study of the biological function, and molecular genetic progress of stress resistance in forest trees provides genetic resources.

Full Text

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Figures

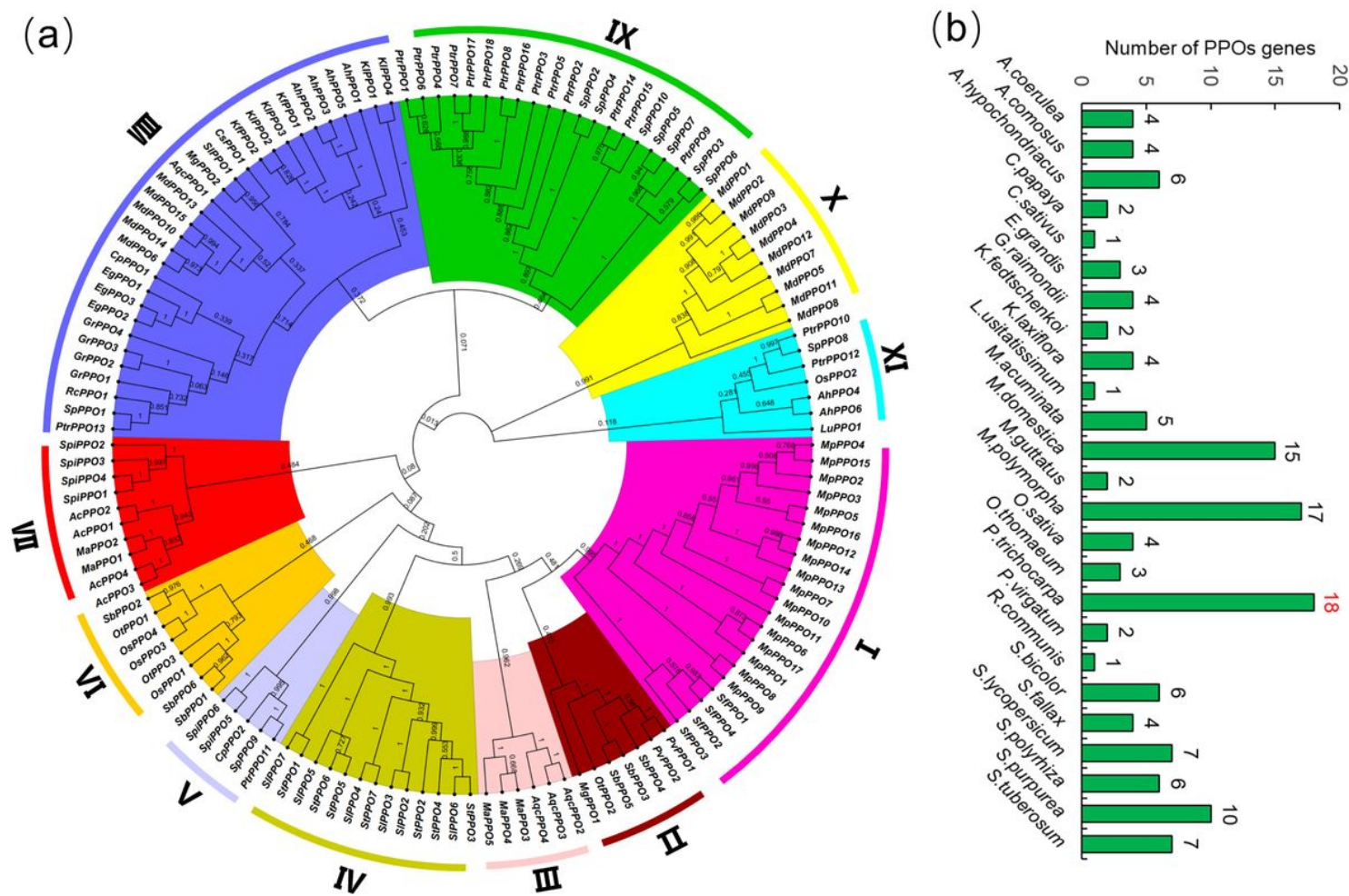


Figure 1

Evolutionary and phylogenetic analysis of the PPOs family in diverse plant species. (a) The phylogenetic tree of PPO proteins from *A.coerulea*, *A.comosus*, *A.hypochondriacus*, *C.papaya*, *C.sativus*, *E.grandis*, *G.raimondii*, *K.fedtschenkoi*, *K.laxiflora*, *L.usitatissimum*, *M.acuminata*, *M.domestica*, *M.guttatus*, *M.polymorpha*, *O.sativa*, *O.thomaeum*, *P.trichocarpa*, *P.virgatum*, *R.communis*, *S.bicolor*, *S.fallax*, *S.lycopersicum*, *S.polyrhiza*, *S.purpurea*, and *S.tuberosum*. (b) Comparisons of PPO proteins number across 25 species of plant.

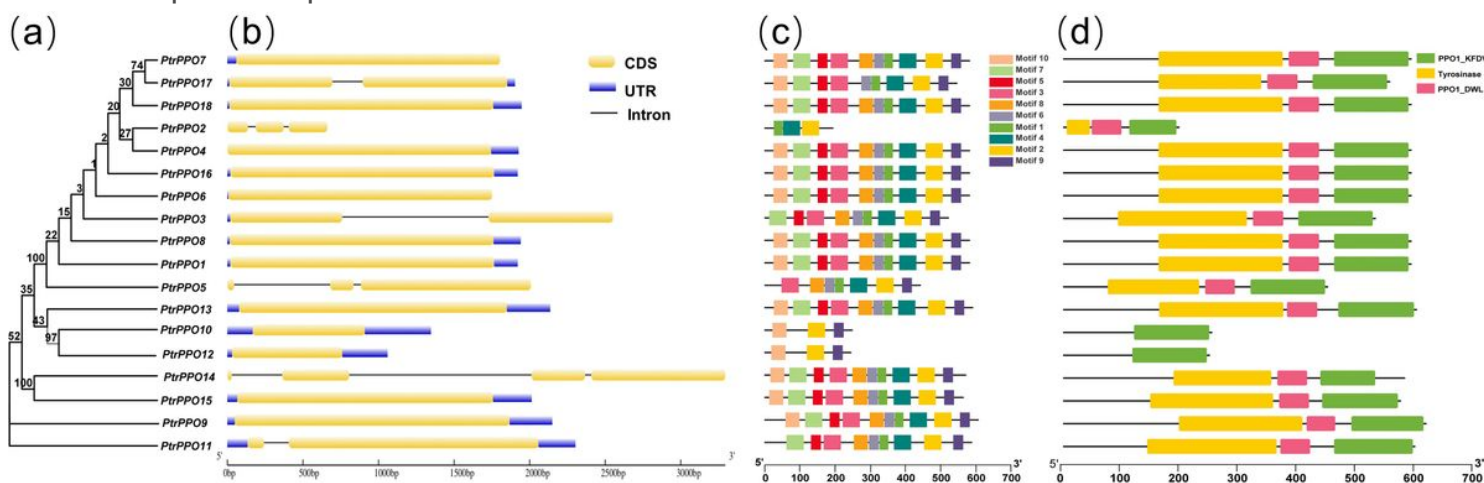


Figure 2

Phylogenetic, gene structure, conserved protein structure and motif analyses of PtrPPOs gene. (a) Phylogenetic tree constructed from full-length amino acid sequences from 18 PtrPPOs. (b) Exon-intron structure analysis of PtrPPOs genes. Blue boxes represent UTR regions; yellow boxes indicate exons; black lines represent introns. (c) Motif distribution of PtrPPOs members. (d) conserved protein domain analysis of PtrPPOs. The length of each pattern is displayed proportionally.

