Supplementary Figures:

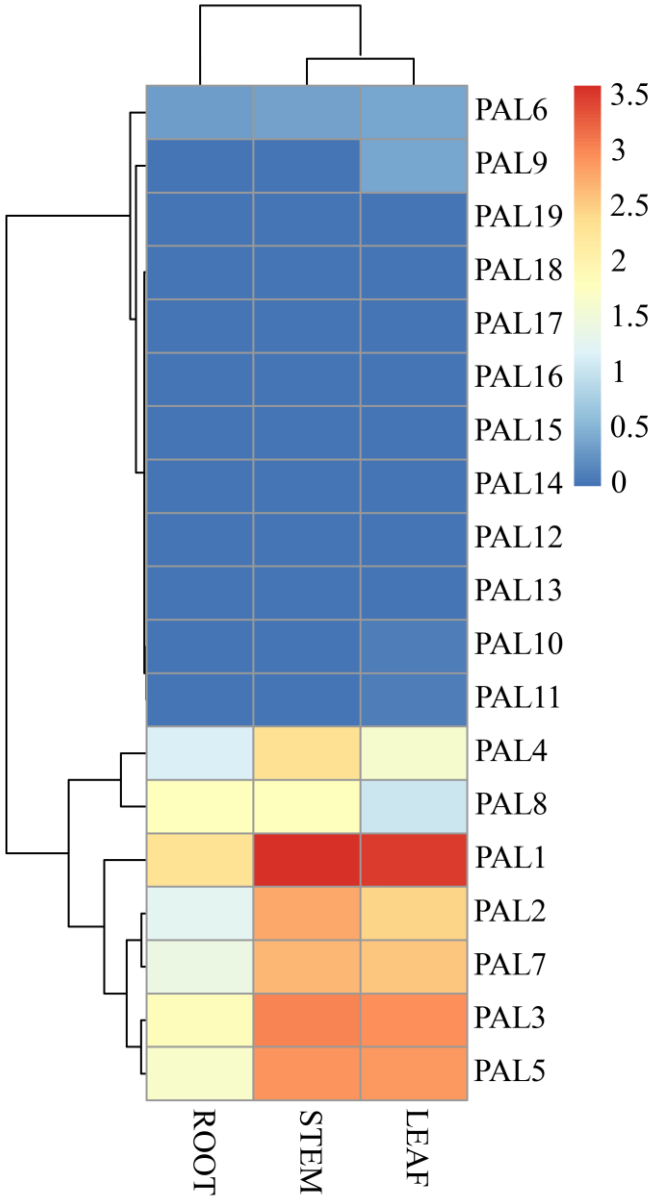

Figure S1. Expression of *PAL* genes in the putative pathway of acteoside biosynthesis across three tissues in *C. grandiflora* benth. The expression level is the sum of all the unigenes for each gene, and $\log_{10}$(sum(FPKM)+1) was used to plot the heatmap. Candidate *PAL* unigenes were selected according to the annotation. Abbreviation: PAL, phenylalanine ammonia-lyase.

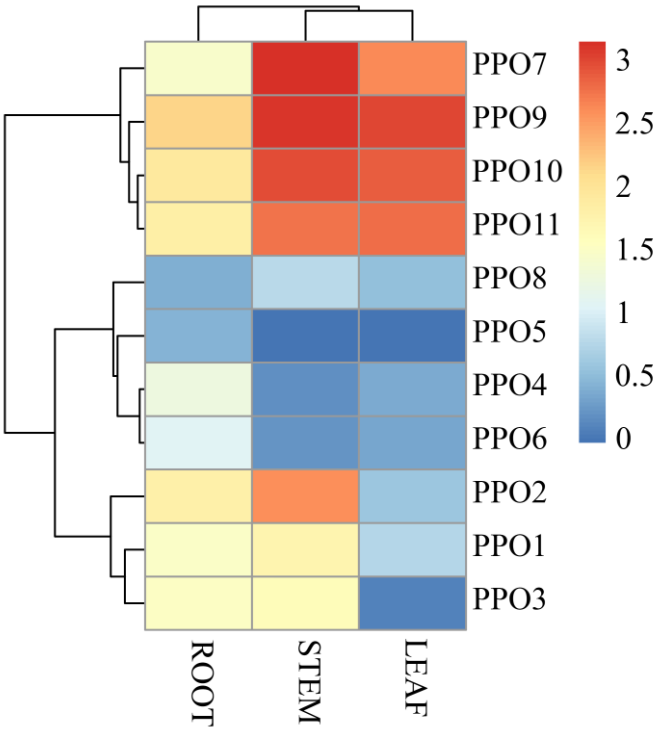

Figure S2. Expression of *PPO* genes in the putative pathway of acteoside biosynthesis across three tissues in *C. grandiflora* benth. The expression level is the sum of all the unigenes for each gene, and $\log_{10}$(sum(FPKM)+1) was used to plot the heatmap. Candidate *PAL* unigenes were selected according to the annotation. Abbreviation: PPO, polyphenol oxidase.