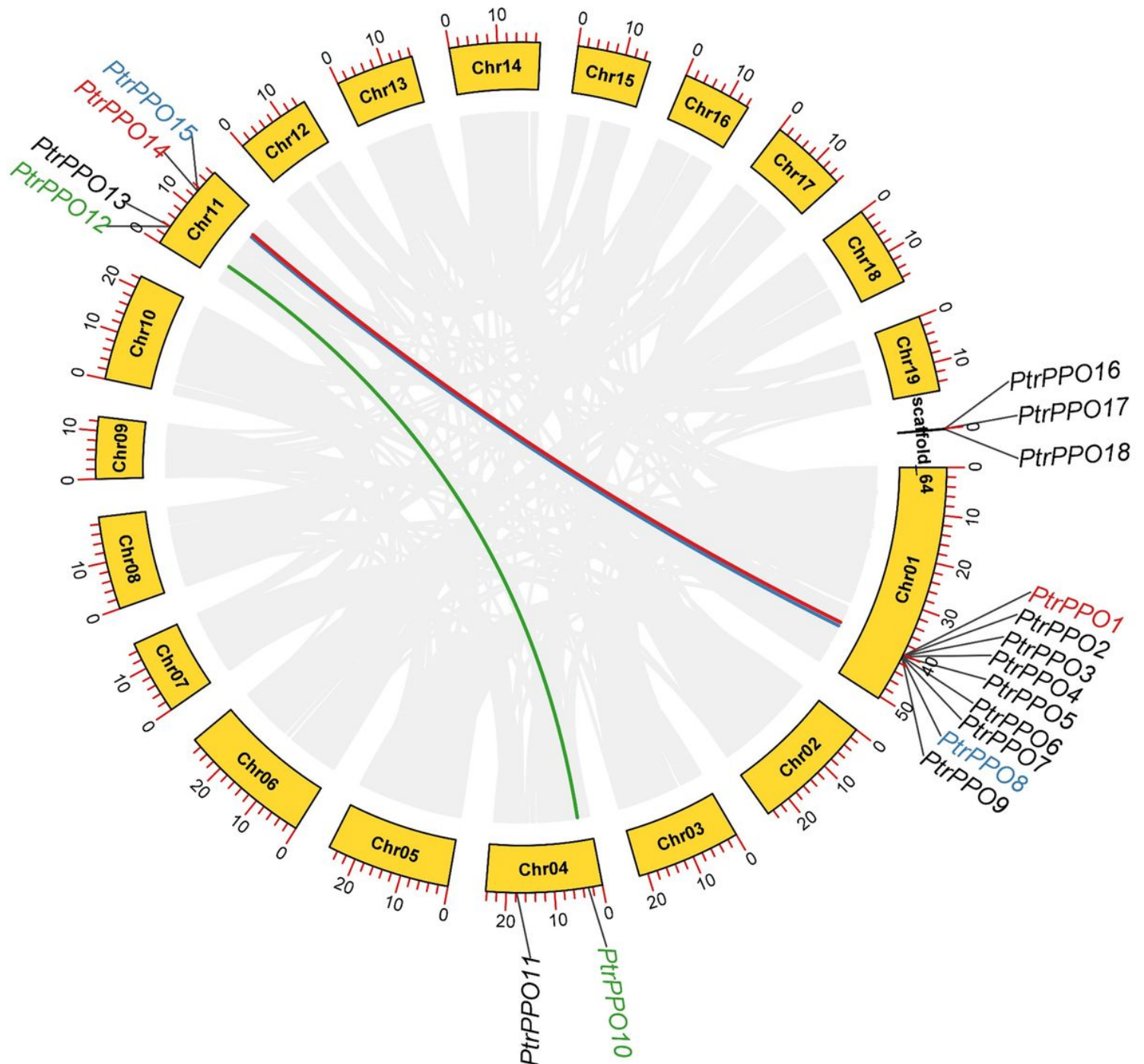


Figure 3

Schematic diagram of PPOs gene distribution and Inter-chromosomal relationships in *Populus trichocarpa* chromosomes. The gray lines represent all syntenic blocks in the chromosome of *Populus trichocarpa*. Red, blue, and green lines show duplicated PPOs gene pairs in *Populus trichocarpa*. The chromosome number is shown in the middle of the arc square. The length of each arc corresponds to the length of the chromosome (Mb).

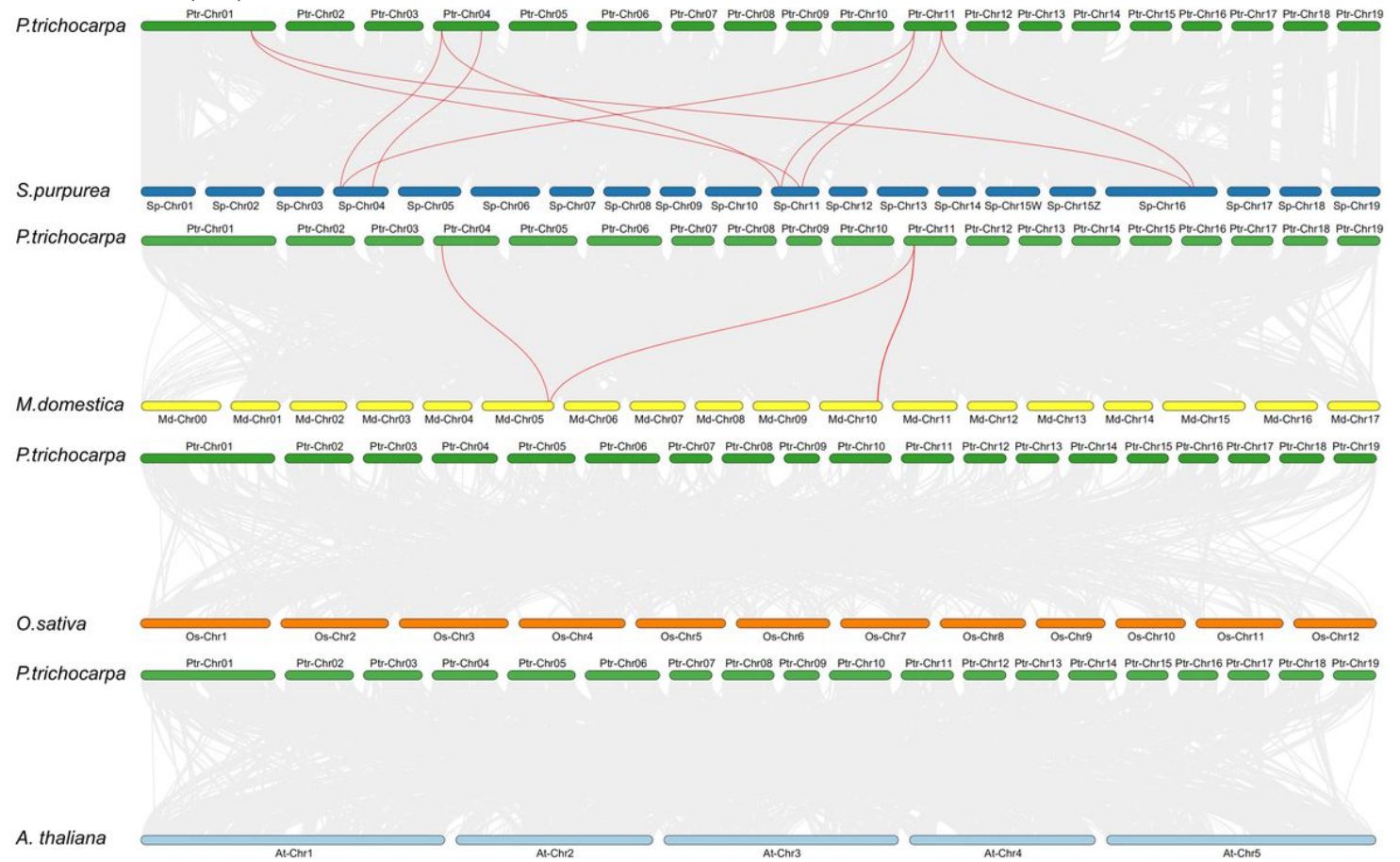


Figure 4

Collinearity analysis of PPOs gene in Poplar and four typical plant species. The gray lines in the background represent collinear blocks between populus and another specie genomes, while the red lines highlight the syntenic PPO gene pairs. *P.trichocarpa*, *Populus trichocarpa*; *S.purpurea*, *Salix purpurea*; *M.domestica*, *Malus domestica* ; *O. sativa*, *Oryza sativa*;