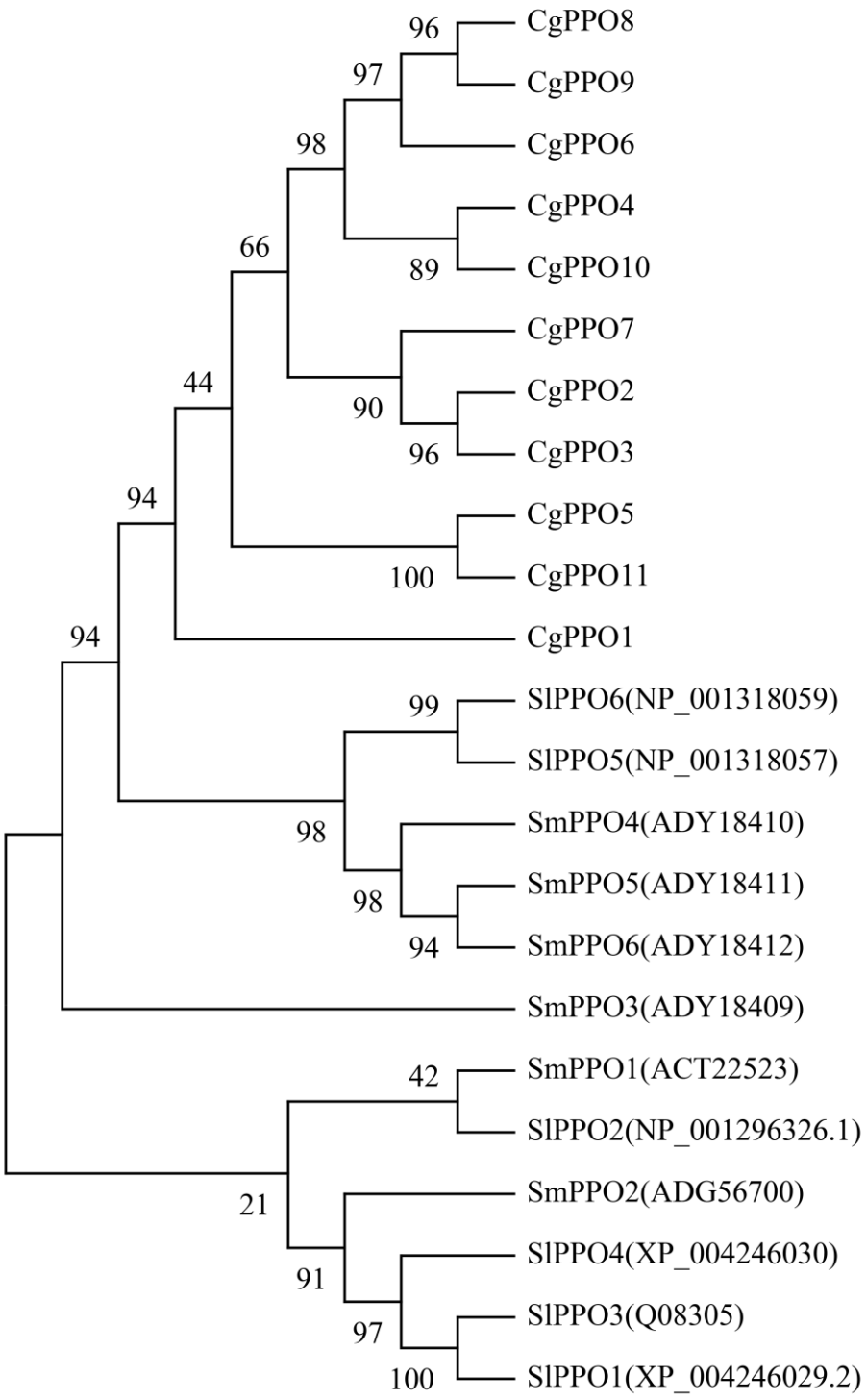

Figure S3. Phylogenetic analysis and expression level of PPOs from *C. grandiflora* Benth. Amino acid sequences were aligned using the ClustalX2 program, and evolutionary distances were calculated using phyML software with the Maximum Likelihood statistical method.

Note: Supplementary tables S1-S14 are too big (277 Mb) to upload at present.

Now the fourteen tables are uploaded into Zenodo website, please download them using this link:

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November 21, 2019

Journal article Open Access

Analysis of Centranthera grandiflora benth Transcriptome Explores Genes of Catalpol, Acteoside and Azafrin Biosynthesis

Zhang, Xiaodong

Supplementary tables for the article "Analysis of ***Centranthera grandiflora*** benth Transcriptome Explores Genes of Catalpol, Acteoside and Azafrin Biosynthesis" in International Journal of Molecular Sciences.

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