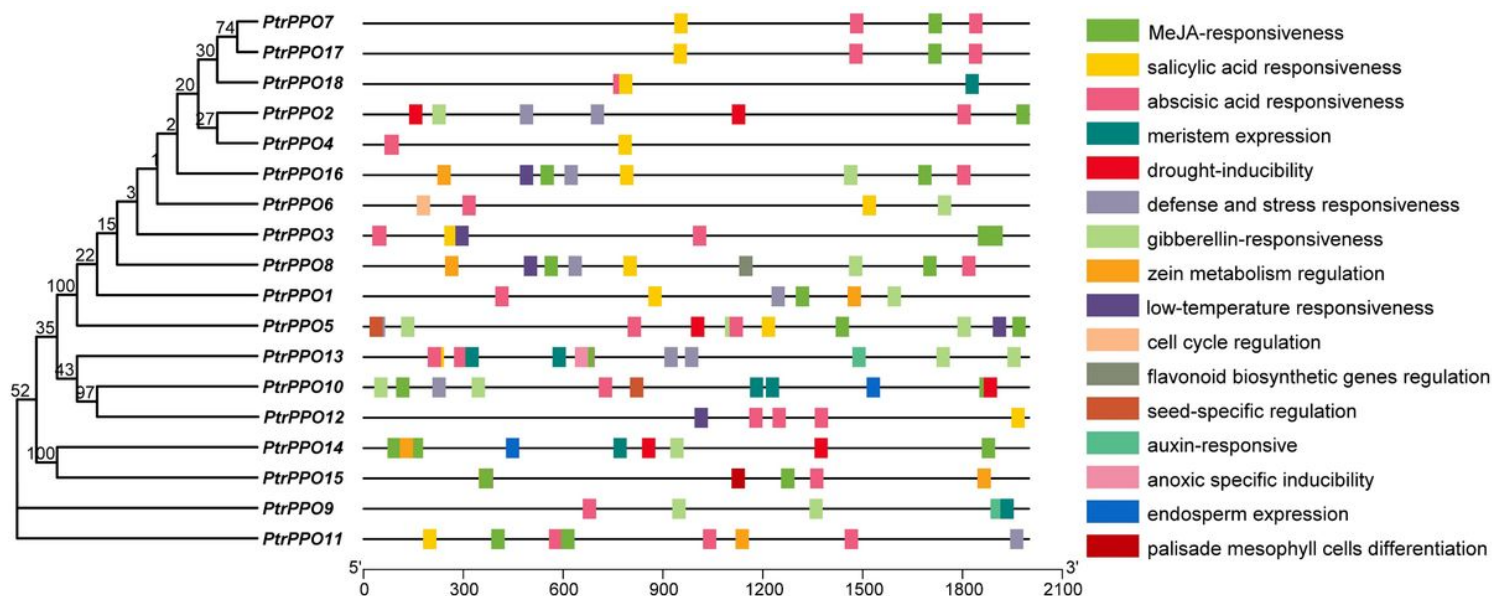


Figure 5

Cis-elements analysis of the *PtrPPO*s. The relative locations of stress and growth related cis-elements in *PtrPPO*s promoter region. Different colors represent different cis-acting elements, and their position corresponds to the corresponding position of the promoter.

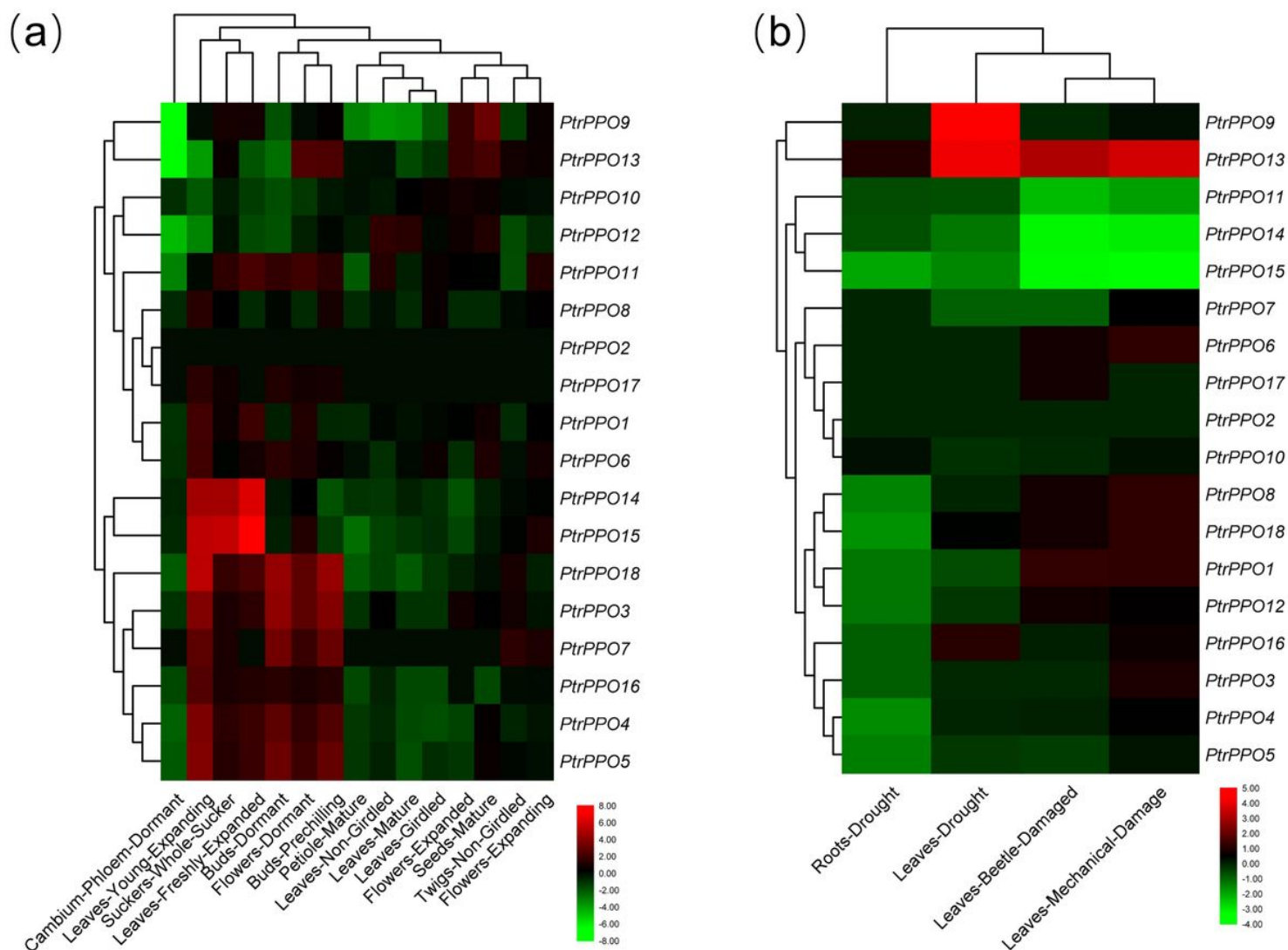


Figure 6

Expression profile of PPOs gene under development and stress. (a) Heat maps showing the expression levels of 18 *PtrPPO*s gene in different tissues at different developmental stages based on transcriptome data. (b) Heat maps of the expression levels of 18 *PtrPPO*s genes in drought, beetle damage, and mechanical damage. The colour bar represent the range of maximum and minimum values of relative expressions in the heat map.

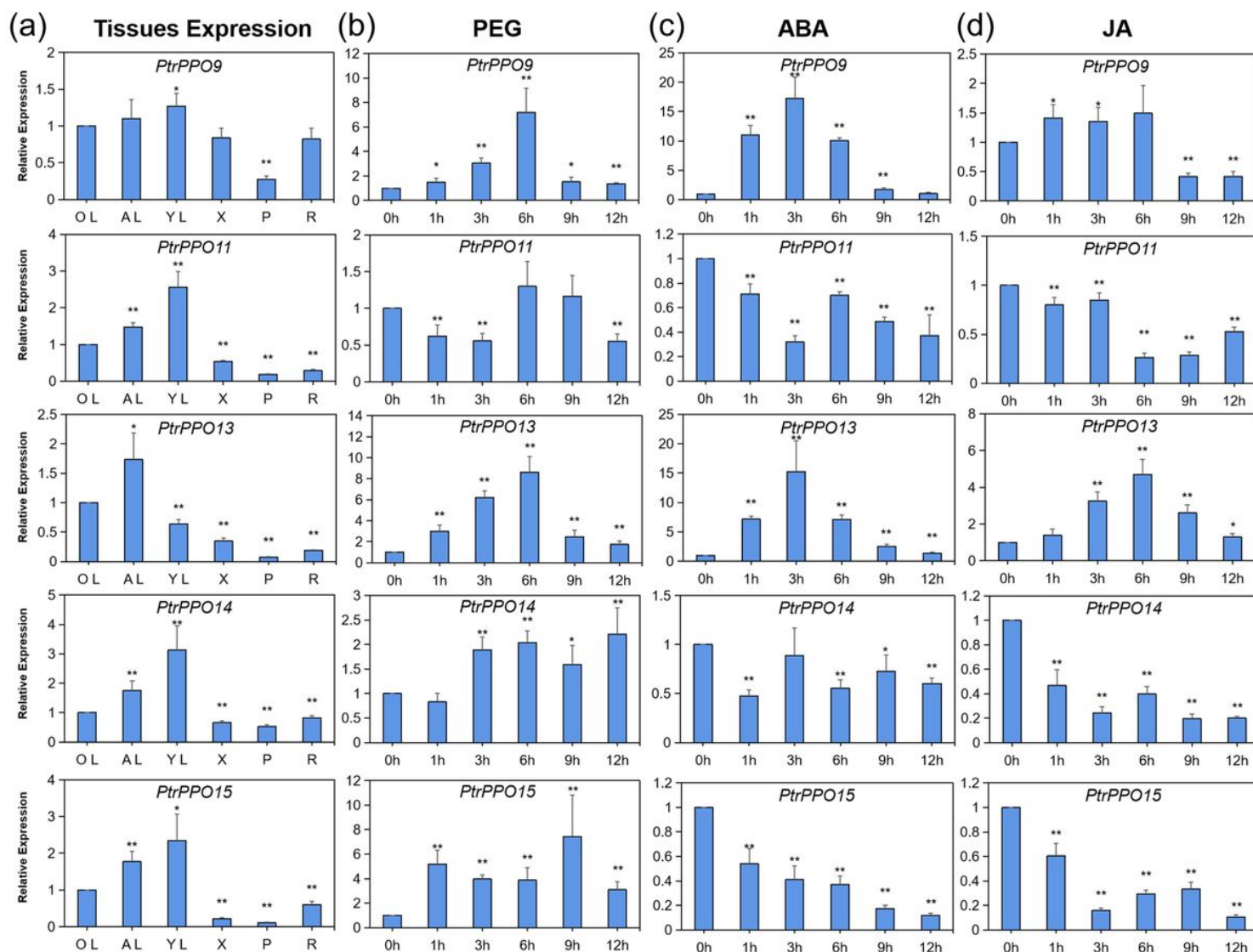


Figure 7

RT-qPCR analysis of the expression profile of PPOs gene. (a) Transcript levels analysis of 5 PtrPPOs in various tissue. YL, young leaf; AL, adult leaf; OL, old leaf; P, phloem; X, xylem; R, root. Transcript levels of 5 PtrPPOs were measured by RT-qPCR in response to PEG (b), ABA (c), and JA(d). Values are means + SE (n = 20). Asterisks denote significant differences: * $P \leq 0.05$; ** $P \leq 0.01$.

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